Invicro

VivoQuant™ 5.2.0
User Manual

Invicro Imaging Services and Software

Last updated: August 14, 2024

Table of Contents

- Installation
  - Installation QuickGuide
  - Installation Details
- Getting Around
  - Keyboard Shortcuts
- Configuration
  - VivoQuant Configuration
  - Display
  - Data
  - DICOM Settings
  - Network
  - Licensing
  - Restricted tags
- File Management
  - Opening DICOM Data
  - Open Reference Data
  - Append Data
  - Open Raw Data
  - Session
- Operators
  - Navigation
  - 3D ROI Tool
  - Projection
  - Reorientation / Registration
  - Time Series
  - Distance / Annotation
  - Checker Board
  - Cropping
  - Arithmetics
  - Filtering
  - Modeling
  - Splitting
- UI Elements
  - Data selector
  - MIP tool
- Viewing and Layout
  - Main window
  - Save Image
  - Save Movie
  - Docks
- View Modes
    - Slice View
    - Tile View
    - Multi View
    - Capture Viewer
- View Menu

    - Show Reference / Input
    - Crosshairs
    - Position Labels
    - Corner Information
    - Active Indicator
    - Layout
    - Zoom

Tools

- VQ Script
- View Control
- MIP Control
- Min/Max Tool
- Histogram
- Preprocessing Tool
- Resample Data
- DICOM Tools
- Autoradiography Calibration
- Worklist Tool

Data Manager

    - Data Manager interface
    - Annotation
    - Save data

Image and Movie

    - Image Magick
- Frame Time Editor
- Update Check

Advanced Modules

- Getting Started

Plug-In Modules

    - Overview
    - Multi-Atlas
    - 3D Brain Atlas
    - Pharmacokinetic Modeling

NanoSPECT Tools

    - Overview
    - QuaniCalc
    - Specific Activity Calculator
    - SUV Calculator
    - Cosstalk Removal
    - Biodist. Visualization
    - Split Projections

Calibration

    - Overview
    - CT Geometrical Calibration
    - MMP SPECT Calibration
    - Near-Field Uniformity QC
- Dosimetry Calc
- Treatment of Quantitative Data

Help

- Logging
- Manual

About
Reporter Tool

iPACSSync Tool

Overview
iPACS Sync Configuration Screen
Syncing data to iPACS

How to guides

Create a custom brain atlas

Troubleshooting

Hardware Requirements
Corrupted Data
Memory Allocation Error
Disabled MIP
Image Distortion and Mirroring

Installation Quick Guide

This document should guide you through the first steps to get VivoQuant running on your system:

Downloading

Please point your favorite web browser to the VivoQuant Home Page for access to the latest release.

VivoQuant^{TM}: Pre-clinical Image Post-processing

VivoQuant^{TM} is Invicro's multi-modality post-processing suite for SPECT, CT, PET, MR, Optical and and Autoradiography imaging data. DICOM, NifTI, and raw data can be imported as well as many proprietary formats from pre-clinical imaging equipment. VivoQuant combines fundamental viewing functionality with powerful tools for fine-tuning images, isolating and analyzing regions of interest, and more. Multiple display modes including orthogonal views, slice views, special co-registration multi-views as well as 3D MIP and volume renderings allow users to optimally view information of interest. Built-in tools allow the imaging scientist to extract the information she or he needs with minimal effort.
Please contact us at support@invicro.com for more details on how to **trial VivoQuant**.

2020-08-06 » VivoQuant 2020 Release

Invicro is pleased to announce the official release of **VivoQuant™ 2020** which includes many new functional enhancements to support multi-modality, multi-species image processing applications. As a vendor neutral software, VivoQuant 2020 streamlines image analysis research studies across all phases of drug discovery and development.

VivoQuant Home Page

Installing

A. Windows

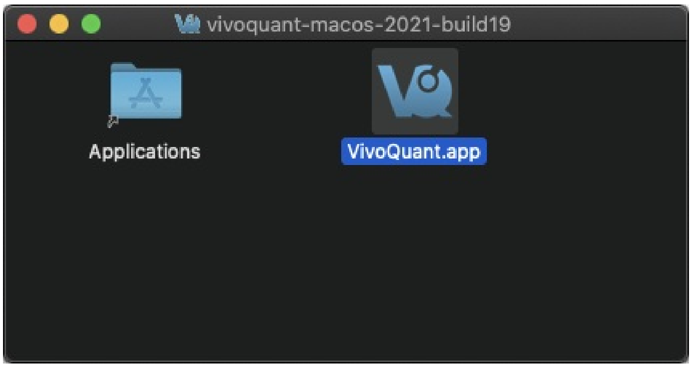
Double-click the VivoQuant install icon to start the installer.

Windows Install

Follow the sequence of set-up steps carried out by the Installer. Please accept the default settings, or change the options according to your needs. A detailed description of the install options can be found in Installation Details.

B. Mac OS X

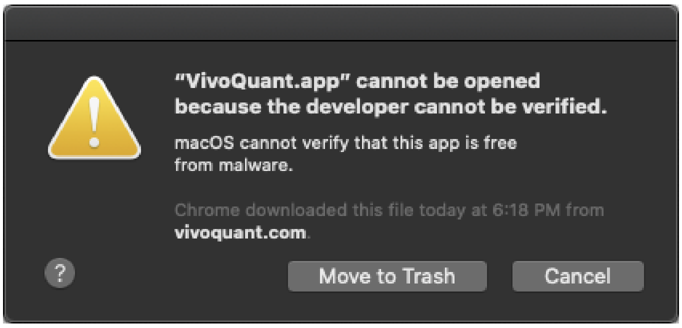
1. Double-click and unzip the VivoQuant zip archive.
2. Locate the VivoQuant installer in the Applications folder.



Mac OS Install

Troubleshooting Mac OS Install

On some occasions, Mac OS will not recognize VivoQuant as a verified application:

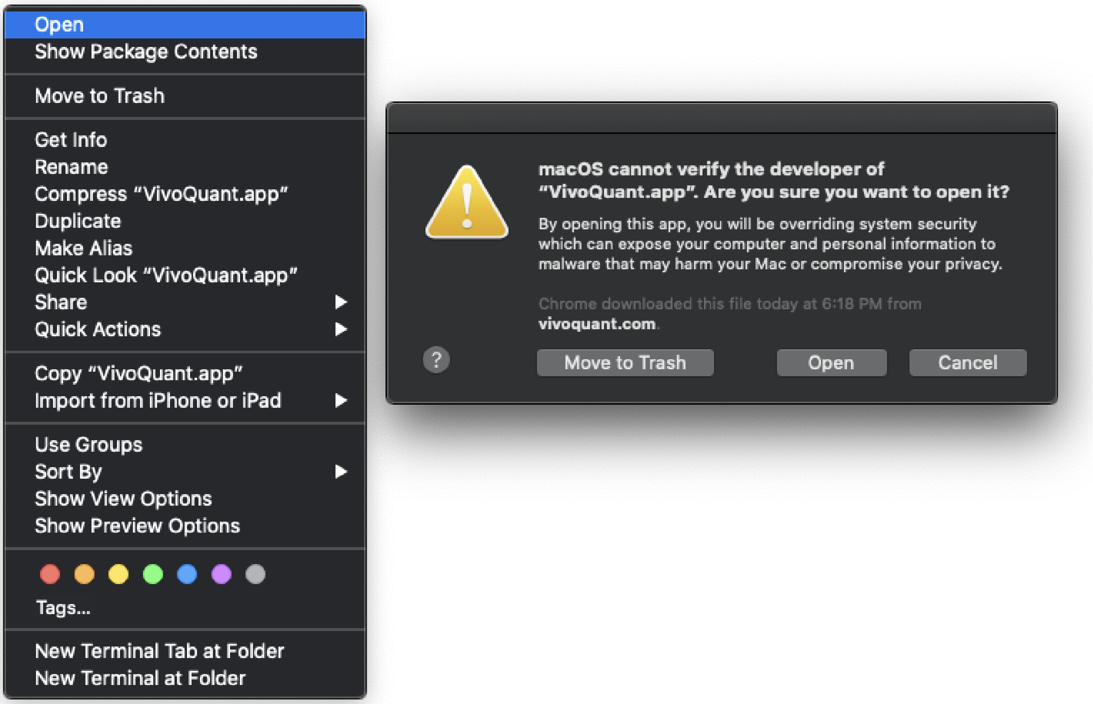

"VivoQuant.app" cannot be opened because the developer cannot be verified.

macOS cannot verify that this app is free from malware.

Chrome downloaded this file today at 6:18 PM from **vivoquant.com**.

Mac OS Warning

To make the **Open** option appear, simply the right-click on the warning message and select **Open**.



macOS cannot verify the developer of "VivoQuant.app". Are you sure you want to open it?

By opening this app, you will be overriding system security which can expose your computer and personal information to malware that may harm your Mac or compromise your privacy.

Chrome downloaded this file today at 6:18 PM from **vivoquant.com**.

Open VivoQuant

C. Linux

Double-click and unzip the VivoQuant zip archive, then move the VivoQuant folder to the desired location. To run VQ, double-click the VivoQuant script contained in this folder.

Licensing

I. Active Accounts

VivoQuant supports two licensing methods: a machine locked file-based license and a floating license. Users should consult their latest purchase agreement for the license to determine which type was purchased.

Floating licenses

The floating license uses an alpha-numeric license key and an internet connection to provide licensed access to VivoQuant. To add a floating license key:

1. Start VivoQuant
2. Go to Configuration > Licensing > Floating license tab
3. Enter the license key in the field provided.
4. Click Ok to close the Configuration dialog.
5. Restart VivoQuant, and the license will be activated in the next session.

Heartbeat pings

To prevent issues with license activations becoming stuck on a user's machine, VivoQuant requires a constant internet connection to send pings to the license server in order to confirm that the activated VivoQuant instance is still in a working state. If the process can no longer communicates with the license server, VivoQuant will notify the user to resolve the connection issue before eventually closing.

File-based Licenses

VivoQuant License Manager manages file-based licenses allocated to an account. An on-site license manager login credential will be provided to each account to access the VivoQuant License Manager. For detailed information on how to manage your account's VivoQuant licenses click Here.

Installing a file-based license

If the end-user's computer has internet access, VivoQuant will automatically detect and install a pre-approved license file. If the end-user's computer does not have internet access, they will need to download the license provided in the link and install manually. To install a license file manually, go to Help > Licensing within VivoQuant and click on **Install key**. VivoQuant is now registered and fully operational.

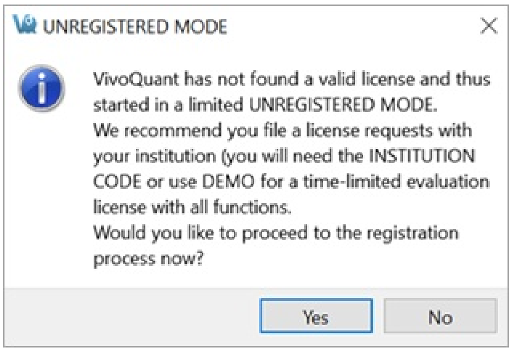
II. Trial Accounts

Methods for Obtaining a Trial License

If you are a current end-user and have an active software account, contact your account representative for a trial license of a plugin module. Your account representative will pre-approve the trial license and you should follow section II.b. below. If you do not have an active account, please follow the below steps.

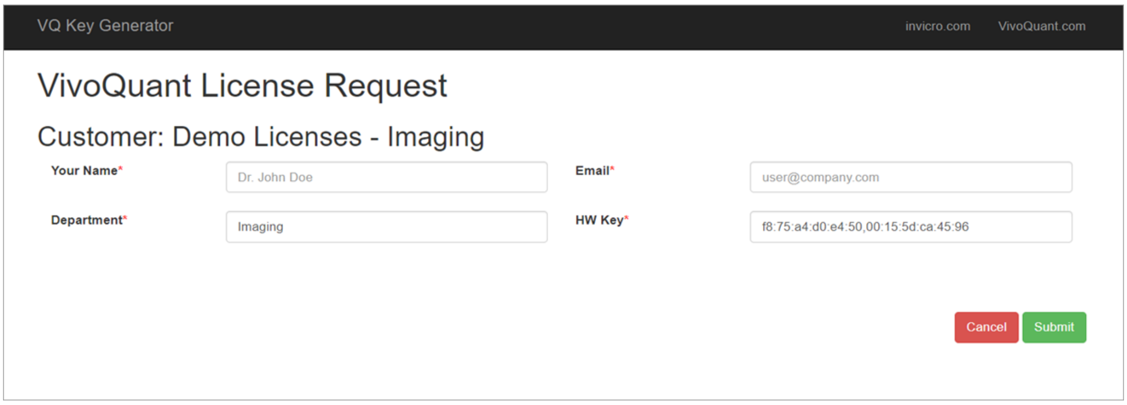
a. Requesting a Trial License

1. Download the latest stable version of VivoQuant. Once you have successfully installed VivoQuant, you will be prompted to register your computer. Click **Yes**.



VivoQuant has not found a valid license and thus started in a limited UNREGISTERED MODE.
We recommend you file a license requests with your institution (you will need the INSTITUTION CODE or use DEMO for a time-limited evaluation license with all functions.
Would you like to proceed to the registration process now?

1. Make sure the company code is DEMO. Enter a value to identify your department (or company) in the **Department** field. The license file will be sent to the email address specified in **Contact address**.
2. After clicking **Register**, your internet browser will load and navigate to the license registration confirmation page.



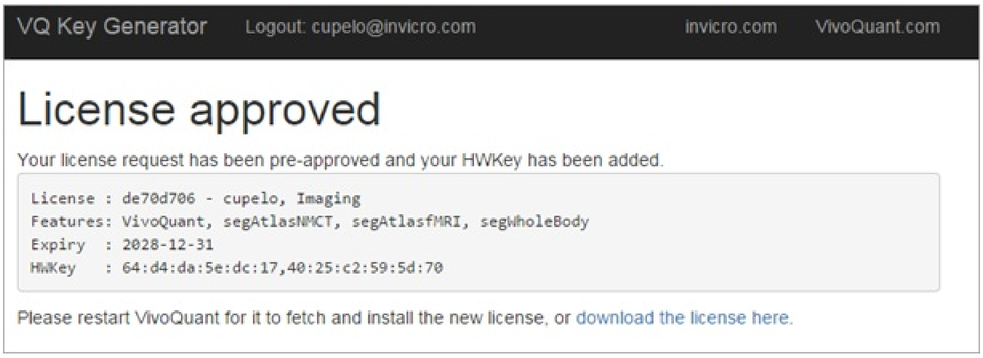
VivoQuant License Request

Customer: Demo Licenses - Imaging

Your Name*: Dr. John Doe
Email*: user@company.com
Department*: Imaging
HW Key*: f8:75:a4:d0:e4:50,00:15:5d:ca:45:96

b. Pre-approved Licenses

1. An account manager can issue a license to an end-user. Upon issuing a license, an email notification will be sent with instructions for downloading the VivoQuant software and installing the license key. After the software has been successfully installed, you will be prompted to register your computer for a license. Click **Yes**.
2. Enter the company code provided in the email along with the email address to which the registration email was sent.
3. After clicking **Register**, your Internet Browser will load and navigate to the license registration confirmation page. You will need to enter the password provided in your email to finalize the process.
4. After you click **Submit**, the system will validate the request. If successful, the below page will appear.



License approved

Your license request has been pre-approved and your HWKey has been added.

```
License : de70d706 - cupelo, Imaging
Features: VivoQuant, segAtlasNMCT, segAtlasfMRI, segWholeBody
Expiry  : 2028-12-31
HWKey   : 64:d4:da:5e:dc:17,40:25:c2:59:5d:70
```

Please restart VivoQuant for it to fetch and install the new license, or download the license here.

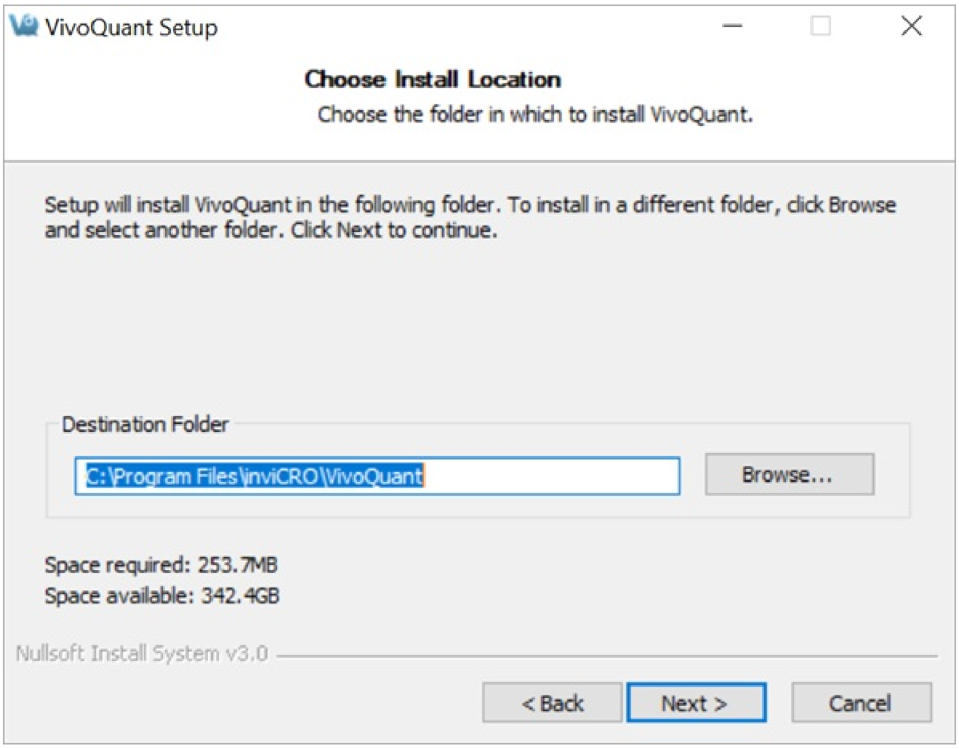
If you experience any problems, please contact support@invicro.com.

Installation Details

After accepting the VivoQuant license, you have the option to choose the install location and components, which allows you to tailor the installation to your specific needs.

Choose Install Location

For the destination folder, it is recommended to keep the default settings. However, if you would like to install multiple versions of VivoQuant on your system, you can choose a different install location here.



Choose Install Location

Choose the folder in which to install VivoQuant.

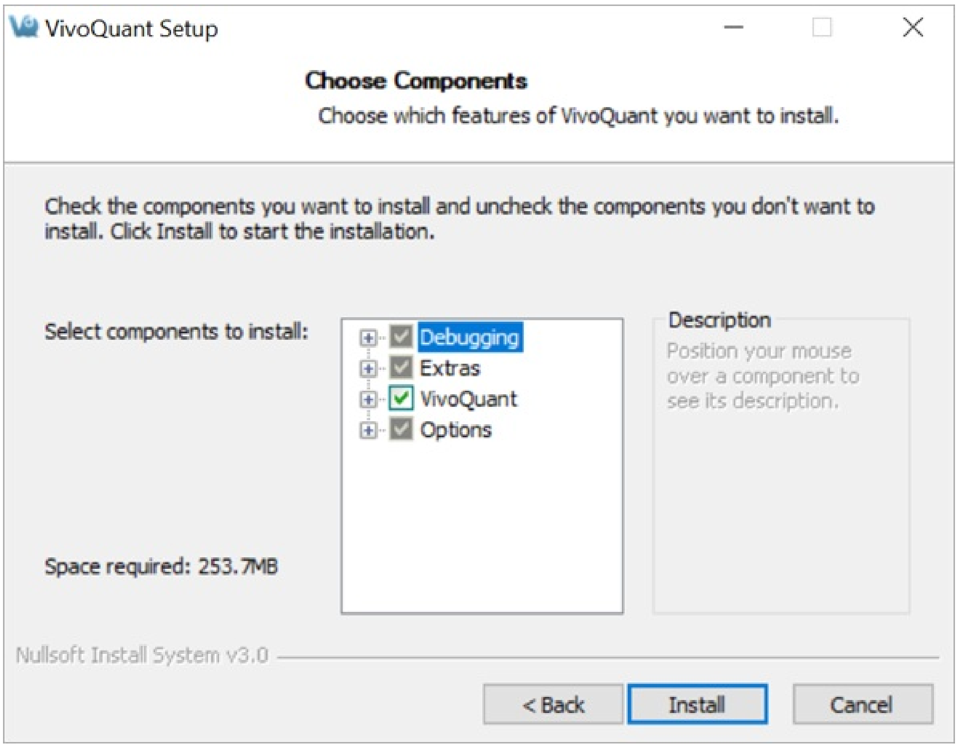
Setup will install VivoQuant in the following folder. To install in a different folder, click Browse and select another folder. Click Next to continue.

Destination Folder: C:\Program Files\inviCRO\VivoQuant

Space required: 253.7MB
Space available: 342.4GB

Install Location

Choose Components



Choose Components

Choose which features of VivoQuant you want to install.

Check the components you want to install and uncheck the components you don't want to install. Click Install to start the installation.

Select components to install:

- ☑ Debugging
- ☑ Extras
- ☑ VivoQuant
- ☑ Options

Description

Position your mouse over a component to see its description.

Space required: 253.7MB

Choose Components

Component	Description
Qt libraries	Unless you already have Qt installed on your system, it is highly recommended that you use the version coming with VQ.
ImageMagick binaries	It installs the IM programs `mpeg2encode` (required for generation of MPEG movies) and `convert` (general tool to convert image formats, not required by VQ).
Manual	After installation, the manual is available by pressing <F1> on the main VQ screen, or using the *Help|Manual* menu. Alternatively, you can also find the manual online.

<table>
<tr><td>Options</td><td>
<table>
<tr><td>Shortcut on desktop</td><td>Installs a VQ icon on Windows desktop.</td></tr>
<tr><td>DicomBrowser shortcut on desktop</td><td>Allows starting of VQ with opened DicomBrowser quickly. Open DICOM data</td></tr>
<tr><td>Add local DICOM folder</td><td>Adds an example DICOM folder to the list of repositories.</td></tr>
<tr><td>Add DEMO iPACS</td><td>Allows access to an online PACS system to download example data and share your data with other users.</td></tr>
<tr><td>Add Service iPACS</td><td>Adds a write-only online PACS system (reading requires password) to allow you to send data to our service engineers.</td></tr>
<tr><td>Enable update check</td><td>When enabled, VQ regularly checks for the availability of new versions and offers you to download and install them.
See Update Check for details.</td></tr>
</table>
</td></tr>
<tr><td>Debugging</td><td>These options allows for debugging issues in VQ.</td></tr>
</table>

Keyboard Shortcuts

General Keyboard Shortcuts

Windows / Linux Shortcut	Mac Shortcut	Shortcut Function
Ctrl + O	⌘ + O	Open Reference
Ctrl + N	⌘ + N	Open input 1
Ctrl + Shift + N	⌘ + Shift + N	Open input 2
Ctrl + D	⌘ + D	Open DICOM Data
Ctrl + I	⌘ + I	Save Image
Ctrl + M	⌘ + M	Save Movie
Ctrl + S	⌘ + S	Save Data (DICOM format)
F1	fn + F1	Manual
F2	fn + F2	Show Reference
F3	fn + F3	Show input 1
F4	fn + F4	Show input 2
F5	fn + F5	Slice Control
F6	fn + F6	MIP Control
F7	fn + F7	Data Manager
Ctrl + +	⌘ + +	Zoom in
Ctrl + -	⌘ + -	Zoom out
Ctrl + 0	⌘ + 0	Normal Size
Ctrl + F	⌘ + F	Full Screen
Ctrl + U	⌘ + U	Auto Zoom
Ctrl + Z	⌘ + Z	Undo Operation
Ctrl + Shift + Z	⌘ + Shift + Z	Redo Operation
Ctrl + I	⌘ + I	Save Image
Ctrl + Shift + D	⌘ + Shift + D	DICOM Dump
Ctrl + Shift + H	⌘ + Shift + H	Histogram

Windows / Linux Shortcut	Mac Shortcut	Shortcut Function
Ctrl + Shift + U	⌘ + Shift + U	Update Check
Ctrl + Shift + C	⌘ + ,	Configuration Panel
Ctrl + Shift + P	⌘ + Shift + P	Preprocessing Tool
Ctrl + Shift + W	⌘ + Shift + W	Worklist Tool
Ctrl + B	⌘ + B	Base NanoSPECT Configuration
Ctrl + Q	⌘ + Q	Quit MMP Calibration Tool
Ctrl + T	⌘ + T	Toggle between pre- and post-correction images in the Near-Field Uniformity panel
←,→,↑,↓	←,→,↑,↓	Scroll through slices in either the Slice View or Tile View.
PageUp,PageDn	fn + ↑, fn + ↓	Scroll through slices in either the Slice View or Tile View.

3D ROI Tool Specific Keyboard Shortcuts

Windows / Linux Shortcut	Mac Shortcut	Shortcut Function
N	N	Navigate to the Navigation tab in the 3D ROI Operator
P	P	Navigate to the Manual Painting tab in the 3D ROI Operator
S	S	Navigate to the Spline Tool tab in the 3D ROI Operator
M	M	Navigate to the Magic Segmentation tab in the 3D ROI Operator
X	X	Navigate to the Expert tab in the 3D ROI Operator
Shift + =	Shift + =	Add a ROI
-	-	Reset the active ROI
E	E	Edit the active ROI
v	v	Toggle visibility of the active ROI
R	R	Rotate through the ROI list in the active ROI drop down menu
Right Click of Mouse	Right Click of Mouse	Rotate through the ROI list in the active ROI drop down menu
T	T	Display quantification table
H	H	Display 3D ROI Histogram Tool
Enter	Return or Enter	Within the Spline tool, confirm classification of voxels within contour to active ROI
Shift + Enter	Shift + Return or Enter	Within the Spline tool, confirm classification of voxels within contour to active ROI and move to next slice
Space	Space	Within the Spline tool, scroll through Spline, Freehand, Bully and Thresholding tools
C	C	Within the Spline tool, clear the currently drawn contour

Slice View - Intraframe Zoom And Pan

Key	Mouse Button and Action	Context	Description
Shift	Left down and drag	Cursor over slice frame	Translates
Shift	Midel down and drag	Cursor over slice frame	Translates
Shift	Scroll wheel	Cursor over slice frame	Zooms within display bounds

VivoQuant Configuration

The VivoQuant Configuration window has several panels that provide access to customizable features as well as important licensing and set-up information.

Getting There

Windows and Linux

The Configuration window is accessible from the **Tools** menu under **Configuration** or by using the keyboard shortcut Ctrl+Shift+C.

MacOS

On Mac, the Configuration window is accessible from the **VivoQuant** menu under **Preferences** or by using the keyboard shortcut ⌘ + ,.

For more on keyboard shortcuts in VivoQuant, see Keyboard Shortcuts.

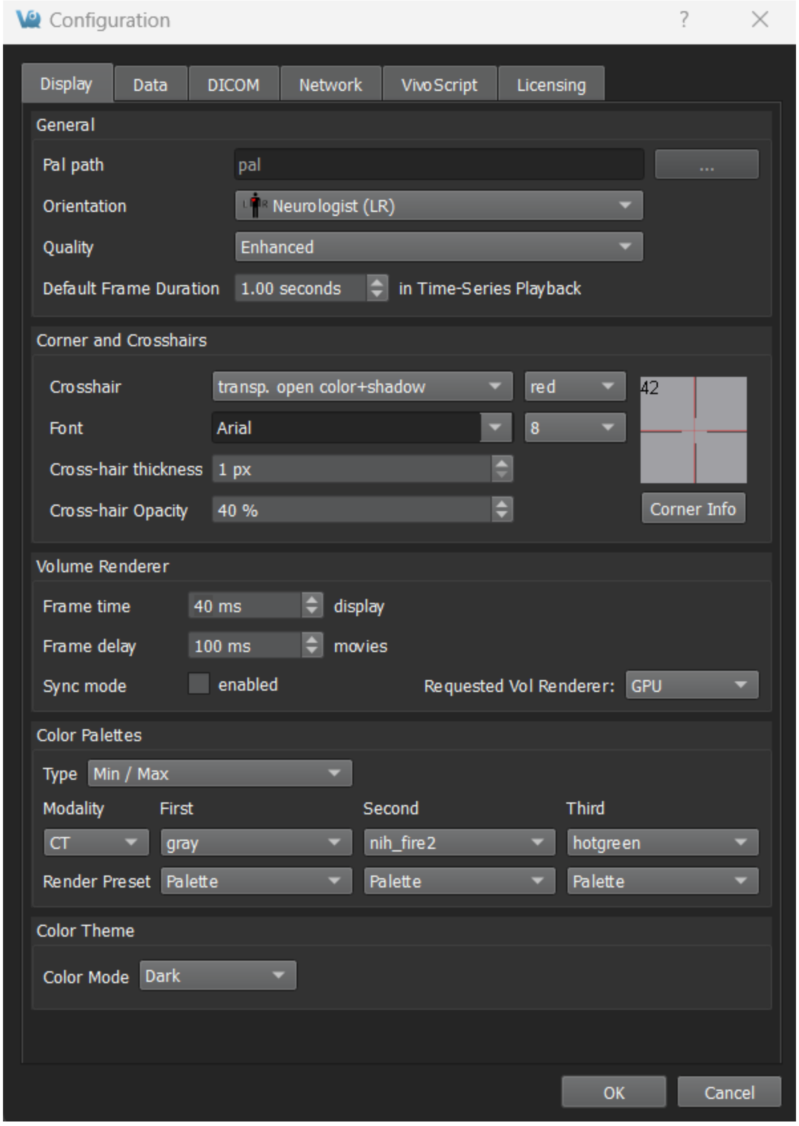
Configuration Panels

The Configuration window consists of six panels:

- Display
- Data
- DICOM Settings
- Network
- Licensing
- VivoScript

Display

Several appearance features may be customized in the Display panel, including General display information, Maximum Intensity Projection attributes, and Color Palette defaults.



General

Pal path: pal

Orientation: Neurologist (LR)

Quality: Enhanced

Default Frame Duration: 1.00 seconds in Time-Series Playback

Corner and Crosshairs

Crosshair: transp. open color+shadow, red

Font: Arial, 8

Cross-hair thickness: 1 px

Cross-hair Opacity: 40 %

Volume Renderer

Frame time: 40 ms display

Frame delay: 100 ms movies

Sync mode: ☐ enabled

Requested Vol Renderer: GPU

Color Palettes

Type: Min / Max

Modality	First	Second	Third
CT	gray	nih_fire2	hotgreen
Render Preset	Palette	Palette	Palette

Color Theme

Color Mode: Dark

Display Panel

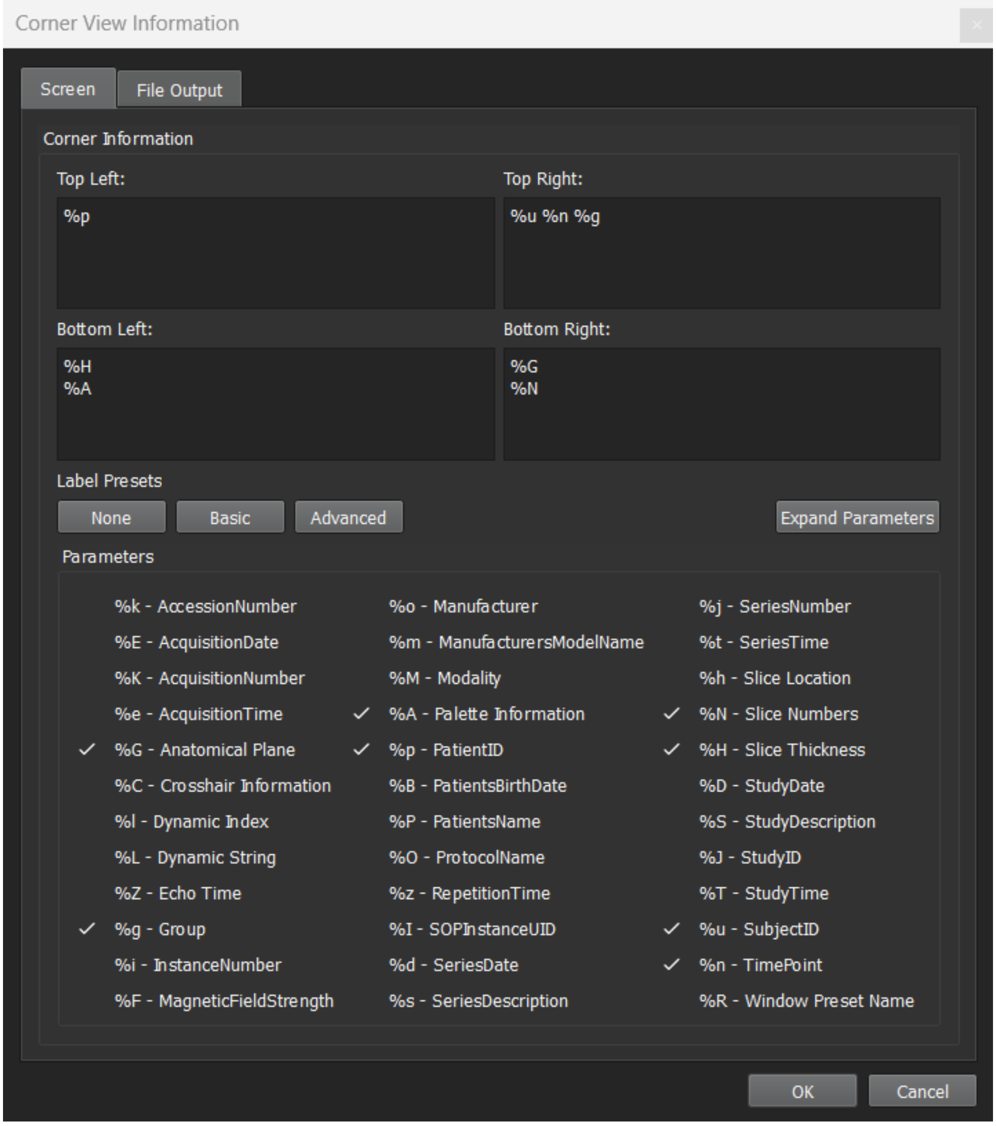
General

Option	Description
Pal Path	Pal files hold the color map information for the different Color Palettes available in VivoQuant.
Orientation	Provides an option to view the data whether in Radiologist View (face to face) or Neurologist View (mirror). Diagrams are used to show the difference.
Quality	Provides an option to view the data whether in Native or Enhanced quality. With Native quality, voxels are always displayed as they are defined in the image, with no smoothing applied. With Enhanced quality, smoothing is applied to the image when a voxel is displayed using multiple pixels on the screen. There is no effect on quantification.
Default Frame Duration	Establish a default value for the ‘Frame Duration’ parameter in the Time Series operator.

Corner and Crosshairs

Option	Description
Crosshair style	Sets the visual style of the crosshair to be used in the Main Window.
Crosshair color	Sets the colors of the crosshair to be used in the Main Window. Crosshair color options include red, yellow, magenta, white, green, and blue.
Font Style	Controls the font style of the displayed text in the Main Window.
Font Size	Controls the size of the text displayed in the Main Window
Crosshair thickness	Controls the pixel width of the crosshair lines
Crosshair Opacity	Controls the opacity of the crosshair lines
Preview Panel	Displays a preview of the font and cross-hair selections.
Corner Info	Launches the **Corner View Information** dialog which controls the information to be displayed on each corner of the slice views.

The **Corner View Information** is organized into two tabs: one for information shown on the screen view and one for information that will show on the image when it is saved out. The corner information is organized into the four corners of the image as can be seen in the corresponding four editable text areas. These text areas support a combination of regular text input and also field expansion by the use of tokens prefaced by the percent character. As you add tokens a helpful check mark will be shown next to the field indicating that it is included in one of the four corners. We also have added a helpful **Expand Parameters** button so you may more easily read through the included fields. Also included are three preset buttons for common corner view settings: None, Basic and Advanced. These were determined by Image Analysts to be commonly used templates; which can be configured through the registry settings.



Corner Information

Top Left: %p

Top Right: %u %n %g

Bottom Left:
%H
%A

Bottom Right:
%G
%N

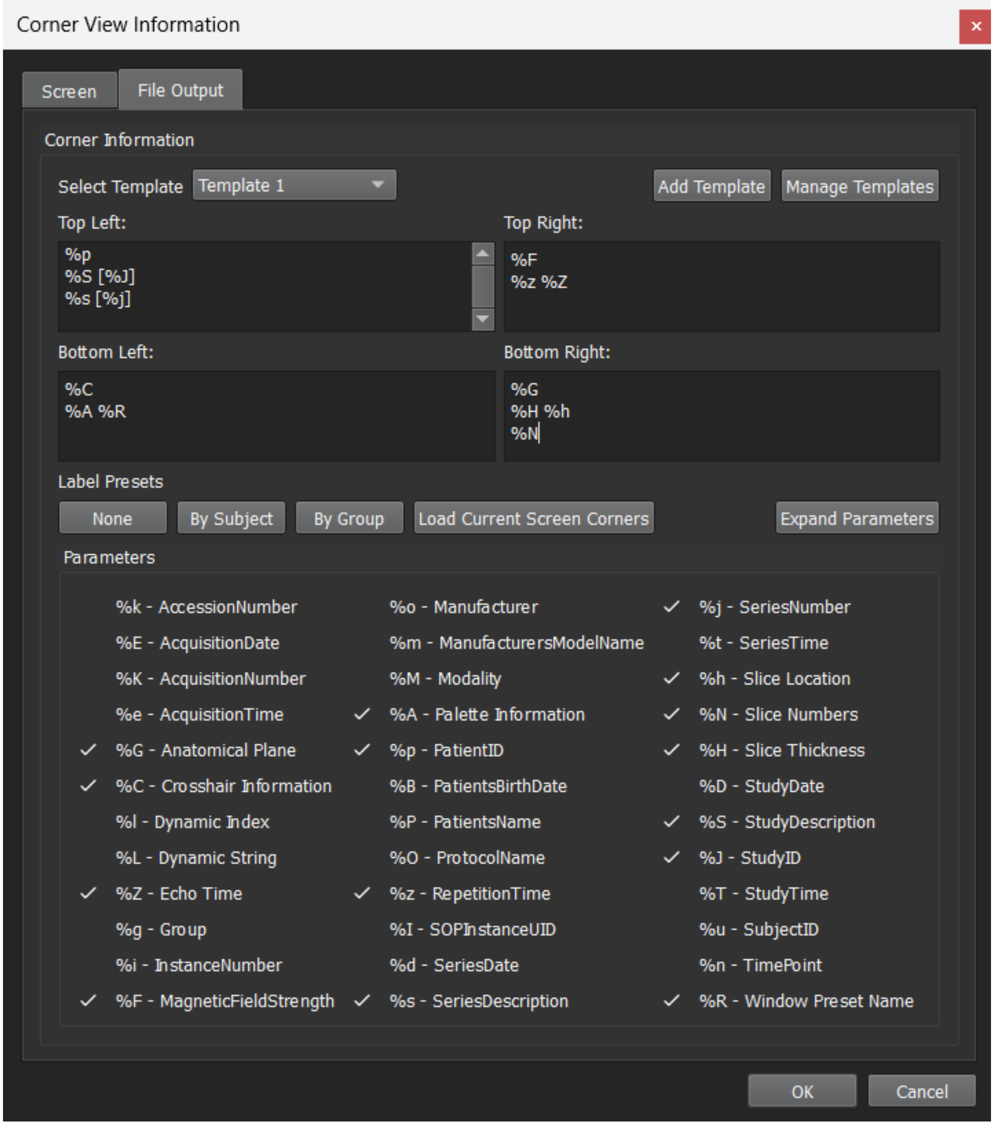
Label Presets

Parameters

- %k - AccessionNumber
- %E - AcquisitionDate
- %K - AcquisitionNumber
- %e - AcquisitionTime
- ✓ %G - Anatomical Plane
- %C - Crosshair Information
- %l - Dynamic Index
- %L - Dynamic String
- %Z - Echo Time
- ✓ %g - Group
- %i - InstanceNumber
- %F - MagneticFieldStrength
- %o - Manufacturer
- %m - ManufacturersModelName
- %M - Modality
- ✓ %A - Palette Information
- ✓ %p - PatientID
- %B - PatientsBirthDate
- %P - PatientsName
- %O - ProtocolName
- %z - RepetitionTime
- %I - SOPInstanceUID
- %d - SeriesDate
- %s - SeriesDescription
- %j - SeriesNumber
- %t - SeriesTime
- %h - Slice Location
- ✓ %N - Slice Numbers
- ✓ %H - Slice Thickness
- %D - StudyDate
- %S - StudyDescription
- %J - StudyID
- %T - StudyTime
- ✓ %u - SubjectID
- ✓ %n - TimePoint
- %R - Window Preset Name

Corner View Screen Layout

The **File Output** tab expands on the **Screen** tab functionality with the addition of more configurable templates. There is also a handy **Load Current Screen Corner** button to copy the corner screen information over to the current template you are configuring.



Corner Information

Select Template: Template 1

Top Left:
%p
%S [%J]
%s [%j]

Top Right:
%F
%z %Z

Bottom Left:
%C
%A %R

Bottom Right:
%G
%H %h
%N

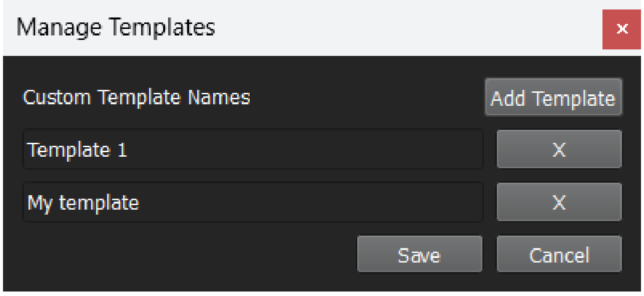
Label Presets

Parameters

%k - AccessionNumber
%E - AcquisitionDate
%K - AcquisitionNumber
%e - AcquisitionTime
✓ %G - Anatomical Plane
✓ %C - Crosshair Information
%I - Dynamic Index
%L - Dynamic String
✓ %Z - Echo Time
%g - Group
%i - InstanceNumber
✓ %F - MagneticFieldStrength
%o - Manufacturer
%m - ManufacturersModelName
%M - Modality
✓ %A - Palette Information
✓ %p - PatientID
%B - PatientsBirthDate
%P - PatientsName
%O - ProtocolName
✓ %z - RepetitionTime
%I - SOPInstanceUID
%d - SeriesDate
✓ %s - SeriesDescription
✓ %j - SeriesNumber
%t - SeriesTime
✓ %h - Slice Location
✓ %N - Slice Numbers
✓ %H - Slice Thickness
%D - StudyDate
✓ %S - StudyDescription
✓ %J - StudyID
%T - StudyTime
%u - SubjectID
%n - TimePoint
✓ %R - Window Preset Name

Corner View File Layout

The **Manage Templates** dialog allows you to create up to seven templates, delete and rename them. Once you save the current list you will access to them via the **Select Templates** dropdown option.



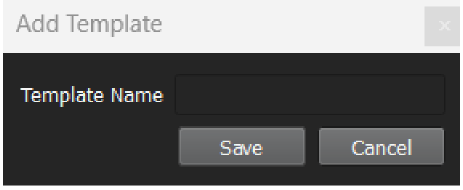
Custom Template Names

Template 1

My template

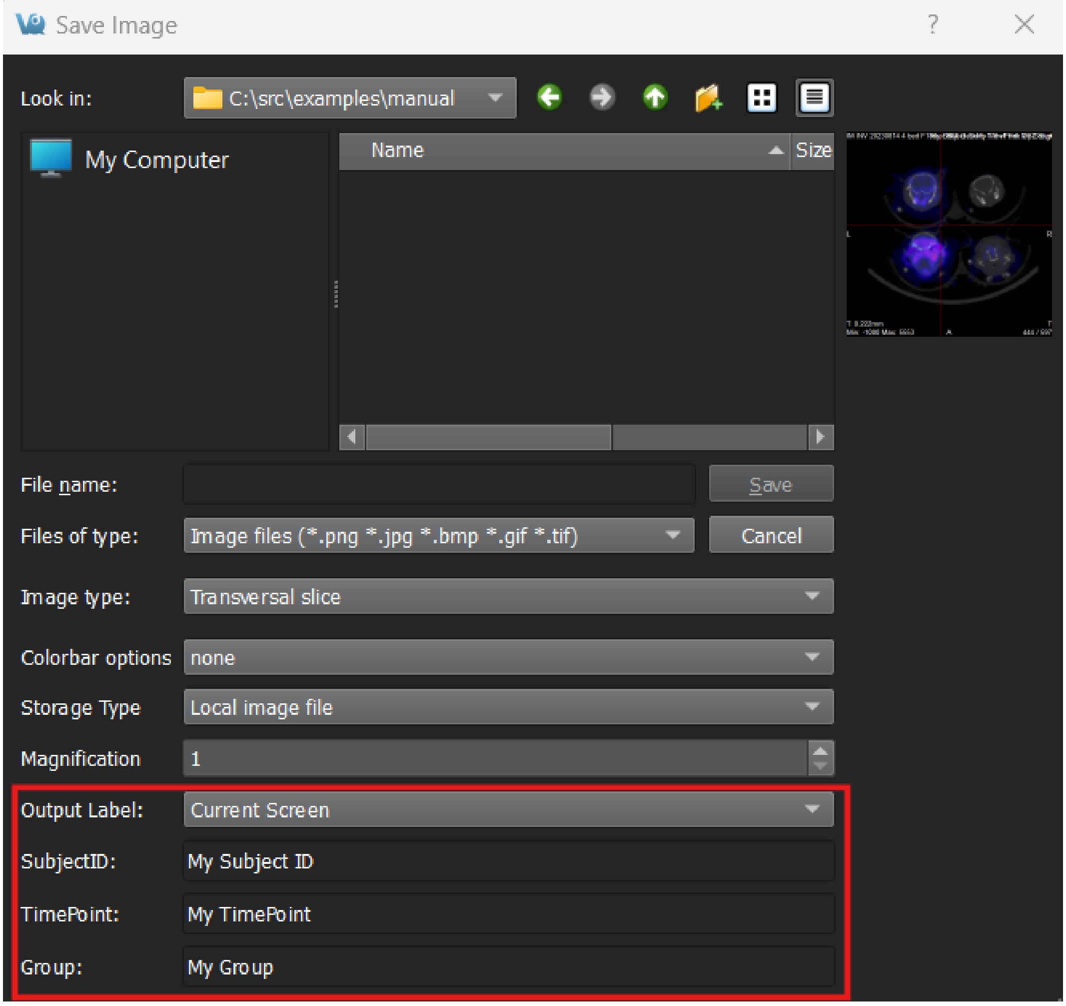
Manage Templates

The **Add Template** option can be accessed either from the **Manage Templates** dialog or on the upper right of the **File Output** tab.



Add Corner Template

One additional feature is the addition of three customizable corner fields that can be changed via the **Save Image** and **Save Movie** dialog. These custom fields are called: SubjectID, TimePoint, and Group. If any of these field parameters are present in the currently selected corner view template then the corresponding editable text fields will show up in the save dialogs. This feature was requested as a time saver when the user is spending a lot of time saving images and needs to make quick label adjustments. Although the use case was specific to these three field names anyone can use these fields for their own custom information; the three names are only mappings from the corner template to these save dialog fields.



Look in: C:\src\examples\manual

File name:

Files of type: Image files (*.png *.jpg *.bmp *.gif *.tif)

Image type: Transversal slice

Colorbar options none

Storage Type Local image file

Magnification 1

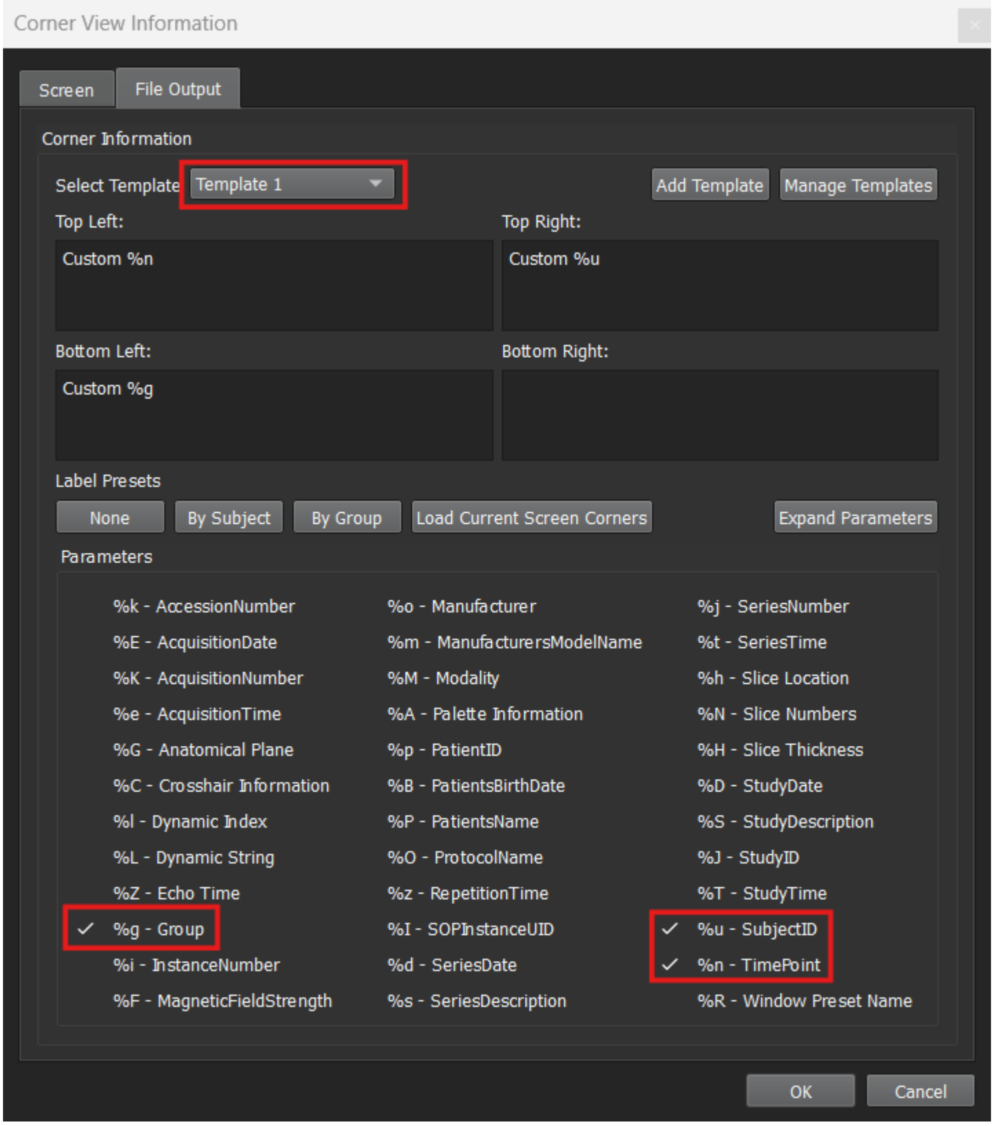
Output Label: Current Screen

SubjectID: My Subject ID

TimePoint: My TimePoint

Group: My Group

Save Corner Label Extra Options



Select Template: Template 1

Top Left: Custom %n

Top Right: Custom %u

Bottom Left: Custom %g

Bottom Right:

Parameters

%k - AccessionNumber	%o - Manufacturer	%j - SeriesNumber
%E - AcquisitionDate	%m - ManufacturersModelName	%t - SeriesTime
%K - AcquisitionNumber	%M - Modality	%h - Slice Location
%e - AcquisitionTime	%A - Palette Information	%N - Slice Numbers
%G - Anatomical Plane	%p - PatientID	%H - Slice Thickness
%C - Crosshair Information	%B - PatientsBirthDate	%D - StudyDate
%I - Dynamic Index	%P - PatientsName	%S - StudyDescription
%L - Dynamic String	%O - ProtocolName	%J - StudyID
%Z - Echo Time	%z - RepetitionTime	%T - StudyTime
✓ %g - Group	%I - SOPInstanceUID	✓ %u - SubjectID
%i - InstanceNumber	%d - SeriesDate	✓ %n - TimePoint
%F - MagneticFieldStrength	%s - SeriesDescription	%R - Window Preset Name

File Output Custom Fields

Volume Renderer

Option	Description
Frame Time - Display	Sets the display duration for each MIP projection image during MIP Controller playback.
Frame Delay - Movie	Sets the delay time between MIP frames in a saved movie.
Sync mode	If enabled, only completed MIP frames will be displayed. If disabled, the MIP will freely rotate at all times but will display a message in place of the MIP for uncompleted frames.
Requested Vol Rendered	Sets the MIP image volume rendering unit. Options are: Smart, CPU and GPU.

Color Palettes

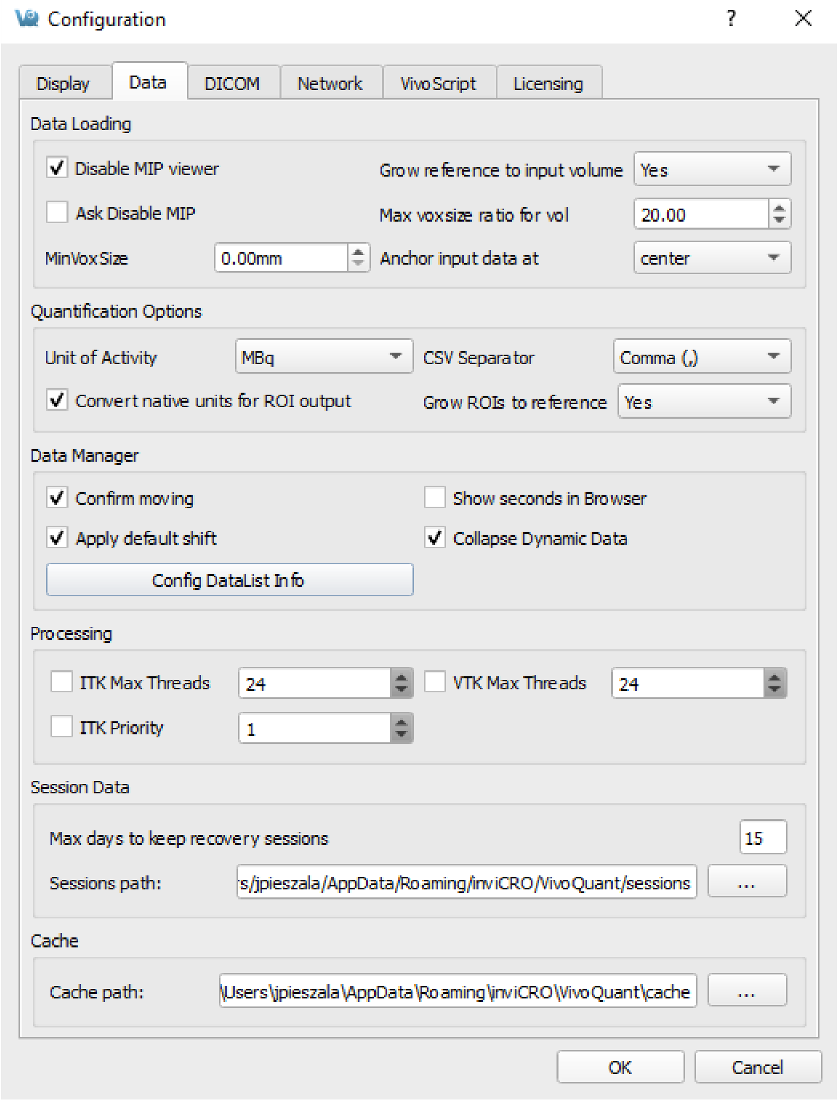
Option	Description
Type	Sets the method for determining the color palette range.
Palette	The default Color Palettes for the first three loaded volumes of each Modality are set. Inputs beyond the third loaded volume of a particular modality follow the palette of the third one.

Color Theme

Option	Description
Color Mode	Changes the general appearance of VivoQuant's menus, buttons and windows: - Default (use the native appearance of the Operating System) - Dark - Light **Note: On MacOS only, the **Default** option is replaced by the **System** option which will follow the Dark/Light system's configuration from **System Preferences** -> **General** -> **Appearance**. It is not yet supported on other Operating Systems.*

Data

The Data panel contains options for data handling, including data loading, quantification, management and processing.



Data Loading

☑ Disable MIP viewer

Grow reference to input volume: Yes

☐ Ask Disable MIP

Max voxsize ratio for vol: 20.00

MinVoxSize: 0.00mm

Anchor input data at: center

Quantification Options

Unit of Activity: MBq

CSV Separator: Comma (,)

☑ Convert native units for ROI output

Grow ROIs to reference: Yes

Data Manager

☑ Confirm moving

☐ Show seconds in Browser

☑ Apply default shift

☑ Collapse Dynamic Data

Processing

☐ ITK Max Threads: 24

☐ VTK Max Threads: 24

☐ ITK Priority: 1

Session Data

Max days to keep recovery sessions: 15

Sessions path: s/jpieszala/AppData/Roaming/inviCRO/VivoQuant/sessions

Cache

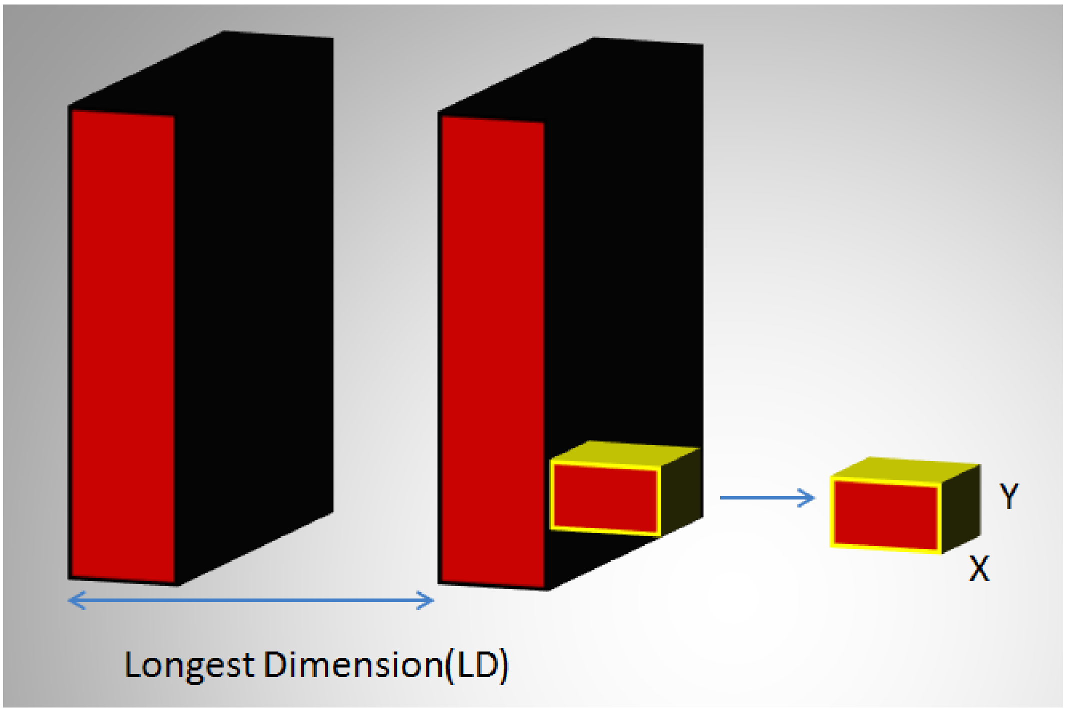
Cache path: \Users\jpieszala\AppData\Roaming\inviCRO\VivoQuant\cache

Data Panel

Data Loading

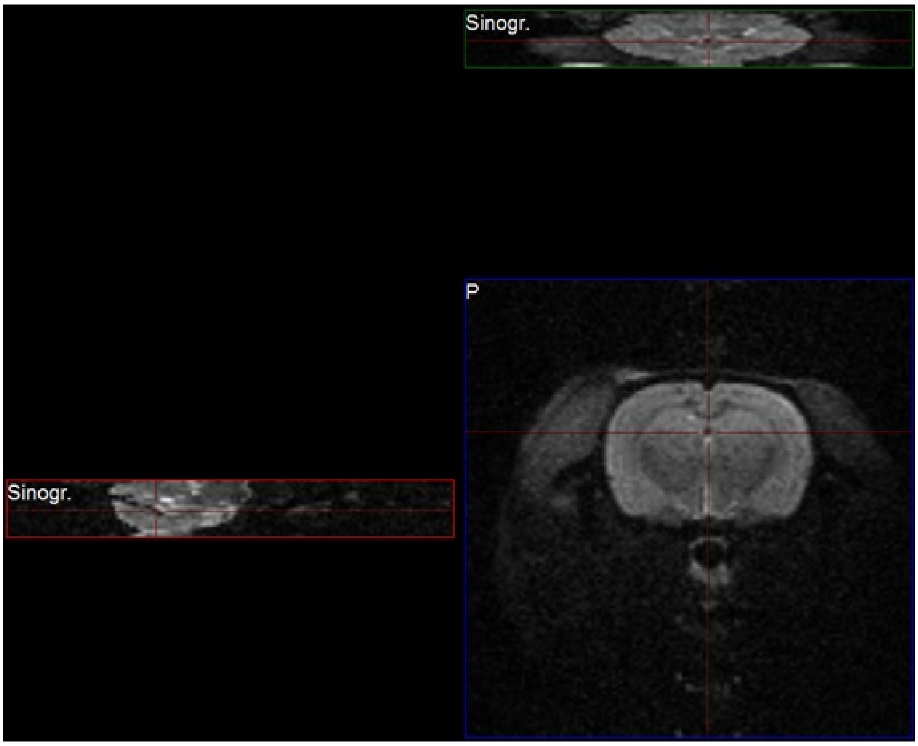
Use the **Data Loading** panel to set loading options.

Option	Description
Disable MIP viewer	Check the box to disable the MIP viewer upon loading. For large datasets, this can improve the loading speed.
Ask Disable MIP	If enabled, VivoQuant will ask for your permission to initialize the MIP viewer upon loading. For large datasets, this can improve the loading speed.
Grow reference to input volume	Choose ‘yes’ to allow the addition of zero-padding to a reference image for it to match the volume of an input image, or ‘no’ to keep the reference image size static (and potentially crop the input image if it is larger than the reference). Choose ‘ask’ to allow a window to appear upon loading, in an input, a data set that is larger than the image in the reference position.
Max voxsize ratio for vol.	Specify the maximum pixel ratio (largest pixel dimension / smallest pixel dimension) by which a data set is interpolated as a volume image file.
MinVoxSize	Specify the minimum allowed voxel width. Data will be resampled upon loading if their voxel width is less than the specified minimum. The voxel width will be doubled until it exceeds the minimum.
Anchor input data	Specify where to anchor the input data. Data can be anchored at the following options: center, head, or foot.



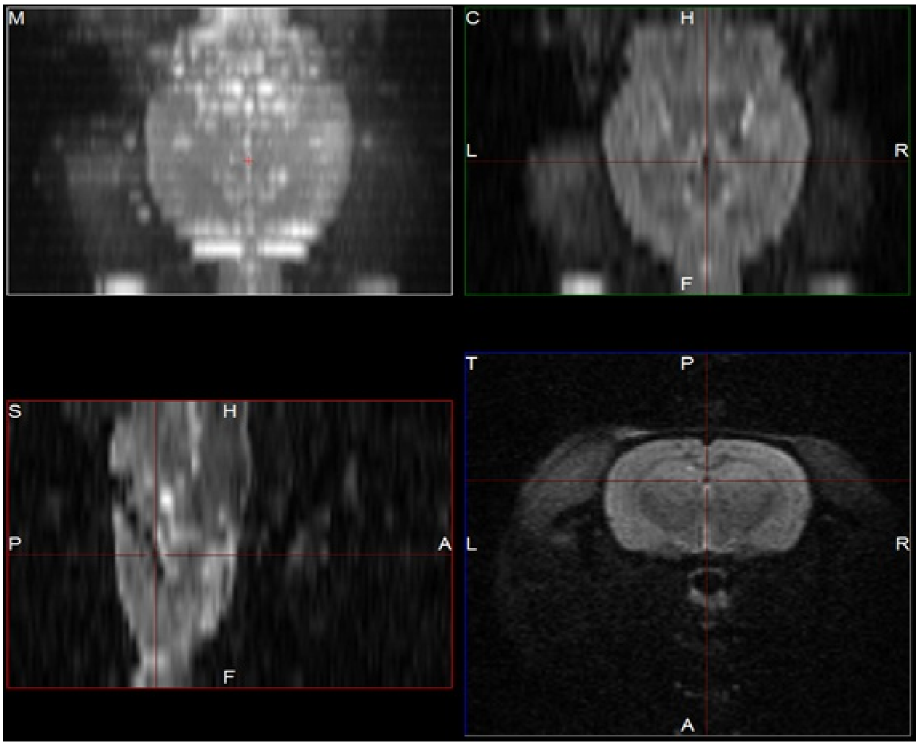
Longest Dimension

In the above image, LD represents the out-of-plane resolution and the X and Y represent the in-plane resolution. If the pixel ratio of the loaded image exceeds the given threshold, i.e. MaxVoxSizeRatio < LD/X, the data set will be loaded as a planar 2D by n file. Below is an example MR image loaded as a planar 2D by n file.



Planar

If the pixel ratio of the loaded image is less than the given threshold, i.e. MaxVoxSizeRatio > LD/X, the data set will be loaded as an interpolated volume image with isotropic voxels. Below is an example MR image loaded as an interpolated volume file.



Interpolated Volume Image

🛈 **Note:** Other modalities besides MR can be loaded into VQ as planar or interpolated volume files based on the Max voxsize ratio for volume setting specified in the configuration window.

As described on the Open DICOM Data help page:

- If the **'Force Planar'** check box is checked in the Data Browser, then the image will load in planar mode regardless of the value set for MaxVoxSizeRatio.
- If the **'Force Planar'** check box is unchecked in the Data Browser, then the image will load in the appropriate mode according to the value set for MaxVoxSizeRatio.

Quantification Options

Use the **Quantification Options** panel to set options used by the Projection++ Operator and the 3D ROI Operator.

Option	Description
Units of Activity	Select the unit to be used for quantifying both PET and SPECT data. Options include MBq, kBq, mCi, and µCi. Note: Concentration units (e.g. nCi/cc) will not be converted to the unit of activity specified. The Multi-Atlas Segmentation and 3D Brain Atlas Tool plugin modules do support converting from concentration units to units of µCi.
CSV Separator	Choose the CSV file delimiter of their choice, applied when saving Quantification data.
Convert native units for ROI output	Enable this option if would like ROI output operations to attempt to convert your data to the unit specified in the **Units of Activity** drop down box mentioned above.
Grow ROIs to reference	Choose if the ROI object should be resampled when the dimensions and or voxel sizes of the reference image are changed. - Ask (a prompt will be displayed to ask for the desired behavior) - Yes (ROIs will be resampled to match the reference's dimension) - No (ROIs will be embedded into an object matching the reference's dimension)
Quant. Table Items	Available here on MacOS only. See the Projection++ Operator and 3D ROI Operator sections for other Operating Systems.

Data Manager

The **Data Manager** panel contains options for handling data.

Option	Description
confirm moving	Check to enable a confirmation message when rearranging data in the Data Manager.
Show seconds in Browser	Check to display the seconds in the study date column in the DICOM browser. VQ has to be restarted to configure this change.
Apply default shift	Check to apply a default reorientation to data being loaded into VQ. The default shift can be defined in the Reorientation/Registration operator. For more on this, please see the Reorientation/Registration page.
Collapse Dynamic Data	If enabled, dynamic frames from the same series will be loaded into the data manager as a single input. If disabled, each dynamic frame will be loaded into the data manager as a separate input. Regardless of the setting, the data manager allows you to manually expand collapsed dynamic data, or collapse a set of dynamic frames into a single input.
Config DataList Info	This button will launch the **Data Manager Text Configuration** dialog; within which, you will be able to customize what meta data is shown listed for your data sources in the Data Manager.

Processing

Use the **Processing Panel** to set resource limits on data processing.

Option	Description
ITK Max Threads	If enabled, you can customize the number of threads used by ITK at runtime. If disabled, ITK thread number will be set to its default value.
VTK Max Threads	If enabled, you can customize the number of threads used by VTK at runtime. If disabled, VTK thread number will be set to its default value.
ITK Priority	If enabled, you can customize ITK thread priority. If disabled, ITK thread priority will be set to its default value.

☑ **Tip:** Setting limits on image processing is particularly useful to prevent performance issues in multi-user setups.

Session data

VivoQuant may at times save a local backup of the current session state so that users can recover their session data. The behavior of the recovery session mechanism can be controlled in the **Session data** panel.

Option	Description
Max days to keep recovery sessions	Recovery sessions older than the set days will be deleted on startup.

Cache

Vivoquant allows users to have more control over system resources by allowing the user to adjust the location of the VQ cache.

Option	Description
Cache Path	Various VQ utilities will be using this location in support of computations and data handling.

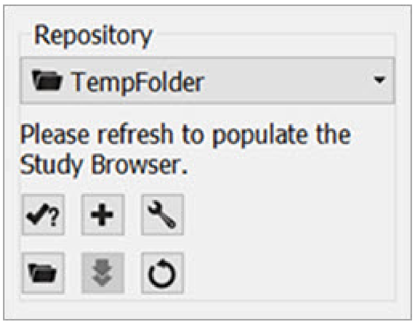
DICOM Settings

The DICOM configuration allows the user to add/edit DICOM repositories. These repositories can be local folders containing DICOM files, or DICOM network servers located whether on a local or a remote computer. The DICOM Dump uses the DICOM Dictionary to identify information in the DICOM header. Check the How-To guide for more information on configuring the NanoSPECT's DICOM Servers in VivoQuant.

Getting There

The DICOM Repository can be accessed in three different ways.

Ddex is accessible via the **Repository** panel in the Data Browser. To open the **Data Browser**, click the icon.

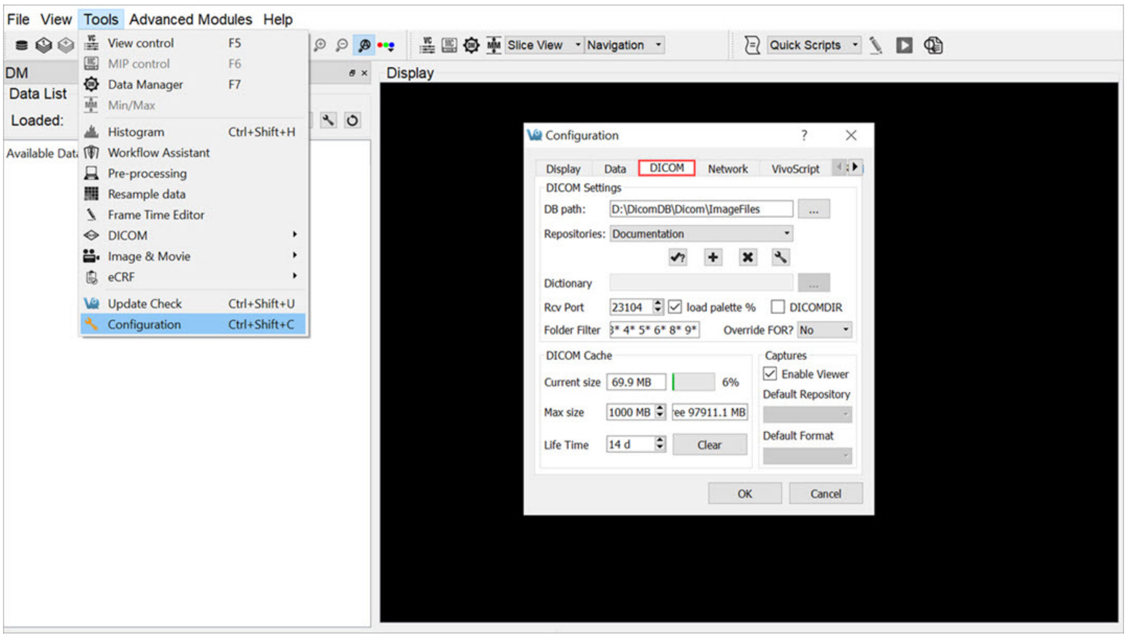


TempFolder

Please refresh to populate the Study Browser.

Repository Panel

The second method is by selecting the Configuration option in the **Tools** menu, and then click on the **DICOM** panel.



DB path: D:\DicomDB\Dicom\ImageFiles

Repositories: Documentation

Dictionary

Rcv Port 23104 ☑ load palette % ☐ DICOMDIR

Folder Filter 3* 4* 5* 6* 8* 9* Override FOR? No

Current size 69.9 MB 6%

Max size 1000 MB ree 97911.1 MB

Life Time 14 d

☑ Enable Viewer

Default Repository

Default Format

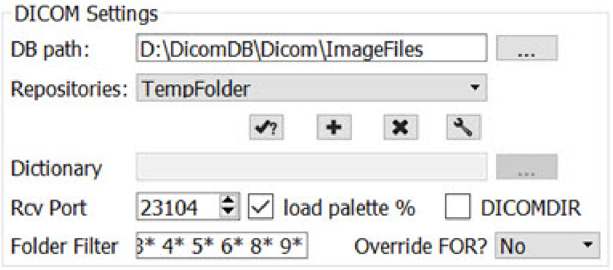
Configuration Option

The third method is by opening the Configuration panel using the "Ctrl+Shift+C" shortcut. For more information on keyboard shortcuts in VQ, please see Keyboard Shortcuts.

Configuration Dialog

The **DICOM** panel in the **Configuration** dialog box provides the most in-depth DICOM information available in VivoQuant. The **DICOM** panel consists of three sections: DICOM Settings, DICOM Cache, and Captures.

DICOM Settings



DICOM Settings

DB path: D:\DicomDB\Dicom\ImageFiles

Repositories: TempFolder

Dictionary

Rcv Port 23104 ☑ load palette % ☐ DICOMDIR

Folder Filter 3* 4* 5* 6* 8* 9*

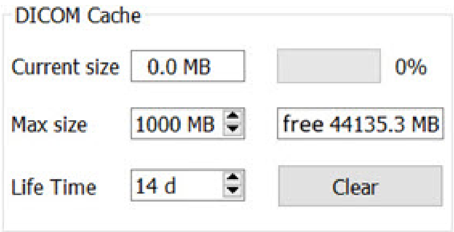
Override FOR? No

DICOM Settings

Option	Description
DB path	Location of local DICOM database. Allows optimized internal access to the Mediso DICOM database. See Optimized local access, for details.
Repositories	List of available repositories. The bank of buttons immediately beneath the pulldown menu operate on the selected repository in this field:
✓?	Checks connection to DICOM repository. Local folders are verified to exist and a C-ECHO is sent to DICOM servers.
⊞	Adds a new repository
☒	Deletes selected repository
🔧	Opens the DICOM repository editor DICOM repository editor
Dictionary	Shows list of additional dictionaries used by the DICOM library. Please set environment variable DCMDICTPATH to set this value. For more information on the DICOM dictionary, see DICOM Dump
Rcv Port	Port over which the DICOM peer sends data.
load palette %	If enabled, the palette window will be loaded in accordance with the image data. If disabled, the palette window will be set to whatever the window was set to last.
DICOMDIR	Checking this box enables support for DICOMDIR files.
Folder Filter	Allows users to specify the type of DICOM files loaded into VivoQuant. Users can configure loading extensionless dicom data by adding a space and * to the end of the default settings:  Folder Filter * *.dcm *.dc3 *.dicom IM_* S_*
Override FOR	A **Frame of Reference** (FOR) is a coordinate system that ensures the spatial relationship of images within a series. It also allows for images across multiple series to share the same FOR. VivoQuant allows users to choose among different behaviors regarding this setting. **Yes:** the system will always overwrite the FOR settings and apply co-registration when loading a DICOM series of images. **No:** the system will never overwrite the FOR settings of the DICOM image series and will always apply co-registration. **Ignore:** the system will neither overwrite the FOR settings nor apply co-registration. **Ask:** the system will provide the user with the option of choosing one of the previous options when loading a DICOM image series.

DICOM Cache

The DICOM cache allows for the storage of frequently used data sets locally, thus improving load time into VivoQuant. Every time VivoQuant is started, it checks the current size of the cache against the maximum cache size. If the current cache size exceeds the maximum cache size, then older files (those opened least recently) are removed.


DICOM Cache

Current size 0.0 MB 0%

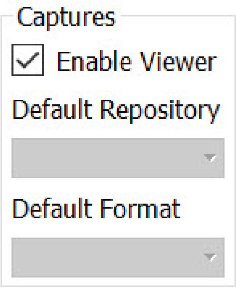
Max size 1000 MB free 44135.3 MB

Life Time 14 d

DICOM Cache

Option	Description
Current Size	Size in Mb of the data currently stored in the DICOM Cache. The percentage to the right of the field indicates how close the cache is to capacity.
Max size	Maximum amount of memory that can be made available for the DICOM Cache (default = 1000.0 MB).
Life Time	Length of time over which data will be stored in the DICOM Cache (default = 14 days).
Clear	Empties the DICOM Cache.

Captures


Captures

☑ Enable Viewer

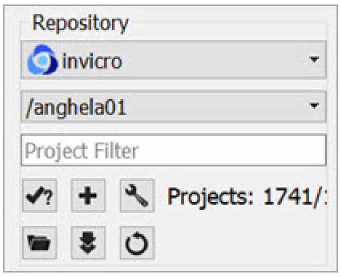
Default Repository

Default Format

Captures

Data Browser Repository Panel

The DICOM Repository panel, in the Data Browser, is the most convenient location for adding and editing repositories, including DICOM Servers, local folders, and PACS Servers.


Repository

invicro

/anghela01

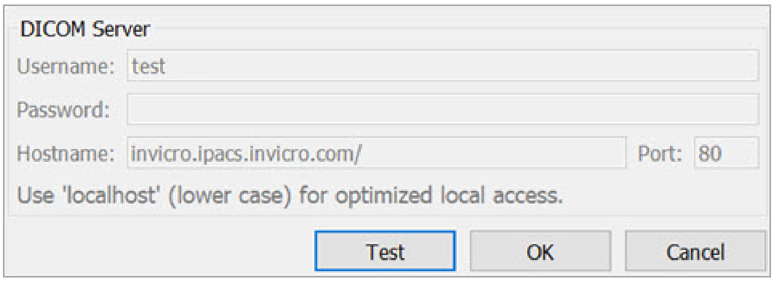
Projects: 1741/:

Repository Panel

Option	Description
Repositories	List of available repositories. The bank of buttons immediately beneath the pulldown menu operate on the selected repository in this field. Please click here to learn more about the DICOM repository section of the DICOM browser:
✓?	Checks connection to DICOM repository. Local folders are verified to exist and a C-ECHO is sent to DICOM servers.
➕	Adds a new repository.
🔧	Edit: Opens the DICOM repository editor.
📂	Opens a Windows Browser that can be used to select a local folder as a repository.
⏬	Fetches all DICOM meta data.
⟳	Removes repository from list.

DICOM repository editor

The DICOM repository editor is used to add repositories, including local folders, DICOM Servers, or iPACS Servers.


DICOM Server

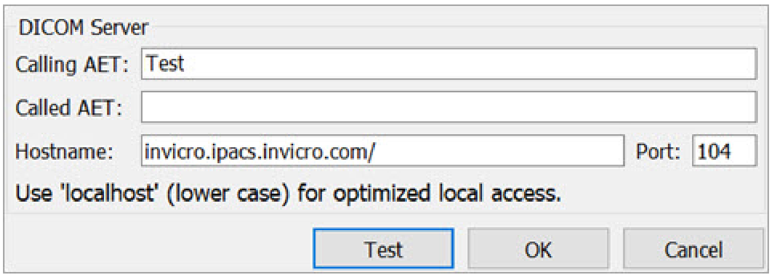
Username: test

Password:

Hostname: invicro.ipacs.invicro.com/ Port: 80

Use 'localhost' (lower case) for optimized local access.

Local Folder


DICOM Server

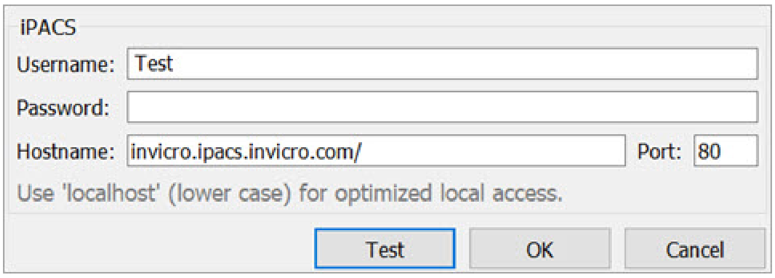
Calling AET: Test

Called AET:

Hostname: invicro.ipacs.invicro.com/ Port: 104

Use 'localhost' (lower case) for optimized local access.

DICOM Server


iPACS

Username: Test

Password:

Hostname: invicro.ipacs.invicro.com/ Port: 80

Use 'localhost' (lower case) for optimized local access.

iPACS Server

Option	Description
Displayed Name	Name as shown in the repository selection box. Can contain any alphanumeric character.
Repository Type	Indicates the type of repository containing the study data to be loaded into VivoQuant.
	Local folders are directories available on the local computer (also via a shared network). Directories containing many files might take longer to scan. In this case, a DICOM server will perform better.
	DICOM servers are network services on the local or a remote computer. They provide a database to efficiently browse study data.
	An **iPACS server** is an online PACS servers, a regularly used archiving and retrieval system for medical images.
Local DICOM folder	Allows for browsing and selecting a local directory. All sub-folders will be displayed as projects in the second repository drop-down window.
DICOM server	AET is an Application Entity Title.
	Calling AET: must be a valid AET configured on the server.
	Called AET: name of the DICOM servers application entity.
iPACS server	**Username** and **Password** are specific to the user of the site's iPACS system.
	Hostname is the site of the server for the iPACS, and **Port** is the communication channel.

DICOM server

A DICOM server is specified by a calling AET, a Called AET, as well as a TCP address consisting of a host name and a port (the default settings are localhost:104). The AETs must be configured on the DICOM server. For VivoQuant, use port 23104 on the remote server.

iPACS server

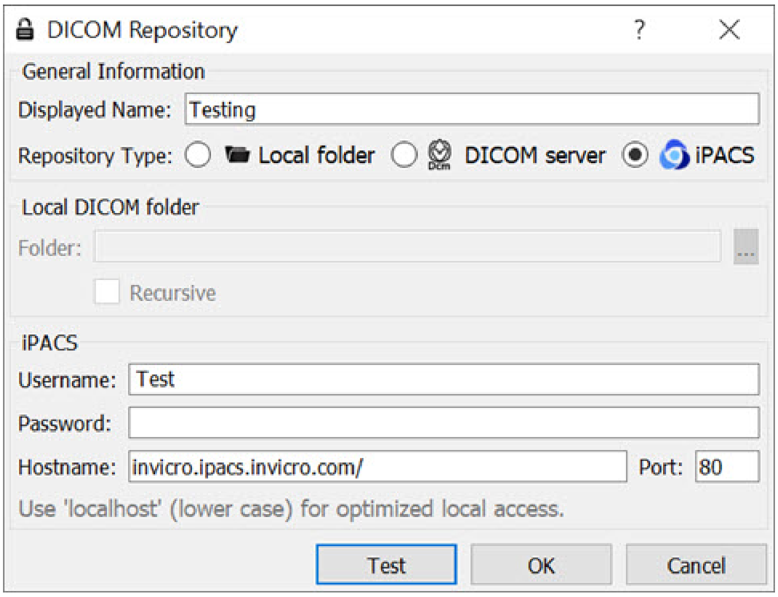
An iPACS server is specified by setting the appropriate Hostname and Port and by entering user-specific Username and Password. A DEMO iPACS server may be registered by using Hostname: demo.ipacs.invicro.com, Port 80, and leaving Username and Password blank. iPACS servers also enable the use of Projects, a useful tool for organizing DICOM data.

Optimized local access

The optimized local access allows for a much faster access to DICOM data. To use this option enter 'localhost' (all lower case) as the hostname, and define the ‘DB path’.

iPACS Projects

The iPACS repositories allow for the use of projects. A project represents a directory structure for DICOM repositories. Data may be stored and accessed via different projects, aiding organization of DICOM data. In the example below, an iPACS repository for “bioscan/demo” is being configured. The “bioscan/demo” repository contains three projects.


DICOM Repository

General Information

Displayed Name: Testing

Repository Type: ○ Local folder ○ DICOM server ● iPACS

Local DICOM folder

Folder:

☐ Recursive

iPACS

Username: Test

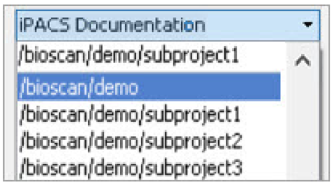
Password:

Hostname: invicro.ipacs.invicro.com/ Port: 80

Use 'localhost' (lower case) for optimized local access.

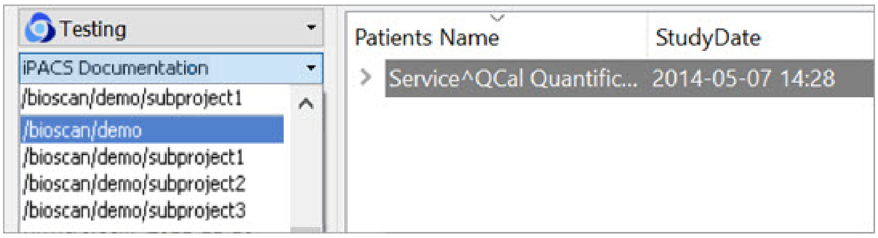
iPACS Repository

If any projects are present within a configured iPACS repository, a second pulldown menu will appear in the Repository panel of the DICOM browser. All projects within that repository are available via the second pulldown menu. The three projects associated with the “bioscan/demo” repository are shown in the screenshot below.



Repository Projects

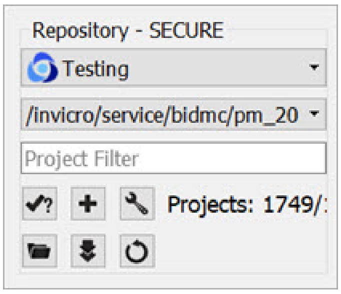
Select a project to view data associated with that project only.



Patients Name	StudyDate
Service^QCal Quantific...	2014-05-07 14:28

Select Project

By default, data will only be displayed when the project to which it belongs is selected from the second pulldown menu. For example, in this screenshot, no data appears in the “bioscan/demo” repository because all data within the larger repository belongs to individual projects.



Repository - SECURE

Testing

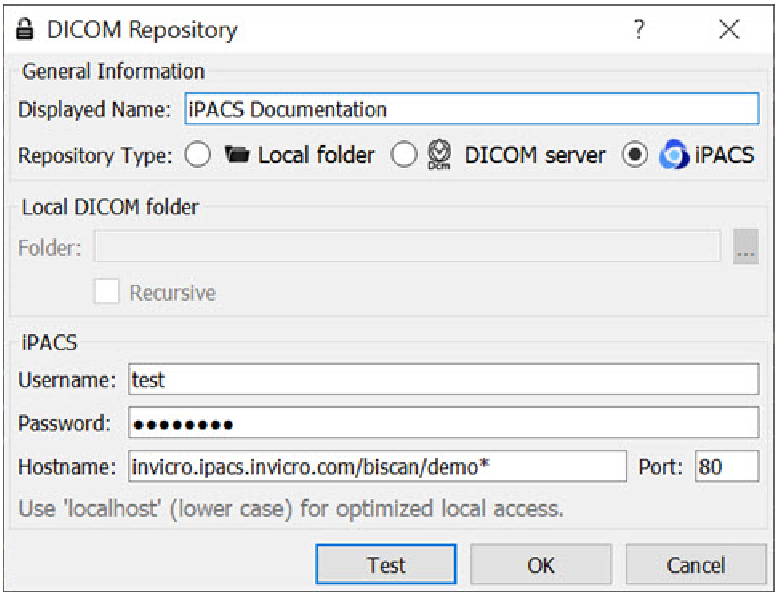
/invicro/service/bidmc/pm_20

Project Filter

Projects: 1749/

Larger Repository

To simultaneously view all data belonging to a repository AND its projects, place an asterisk (*) at the end of the hostname during repository configuration. The asterisk will cause all data within the repository and its projects to be displayed recursively. This behavior applies across all repository and project levels.



DICOM Repository

General Information

Displayed Name: iPACS Documentation

Repository Type: ○ Local folder ○ DICOM server ● iPACS

Local DICOM folder

Folder:

☐ Recursive

iPACS

Username: test

Password: •••••••••

Hostname: invicro.ipacs.invicro.com/biscan/demo*

Port: 80

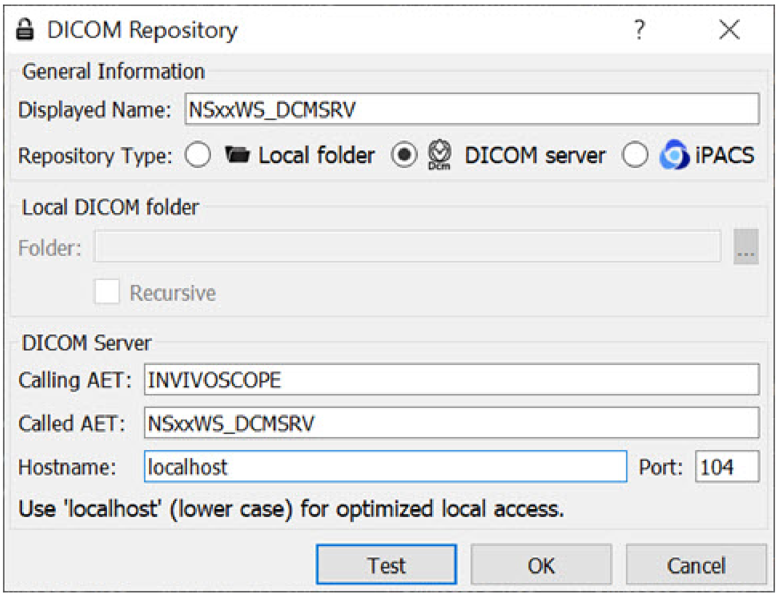
Use 'localhost' (lower case) for optimized local access.

Repository Data Display

How to configure the NanoSPECT's DICOM Servers

First, open the Data Browser. Find the Repository panel and either select the pre-existing repository from the pulldown menu or select "new" to create a new repository.

For the standard access on the NS Workstation (WS), use:



DICOM Repository

General Information

Displayed Name: NSxxWS_DCMSRV

Repository Type: ○ Local folder ● DICOM server ○ iPACS

Local DICOM folder

Folder:

☐ Recursive

DICOM Server

Calling AET: INVIVOSCOPE

Called AET: NSxxWS_DCMSRV

Hostname: localhost Port: 104

Use 'localhost' (lower case) for optimized local access.

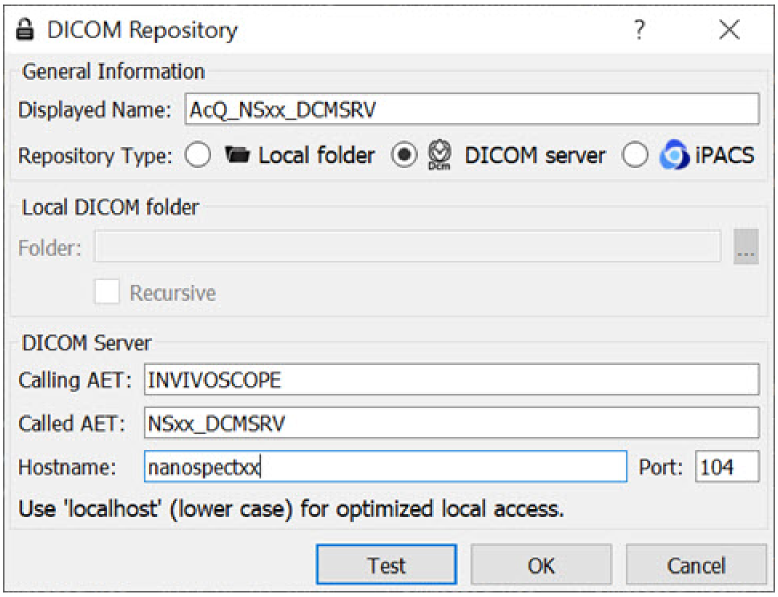
Workstation DICOM Server

Option	Description
Displayed Name	NSxxWS_DCMSRV (or customer’s preference)
Type	DICOM Server
AET	INVIVOSCOPE
Called AET	NSxxWS_DCMSRV
Hostname	localhost
Port	104

where xx is replaced with the **NanoSPECT** number, typically no leading 0 for numbers \< 10.

The local access VivoQuant is able to access the DICOM Server directly, so there is no need to add the VQ as a client on the DICOM Server.

The above table described configuring VivoQuant to access the **Workstation DICOM Server**. VivoQuant may also be configured to access the Acquisition computer’s DICOM Server. The procedure is similar, but there is no WS in the naming convention.



General Information

Displayed Name: AcQ_NSxx_DCMSRV

Repository Type: ○ Local folder ● DICOM server ○ iPACS

Local DICOM folder

Folder:

☐ Recursive

DICOM Server

Calling AET: INVIVOSCOPE

Called AET: NSxx_DCMSRV

Hostname: nanospectxx Port: 104

Use 'localhost' (lower case) for optimized local access.

Acquisition computer's DICOM Server

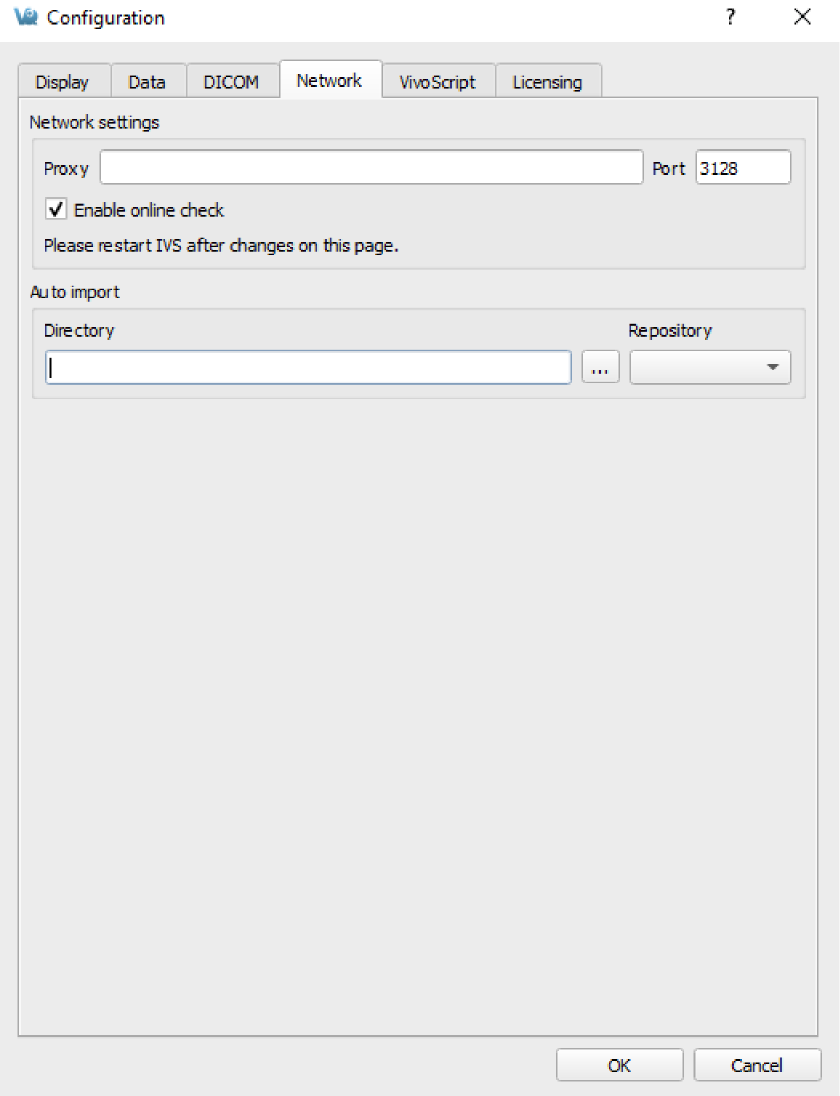
Options	Description
Displayed Name	ACQ_NSxx_DCMSRV (or customer’s preference)
Type	DICOM Server
Calling AET	INVIVOSCOPE
Called AET	NSxx_DCMSRV
Hostname	nanospectxx
Port	104

where xx is replaced with the **NanoSPECT** number, typically no leading 0 for numbers \< 10.

In place of hostname (i.e., nanospectxx), it is also possible to use IP addresses (i.e., 192.168.1.1 for local WS-ACQ computer connections). Please verify that the hostname resolves by using ping hostname in a Command window. Also, in order to access the ACQ computer from the WS computer, you must configure the DICOM Server on the ACQ computer.

Network

The Network panel consists of two sections: Network Settings and Auto Import.



Network settings

Proxy

Port 3128

☑ Enable online check

Please restart IVS after changes on this page.

Auto import

Directory

Repository

Network Panel

Network Settings

The Network Settings section includes an option for enabling a proxy server to be used with VivoQuant. There are fields for entering a proxy and a port number associated with that proxy. The "Enable Online Check" checkbox will automatically detect any available proxy servers. If you believe a proxy server is needed, please contact your local IT representative.

Auto Import

The Auto Import allows you to designate a folder through which files can be automatically transferred into a Repository. According to the setup in the above screenshot, DICOM files placed in the VQ-AutoImport directory will be automatically imported into the NS00WS_DCMSRV repository upon the next restart of VivoQuant.

Licensing

Getting There

The Licensing panel is available in the Configuration Window. Alternatively, it may be reached directly via the Help menu.

Contents

The Licensing panel contains information about the current active license type (either machine-locked file-based or a floating license) as well as selected information about the user who owns the license.

Licensing is required to unlock most of VivoQuant features. Please see the Licensing Quick Guide for more details.

Restricted tags

VivoQuant can be configured to disallow editing of specific DICOM tags. To control which tags can be edited, users can modify the restricted_tags.cfg file included next to the VivoQuant executable in the installation folder.

Consult the DICOM standard for the names of tags that can be included in this file.

ℹ **Note:** The macOS installer .dmg bundle is not write-able by default. Users should investigate tools like hdiutil to create a write-able version of the installer with this file modified to distribute to end-users.

Opening DICOM Data

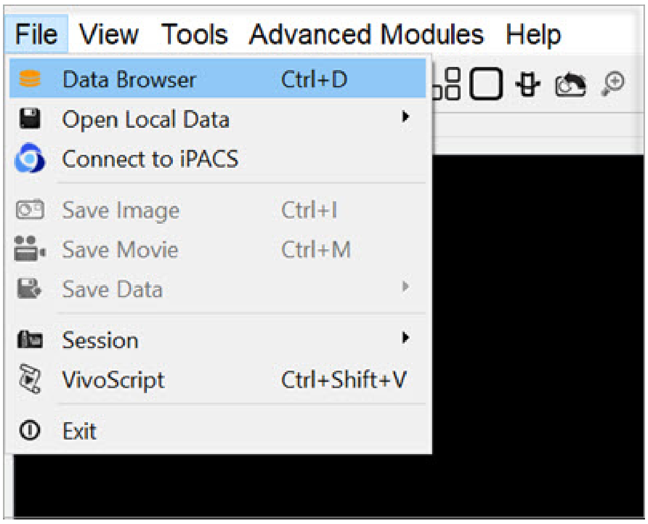
The **Data Browser** provides convenient access to files in a DICOM server or any other specified iPACS Browser. From the **Data Browser**, reconstructions can be started and files can be exported.

Getting There

There are three different methods to access the **Data Browser**.

The first method is by clicking the icon in the Main Window.

The second method is to go to **File** > **Data Browser**.

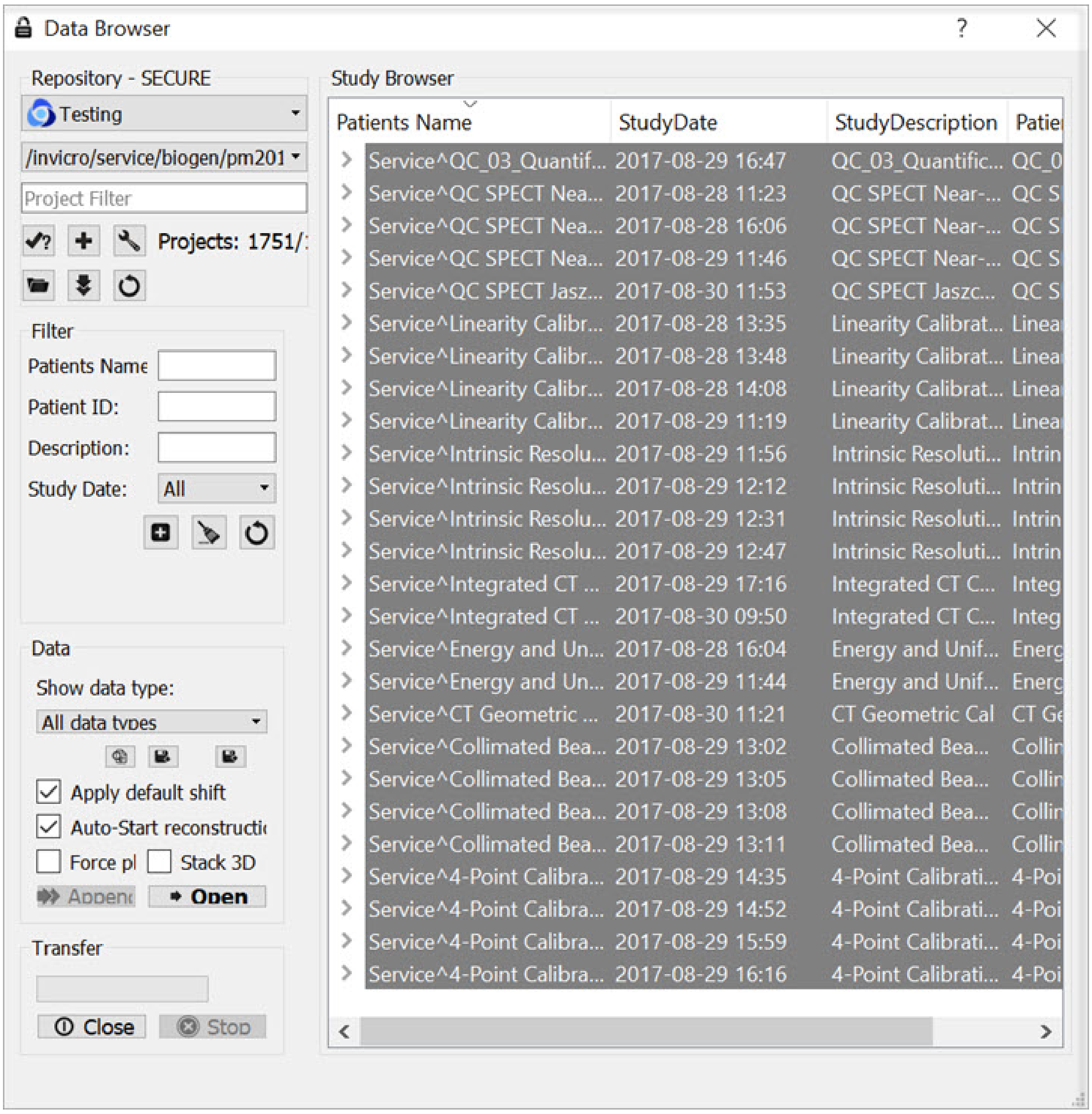


Data Browser

The third method is to use the keyboard shortcut Ctrl+D. For more on keyboard shortcuts in VivoQuant, see Keyboard Shortcuts.

Function

The **Data Browser's** main window is split into five sections: Repository, Filter, Data, Study Browser, and **Transfer**.



Testing

/invicro/service/biogen/pm201

Projects: 1751/:

Patients Name:

Patient ID:

Description:

Study Date: All

Show data type: All data types

☑ Apply default shift

☑ Auto-Start reconstructi

☐ Force pl ☐ Stack 3D

Patients Name	StudyDate	StudyDescription	Patie
Service^QC_03_Quantif...	2017-08-29 16:47	QC_03_Quantific...	QC_0
Service^QC SPECT Nea...	2017-08-28 11:23	QC SPECT Near-...	QC S
Service^QC SPECT Nea...	2017-08-28 16:06	QC SPECT Near-...	QC S
Service^QC SPECT Nea...	2017-08-29 11:46	QC SPECT Near-...	QC S
Service^QC SPECT Jasz...	2017-08-30 11:53	QC SPECT Jaszc...	QC S
Service^Linearity Calibr...	2017-08-28 13:35	Linearity Calibrat...	Linea
Service^Linearity Calibr...	2017-08-28 13:48	Linearity Calibrat...	Linea
Service^Linearity Calibr...	2017-08-28 14:08	Linearity Calibrat...	Linea
Service^Linearity Calibr...	2017-08-29 11:19	Linearity Calibrat...	Linea
Service^Intrinsic Resolu...	2017-08-29 11:56	Intrinsic Resoluti...	Intrin
Service^Intrinsic Resolu...	2017-08-29 12:12	Intrinsic Resoluti...	Intrin
Service^Intrinsic Resolu...	2017-08-29 12:31	Intrinsic Resoluti...	Intrin
Service^Intrinsic Resolu...	2017-08-29 12:47	Intrinsic Resoluti...	Intrin
Service^Integrated CT ...	2017-08-29 17:16	Integrated CT C...	Integ
Service^Integrated CT ...	2017-08-30 09:50	Integrated CT C...	Integ
Service^Energy and Un...	2017-08-28 16:04	Energy and Unif...	Energ
Service^Energy and Un...	2017-08-29 11:44	Energy and Unif...	Energ
Service^CT Geometric ...	2017-08-30 11:21	CT Geometric Cal	CT Ge
Service^Collimated Bea...	2017-08-29 13:02	Collimated Bea...	Collin
Service^Collimated Bea...	2017-08-29 13:05	Collimated Bea...	Collin
Service^Collimated Bea...	2017-08-29 13:08	Collimated Bea...	Collin
Service^Collimated Bea...	2017-08-29 13:11	Collimated Bea...	Collin
Service^4-Point Calibra...	2017-08-29 14:35	4-Point Calibrati...	4-Poi
Service^4-Point Calibra...	2017-08-29 14:52	4-Point Calibrati...	4-Poi
Service^4-Point Calibra...	2017-08-29 15:59	4-Point Calibrati...	4-Poi
Service^4-Point Calibra...	2017-08-29 16:16	4-Point Calibrati...	4-Poi

Data Browser Main Window

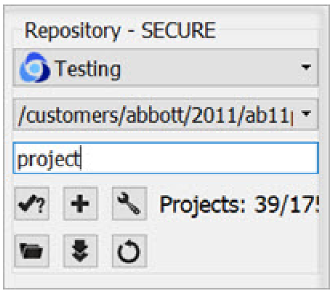
Repository

The **Repository** section displays the **Data Browser** or local folder from which data files are currently being displayed in the **Study Browser**. See DICOM Configuration for more information on configuring your **Data Browser**, including the use of projects in an iPACS repository.

This section contains a filter that allows users to reduce the project list to more easily search for a desired project. There are three ways to filter the project list, as described in the following table:

Filter Option	Description	Example
word	Reduces project list to all projects that contain the given word in their path.	Type exampledata in the projects filter to reduce the projects list to all projects with the word exampledata in their path.
!word	Reduces project list to all projects that do not contain the given word in their path.	Type !exampledata in the projects filter to reduce the projects list to all projects that do not contain exampledata in their path.
&regexp	Reduces project list to all projects that match the given regular expression.	An example of a commonly used regular expression is the choice operator "|", which matches either the expression before or the expression after the operator. For example, if the user types &exampledata|test in the projects filter, the project list will reduce to all projects that have the word exampledata and all projects with the word test in their path.

Press enter on the keyboard to apply the filter. The filtered number of projects over the total number of projects is displayed. For example, the image below displays 7 out of 1743 projects with the word demo in their path.



Repository - SECURE
Testing
/customers/abbott/2011/ab11|
project
Projects: 39/17!

Repository Filter

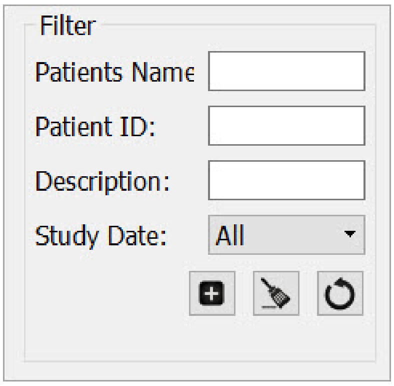
☑ **Tip:** For more examples of regular expressions supported by the projects filter, click here .

Filter

As the database grows, the **Filter** tool becomes useful for sifting through studies to find just the right one. Options for filtering include **Patient's Name**, **Patient ID**, **Study Description**, and **Study Date**. After entering values in these available fields, simply hit the refresh filter settings button ⟳ to refresh the **Study Browser**. To view all the data again, hit the clear filter button to empty the fields, and hit ⟳ again to refresh the **Study Browser**.

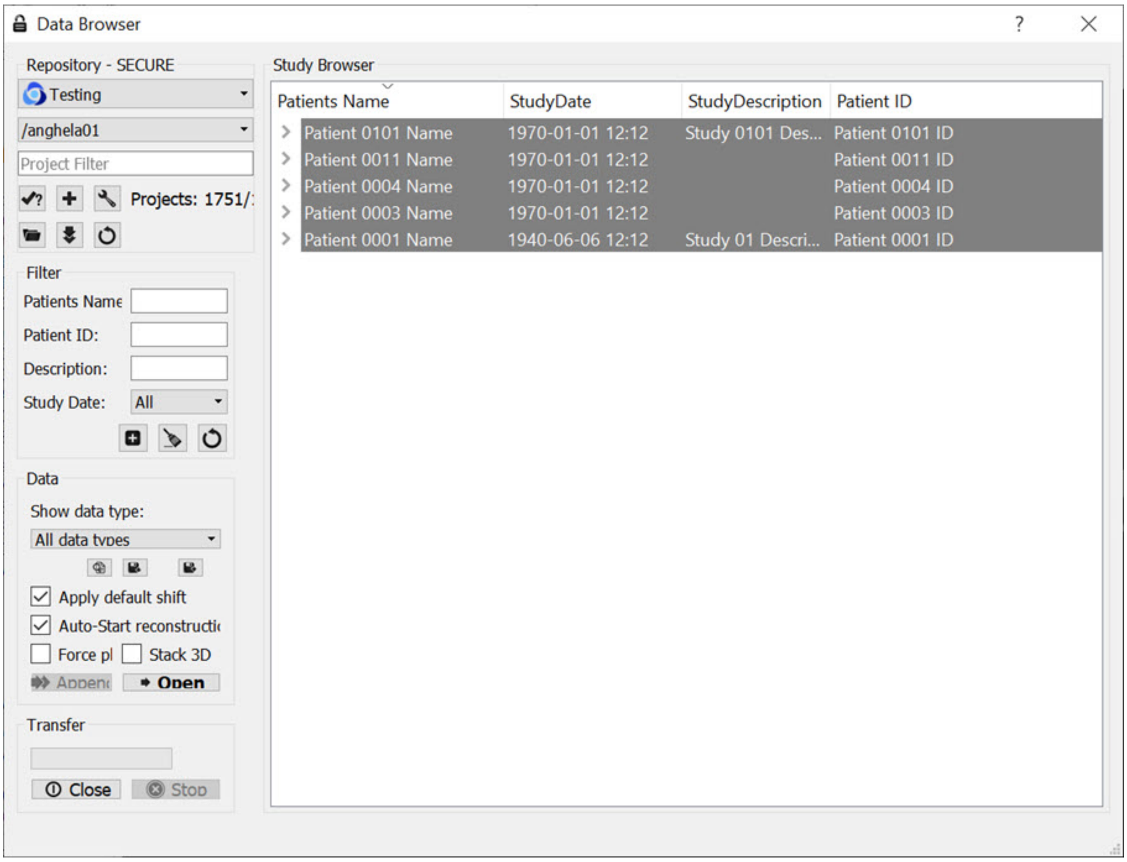
ℹ **Note:** filtering uses a Unix-like naming structure. For example, to find all studies that begin with **Mouse**, enter **Mouse*** in the filter for **Patient's Name**. To find any study containing **I123**, enter ***I123*** in the filter for Patient's Name.

Also available in the filter options is the ⊞ function, used to expand or collapse the entries currently displayed in the **Data Browser**. The first click will expand all data at the patient/study level; the second click will then expand at the series level; the third click will collapse the series level; the fourth click will collapse patients/studies.



Plus Function

The image below shows the project list on the **Study Browser** before expansion:



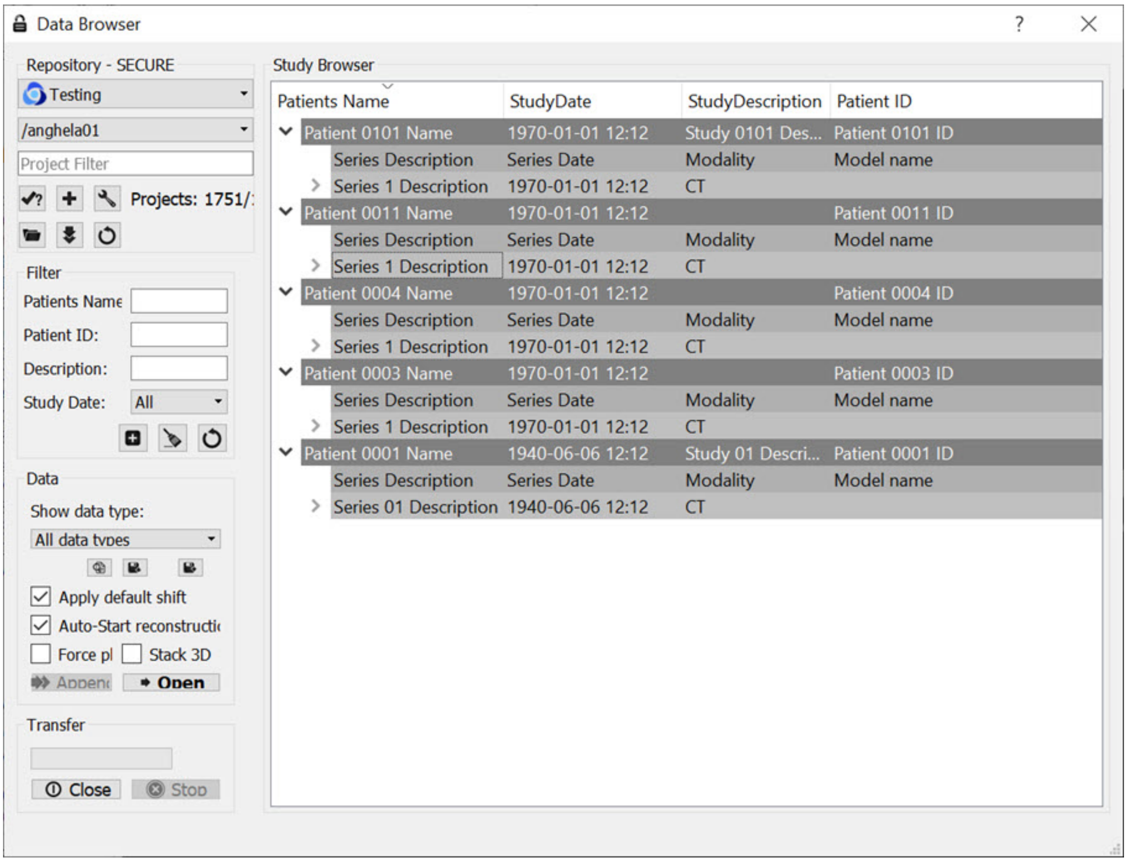
Patients Name	StudyDate	StudyDescription	Patient ID
Patient 0101 Name	1970-01-01 12:12	Study 0101 Des...	Patient 0101 ID
Patient 0011 Name	1970-01-01 12:12		Patient 0011 ID
Patient 0004 Name	1970-01-01 12:12		Patient 0004 ID
Patient 0003 Name	1970-01-01 12:12		Patient 0003 ID
Patient 0001 Name	1940-06-06 12:12	Study 01 Descri...	Patient 0001 ID

Repository - SECURE: Testing, /anghela01

☑ Apply default shift
☑ Auto-Start reconstructi
☐ Force pl ☐ Stack 3D

Before Expansion

After one click of the ⊞ button, the project list will be displayed as follows:



Repository - SECURE: Testing

/anghela01

Projects: 1751/

Patients Name:

Patient ID:

Description:

Study Date: All

Show data type: All data types

☑ Apply default shift

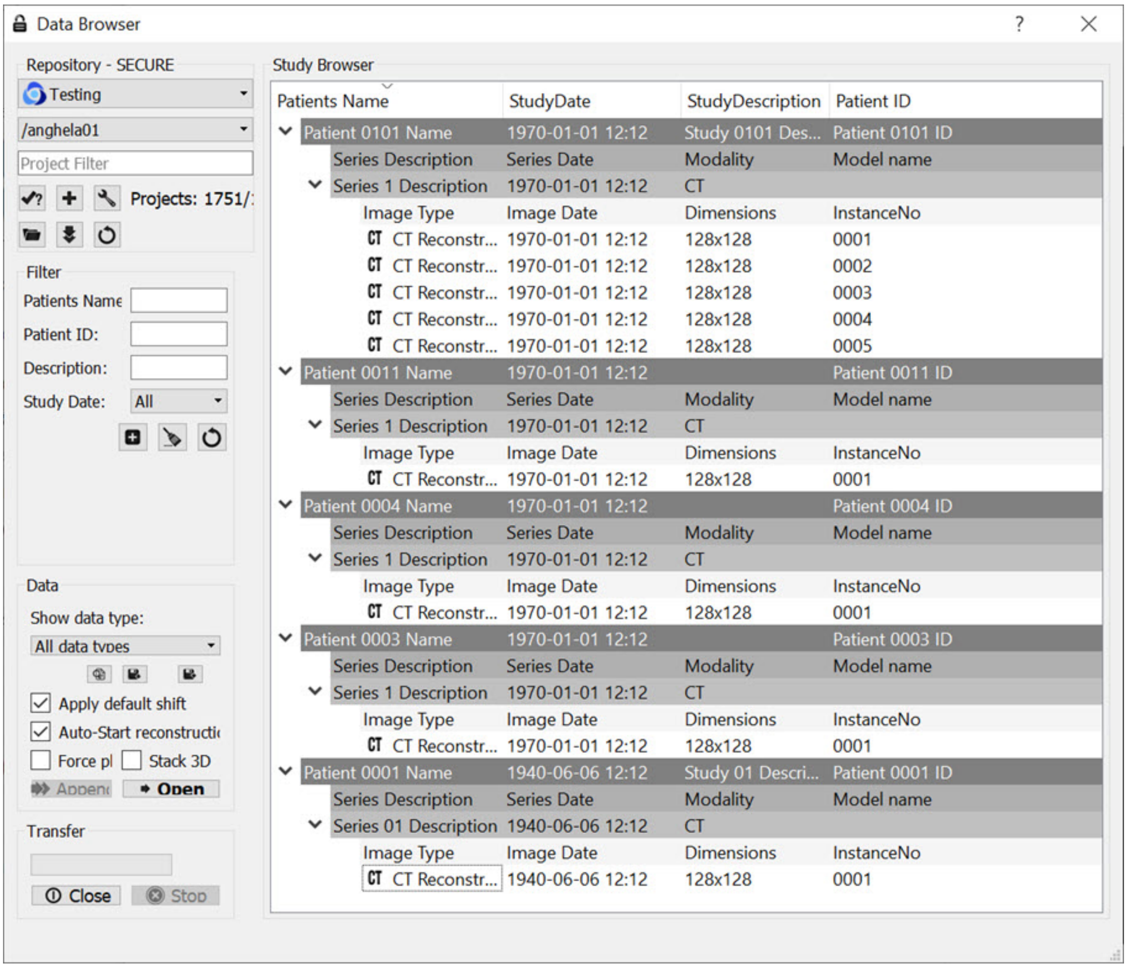
☑ Auto-Start reconstructi

☐ Force pl ☐ Stack 3D

Patients Name	StudyDate	StudyDescription	Patient ID
Patient 0101 Name	1970-01-01 12:12	Study 0101 Des...	Patient 0101 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Patient 0011 Name	1970-01-01 12:12		Patient 0011 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Patient 0004 Name	1970-01-01 12:12		Patient 0004 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Patient 0003 Name	1970-01-01 12:12		Patient 0003 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Patient 0001 Name	1940-06-06 12:12	Study 01 Descri...	Patient 0001 ID
Series Description	Series Date	Modality	Model name
Series 01 Description	1940-06-06 12:12	CT	

First Expansion

After the second click of the ⊞ button, the series level will be displayed in the **Study Browser**:



Repository - SECURE: Testing

/anghela01

Study Date: All

Show data type: All data types

☑ Apply default shift

☑ Auto-Start reconstructi

☐ Force pl ☐ Stack 3D

Patients Name	StudyDate	StudyDescription	Patient ID
Patient 0101 Name	1970-01-01 12:12	Study 0101 Des...	Patient 0101 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Image Type	Image Date	Dimensions	InstanceNo
CT CT Reconstr...	1970-01-01 12:12	128x128	0001
CT CT Reconstr...	1970-01-01 12:12	128x128	0002
CT CT Reconstr...	1970-01-01 12:12	128x128	0003
CT CT Reconstr...	1970-01-01 12:12	128x128	0004
CT CT Reconstr...	1970-01-01 12:12	128x128	0005
Patient 0011 Name	1970-01-01 12:12		Patient 0011 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Image Type	Image Date	Dimensions	InstanceNo
CT CT Reconstr...	1970-01-01 12:12	128x128	0001
Patient 0004 Name	1970-01-01 12:12		Patient 0004 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Image Type	Image Date	Dimensions	InstanceNo
CT CT Reconstr...	1970-01-01 12:12	128x128	0001
Patient 0003 Name	1970-01-01 12:12		Patient 0003 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Image Type	Image Date	Dimensions	InstanceNo
CT CT Reconstr...	1970-01-01 12:12	128x128	0001
Patient 0001 Name	1940-06-06 12:12	Study 01 Descri...	Patient 0001 ID
Series Description	Series Date	Modality	Model name
Series 01 Description	1940-06-06 12:12	CT	
Image Type	Image Date	Dimensions	InstanceNo
CT CT Reconstr...	1940-06-06 12:12	128x128	0001

Second Expansion

ℹ **Note:** Expanding large numbers of datasets can take several minutes.

Data

The **Data** section provides several functions for manipulating data, including sorting, finding, and opening.

Show Data Type	This pull-down menu is used to limit the data displayed in the **Study Browser** to a single modality (i.e., CT) or data type (i.e.,reconstructions).
Open ➡ Open	Opens the data highlighted in the **Study Browser**. If a single data file is highlighted, it will be opened as the Reference image. If an entire Study is highlighted, the **Open** button recognizes which data file is the CT and sets it as the Reference. The **Open** button unloads data currently in VivoQuant and replaces it with the highlighted data. More information on the relationship between the **Study Browser** and the **Open** button can be found in the Study Browser documentation.
Append ➡➡ Append	Appends the data highlighted in the **Study Browser** to the data sets already loaded into VivoQuant. For example, if two data sets are selected in the **Data Browser** and three data sets are already loaded into VivoQuant, then appending the two highlighted data sets will cause them to appear as data sets 4 and 5 in the Data Manager. Use the **Open** button to unload data currently loaded in VivoQuant and replace it with the highlighted data.
Find	Enables a search of the **Study Browser** by looking for user-defined text in one of the available columns (**Patient's Name**, **Study Date**, **Study Description**, or **Patient ID**).
Import	Allows data from a local folder to be imported into another local folder, database, or iPACS repository.
Export	Allows data to be copied to a local folder.
Apply default shift	If checked, a pre-defined shift will be applied to reconstructed SPECT data when it is opened. See Reorientation for more details on setting default shift values.
Auto-start reconstruction	If checked, CT and NM reconstructions will begin automatically when the Open button is applied to projection data in the **Study Browser**.
Force planar	If checked, it prevents interpolation from being performed on data with non-isotropic voxels. By default, data with voxel widths greater in the z dimension than in the x and y dimensions will be interpolated to have isotropic voxels when the **Open** button is applied.
Stack 3D	If checked, each 3D volume is loaded one on top of the other in a single series of images. If unchecked, each 3D volume is loaded in the same space, as a separate series.

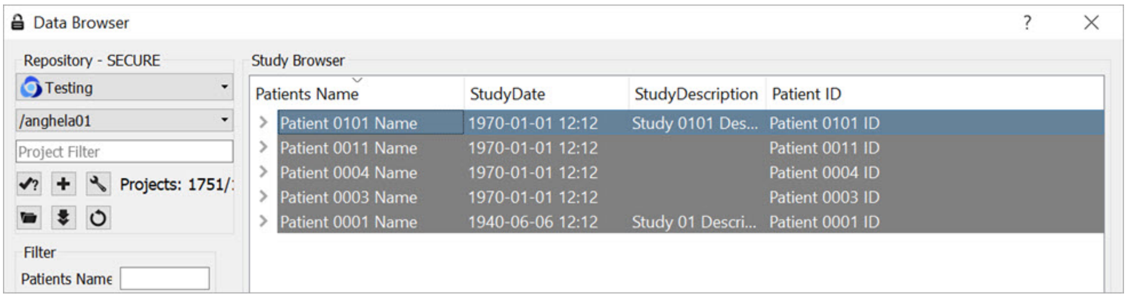
Data Formats

By default, the **Data Browser** supports data with *.dcm, *.dc3 or *.dicom extensions. To edit this setting and configure loading in extension-less data from the **Data Browser**, navigate to the DICOM Settings page.

Study Browser

The **Study Browser** displays the data found in the selected Repository. The Filter, Show Data Type, and Find options can be used to limit the data displayed in the **Study Browser**. In all cases, the data is opened with either the Open button or the Append button. The **Open** button will unload data currently open in VivoQuant and load the highlighted data as Reference, Input 1, Input 2, etc. The **Append** button will leave the currently loaded data unchanged and append the highlighted data. This appended data may be accessed via the Data Manager.

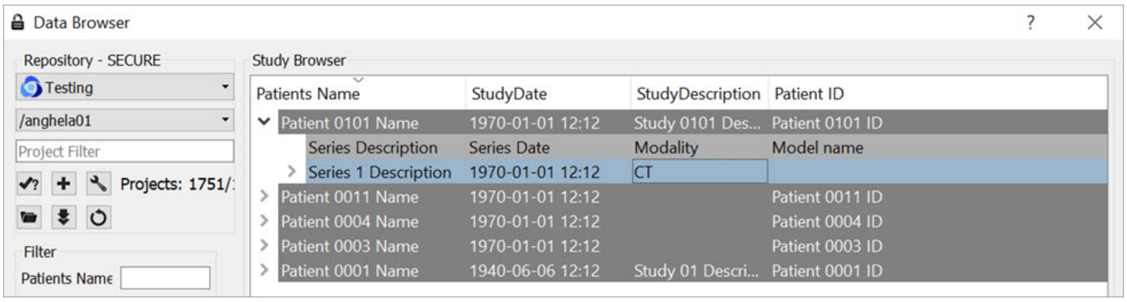
At the top level, multiple files may be opened into the **Main Window** simultaneously. The **Data Browser** recognizes the files in the study and opens them accordingly, setting the CT image as the Reference. If extra data is found, the **Data Browser** provides the message: Ignoring extra data sets.



Patients Name	StudyDate	StudyDescription	Patient ID
Patient 0101 Name	1970-01-01 12:12	Study 0101 Des...	Patient 0101 ID
Patient 0011 Name	1970-01-01 12:12		Patient 0011 ID
Patient 0004 Name	1970-01-01 12:12		Patient 0004 ID
Patient 0003 Name	1970-01-01 12:12		Patient 0003 ID
Patient 0001 Name	1940-06-06 12:12	Study 01 Descri...	Patient 0001 ID

Top Level

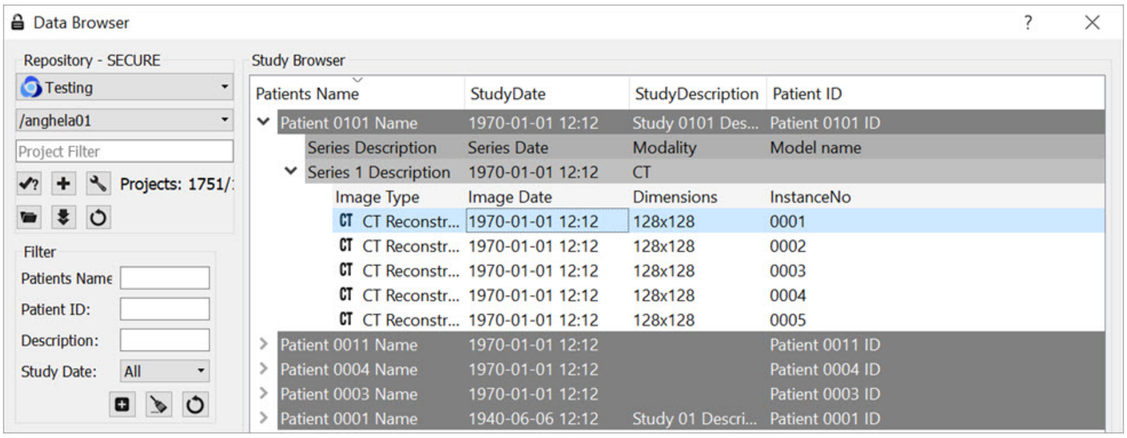
At the next level, single data sets from a study may be selected for viewing.



Patients Name	StudyDate	StudyDescription	Patient ID
Patient 0101 Name	1970-01-01 12:12	Study 0101 Des...	Patient 0101 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Patient 0011 Name	1970-01-01 12:12		Patient 0011 ID
Patient 0004 Name	1970-01-01 12:12		Patient 0004 ID
Patient 0003 Name	1970-01-01 12:12		Patient 0003 ID
Patient 0001 Name	1940-06-06 12:12	Study 01 Descri...	Patient 0001 ID

Second Level

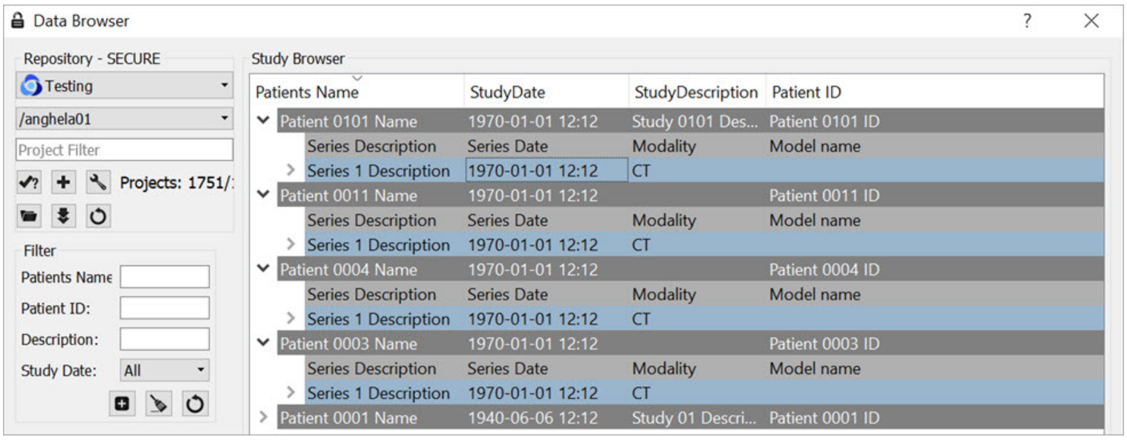
This nested structure continues, depending on the format in which the data is saved. For example, for CT data saved in **Single Frame** format, single slices may be selected for viewing.



Patients Name	StudyDate	StudyDescription	Patient ID
Patient 0101 Name	1970-01-01 12:12	Study 0101 Des...	Patient 0101 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Image Type	Image Date	Dimensions	InstanceNo
CT CT Reconstr...	1970-01-01 12:12	128x128	0001
CT CT Reconstr...	1970-01-01 12:12	128x128	0002
CT CT Reconstr...	1970-01-01 12:12	128x128	0003
CT CT Reconstr...	1970-01-01 12:12	128x128	0004
CT CT Reconstr...	1970-01-01 12:12	128x128	0005
Patient 0011 Name	1970-01-01 12:12		Patient 0011 ID
Patient 0004 Name	1970-01-01 12:12		Patient 0004 ID
Patient 0003 Name	1970-01-01 12:12		Patient 0003 ID
Patient 0001 Name	1940-06-06 12:12	Study 01 Descri...	Patient 0001 ID

Third Level

Ctrl-click and Shift-click options are also implemented to simplify data selection. This feature is useful for selecting multiple subsets of studies for both loading them into the **Main Window** and exporting them.



Patients Name	StudyDate	StudyDescription	Patient ID
Patient 0101 Name	1970-01-01 12:12	Study 0101 Des...	Patient 0101 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Patient 0011 Name	1970-01-01 12:12		Patient 0011 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Patient 0004 Name	1970-01-01 12:12		Patient 0004 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Patient 0003 Name	1970-01-01 12:12		Patient 0003 ID
Series Description	Series Date	Modality	Model name
Series 1 Description	1970-01-01 12:12	CT	
Patient 0001 Name	1940-06-06 12:12	Study 01 Descri...	Patient 0001 ID

Multiple Selection

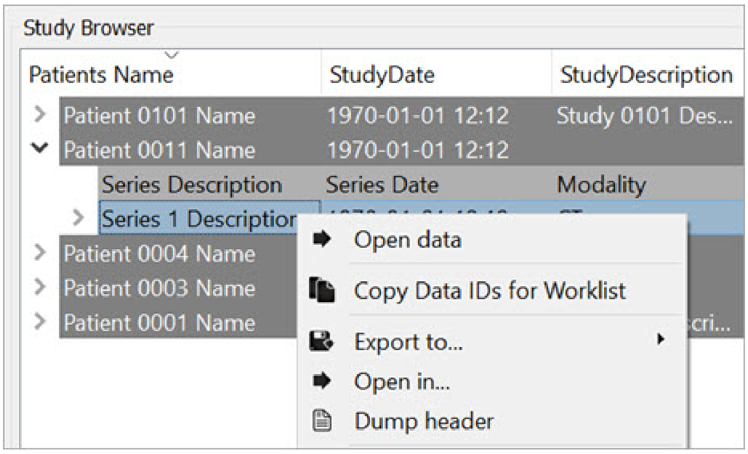
Right-Click function

The right-click function of the **Data Browser** is used as a shortcut for opening/exporting CT or NM data and sending it to a batch job (HiSPECT or BatchCT for SPECT and CT data, respectively), reconstruction or DICOM dump. When working in a local repository, the right-click option may be used to delete data.

To use this function, highlight either the CT or NM data and right-click. A box with a number of functions is then displayed. The options vary depending on the type of projection data selected.

Within Database or iPACS Server

Right-click on the Helical CT or Helical SPECT scan of interest.



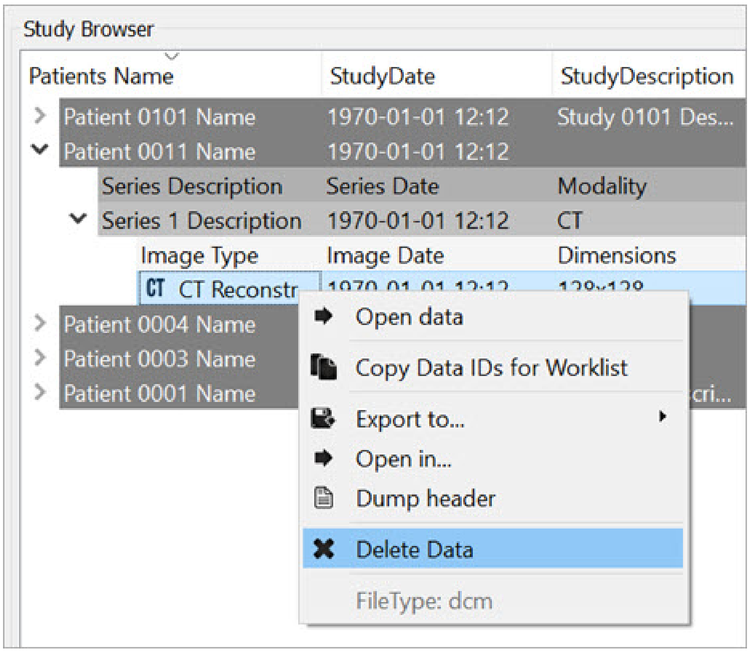
Right-Click

The Right-Click function provides various options, depending on the data type available.

Option	Description
Open data	Opens the selected data set in VivoQuant and loads it as the reference (see Open Reference).
Export to...	Allows data to be copied to a local folder or to another **Data Browser** or iPACS repository.
Open in...	Allows the data to be opened in an external Application.
Dump Header	Sends the file to the DICOM dump tool, which displays the information contained in the DICOM headers.

Within a Local Repository

When working in a local repository, the right-click button may also be used to delete data.

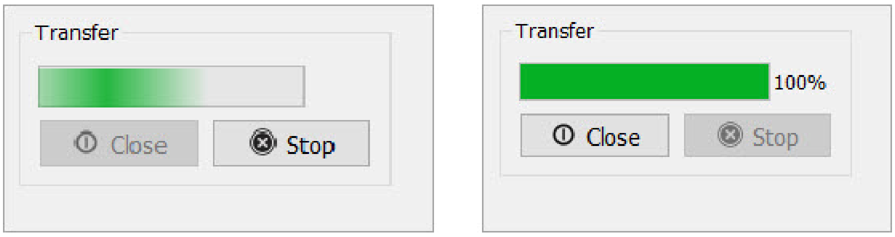


Patients Name	StudyDate	StudyDescription
Patient 0101 Name	1970-01-01 12:12	Study 0101 Des...
Patient 0011 Name	1970-01-01 12:12	
Series Description	Series Date	Modality
Series 1 Description	1970-01-01 12:12	CT
Image Type	Image Date	Dimensions
CT Reconstr		
Patient 0004 Name		
Patient 0003 Name		
Patient 0001 Name		cri...

Delete Local Data

Transfer

The **Transfer** section of the **Data Browser** features a progress bar that shows the percentage of completion of the current process.



Transfer Bar

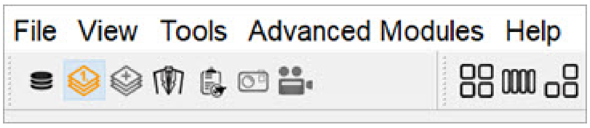
Click the Stop button to cancel the current process. Click the Close button to exit the **Data Browser**.

Open Reference Data

The first data set loaded into VivoQuant is called the **Reference** because it is often a CT image used for anatomical reference. When loading multiple data sets from the Data browser, VivoQuant recognizes CT data and automatically sets it as the **Reference**. VQ is capable of handling several file formats.

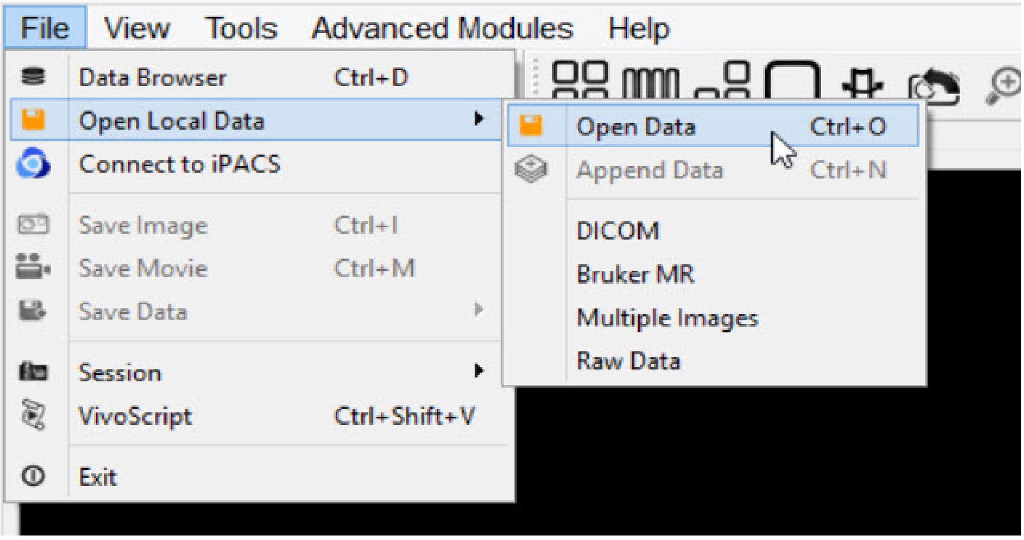
Getting There

There are three different methods for opening data. The first method is to use the **Open Data** or the **Append Data** thumbnails in the Main Window.



Main Window

The second method is to go to **Open Data** under the File menu.

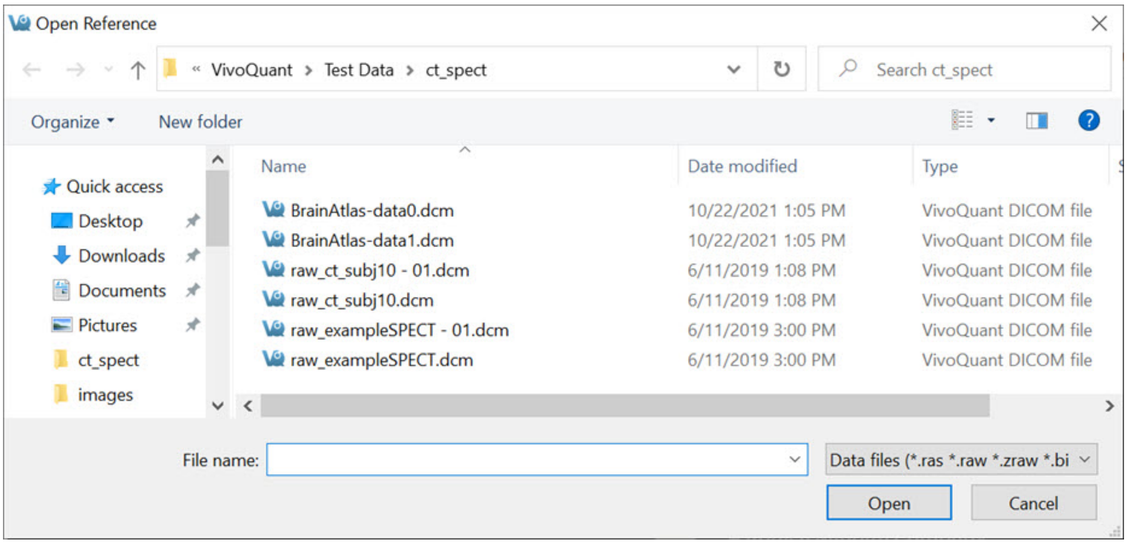


Open Local Data

The third method is to use the keyboard shortcut Ctrl+O. For more on keyboard shortcuts in VivoQuant, please see Keyboard Shortcuts.

Function

Selection of the **Open Data** option opens a navigation window from which the **Reference** data set may be selected.



Name	Date modified	Type
BrainAtlas-data0.dcm	10/22/2021 1:05 PM	VivoQuant DICOM file
BrainAtlas-data1.dcm	10/22/2021 1:05 PM	VivoQuant DICOM file
raw_ct_subj10 - 01.dcm	6/11/2019 1:08 PM	VivoQuant DICOM file
raw_ct_subj10.dcm	6/11/2019 1:08 PM	VivoQuant DICOM file
raw_exampleSPECT - 01.dcm	6/11/2019 3:00 PM	VivoQuant DICOM file
raw_exampleSPECT.dcm	6/11/2019 3:00 PM	VivoQuant DICOM file

Data files (*.ras *.raw *.zraw *.bi

Navigation Window

File Formats

VivoQuant can handle a variety of file formats. The default options include:

1. **DICOM**: *.dcm, *.dicom, 1.*
2. **TRaster**: *.ras, *.res., *.bin
3. **Raw**: *.raw
4. **Image Files**: *.png, *.tif, *.tiff, *.jpg, *.jpeg, *.bmp
5. **Other**: *.img, *.nii, *.mhd, *.mha, *.fdf, *.dc3, *.vol

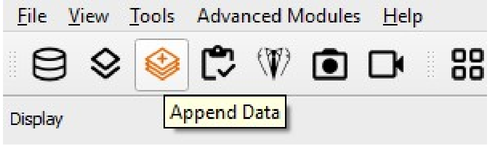
The navigation window also provides an option for displaying **All Files**, without specifying any of the above formats.

Append Data

The second data set loaded into VivoQuant is called the Input data and refers to the SPECT data. When loading multiple data sets from the Data browser, VivoQuant recognizes SPECT/PET data and automatically sets it as the input file. For dual isotope imaging, two input data sets can be added simultaneously. VivoQuant is capable of handling several file formats.

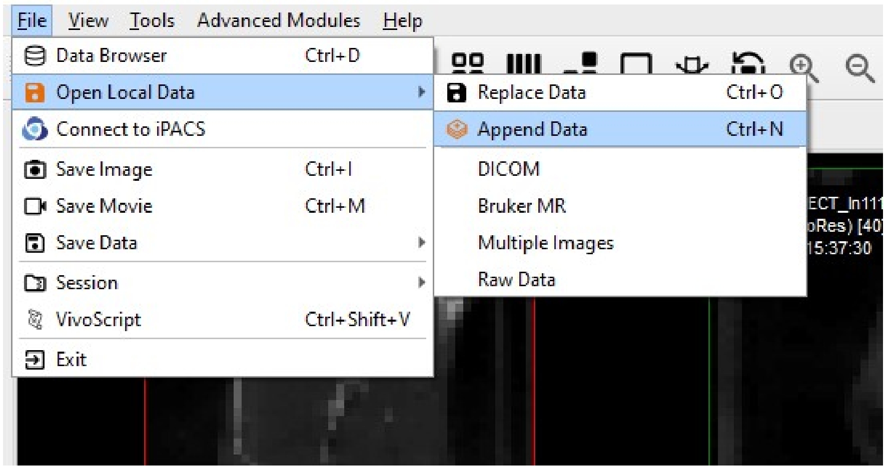
Getting There

There are different methods for appending data. The first method is to use the “Append Data” thumbnails in the Main Window.



Append Data

The second method is to go to **File** > **Append Data**.



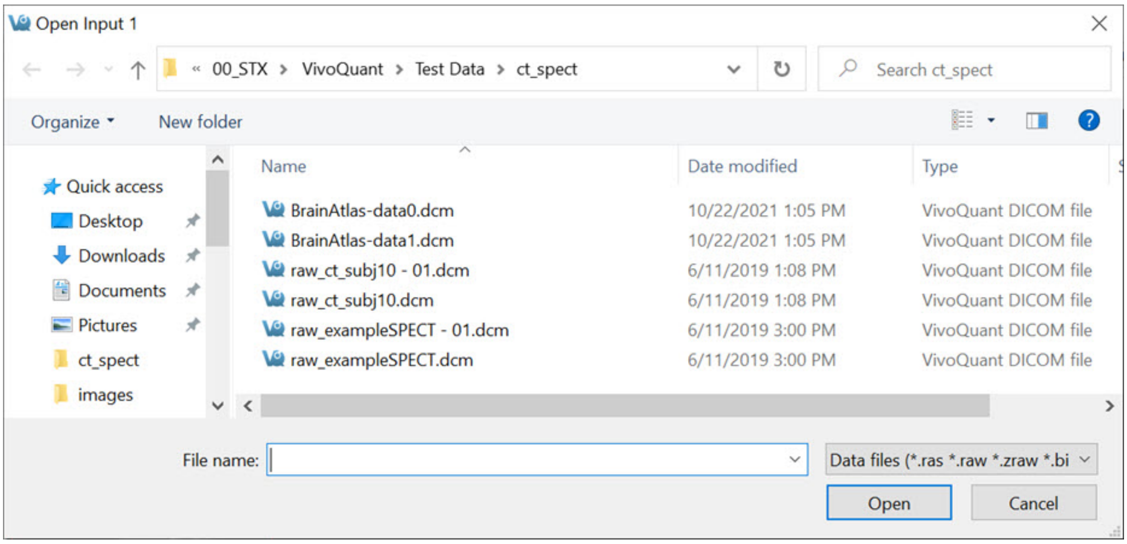
Main Window

The third method is to use the keyboard shortcut Ctrl+N to load input 1, and Ctrl+Shift+N to load additional inputs. For more on keyboard shortcuts in VivoQuant, please see Keyboard Shortcuts.

ℹ **Note:** An initial data set must be loaded into the **Data Manager** prior to appending data.

Function

Selection of the **Append Data** option opens a navigation window from which the input data set may be selected.



Name	Date modified	Type
BrainAtlas-data0.dcm	10/22/2021 1:05 PM	VivoQuant DICOM file
BrainAtlas-data1.dcm	10/22/2021 1:05 PM	VivoQuant DICOM file
raw_ct_subj10 - 01.dcm	6/11/2019 1:08 PM	VivoQuant DICOM file
raw_ct_subj10.dcm	6/11/2019 1:08 PM	VivoQuant DICOM file
raw_exampleSPECT - 01.dcm	6/11/2019 3:00 PM	VivoQuant DICOM file
raw_exampleSPECT.dcm	6/11/2019 3:00 PM	VivoQuant DICOM file

File name:
Data files (*.ras *.raw *.zraw *.bi

Navigation Window

File Formats

VivoQuant can handle a variety of file formats. The default options include:

1. **DICOM**: *.dcm, *.dicom, 1.*
2. **TRaster**: *.ras, *.res., *.bin
3. **Raw**: *.raw
4. **Image Files**: *.png, *.tif, *.tiff, *.jpg, *.jpeg, *.bmp
5. **Other**: *.img, *.nii, *.mhd, *.mha, *.fdf, *.dc3, *.vol

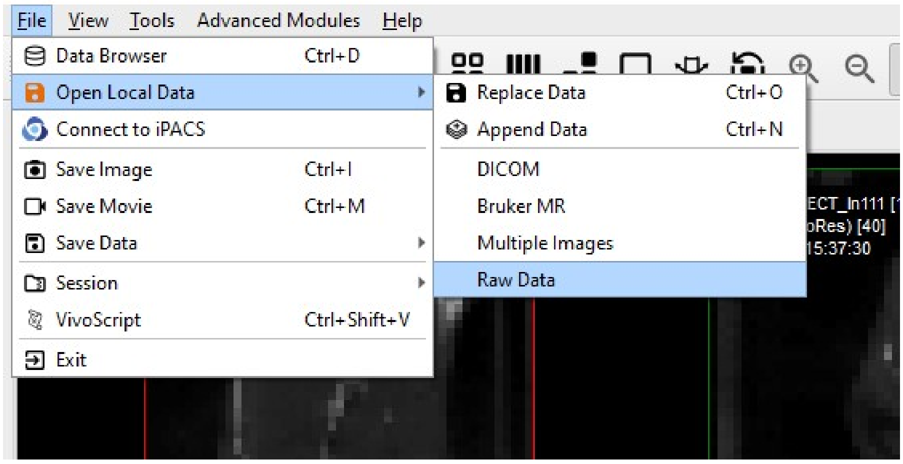
The navigation window also provides an option for displaying **All Files**, without specifying any of the above formats.

Open Raw Data

This option is used to load the raw data from studies.

Getting There

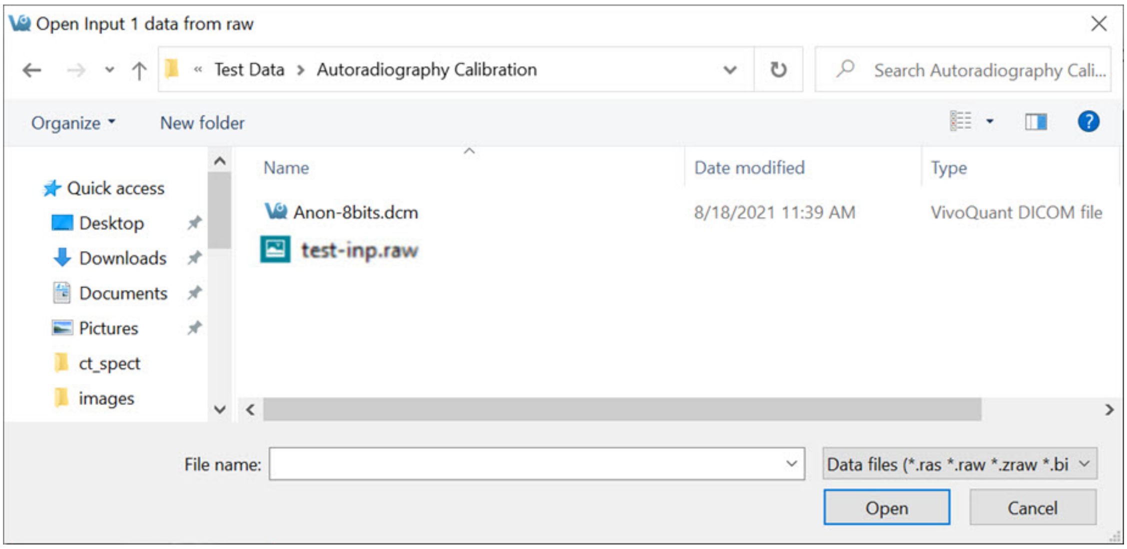
To load raw data, go to **File** > **Open Local Data** > **Raw Data**.



Open Raw Data

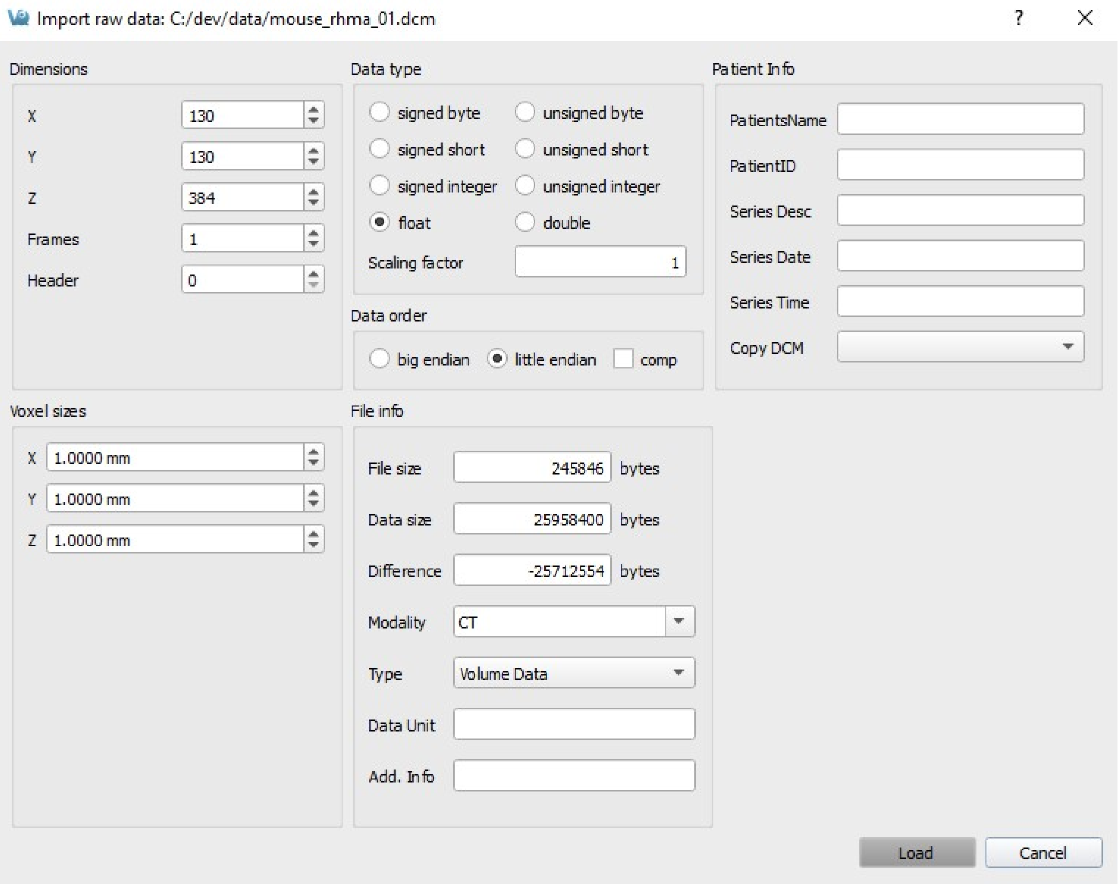
Function

Selection of the **Open Raw Data** option opens a navigation window from which the raw data may be selected.



Navigation Window

Once the raw data has been selected, a **Raw Data Importer** window appears which contains information about the data, such as dimensions, voxel size, data type and file information. Most data is automatically populated from the file. Other data fields have to be filled in by the user in order to provide VivoQuant with information on how to interpret the file. Once all the data fields have been completed, click **Load** to import the raw data is imported.



Import raw data: C:/dev/data/mouse_rhma_01.dcm

Dimensions

X 130
Y 130
Z 384
Frames 1
Header 0

Data type

○ signed byte ○ unsigned byte
○ signed short ○ unsigned short
○ signed integer ○ unsigned integer
● float ○ double
Scaling factor 1

Data order

○ big endian ● little endian ☐ comp

Patient Info

PatientsName
PatientID
Series Desc
Series Date
Series Time
Copy DCM

Voxel sizes

X 1.0000 mm
Y 1.0000 mm
Z 1.0000 mm

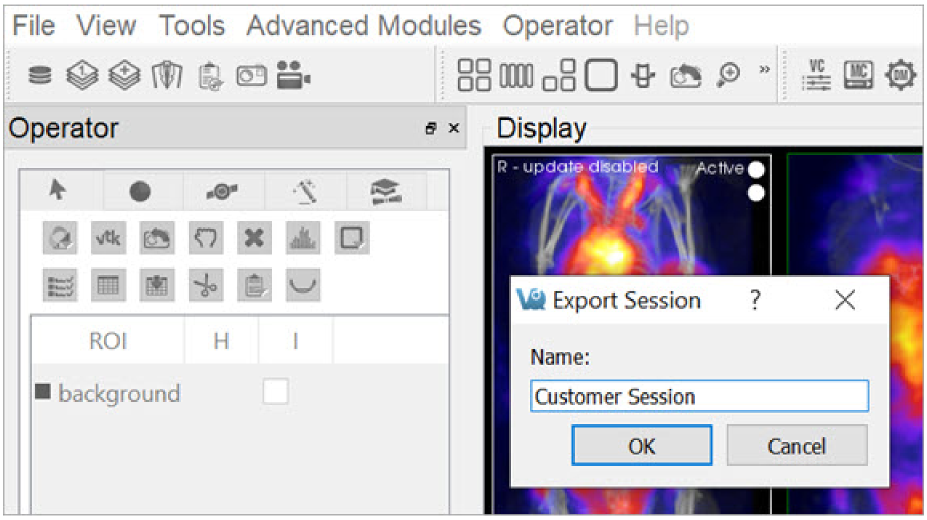
File info

File size 245846 bytes
Data size 25958400 bytes
Difference -25712554 bytes
Modality CT
Type Volume Data
Data Unit
Add. Info

Raw Data Importer

Session

Sessions allow the user to save the current working environment. The exact location in the software is saved along with the image data that is currently loaded in the **Data Manager**. The operator or tool and parameters being used are saved as well. A session can be saved to the local cache or exported as a compressed zipacs folder structure that can be used to share with colleagues.

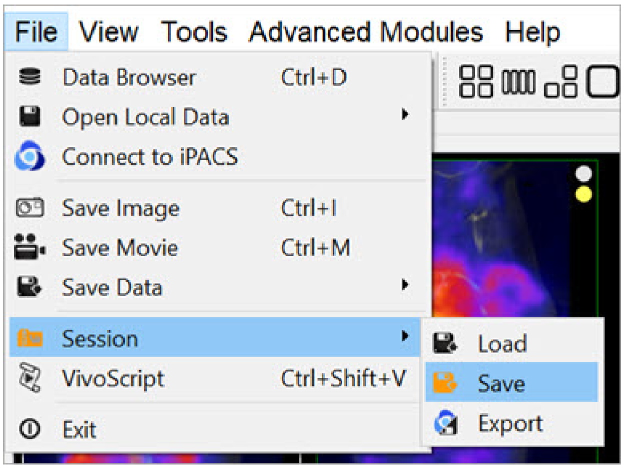


Name: Customer Session

Sessions

Getting There

A session can be saved, loaded, or exported by selecting the appropriate option under **File** > **Session** in the main menu.

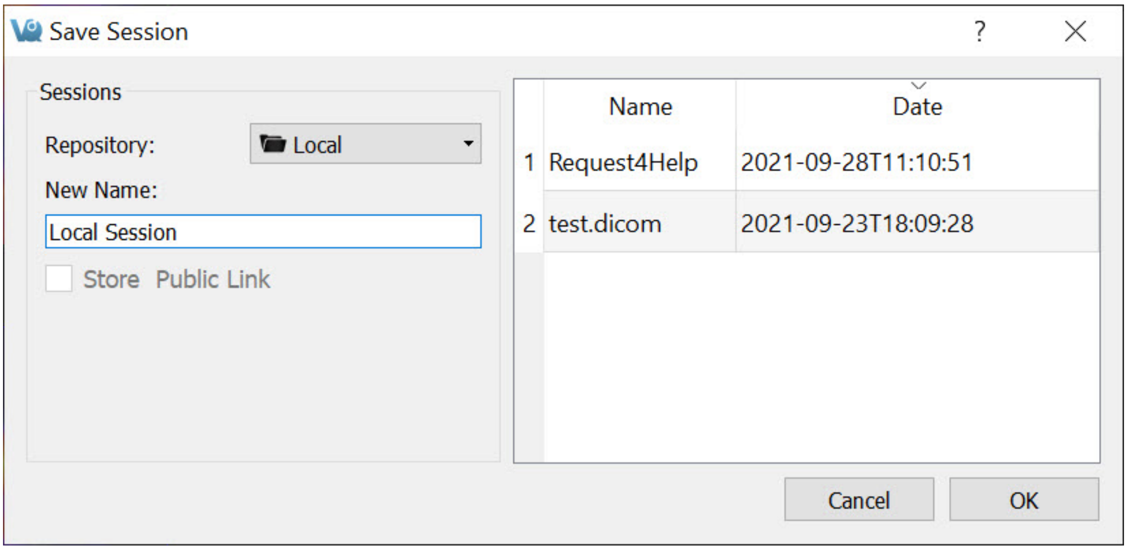


Save Session

Session Manager

The **Session Manager** allows users to load previously saved sessions, save new sessions and export sessions to save them locally and/or on any iPACS available.

When saving a session, users can specify the desired repository and session name for easy sorting later.



Repository: Local

New Name:

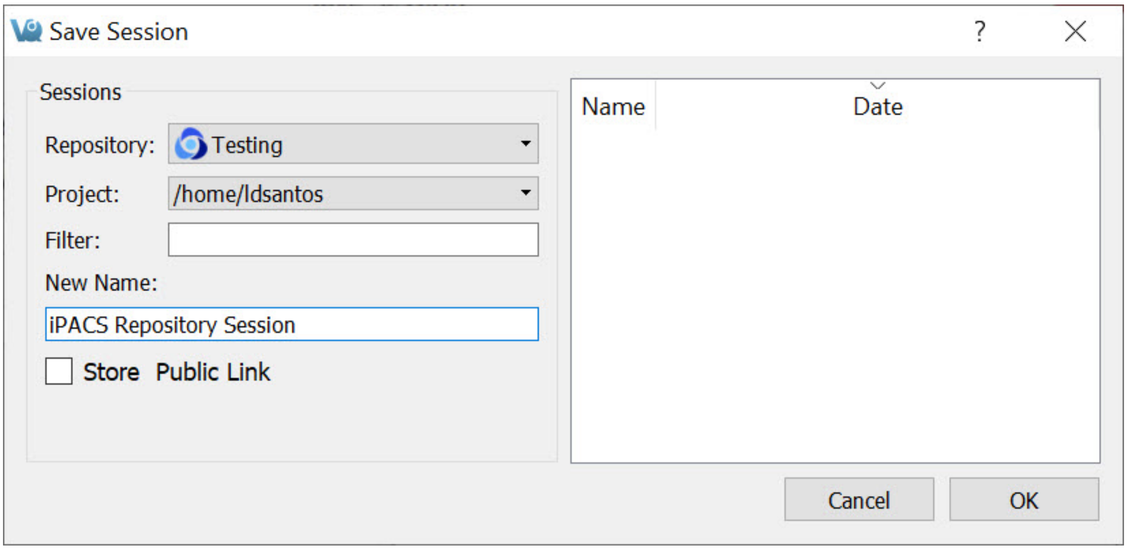
Local Session

☐ Store Public Link

	Name	Date
1	Request4Help	2021-09-28T11:10:51
2	test.dicom	2021-09-23T18:09:28

Session Manager

In addition to saving sessions locally or to a desired repository, users may also associate the saved session with a specific project from within their desired iPACS repository. This allows for a more efficient access and organization of various sessions across multiple projects.



Repository: Testing

Project: /home/ldsantos

Filter:

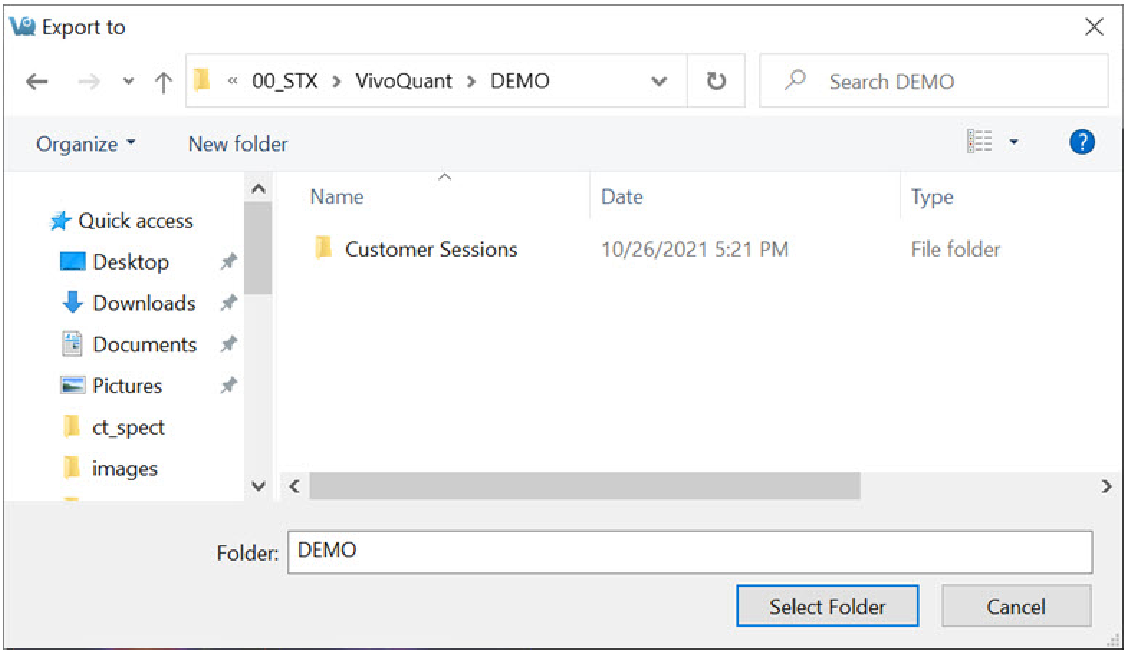
New Name:

iPACS Repository Session

☐ Store Public Link

iPACS Repository Session

When exporting a session, specify a location on the local where the compressed zipacs folder will be saved.

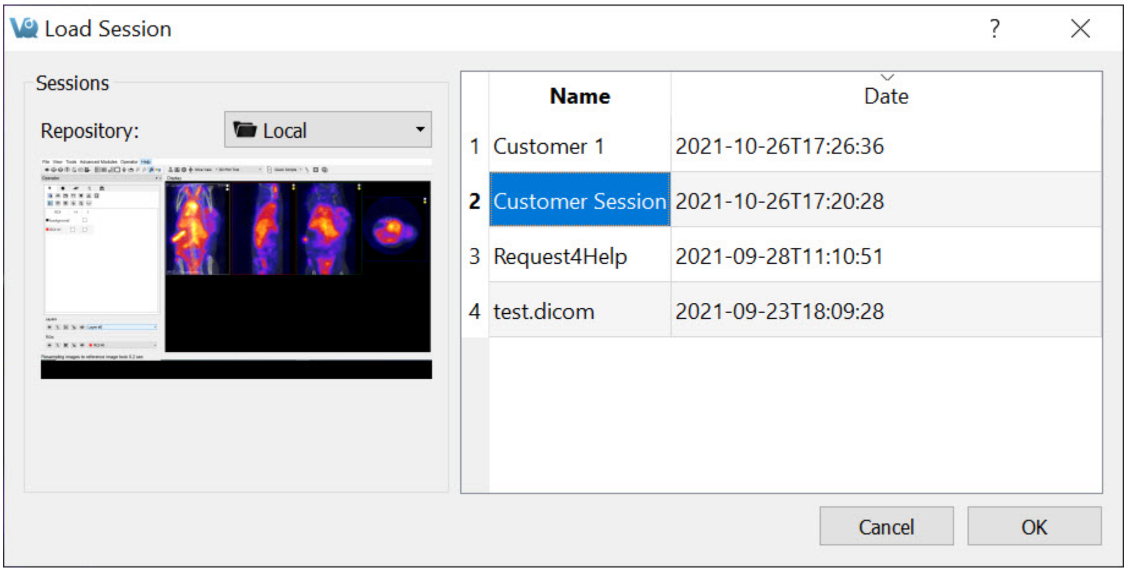


Name	Date	Type
Customer Sessions	10/26/2021 5:21 PM	File folder

Folder: DEMO

Export Session

To load a compressed zipacs folder, go to **File** > **Session** > **Load**, and select the session from the appropriate folder. When loading a previously saved session, the session GUI displays the name and date of each study and allows for easy sorting of files . Users can click on any session to see a **Preview** of that session in the window.

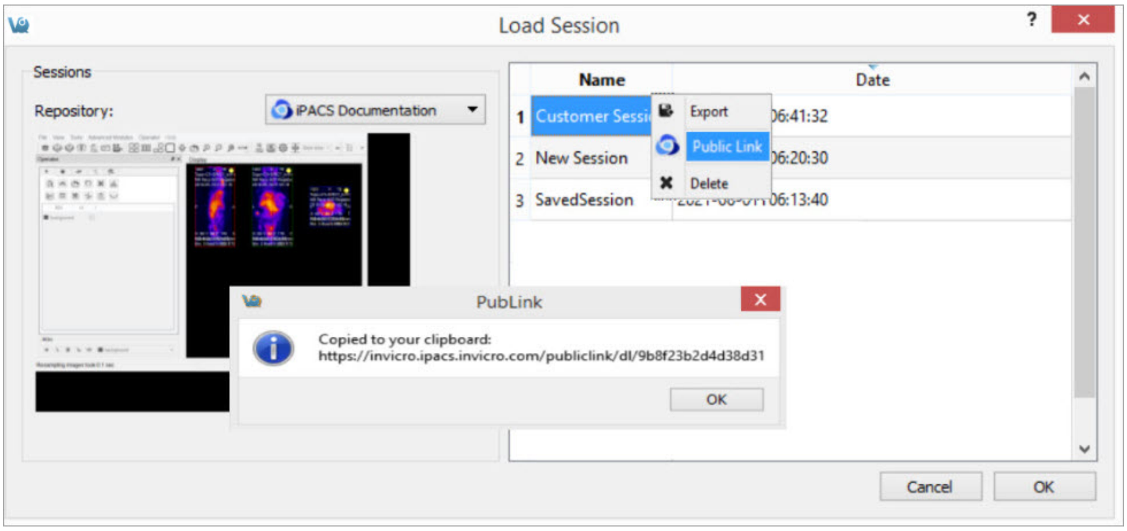


Repository: Local

	Name	Date
1	Customer 1	2021-10-26T17:26:36
2	Customer Session	2021-10-26T17:20:28
3	Request4Help	2021-09-28T11:10:51
4	test.dicom	2021-09-23T18:09:28

Load Session

Right-clicking on a session in the **Session Manager** allows the user to delete that session, export it as a compressed zipacs folder to a local storage location, or create a **Public Link** to the session. Public links can be copied to the user's clipboard and pasted into a report, email, etc., as desired.



Repository: iPACS Documentation

Copied to your clipboard:
https://invicro.ipacs.invicro.com/publiclink/dl/9b8f23b2d4d38d31

Public Link

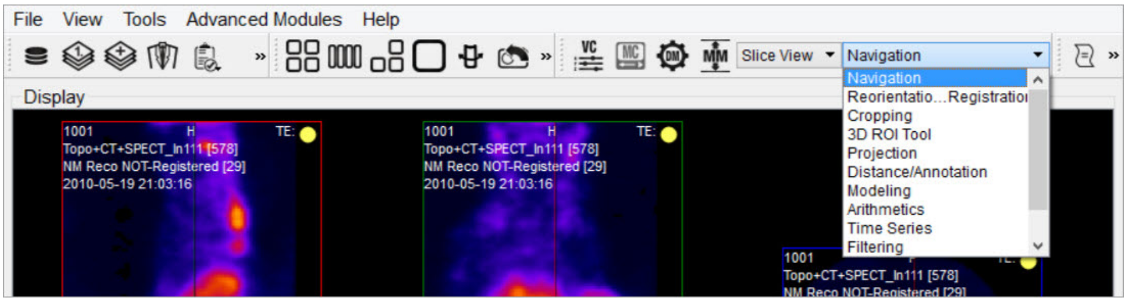
Navigation

The **Navigation** operator is selected by default when VivoQuant is opened. This tool enables the user to manually scroll through the image slices and rotate the Maximum intensity Projection (MIP). Similar functionality is available via the View Control tool.

ℹ **Note:** this page is concerned with Navigation in Slice View. While navigation is similar in other view modes, the keystrokes and movements described below may not produce identical behavior. For information regarding navigation in other view modes, see the Tile View, Multi View, or MPR View sections.

Getting There

To enter the **Navigation Panel**, select **Navigation** from the pull-down menu on the VivoQuant front panel.

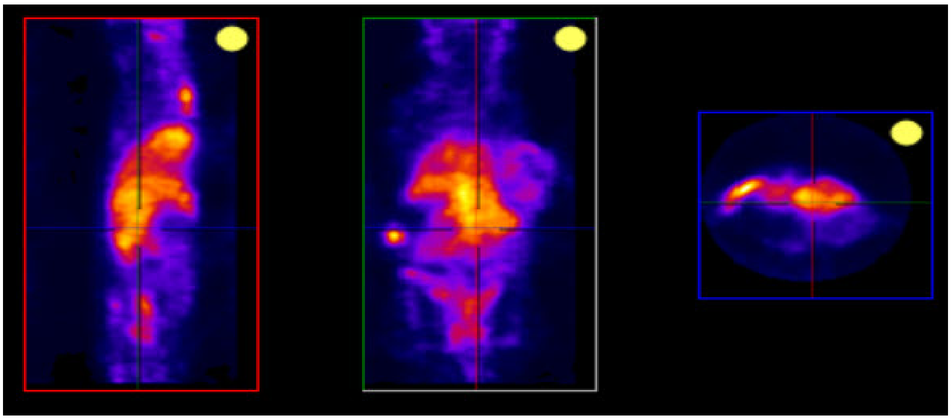


Navigation Panel

There are several methods for operating the slice control navigator. This section describes manual manipulation using a mouse device. The View Control tool offers a wider array of options for controlling the Navigator window.

Function

Navigation through the viewports includes scrolling through slices, zooming and panning.



Navigation Function

Scrolling

To scroll through the individual slices, left click and move the mouse cursor up and down or to the side on the different viewports (sagittal, coronal or transverse).

When in Slice View or in Multi View with **Link Views** checked, scrolling is *not* independent across viewports: scrolling in one viewport will affect the other viewports.

Zooming

To zoom in or out within a viewport, hold the Shift key and move the mouse wheel forward or backward, respectively.

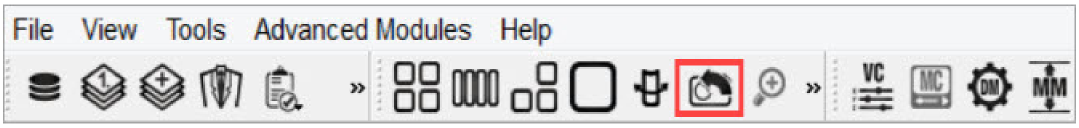
Zooming is independent across viewports: zooming in one viewport will not affect the others, and all viewports may be zoomed to different amounts.

Panning

To pan within a viewport, hold the Shift key and click and drag the mouse. Panning is independent across viewports: panning in one viewport will not affect the others, and all viewports may panned to different amounts.

Resetting Viewport

At any time, the zooming and panning within viewports may be reset to their default positions by clicking the icon located on the toolbar.



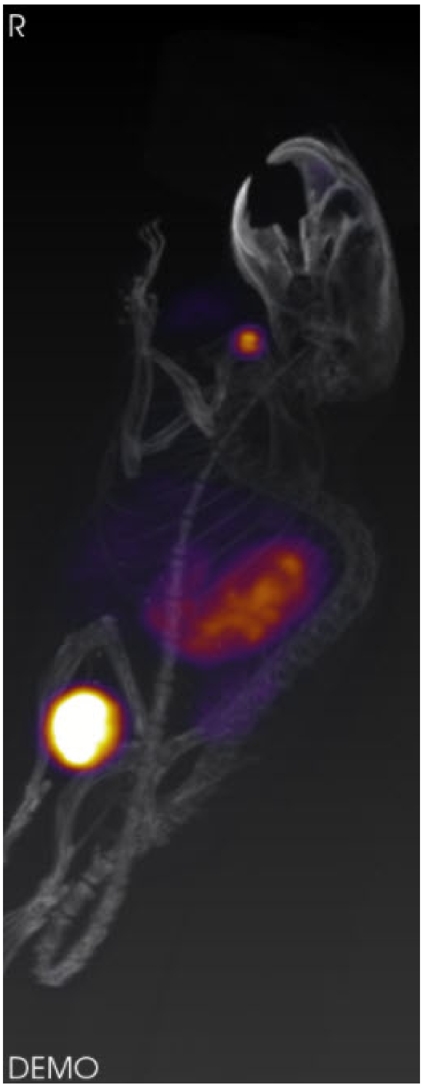
Reset to Default

MIP-Specific Function

The functions for controlling the MIP are slightly different than the functions that control the slices.

VTK MIP

To freely rotate the VTK MIP, click and drag the mouse across the MIP. To zoom in and out, scroll the mouse wheel forward and backward. To pan around the MIP, hold the Shift key and drag the mouse across the MIP. To rotate the MIP about a fixed axis of rotation, hold the Ctrl key and drag the mouse in a circular motion across the MIP.

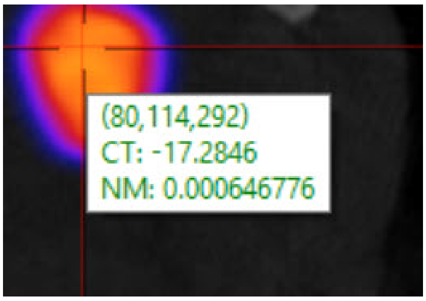


VTK MIP

This information is also found in the **MIP Control** tool. For more information on using this tool, see the MIP Control page.

Tooltip

The tooltip feature is available by briefly holding a mouse left click on any of the three slice views (transverse, sagittal, coronal) in the **Navigator** window. The tooltip feature displays (x,y,z) coordinate locations and voxel values for each displayed data set for that (x,y,z) position.


(80,114,292)
CT: -17.2846
NM: 0.000646776

Tooltip

This information is also found in the **View Control** tool. For more information on using this tool, see the View Control page.

3D ROI Tool

Overview

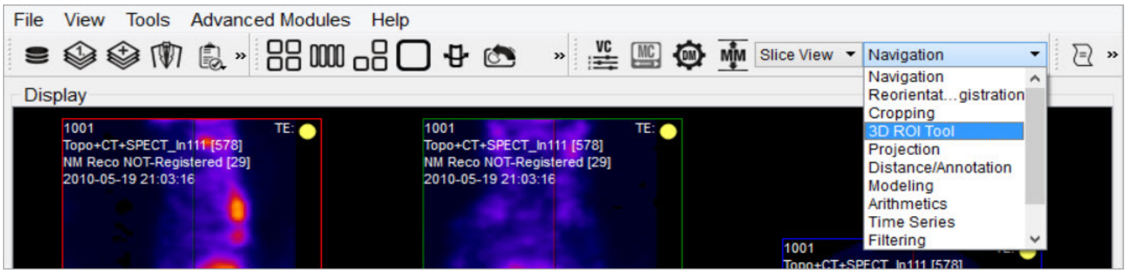
ROI stands for **Region of Interest** and is used to describe a particular area or volume within an image for which the user wishes to characterize some quantity or quality. The 3D ROI operator provides advanced tools for drawing, visualizing, saving, and quantifying both 2- and 3-dimensional regions. This tool allows for having a voxel belonging to more than one ROI. For example, a user could have an ROI that contains the whole brain and other ROIs for regions of the brain, meaning that each voxel of the whole brain ROI would need to simultaneously be part of two different ROIs.

Invicro implemented overlapping of ROIs by adding layers. The user is able to add new layers in the 3D ROI Operator, select an active layer, and create and modify ROIs in that layer independent of the contents of other layers. Overlapping is then possible as each voxel can belong to various ROIs on each layer.

The previous ROIs approach limited the user to 256 ROIs, as it used an internal buffer of unsigned chars (1 byte per voxel). To allow for multiple layers, the new approach keeps a list of buffers of unsigned chars that can be increased on demand by the user up to a potential of 8 layers if the RAM allows it. The new maximum total number of ROIs was then increased to 2048, and each voxel now supports up to 8 overlapping ROIs. However, the allocated RAM for the ROIs object increases significantly as the user adds more layers. We can also expect a small overhead execution cost when drawing the ROIs on the image for display purposes, as the blending or the handling of the different layer will require more processing.

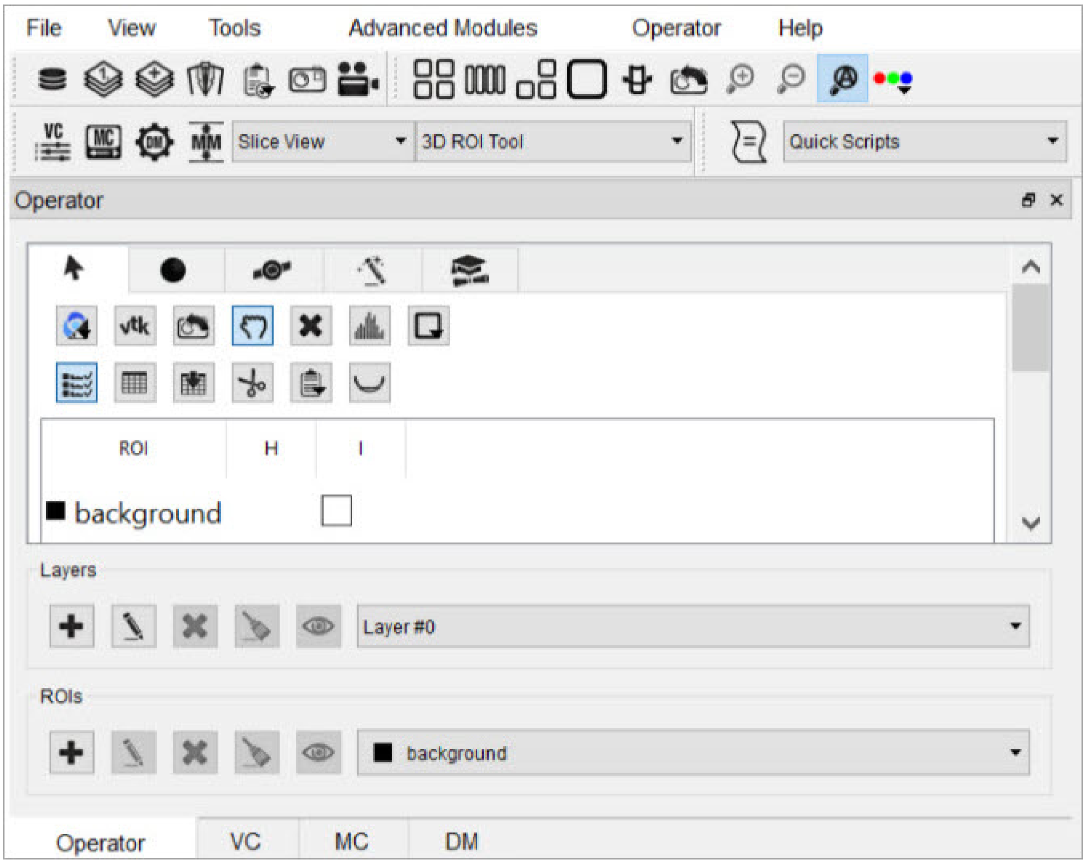
Getting There

The 3D ROI tool can be accessed via the operators pull-down menu on the VivoQuant front panel.



3D ROI Tool

When the 3D ROI Tool is selected, a 3D ROI Tool operator window is displayed.



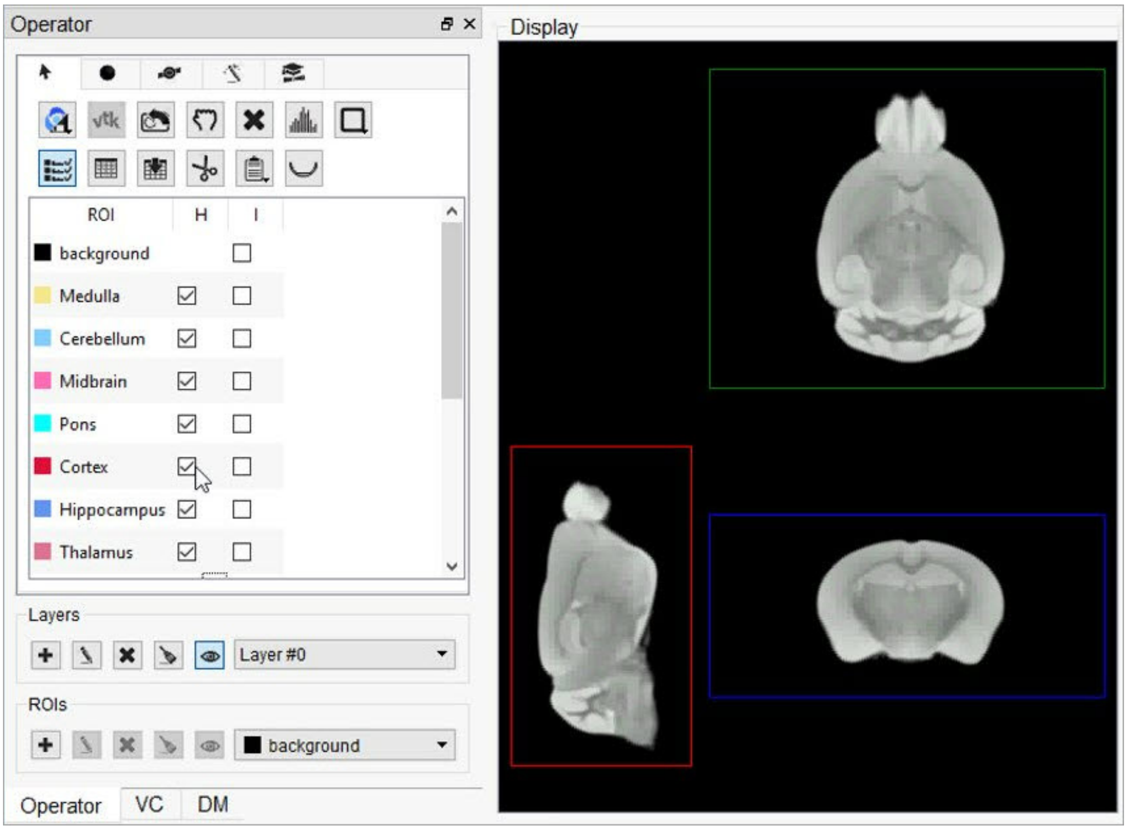
3D ROI Operator Window

Each tab of the 3D ROI Operator window provides a grouped set of functionalities.

Tab	Description
➤	ROI Loading, Saving, and Quantification Tools
●	Painting Tools
◉	2D Drawing Tools
✧	3D Segmentation Tools
🎓	Expert Settings

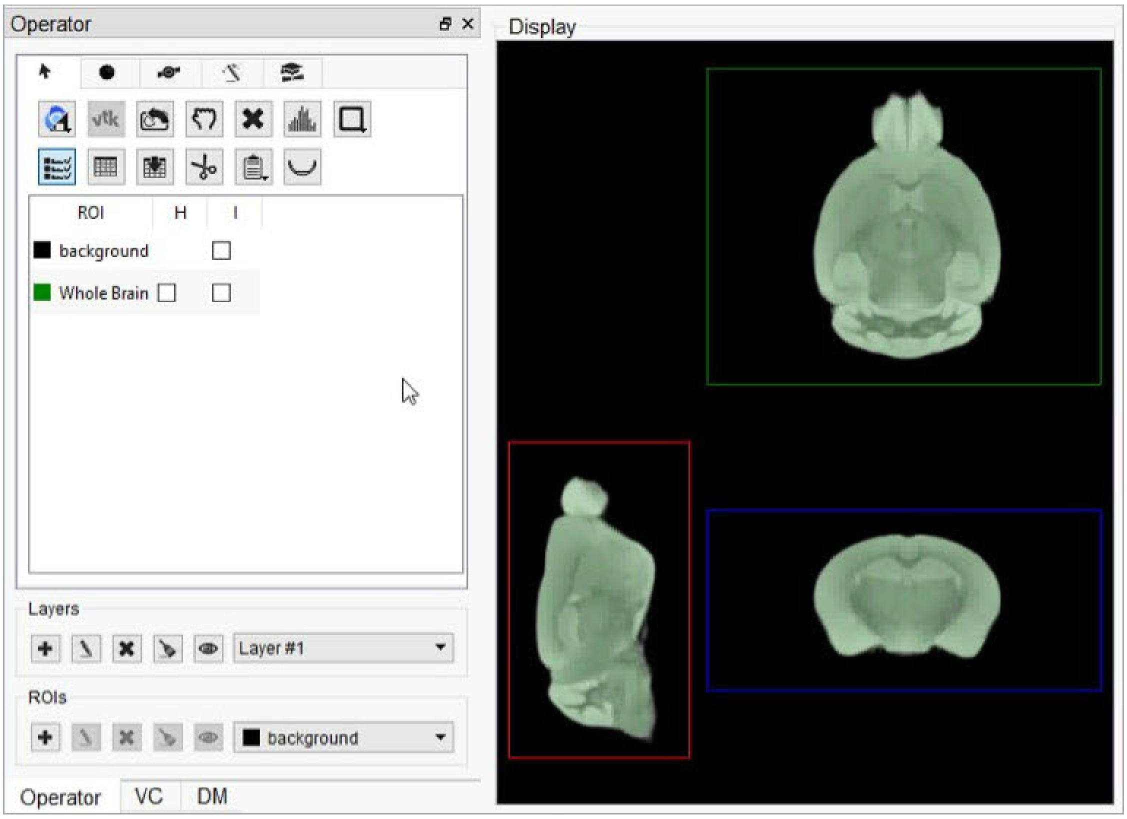
Layers

We use ROIs to label voxels in the image as belonging to a region, so we can extract quantitative information about that region from the image. Layers allow the user to specify that a particular voxel belongs to multiple regions. Within a layer, a given voxel can only belong to one region; that is, ROIs are associated with a layer. For example, one layer could contain different brain sections, while another layer defines the entire brain.



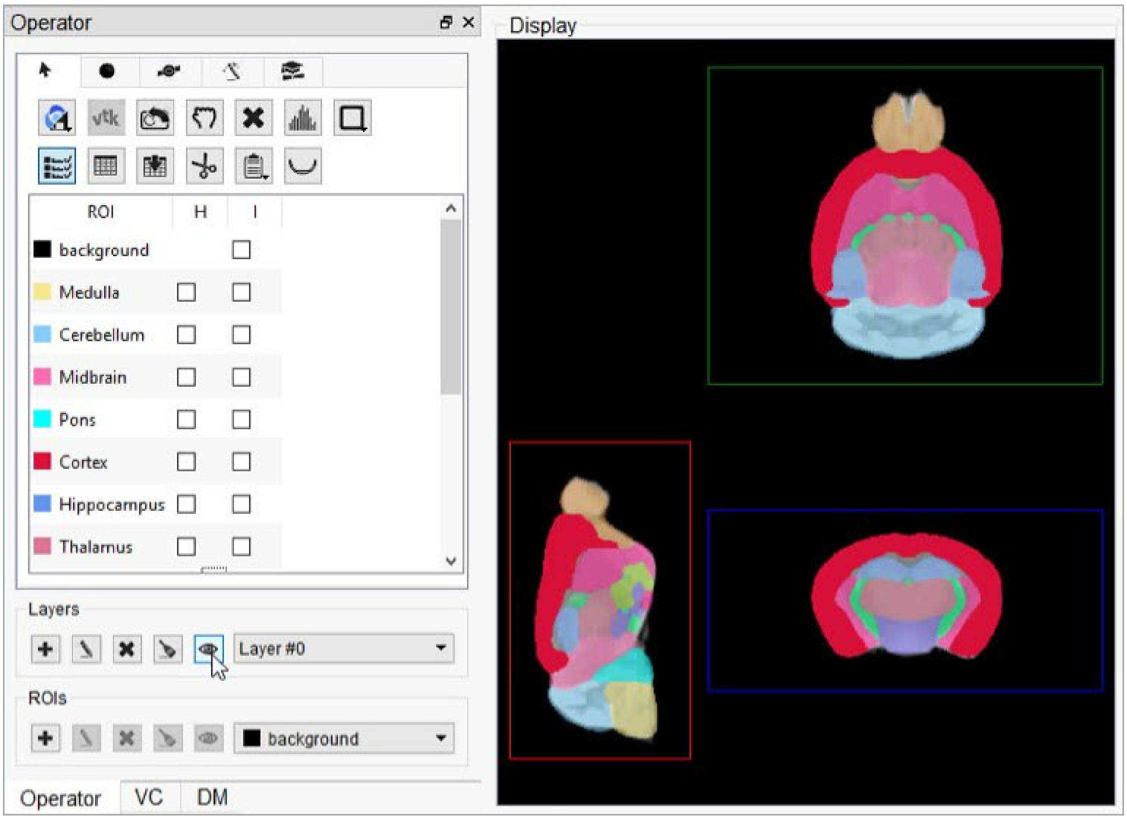
ROI	H	I
■ background		☐
Medulla	☑	☐
Cerebellum	☑	☐
Midbrain	☑	☐
Pons	☑	☐
Cortex	☑	☐
Hippocampus	☑	☐
Thalamus	☑	☐

No brain sections defined



ROI	H	I
■ background		☐
🟩 Whole Brain	☐	☐

Whole brain ROI (green) defined in Layer 1

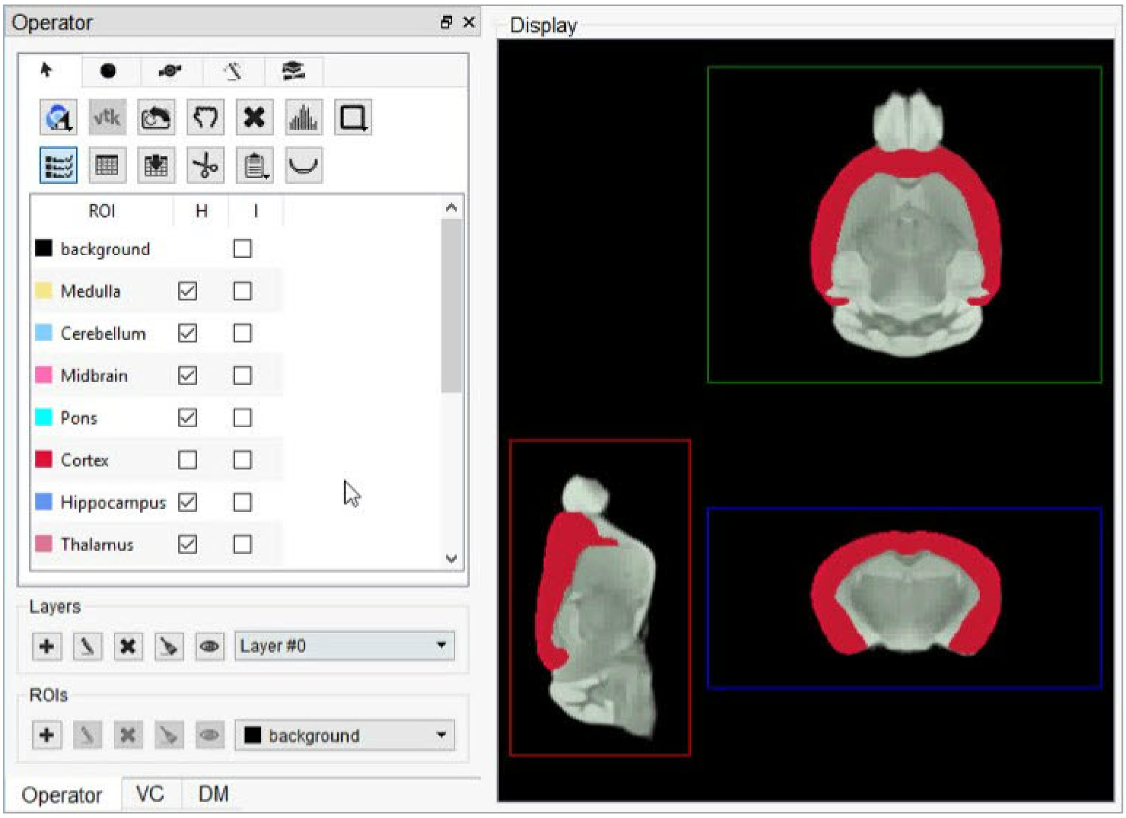


ROI	H	I
background		☐
Medulla	☐	☐
Cerebellum	☐	☐
Midbrain	☐	☐
Pons	☐	☐
Cortex	☐	☐
Hippocampus	☐	☐
Thalamus	☐	☐

Layer #0

background

Brain sections separately defined as ROIs in Layer 0

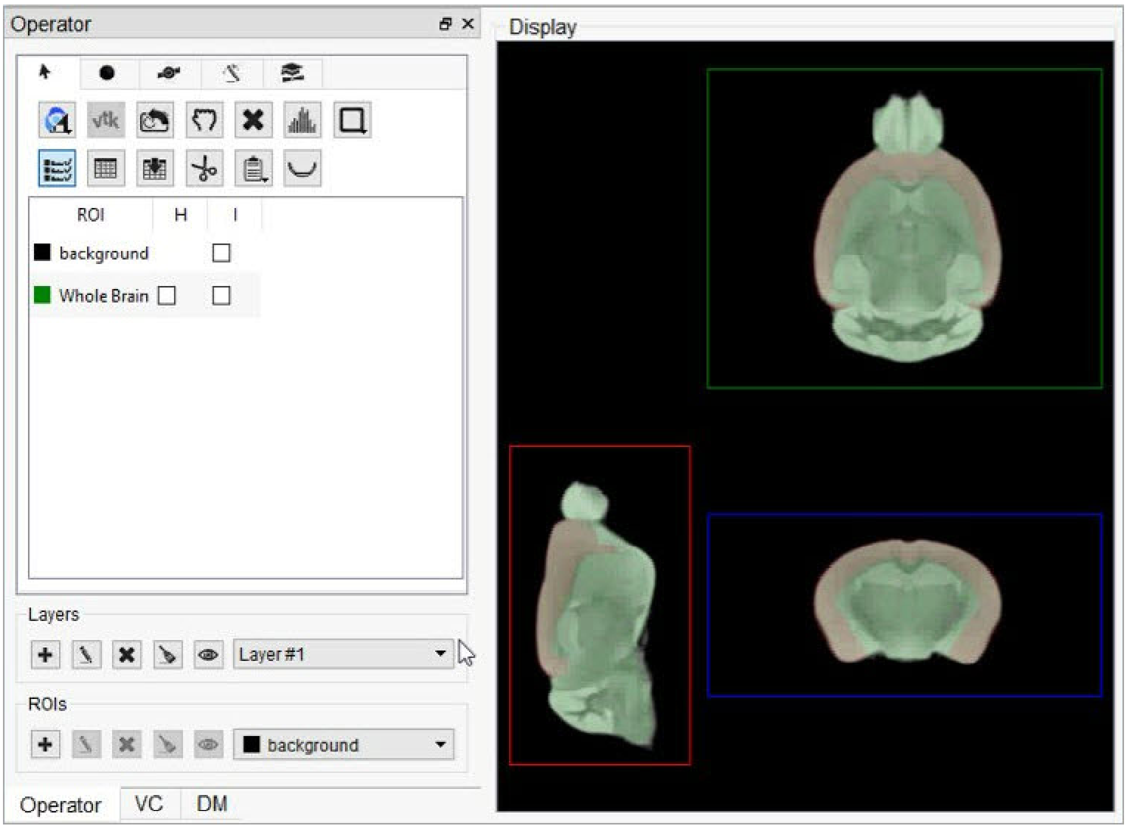


ROI	H	I
background		☐
Medulla	☑	☐
Cerebellum	☑	☐
Midbrain	☑	☐
Pons	☑	☐
Cortex	☐	☐
Hippocampus	☑	☐
Thalamus	☑	☐

Layer #0

background

Cortex brain section (red) defined in Layer 0 over whole brain (green) of Layer 1



Whole brain section (green) layered over cortex brain section (red)

Layers can be created and deleted from the strip of icons at the bottom of the 3D ROI Operator.

Layer Options

Relevant layer actions are described in the table below.

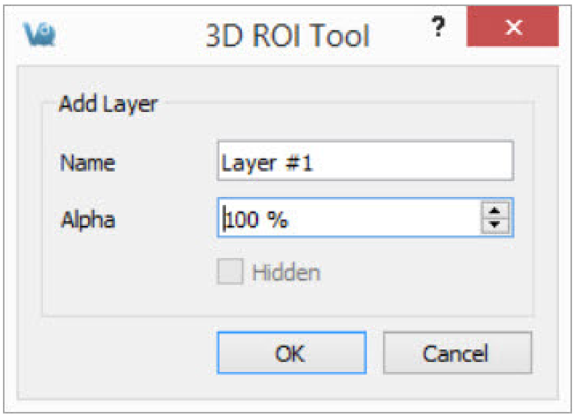
Icon	Description
⊞	Add a Layer
✎	Edit a Layer
👁	Hide a Layer
⟲	Reset a Layer
☒	Delete a Layer

Add a Layer

Click the **Add Layer** button ⊞ to create a new layer.

A popup window will open, prompting the user to name the new layer and set the transparency of the ROIs by selecting an alpha value.

- Decrease the alpha value to increase the transparency of all ROIs in the layer.
- Values range from 0% - 100% and change by 10% increments.
- The option to make the layer hidden is not available during the layer creation process and appears greyed-out.



Name Layer #1

Alpha 100 %

☐ Hidden

Add Layer

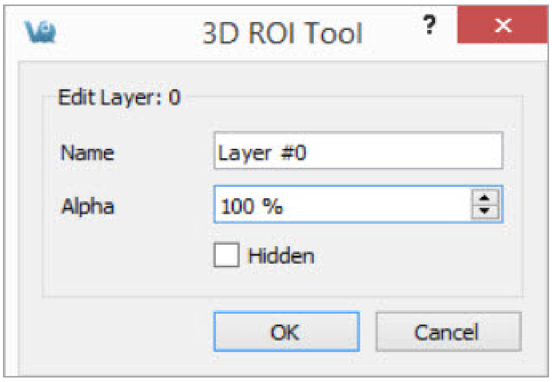
ℹ **Note:** The maximum limit of layers in one session is 8.

Edit a Layer

Click the **Edit Layer** button ✎ to edit a existing layer.

A popup window will open, allowing the user to edit the name of the selected layer, change the transparency of the ROIs by adjusting the alpha value, or hide/unhide the layer.

- Decrease the alpha value to increase the transparency of all ROIs in the layer.
- Values range from 0% - 100% and change by 10% increments.



Name Layer #0

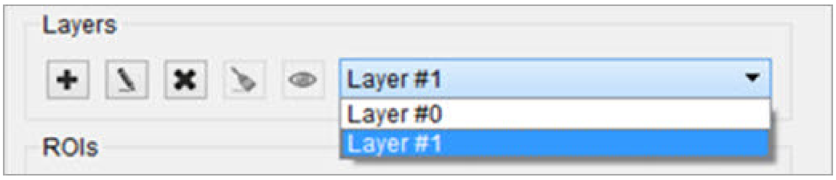
Alpha 100 %

☐ Hidden

Edit Layer

Select Active Layer

Select the layer of interest from the dropdown Layer to set it as the **Active Layer**. The display will show the active layer, and any layer actions, such as editing or deleting, will be performed on the current active layer.



Active Layer

Hide a Layer

Click the **Hide Layer** button to hide the active layer. Click the **Hide Layer** button again to show the layer.

Hide / Show Layer

Reset a Layer

Click the **Reset Layer** button to clear the contents of all ROIs in the active layer.

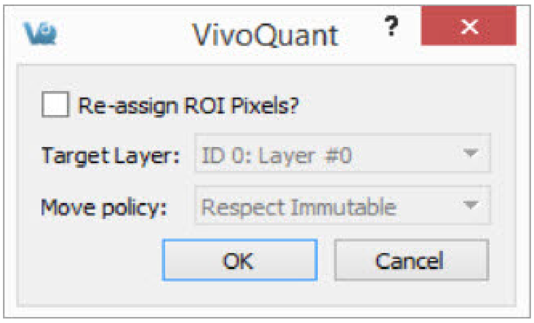
Reset Layer

Delete a Layer

Click the **Delete Layer** button to open options for the active layer.

Delete Layer

A popup window will open, prompting the user to delete or reassign the ROIs associated with the specified layer.



☐ Re-assign ROI Pixels?

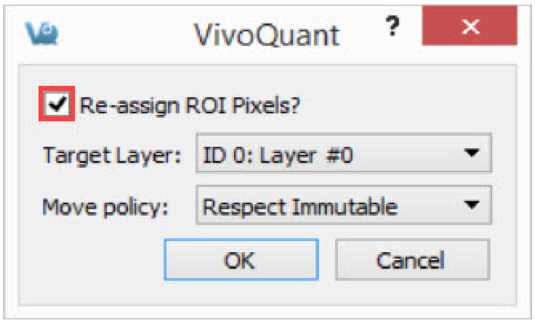
Target Layer: ID 0: Layer #0

Move policy: Respect Immutable

Delete Layer

- To delete all ROIs in the layer, click OK.
- To reassign the ROIs to another layer, click the Re-assign ROI Pixels check box and the greyed-out options underneath

will become active.



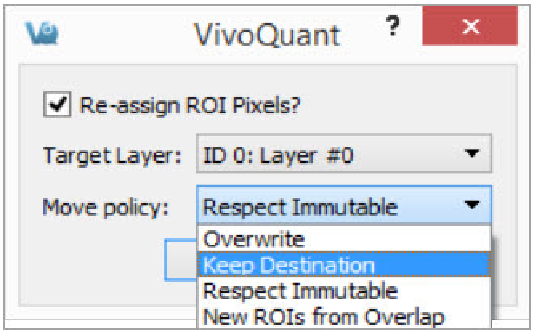
☑ Re-assign ROI Pixels?

Target Layer: ID 0: Layer #0

Move policy: Respect Immutable

Re-assign ROI Pixels

Verify that the layer selected in **Target Layer** is the layer of interest then select the **Move Policy** to apply.



☑ Re-assign ROI Pixels?

Target Layer: ID 0: Layer #0

Move policy: Respect Immutable

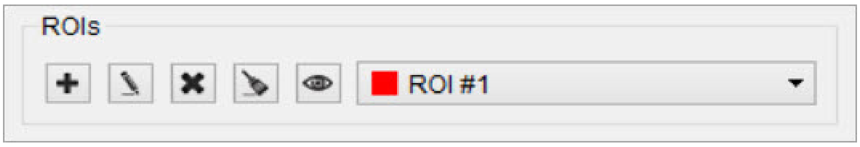
Select Move Policy

Available Move Policies are described in the table below.

Move Policy	Description
Overwrite	ROIs from the layer being deleted (active layer) will trump any overlapping ROIs existing on the destination layer. Use this option if you do not want any of the ROIs being moved to be changed.
Keep Destination	ROIs on the destination layer will trump any overlapping ROIs existing on the layer being deleted (active layer). Use this option if you do not want the ROIs in the destination layer to be changed.
Respect Immutable (default)	Use this option if the user wants ROIs from both the destination layer and layer being deleted (active layer) to be preserved or overwritten based on pre-specified information. ROIs marked immutable from the destination layer will trump any overlapping ROIs. ROIs not marked immutable from the destination layer will be trumped by the ROIs from the source layer if overlapping.
New ROIs from Overlap	Using this option will create new ROIs in areas where the destination ROIs and the ROIs being moved overlap. Use this option if you want the flexibility to decide how the overlap is handled.

ROI Creation and Deletion

ROIs can be created and deleted from the strip of icons at the bottom of the 3D ROI Operator.



ROI Creation and Deletion

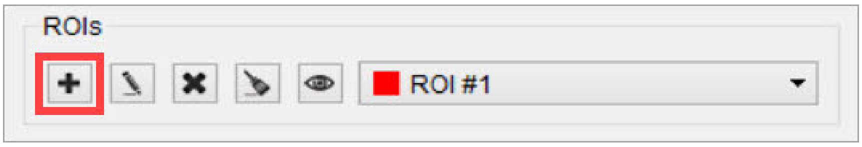
Icon	Description
⊞	Add an ROI
✎	Edit an ROI
☒	Delete an ROI
↺	Reset an ROI
👁	Hide an ROI

Add an ROI

There are two methods for adding an ROI:

1. Add Via ROI Section Buttons

Click the **Add ROI** button ⊞ to open options for adding a new ROI.

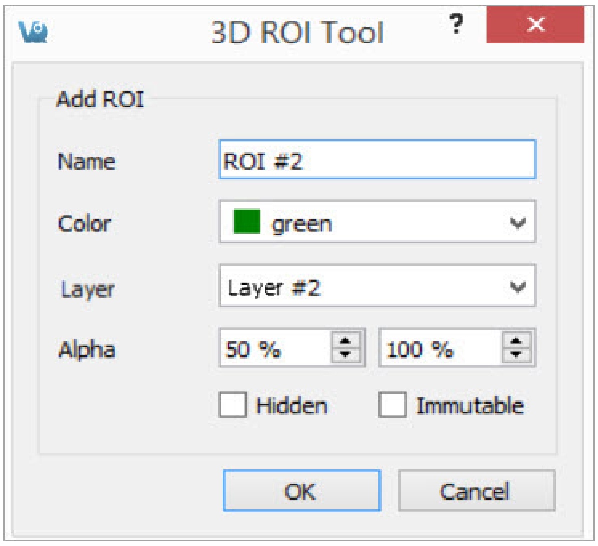


Add ROI

A popup window will open, prompting the user to provide specific information for the new ROI, including:

- The ROI's name and color.
- The layer to which the ROI should be added

  ℹ **Note:** The Number of ROIs per layer should not exceed the limit of 256.
- The transparency of the ROI in the slice and MIP views.
  - To alter the transparency, increase or decrease the alpha values (a lower percentage will increase the transparency of an ROI).
- The ROI's visibility by checking "Hidden" to turn the ROI off in all views.
- The ROI's ability to be edited by selecting "Immutable."



Name: ROI #2

Color: 🟩 green

Layer: Layer #2

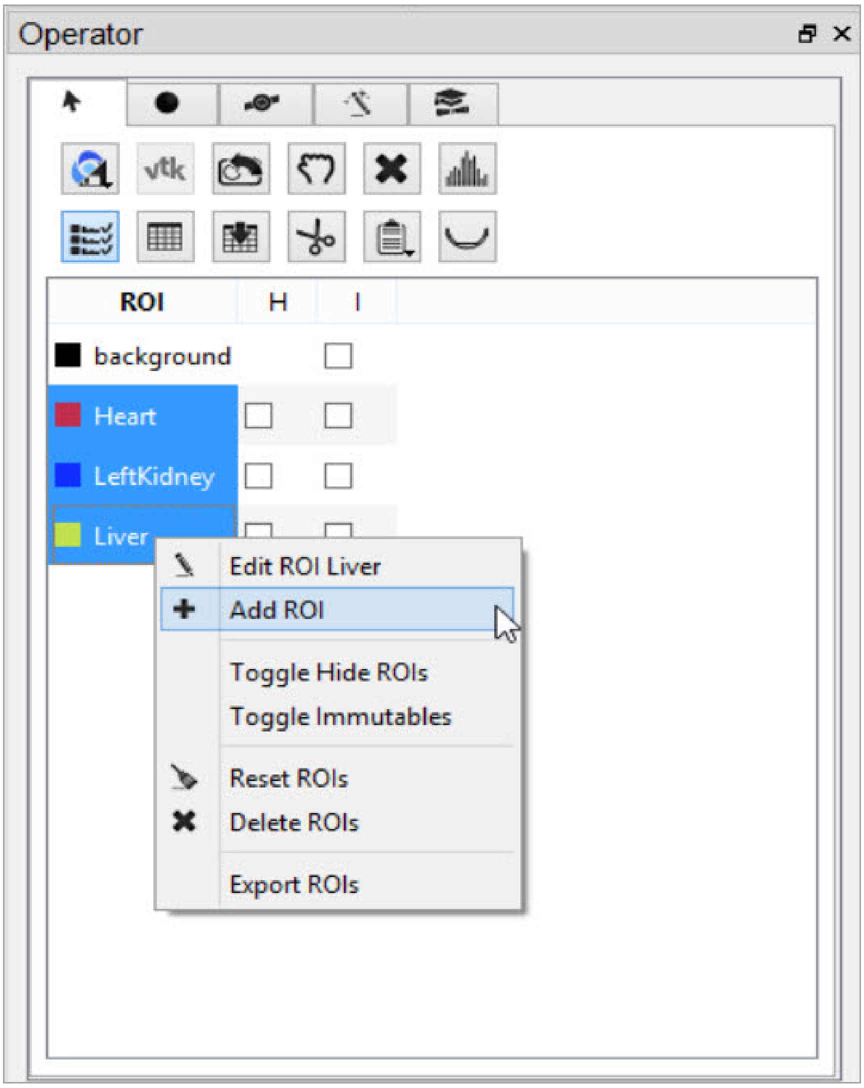
Alpha: 50 % 100 %

☐ Hidden ☐ Immutable

ROI Popup Window

2. Add Via Right-Clicking the Navigation Pane

Another option is to select any (or many) of the existing ROIs is to right click and select **Add ROI**. This will append a new ROI to the end of the list.

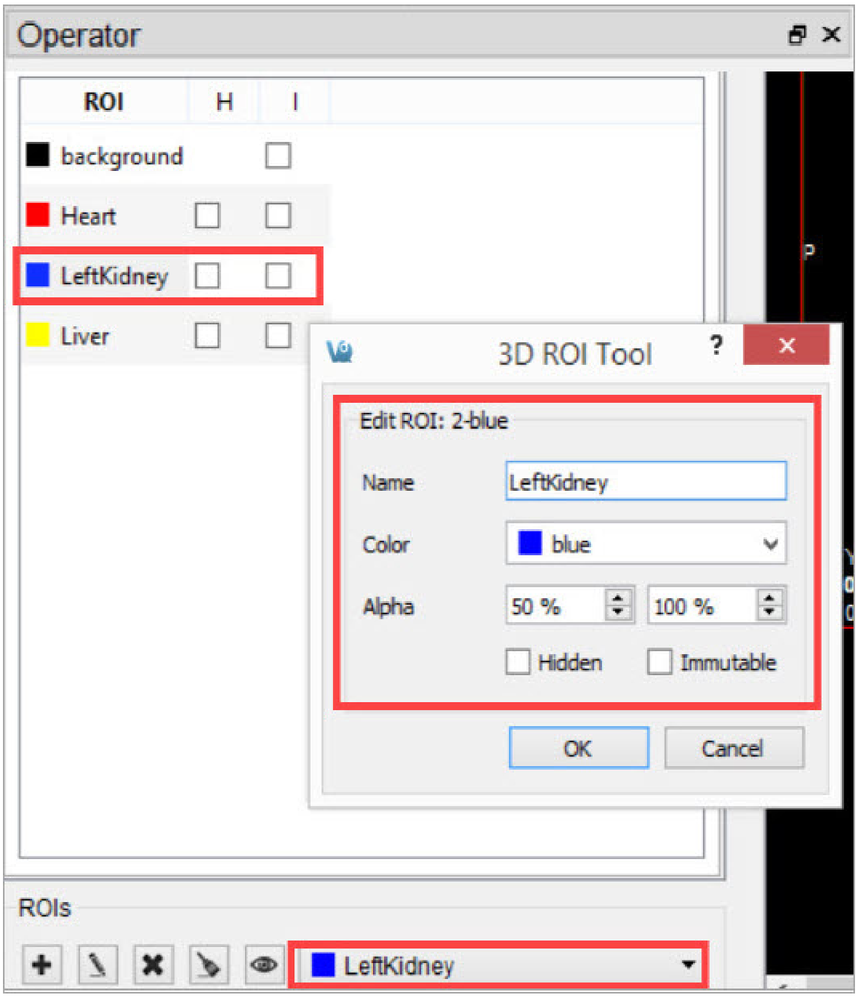


ROI	H	I
■ background		☐
🟥 Heart	☐	☐
🟦 LeftKidney	☐	☐
🟩 Liver	☐	☐

Right-click Add ROI

Edit an ROI

To edit an ROI, double-click the ROI to be edited to select it and click on the **Edit ROI** button ✎. A popup window will opens and allow the user to change the name, color, transparency (Alpha), visibility, and state of immutability of the ROI. To make ROIs immutable, check the boxes in the 'I' column.



ROI	H	I
■ background		☐
🟥 Heart	☐	☐
🟦 LeftKidney	☐	☐
🟨 Liver	☐	☐

Edit ROI: 2-blue

Name: LeftKidney

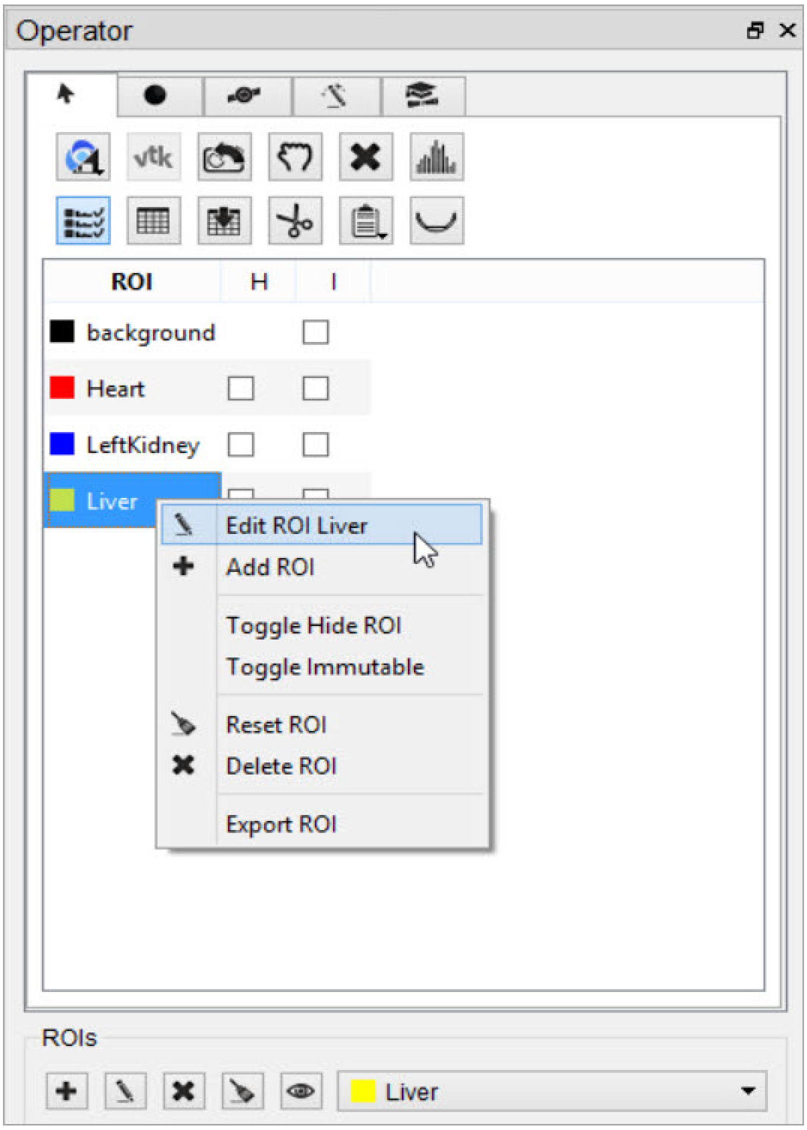
Color: 🟦 blue

Alpha: 50 % 100 %

☐ Hidden ☐ Immutable

Edit ROI

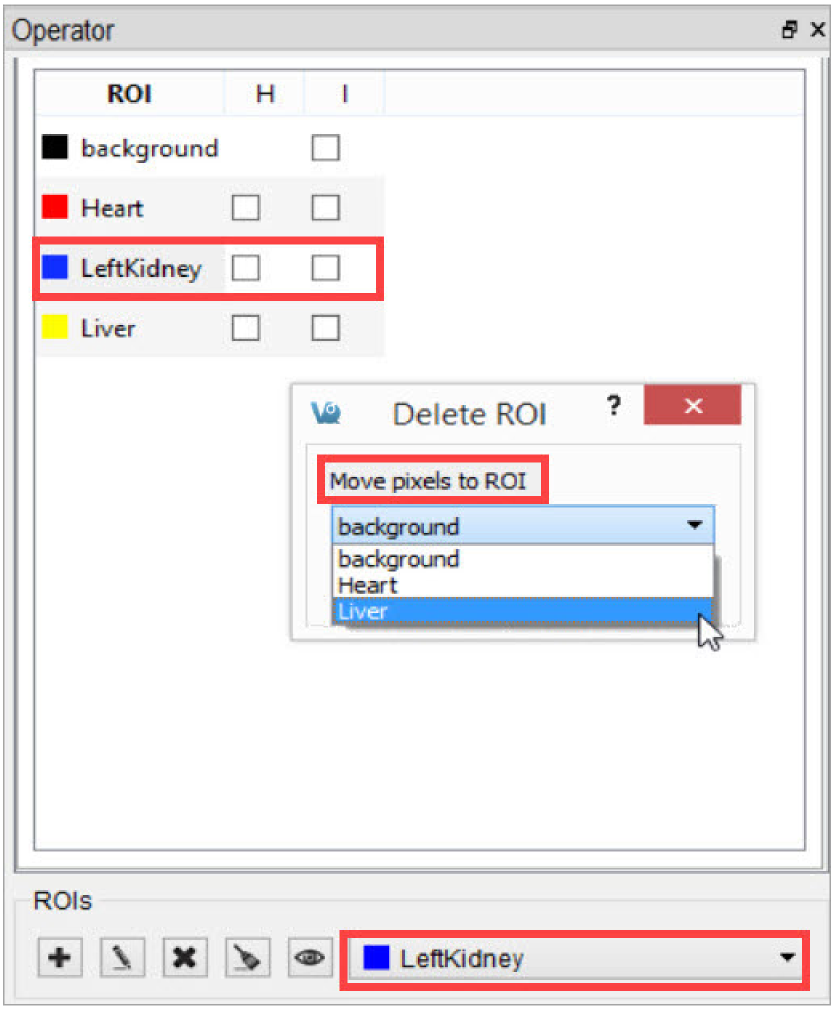
Another option is to right-click on any ROI in the operator and select **Edit ROI**.



Right-click Edit ROI

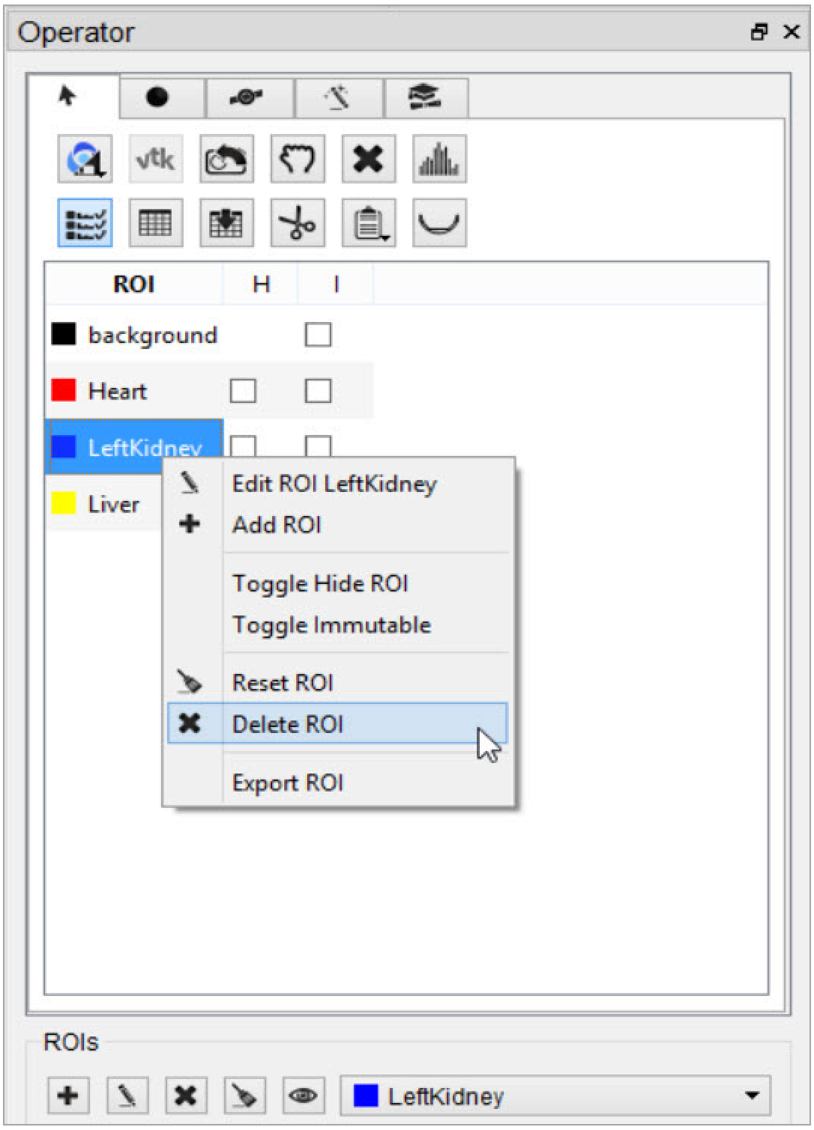
Delete an ROI

To delete an ROI, double-click the ROI to be deleted to select it and click on the **Delete ROI** button ☒. A popup window will open and allow the user to move the pixels of the selected ROI to either the background or another ROI.



Delete ROI

Another option is to select one or many of the existing ROIs, right click, and select **Delete ROI**.

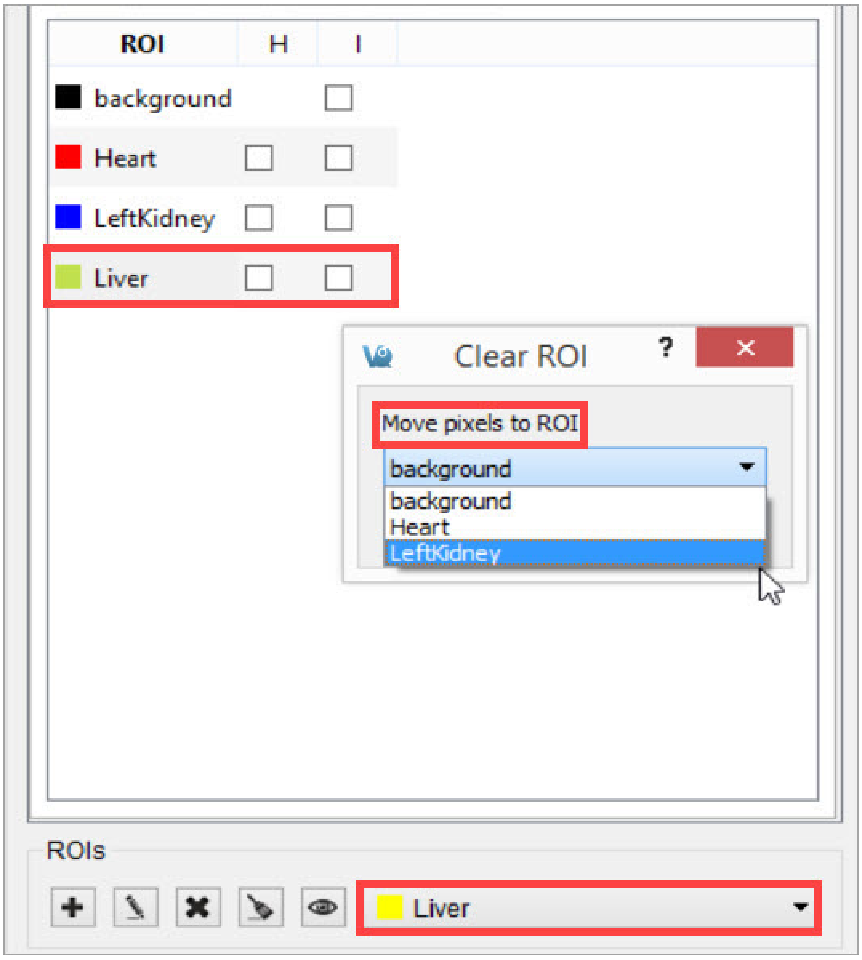


Right-click Delete ROI

Note: The ROI will no longer appear in the drop-down menu after being deleted.

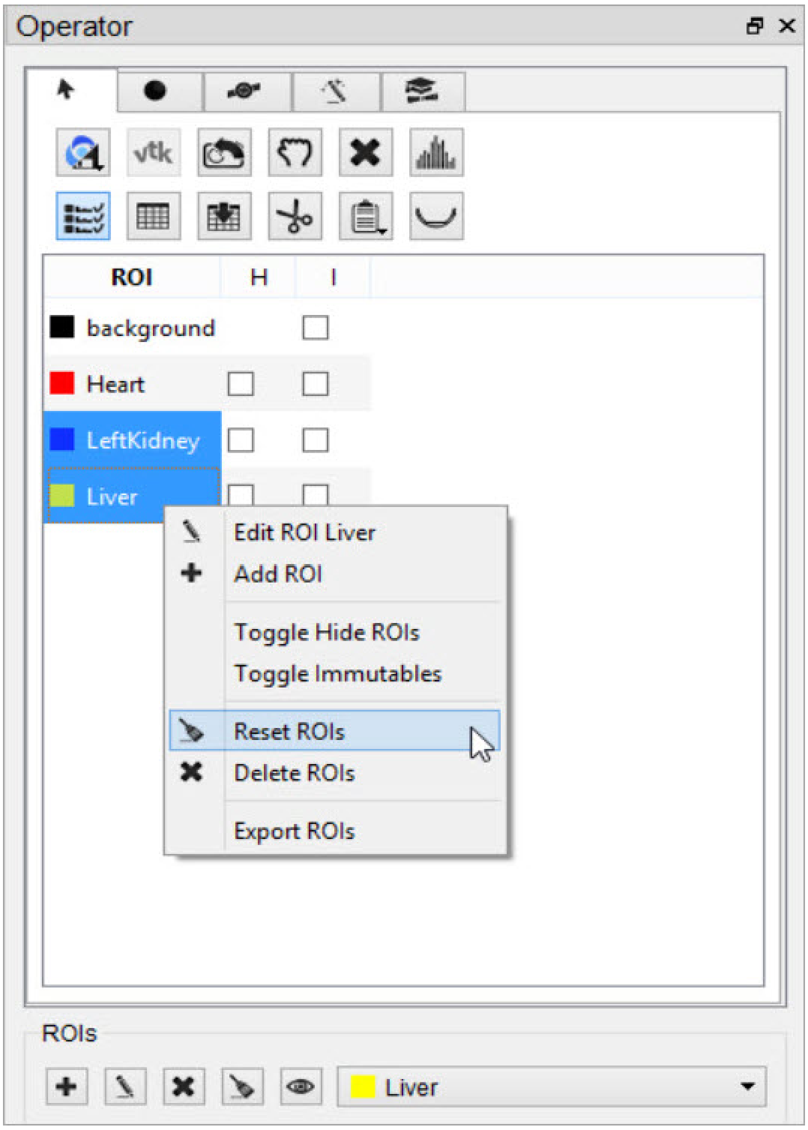
Reset an ROI

To reset an ROI, double-click the ROI to be reset to select it and click on the **Reset ROI** button . A popup window will open and allow the user to move the pixels of the selected ROI to either the background or another ROI.



Reset ROI

Another option is to select one or many of the existing ROIs, right click, and select **Reset ROI**.



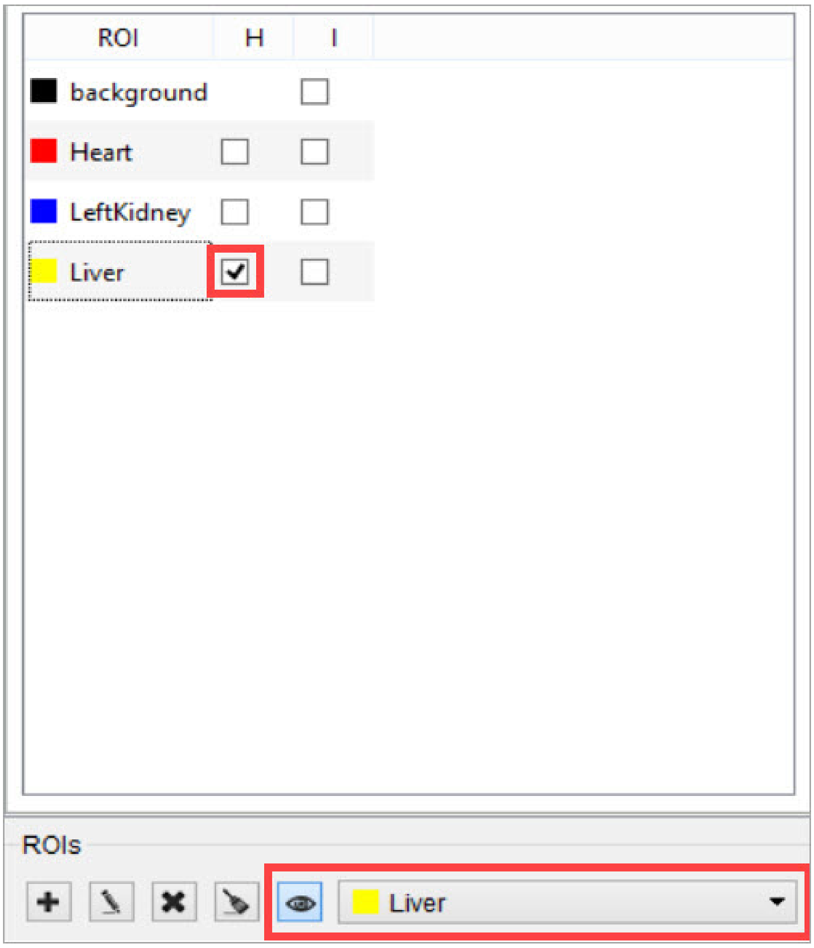
ROI	H	I
■ background		☐
🟥 Heart	☐	☐
🟦 LeftKidney	☐	☐
🟨 Liver	☐	☐

Right-click Reset ROI

ℹ **Note:** The ROI will still exist after it has been reset, but it will no longer have any voxels associated with it.

Hide an ROI

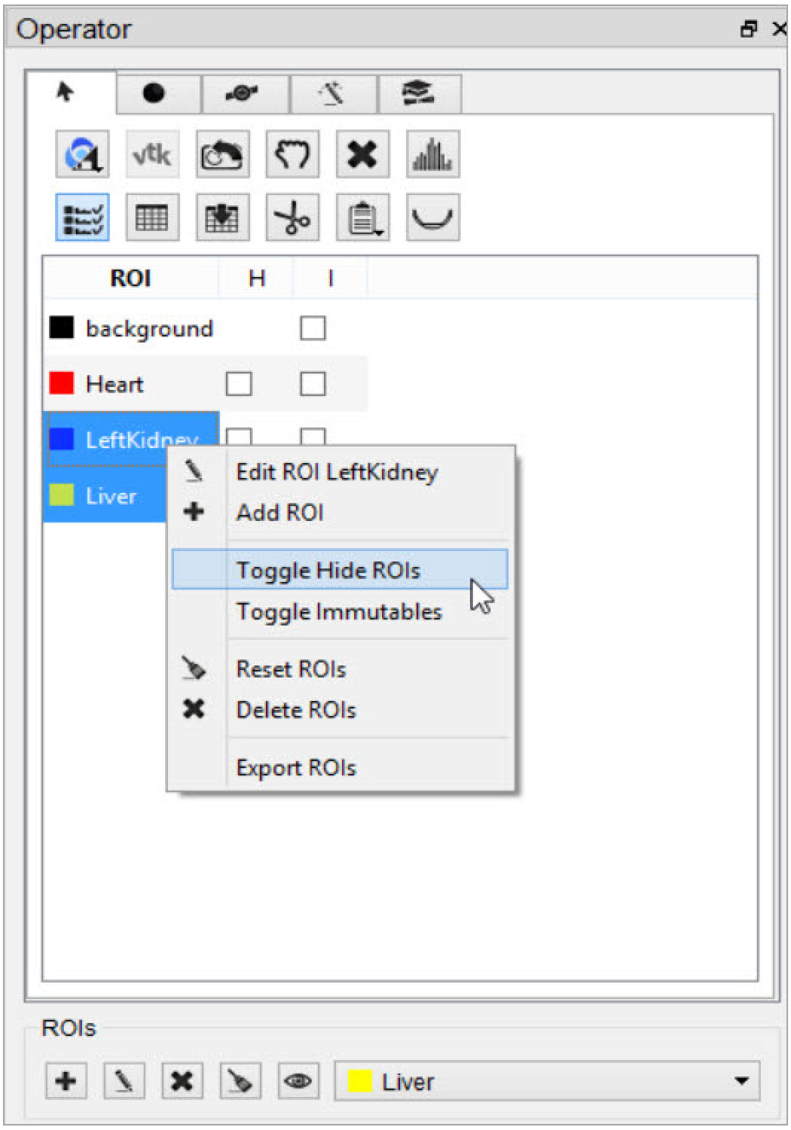
To hide an ROI in the slice and MIP views without deleting it, double-click the ROI to select it and click on the **Hide ROI** button 👁.



ROI	H	I
⬛ background		☐
🟥 Heart	☐	☐
🟦 LeftKidney	☐	☐
🟨 Liver	☑	☐

Hide ROI

Another option is to select any one or all of the desired ROIs, right click, and select **Toggle Hide ROI(s)**. All selected ROIs will become hidden.

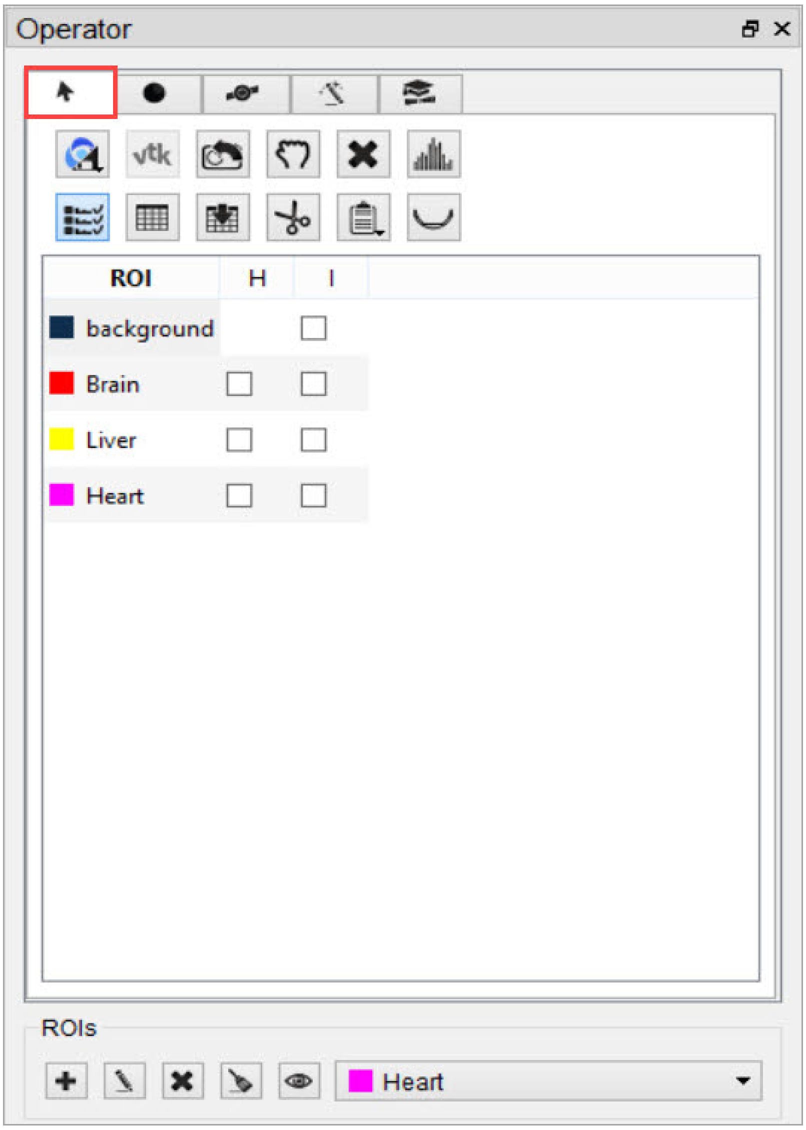


Right-click Hide ROI

Note: If the ROI is not immutable, it can be edited even if it is hidden.

ROI Loading, Saving, and Quantification Tools

The first tab in the 3D ROI Operator window features tools for basic input/output operations, quantification, and viewing functionality. To freely navigate through the slices with the cursor, this panel must be active.



ROI	H	I
background		☐
Brain	☐	☐
Liver	☐	☐
Heart	☐	☐

Heart

Basic ROI Functions

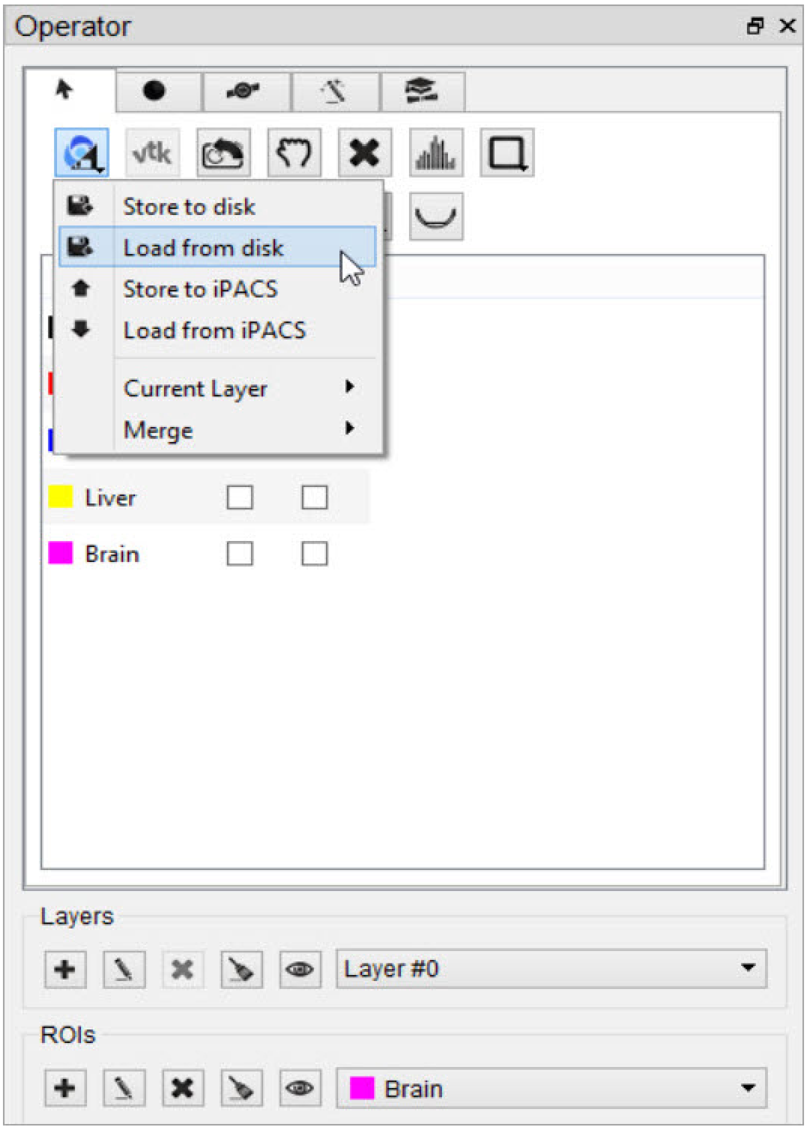
The buttons in this tab perform several functions within the operator.

Button	Function
🌐	Load or save an ROI from disk or iPACS
vtk	Render ROIs in the MIP view
↺	Reset the camera view
✖	Reset all ROIs
📊	Show the image histogram
▦	Show the quantification table
▦	Export the quantification table to disk
✂	Perform a cut on an image using an ROI
📋	Perform a copy or paste on an image using an ROI
◡	Export ROIs into the Bed Removal tool

Load an ROI from Disk

The 3D ROI tool supports file formats of VQ 3D ROI (.rmha), RTSTRUCT DICOM (.dcm), and vtkStructuredPoints (.vtk). To load an ROI from disk, click the **Load ROI** button 🌐, select the **Load from disk** option and choose the desired ROI from the file browser.

Although RTSTRUCT files are intended to be paired with a referenced image, VQ allows you to load any RTSTRUCT even if it was not created for that image. If contours in the RTSTRUCT file overlap, the ROIs will be loaded in separate layers.

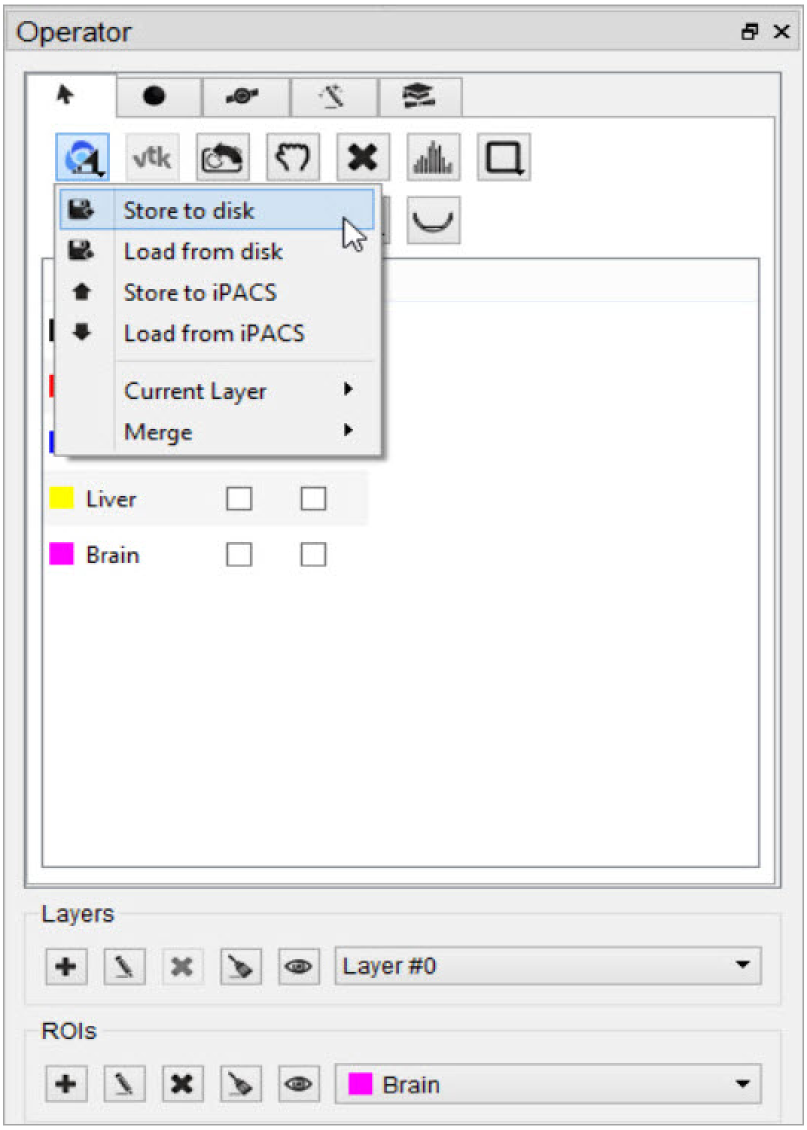


Load ROI from Disk

Save an ROI to Disk

To save an ROI to disk, click the **Load ROI** button, select the **Store to disk** option and specify a name and location for the file. All existing regions will be written to the same ROI file.

When saving RTSTRUCT files, keep in mind that the RTSTRUCT file format specifies contours using locations from a referenced image. If the referenced image was resampled, the origin was moved, or any other changes were made to the image in VQ that would change the coordinate space of the image, the currently loaded image will need to be saved as well. This is to enforce that the locations of the contour points in the RTSTRUCT file match the coordinate space of the new referenced image.

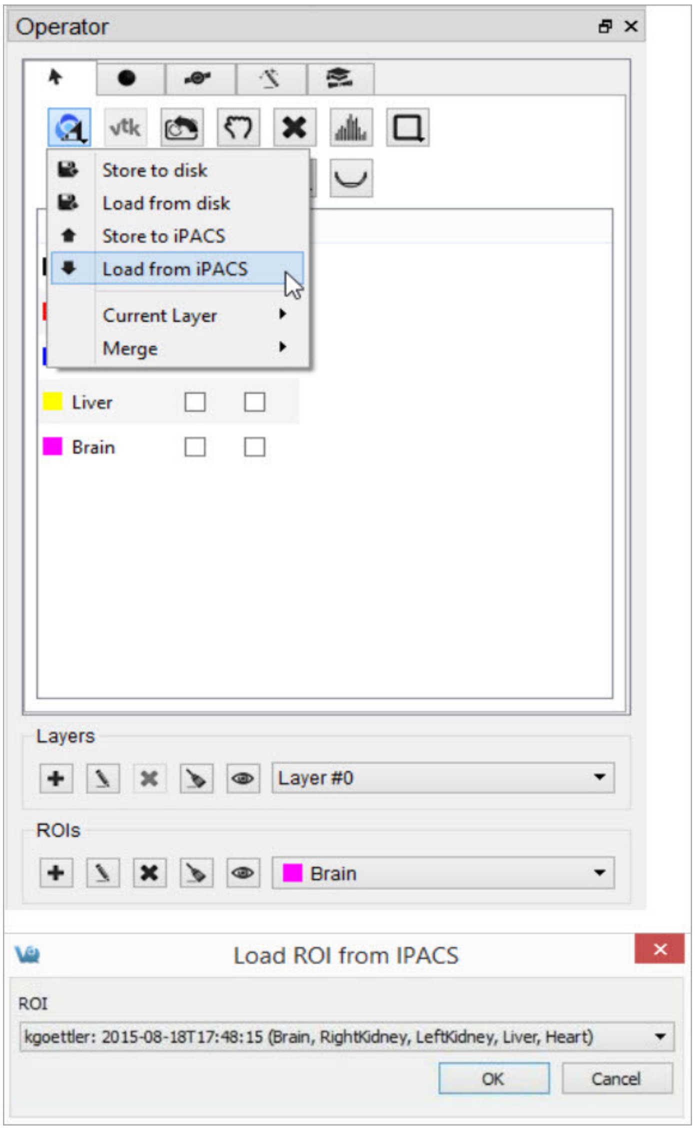


Save ROI to Disk

Load an ROI from an iPACS

To load an ROI from an iPACS, click the **Load ROI** button and select the **Load from iPACS** option. The image data currently loaded must have been retrieved from an iPACS, and there must be an ROI associated with that image already stored on the iPACS.

If only one ROI exists for the image, that ROI will automatically be loaded. If multiple ROIs exist, the user will be given a drop-down menu of available ROIs to choose from. The choices can be distinguished by the ROI creator's iPACS username, date and time of creation, region names, and file type (RMHA or RTSTRUCT).



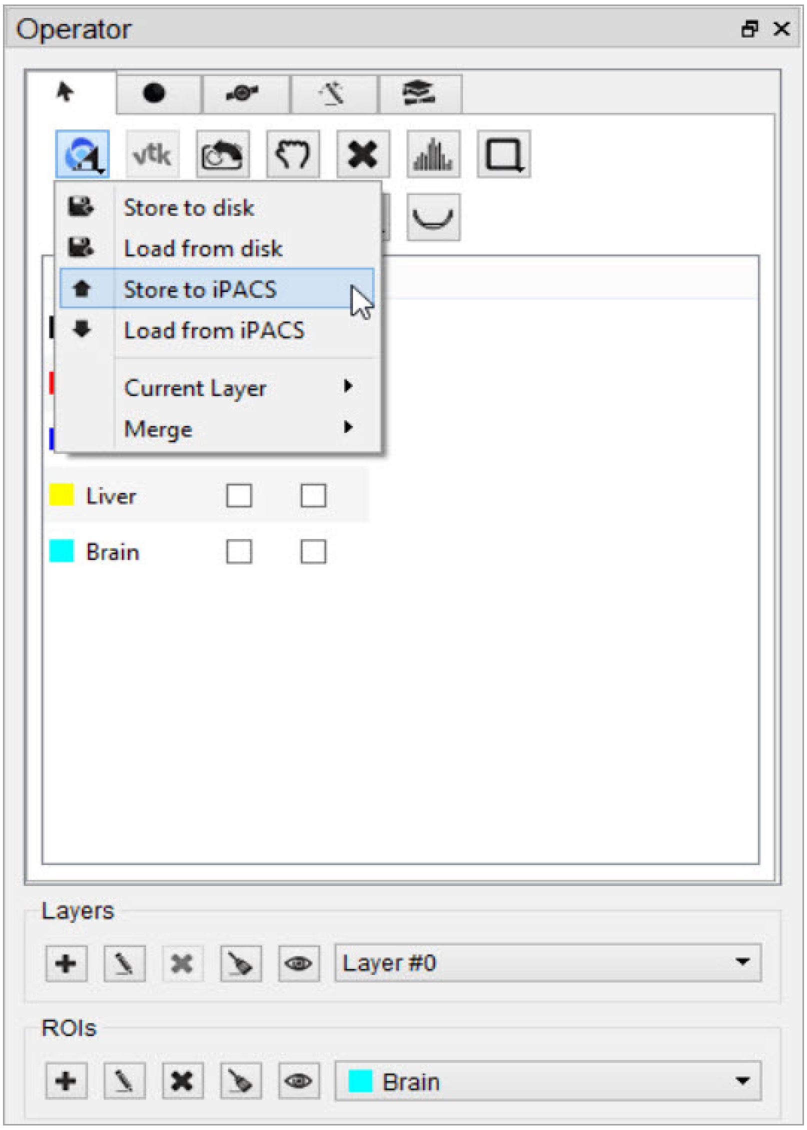
ROI: kgoettler: 2015-08-18T17:48:15 (Brain, RightKidney, LeftKidney, Liver, Heart)

Load ROI from iPACS

Save an ROI to an iPACS

To save an ROI to an iPACS, click the **Load ROI** button, select the **Store to iPACS** option, and select the desired format (RMHA or RTSTRUCT) of the file that will be uploaded. The ROI will be automatically associated with the current image. Unique filenames will be generated based on the creator's username and the patient's name from the image header. Previously saved ROIs will not be overwritten. The files will be saved to a subdirectory of the current project on the WebDisk, named roi.

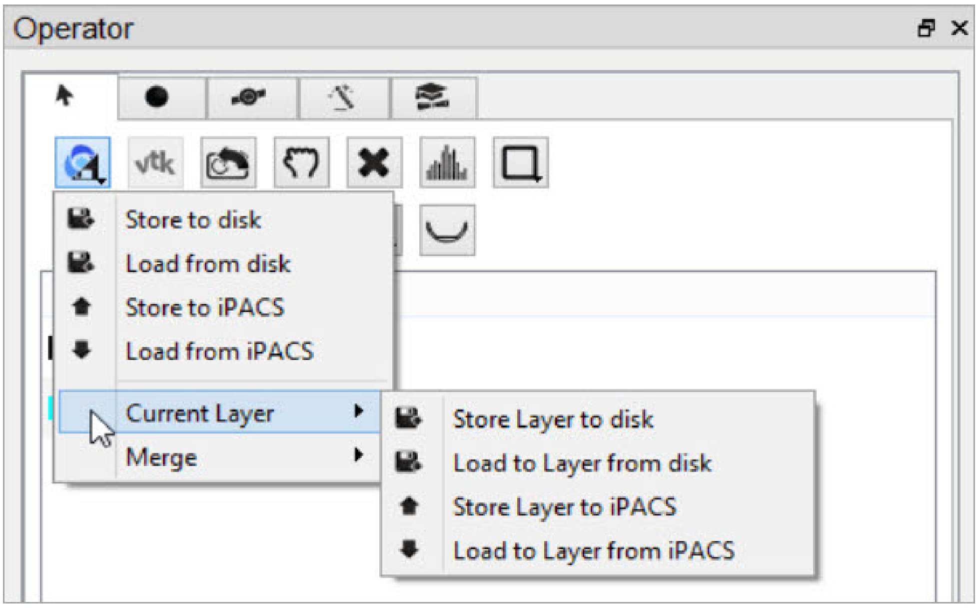
Similarly to saving RTSTRUCT files locally, the contour points in the generated RTSTRUCT will be in the coordinate space of the current image, so if resampling or other changes that affect the image's coordinate space were performed on the image in VQ, the current image will now be the referenced image for any RTSTRUCT. The reference image should be saved to the iPACS before saving the RTSTRUCT so that the RTSTRUCT files are associated with the referenced image matches their coordinate space.



Save ROI to iPACS

Select Current Layer

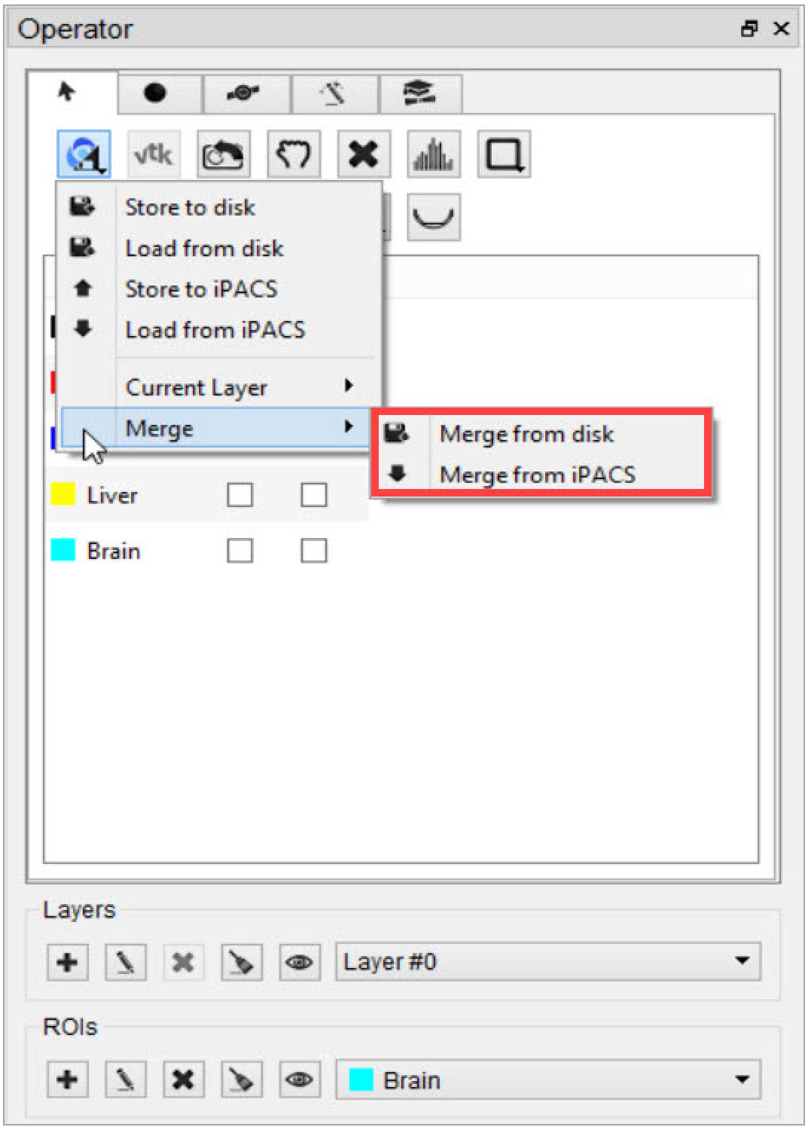
By default, all layers are loaded or saved when loading or saving an ROI. However, the user can specify to save only a single layer by loading or saving the current layer. This functionality is only supported for RMHA files. The RTSTRUCT file format does not support layers because contours can be overlapping.



Load or Save Current Layer

Merge ROIs from an iPACS or Disk

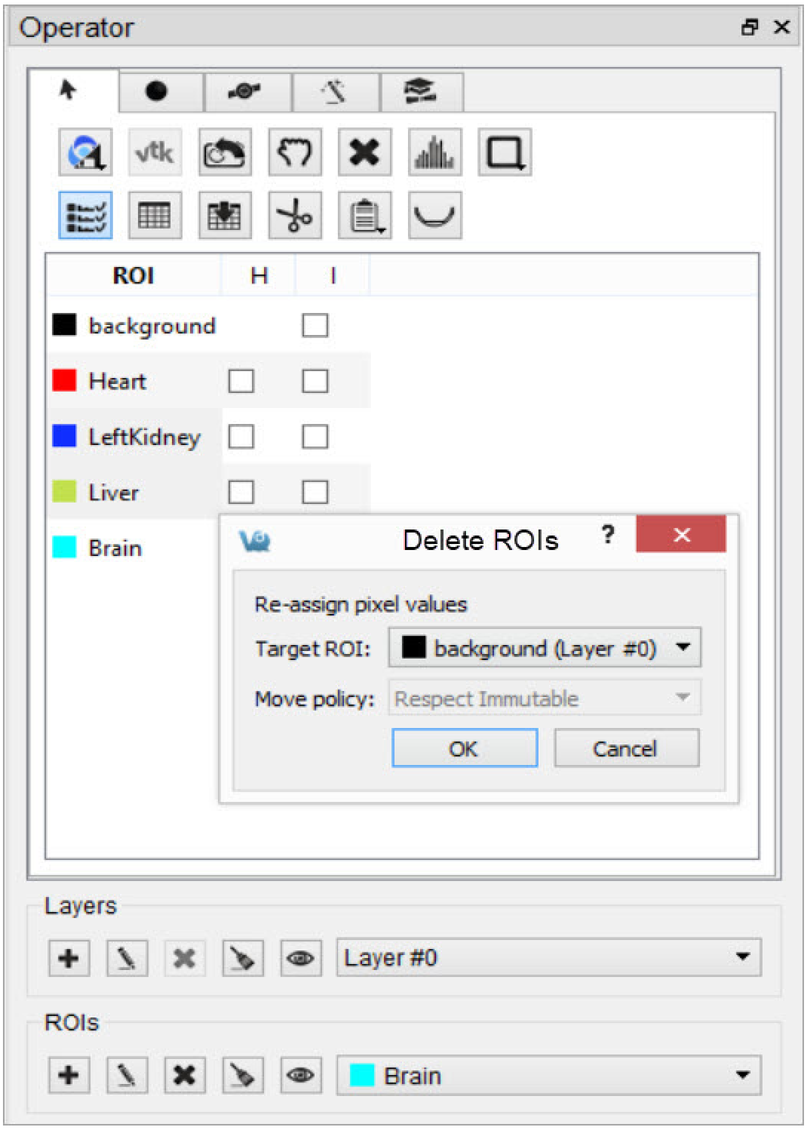
To append previously stored ROIs to a set of ROIs currently open in the 3D ROI tool, click the**Load ROI** button and select **Merge from iPACS** or **Merge from disk**, depending on where the additional ROIs are stored. The additional ROIs associated with that image will be appended to the currently open ROI set in the 3D ROI viewer. Previously saved ROIs will not be overwritten.



Merge ROI

If there is any overlap of existing and merged ROIs, a new ROI will be created and named as a combination of the two ROIs listed names. For example, if a portion of a “Heart” and “Liver” ROI overlap after a merge, the new combined ROI created will be named “Heart/Liver”, and consist of only the specific volume of Heart and Liver that overlap.

To associate the combined ROI with the proper ROI, right-click the combined ROI and select **Delete ROI**. A popup window will open and allows the user to move the pixels of the selected ROI to either the background or another ROI. Selecting “background” will delete the ROI all together.



ROI	H	I
■ background		☐
🟥 Heart	☐	☐
🟦 LeftKidney	☐	☐
🟩 Liver	☐	☐
🟦 Brain		

Target ROI: ■ background (Layer #0)

Move policy: Respect Immutable

Layer #0

Brain

Associate Combined ROIs

Center view on ROI

To center the field of view on the center of mass of a particular ROI, double click the ROI in the ROI Table.

Render ROIs in the MIP View

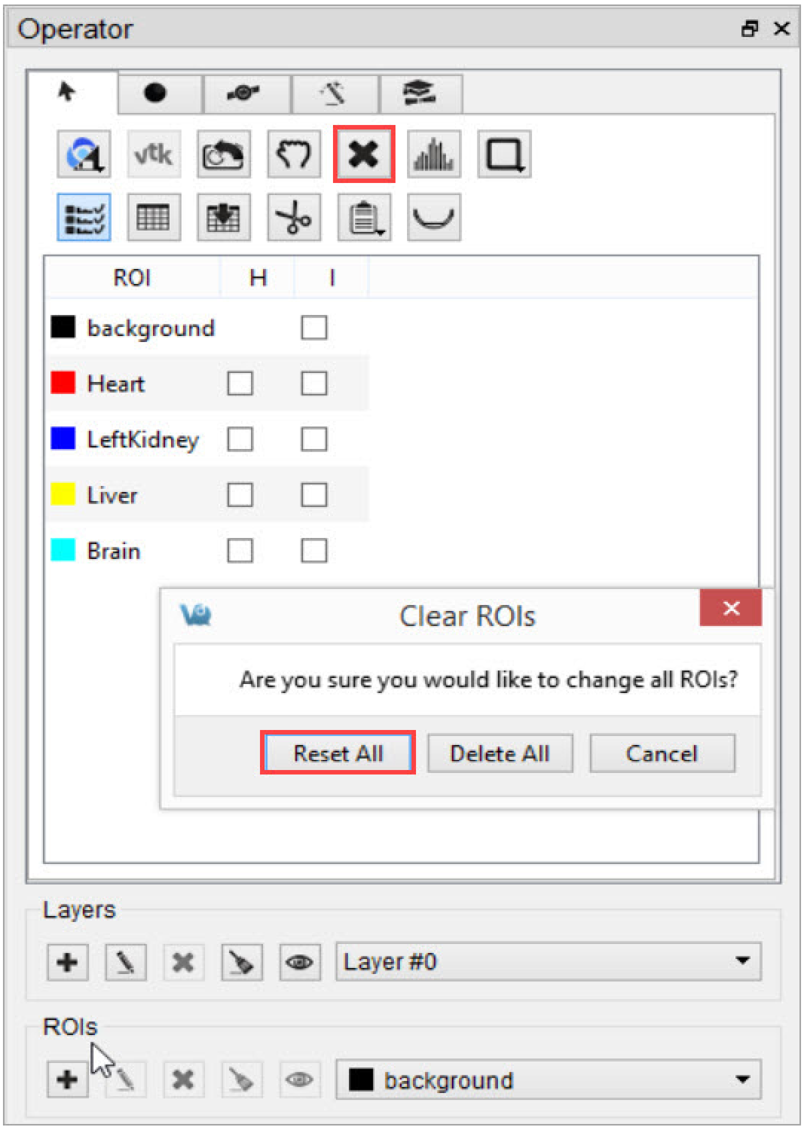
To trigger a new rendering of the current viewed ROIs in the MIP view, click the **VTK** button vtk .

Reset the Camera View

To reset the MIP view to the original orientation and size, click the **Reset Camera** button 📷 .

Reset all ROIs

To reset all existing ROIs, click the ✖ button and select **Reset All**. Empty ROIs will still exist under the same naming and coloring scheme.

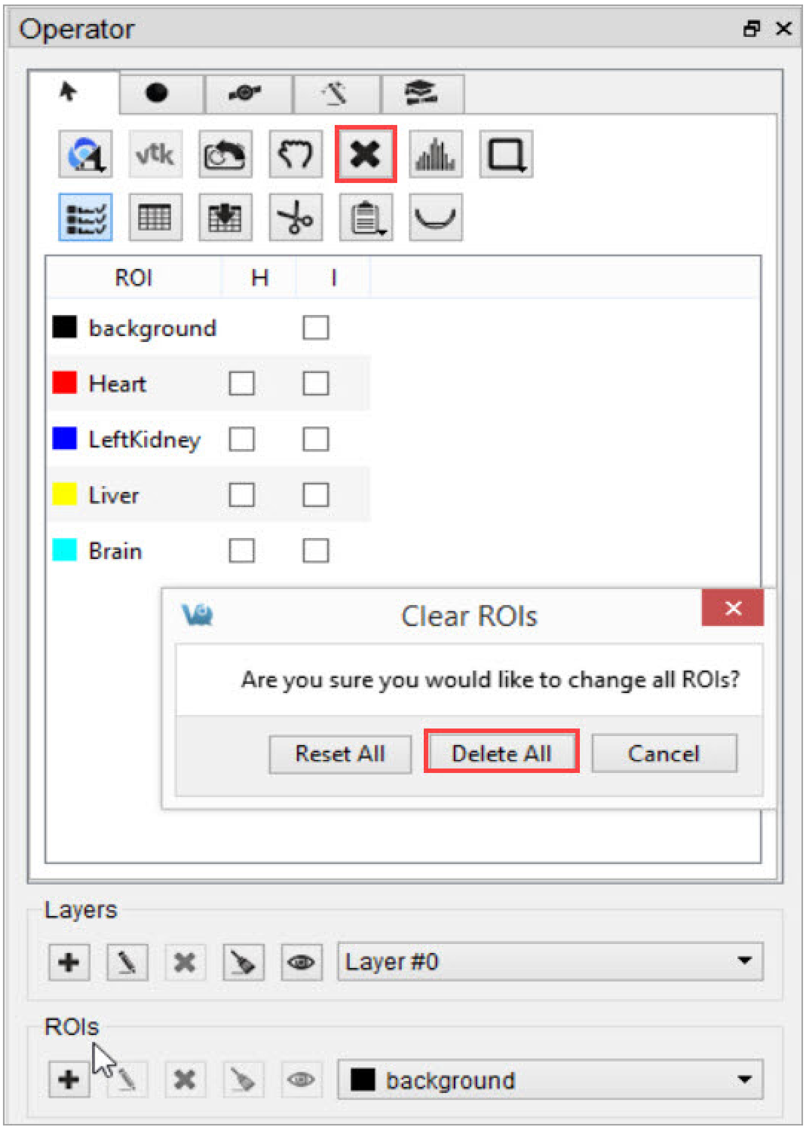


ROI	H	I
■ background		☐
🟥 Heart	☐	☐
🟦 LeftKidney	☐	☐
🟨 Liver	☐	☐
🟦 Brain	☐	☐

Are you sure you would like to change all ROIs?

Reset All ROIs

To delete all ROIs completely, click ☒ and select **Delete All**. The background will be the only thing left in the ROI menu.



ROI	H	I
■ background		☐
🟥 Heart	☐	☐
🟦 LeftKidney	☐	☐
🟨 Liver	☐	☐
■ Brain	☐	☐

Are you sure you would like to change all ROIs?

Delete All ROIs

Show the Image Histogram

To view a histogram of the image or any subset of the image determined by an ROI, click the **Show Histogram** button. Choose the image used to generate the histogram by selecting it from the **Data Set** drop-down menu. The portion of the image contributing to the histogram can be set under the **ROI Controls** by selecting an ROI from the drop-down menu.

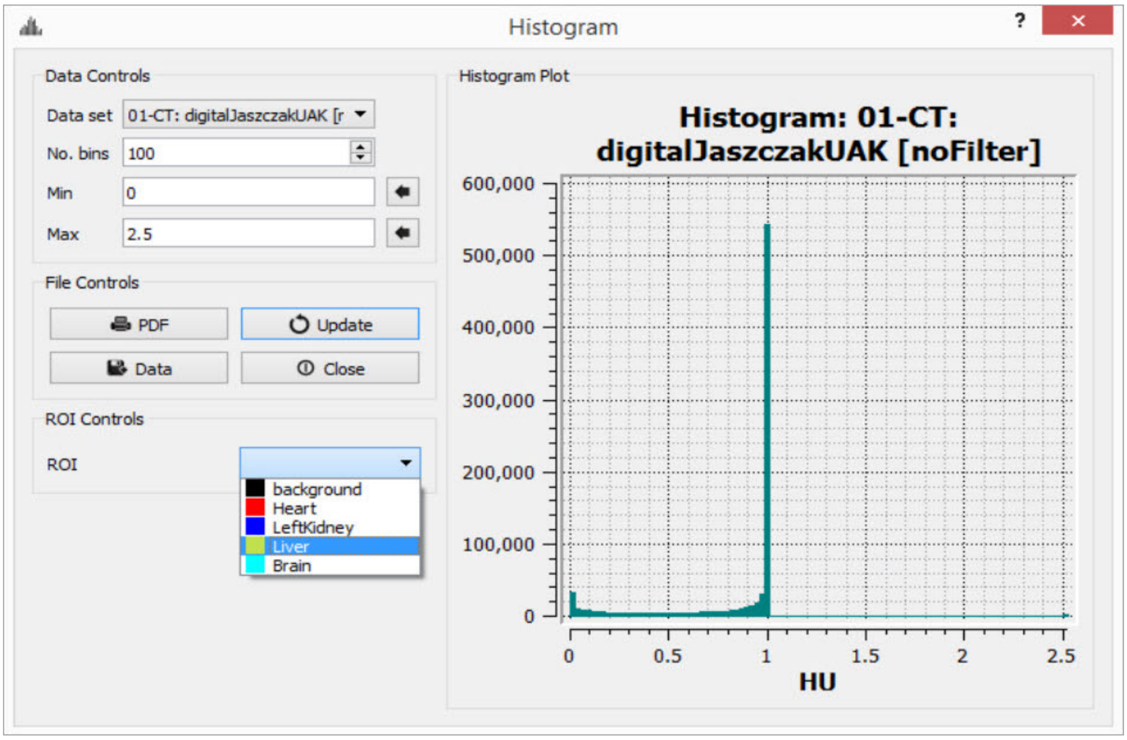
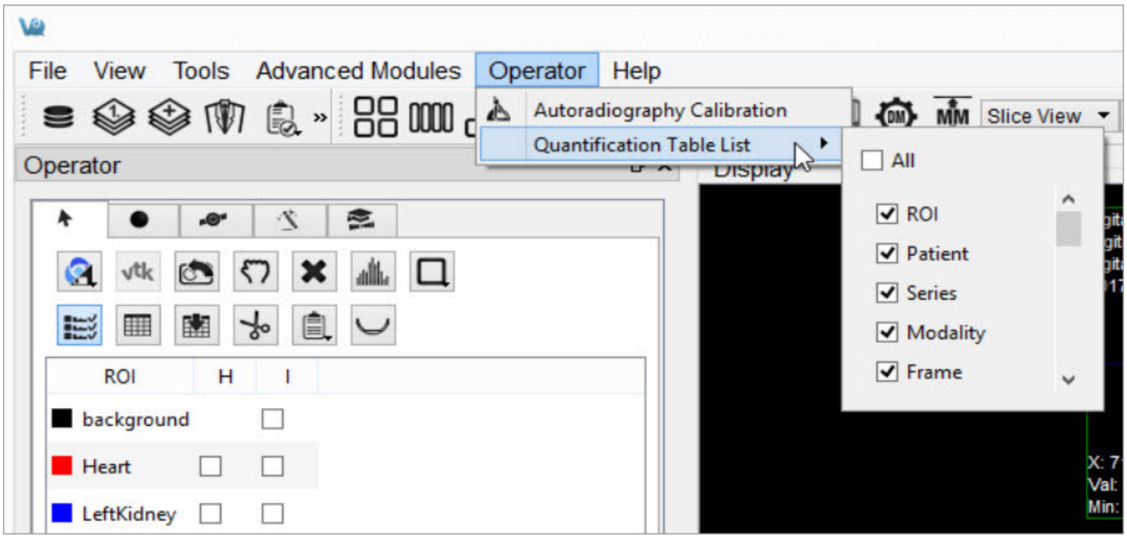

Data set 01-CT: digitalJaszczakUAK [r
No. bins 100
Min 0
Max 2.5

Image Histogram

Set Quantification Table Columns

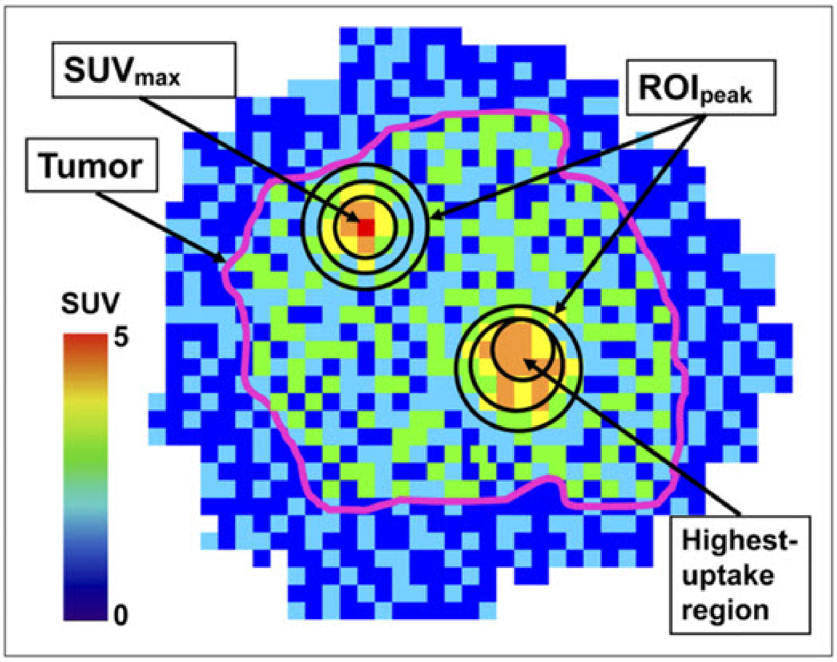
To determine which quantitative fields will be displayed in the quantification table and stored to the iPACS, if applicable, go to the Operator tab on the main menu, then select **Quantification Table List**.



Set Quantification Table Columns

The available quantification values are described below:

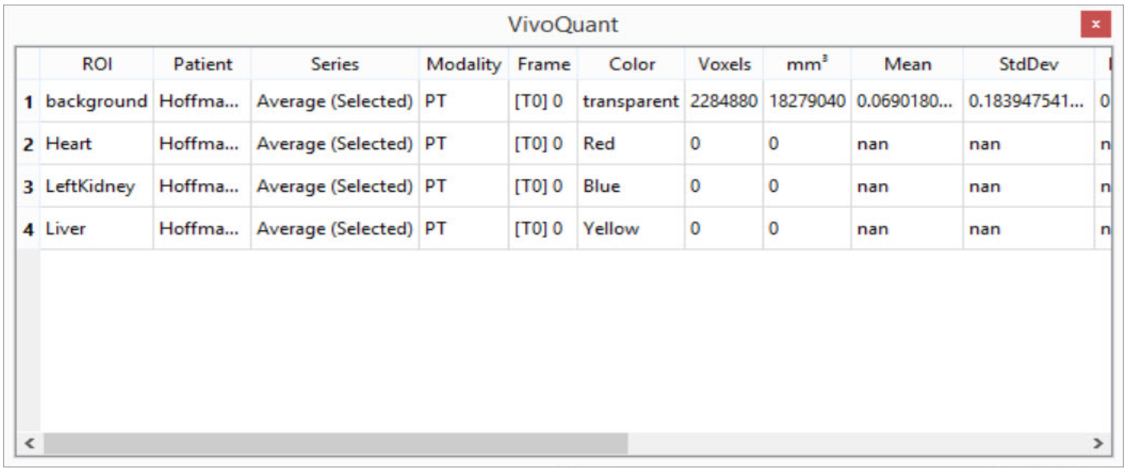
Option	Description
ROI	Name of the ROI. You can left-click this field to enter comments.
Patient	Patient’s name for the current study.
Series	Specific data set in the study from which the data was calculated.
Modality	Modality from which the data values for the row were calculated.
Color	Color of the ROI as drawn in the display.
Voxels	Total number of voxels contained in the selected ROI.
Volume	Volume of the selected ROI in units of cubic millimeters.
Mean	Arithmetic mean of values of voxels contained in the ROI.
StdDev	Standard Deviation of values of voxels contained in the ROI.
Min	Minimum value of all voxels contained in the ROI.
Max	Maximum value of all voxels contained in the ROI.
Median	Median value of all voxels contained in the ROI.
Sum	Sum of all voxels contained in the ROI, sometimes interchangeable with ‘Uptake’
Unit	Unit of voxels in the selected dataset.
Conc 10%	Concentration (mean/volume) of the 10th Percentile of voxels contained in the ROI.
Conc 50%	Concentration (mean/volume) of the 50th Percentile of voxels contained in the ROI.
Conc Peakregion	Concentration (mean/volume) of the 3x3x3 cube of voxels with the greatest mean of all 3x3x3 cubes of voxels contained within the ROI. Referred to below as Highest-uptake region.
Conc Peakmax	Concentration (mean/volume) of the 3x3x3 cube of voxels that has at its center the maximum voxel of the voxels contained in the ROI. Referred to below as SUVmax.
Conc Max	Concentration (mean/volume) of the maximum voxel of the voxels contained in the ROI.
Conc	Concentration (mean/volume) of all the voxels contained in the ROI.
Conc Unit	Unit of voxels in the selected data set over volume (mm3).



"Impact of the Definition of Peak Standardized Uptake Value on Quantification of Treatment Response". Vanderhoek, et al. J Nuclear Medicine, 2012. [Link](#) .

Show the quantification table.

To display the quantification table, including all existing ROIs, click the **Show Table** button ▦ .



	ROI	Patient	Series	Modality	Frame	Color	Voxels	mm³	Mean	StdDev
1	background	Hoffma...	Average (Selected)	PT	[T0] 0	transparent	2284880	18279040	0.0690180...	0.183947541...
2	Heart	Hoffma...	Average (Selected)	PT	[T0] 0	Red	0	0	nan	nan
3	LeftKidney	Hoffma...	Average (Selected)	PT	[T0] 0	Blue	0	0	nan	nan
4	Liver	Hoffma...	Average (Selected)	PT	[T0] 0	Yellow	0	0	nan	nan

Show Quantification Table

Export the quantification table to disk.

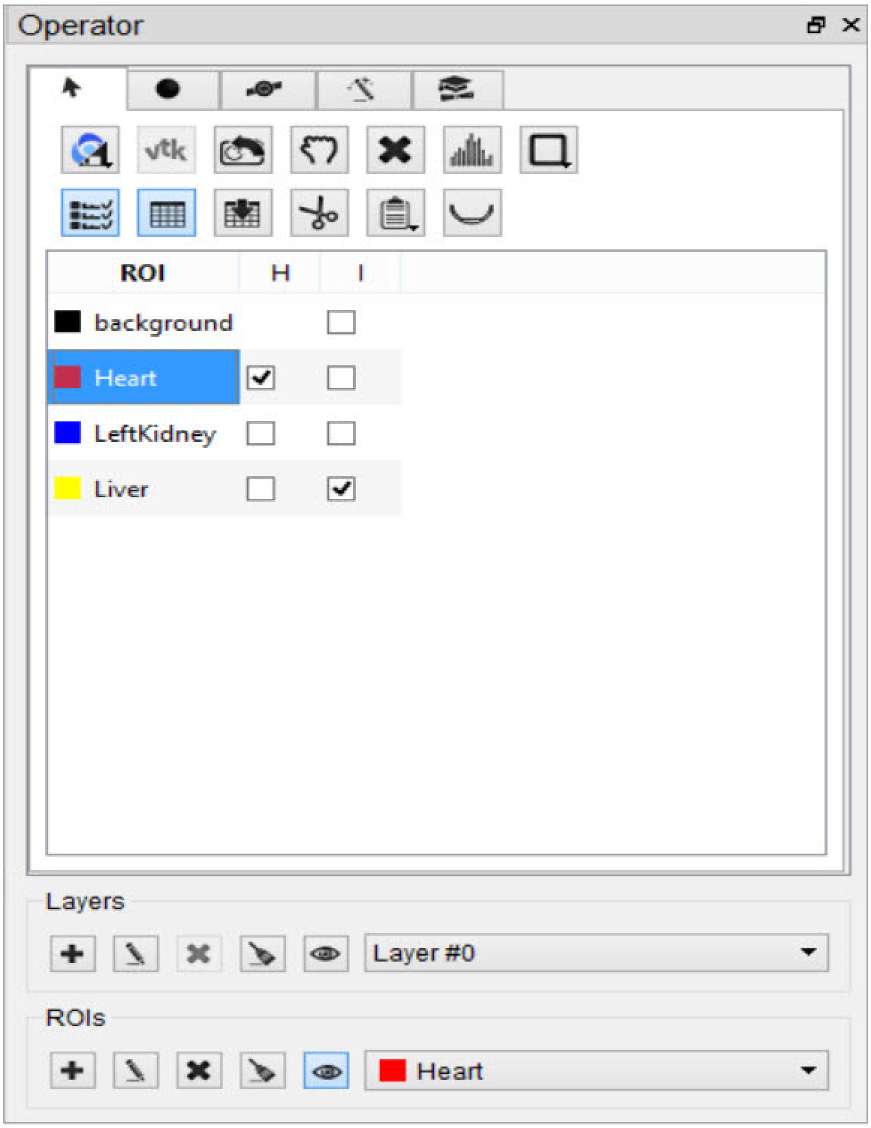
To export the quantification table to disk as a comma-separated values (.csv) file, click the **Export Table** button ▦ .

Perform a cut on an image using an ROI.

To remove voxels from image data based on an ROI, choose the desired ROI from the ROI selector and click the **Cut ROI** button ✂ . All visible images will be cut and the ROI will remain unchanged. The cut tool is useful for eliminating undesired features in images, such as metal instrumentation that may appear in some CTs.

Show or Hide an ROI

To hide an ROI, Check the boxes in the **H** column. An ROI can also be hidden by selecting it and clicking on the **Hide/Show** button .



ROI	H	I
⬛ background		☐
🟥 Heart	☑	☐
🟦 LeftKidney	☐	☐
🟨 Liver	☐	☑

Show/Hide ROI

Copy or Paste the 3D ROI

Click the **Copy/Paste ROI** button to copy and/or paste ROIs between instances of VivoQuant.

Export ROIs into the Bed Removal Tool

Click the **Export to Bed Removal** button to export ROIs into VivoQuant's **Bed Removal** tool.

Import Layers and ROIs with Overlapping Regions

Certain image formats, such as PMOD VOI and DICOM RTSTRUCT, support overlapping regions inherently. VivoQuant's 3D ROI tool loaders handle the overlap appropriately.

ℹ **Note:** Overlapping ROIs should be assigned to different layers.

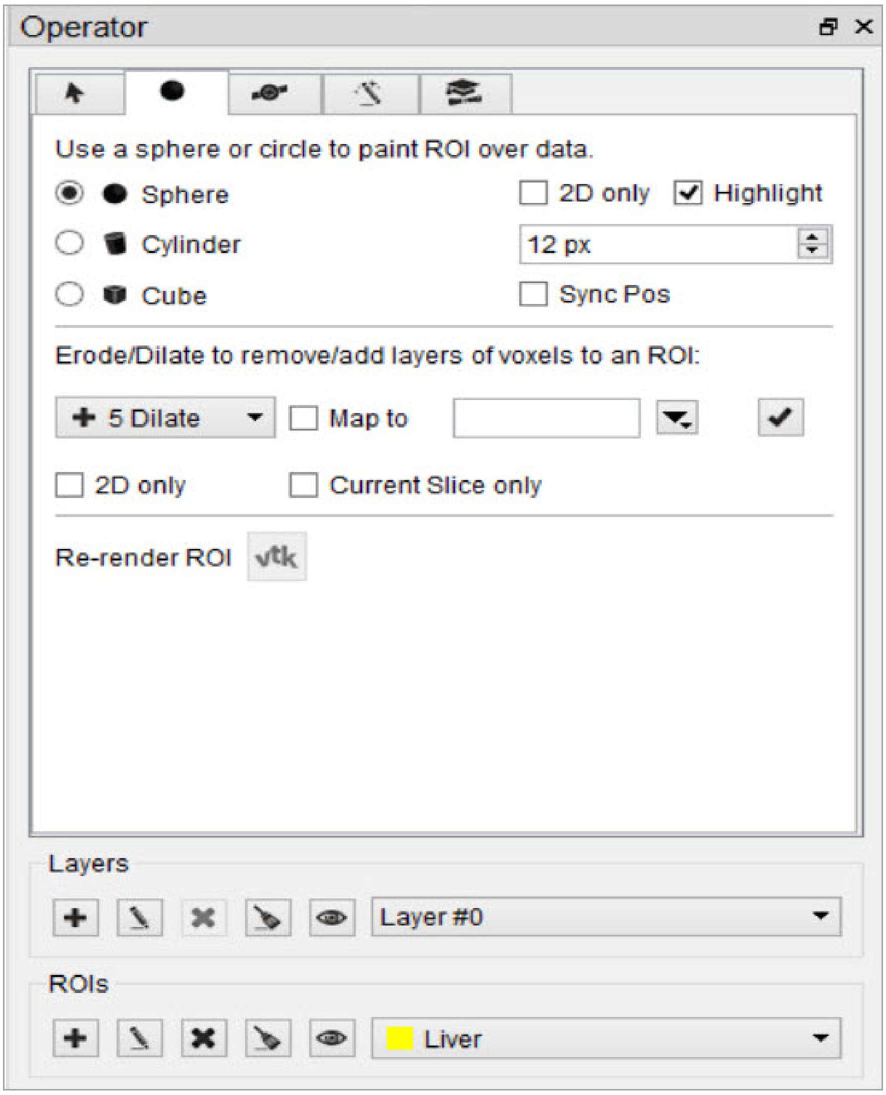
Not only has the **3D ROI Tool** been updated to be compatible with overlapping ROIs, but numerous pre-existing features also successfully operate on the active layer supporting overlapping ROIs. These include: Segmentation Algorithms, Painting in the slice views, Tooltip Pixel hovers, Reorientation Operator, Modeling Operator, Multi-view Visibility, VTK MIP, AutoRAD, MAS, Brain Atlas and Smoothing Operator.

☑ **Tip:** The number of imported layers should not exceed the limit of 8. Number of layers should be **efficient**. Do not create one layer per region; but rather, collapse regions to the same layer where possible.

Painting Tools

There are several paintbrushes to choose from when creating an ROI. The sphere ●, cylinder, or cube paintbrush can be selected by clicking the corresponding radiobutton on the Painting tab ●. The radius of the paintbrush can be set by changing the number of pixels shown in the numerical spin box. These 3D paintbrushes extend across multiple slices. To activate 2D mode, mark the '2D only' checkbox. In 2D mode, the paintbrush will only paint on the current slice.

Note: An ROI must be added before the painting tools can be used.



Use a sphere or circle to paint ROI over data.

● Sphere ☐ 2D only ☑ Highlight
○ Cylinder 12 px
○ Cube ☐ Sync Pos

Erode/Dilate to remove/add layers of voxels to an ROI:

+ 5 Dilate ☐ Map to

☐ 2D only ☐ Current Slice only

Re-render ROI

Layers: Layer #0

ROIs: Liver

Painting Tools

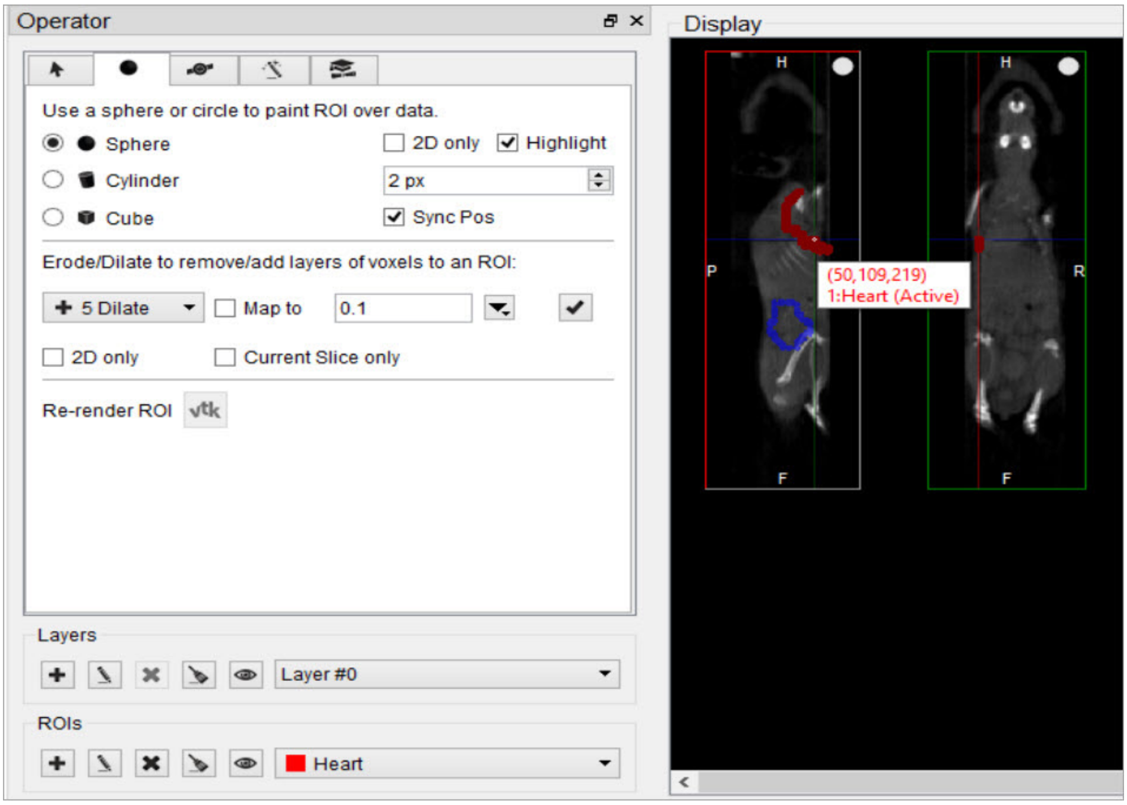
ROIs can be drawn freely on any of the three slice views. The view currently being drawn in will be denoted as Active in the upper left corner.

Each voxel can only belong to a single ROI. Painting over an existing ROI with a new ROI will place the painted voxels in the new ROI, unless the existing ROI is immutable. (See Edit an ROI to learn how to make an ROI immutable.)

To erase voxels from an existing ROI, paint over the existing ROI with the ROI selector set to Background. Alternatively, set the ROI selector to the existing ROI (from which to erase voxels) and hold down the Shift key while drawing. The Shift key activates the background ROI for the painting tool, even if another ROI is set in the ROI selector.

Sync Pos

If "Sync Pos" is checked, then the non-Active slice views will be updated in real time to match the position of the drawing tool on the Active slice. When this option is selected, drawing times will typically be slower.



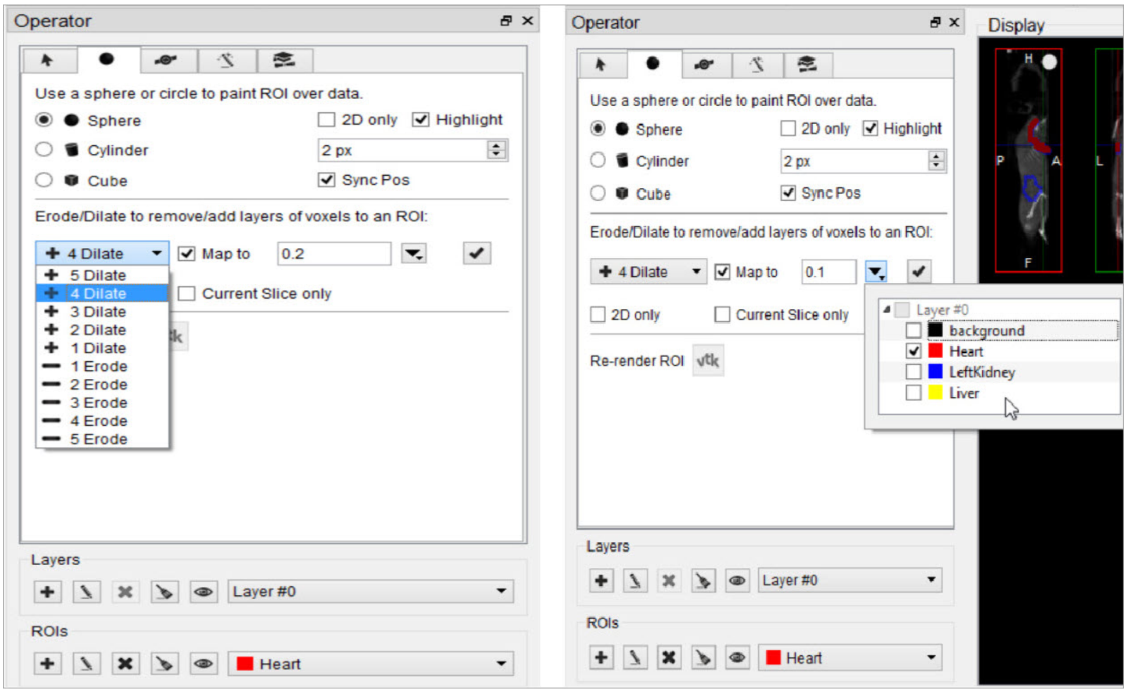
Sync Pos Option

Erode/Dilate.

The Erode/Dilate tool can be used to remove or add up to 5 layers of voxels from the input ROI. The erosion or dilation will be applied to the currently selected ROI in the ROI selector.

If you would like the voxels that are being added or removed from the ROI to be put in an ROI other than the one currently selected, mark the ‘Map to’ checkbox and choose the ROI to put the new voxels in from the drop-down menu to the right ▼
.

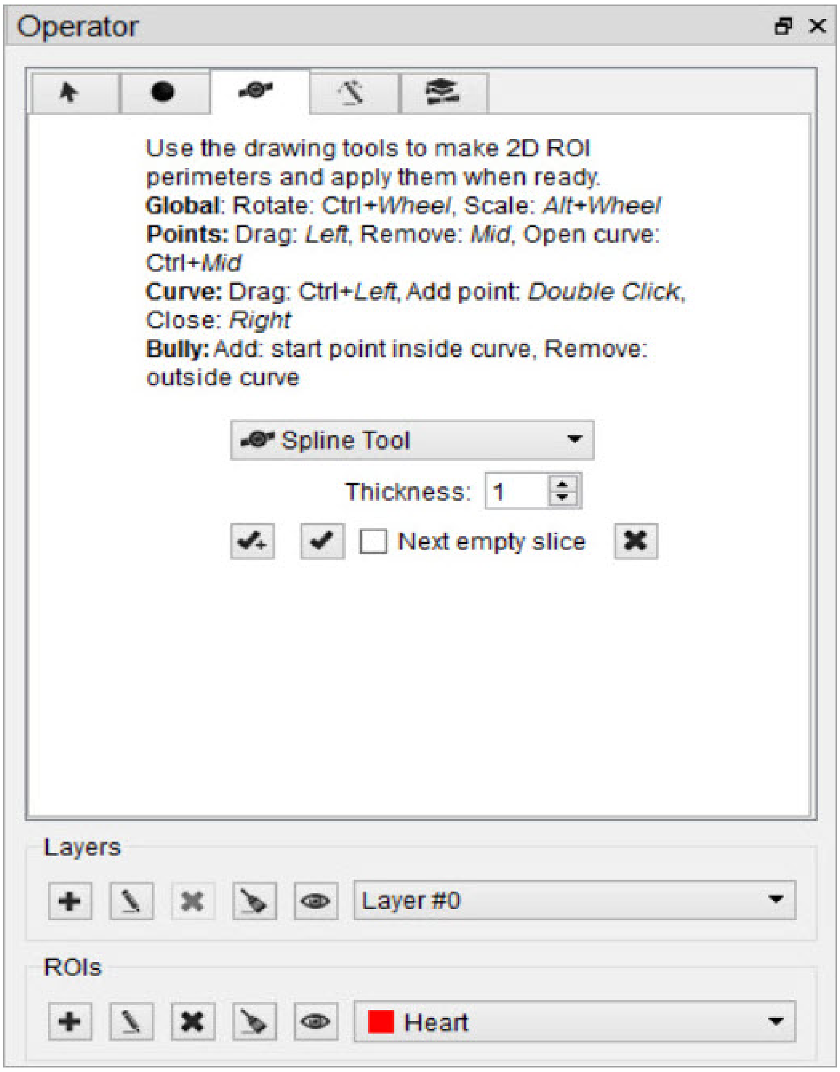
To perform the erosion or dilation, click the **Checkmark** button ✓ .



Perform Erosion/Dilation

2D Drawing Tools

The 2D drawing tools match the options available within the Projection++ Tool.



Use the drawing tools to make 2D ROI perimeters and apply them when ready.
Global: Rotate: Ctrl+*Wheel*, Scale: *Alt+Wheel*
Points: Drag: *Left*, Remove: *Mid*, Open curve: Ctrl+*Mid*
Curve: Drag: Ctrl+*Left*, Add point: *Double Click*, Close: *Right*
Bully: Add: start point inside curve, Remove: outside curve

Spline Tool

Thickness: 1

☐ Next empty slice

Layers

Layer #0

ROIs

Heart

2D Drawing Tools

Choose the desired tool from the drop-down menu to begin drawing. Use the ☒ button to delete a contour (this will not delete the ROI). Use the ☑ button to add the voxels within a drawn contour to the currently selected ROI.

	Spline tool
	Bully tool
	Freehand tool
	2D Thresholding tool

Spline Tool

Use the spline tool to define points between which smooth curves will be filled in. The base points can be moved by using the left mouse button to drag them. Additionally, points can be deleted by click on a middle point, or added by double clicking on a curve. Once a shape has been closed by clicking the right mouse button, it can be re-opened by hitting Shift + middle click on a point.

Bully Tool

Use the bully tool to nudge the drawn boundary inward or outward with a circle-shaped cursor. The cursor size can be changed using the paintbrush size selector in the Painting Tools panel. This mode provides an efficient way to fine-tune an ROI made in Spline or Freehand mode. You may select which image data you want to use as the input ("Ref" is the first image loaded in the Data Manager, "Inp1" is the second, etc.) and the thickness of the tool, in the bully tool and for the following three tools as well.

Freehand Tool

A freehand region may be drawn by moving the mouse while holding down the left mouse button. The region may be drawn in segments through a series left clicks and closed with a right click.

2D Thresholding Tool

Use the Percentage selector field to set a threshold for the ROI. Specify the image on which to base the thresholding using the drop-down menu.

☑+	Apply Spline Path to ROI and move to next slice
☑	Apply Spline Path to ROI
☒	Clear Spline Path

Apply Spline Path to ROI and move to next slice.

This button creates a 2D ROI within the spline path and moves to next slice.

Apply Spline Path to ROI

This button creates a 2D ROI within the spline path.

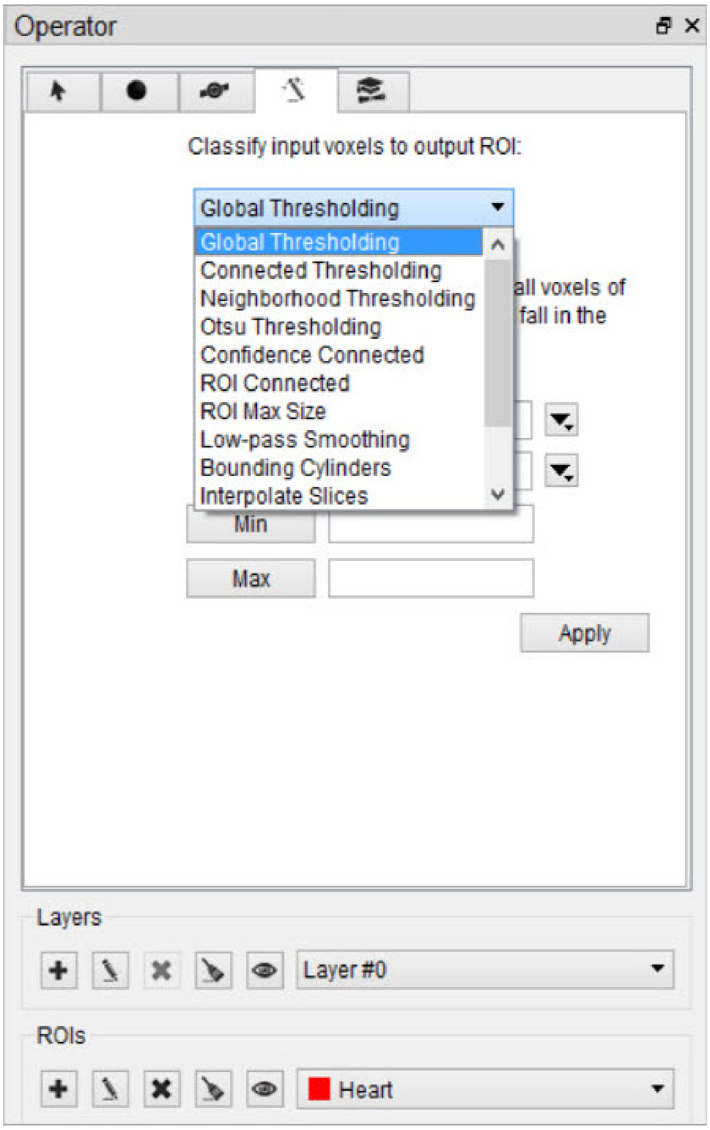
Clear Spline Path

This button clears the spline path and all points.

3D Segmentation Tools

The 3D Segmentation Tools are located in the Segmentation Algorithms tab . They be used to apply different thresholding techniques across input images and user-defined ROIs, as well as advanced ROI processing.

ℹ **Note:** An ROI must be added before the segmentation tools can be used.



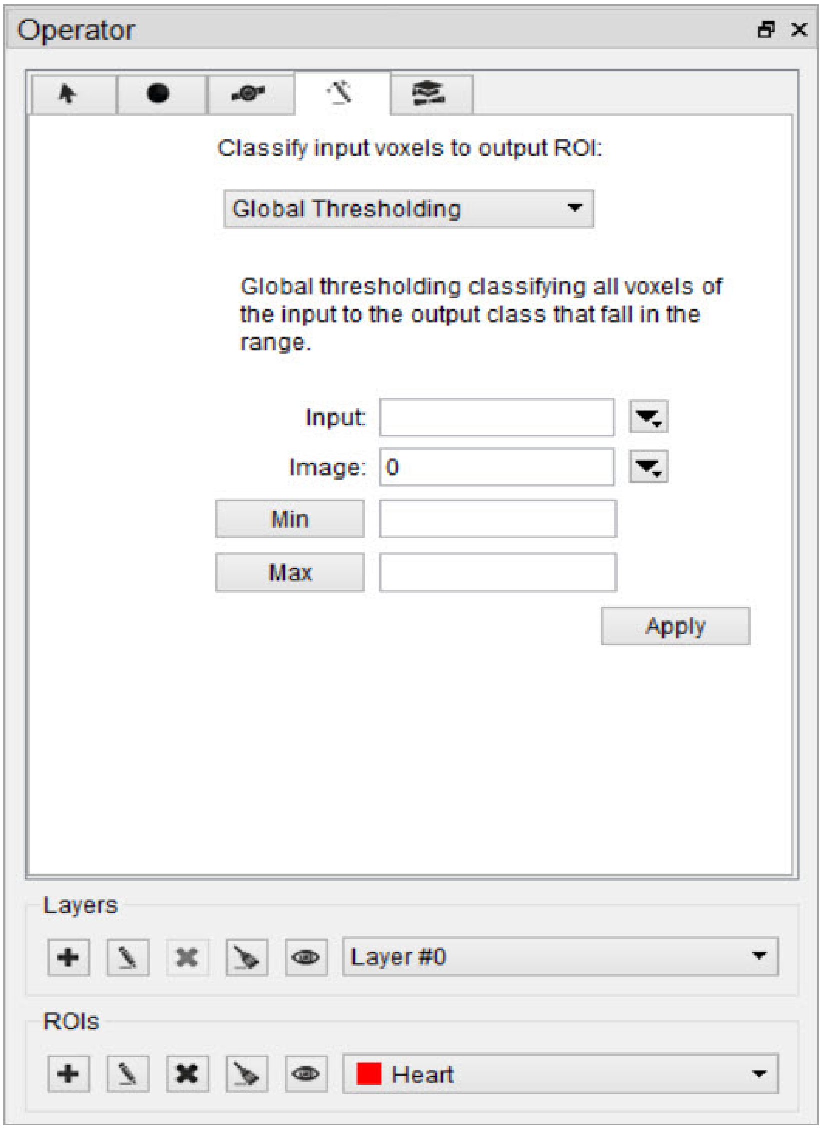
3D Segmentation Tools

Setting the Input and Output ROI

The Input ROI must be selected from the **Input** drop-down menu before applying thresholding. If an ROI other than the background is selected, only image pixels within the chosen ROI will be considered when thresholding is performed.

The Output ROI is the ROI specified in the ROI drop-down menu located at the bottom of the 3D ROI Operator window. If the Output ROI is not empty prior to thresholding, the result of the thresholding will be added to the existing voxels of the Output ROI.

Keep in mind that other ROIs may be overwritten if the result of a thresholding technique intersects them. To prevent other ROIs from being altered, set them to immutable. (See Edit an ROI to learn how to make an ROI immutable.)



Classify input voxels to output ROI:

Global Thresholding

Global thresholding classifying all voxels of the input to the output class that fall in the range.

Input:

Image: 0

Layer #0

Heart

Set Input/Output ROI

Choosing the Image Data

The segmentation algorithm will work on the data from the image specified in the Image drop-down.

Setting the Seed Point

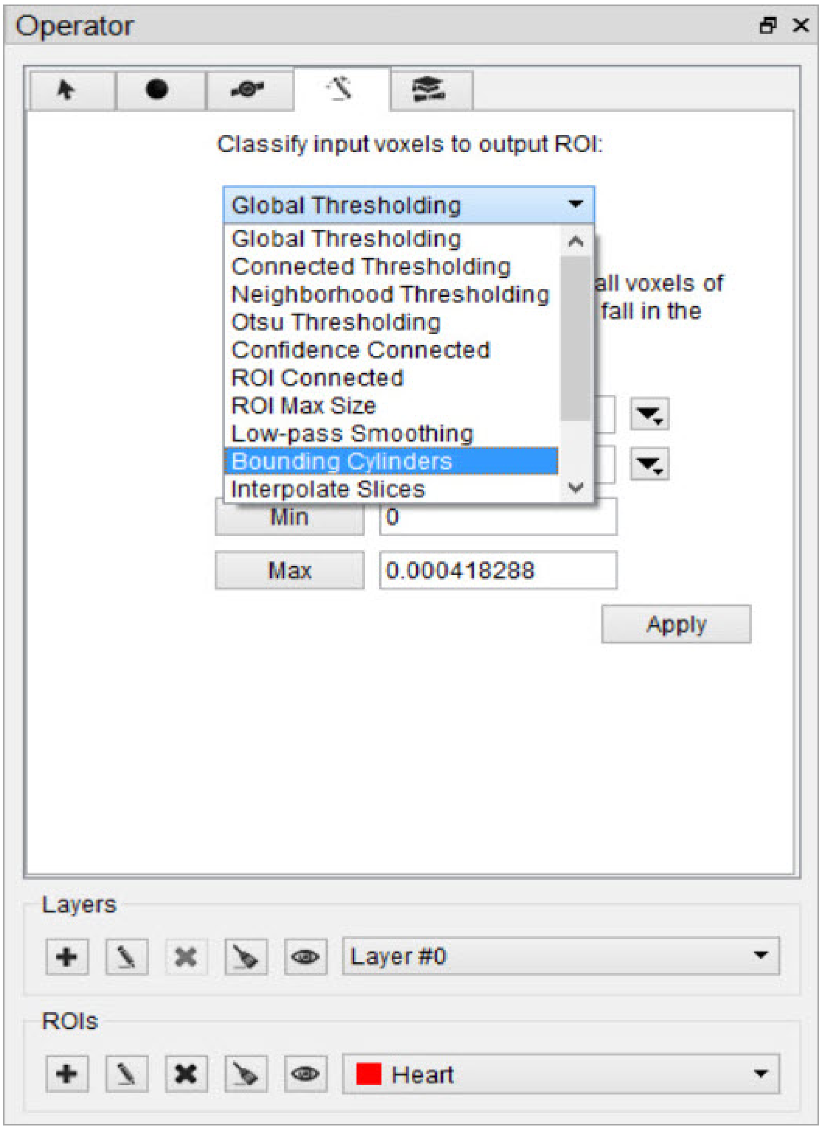
For methods that require a seed, the cursor location at the time the thresholding is performed will be used.

Setting the Thresholds

For methods that require thresholds, use the number fields beneath the Image Selection drop-down. Click the**Min** and **Max** buttons to the left of each threshold field to fill in the minimum and maximum values, respectively, from the selected image. The unit is assumed to match that specified in the header.

Available Thresholding Methods

The thresholding methods available can be selected from the **Segmentation Algorithm** drop-down menu. After selecting a seed and thresholds as necessary, click ‘Apply’ to perform the segmentation. The thresholding operation may take about a minute to complete.



Classify input voxels to output ROI:

Global Thresholding

Min 0

Max 0.000418288

Layers: Layer #0

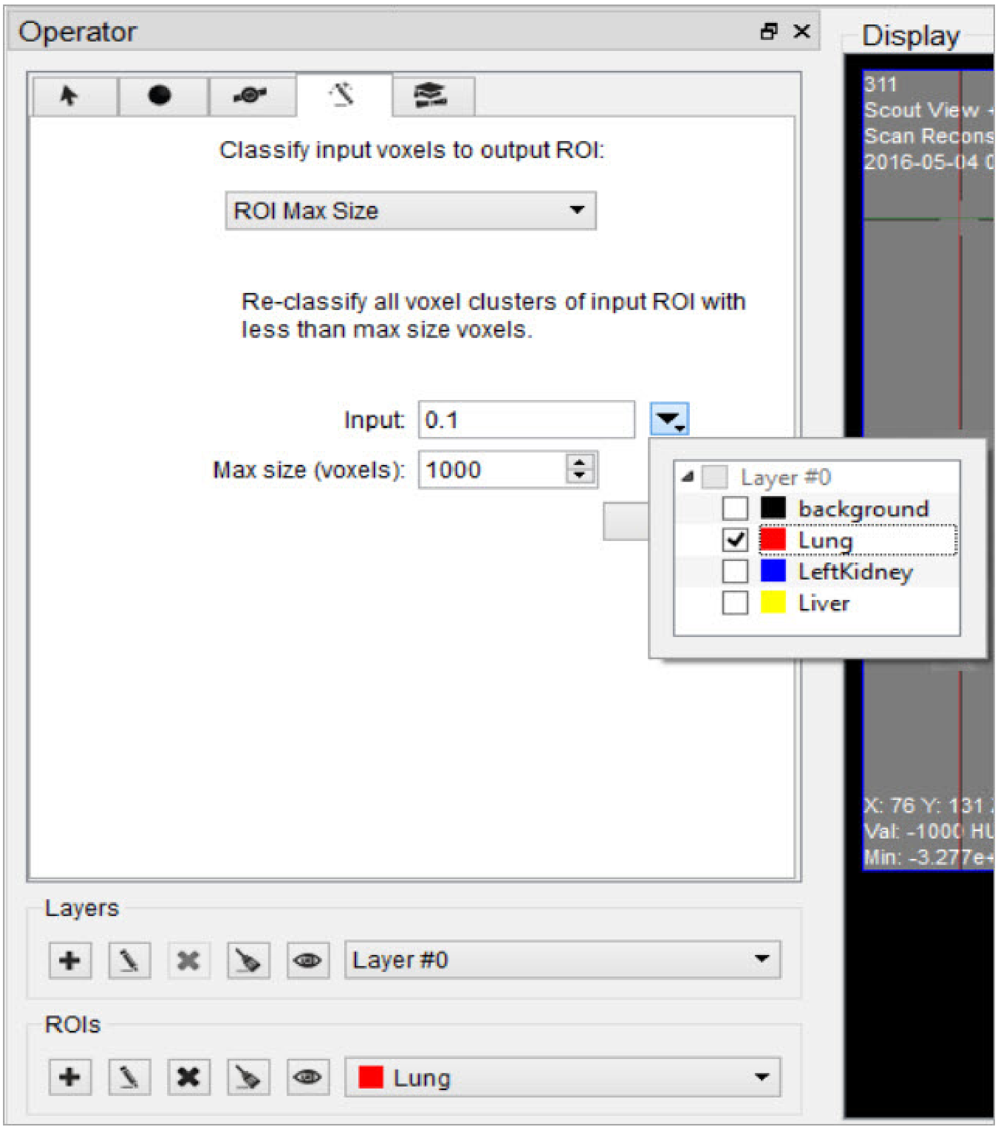
ROIs: Heart

Thresholding Methods

	Requires Seed?	Requires Thresholds?
Global Thresholding	No	Yes
Connected Thresholding	Yes	Yes
Neighborhood Thresholding	Yes	Yes
Otsu Thresholding	No	Yes
Confidence Connected	Yes	No
ROI Connected	Yes	No
ROI Max Size	No	No
Low-pass Smoothing	No	No
Bounding Cylinders	No	No
Interpolate Slices	No	No
Modal Smoothing	No	No
Connected Components	No	No
K-Means Clustering	Yes	No

ROI Max Size

The ROI Max Size filter can be used to fill holes in existing ROIs. Any connected components in the Input ROI that are comprised of fewer voxels than the **Max size** specified will be mapped to the output ROI.



Classify input voxels to output ROI:

ROI Max Size

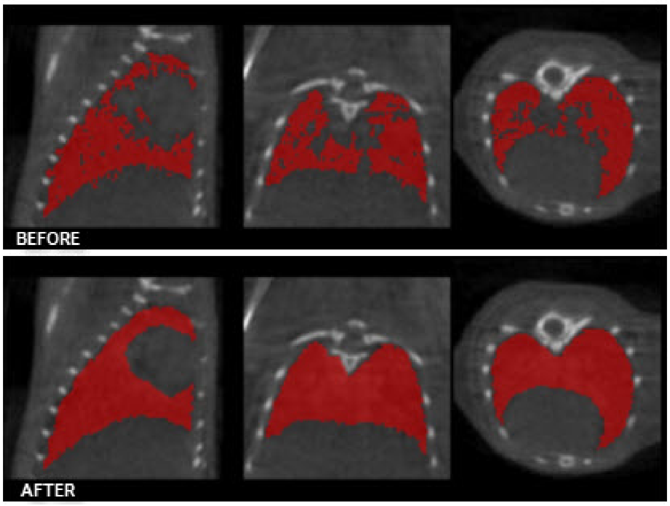
Re-classify all voxel clusters of input ROI with less than max size voxels.

Input: 0.1

Max size (voxels): 1000

☐ 🟥 background
☑ 🟥 Lung
☐ 🟦 LeftKidney
☐ 🟨 Liver

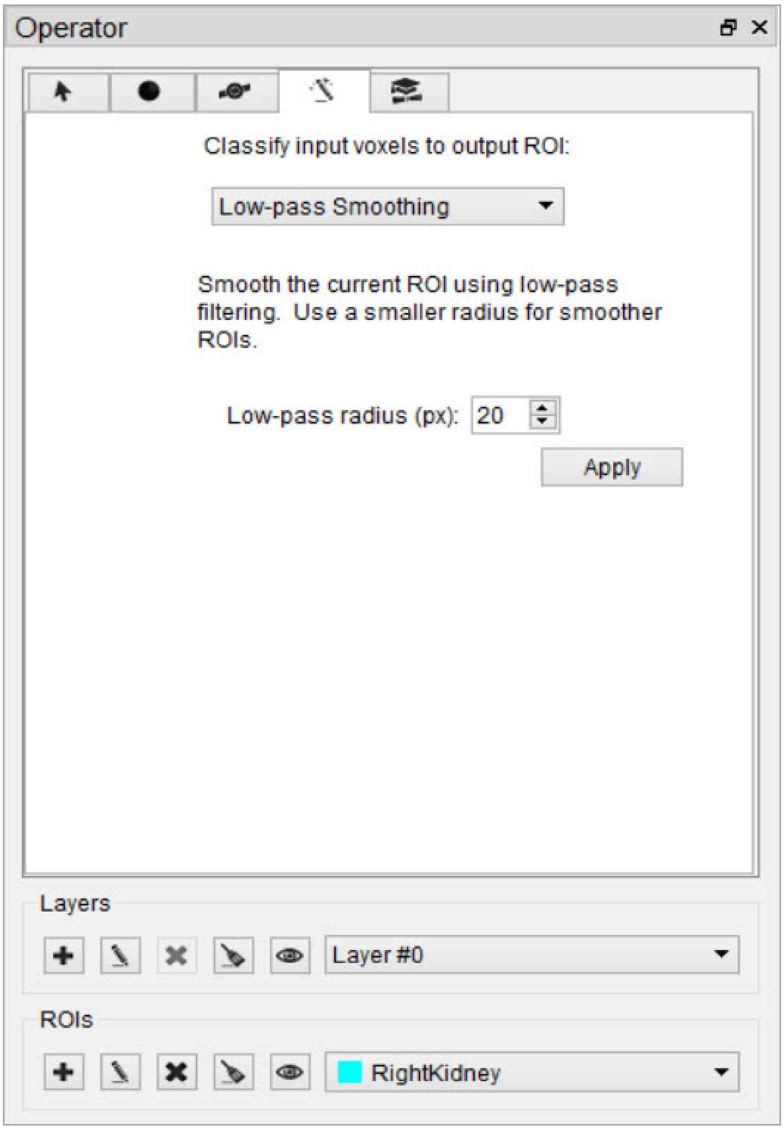
ROI Max Size



Before/After ROI Max Size

Low-pass Smoothing

Use the Low-pass Smoothing filter to remove jagged surfaces from manually created ROIs. The amount of smoothing can be controlled with the Low-pass radius parameter. Smaller radii will result in smoother ROIs.



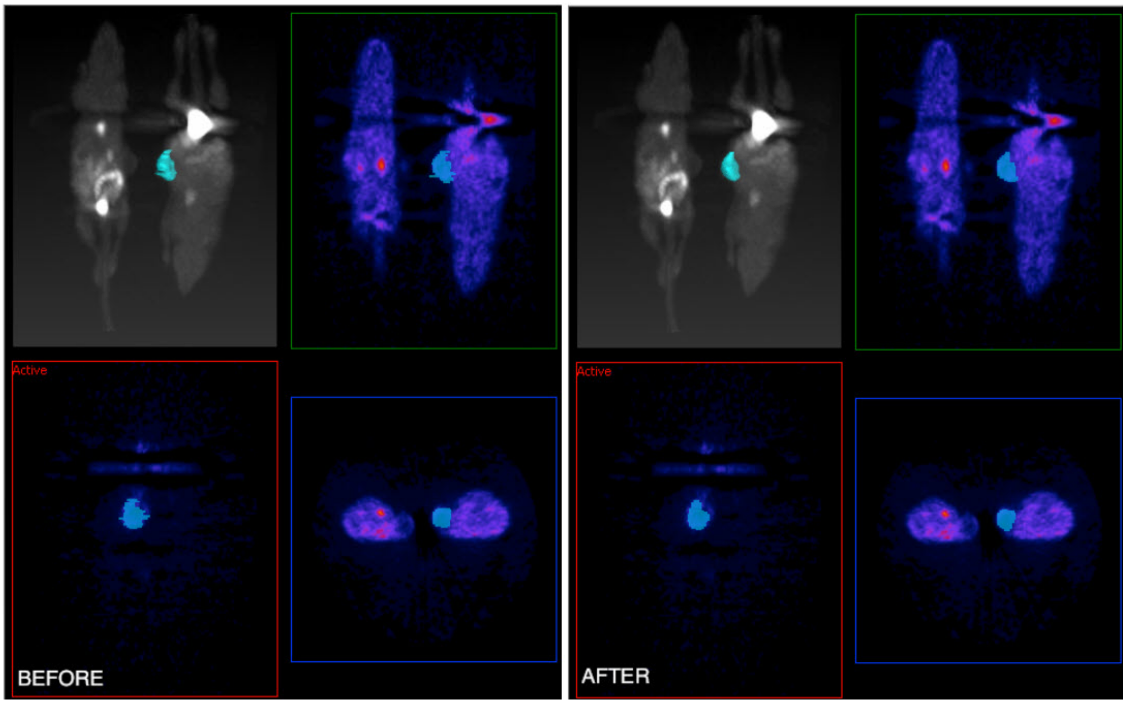
Classify input voxels to output ROI:

Low-pass Smoothing

Smooth the current ROI using low-pass filtering. Use a smaller radius for smoother ROIs.

Low-pass radius (px): 20

Low Pass Smoothing

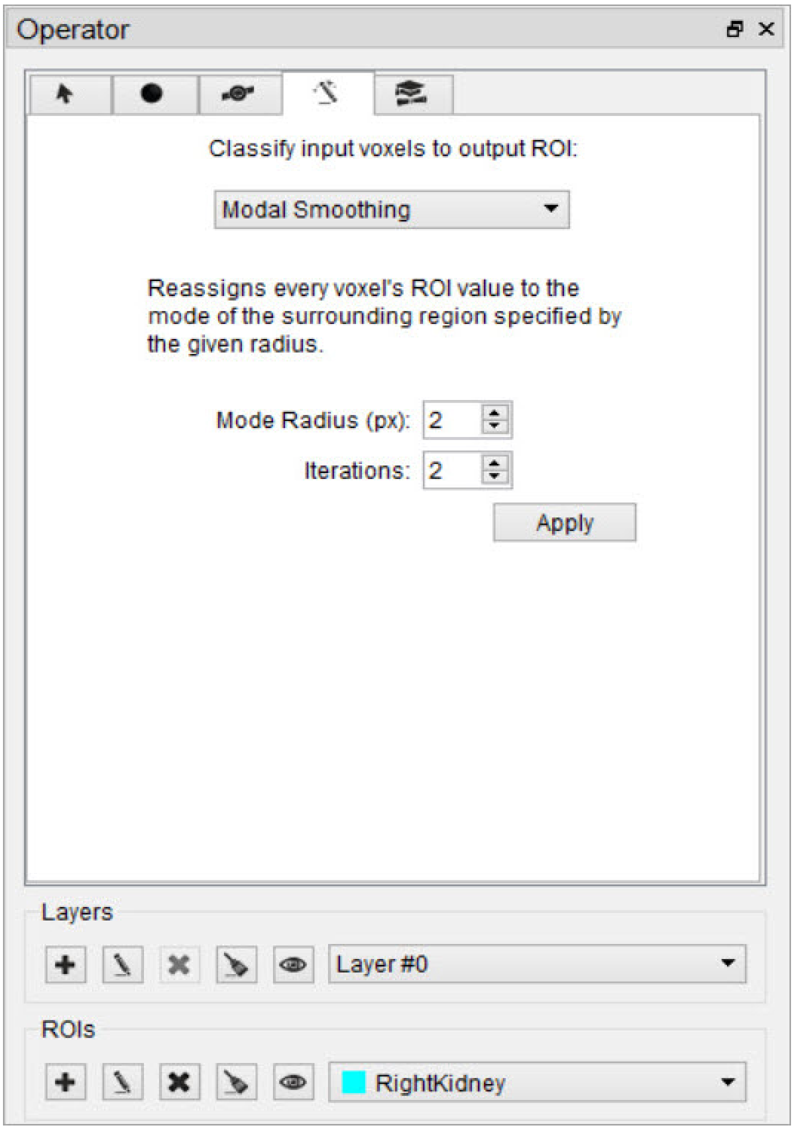


Before/After Low Pass Smoothing

ℹ **Note:** Smoothing ROIs contained in images with large dimensions can take upwards of 30 seconds.

Modal Smoothing

Use modal smoothing to reassign every voxel's ROI value to the mode of the surrounding region specified by the given radius. The amount of smoothing can be controlled by the Mode Radius and Iterations parameters.



Classify input voxels to output ROI:

Modal Smoothing

Reassigns every voxel's ROI value to the mode of the surrounding region specified by the given radius.

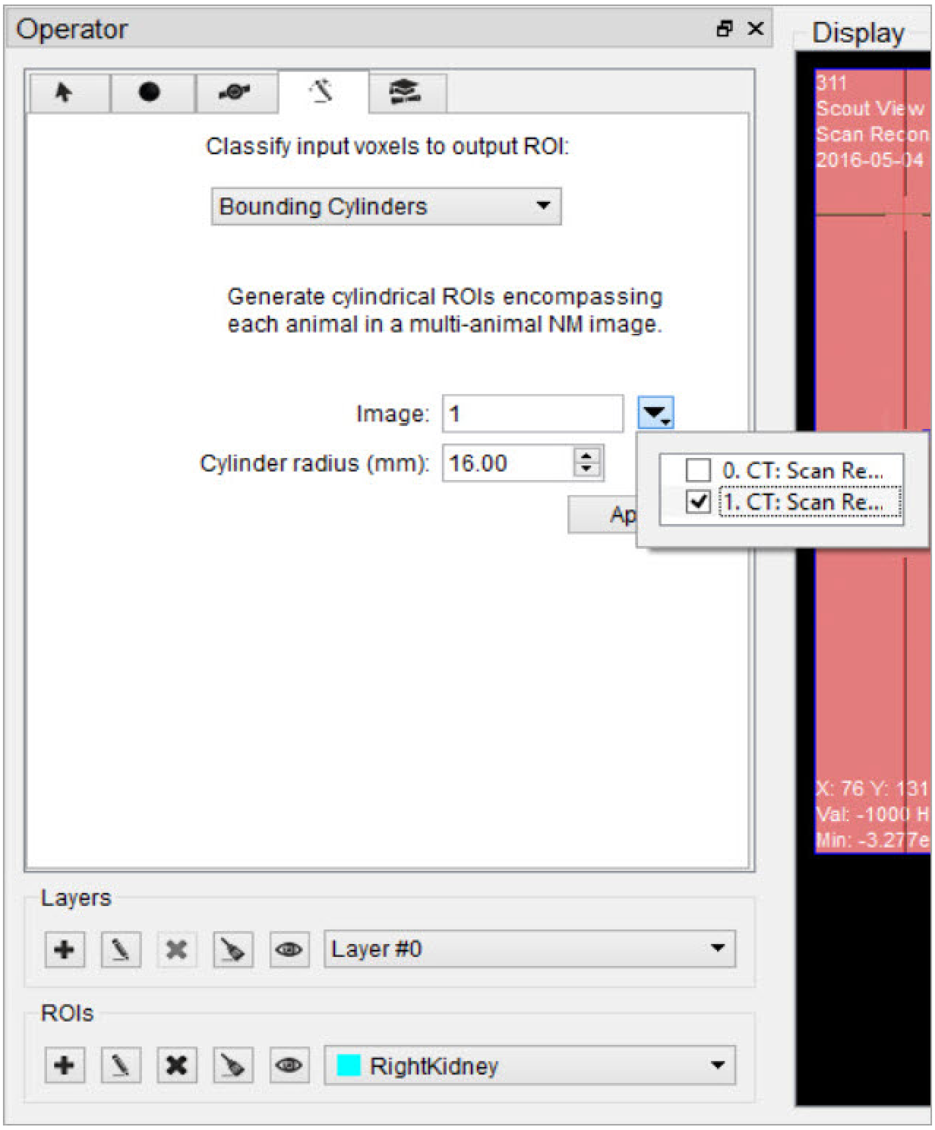
Mode Radius (px): 2

Iterations: 2

Modal Smoothing

Bounding Cylinders

The Bounding Cylinders tool can be used to generate cylindrical ROIs that encompass each animal of a multi-animal image. The number of animals is automatically determined and the cylinder radius can be configured. This algorithm works best on NM images, but may also work on some CT images.



Classify input voxels to output ROI: Bounding Cylinders

Generate cylindrical ROIs encompassing each animal in a multi-animal NM image.

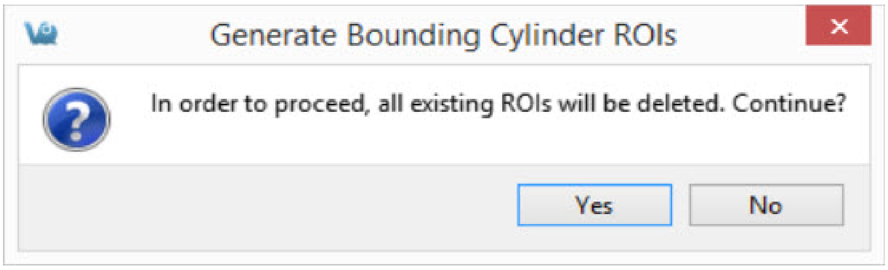
Image: 1

☐ 0. CT: Scan Re...
☑ 1. CT: Scan Re...

Cylinder radius (mm): 16.00

Bounding Cylinders

Note: If there are any ROIs present prior to using this tool, they will be deleted.

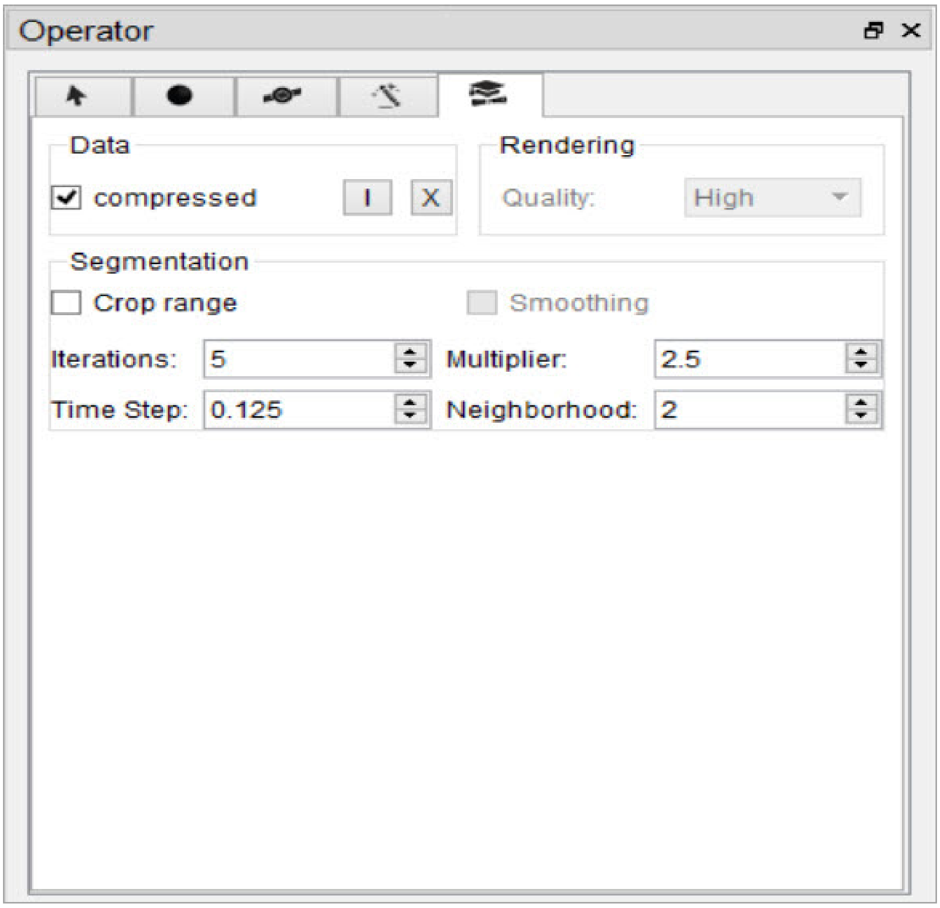


In order to proceed, all existing ROIs will be deleted. Continue?

Generate Bounding Cylinders

Expert Settings

The Expert tab, presents the advanced settings of the 3D ROI Operator. For the typical user, these settings will not need to be changed.



Data
☑ compressed [I] [X]

Rendering
Quality: High

Segmentation
☐ Crop range
☐ Smoothing

Iterations: 5
Multiplier: 2.5
Time Step: 0.125
Neighborhood: 2

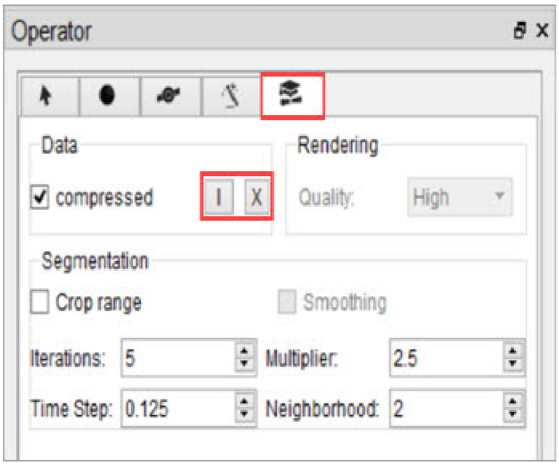
Expert Settings

Data Group

By default, VQ ROIs are written in a compressed format. To extend compatibility with other tools (e.g., ITK), uncheck “compressed.” If the ROI files will only be used within VQ, leave the “compressed” box checked.

Importing and Exporting ROIs

To import an ROI loaded in the **Data Manager** from an image file, click the **Import** button I and select the corresponding dataset to import. To export a 3D ROI as an image to allow manipulations outside of the 3D ROI tool, click the **Export** button X .



Data
☑ compressed [I] [X]

Rendering
Quality: High

Segmentation
☐ Crop range
☐ Smoothing

Iterations: 5
Multiplier: 2.5
Time Step: 0.125
Neighborhood: 2

Import / Export ROIs

Rendering

If “auto” is checked, ROIs will be re-rendered in the MIP view automatically upon certain triggers. When unchecked, rendering will only occur when the VTK button is used. For systems with less speed and memory, it may be helpful to select a less demanding setting from the rendering quality combo box.

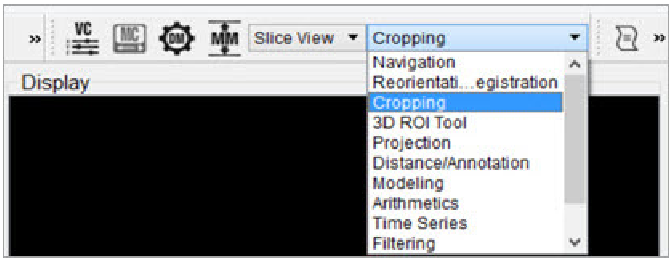
Segmentation

To add a curvature flow smoothing preprocessing step to the segmentation methods, check the “Smoothing” box. Use the Segmentation fields to tune up the parameters of the segmentation methods. The Smoothing filter will use the Iterations and Time Step settings; the Confidence Connected Thresholding will use the Multiplier and NeighborRad (neighborhood radius) settings; the Neighborhoood Thresholding will use the NeighborRad setting.

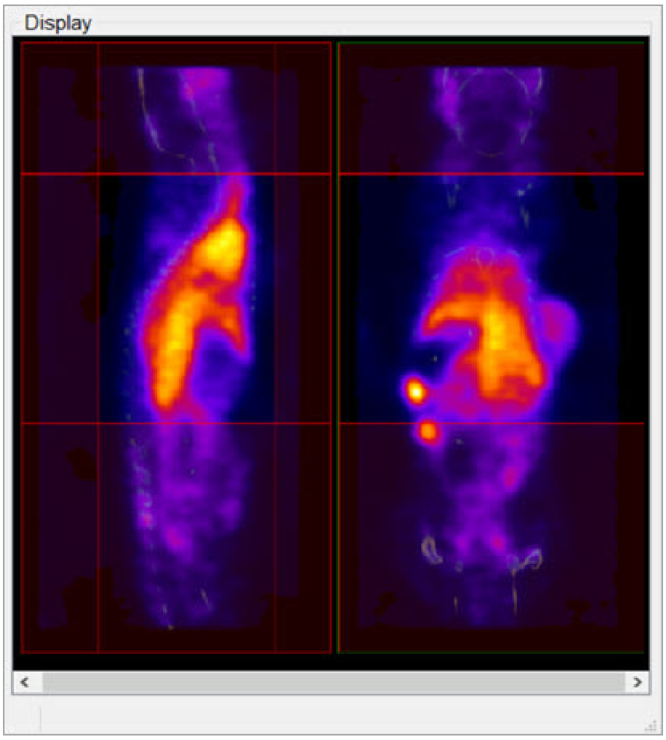
Crop Range

To perform any of the thresholding segmentation methods on only a sub-region of the input image, follow these steps:

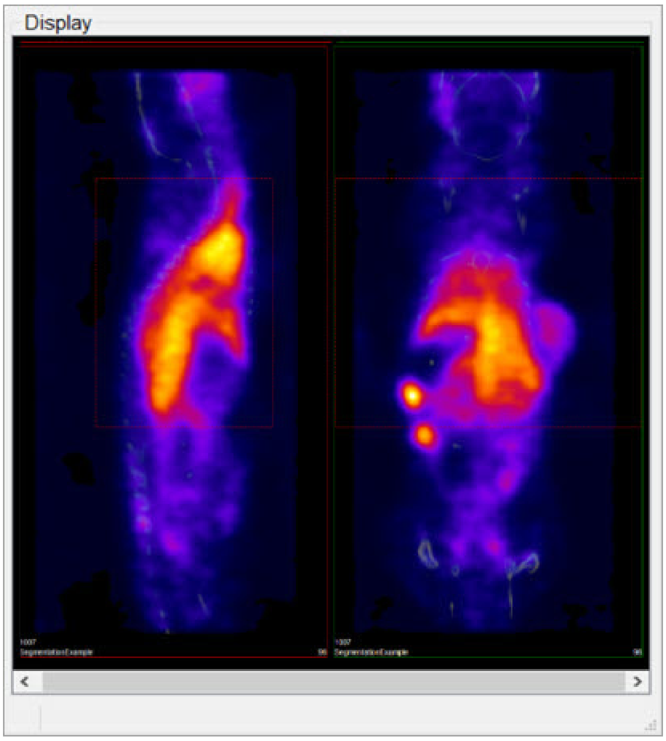
1. Open the Cropping operator from the **Operators** drop-down menu.



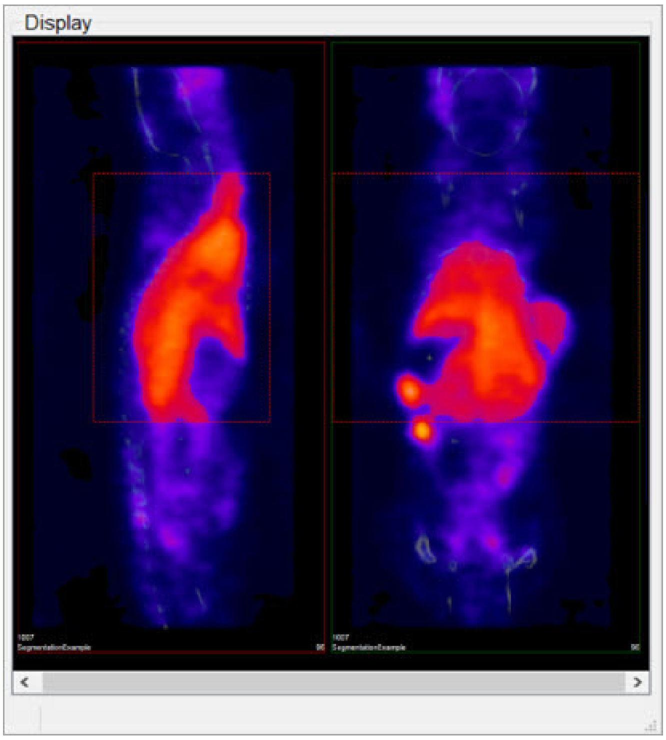
2. Use the red sliders to select the desired region of the image.



3. After you’ve selected the desired region, go back to the 3D ROI tool by selecting the 3D ROI operator from the **Operators** drop-down menu.
4. In the Expert tab of the 3D ROI Operator, mark the Crop Range checkbox. Dashed red lines will appear on the image, indicating the boundaries of the selected region.

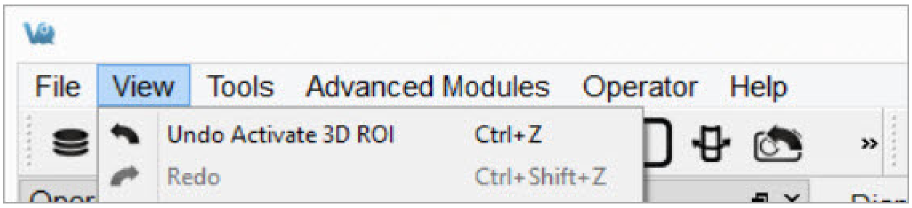


5. When the desired thresholding method is performed (see Segmentation Tools to learn how to use the Segmentation panel of the 3D ROI Operator), only the region within the crop range will be segmented.



Undo/Redo Functionality

To undo/redo operations performed in the 3D ROI tool go to the View tab on ViviQuant’s main menu and click the **Undo** ↶ or **Redo** ↷ button. The operation to be undone or redone will be described in the drop-down menu. Keyboard shortcuts are also available for undoing or redoing an operation.



Undo / Redo

ℹ **Note:** The input ROI will be set to background whenever the undo function is applied.

The undo/redo functionalities are applicable to all functions performed on 3D ROI data itself. Operations performed to actual volume image data cannot be undone or redone. For example, performing a cut on an image using an ROI cannot be undone since it is applied to actual volume data and not just 3D ROI data.

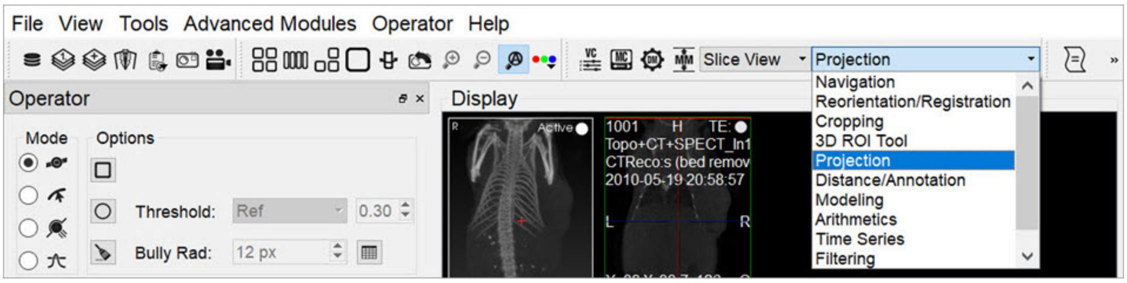
ℹ **Note:** To undo/redo filling a contour in the Spline Tool the user must navigate away from the spine tool window.

Projection

The **Projection Tool** provides a means to quantify density and activity parameters in CT and NM, MR, PET, or SPECT images. The tool provides several options for generating quantification data. There are multiple methods for setting the region of interest, flexibility in selection of the quantification view direction, easy-to-read presentation of data found in the Quantification Table, and options for saving and loading ROIs or plotting data.

Getting There

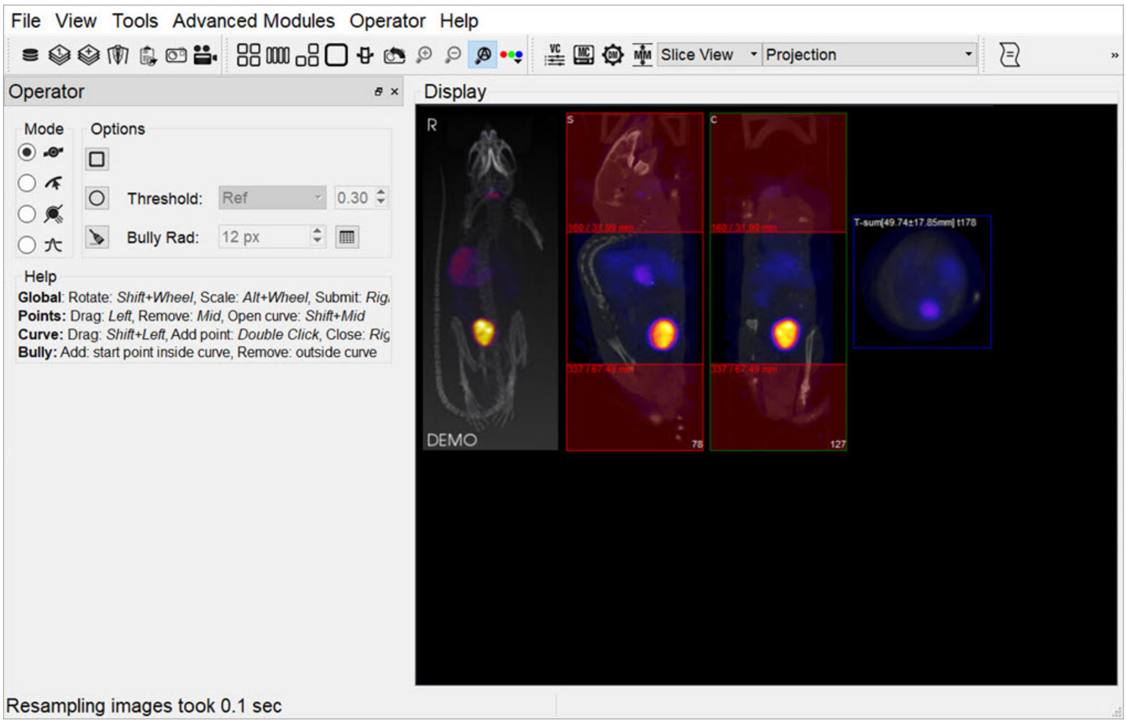
To access the **Projection** tool, use the **View** sub-menu in the **Operator** section of the main menu.



Access Projection

Using the Tool

Upon selection of the tool, the **Projection** panel appears. The first step in using the projection tool is to define a Region-of-interest (ROI).



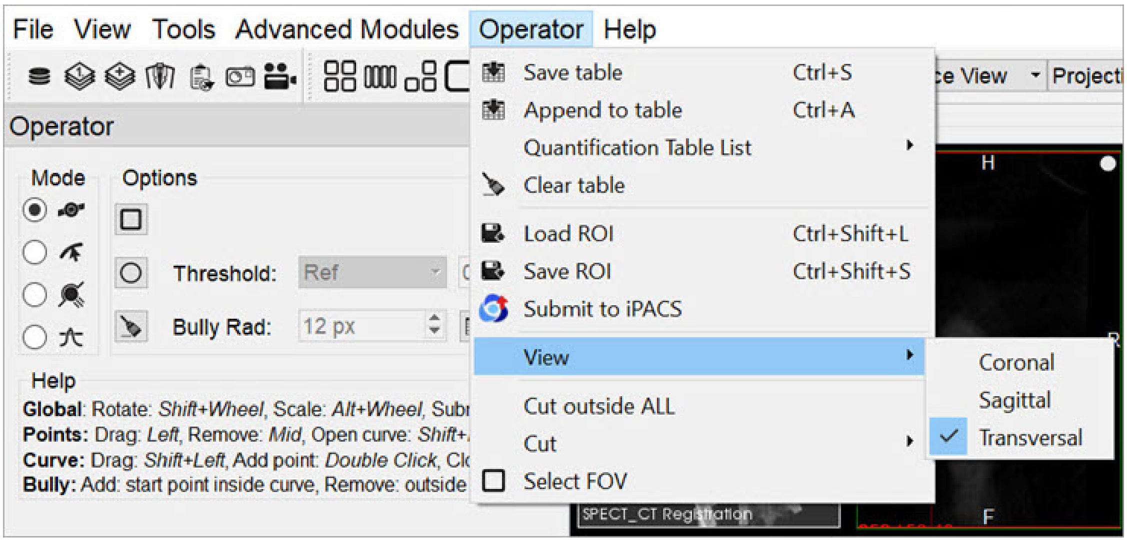
Global: Rotate: *Shift+Wheel*, Scale: *Alt+Wheel*, Submit: *Rig*
Points: Drag: *Left*, Remove: *Mid*, Open curve: *Shift+Mid*
Curve: Drag: *Shift+Left*, Add point: *Double Click*, Close: *Rig*
Bully: Add: start point inside curve, Remove: outside curve

Resampling images took 0.1 sec

Define ROI

Choosing the View Direction

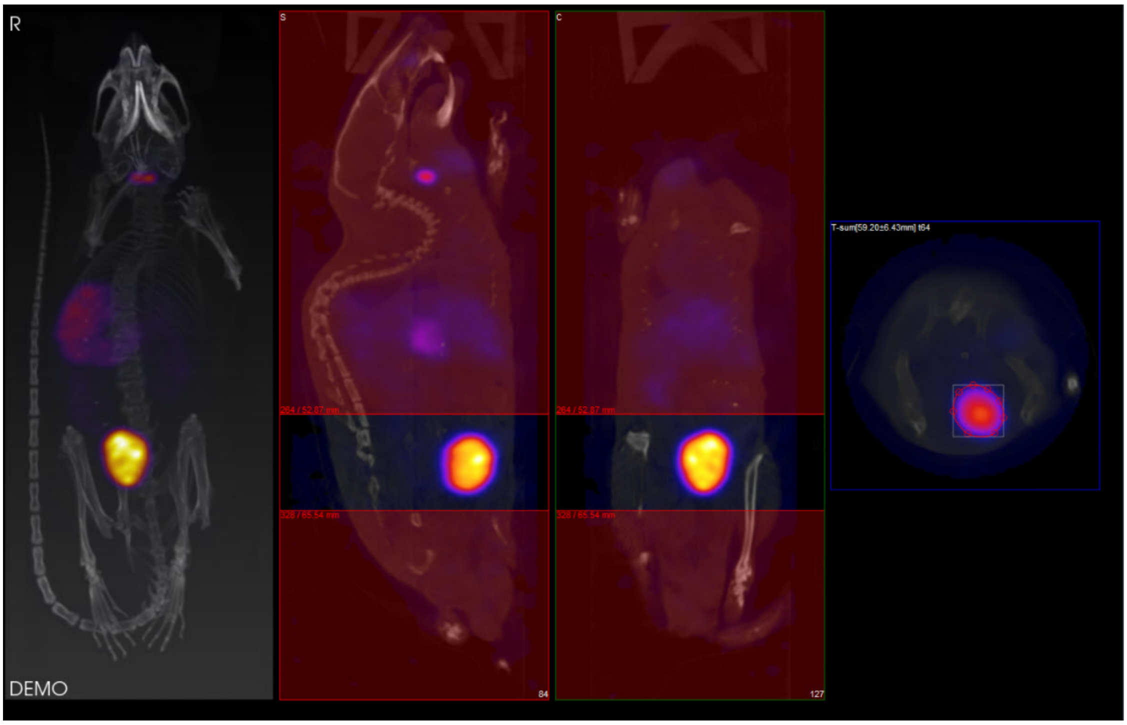
The ROI may be drawn in either the transverse (default), coronal, or sagittal plane. To toggle between these options, use the **View** menu in the **Operator** tab of the main menu.



Help
Global: Rotate: *Shift+Wheel*, Scale: *Alt+Wheel*, Subr
Points: Drag: *Left*, Remove: *Mid*, Open curve: *Shift+*
Curve: Drag: *Shift+Left*, Add point: *Double Click*, Cl
Bully: Add: start point inside curve, Remove: outside

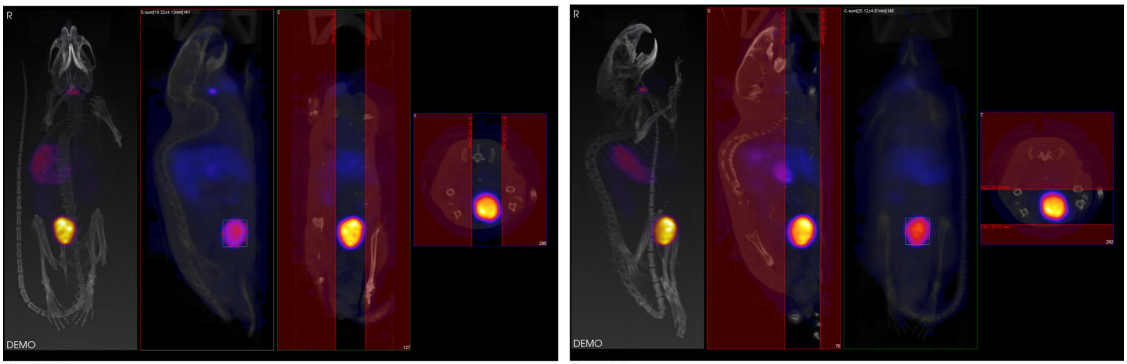
Choose View Direction

In this example, using the default settings, the axial sliders determine the extent of the ROI in the axial direction. The region or pre-defined shape described below determines the bounds of the ROI in the **transverse plane**.



Transverse Plane

By using the **View** menu, it is also possible to draw ROI boundaries in the **sagittal plane** or **coronal plane**:



Sagittal Plane

Coronal Plane

Sagittal and Coronal Planes

Choosing the ROI type

There are four ROI types, labeled as **Modes**:

	Spline	Points are defined, and smooth curves are drawn in between. The base points can be moved by using the left mouse button to drag them. Additionally, points can be deleted (middle click point) or added (double click position on curve). Once a shape has been closed (right mouse button), it can be re-opened by using **Shift + middle click** on a point.
	Freehand	A freehand region may be drawn by moving the mouse while holding down the left mouse button. The region may be drawn in segments through a series of **left clicks** of the mouse.
	Bully	Push lines out or into the object with a circle-shaped cursor. The size of the cursor is defined by setting the **Bully Rad** field in the **Options** section. This mode provides an efficient way to fine-tune an ROI made in **Spline** or **Freehand** mode.
	Threshold	A reference voxel is determined with a **left click** in the transverse window. The ROI is determined by finding the region of voxels surrounding the reference voxels that share similar values to the reference voxels. The threshold value establishes how near in value the boundary voxels must be to the reference voxel.

Mouse Actions

Action	Mouse Shortcut
Rotate ROI	Shift + mouse wheel
Scale ROI	Alt + mouse wheel
Move ROI	Shift + left click

Once the desired ROI has been defined, click the **Show Table** button or right-click on the ROI to open the Quantification Table. This table contains a wide range of information, as described below.

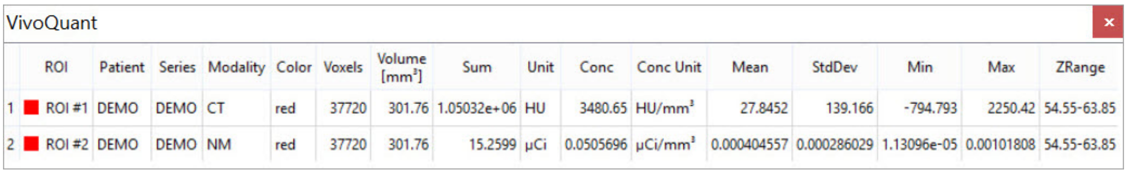
Click the **Clear** button in the **Options** section to clear the current ROI and begin drawing another.

Note: The unit used for measuring CT attenuation is the Hounsfield Unit (HU), while the unit used for measuring activity in the NM, MR, PET, and SPECT images is Mega-Becquerel (MBq), kilo-Becquerel (kBq), or micro-Curie (uCi).

VQ maintains the most recent ROI until a new ROI is defined. Each ROI for which data is collected is assigned a new color. Note, for example, that editing a ROI following data calculation results in a change to the color of the ROI. Also, the MIP reflects the currently selected ROI by shading the region encompassed by the ROI according to the appropriate color.

Quantification Table

After defining the ROI, the quantification table will fill the following fields.



VivoQuant

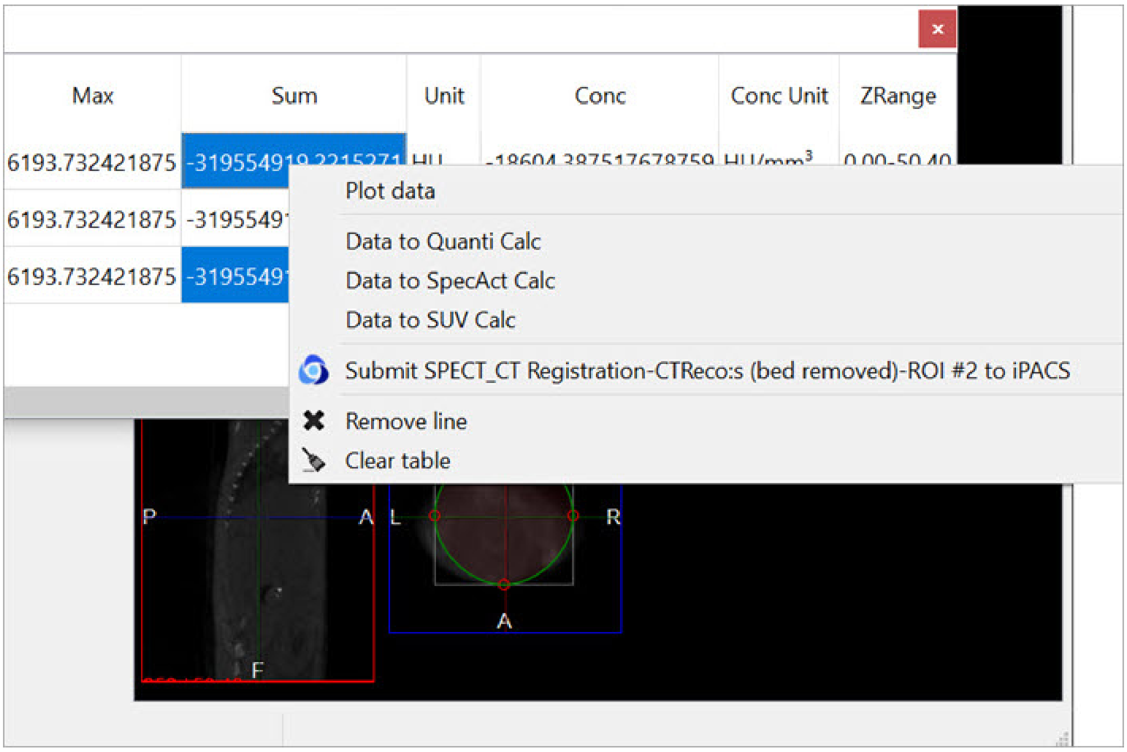
	ROI	Patient	Series	Modality	Color	Voxels	Volume [mm^3]	Sum	Unit	Conc	Conc Unit	Mean	StdDev	Min	Max	ZRange
1	🟥 ROI #1	DEMO	DEMO	CT	red	37720	301.76	1.05032e+06	HU	3480.65	HU/mm^3	27.8452	139.166	-794.793	2250.42	54.55-63.85
2	🟥 ROI #2	DEMO	DEMO	NM	red	37720	301.76	15.2599	µCi	0.0505696	µCi/mm^3	0.000404557	0.000286029	1.13096e-05	0.00101808	54.55-63.85

Quantification Table Fields

Field	Description
ROI	Name of the ROI. You can left-click this field to enter comments.
Patient	Patient’s name for the current study.
Series	Specific data set in the study from which the data was calculated.
Modality	Modality from which the data values for the row were calculated.
Color	Color of the ROI as drawn in the display.
Voxels	Total number of voxels contained in the selected ROI.
Volume [mm3]	Volume of the selected ROI in units of cubic millimeters.
Sum	Total amount of attenuation/activity in the selected ROI for CT and NM, MR, PET, or SPECT data sets, respectively.
Unit	Unit of voxels in the selected dataset. CT data use Hounsfield units (HU). You can specify the units used by SPECT data in the Data Panel of the Configuration Tool. Options include MBq, kBq, mCi, and µCi.
Concentration	Total amount of attenuation/activity in the selected ROI for CT and NM, MR, PET, or SPECT data sets, respectively, divided by the ROI volume.
Conc Unit	Unit of voxels in the selected data set over volume. CT data use Hounsfield units (HU/mm^3). You can specify the units used by SPECT data in the Data Panel of the Configuration Tool. Options include MBq/mm3, kBq/mm3, mCi/mm3, and µCi/mm3.
Mean	Average amount of attenuation/activity in the selected ROI.
StdDev	Standard deviation is a measurement of the variability in attenuation/activity in the selected ROI from voxel-to-voxel. The smaller this value, the more uniform the distribution of attenuation/activity in the ROI.
Min	Minimum attenuation/activity value of the voxels in the selected ROI.
Max	Maximum attenuation/activity value of the voxels in the selected ROI.
ZRange	Distance spanned by the axial sliders specified via slice numbers.

Quantification Table Options

Right-click on one or more entries in the Quantification table to view the following options:



Max	Sum	Unit	Conc	Conc Unit	ZRange
6193.732421875	-319554919.2215271	HU	-18604.387517678759	HU/mm³	0.00-50.40
6193.732421875	-3195549				
6193.732421875	-3195549				

Quantification Table Options

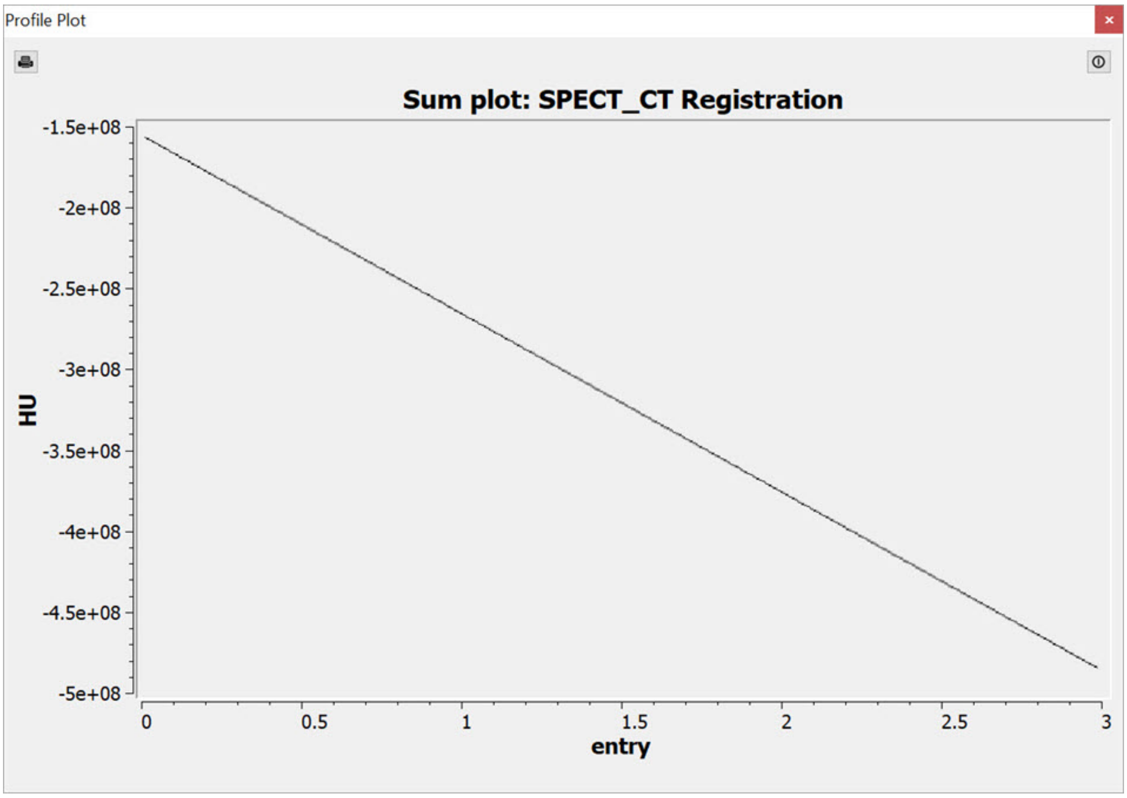
Menu Item	Description
Plot data	Plots the selected data on a line graph.
Data to Quanti Calc	Calculates the Quantification factor with the acquired data.
Data to SpecAct Calc	Calculates the specific activity with the acquired data.
Data to SUV Calc	Calculates the standarized uptake value with the acquired data.
Submit ROI #* to iPACS	Submits #* ROI (the selected ROI) to iPACS.
Remove line	Deletes the entire row of the corresponding selected cell.
Clear table	Deletes all information from the table, but not permanently. The table can be reopened by right-clicking and the data for the corresponding selection will reappear.

Plot data

It is possible to plot the quantified data. This function is useful to look at changes in activity, concentration, volume, etc., particularly in gated, dynamic, and longitudinal studies.

To plot data from the quantification tool, select the column of interest (i.e., Sum, Mean, etc.), right-click on any element in the column, and then select **Plot Data**.

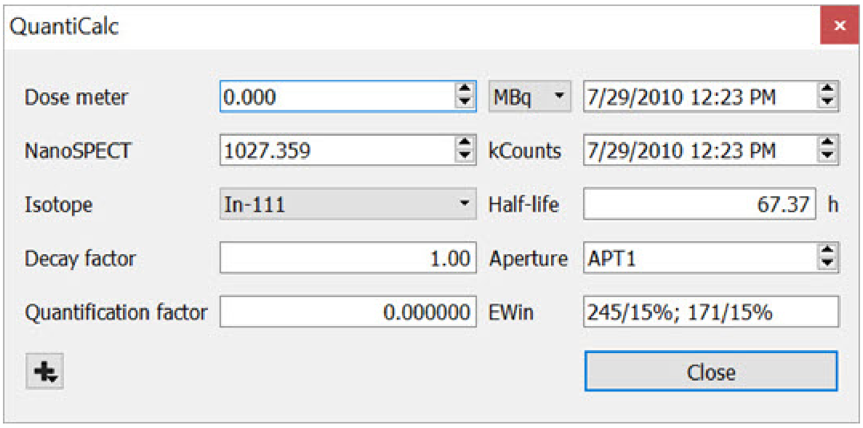
The plotted data will open in a new window and may be saved into an output PDF file.



Plot Data

Data to Quanti Calc

The calculator will automatically import the associated data.

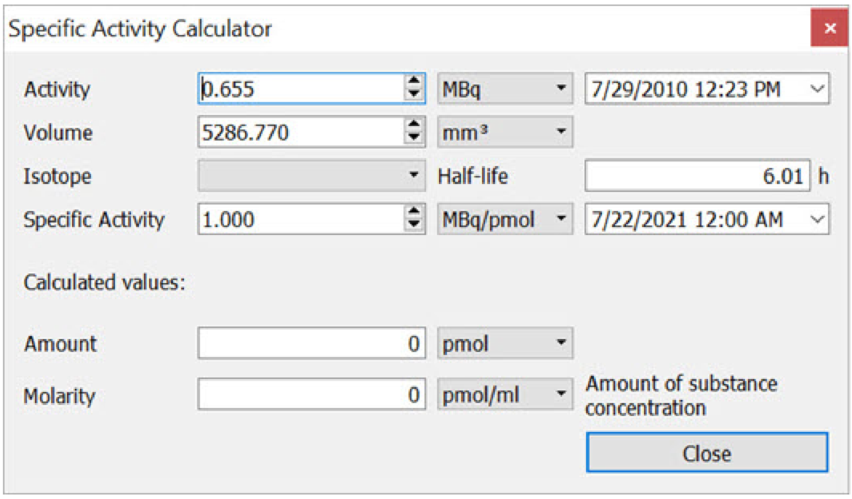


Dose meter	0.000	MBq	7/29/2010 12:23 PM
NanoSPECT	1027.359	kCounts	7/29/2010 12:23 PM
Isotope	In-111	Half-life	67.37 h
Decay factor	1.00	Aperture	APT1
Quantification factor	0.000000	EWin	245/15%; 171/15%

Quantification Calculator

Data to SpectAct Calc

The calculator will automatically import the associated data.



Specific Activity Calculator

Activity: 0.655 MBq 7/29/2010 12:23 PM
Volume: 5286.770 mm³
Isotope:
Half-life: 6.01 h
Specific Activity: 1.000 MBq/pmol 7/22/2021 12:00 AM

Calculated values:

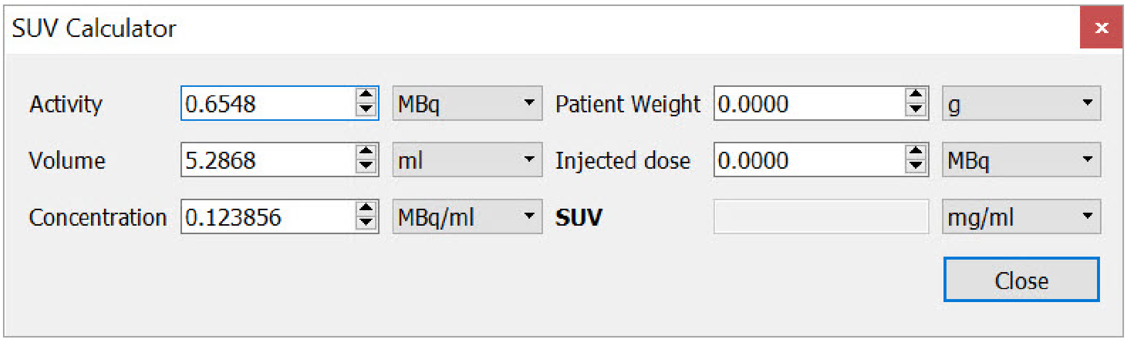
Amount: 0 pmol
Molarity: 0 pmol/ml

Amount of substance concentration

Specific Activity Calculator

Data to SUV Calc

The calculator will automatically import the associated data.



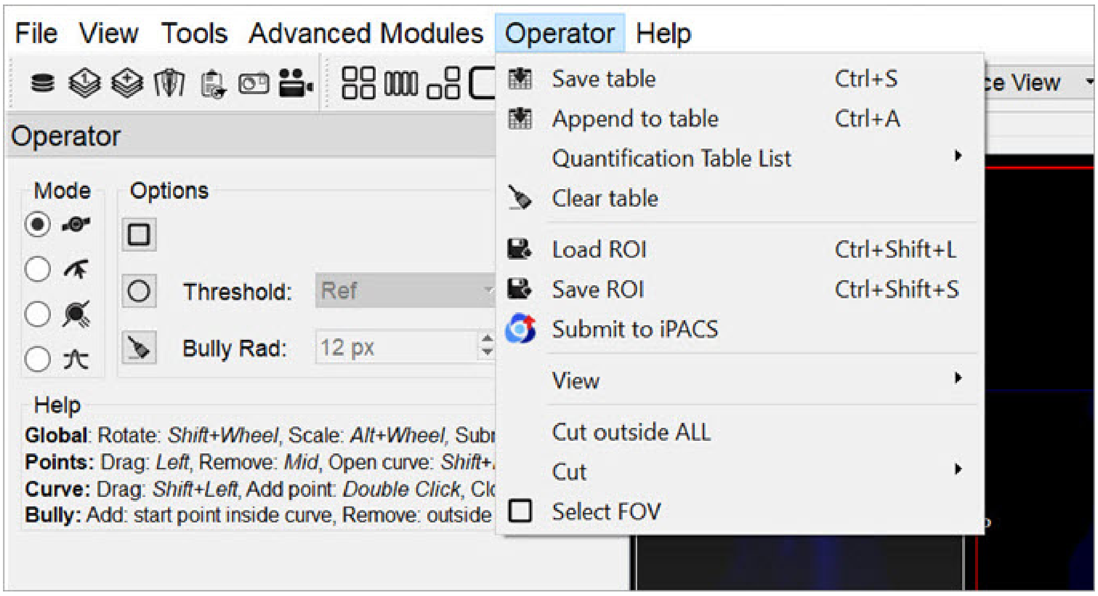
SUV Calculator

Activity: 0.6548 MBq
Volume: 5.2868 ml
Concentration: 0.123856 MBq/ml
Patient Weight: 0.0000 g
Injected dose: 0.0000 MBq
SUV: mg/ml

SUV Calculator

Operator Menu

The **Projection** operator also provides several options for saving quantification and ROI information, as well as viewing and cutting options, and miscellaneous ROI functions. To access these options, click on the **Operator** section in the main menu.



Threshold: Ref
Bully Rad: 12 px

Help
Global: Rotate: *Shift+Wheel*, Scale: *Alt+Wheel*, Subr
Points: Drag: *Left*, Remove: *Mid*, Open curve: *Shift+*
Curve: Drag: *Shift+Left*, Add point: *Double Click*, Cl
Bully: Add: start point inside curve, Remove: outside

File Menu

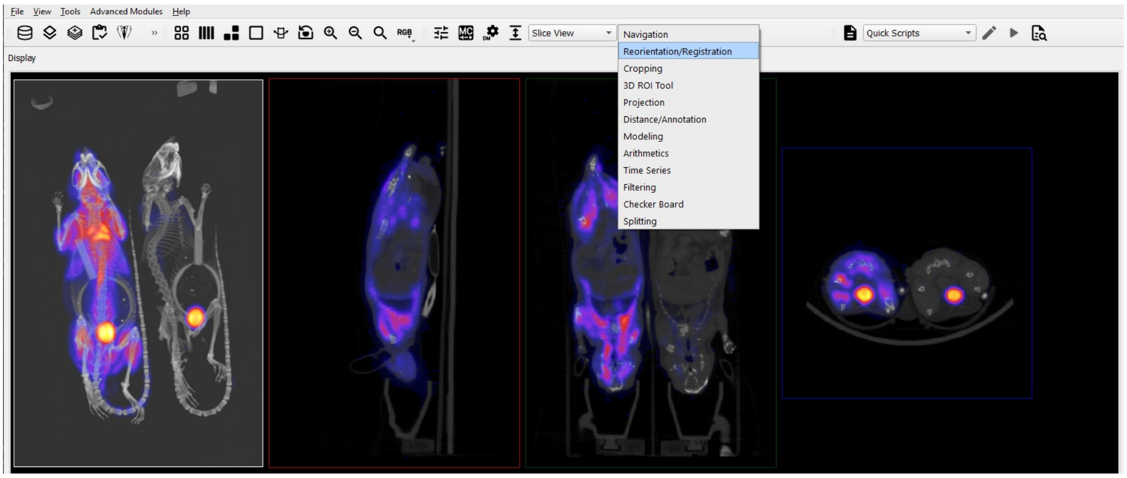
Menu Item	Description
Save table	Saves the current Quantification table to a local file. Accepted formats include .csv, .txt, and .xls.
Append to table	Appends the current Quantification table to a previously saved table.
Quantification table list	Allows users to choose what fields to be displayed in the Quantification table.
Clear table	Clears the current Quantification table.
Load ROI	Loads a previously saved ROI.
Save ROI	Saves the current ROI as a .roi file.
Submit to iPACS	Submit the quantification data as a Data Point to the associated image on the iPACS.
View	Allows users to choose the ROI view direction.
Cut outside ALL	Clears all voxels outside the ROI within the currently selected slices, and all voxels outside the currently selected slices. Slices outside the set axial range will be cleared entirely.
Cut	Clears all voxels inside/outside the ROI within the currently selected slices, depending on which direction (inside/outside) is selected. Slices outside the set axial range will not be affected. - **Apply ROI to all slices:** Applies the ROI to every slice in the image.
Select FOV	Creates a new ROI entry representing the field-of-view (the entire volume of the image). The quantification table will be populated with this entry, labelled as **FOV**.
Copy table	Copies the data in the Quantification table to the clipboard.
Close	Closes the Quantification panel and returns the VQ to the Navigation screen.

Reorientation / Registration Tool

The **Reorientation/Registration** Tool enables manual and automatic realignment of image data via translation, rotation, or flipping. Reference and input data may be manipulated separately, and specific translation settings may be saved and/or loaded for future studies, including the option for setting automatically applied default image shifts.

Getting There

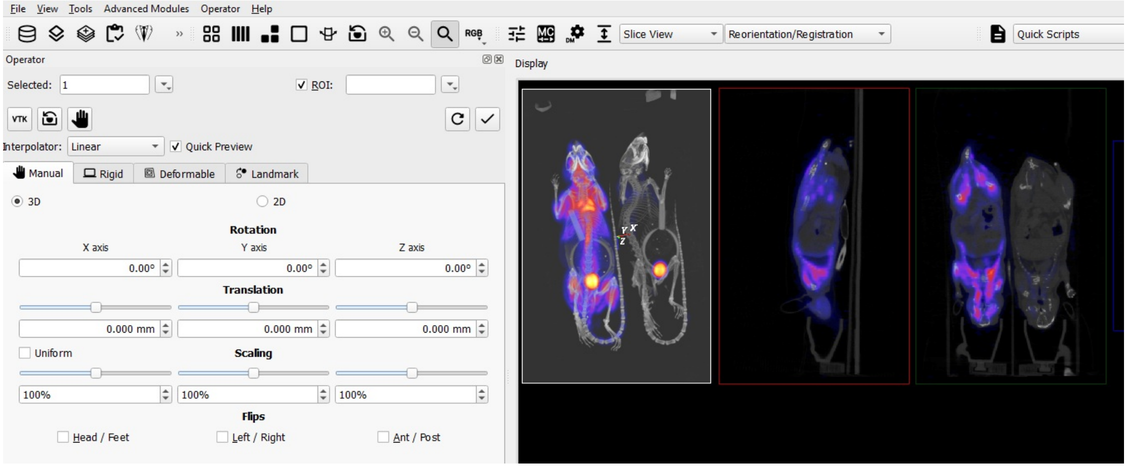
The **Reorientation/Registration** Tool can be accessed via the tool pull-down menu on VivoQuant's front panel.



Reorientation / Registration Tool

Using the Tool

Upon selecting the tool, the **Reorientation/Registration** operator window is displayed.

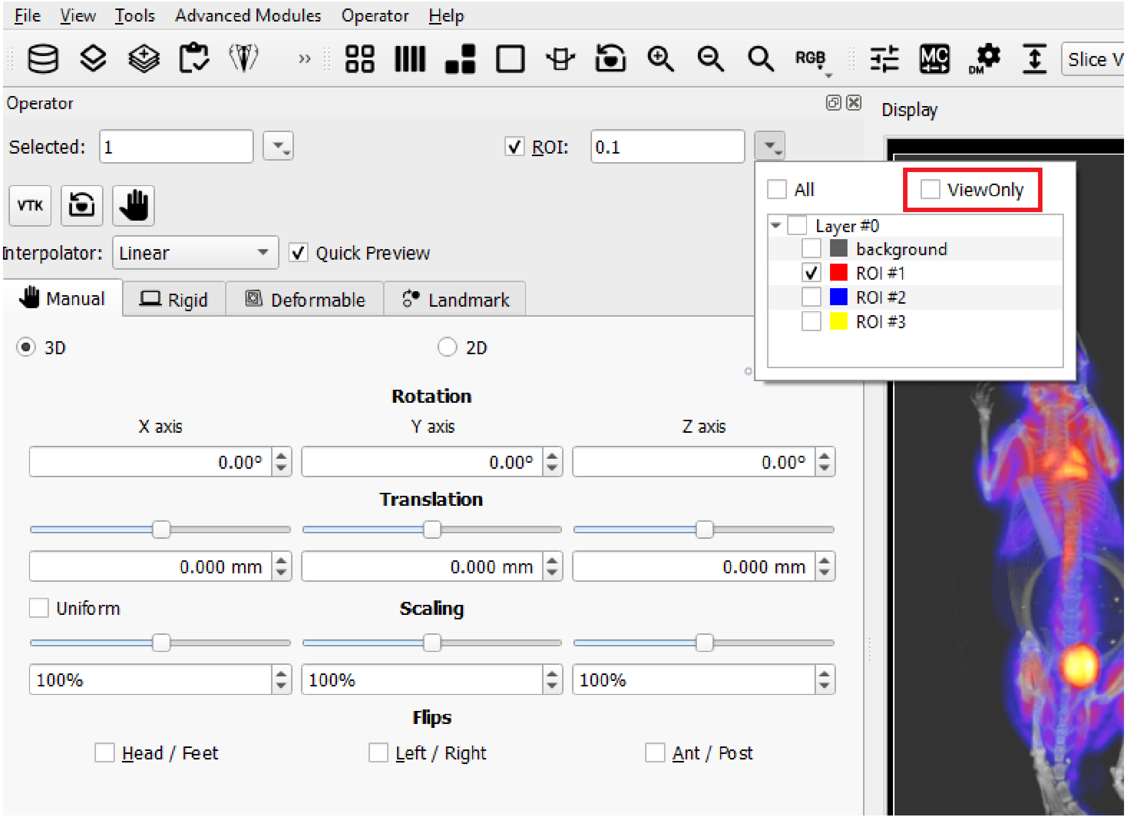


Selected: 1
☑ ROI:
Interpolator: Linear
☑ Quick Preview
● 3D ○ 2D
Rotation: X axis 0.00° Y axis 0.00° Z axis 0.00°
Translation: 0.000 mm 0.000 mm 0.000 mm
☐ Uniform
Scaling: 100% 100% 100%
Flips: ☐ Head / Feet ☐ Left / Right ☐ Ant / Post

Reorientation / Registration Window

The Data Selector Widget is used to determine which inputs will be reoriented by the Operator.

ROIs can be selected by checking the **ROI** checkbox. By default, all ROIs will be subject to reorientation when the ROI box is checked. If you wish to select only specific ROIs, click on the pull-down menu and select the desired ROIs. You may also choose to simply view the ROIs while performing a reorientation, without performing the reorientation on the ROIs themselves, by selecting **View Only** from the **ROI** pull-down menu.



Selected: 1

☑ ROI: 0.1

Interpolator: Linear ☑ Quick Preview

● 3D ○ 2D

X axis	Y axis	Z axis
0.00°	0.00°	0.00°
0.000 mm	0.000 mm	0.000 mm
100%	100%	100%

☐ Uniform

☐ Head / Feet ☐ Left / Right ☐ Ant / Post

Select ROIs

The buttons at the top of the operator window perform various functions within the operator.

Option	Description
vtk	Force re-render of VTK Viewer
⟲	Reset VTK Viewer position
✋	Toggle ability to perform reorientation in VTK Viewer
↻	Resets current reorientation operation
☑	Apply current reorientation operation

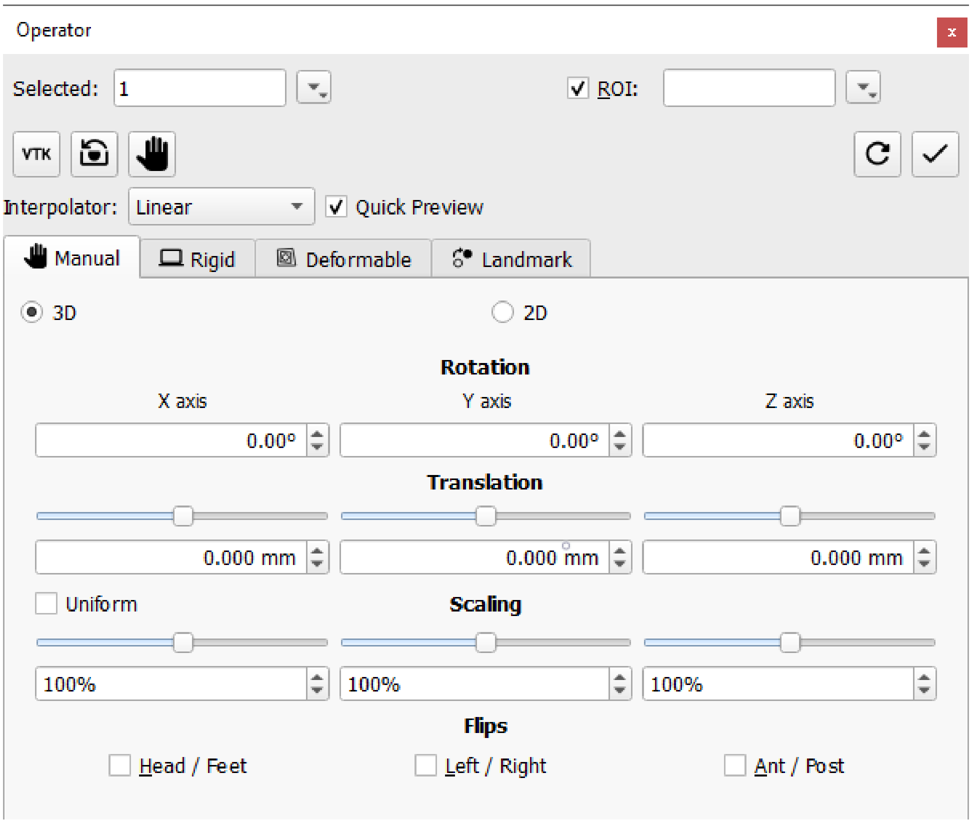
The **Interpolator** drop down menu designates which interpolator will be used during the transformation. The default interpolator value is **Linear**.

☑ **Tip:** When manipulating atlases and other integer-only datasets, linear interpolation may be detrimental. The Nearest-Neighbor (NNB) interpolator is recommended in these cases to preserve integer values upon transformation.

The **Quick Preview** option enables VivoQuant to render a low resolution version of the registration. Note: this toggle does not execute a registration but only allows a faster low resolution rendering after a registration as been computed via the **Register** button. Users can apply by clicking **Apply** in the **Operator** menu.

3D and 2D Manual Options

3D and 2D manual registration options are available in the first tab of the operator. Images/ROIs can be rotated up to 360 degrees around their X, Y and Z axis; translated in any direction along their X, Y and Z axis; and scaled in any dimension. The reorientation will be performed on all images/ROIs selected at the top of the operator window.



Selected: 1

☑ ROI:

Interpolator: Linear

☑ Quick Preview

● 3D ○ 2D

	X axis	Y axis	Z axis
Rotation	0.00°	0.00°	0.00°
Translation	0.000 mm	0.000 mm	0.000 mm
Scaling	100%	100%	100%

☐ Uniform

☐ Head / Feet ☐ Left / Right ☐ Ant / Post

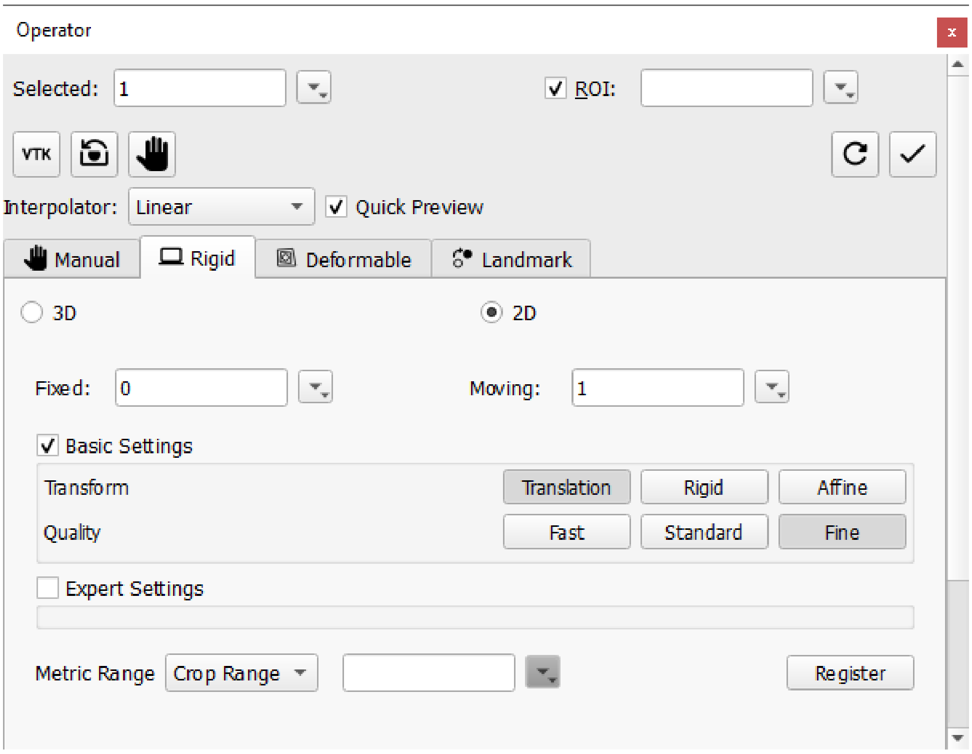
3D and 2D Manual Registration

- **Rotation** is completed by either using the up and down buttons next to the box or by typing in the number of degrees you wish to rotate the image. Once the desired positioning has been achieved, click ‘OK’ to apply the transformation.
- **Translation** is achieved by scrolling the bar to the left or the right or typing in the number of mm to be moved in the box below. Translation can also be achieved by holding the “Ctl” button on the keyboard and dragging images in the Viewports.
- **Flips** can be performed about any of the three axes by selecting the check box for Head/Foot, Left/Right, or Anterior/Posterior.
- **Scaling** can be enabled in the Operator menu. When enabled, images and ROIs can be scaled during reorientation by scrolling the bar to the left or right or typing in the % by which to scale. To scale uniformly in all three dimensions, check the “Uniform” box.

❗ **Warning:** When scaling data, please use caution, as scaling can lead to errors in quantitation. For more information, refer to the Treatment of Quantitative Data page.

3D and 2D Automatic Options

3D and 2D automatic registration options can be found in the second tab of the operator. There are **Basic Settings** (default) and **Expert Settings** available for each type of automatic registration.



Selected: 1

☑ ROI:

Interpolator: Linear

☑ Quick Preview

○ 3D ● 2D

Fixed: 0

Moving: 1

☑ Basic Settings

Transform: Translation

Quality: Fine

☐ Expert Settings

Metric Range: Crop Range

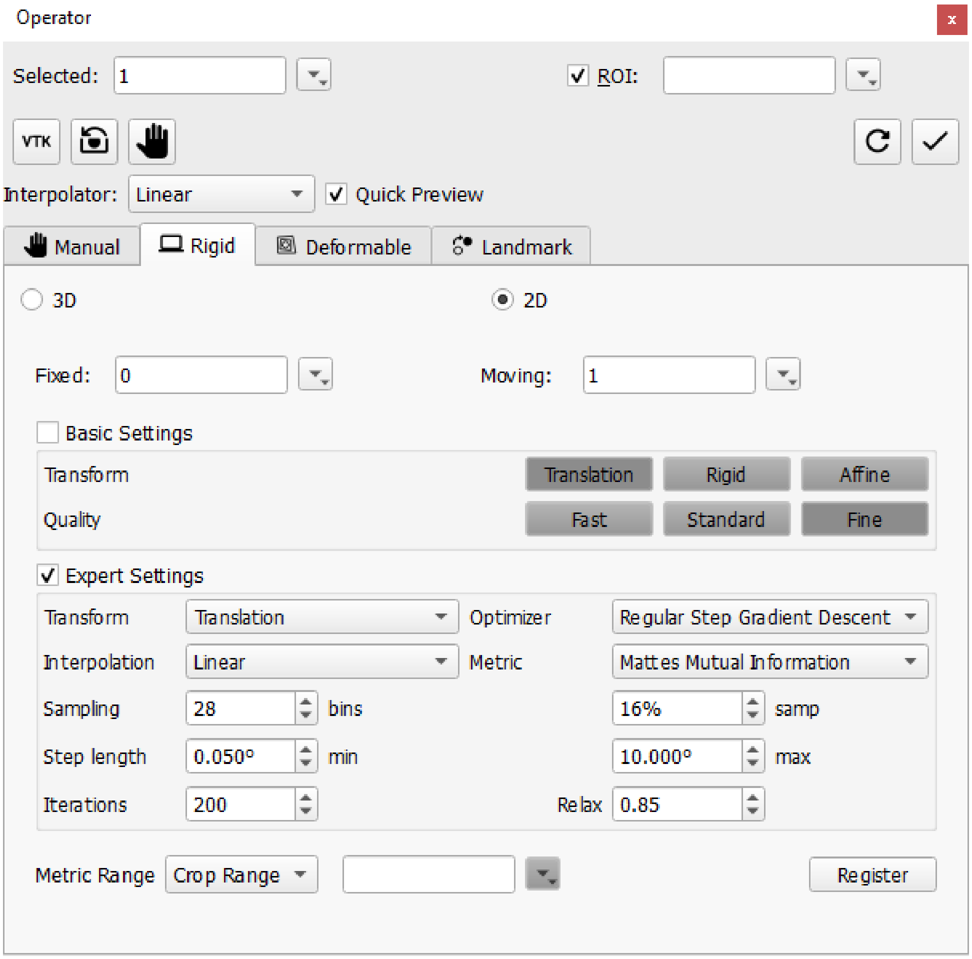
3D and 2D Automatic Registration

The default options for registering data include **Translation**, **Rigid** and **Affine**. The **Translation** registration is a rigid registration which will shift the input data set in the (x,y,z) directions. The **Rigid** registration will rotate and translate the input data set. The **Affine** registration is a linear transformation which will rotate, translate, shear and scale the input data set.

Transform	Description
Translation	Translations only
Rigid	Translations and rotations only
Affine	Translations, rotations, scalings, and shearings

Quality	Description
Fast	Fastest, but least detailed
Standard	Average
Fine	Slowest, but most detailed

The **Expert Settings** are intended for experienced users only and provide access to a variety of transform, optimization, interpolation, and metric (figure-of-merit) schemes. User-configurable fields are also provided for the number of sampling bins, minimum and maximum step length, maximum number of iterations, percentage of voxels to be used for registration, and a relaxation factor.



Selected: 1

☑ ROI:

Interpolator: Linear

☑ Quick Preview

○ 3D ● 2D

Fixed: 0

Moving: 1

☐ Basic Settings

Transform

Quality

☑ Expert Settings

Transform: Translation

Optimizer: Regular Step Gradient Descent

Interpolation: Linear

Metric: Mattes Mutual Information

Sampling: 28 bins

16% samp

Step length: 0.050° min

10.000° max

Iterations: 200

Relax: 0.85

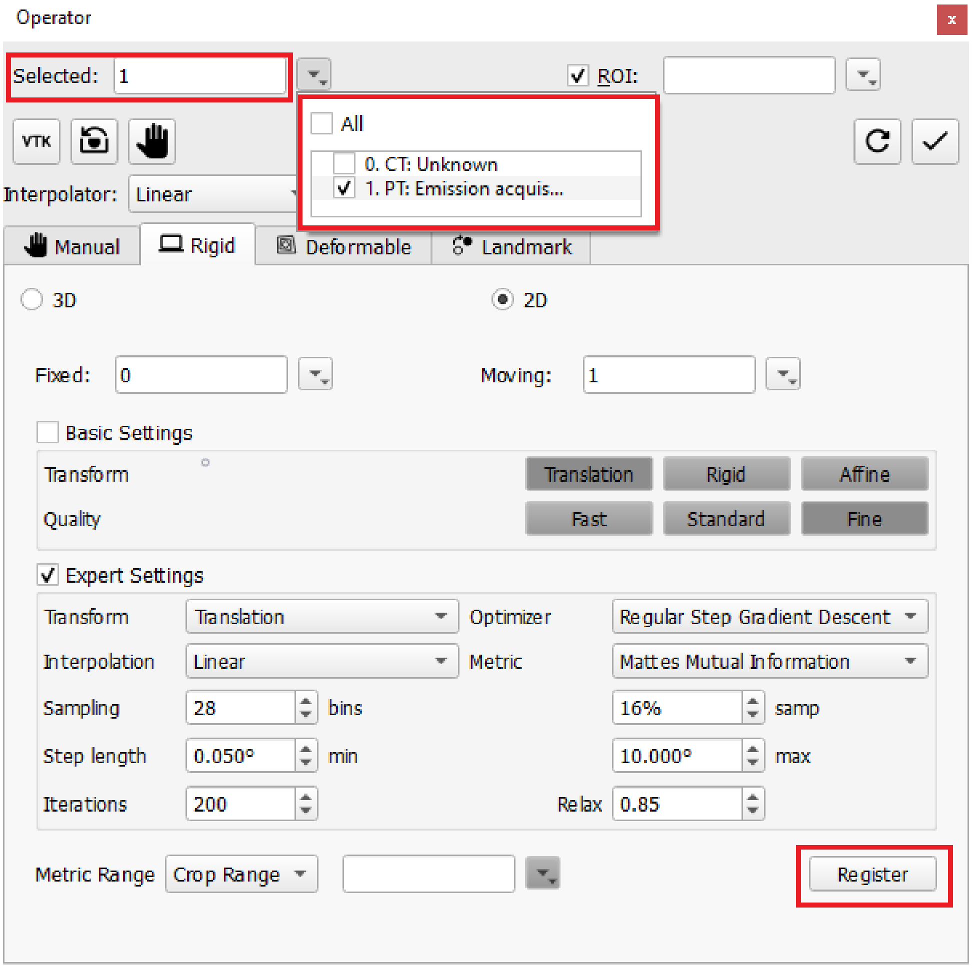
Metric Range: Crop Range

Expert Settings

Option	Description
Transform	Type of transform used
Optimizer	Method used to determine how to move image in response to changes in metric
Interpolation	Interpolator used during the registration procedure
Metric	Metric used when calculating the similarity between moving and fixed images
Sampling Bins	Number of bins used for calculating the histogram in the Mattes MI metric (only applies when Metric is Mattes Mutual Information)
Sampling Percent	Percentage of voxels in the image to use when calculating the metric (only applies when Metric is Mattes Mutual Information, or Mutual Information)
Step Length (min)	Minimum step size the optimizer is permitted to take
Step Length (max)	Maximum step size the optimizer is permitted to take
Iterations	Maximum number of iterations the registration process is permitted to take
Relax	Scaling factor applied to the step size when the optimizer changes direction

A crop range can also be defined which, when enabled, will perform the registration optimization calculations based solely on the voxels within the crop range. This can be useful when images have noise, regions of little to no signal, or other artifacts that may affect optimization calculations. For information about setting a crop range, see **Crop Range** under Expert Settings on the 3D ROI Tool page.

To begin the registration, select the desired dataset and click **Register**. A window will appear that shows information about the progress of the optimization.



Selected: 1

☑ ROI:

☐ All
☐ 0. CT: Unknown
☑ 1. PT: Emission acquis...

Interpolator: Linear

○ 3D
● 2D

Fixed: 0
Moving: 1

☐ Basic Settings

☑ Expert Settings

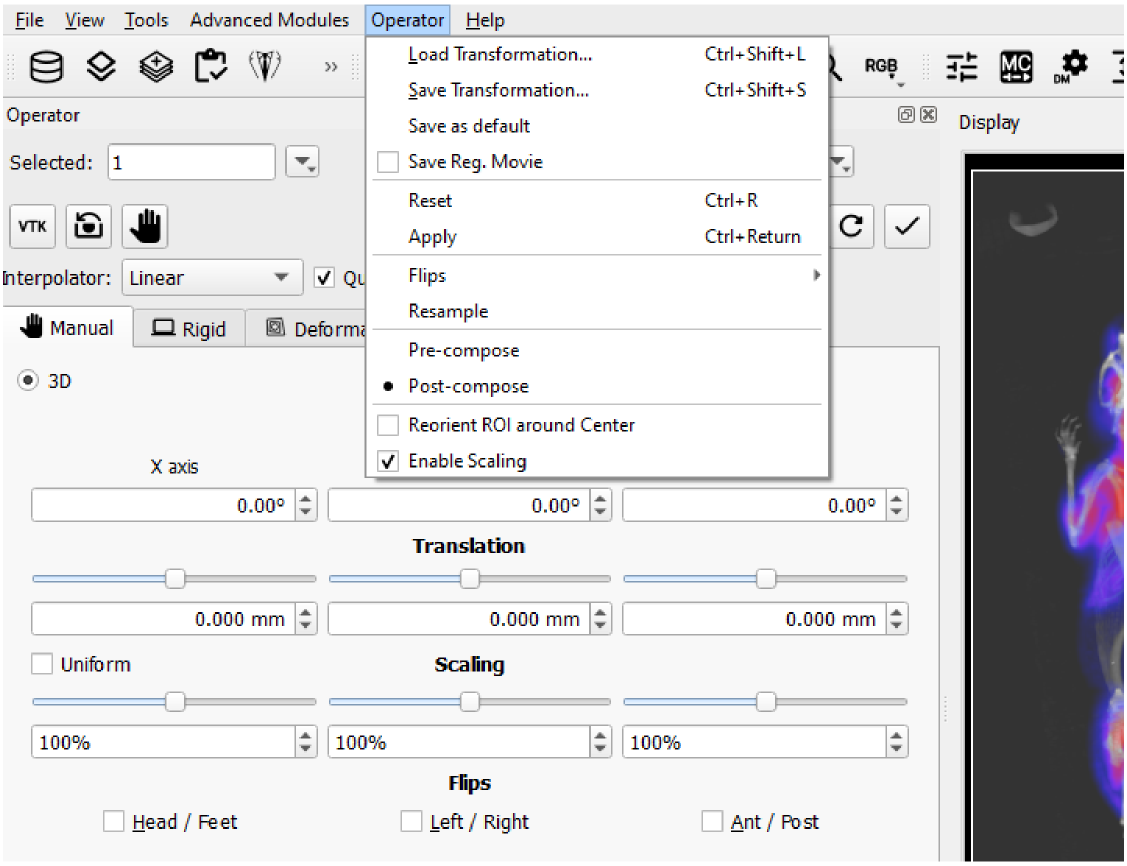
Transform: Translation
Optimizer: Regular Step Gradient Descent
Interpolation: Linear
Metric: Mattes Mutual Information
Sampling: 28 bins
16% samp
Step length: 0.050° min
10.000° max
Iterations: 200
Relax: 0.85

Metric Range: Crop Range

Begin Registration

Menu Options

The **Reorientation/Registration** operator menu can be used for storing transformations, setting a default image transformation, and controlling the behavior of the operator.



Selected: 1

Interpolator: Linear

☑ Qu

● 3D

0.00° | 0.00° | 0.00°

0.000 mm | 0.000 mm | 0.000 mm

☐ Uniform

100% | 100% | 100%

☐ Head / Feet ☐ Left / Right ☐ Ant / Post

Operator Menu

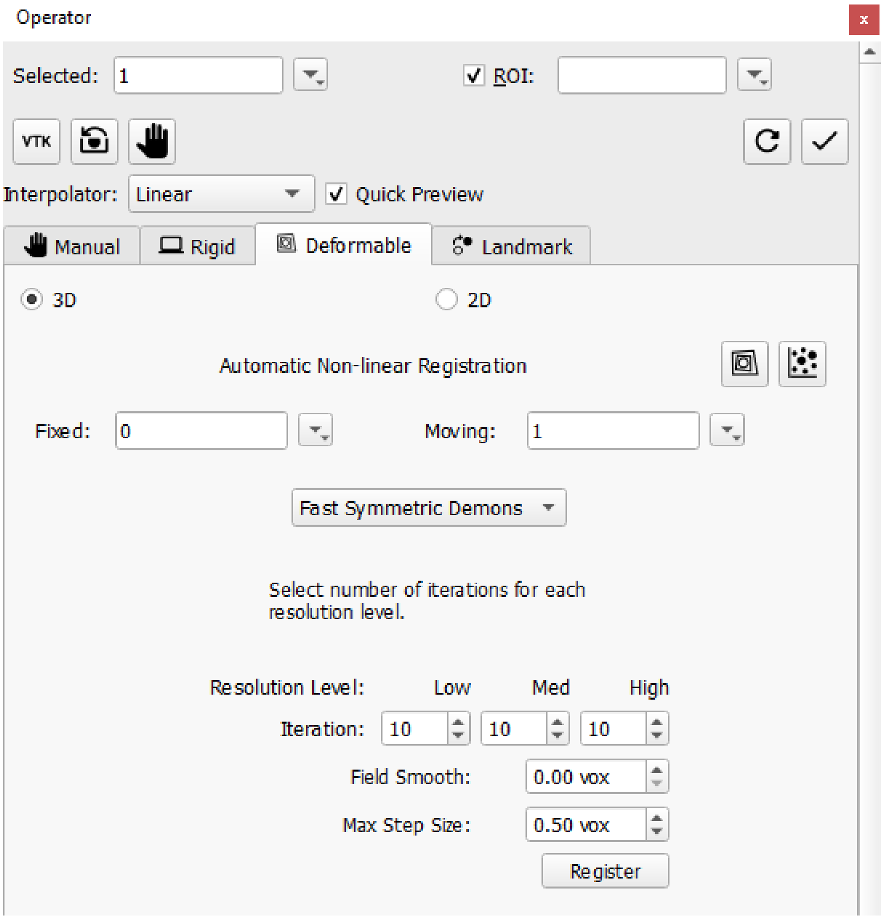
Option	Keyboard Shortcut	Description
Load Transformation...	Ctrl+Shift+L	Applies a pre-defined transformation to the active data set.
Save Transformation...	Ctrl+Shift+S	Saves the current transformation settings (rotation, translation, flips) into a .xml file.
Save as default		Saves the current transformation settings (rotation, translation, flips) as default settings for image data. If the **Apply Default Shift** checkbox is selected, these settings will be automatically applied to any image data that then gets loaded. See the How To Guide for more on setting a default image shift.
Reset	Ctrl+R	Resets all transformation settings (rotation, translation, flips) back to the default values.
Apply	Ctrl+Return	Applies the current transformation settings (rotation, translation, flips) to the active data set.
Flips		Provides the option of flipping the data in any of three directions, described as Head/Feet, Left/Right, and Anterior/Posterior.
Resample		Directs the user to the Resample Data tool. The Resample Data tool allows rebinning of reconstructed data into an arbitrary voxel size.
Pre-compose		Transformation which applies T1 to the source, and then applies T2 to that result to obtain the target.
Post-compose		Transformation which applies T2 to the source, and then applies T1 to that result to obtain the target.
Reorient ROI around center		Sets reference point for transformation as center of ROI instead of center of image.
Enable scaling		Toggles appearance of Scaling under 3D and 2D manual registration panels.

Automatic Non-Linear Registration

The **3D Automatic Non-Linear Registration** tool provides deformable registration of the data by computing a unique transformation matrix for all voxels of data represented. After selecting your preference from the dropdown, the number of iterations for each resolution level can be adjusted. Drop-down preferences include: Fast Symmetrical Demons, Symmetric Demons, Diffeomorphic Demons, and Demons. To show the deformed grid overlaid or a heatmap of the Deformable vector field over of the image, use the toggle buttons.

To learn more about the Non-Linear Registration techniques please visit the link below:

- http://www.insight-journal.org/browse/publication/154



Selected: 1

☑ ROI:

Interpolator: Linear

☑ Quick Preview

● 3D ○ 2D

Fixed: 0

Moving: 1

Fast Symmetric Demons

Select number of iterations for each resolution level.

Resolution Level:	Low	Med	High
Iteration:	10	10	10

Field Smooth: 0.00 vox

Max Step Size: 0.50 vox

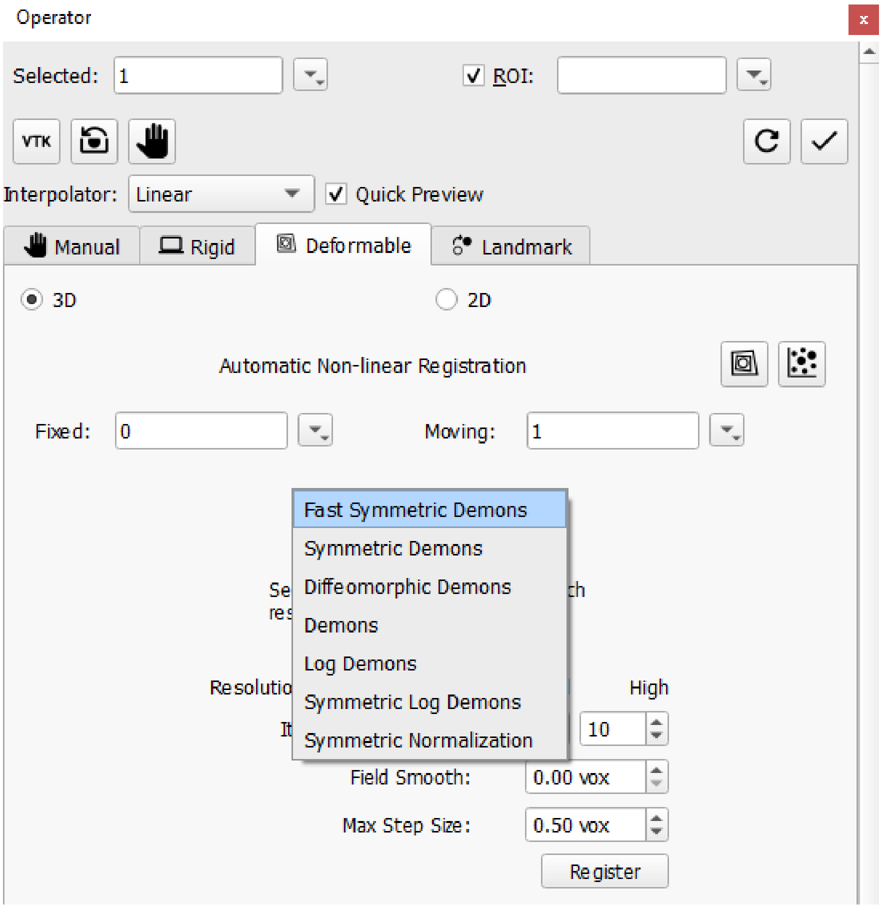
Non-Linear Registration

Automatic Slice-by-Slice Non-Linear Registration

The **2D Automatic Slice-by-Slice Non-Linear Registration** tool provides deformable registration of the data by computing individual transformation matrices for each voxel of data represented. After selecting your preference from the dropdown, the number of iterations for each resolution level can be adjusted.

To learn more about the Non-Linear Registration techniques please visit the link below:

- http://www.insight-journal.org/browse/publication/154



Selected: 1

☑ ROI:

Interpolator: Linear

☑ Quick Preview

● 3D ○ 2D

Fixed: 0

Moving: 1

10

Field Smooth: 0.00 vox

Max Step Size: 0.50 vox

Slice-by-Slice Non-Linear Registration

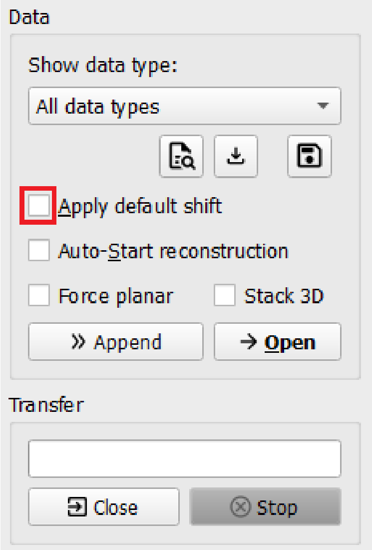
How to Set a Default Image Shift

One of the most powerful features of the NanoSPECT is its ability to automatically register SPECT and CT data to create anatomically and functionally valuable fused images. Imaging without the application of any transformation typically results in data that are fused well within 1.5mm in any direction. However, taking the time to set up a default image shift can help insure that all image acquisitions are perfectly fused.

Make a simple phantom, but one that breaks symmetry along multiple directions. A syringe with an air bubble, placed in the bed at an angle works well.

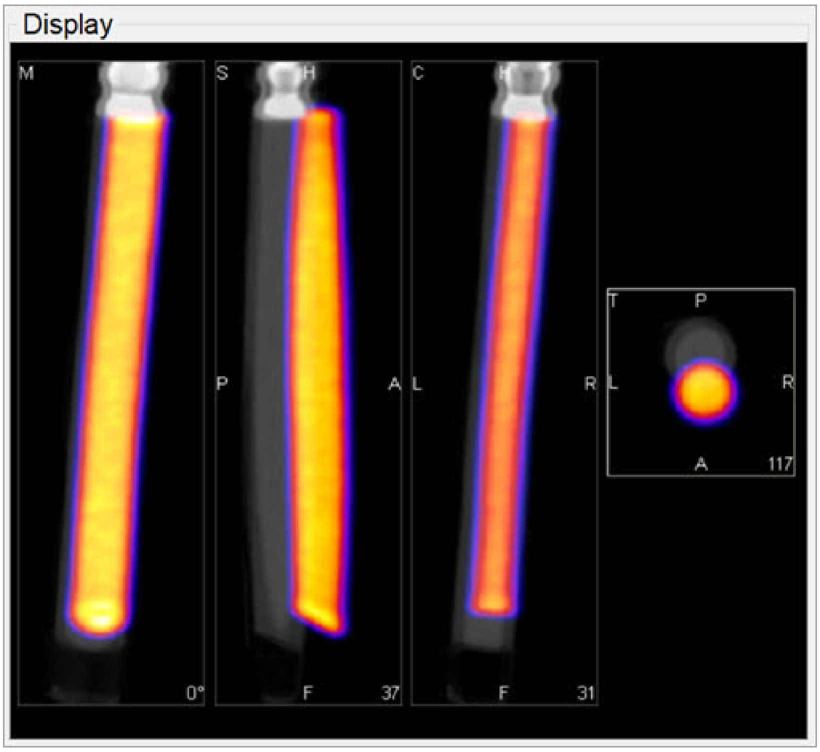
Collect an image/CT of the phantom. It is recommended that standard reconstructions (or better) are used for both the image and the CT to enable more precise transformation settings.

1. Uncheck the **Apply Default Shift** box located in the DICOM browser.



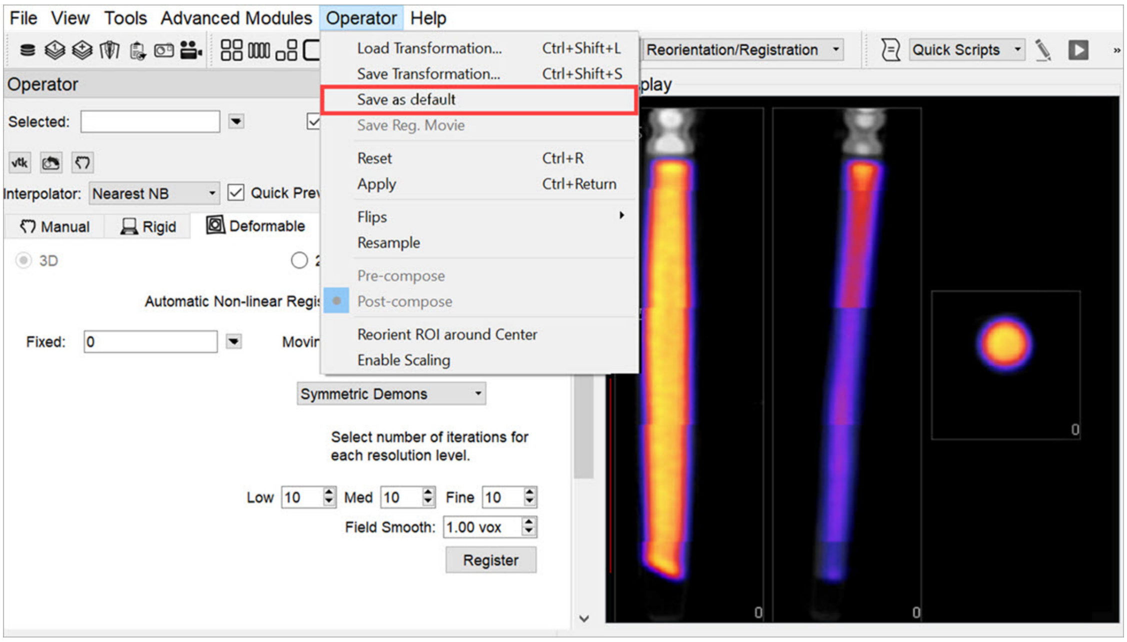
Open Data

2. Load the data into VivoQuant.



Load Data

3. Use the reorientation tool to shift and/or rotate the image data set (Input 1) so that the image and CT data are perfectly aligned. Typically, only shifts are needed for this operation. If rotations are needed, they should be only plus/minus 1 degree. Before clicking **Apply**, go to **Operator** > **Save As Default** and save the transformation



Interpolator: Nearest NB

Fixed: 0

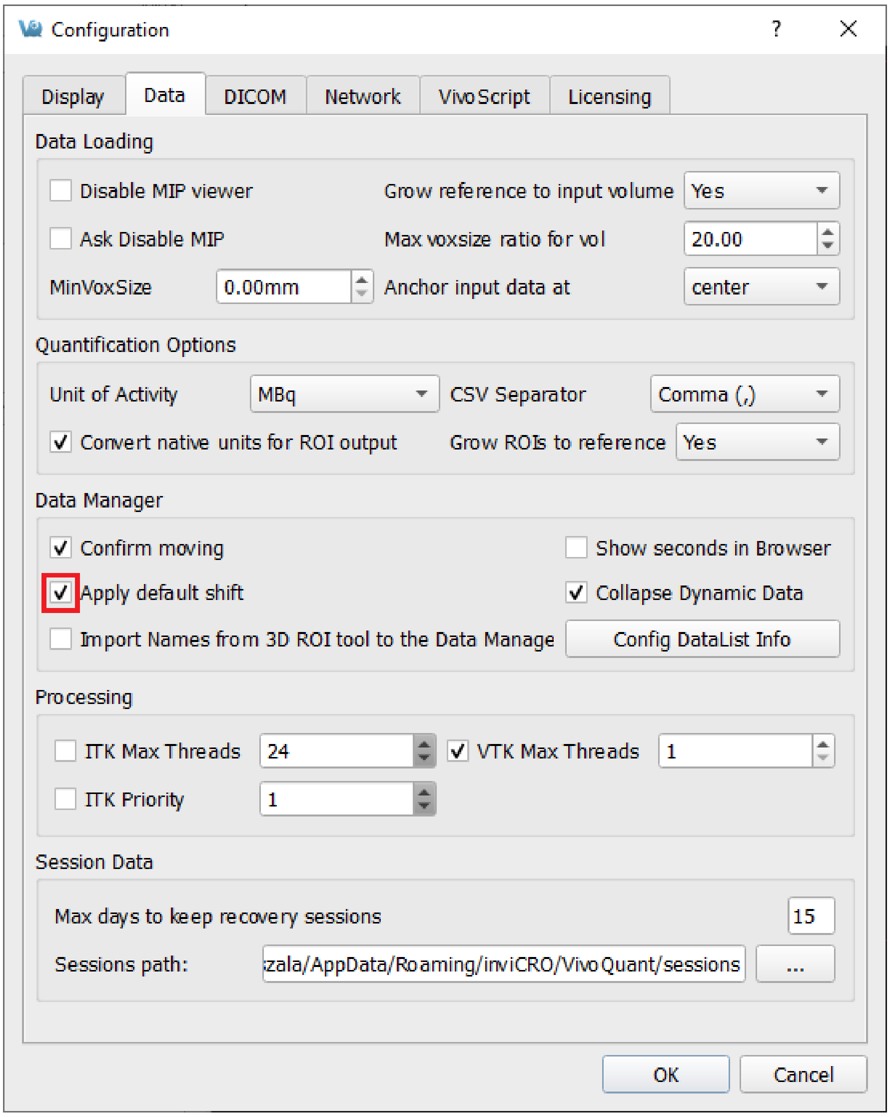
Symmetric Demons

Low 10 Med 10 Fine 10

Field Smooth: 1.00 vox

Save as Default

4. Return to the Data Browser or go to the Tools Menu and re-check the **Apply Default Shift** box.



☐ Disable MIP viewer

Grow reference to input volume: Yes

☐ Ask Disable MIP

Max voxsize ratio for vol: 20.00

MinVoxSize: 0.00mm

Anchor input data at: center

Unit of Activity: MBq

CSV Separator: Comma (,)

☑ Convert native units for ROI output

Grow ROIs to reference: Yes

☑ Confirm moving

☐ Show seconds in Browser

☑ Apply default shift

☑ Collapse Dynamic Data

☐ Import Names from 3D ROI tool to the Data Manage

☐ ITK Max Threads: 24

☑ VTK Max Threads: 1

☐ ITK Priority: 1

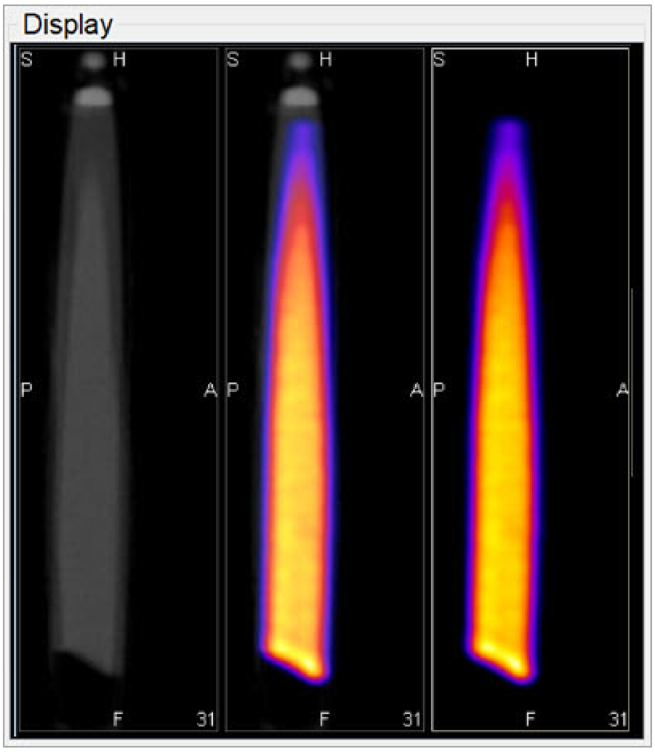
Max days to keep recovery sessions: 15

Sessions path: zala/AppData/Roaming/inviCRO/VivoQuant/sessions

Apply Default Shift

5. Reload the image/CT phantom data that were just acquired. They – and all other data sets – will now be perfectly

fused.



Reload Data

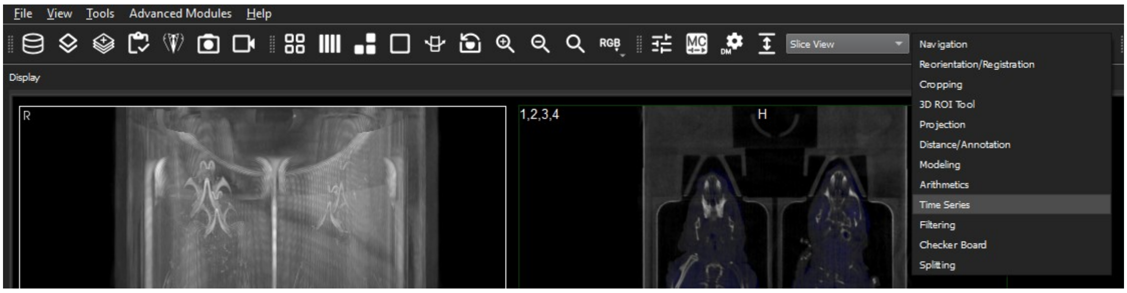
ℹ **Note:** This same formalism may be used to generate other Transformation files. Instead of choosing **Save as Default** in the operator menu, choose **Save Transformation**. Then, it is possible to later load that transformation (using the **Load Transformation** option in the operator menu). These saved transformations are useful when fusing data from other modalities with NanoSPECT CT data, for example.

Time Series

The **Time Series** operator provides an easy way to visualize sets of dynamic data as a time series. This operator can be used to play slice views of each image of a collection in sequence.

Getting There

The **Time Series** operator can be accessed via the pull-down menu on VivoQuant's front panel.

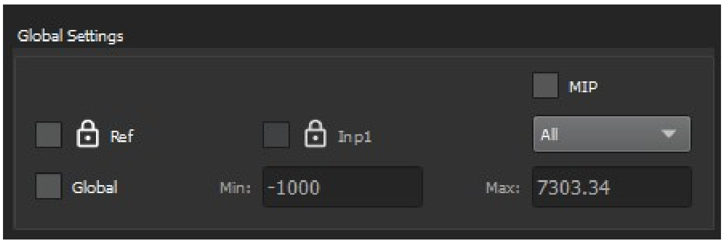


Time Series Operator

Using the Operator

Data must be loaded into VivoQuant in the correct time-order, with the reference image (if any) loaded first. Use the **Data Manager** to sort the datasets as necessary.

If there is a reference image loaded, check **Lock Ref** to keep the reference image visible with all other images of the series. Check **Lock Inp1** to keep the image in the **Input 1** position visible with all other images of the series.



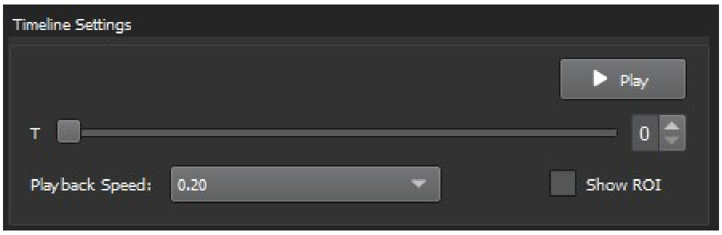
Min: -1000

Max: 7303.34

Lock Image

The **Time Series** operator also enables users to set a global windowing, which will apply to all loaded images. The windowing format (either Min/Max or Level/Width) is determined by the Display Configuration. To set it, simply check the **Global** box and enter appropriate windowing values into the respective boxes.

Timeline Settings



T: 0

Playback Speed: 0.20

Timeline Settings

Use the slider or image index field to manually scroll through the datasets of the series. Click **Play** to run the sequence in a loop.

The Playback Speed pull-down menu allows you to select the frame duration for all frames. There are two groups available:

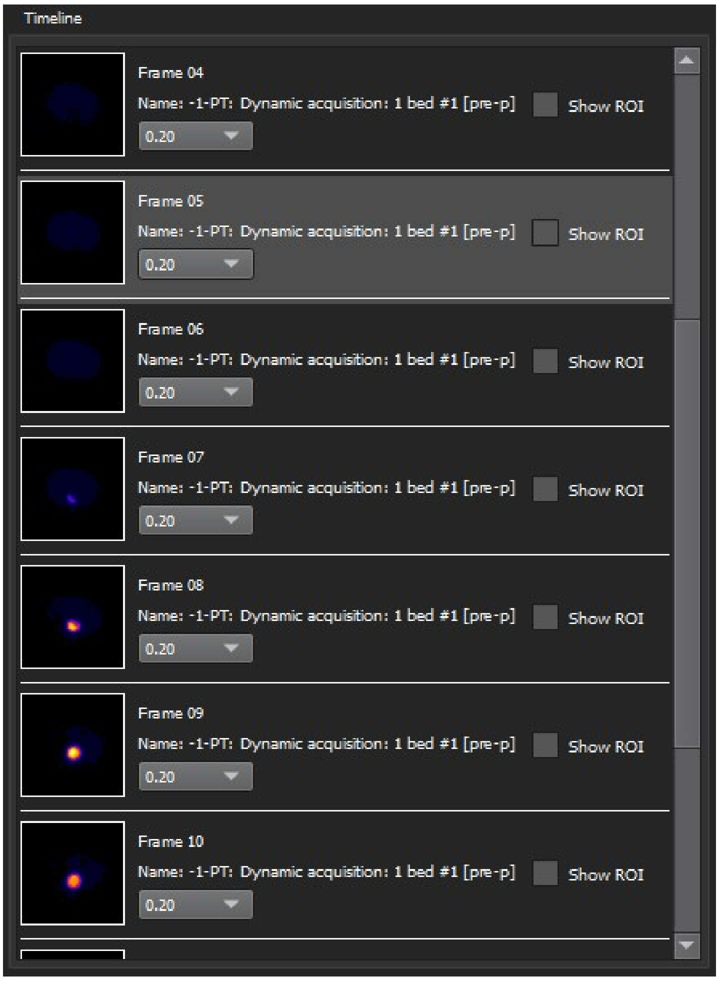
1. **Uniform Frame Duration**: Select a fixed frame duration to apply to all frames.
2. **Variable Frame Duration**: Choose between the following options:
    - Standard: Use the FrameAcquisitionDuration or ActualFrameDuration as obtained from the DICOM Header.
    - Logarithmic: Apply a logarithmic function to each frame duration obtained from the DICOM Header.
    - Square Root: Apply a square root function to each frame duration obtained from the DICOM Header.
    - Reduce Min to Sec: Reduce the duration of each frame obtained from the DICOM Header by a factor of 60.

ℹ **Note:** The **Variable Frame Duration** option retrieves frame duration information from the DICOM Header. If this data is unavailable or needs to be modified, the user can open the Frame Time Editor from the **Tools** menu to add or modify these values.

The user can select the **Other...** option to add a custom frame duration.

The Show ROI option in **Timeline Settings** section enables or disables ROI's on all frames.

Timeline



Frame 04
Name: -1-PT: Dynamic acquisition: 1 bed #1 [pre-p] ☐ Show ROI
0.20

Frame 05
Name: -1-PT: Dynamic acquisition: 1 bed #1 [pre-p] ☐ Show ROI
0.20

Frame 06
Name: -1-PT: Dynamic acquisition: 1 bed #1 [pre-p] ☐ Show ROI
0.20

Frame 07
Name: -1-PT: Dynamic acquisition: 1 bed #1 [pre-p] ☐ Show ROI
0.20

Frame 08
Name: -1-PT: Dynamic acquisition: 1 bed #1 [pre-p] ☐ Show ROI
0.20

Frame 09
Name: -1-PT: Dynamic acquisition: 1 bed #1 [pre-p] ☐ Show ROI
0.20

Frame 10
Name: -1-PT: Dynamic acquisition: 1 bed #1 [pre-p] ☐ Show ROI
0.20

Timeline

The **Timeline** section displays a list of frames with preview images. Here, users can select the duration and enable or disable ROIs for each individual frame. Multiple frames can be selected to apply changes simultaneously.

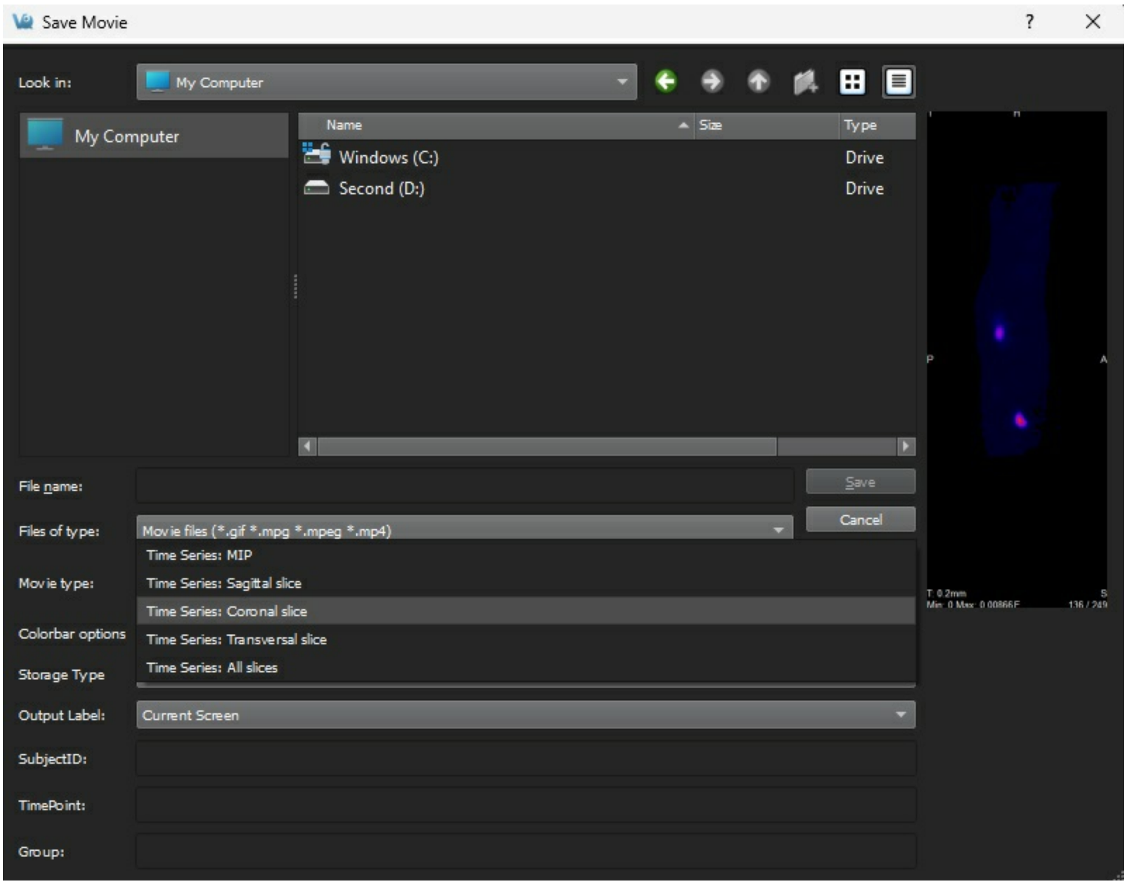
Default Frame Duration

When the **Time Series** is opened, it uses a default frame duration. This value can be changed in the **Configuration Tool** under the **Display** tab in the **General** section.

Saving a Movie

To save a **Time Series** movie, open the **Save Movie** dialog with the **Time Series** operator. This can be done by clicking the **Save Movie** icon in the toolbar ; by navigating to **File** > **Save Movie**, or by the keyboard shortcut **Ctrl + M**.

The options for the output movie are similar to those in the regular Save Movie dialog box. The only difference is that the options in the **Movie Type** drop-down box reflect the **Time Series** movie types. Once the desired options are set, click **Save** to save the movie file.



Look in: My Computer

Files of type: Movie files (*.gif *.mpg *.mpeg *.mp4)

Output Label: Current Screen

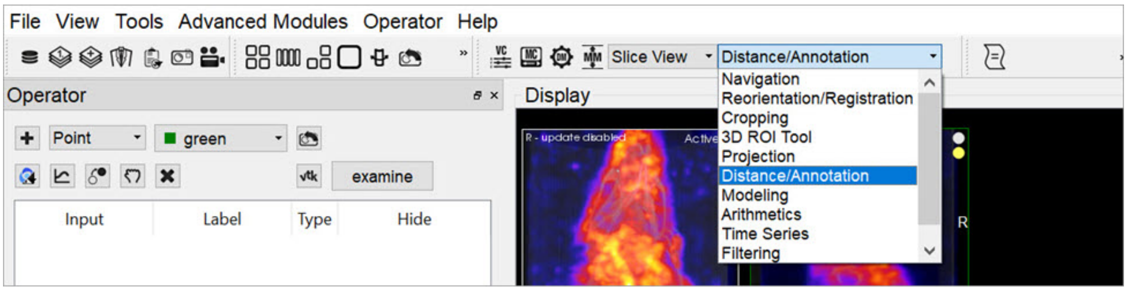
Save Movie

Distance / Annotation Tool

The **Distance/Annotation** tool enables you to measure the distance between two points in any image. For example, it can be used to measure the size of a tumor by measuring its length, depth and width. One of the most powerful options available with the distance measure is the capability to perform landmark co-registration.

Getting There

The **Distance/Annotation** tool can be accessed via the tool pull-down menu on VivoQuant's front panel.



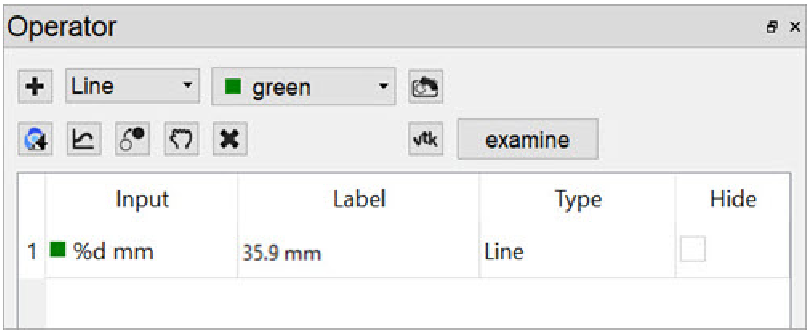
Input	Label	Type	Hide

Distance / Annotation Tool

Using the tool

Upon selecting the tool, the**Distance/Annotation** operator is displayed. The physical distance between two points can be measured by clicking on the **Add New** icon + to add an object. To measure distance, left-click on two points of the image. A line is displayed between the two points to show what is being measured.

In the **Distance/Annotation** operator, each line is identified by a unique color tag. For each line, the 3D start and end points of the line are displayed as well as the length of the line (in mm). Multiple distances can be measured on the same image and are easily distinguished by their unique color. The results can be saved into an Excel file by clicking **Save**. The Profile function enables a graphic plot of the distance to be displayed for both the reference and the input data.



	Input	Label	Type	Hide
1	🟩 %d mm	35.9 mm	Line	☐

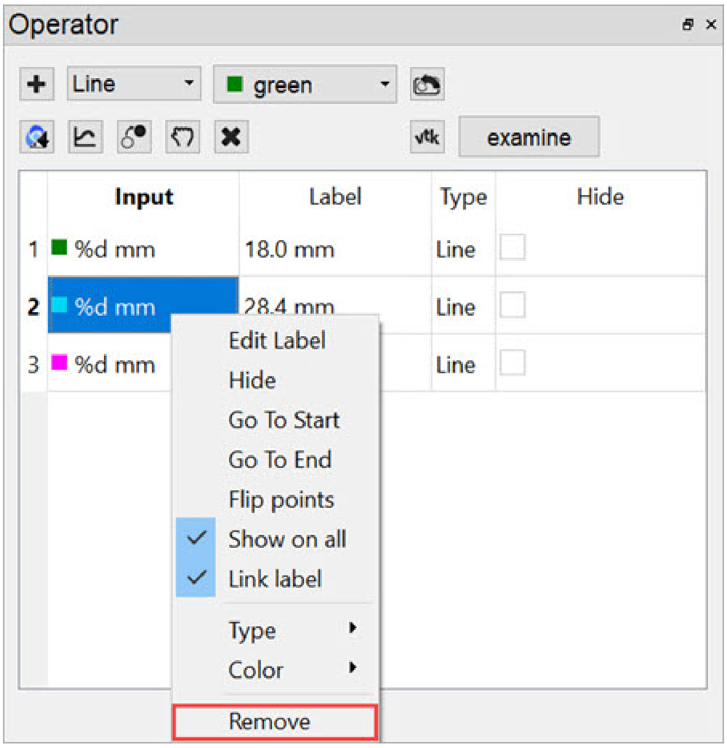
Add Object

Goto with-in the object

Since a single left click sets a new point, you have to use a single middle mouse button click to go to the given position in the two respective other slices.

Removing Distance Measures

Right-click on any of the distance measures and click **Remove** to delete the distance measure completely.

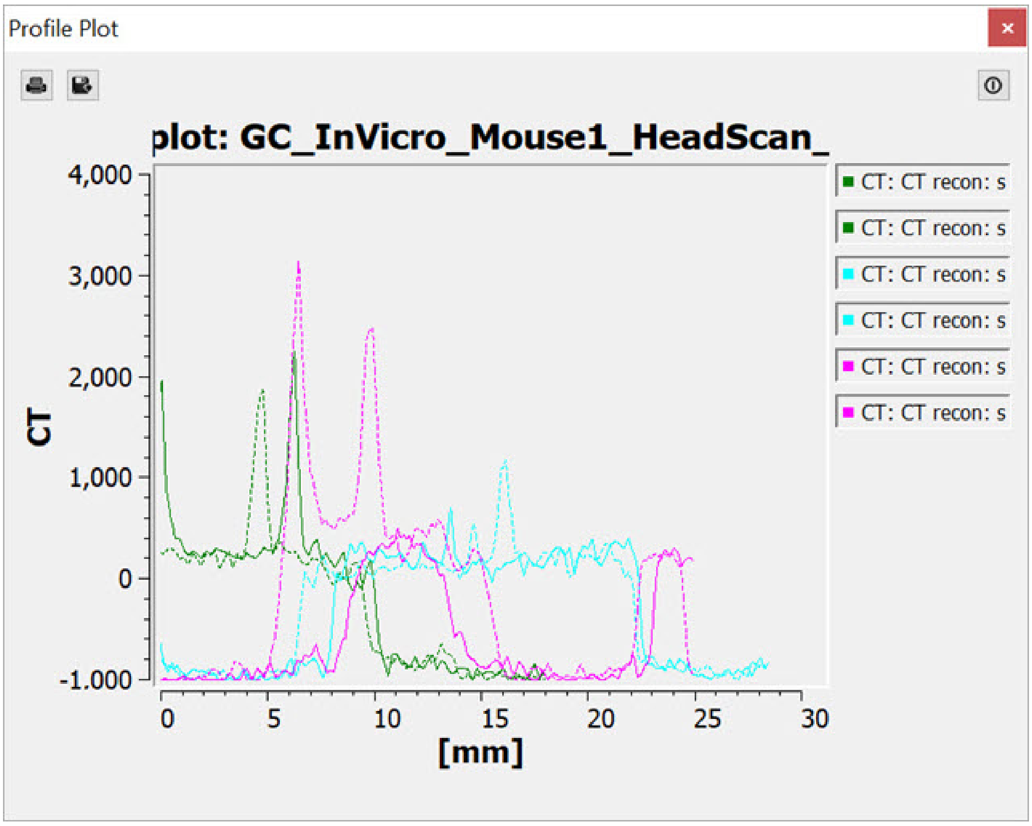


	Input	Label	Type	Hide
1	🟩 %d mm	18.0 mm	Line	☐
2	🟦 %d mm	28.4 mm	Line	☐
3	🟪 %d mm		Line	☐

Remove Distance Measure

Profile

The **Profile** tool plots the values in each voxel through which the line passes. Values are displayed for both Reference and Input data sets and, given proper calibration, the plot values will be in Houndsfield units and MBq for CT and NM data sets, respectively. The **File** menu provides an option to save the Profile data as a PDF.



Profile Tool

Landmark Circle Detection

This feature is triggered via the **Landmark Circle Detection** icon. Landmark Circle Detection is basically a way to find circles in the image slices that can be used as anchor points for image registration, and is effectively used by Reorientation / Registration via the Landmark tab option.

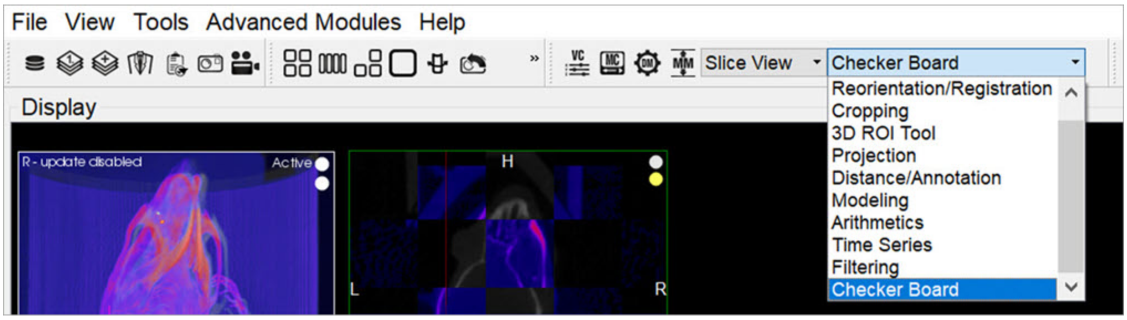
Landmark circle detection employs an algorithm known as **Hough Circle Detection**. This algorithm works best if you first create circle annotations around the circles in one slice of the image; this helps the algorithm by seeding it. The more circle annotations the better the registration will be. When you click the button the algorithm will use your annotations as known circles and will try to interpolate and detect the same circle in all other image slices, populating new annotation shapes into the list for each. Without any supplied annotation circles the Hough settings dialog will appear and allow to you to tailor the algorithm for automatic circle detection.

Checker Board

In **Checker Board** mode, the reference and input data sets are arrayed in a pattern of alternating squares. This mode is especially useful when checking image registration.

Getting There

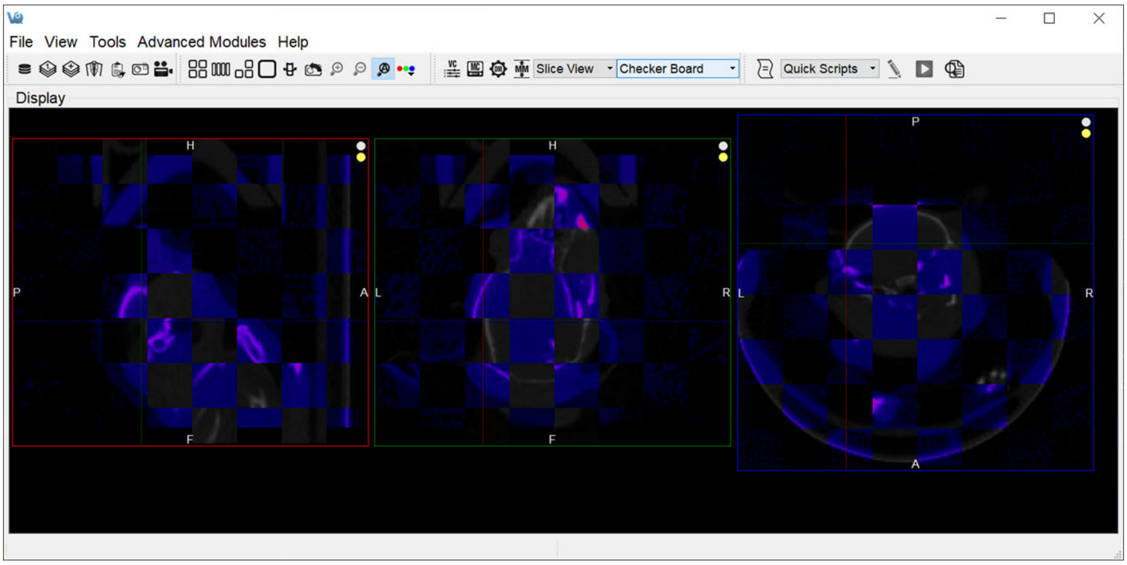
The **Checker Board** tool can be accessed via the tool pull-down menu on VivoQuant's front panel.



Checker Board Tool

Using the Tool

Upon selecting the **Checker Board** tool, the display of the coronal, sagittal, and transverse windows is automatically updated. In these windows, the reference and input data sets are displayed in an alternating grid pattern. Both the **Input 1** and **Input 2** data sets are displayed in the same squares of the checkerboard. To return to normal viewing, select Navigation in the **Tools** menu. To adjust the size of the tiles, hold Shift and use the mouse wheel.



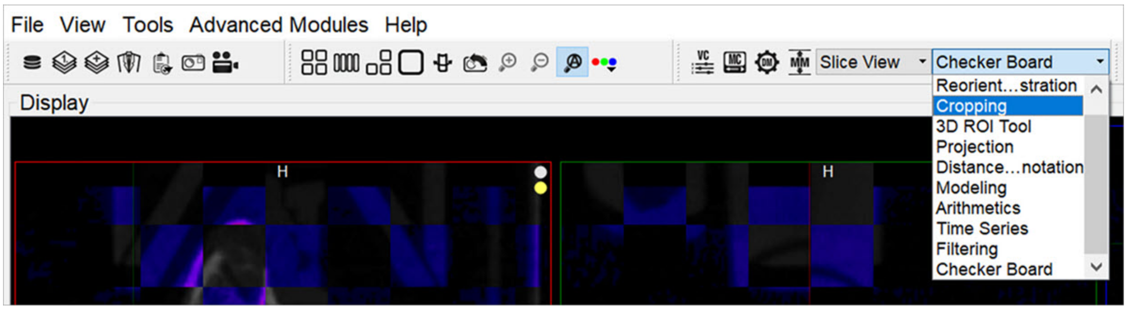
Using the Tool

Cropping Tool

The **Cropping Tool** allows images to be made smaller by removing any unwanted areas. For example, if an image has been cut, then the cropping function can be used to trim away the blank areas of the image.

Getting There

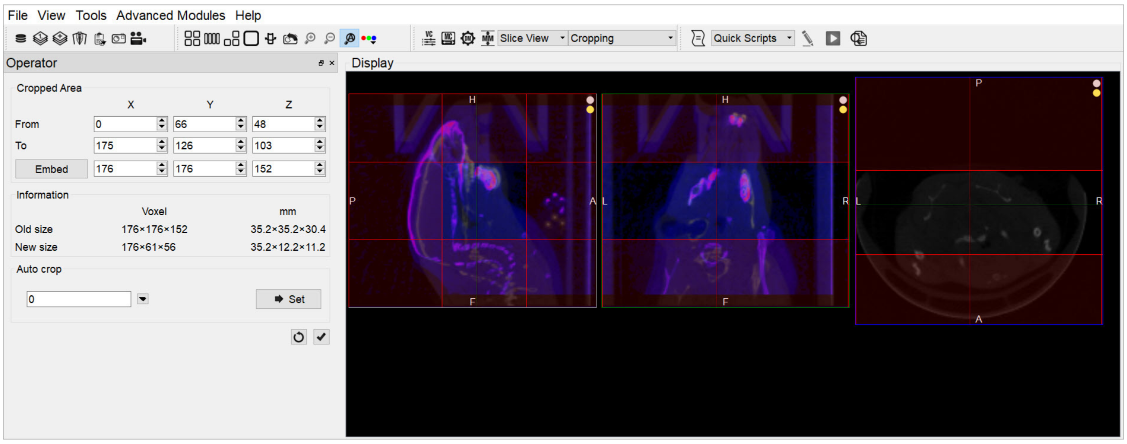
The **Cropping** tool can be accessed via the tool pull-down menu on VivoQuant's front panel.



Cropping Tool

Using the Tool

Upon selecting the **Cropping** tool, the standard view options disappear and red sliders are displayed in their place.



Cropped Area

	X	Y	Z
From	0	66	48
To	175	126	103
Embed	176	176	152

Information

	Voxel	mm
Old size	176×176×152	35.2×35.2×30.4
New size	176×61×56	35.2×12.2×11.2

Auto crop

0

Cropping Sliders

Two red sliders appear for each view direction (i.e., coronal, sagittal, and transversal). The red sliders may be moved using the mouse (click and hold on a slider and then move the mouse to move the slider) or by using the arrow keys in the cropping dialog. Manipulation of the red sliders creates a three-dimensional rectangular cropping volume. The current voxel position of the red sliders is displayed in the **Cropped Area** section of the operator window.

To apply the crop, once the red sliders are in the desired positions, click the **Crop** button ☑.

To reset the crop range sliders to their original positions, click the **Refresh** button ⟳.

The **Cropping** dialog provides information about the pixel location of each red slider (x, y, z), and current and cropped image size information in both voxels and mm. The embed function will pad background slices to increase the dimensions of the image. The auto-crop feature starts its search at the end slices of the image and adjusts the sliders towards the center of the image until a non-background voxel is detected from all 6 faces.

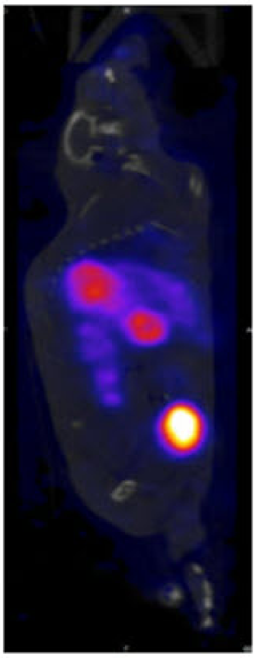


Image before cropping

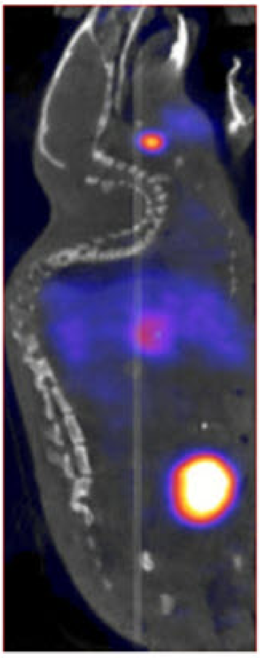


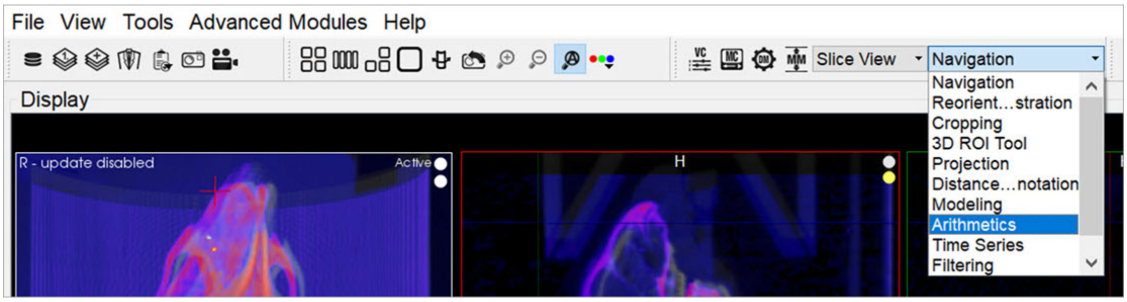
Image after cropping

Arithmetics

The **Arithmetics** operator can be used to add, subtract, multiply, divide, average or merge multiple images. Additionally, a scalar multiplier or addend can be applied to all voxels of an image with the **Arithmetic** operator.

Getting There

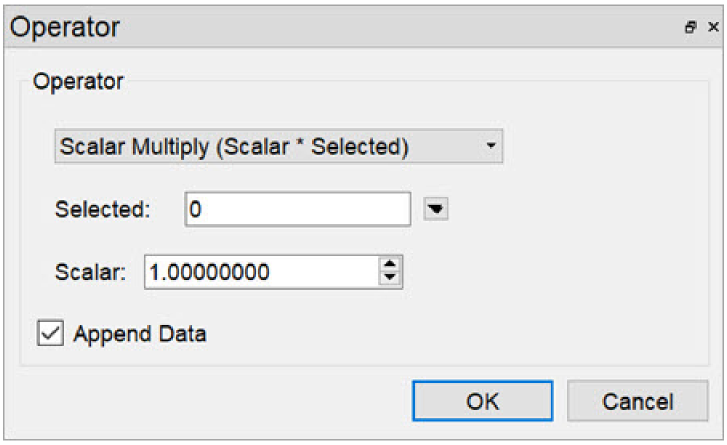
The **Arithmetics** operator can be accessed via the tool pull-down menu on VivoQuant's front panel.



Arithmetics Tool

Using the Tool

Upon selecting the operator, the **Arithmetics** window is displayed.



Scalar Multiply (Scalar * Selected)

Selected: 0

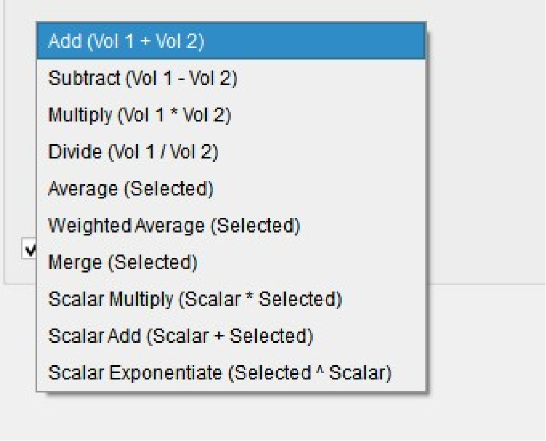
Scalar: 1.00000000

☑ Append Data

Arithmetics Tool Window

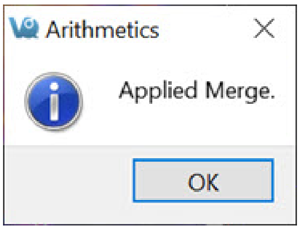
The main drop-down menu in the operator window contains a selection of the available operators. In some cases, multiple images can be selected for the operation via the Data Selector Widget.

- **Add**, **Subtract**, **Multiply**, **Divide**, and **Average**: each of these operates on two images. These operations are performed voxel-wise.
- **Scalar Multiply** and **Scalar Add**: can be applied to any of the loaded images. Set the factor or addend by increasing or decreasing the scalar value.
- **Weighted Average**: applies a time weighted average across the selected dynamic images. Weights can be set manually per-frame or derived from DICOM header entries.
- **Merge** whole integer value phantoms to load into the 3D ROI tool. It can be applied to any of the loaded images. This is very useful for fixed-volume ROI analysis.



Merge

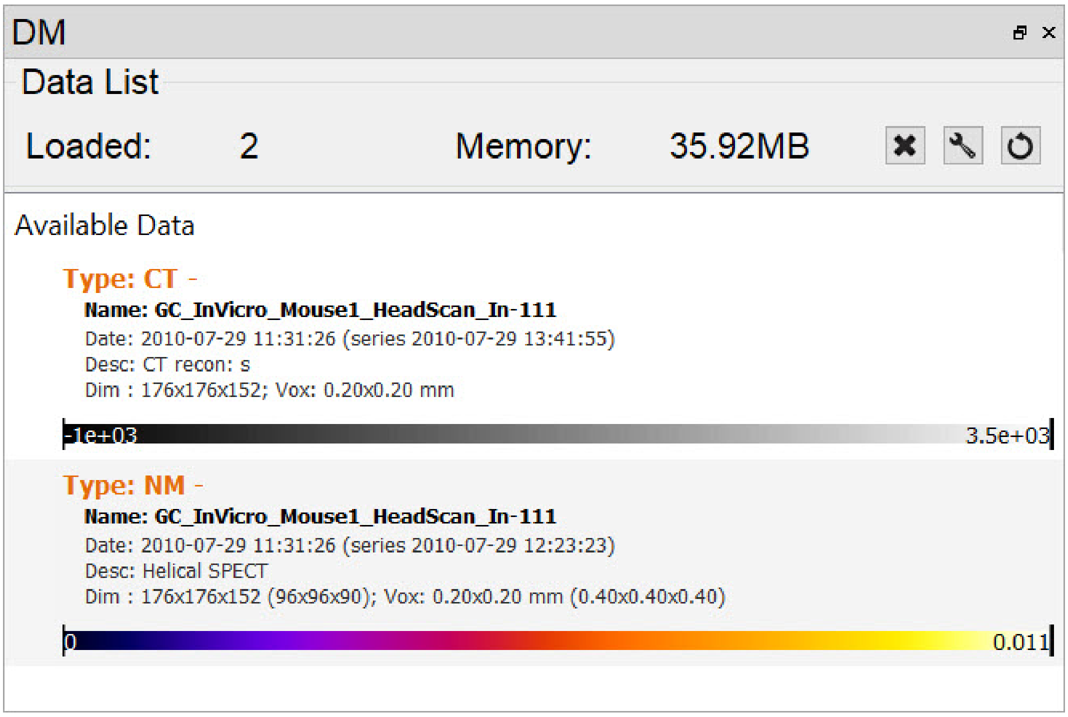
Click **OK** to perform the chosen operation. A dialog will appear to indicate successful application of the chosen function.



Applied Merge.

Operation Applied

For all arithmetic operations, the user has the option to append the resulting volume(s) or perform the function in-place, thus replacing the existing data with the amended data.



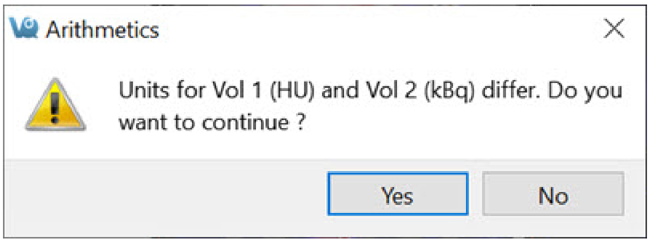
Loaded: 2 Memory: 35.92MB

Type: CT -
Name: GC_InVicro_Mouse1_HeadScan_In-111
Date: 2010-07-29 11:31:26 (series 2010-07-29 13:41:55)
Desc: CT recon: s
Dim : 176x176x152; Vox: 0.20x0.20 mm

Type: NM -
Name: GC_InVicro_Mouse1_HeadScan_In-111
Date: 2010-07-29 11:31:26 (series 2010-07-29 12:23:23)
Desc: Helical SPECT
Dim : 176x176x152 (96x96x90); Vox: 0.20x0.20 mm (0.40x0.40x0.40)

Data List

Units are considered by the **Arithmetics** operator. A warning will be displayed if an attempt is made to add, subtract, multiply, divide or average two images of differing units and will allow the user to halt the operation.



Units for Vol 1 (HU) and Vol 2 (kBq) differ. Do you want to continue ?

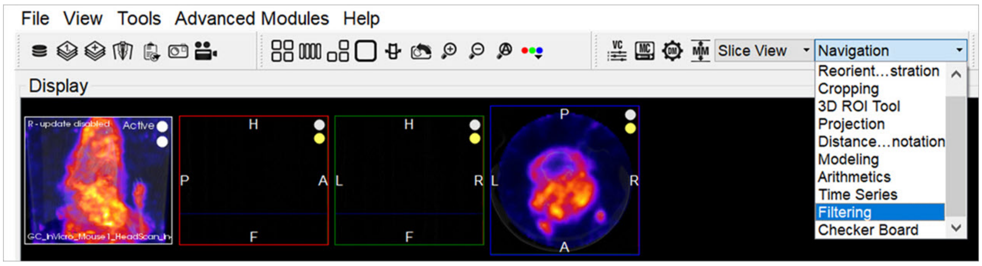
Arithmetic Units

Filtering

The **Filtering** operator offers a variety of smoothing filters with configurable input parameters and can be applied to any of the loaded images.

Getting There

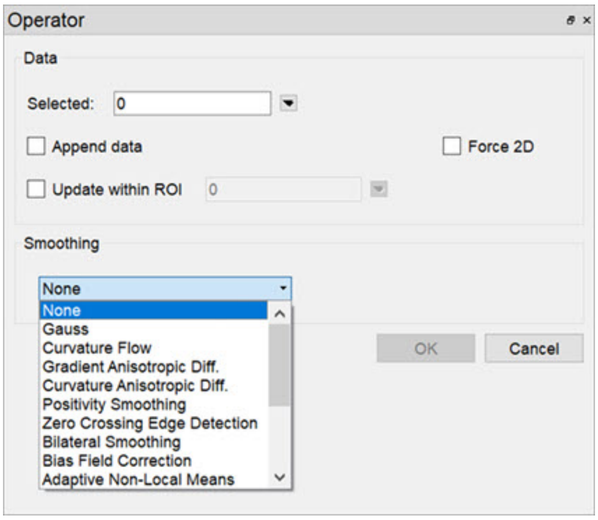
The **Filtering** operator can be accessed via the tool pull-down menu on VivoQuant's front panel.



Filtering operator

Using the Tool

Upon selecting the tool, the **Filtering** operator window is displayed.


Operator

Data

Selected: 0

☐ Append data ☐ Force 2D

☐ Update within ROI 0

Smoothing

None

Filtering operator window

Using this tool, any loaded data can be selected for smoothing via the Data Selector Widget.

Select the desired smoothing algorithm from the available options in the **Smoothing** drop-down menu. Use the parameter fields to set appropriate values. The effect of the chosen smoothing filter will be previewed in 2D in the slice views. To remove the 2D preview, go back to **None** in the drop-down menu of smoothing filters.

Currently available filters include:

- Gaussian Smoothing
- Curvature Flow
- Gradient Anisotropic Diffusion
- Curvature Anisotropic Diffusion
- Positivity Smoothing (to remove negativity from FBP reconstructions)
- Zero Crossing Edge Detection
- Bilateral Smoothing
- Bias Field Correction

Each filter uses a different subset of the configurable parameters. See the table below if parameters other than the default settings are desired.

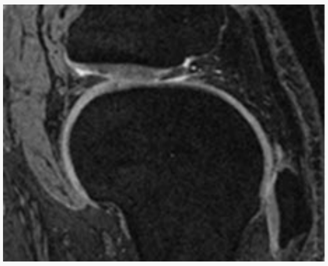
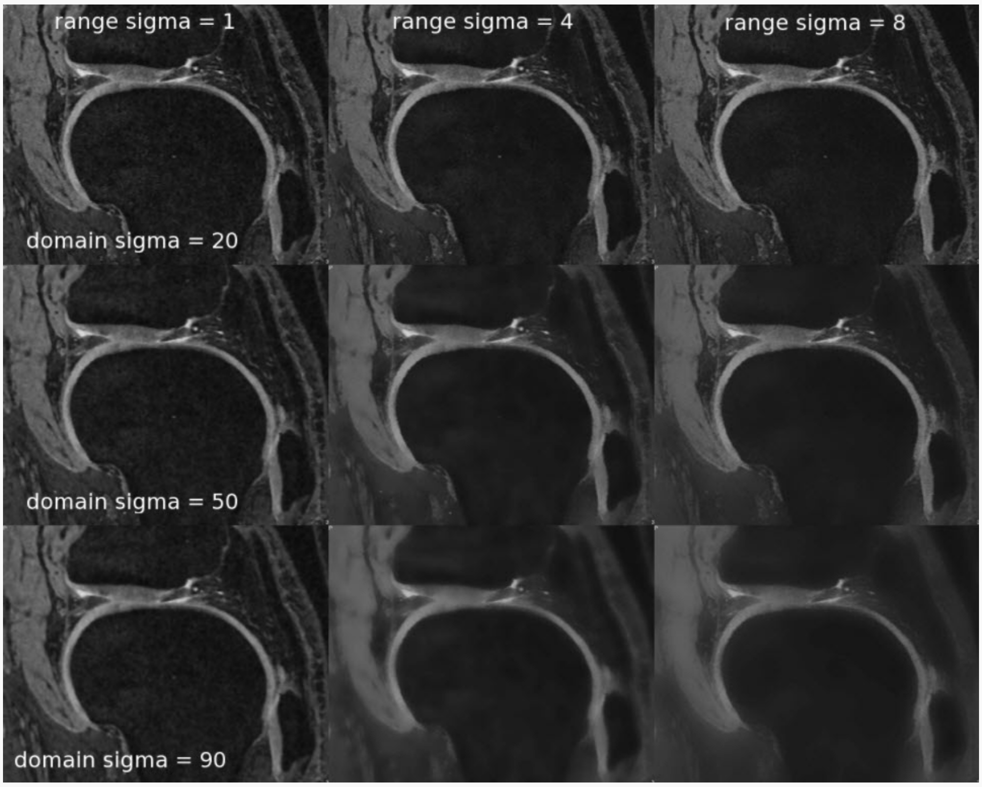
Parameter	Description	Used by	Default Value
Append Bias Field	Append the estimated bias field as an image	Bias Field Correction	not checked
FWHM	Full-width half-maximum kernel size	Gauss, Zero Crossing Edge Detection	1.00mm
Conductance	Parameter governing sensitivity to edge contrast	Gradient Anisotropic Diffusion, Curvature Anisotropic Diffusion	1
Control Points	Set the control point grid size defining the B-spline estimate of the scalar bias field	Bias Field Correction	
Converge Threshold	Minimum difference between estimates needed to end iterations	Bias Field Correction	0.001
Downsample Factor	Factor by which image voxels will be downsampled before calculating the filter	Bias Field Correction	2.0
Iter, **Max Iter**	Number of iterations	Curvature Flow, Gradient Anisotropic Diffusion, Curvature Anisotropic Diffusion, Positivity Smoothing, Bias Field Correction	5
Iterative Otsu	Toggles option to use ROIs as a mask	Bias Field Correction	checked
CutOffFrac	If the fraction of voxels that are negative falls below this value, further iterations of the filter will not be performed.	Positivity Smoothing	0.005
Time Step	Stepsize, effectively analogous to kernel width	Curvature Flow, Gradient Anisotropic Diffusion, Curvature Anisotropic Diffusion	0.125
Mask	ROI masks to use to limit filter context	Bias Field Correction	background ROI layer
Max Error	Difference between the area under the discrete Gaussian curve and the area under the continuous Gaussian	Zero Crossing Edge Detection	0.5
Range Sigma	The standard deviation of the gaussian blurring kernel in the image range. Units are intensity.	Bilateral Smoothing	50
Domain Sigma	The standard deviation of the gaussian blurring kernel in each dimensional direction. Units match image spacing units.	Bilateral Smoothing	4
Spline order	Sets the spline order defining the bias field estimat	Bias Field Correction	3

The smoothing function is executed by left-clicking on **OK**. Depending on the image size and filter selected, this may take several seconds. Once the smoothing function is applied, any subsequent operations will be based on the smoothed images.

Each filter will have different edge-preserving and noise-reduction properties. Choose the one that best suits your application.

No Smoothing	Gauss	Curvature Flow	Gradient Anisotropic Diffusion	Curvature Anisotropic Diffusion
				

The bilateral smoothing filter could take several minutes for large images in 3D, especially for greater values of domain sigma. Check the **Force 2D** option to speed up this filter.

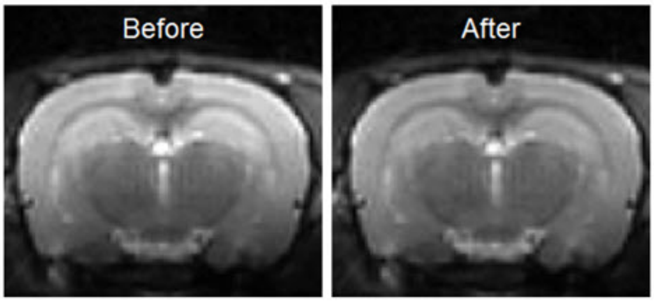
No Filtering Applied	Various Bilateral Smoothing Parameters
	

The positivity smoothing filter will also typically take longer to run than the other smoothing filters, up to several minutes for larger images. This filter was specially designed to redistribute the activity across neighboring voxels such that the total sum of the image is preserved but the number of voxels with negative values is reduced. It is intended to be used to correct images reconstructed with FBP.

Bias Field Correction

Intensity gradient artifacts in magnetic resonance imaging can often cause difficulties with automated segmentation and analysis tools that rely on intensity contrasts, not to mention the detriment to qualitative appearance. The **Bias Field Correction** filter implements the N3 bias correction algorithm (*Tustison 2010*) to estimate the gradient field present in the image and uses this filter to normalize each voxel of the image.

Due to the higher performance cost, a preview of its filtering is not available but the filtering can be applied via the filtering operator. The user may optionally adjust the field smoothness to avoid or allow high spatial frequency corrections and also append the estimated bias field as an image to the DataManager.



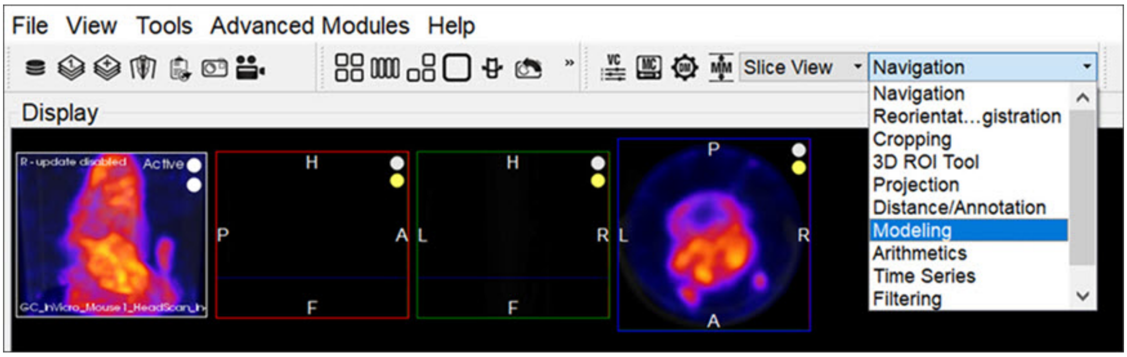
Bias Field Correction

Modeling

The **Modeling** operator provides an integrated solution for representing the loaded data set with one of the following relevant mathematical models to allow for predictions and analysis.

Getting There

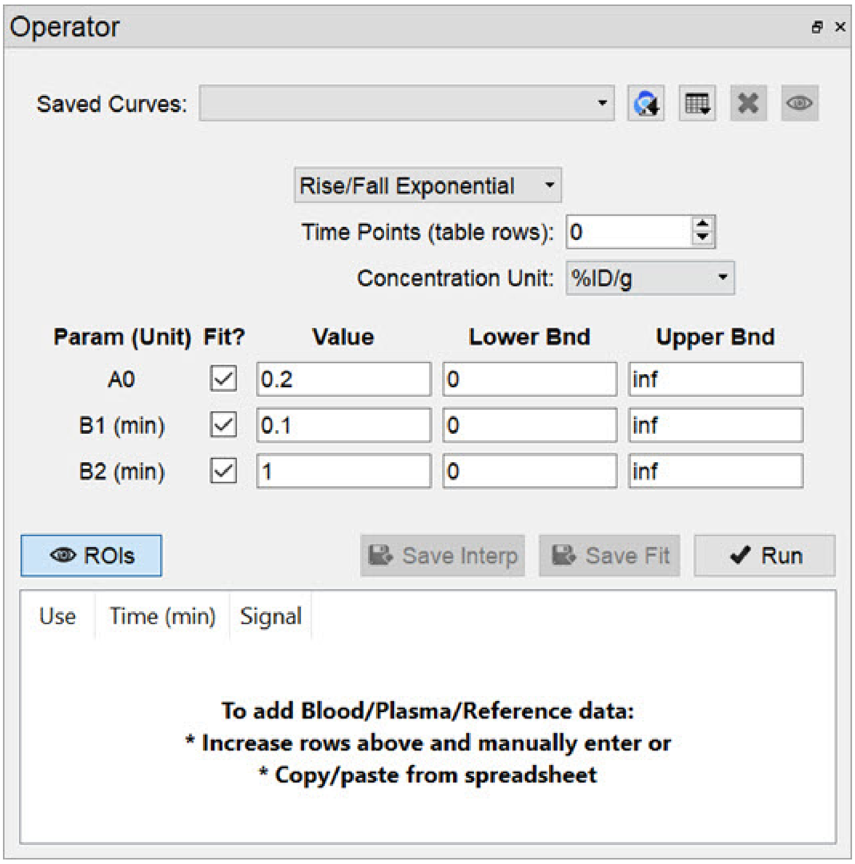
The **Modeling** operator can be accessed via the tool pull-down menu on VivoQuant's front panel.



Modeling Tool

Function

Upon selecting the tool, the **Modeling** operator window is displayed.



Saved Curves:

Rise/Fall Exponential

Time Points (table rows): 0

Concentration Unit: %ID/g

Param (Unit)	Fit?	Value	Lower Bnd	Upper Bnd
A0	☑	0.2	0	inf
B1 (min)	☑	0.1	0	inf
B2 (min)	☑	1	0	inf

Use	Time (min)	Signal

To add Blood/Plasma/Reference data:
*** Increase rows above and manually enter or**
*** Copy/paste from spreadsheet**

Modeling Tool Window

Appropriate data should be loaded into VivoQuant in the correct order, with the reference image (if any) loaded first. Use the Data Manager to sort the datasets as necessary.

From within the **Modeling** operator drop-down, you can select the specific mathematical model applicable to your analysis. Once chosen, the operator window will fill with the model’s parameters and settings.

ℹ **Note:** Access to models depends on your specific VivoQuant license. For information regarding your license, please contact your account manager or email support@invicro.com.

Models

MR Models

MR models are included with every VivoQuant license. These models include T2, T1, ADC, Fat and GLM.

Pharmacokinetic Models

Pharmacokinetic models are available as a plug-in for the **Modeling** operator. These models include the Two-Tissue Compartment Model (2TCM), One-Tissue Compartment Model (1TCM), Logan Graphical Method, Simplified Reference Tissue Model 1 & 2 (SRTM/SRTM2), Logan Non-Invasive Graphical Method, and Patlak Analysis. Detailed information for these models may be found on the Pharmacokinetic Modeling page.

ℹ **Note:** Access to models depends on your specific VivoQuant license. For information regarding your license, please contact your account manager or email support@invicro.com.

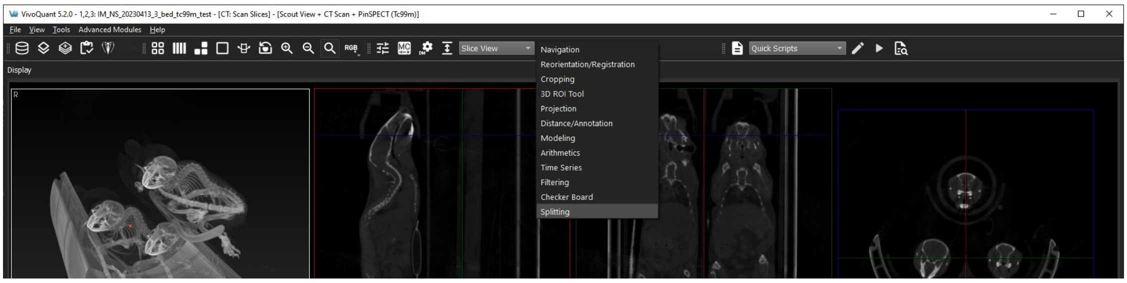
Splitting

Overview

This operator allows the user to create and modify shapes to extract areas of interest. It is at its heart an elaborate cropping operator. The geometric properties of the shapes will ultimately decide the eventual splitting operation while the stylistic options are meant to help the user organize their workflow. Once fine tuning is complete the user can export the areas of interest into new data sources. The exported files can be automatically loaded into the data manager or saved out to the file system. There is also an additional option to control the orientation of the split data to aid in further analysis.

Getting There

The **Splitting Operator** can be accessed and launched via the operator pull-down menu on VivoQuant's front panel.

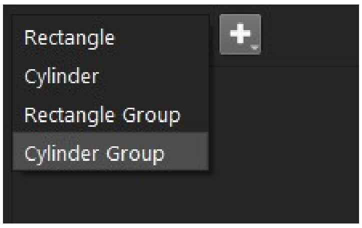


Splitting Operator

The default widget will then populate into a UI pane.

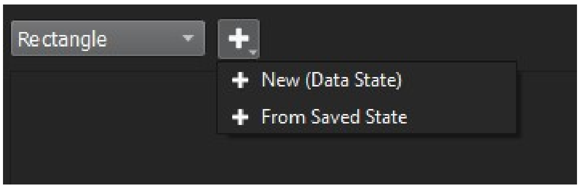
Using the Operator

The first step in using the splitting tool is to choose a geometry, the options are Rectangle, Cylinder, Rectangle Group and Cylinder Group. These basic shapes the user will modify to fit their desired areas of interest. The geometric properties will ultimately determine the final extraction export.



Splitting Operator Geometry

The next step is to click the **+** button and expand the dropdown shape creation options. The option labeled **New (Data State)** will create the shape with initial values that correlate well with the loaded data. The initial defaults in this mode will be based on proportions of the currently loaded data size. This is a good way to start fresh, especially when using a new data source. The second option labeled **From Saved State** allows the user to load a previously saved shape of the current type. If no saved shape of that shape type is found a pop up will alert the user than one was not found and how to go about creating one. See Saving State. A new shape created in this mode will not be automatically correlated with the data and will keep the saved values unchanged.

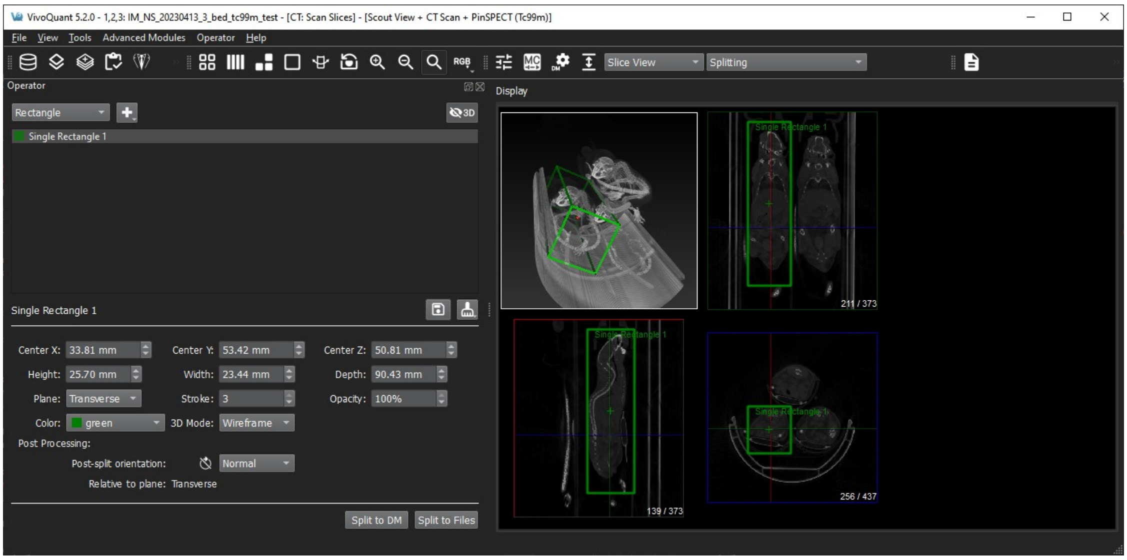


Splitting Operator Creation Mode

Once the shape is created and selected the fields of the shape will populate in the dialog.

Rectangle

The center options will adjust the position of the rectangle in three-dimensional image space, while the height, width, and depth values will be defined relative to the currently selected plane. Stroke and Opacity can be used to change the visibility, color options are provided for visual organization, and the 3D Mode is used for additional adjustments within the 3D view, see 3D Support. The user can also manipulate the shape in the 2D slice views by dragging the corners of the rectangle or the center marker.



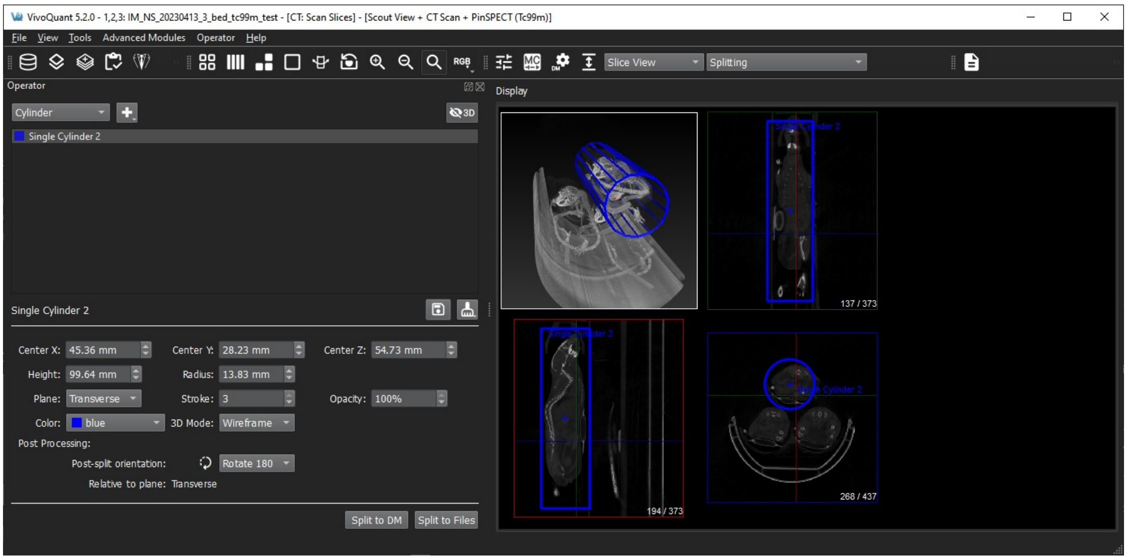
Single Rectangle 1

Center X: 33.81 mm
Center Y: 53.42 mm
Center Z: 50.81 mm
Height: 25.70 mm
Width: 23.44 mm
Depth: 90.43 mm
Plane: Transverse
Stroke: 3
Opacity: 100%
Color: 🟩 green
3D Mode: Wireframe
Post Processing:
Post-split orientation: Normal
Relative to plane: Transverse

Splitting Operator Rectangle

Cylinder

The center options will adjust the position of the cylinder in three-dimensional image space, while the radius and height values will be defined within the currently selected plane. Stroke and Opacity can be used to change the visibility, color options are provided for visual organization, and the 3D Mode is used for additional adjustments within the 3D view, see 3D Support. The user can also manipulate the shape in the 2D slice views by dragging the circle edge of the cylinder, the corners or the center marker.



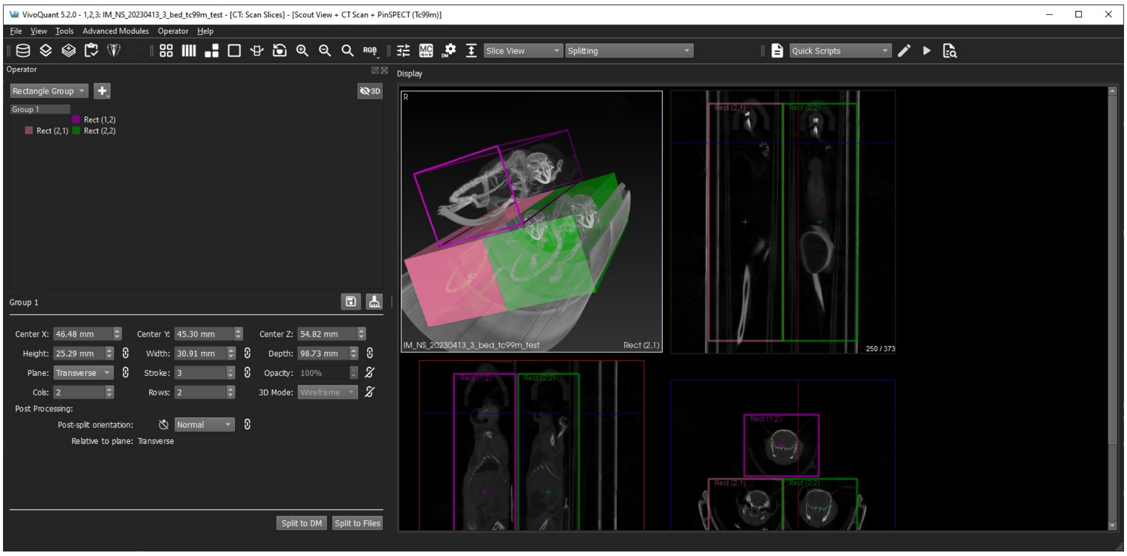
Single Cylinder 2

Center X: 45.36 mm
Center Y: 28.23 mm
Center Z: 54.73 mm
Height: 99.64 mm
Radius: 13.83 mm
Plane: Transverse
Stroke: 3
Opacity: 100%
Color: 🟦 blue
3D Mode: Wireframe
Post Processing:
Post-split orientation: Rotate 180
Relative to plane: Transverse

Splitting Operator Cylinder

Rectangle Group

The Rectangle Group option has two modes based on selection: one for editing the entire group of rectangles and the other for individual rectangle editing. They both work in the same general fashion as discussed in the previous **Rectangle** section. Group editing is performed when the Rectangle Group name is highlighted as shown in the image below. You will notice the additional fields to adjust the number of rectangles via rows and columns. The center values for the Rectangle Group represent the center of mass of all the children's rectangles and can be used to move all the children by the same amount.



Group 1

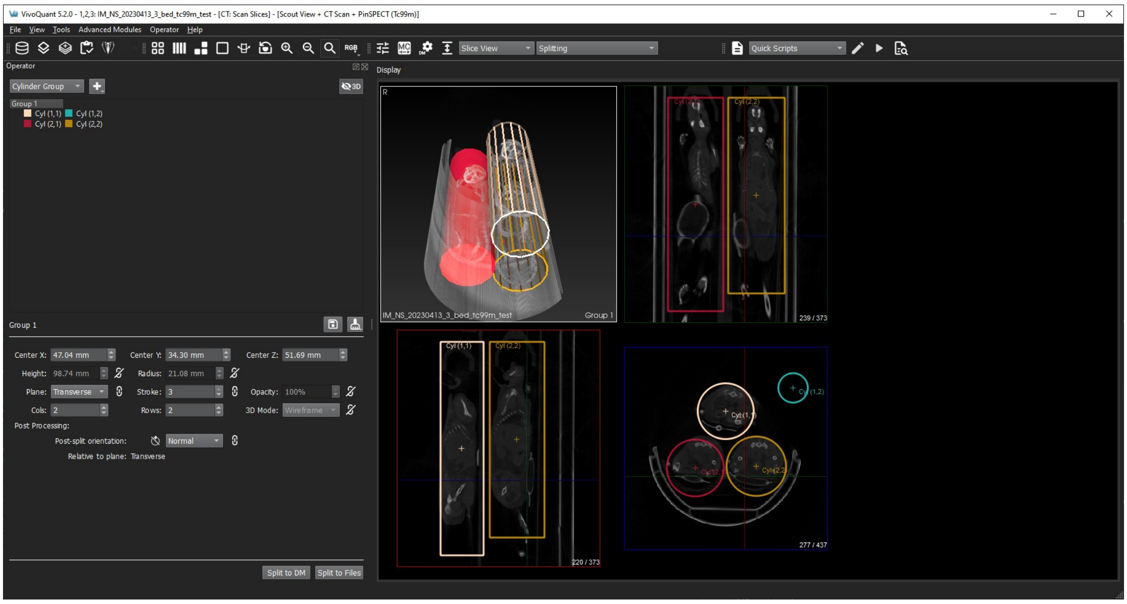
Center X: 46.48 mm
Center Y: 45.30 mm
Center Z: 54.82 mm
Height: 25.29 mm
Width: 30.91 mm
Depth: 98.73 mm
Plane: Transverse
Stroke: 3
Opacity: 100%
Cols: 2
Rows: 2
3D Mode: Wireframe
Post Processing:
Post-split orientation: Normal
Relative to plane: Transverse

Splitting Operator Group Rectangle

Note: Changing the plane in a group will reset position and size for its children.

Cylinder Group

The Cylinder Group option has two modes based on selection: one for editing the entire group of cylinders and the other for individual cylinder editing. They both work in the same general fashion as discussed in the previous **Cylinder** section. Group editing is performed when the Cylinder Group name is highlighted as shown in the image below. You will notice the additional field to adjust the number of cylinders via rows and columns. The center values for the Cylinder Group represent the center of mass of all the children's rectangles and can be used to move all the children by the same amount.



Group 1

Center X: 47.04 mm
Center Y: 34.30 mm
Center Z: 51.69 mm
Height: 98.74 mm
Radius: 21.08 mm
Plane: Transverse
Stroke: 3
Opacity: 100%
Cols: 2
Rows: 2
3D Mode: Wireframe
Post Processing:
Post-split orientation: Normal
Relative to plane: Transverse

Splitting Operator Group Cylinder

Note: Changing the plane in a group will reset position and size for its children.

Group and Child Linking

As can be viewed in the previous two images, there are link icons next to certain shape fields. These links symbolize the current state of the group's children regarding the context of that field and show whether all the children share the same group value or not. If the user wishes to overwrite one of the individual child settings, they need only to relock the corresponding icon.

Output

The image below show the fields that are relevant to the export of the splitting.

Post Processing:

Post-split orientation: Rotate 180

Relative to plane: Transverse

Splitting Operator Output Options

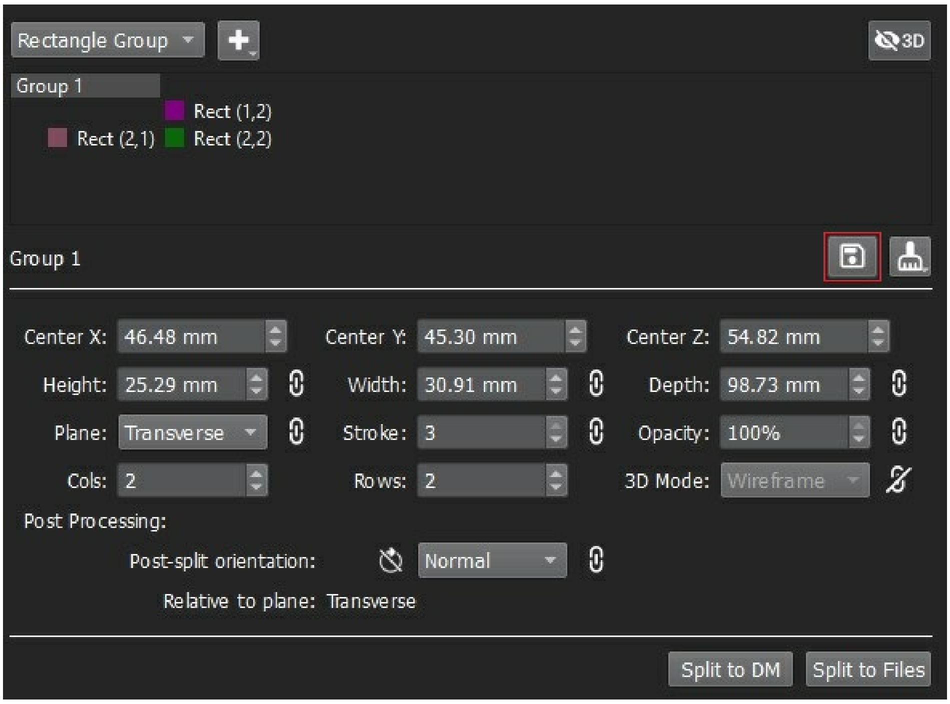
There are two options for exporting the split results. The first is splitting to the Data Manager triggered by the button labeled **Split to DM**. See Data Manager for more information. The second option for export is to **Split to Files**. All geometries that are currently listed will be exported as files. The file name that you specify will be prepended to the name of the geometry. Care should be taken not to overwrite older data that was previously saved.

The post-processing orientation will be applied after the extraction phase and is an additional tool for further analysis and organization.

Note: The **orientation** option will be applied after running the split, it has no visual effect on the screen because it is a post processing step.

Save Shape State

Once a shape has been created you will see a save floppy disc icon to the right of the current shape title as seen in the image below. At any time, the user can click that button to save the current state of that specific shape type. A note should be made here that we currently only support one saved version for each shape type. If the user requires more variety in saved states they can use the Operator Menu capabilities.



Rectangle Group

Group 1

Rect (1,2)

Rect (2,1)

Rect (2,2)

Group 1

Center X: 46.48 mm

Center Y: 45.30 mm

Center Z: 54.82 mm

Height: 25.29 mm

Width: 30.91 mm

Depth: 98.73 mm

Plane: Transverse

Stroke: 3

Opacity: 100%

Cols: 2

Rows: 2

3D Mode: Wireframe

Post Processing:

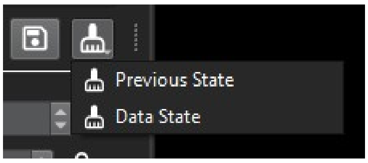
Post-split orientation: Normal

Relative to plane: Transverse

Splitting Operator Save State

Revert Shape State

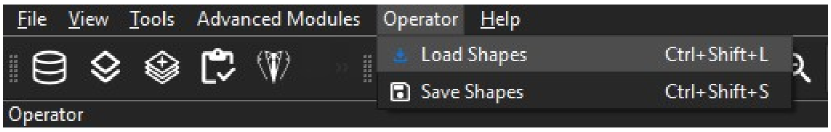
To the right of the save floppy the user will see the broom icon that has two options for reverting state. The first option labeled **Previous State** will set all the shape values back to either the initial state or the state when the saved icon was last clicked. The second option labeled **Data State** is a way for the user to correlate their current shape settings to the currently loaded data source. This option addresses the case where new data has been loaded that maybe doesn't currently correlate well to the current shape. This option is similar to creating a shape with the **New (Data State)** except only the values associated with position and size are updated.



Splitting Operator Revert State

Operator Menu

The Splitting Operator toolbar options consists of a **Load Shapes** option and a **Save Shapes** option. Both options launch a file dialog to complete the requested action. The load option will replace the current splitting shape list with the newly loaded list and correspondingly the save option will save the entire shape list. The file type is XML.



Splitting Operator Toolbar Menu

Sessions Support

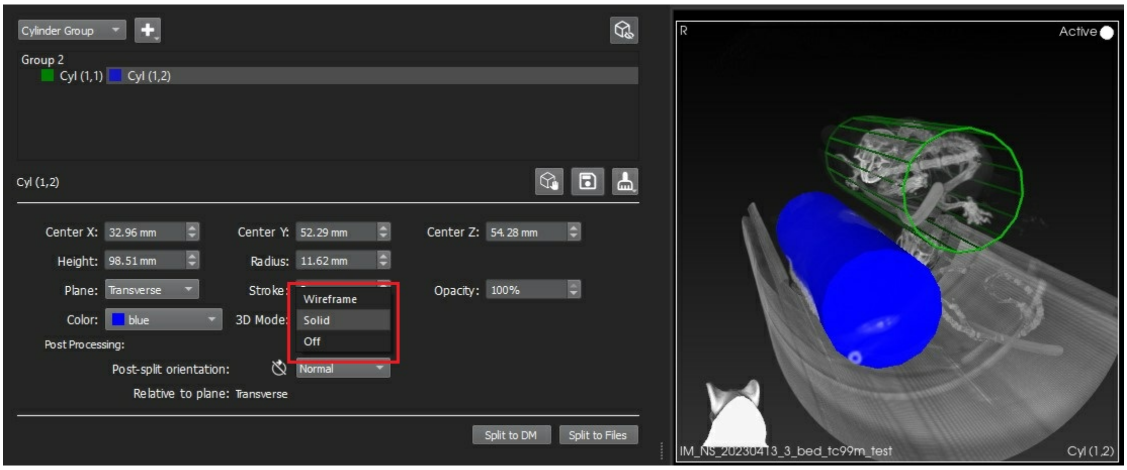
When saving out sessions the entire shape list will be captured in its current state, and when loading a session, the current shape list will be replaced by the shape list in the saved session. See Session for more information.

3D Support

The 3D View supports picking and hovering and will display the current shape name in the status text in the bottom right of the view. If no shape is currently being hovered over the status text will return to the currently selected shape name. Rendering in 3D can be globally turned on and off for all split shapes via the button in the top right corner.

Splitting Operator Show In 3D

Additionally, the individual shapes and shape group have a 3D rendering control which not only includes the ability to turn them off individually but also allows choosing between a solid vs wireframe rendering.



Cyl (1,2)

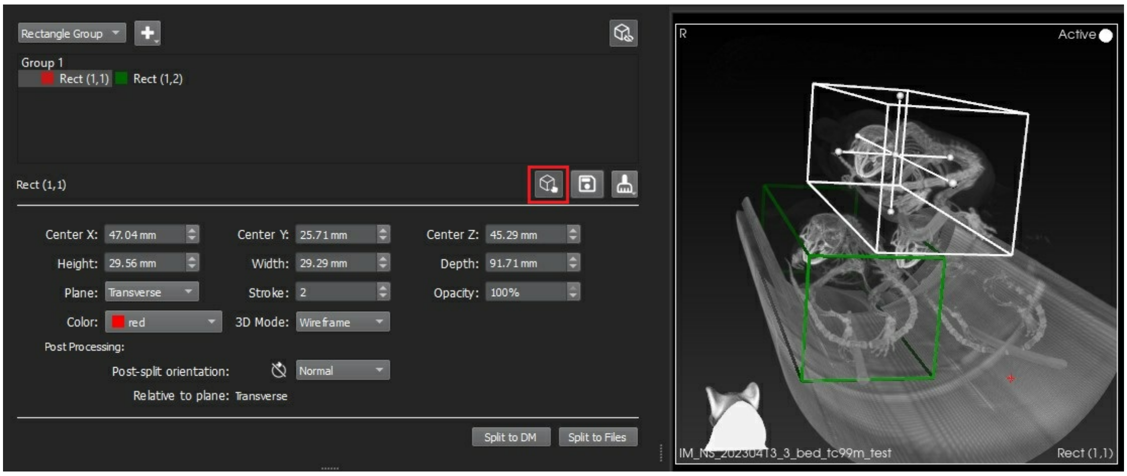
Center X: 32.96 mm
Center Y: 52.29 mm
Center Z: 54.28 mm
Height: 98.51 mm
Radius: 11.62 mm
Plane: Transverse
Opacity: 100%
Color: blue
Post Processing:
Post-split orientation: Normal
Relative to plane: Transverse

Splitting Operator 3D Render Mode

The 3D view supports full editing of the split shapes via the UI field controls or via interacting with the 3D rendering. The editing using the UI field controls is no different than editing in the slice views and should work as expected.

3D Editing

In order to the interact with the 3D shape rendering the user can click the *Edit in 3D* button. This button is present on individual shapes only and is enabled when the main *Show in 3D* button is also enabled. Once the button is depressed the edit widget will appear around the currently selected shape.



Rect (1,1)

Center X: 47.04 mm
Center Y: 25.71 mm
Center Z: 45.29 mm
Height: 29.56 mm
Width: 29.29 mm
Depth: 91.71 mm
Plane: Transverse
Stroke: 2
Opacity: 100%
Color: red
3D Mode: Wireframe
Post Processing:
Post-split orientation: Normal
Relative to plane: Transverse

Splitting Operator Edit In 3D

This edit widget has 7 control points; 6 are for dragging the boundary of the shape and 1 is for dragging the center position of the shape. Other edit widget controls are invoked via the following mouse and keyboard sequences:

Key	Mouse Button and Action	Context	Description
N/A	Right down and drag	Cursor over edit box	Uniform scaling
Shift	Left down and drag	Cursor over edit box	Translates
N/A	Middle down and drag	Cursor over edit box	Translates

3D Quick Editing

We also have provided another means to edit without first clicking the *Edit in 3D* button. This quick edit method should speed up 3D edits where users wish to change center or do a uniform scaling. These behaviors are invoked via the following mouse and keyboard sequences:

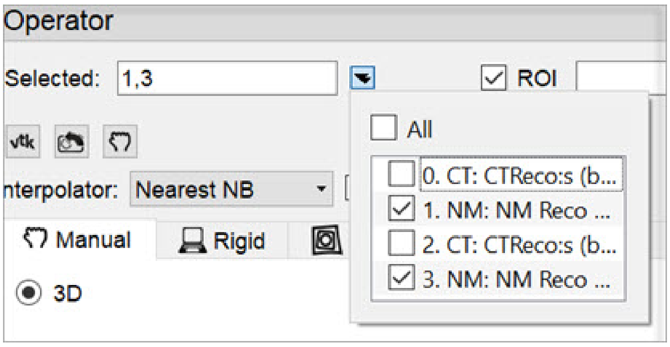
Key	Mouse Button and Action	Context	Description
Alt	Right down and drag	Cursor over any shape	Uniform scaling
Alt	Left down and drag	Cursor over any shape	Translates

Note: The 3D view must be in focus for ALT key to engage.

Once the user enters a quick edit context any current edit widget that may have been visible will be turned off.

Data Selector Widget

The **Data Selector Widget**, which is used by the **Reorientation/Registration**, **Arithmetics**, and **Filtering** operators, provides a flexible method for selecting inputs on which to perform actions.



Selected: 1,3

☑ ROI

nterpolator: Nearest NB

☐ All
☐ 0. CT: CTReco:s (b...
☑ 1. NM: NM Reco ...
☐ 2. CT: CTReco:s (b...
☑ 3. NM: NM Reco ...

Data Selector

Using the Data Selector

The **Data Selector Widget** offers two ways to inform VivoQuant on which inputs the user would like to operate.

- **Option 1**: The user may type the inputs of interest into the text field, using standard list logic. For example, typing [1,2,3,4] will inform VivoQuant the user wishes to operate on Input1, Input2, Input3 and Input4. Alternatively, this same command could be accomplished simply by typing [1-4]. These formats may also be mixed, for example, typing [1-3,5] would indicate the user wishes to operate on Input1 through Input3, and Input5. An important note is that the widget refers to the Reference image as 0.

- **Option 2**: The user may choose to use the widget dropdown, which is the button with the triangle, shown selected, above. This will allow the user to select the check box for the inputs of interest, or the **All** option if so desired. Using the dropdown does not preclude the user from also editing the text field, as it will update according to the selected items.

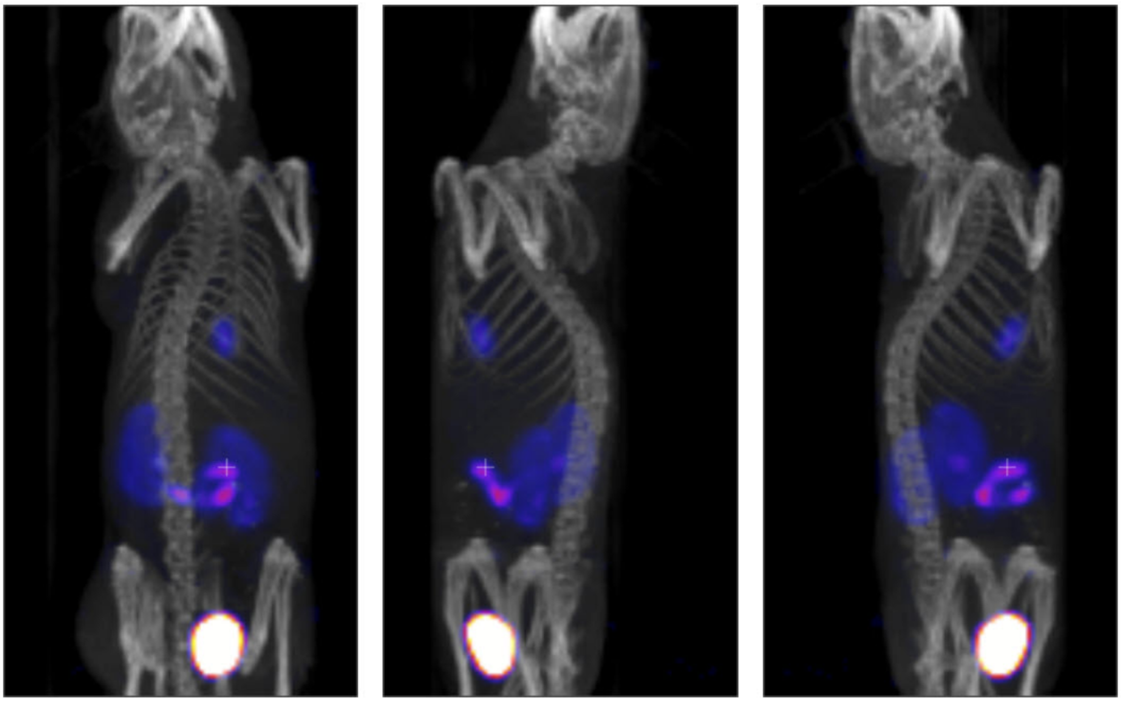
Maximum Intensity Projection (MIP)

A **Maximum Intensity Projection (MIP)** is a series of 2D images generated from a 3D reconstruction by selecting the maximum value through the reconstruction *seen* by each 2D pixel at each of several viewing angles.

Each angular view in a **MIP** has a unique viewing angle which defines the 2D projection plane. Parallel rays emanate from each of the pixels in the projection plane through the reconstruction. The maximum intensity, i.e. largest-valued voxel, encountered by each ray is assigned to the pixel from which that ray emanated. For example, bone typically exhibits a high value in a CT reconstruction. Therefore, in X-Ray CT MIPs, the skeleton is prominent as the bone values are selected from the voxels included in a given ray. Repeating this process for multiple angles around the animal generates what appears to be a "rotating film" of the reconstructed image.

The **MIP tool** enables manipulation of 3-dimensional renderings of SPECT and CT data. This easy-to-use software allows the integration of SPECT and CT data into one image. Data can be viewed as image slices or as a continuous movie. This tool also provides means to modify color, intensity, and zoom of an image as well as various options for saving the data.

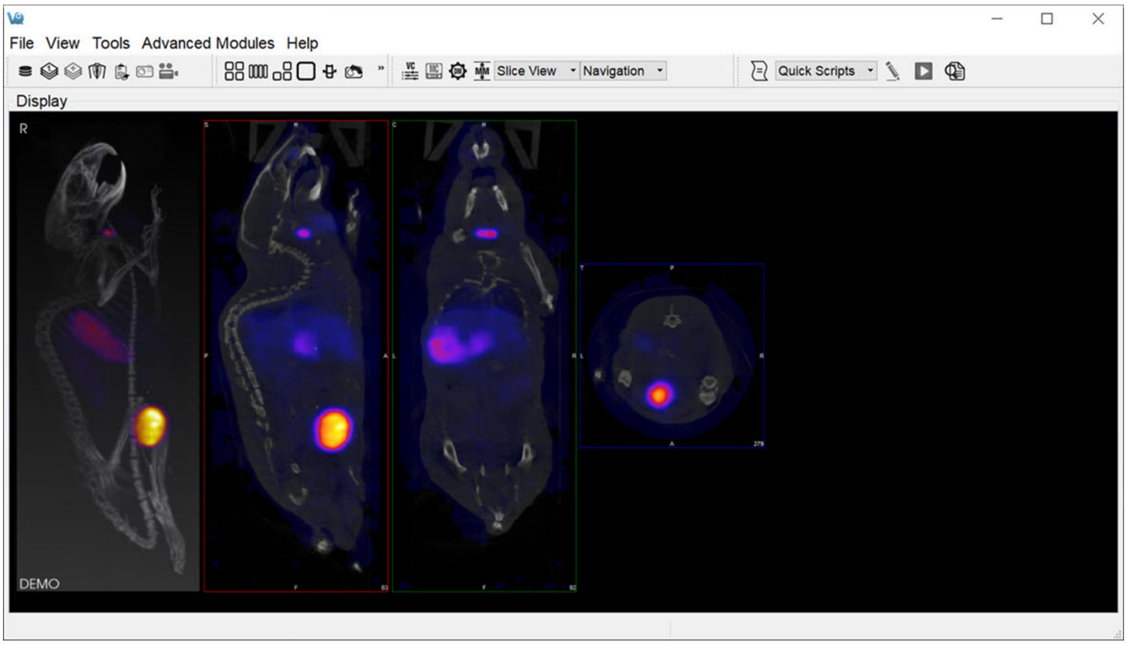
Example MIP projections at three different angles are shown below:



MIP Projections

Main Window

VivoQuant's **Main Window** contains the primary display and is the focal point for reaching all other functions.



Display

Menus

There are five menus across the top of the **Main Window**:

Menu	Function
File	Used for file manipulation and includes options for opening, saving, printing, and publishing files.
View	Used to control the display of data already loaded into the VQ. Entire data sets may be toggled as may a variety of display options, including layout and zoom.
Tools	Provides access to several VQ image processing tools, including data control, reconstruction, calibration, and configuration features.
Advanced Modules	Provides access to more advanced VQ image processing tools, including data control, reconstruction, calibration, and configuration features.
Help	Help content, including licensing information and the manual, are available in this menu.

Docks

The View Control, MIP Control, Data Manager, and **Operators** are automatically placed into Docks upon opening. Docks may be dragged and dropped into and out of the **Main Window** display, and multiple controllers/operators are dockable at any given time.

Thumbnails

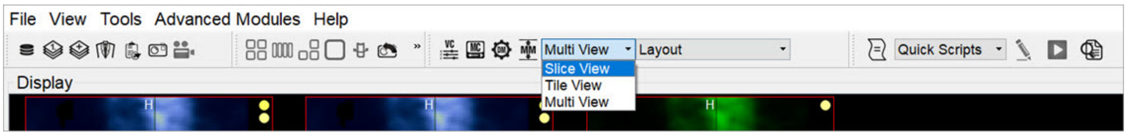
The thumbnail icons described below provide fast access to different features:

Thumbnail Icon	Function
	Opens the Data Browser
	Opens a browser that will unload currently loaded data and replace it with the data selected in the browser.
	Opens a browser that will append data to currently loaded data.
	Opens the Save Image window.
	Opens the Save Movie window.
⊞	Changes the display layout to a 2 x 2 grid layout.
	Changes the display layout to a 1 x 1 grid layout.
	Changes the display layout to show the sagittal, coronal, and transverse data slices but not the MIP.
▢	Changes the display layout to show only the transverse data slices.
	Changes the display layout to show only the MIP.
	Resets the zoom and pan within each viewport in the display.
	Zooms in 25%.
	Zooms out 25%.
	Auto-zooms to fit data to screen.
●●●	Opens RGB color options.
VC	Opens the Viewer Control panel.
MC	Opens the MIP Control panel.
DM	Opens the Data Manager panel.
MM	Opens the Min Max Tool panel.
	Opens the VivoScript Evaluation window.

Thumbnail Icon	Function
✎	Edits the VivoScript file selected in the Quick Scripts menu.
▶	Evaluates the VivoScript file selected in the Quick Scripts menu.
⊗	Aborts the VivoScript in execution.
🔍	Activates the Peek tool, used to reveal names of operator widgets for use in VivoScripts. See the VivoScript page for more.

View Modes

There are three viewing modes available via the pull-down menu located next to the thumbnail icons.

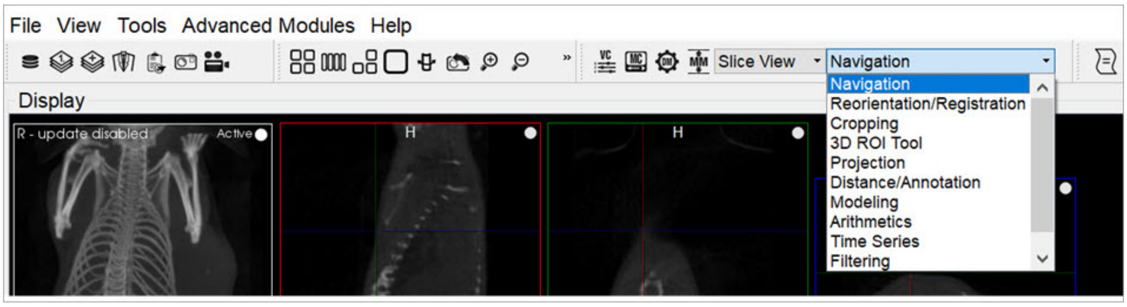


Viewing Modes

View Mode	Function
Slice View	The Slice View (default) simultaneously displays images of single slices for the MIP, sagittal, coronal, and transversal views of the loaded data sets.
Tile View	The Tile View displays an array of slices for either, sagittal, coronal, or transversal view of the loaded data sets.
Multi View	The Multi View displays sagittal, coronal, or transversal slices of each data set adjacent to one another simultaneously.

Operators

The operators are accessible via the pull-down menu located next to the thumbnail icons.



Operators

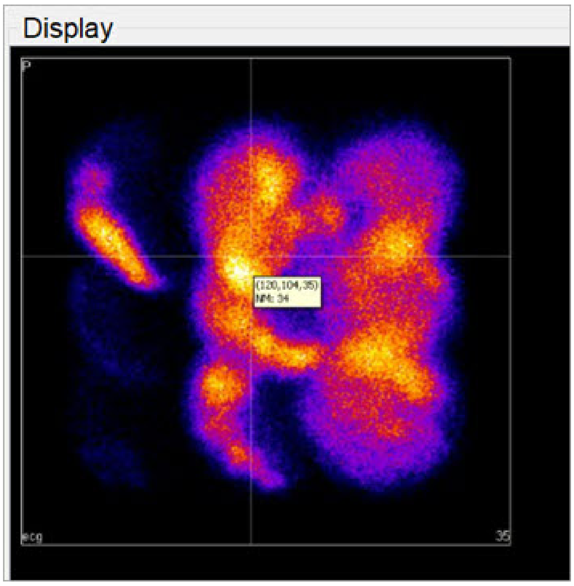
Operator	Function
Navigation	Enables manually scrolling through the image slices and rotation of the Maximum intensity Projection (MIP).
3D ROI Tool	Provides advanced tools for drawing, visualizing, saving, and quantifying both 2- and 3-dimensional regions.
Projection	Provides a means to quantify density and activity parameters in CT and NM scans, respectively.
Reorientation/Registration	Enables realignment of image data via translation, rotation, or flipping. In registration mode, a variety of registration algorithms are available to automatically register data from a wide variety of modalities.
Time Series	Allows sagittal, coronal, and transverse slices of datasets from a time series to be played sequentially in a loop or easily scrolled through manually.
Distance/Annotation	Allows you to measure the distance between two points in any image.
Checkerboard	In checkerboard mode, the reference and input data set(s) are arrayed in a pattern of alternating squares, resembling a checkerboard.
Cropping	Allows images to be made smaller by removing any unwanted areas.
Arithmetics	Allows voxel-wise arimethic operations on two input images, or scalar operations on any number of input images.
Filtering	Uses a selection of built-in smoothing filters with configurable parameters.
Modeling	Provides an integrated solution for representing the loaded data set with one of several mathematical models to allow for predictions and analysis.
Splitting	Provides utility to split the image into a number of distince regions.

Display

The **Display** field is the main component of the **Main Window**. The first three images loaded in the **Data Manager** are visible in the **Display** field. Many tools and image-processing steps are visible in the data sets shown in the **Display** field.

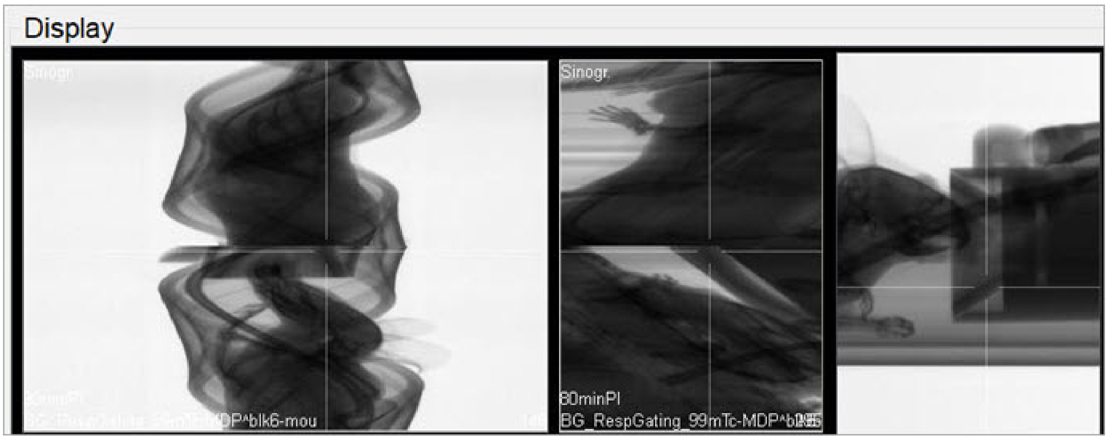
Projections vs. Reconstructions

The **Display** window recognizes whether a loaded data set is projection data or reconstructed data. The default viewing scheme, known as Slice View, for reconstructed data includes an MIP and three separate viewing directions (sagittal, coronal, and transversal). When viewing projection data or sinograms (sets of CT projection data), VivoQuant displays the data accordingly. For example, transverse slices of projection data are displayed with a P in the top-left corner.



Projections vs. Reconstructions

For CT data, selecting the correct layout will display the relevant sinogram data. For the corresponding windows, the data are labeled as sinogr., denoting “sinogram”.



Sinogram

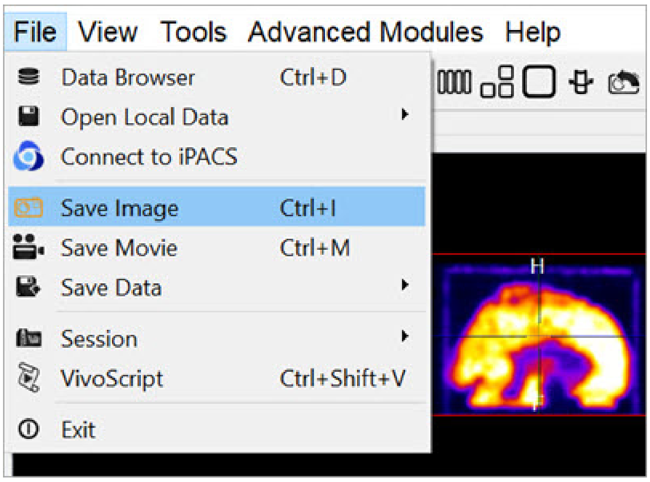
ℹ **Note:** It is not possible to view projection (non-volumetric) and reconstruction (volumetric) data simultaneously. Attempting to append reconstruction data to projection data, or vice versa, will result in an error message.

Save Image Data

This function saves images as picture files. Slices can be saved individually (sagittal, coronal or transversal) or all in one image. This feature can also save a Maximum intensity Projection (MIP) picture (MIP viewer must be active). Images will appear exactly as they do in the viewer.

Getting There

There are three different methods for saving images. The first method is to go to **File** > **Save Image**.



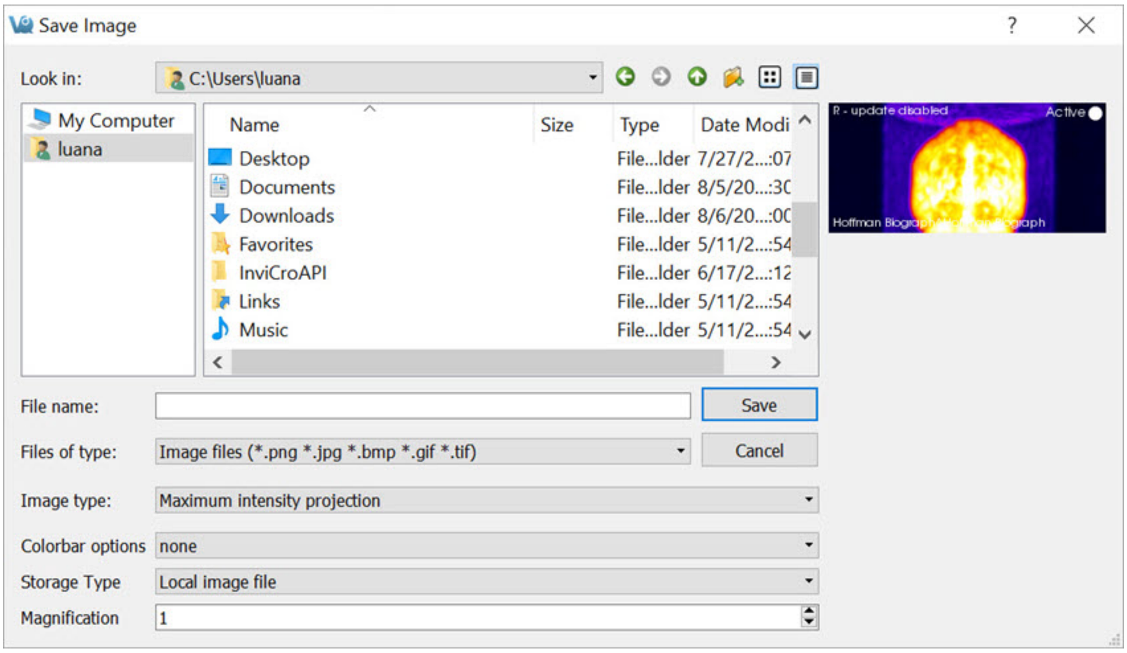
File Menu

The second method is to use the keyboard shortcut Ctrl+I. For more information on keyboard shortcuts, please see Keyboard Shortcuts.

The third method is to click on the **Save Image** button .

Function

Upon selecting any of the above options, the **Save Image** window opens.



Look in: C:\Users\luana

File name:

Files of type: Image files (*.png *.jpg *.bmp *.gif *.tif)

Image type: Maximum intensity projection

Colorbar options none

Storage Type Local image file

Magnification 1

Save Image Window

There are several options for the output images.

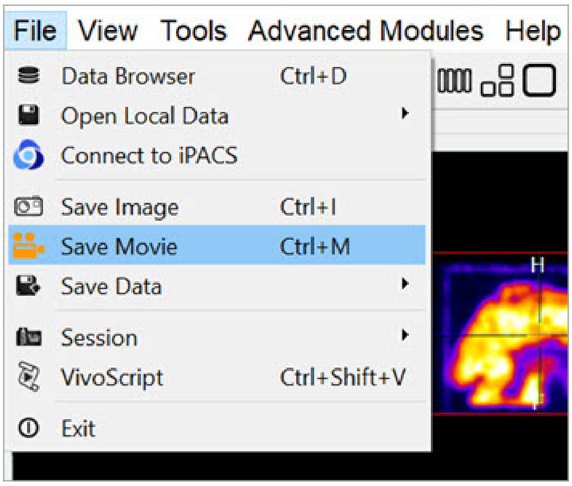
Option	Description
File name	Sets the name of the image file.
Files of type	Sets the type of image file. File types can be: - .png - .jpeg -.bmp - .gif - .tif
Image type	Sets the type of image. Image types can be: - Maximum intensity projection (MIP) - Sagittal slice - Coronal slice - Transversal slice - All views in one image - All images separately
Colorbar options	Sets the colorbar and label options for the image. Options include: - None - no colorbars or labels - No labels - colorbars with no labels - Simple labels - colorbars with one set of evenly distributed gradations placed across all color bars. - Smart labels - colorbars with separate sets of gradations for each color bar incremented with respect to the units of each color bar.
Storage type	Sets whether the image file will be stored as a local image file or as a DICOM Secondary Capture.
Magnification	Sets a scalar magnification factor to be applied to the resulting image. This affects only the magnification of the image file being generated.

Save Movie

This function enables saves images as movie files. The slices can be saved individually (sagittal, coronal or transversal) or all in one movie. This feature can also be save a Maximum intensity Projection (MIP) picture.

Getting There

There are three different methods for saving movies. The first method is to go to **Save Movie** under the **File** menu.



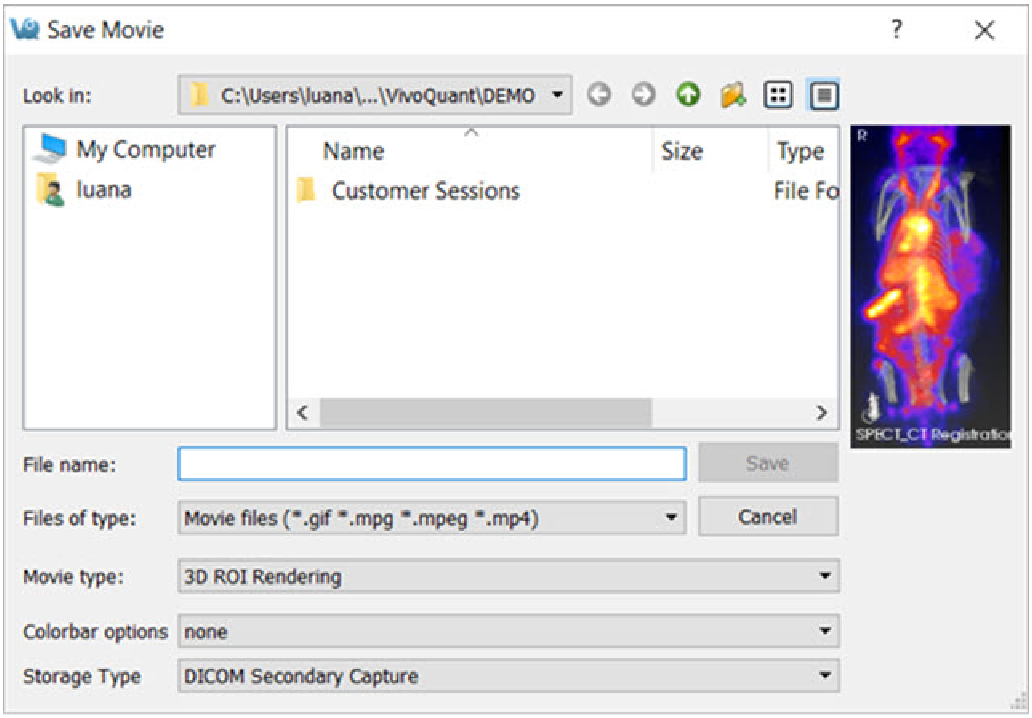
File Menu

The second method is to use the keyboard shortcut Ctrl+M. For more information on keyboard shortcuts, please see Keyboard Shortcuts.

The third method to save **image slices** is to click on the **Save Movie** button in the Main Window.

Function

Upon selecting any of the above options, the **Save Movie** window opens.



Look in: C:\Users\luana\...\VivoQuant\DEMO
File name:
Files of type: Movie files (*.gif *.mpg *.mpeg *.mp4)
Movie type: 3D ROI Rendering
Colorbar options none
Storage Type DICOM Secondary Capture

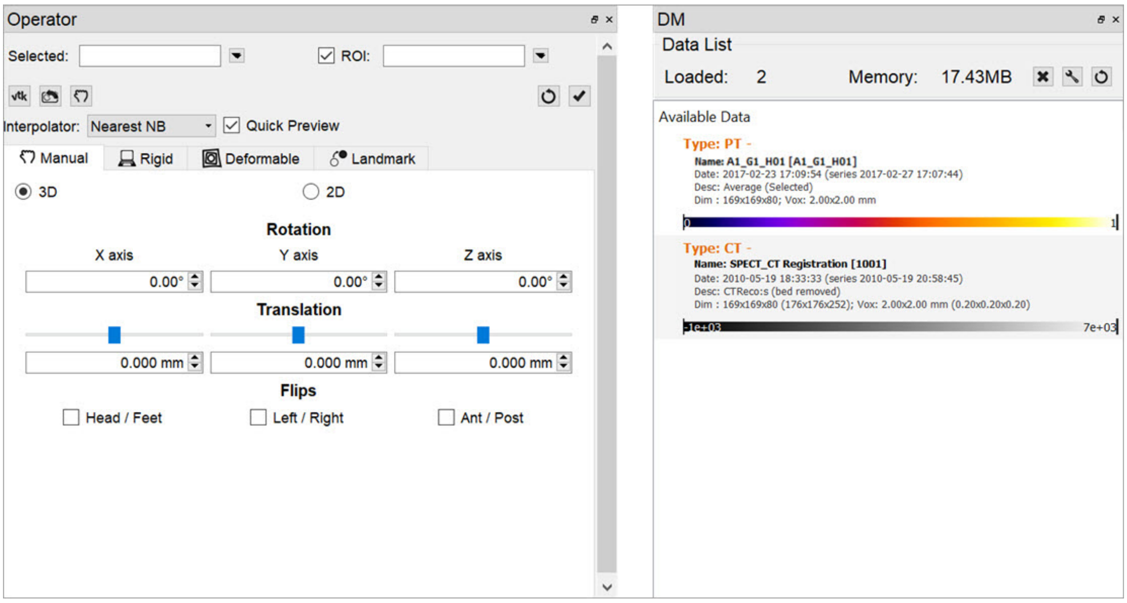
Save Movie Window

There are several options for the output movies.

Option	Description
File name	Sets the name of the movie file.
Files of type	Sets the type of the movie file. File types can be: - .gif - .mpg - .mpeg - .mp4
Movie type	Sets the type of Movie. Movie types can be: - Maximum intensity projection (MIP) - Sagittal slice - Coronal slice - Transversal slice - All movies separately
Colorbar options	Sets the colorbar and label options for the movie. Options include: - None - no colorbars or labels - No labels - colorbars with no labels - Simple labels - colorbars with one set of evenly distributed gradations placed across all color bars. - Smart labels - colorbars with separate sets of gradations for each color bar incremented with respect to the units of each color bar.
Storage type	Sets whether the movie file will be stored as a local movie file or as a DICOM via Secondary Capture.

Docks

The **Viewer Control**, **MIP Control**, **Data Manager**, and all **Operators** are automatically placed into docks upon opening. **Docks** may be dragged and dropped into and out of the **Main Window** display and multiple **Controllers** are dockable at any given time.



Interpolator: Nearest NB ☑ Quick Preview

☑ ROI:

● 3D ○ 2D

Rotation: X axis 0.00°, Y axis 0.00°, Z axis 0.00°

Translation: 0.000 mm, 0.000 mm, 0.000 mm

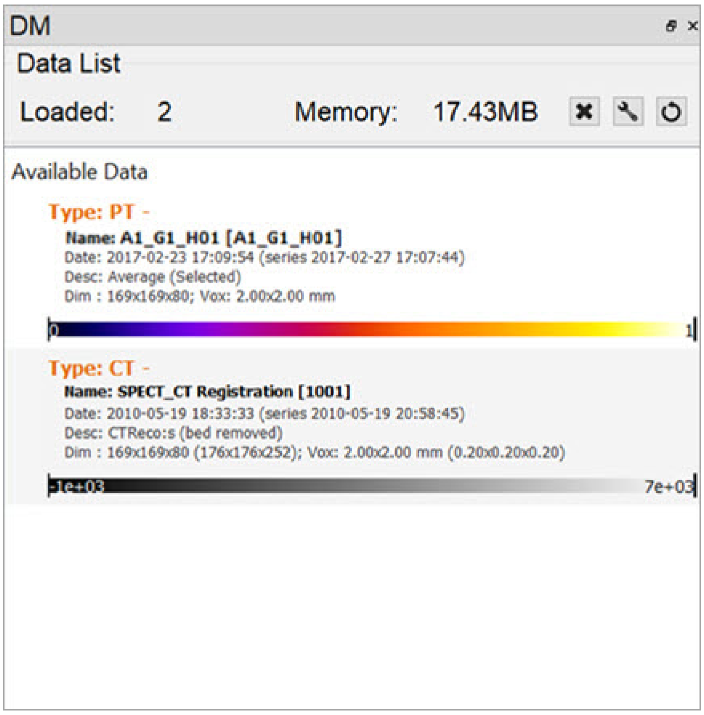
Flips: ☐ Head / Feet ☐ Left / Right ☐ Ant / Post

Loaded: 2 Memory: 17.43MB

Docks

Using Docks

Any controller or operator displayed in a dock may be *popped out* into its own window by dragging and dropping. Similarly, any controller or operator can be re-docked by dragging it back into a docking area (the left, right, or bottom area of the main window).



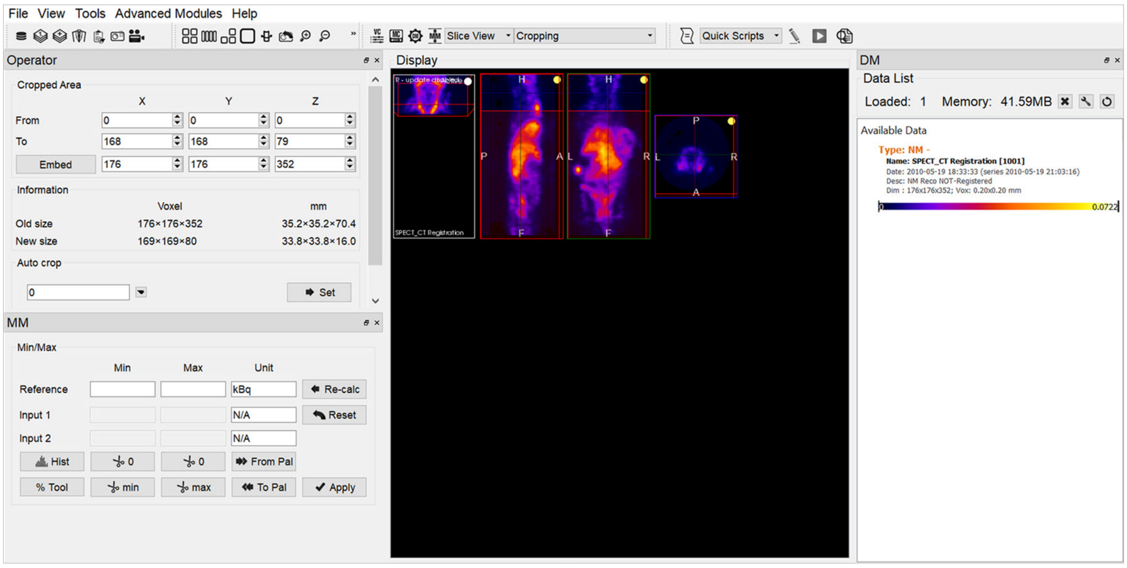
Loaded: 2 Memory: 17.43MB

Type: PT -
Name: A1_G1_H01 [A1_G1_H01]
Date: 2017-02-23 17:09:54 (series 2017-02-27 17:07:44)
Desc: Average (Selected)
Dim : 169x169x80; Vox: 2.00x2.00 mm

Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)
Desc: CTReco:s (bed removed)
Dim : 169x169x80 (176x176x252); Vox: 2.00x2.00 mm (0.20x0.20x0.20)

Docks Pop-In and Pop-Out

Docks may be placed on either side of the main window, allowing immediate access to many VivoQuant tools without changing windows. If you need more main window space for image viewing, close or re-arrange the docks to your preference.



Cropped Area

	X	Y	Z
From	0	0	0
To	168	168	79
Embed	176	176	352

Information

	Voxel	mm
Old size	176×176×352	35.2×35.2×70.4
New size	169×169×80	33.8×33.8×16.0

Auto crop: 0

Min/Max

	Min	Max	Unit
Reference			kBq
Input 1			N/A
Input 2			N/A

SPECT_CT Registration

Data List

Loaded: 1 Memory: 41.59MB

Available Data

Type: NM -

Name: SPECT_CT Registration [1001]

Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)

Desc: NM Reco NOT-Registered

Dim : 176x176x352; Vox: 0.20x0.20 mm

0 0.0722

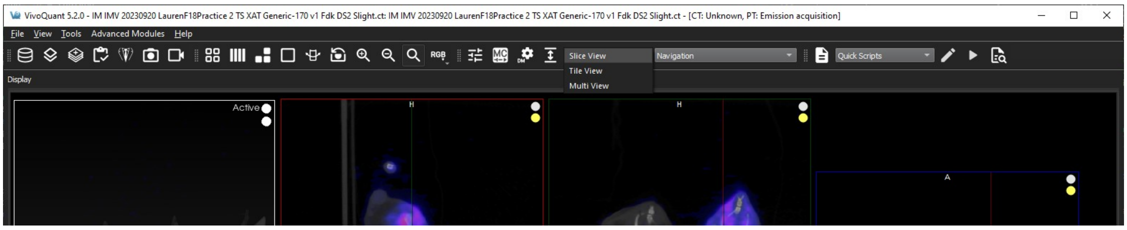
Dual Docks

Slice View

The **Slice View** (default) simultaneously displays images of single slices for the sagittal, coronal, and transversal views of the loaded data sets.

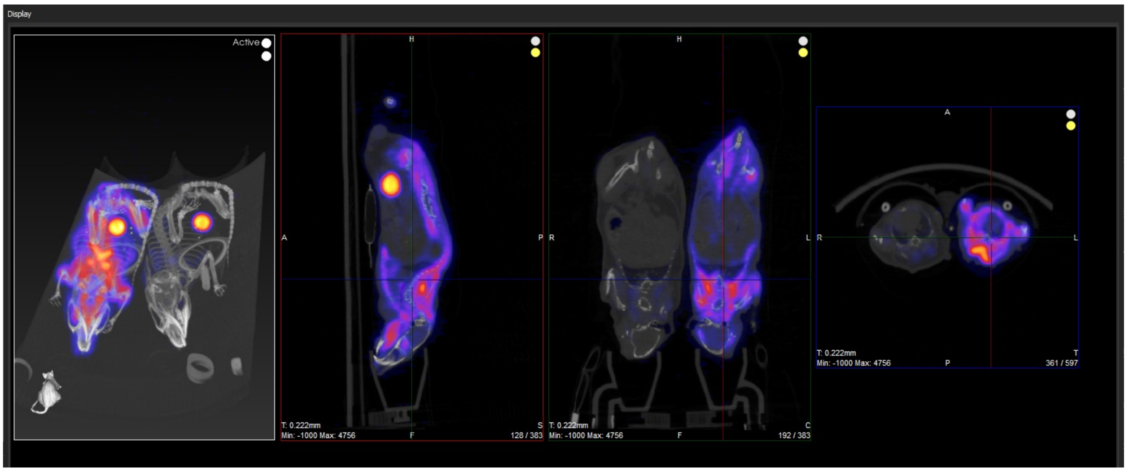
Getting There

The **Slice View** is available via the view pull-down menu on the **Main Window**.



Slice View Display

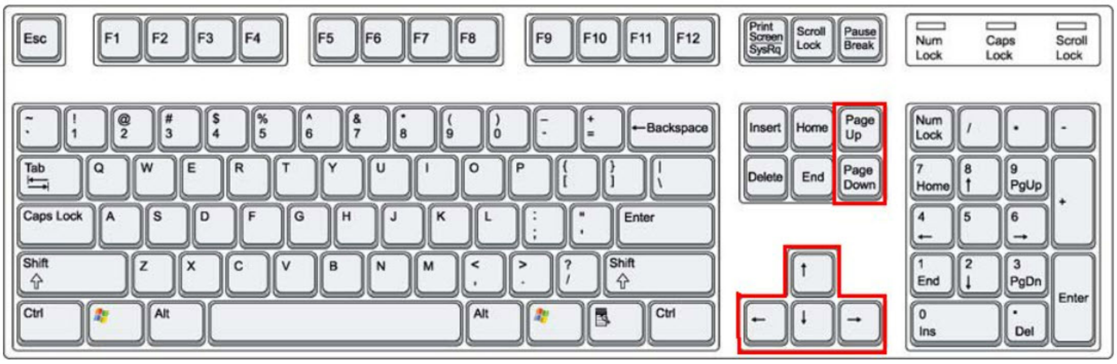
Slice View Display



Slice View

You can scroll through slices in the **Slice View** by using the scroll wheel on a mouse or by using the arrow and paging keys on your keyboard.

The keys control different views (coronal, sagittal, or transversal) depending on the current active view. Click on a view to make it the active view. Generally, you will control the active view with the paging (PageUp, PageDn) keys, and scroll the other two views with the arrow (→, ←, ↑, ↓) keys.



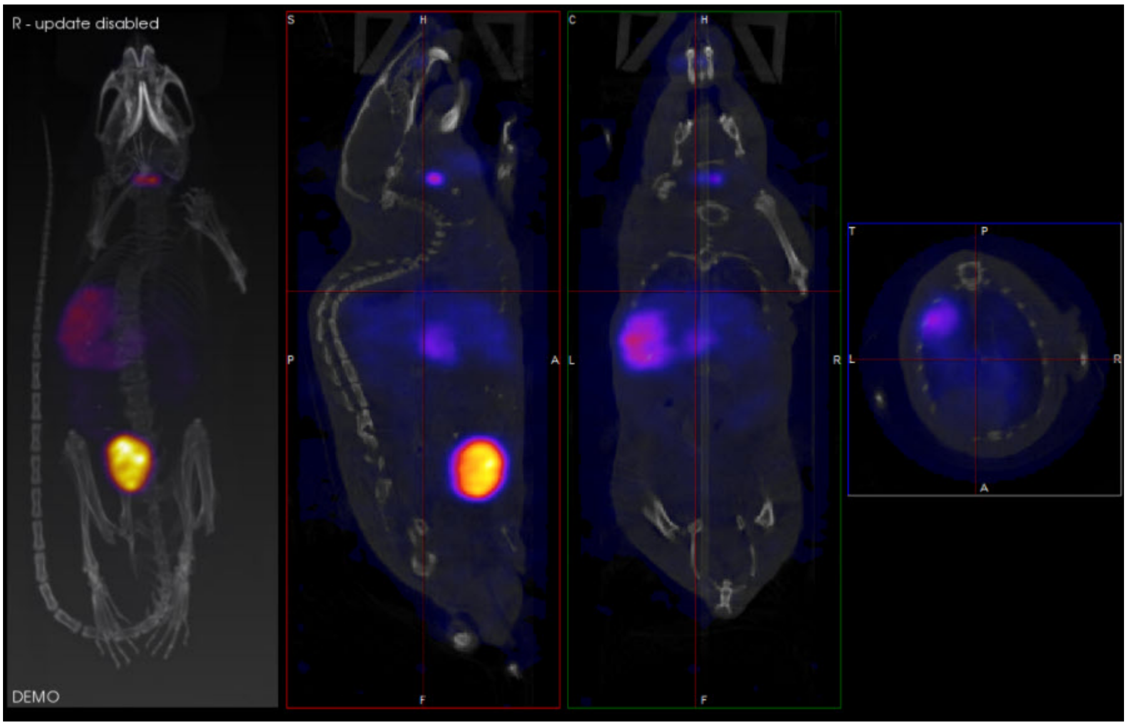
Keyboard Controls

Scrolling Slices Example

You can use the arrow and paging keys to scroll through slices in the **Slice View**.

In the example image below, the transversal view is the active view. The ← and → keys move the crosshairs towards the L (left side) and R (right side) in the transversal slice, respectively. Moving through the object to the left or right steps through the sagittal plane of the object; thus, the sagittal slice changes.

The ↑ and ↓ keys will move the crosshair towards P (posterior side) and A (anterior side). Both these sides are also visible in the sagittal slice of the object (rotated 90-degrees). Using the ↑,↓ keys in the transversal plane will shift the vertical crosshair in the sagittal plane, and step through the coronal views of the object.



Scrolling Slices Example

Scrolling Slices Shortcuts Table

The following table displays the function of the arrow and paging keys for each active view.

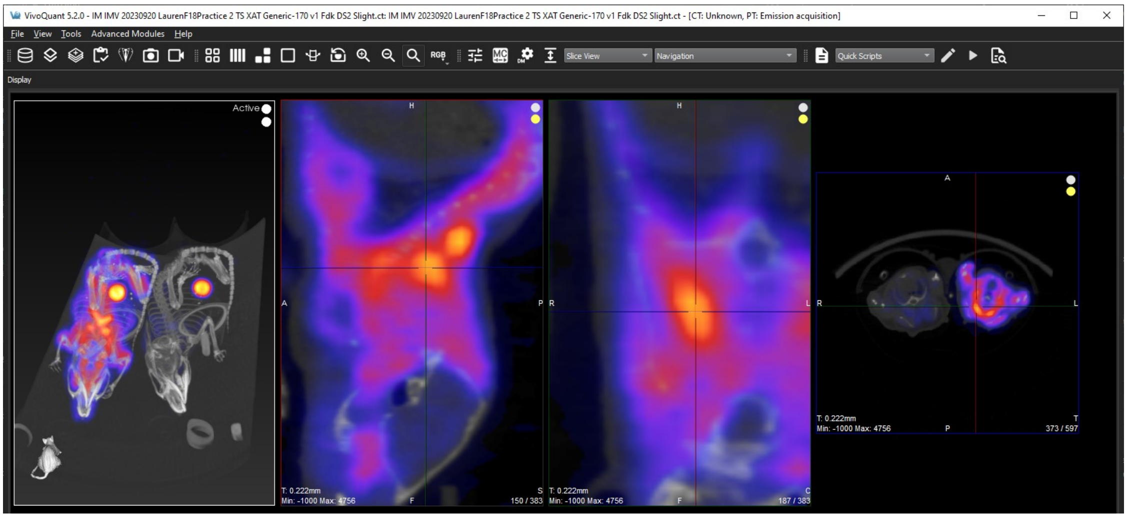
Active View	←	→	↑	↓	PageUp	PageDn
Coronal	Previous sagittal slice	Next sagittal slice	Previous transversal slice	Next transversal slice	Previous coronal slice	Next coronal slice
Sagittal	Previous coronal slice	Next coronal slice	Previous transversal slice	Next transversal slice	Previous sagittal slice	Next sagittal slice
Transversal	Previous sagittal slice	Next sagittal slice	Previous coronal slice	Next coronal slice	Previous transversal slice	Next transversal slice

Slice Intraframe Zoom and Pan

The following key and mouse sequences allow users to pan and zoom within a slice display frame. It is important to note that this zoom behavior differs from the standard Zoom. This zoom keeps the displayed slice bounds fixed and performs the zoom and pan within these bounds. In contrast, other UI zoom controls change the scale and display bounds of the slice.

Slice View - Intraframe Zoom And Pan

Key	Mouse Button and Action	Context	Description
Shift	Left down and drag	Cursor over slice frame	Translates
Shift	Midel down and drag	Cursor over slice frame	Translates
Shift	Scroll wheel	Cursor over slice frame	Zooms within display bounds



Scrolling Zoom

Other Slice View Tools

You can also scroll through slices through the **Viewer Control** panel using the sliders and their associated spin boxes. Additionally, you can use the Layout and Zoom options to control the **Slice View**.

Tile View

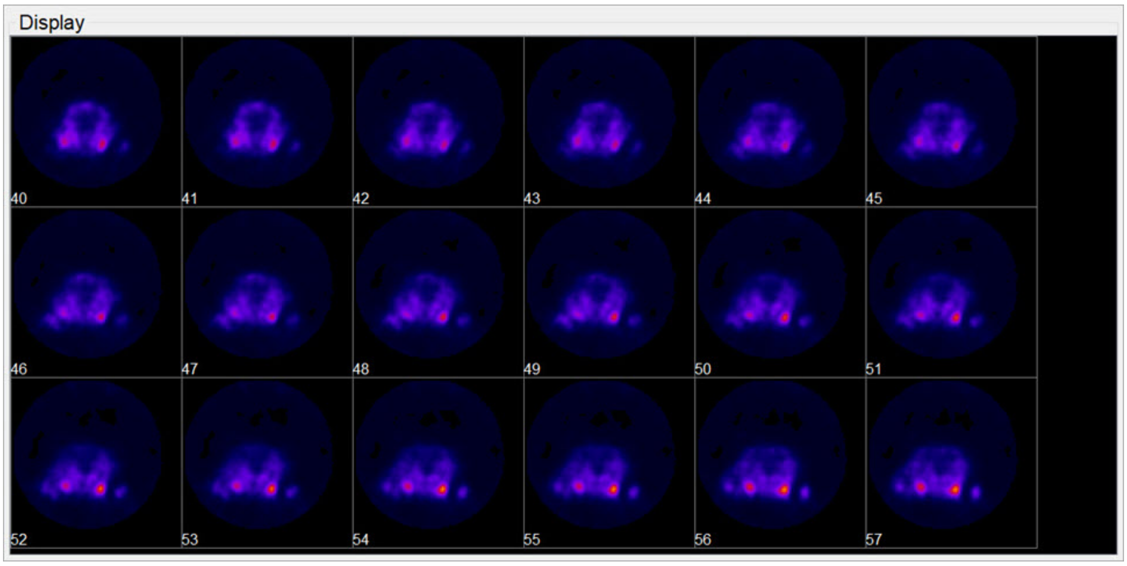
The **Tile View** displays an array of slices for either sagittal, coronal, or transversal view of the loaded data sets. The number of slices displayed depends on the size of the VivoQuant window.

Getting There

The **Tile View** is available via a pull-down menu on the Main Window.

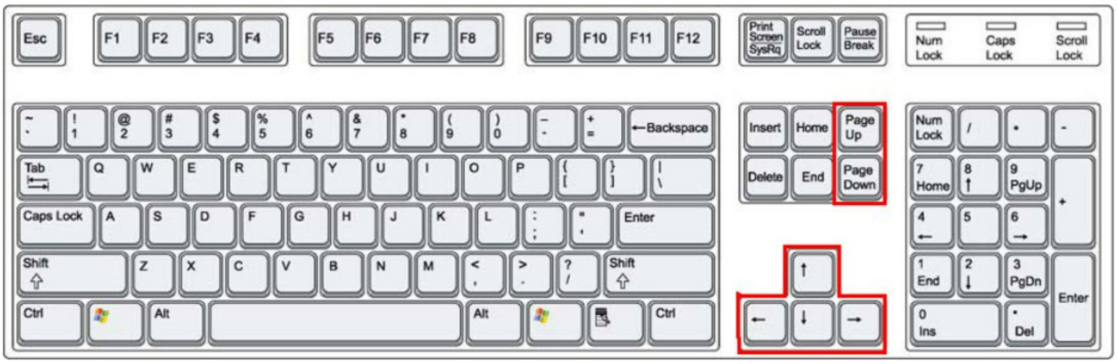
Tile View

Using the Tile View Display



Tile View Display

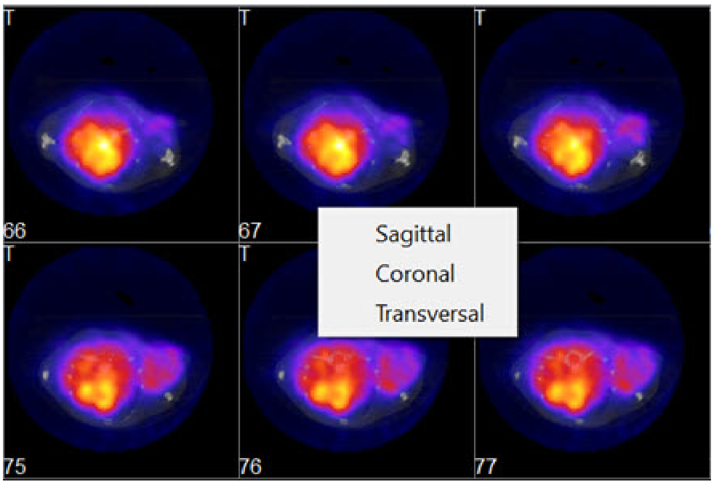
You can scroll through slices in the **Tile View** using the scroll wheel on a mouse or using the arrow and paging keys on your keyboard. The keys control the rate at which the user scroll through the tiles.



Keyboard Controls

←	→	↑	↓	PageUp	PageDn
Previous slice	Next slice	Previous row	Next row	Previous screen	Next screen

To switch between views (coronal, sagittal, transversal) in the **Tile View**, right-click on a tile and choose the desired view.



Switch View

There are two operators available in **Tile View**. The [Time Series]() operator, which enables dynamic data to be viewed as a time series, and the [3D ROI Tool]() operator, which enables ROIs to be displayed in **Tile View**.

ℹ **Note:** ROIs can't be edited in Tile View.

Multi View

Use the **Multi View** to create a fully customized Display for your data. You can select how many Viewports and in what orientation they will be displayed, and which datasets will be rendered in them. This is especially useful if you work with data across multiple image modalities.

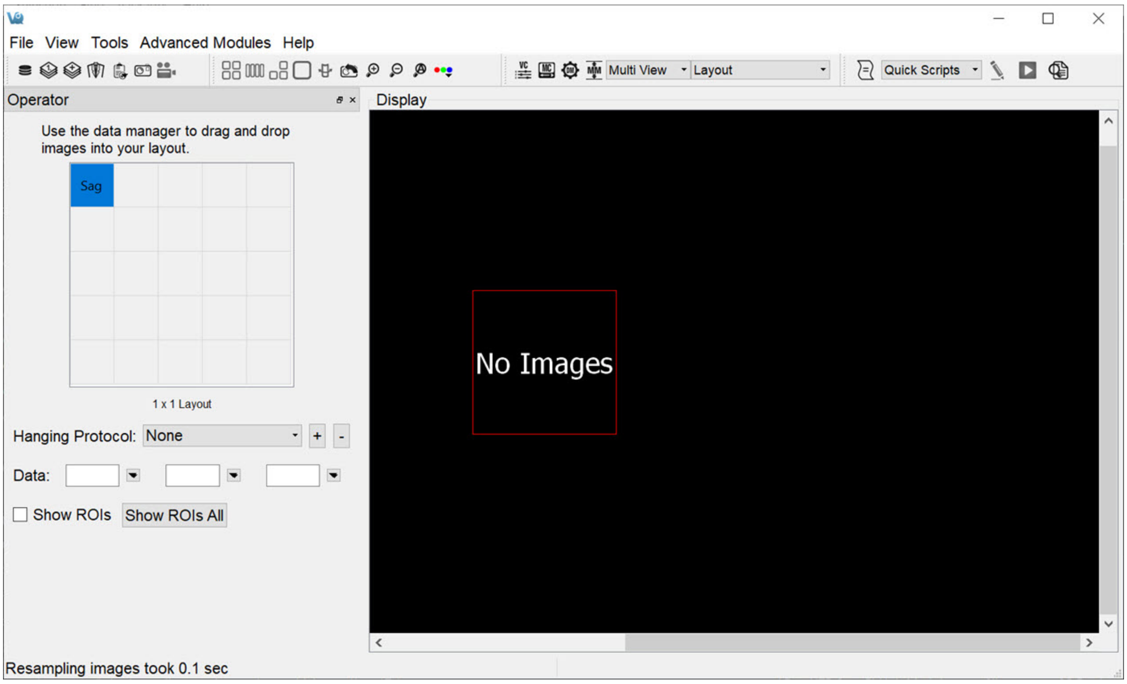
Getting There

The **Multi View** is available via a pull-down menu on the Main Window.

Multi View

Setting Up the Multi View Display

The **Multi View** tool activates a view-specific layout operator.



Use the data manager to drag and drop images into your layout.

Hanging Protocol: None

Data:

☐ Show ROIs

No Images

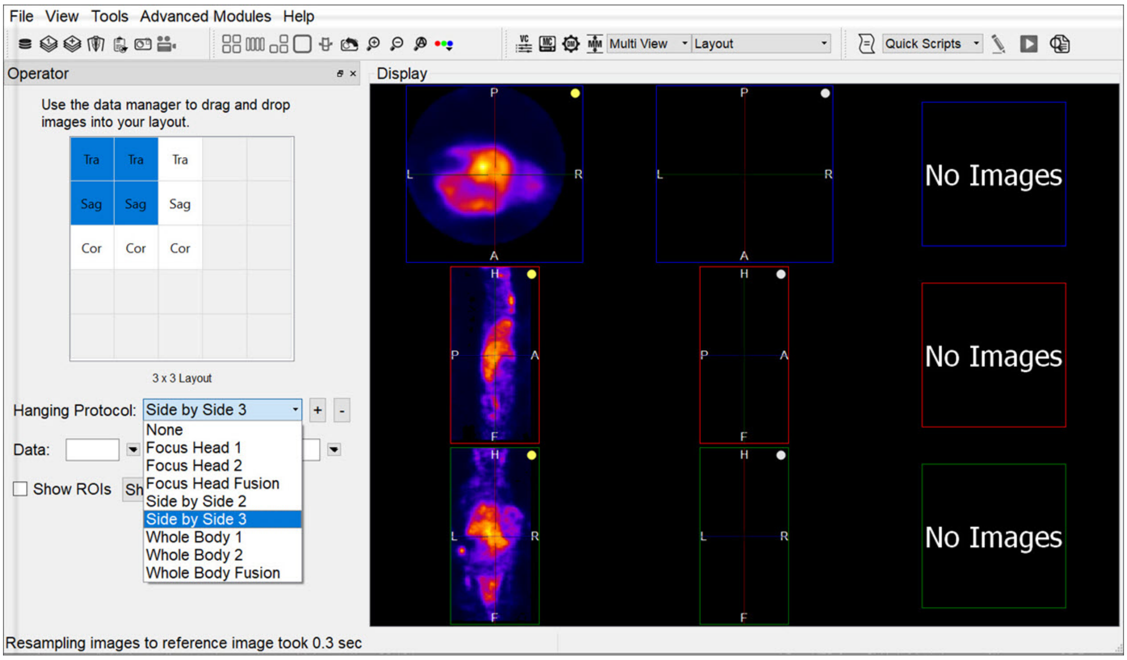
Resampling images took 0.1 sec

Multi View Layout Operator

Use the **Layout** operator to customize the **Multi View** display:

1. Select the desired layout, which will define the number of rows and columns of the **Viewports**.
2. For each viewport, select the datasets and slices that will be displayed.
3. Use the **Hanging Protocol** pull-down menu to set the desired layout.

   The 5x5 grid will populate with the corresponding number of rows and columns, and control both the datasets displayed in each viewport and the slice type.



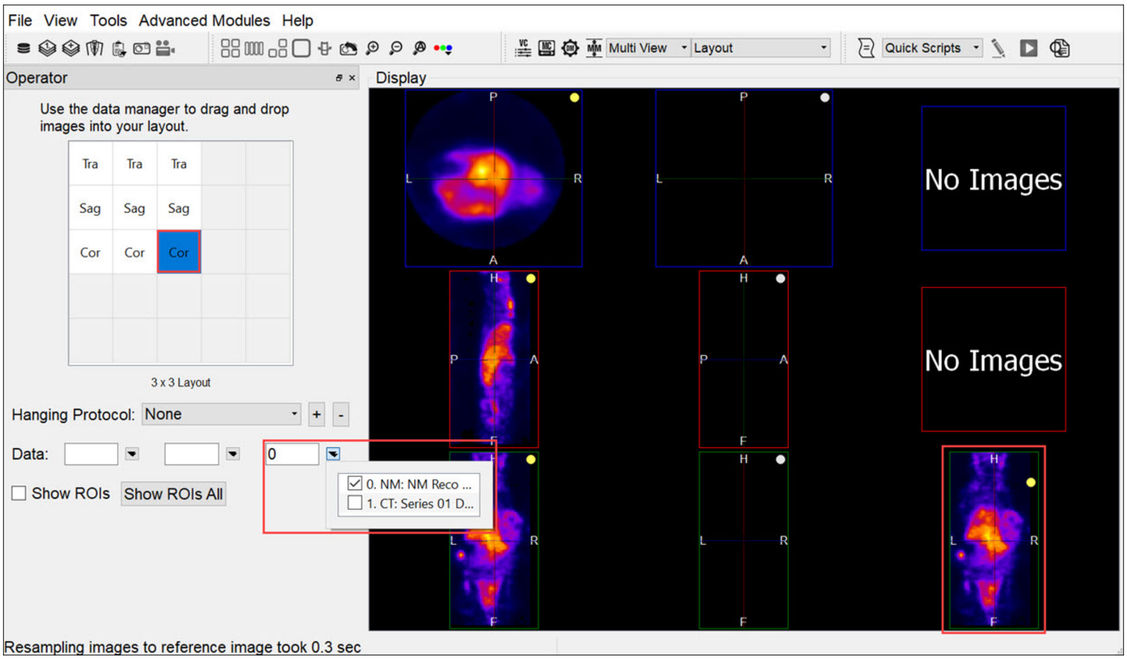
Use the data manager to drag and drop images into your layout.

Hanging Protocol: Side by Side 3

Resampling images to reference image took 0.3 sec

Hanging Protocol

To load data into a particular viewport, click on the corresponding box in the grid, and select the **Reference**, **Input 1** and **Input 2** dataset(s) image from the **Data** pull-down menus. The dataset(s) will be loaded automatically.



Use the data manager to drag and drop images into your layout.

Hanging Protocol: None

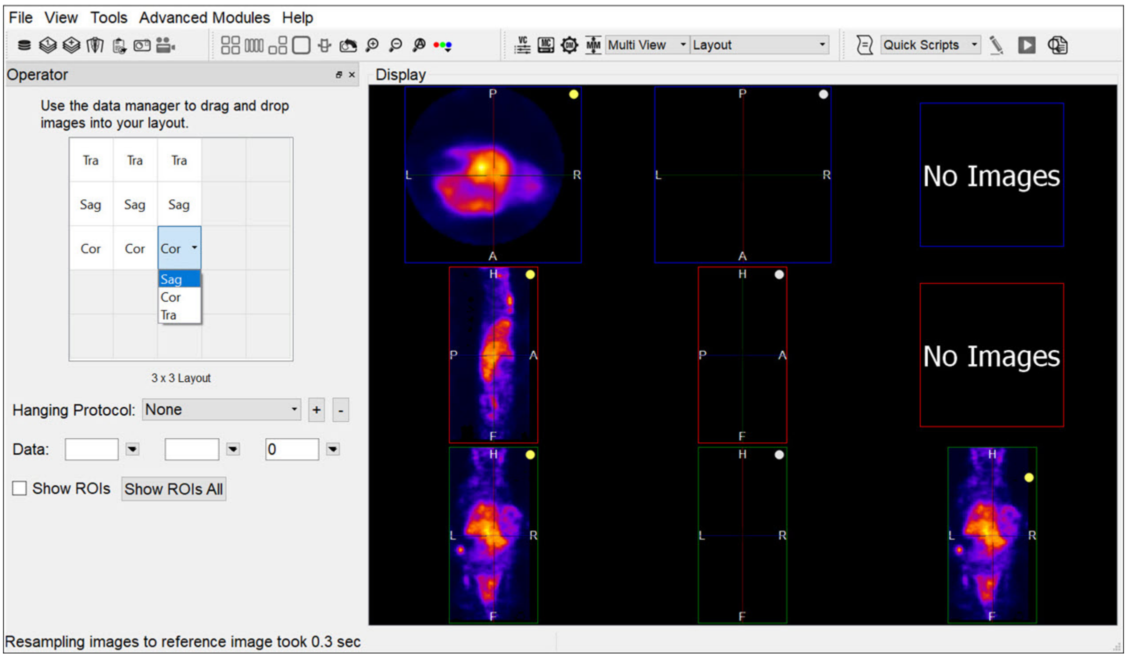
Data: 0

☑ 0. NM: NM Reco ...
☐ 1. CT: Series 01 D...

Resampling images to reference image took 0.3 sec

Load Viewport

The boxes in the 5x5 grid are labelled Cor, Sag, or Tra, indicating the type of slices displayed in the Viewports. To change the type of slice, double click on the corresponding box in the grid and select the desired slice type.



Use the data manager to drag and drop images into your layout.

Hanging Protocol: None

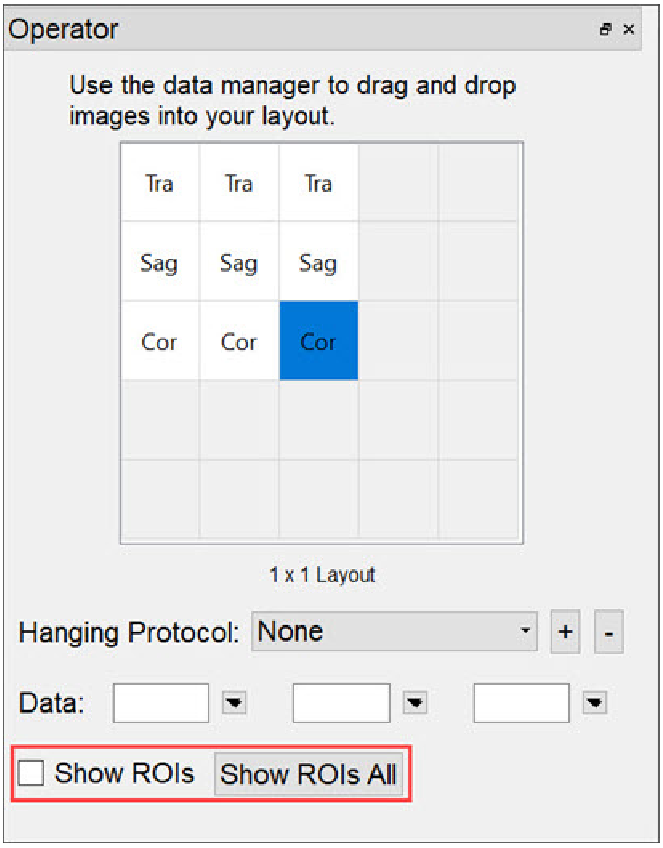
Data: 0

☐ Show ROIs

Resampling images to reference image took 0.3 sec

Select Slice Type

To show ROIs in a Viewport, select the desired Viewport, by either clicking on it in the Display or clicking on the corresponding 5x5-grid box, and check **Show ROIs**. To show ROIs in all viewports, click the **Show ROIs All** button.



Use the data manager to drag and drop images into your layout.

Hanging Protocol: None

Data:

☐ Show ROIs

Show ROIs

Using the Multi View Display

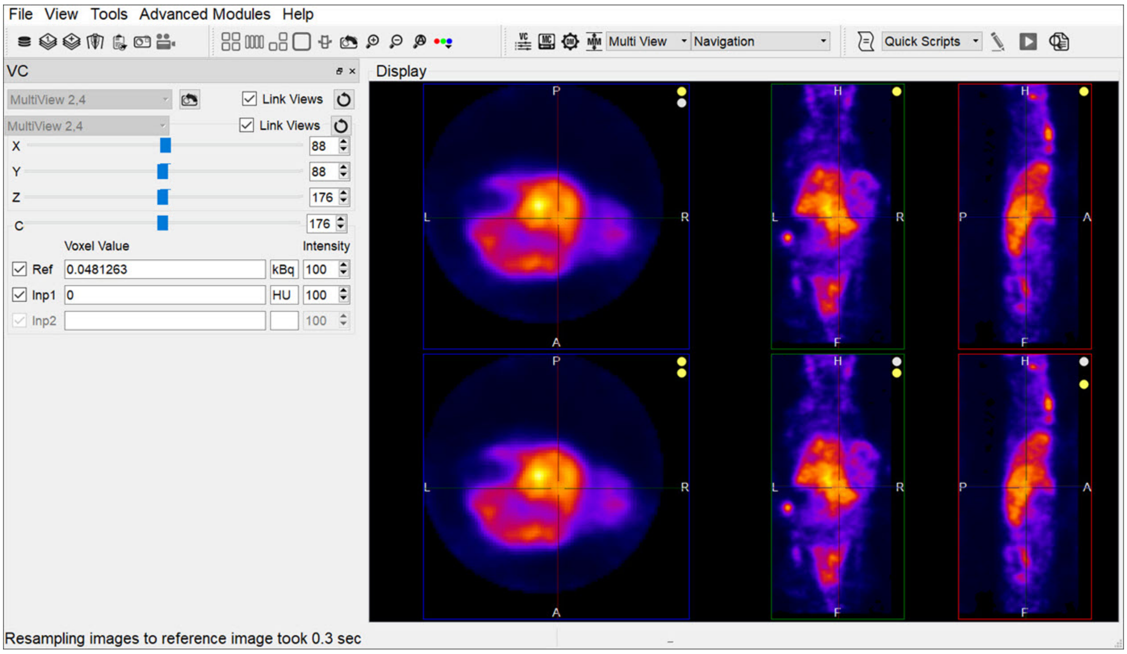
Navigation

To use the **Multi View** in the same way as other Displays, close the **Layout** operator and select the **Navigation** operator. The **Navigation** operator in Multi View has identical functionalities as in Slice View. Mouse and keyboard functions, including

Keyboard Shortcuts, are preserved.

Viewer Control in Multi View

The View Control functionality is extended in **Multi View** to cover the new viewport layout. This includes the ability to view voxel and color information for each viewport in the Display, as well as the ability to unlink the viewports, enabling them to be navigated independently of one another.



MultiView 2,4 ☑ Link Views

MultiView 2,4 ☑ Link Views

X 88

Y 88

Z 176

C 176

	Voxel Value		Intensity
☑ Ref	0.0481263	kBq	100
☑ Inp1	0	HU	100
☑ Inp2			100

Multi View | Navigation

Resampling images to reference image took 0.3 sec

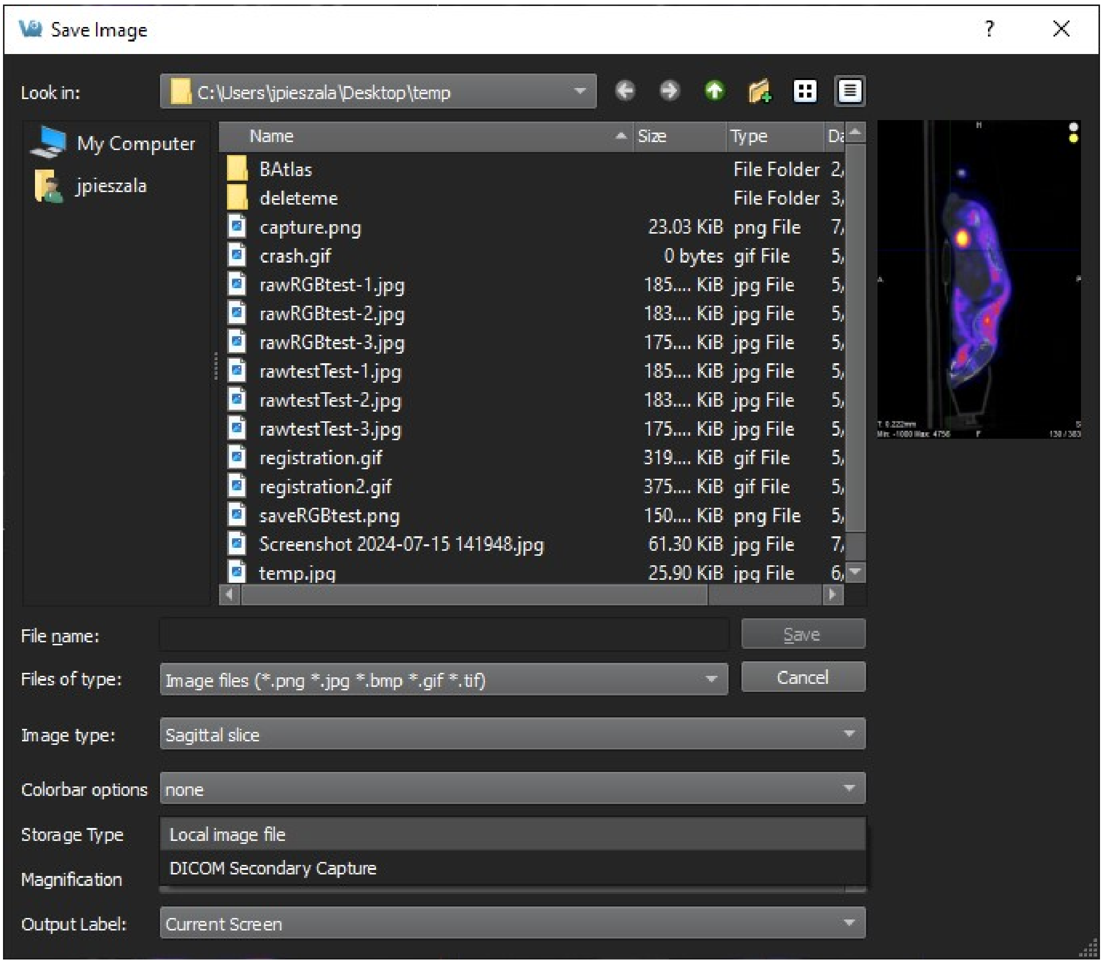
View Control Functionality

Capture Viewer

The **Capture Viewer** allows for editing image and movie files prior to saving.

Getting There

When saving an image or movie file, the second option in the **Storage Type** drop-down menu is **DICOM Secondary Capture**. Select this option and click **Save** to load the data into the **Capture Viewer**.



Look in: C:\Users\jpieszala\Desktop\temp

Name	Size	Type	Da
BAtlas		File Folder	2,
deleteme		File Folder	3,
capture.png	23.03 KiB	png File	7,
crash.gif	0 bytes	gif File	5,
rawRGBtest-1.jpg	185.... KiB	jpg File	5,
rawRGBtest-2.jpg	183.... KiB	jpg File	5,
rawRGBtest-3.jpg	175.... KiB	jpg File	5,
rawtestTest-1.jpg	185.... KiB	jpg File	5,
rawtestTest-2.jpg	183.... KiB	jpg File	5,
rawtestTest-3.jpg	175.... KiB	jpg File	5,
registration.gif	319.... KiB	gif File	5,
registration2.gif	375.... KiB	gif File	5,
saveRGBtest.png	150.... KiB	png File	5,
Screenshot 2024-07-15 141948.jpg	61.30 KiB	jpg File	7,
temp.jpg	25.90 KiB	jpg File	6,

File name:

Files of type: Image files (*.png *.jpg *.bmp *.gif *.tif)

Image type: Sagittal slice

Colorbar options none

Storage Type

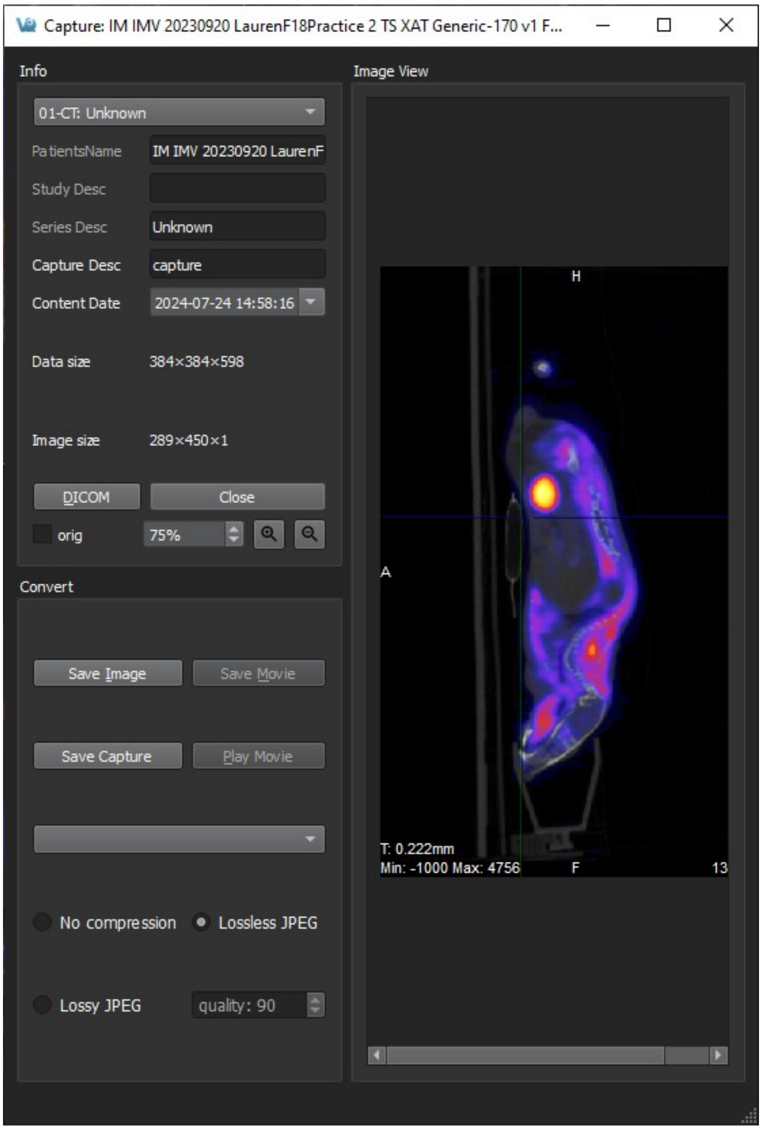
Magnification

Output Label: Current Screen

DICOM Secondary Capture Option

Function

The **Capture Viewer** panel is split into three sections: Info, Convert, and Image View.



Capture: IM IMV 20230920 LaurenF18Practice 2 TS XAT Generic-170 v1 F...

Info

01-CT: Unknown

PatientsName IM IMV 20230920 LaurenF

Study Desc

Series Desc Unknown

Capture Desc capture

Content Date 2024-07-24 14:58:16

Data size 384×384×598

Image size 289×450×1

☐ orig 75%

Convert

○ No compression ● Lossless JPEG

○ Lossy JPEG quality: 90

Capture Viewer Panel

Info

The **Info** field includes functions that affect the output image.

Option	Description
Series Description	Image pull-down menu. The selected image will be reflected in the **Series Desc** field.
PatientsName	Patient name as stored in the **DICOM header**.
Study Desc	Protocol used to collect the data.
Series Desc	Series description including modality.
Capture Desc	Name of image/movie to be saved. Manually entered by the user.
Content Data	Date and time at which the image/movie was loaded into the **Capture Viewer**.
Data Size	Size of the original data referred to in the **Series Description** pull-down menu.
Image Size	Size of image currently being displayed.
DICOM	When pressed, displays the DICOM header for the data.
Close	When pressed, closes the **Capture Viewer** without saving image.
orig	When checked, maintains, or returns to, the original image size.
⊕ and ⊖	Increases/decreases the image size.

Convert

The **Convert** field includes several options that affect the output image.

Option	Description
Save Image	Opens the Save Image screen.
Save Movie	Opens the Save Movie screen.
Play Movie	Plays/stops the movie.
Save Capture	Saves image/movie into the repository specified in the pull-down menu.

Image View

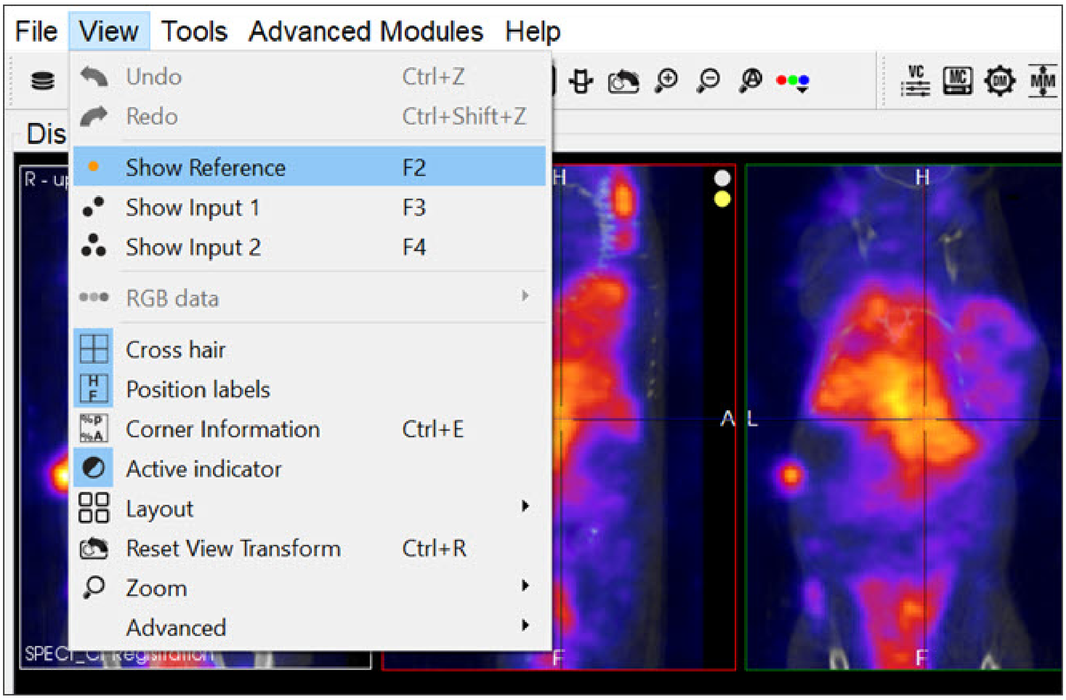
The **Image** field displays of the image or movie that is currently being edited.

Show Reference / Input 1 / Input 2

The datasets rendered in the display (**Reference**, **Input 1** and **Input 2**) may be turned on and off.

Getting There

To toggle the appearance of these datasets, go to the **View** menu and select **Show Reference**, **Show Input 1**, or **Show Input 2**. The change will be immediately visible in the Display.



Show Reference / Input

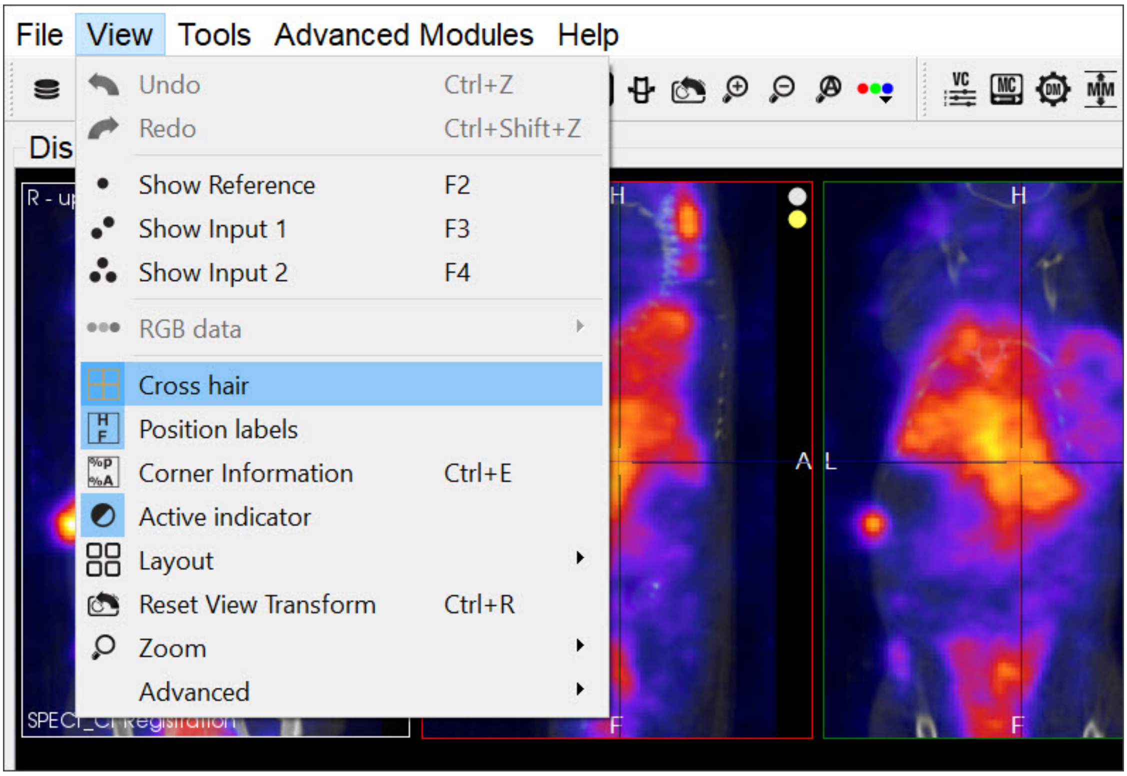
Alternatively, you can use the keyboard shortcuts: F2 for **Reference**, F3 for **Input 1**, and F4 for **Input 2**. For more information on keyboard shortcuts, visit the Keyboard Shortcuts page.

Cross Hair

This function allows for displaying cross hairs on the images to assist navigation through the slices.

Getting There

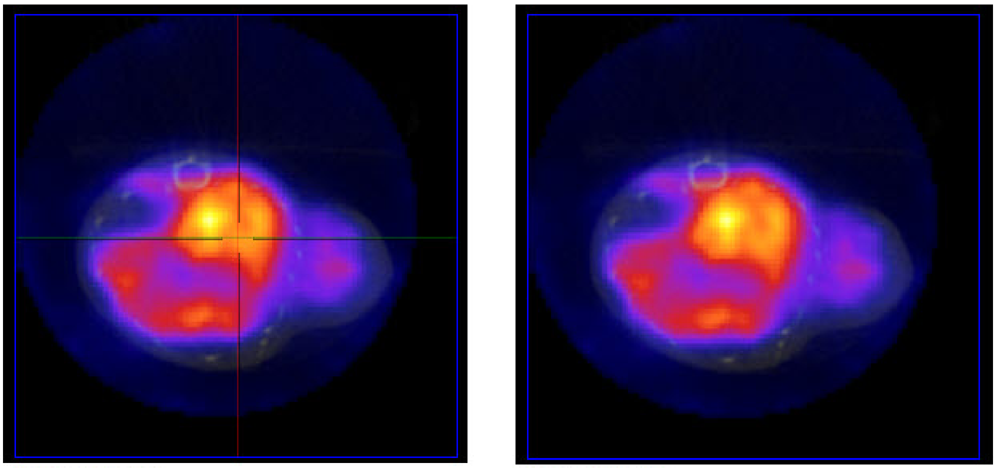
To display the **Cross Hairs** on the image, go to the **View** menu and select **Cross hair**.



Cross Hairs

Function

The **Cross Hairs** are displayed over each cross-sectional image: sagittal, transversal and coronal. To display the cross hairs in the images, go to the **View** menu and select **Cross Hair**. To conceal the cross hairs from view, unselect the **Cross Hair** functionality by left-clicking on it.



Cross Hairs On

Cross Hairs Off

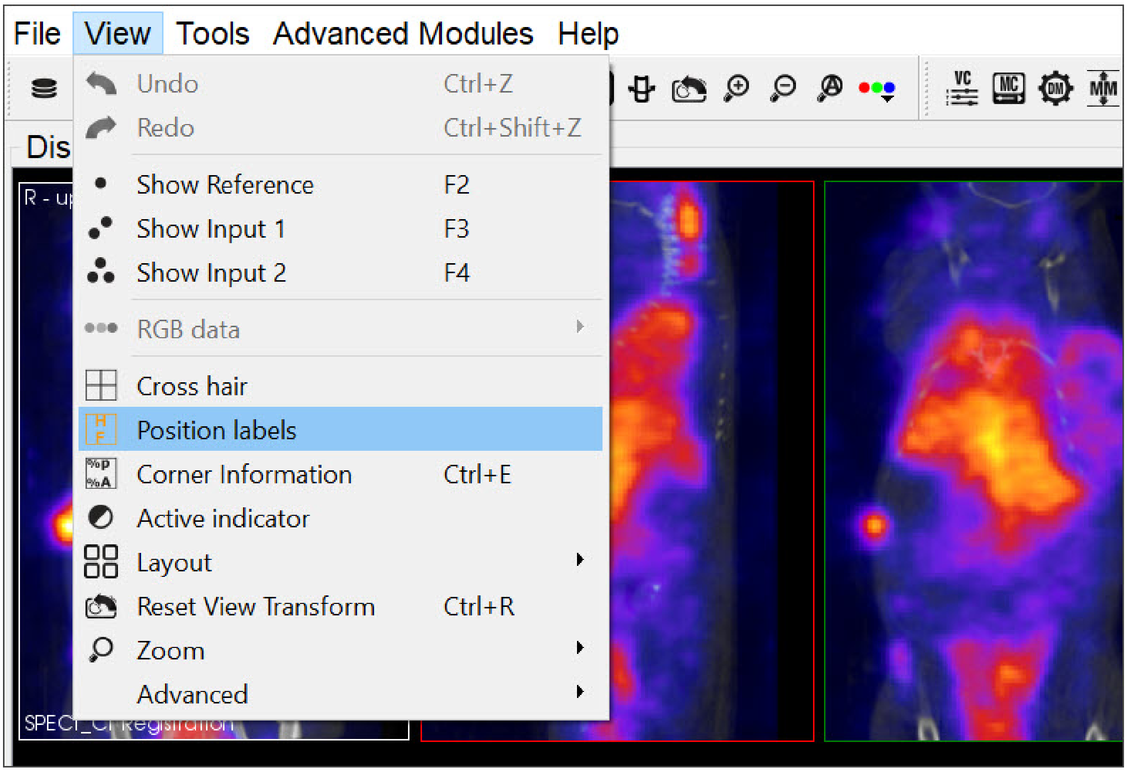
Sow / Hide Cross Hairs

Position Labels

The **Position Labels** are displayed on each image plane and MIP. They indicate which side of the subject is being viewed.

Getting There

To display the position labels on the image, go to the **View** menu and select **Position Labels**.



Position Labels

Function

The labels indicate the plane of view (sagittal, coronal and transversal), and also the left/right and anterior/posterior side of the subject.

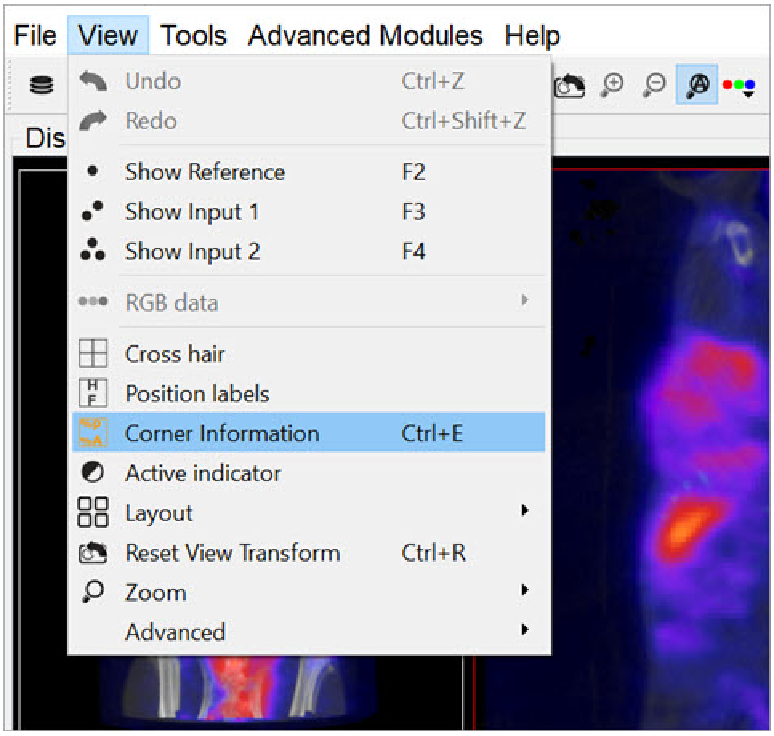
Sagittal	There is an S on the top left corner of the image to indicate that it is the **Sagittal** plane. There is also a P to indicate the posterior side of the subject, and an A to indicate the anterior side of the subject.
Coronal	There is a C on the top left corner of the image to indicate that it is the **Coronal** plane. There is also an H to indicate the head of the subject, and an F to indicate the feet of the subject.
Transversal	There is a T on the top left corner of the image to indicate that is it the **Transversal** plane. There is also an L to indicate the left side of the subject, and an R to indicate the right side of the subject.

Corner Information

This feature allows for configuring the image information to be displayed on the four corners of each viewport.

Getting There

To display the image information, go to the **View** menu and select **Corner Information**.



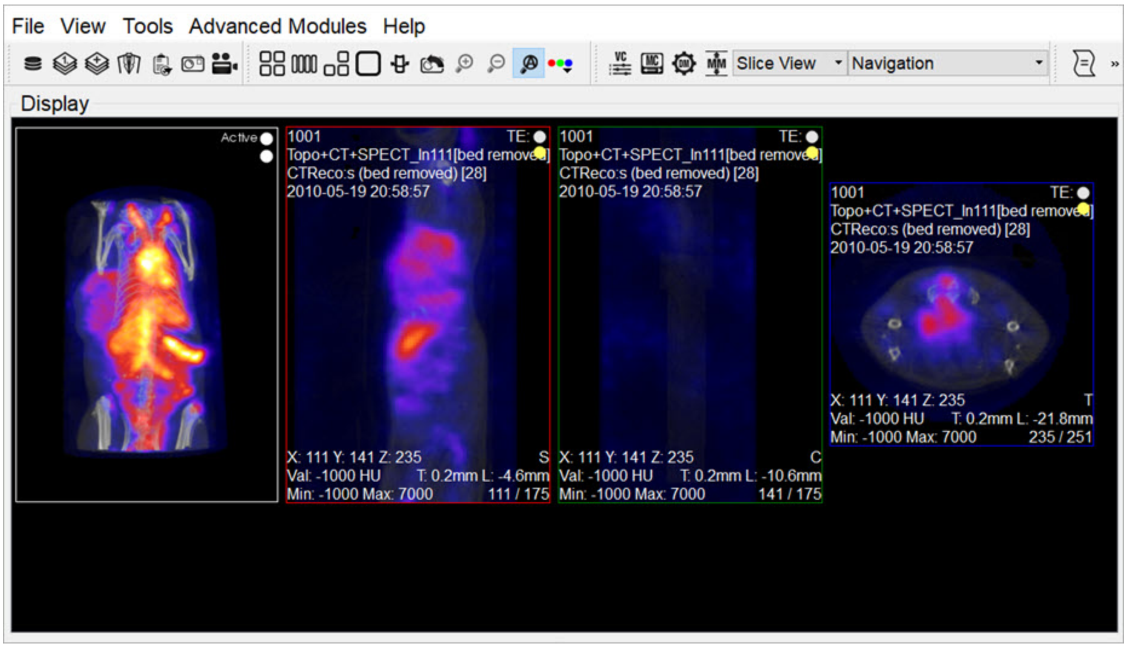
Corner Information

Alternatively, you can use the keyboard shortcut Shift+E to display the image information.

To conceal the information labels from view, unselect the **Corner Information** function by using either of the above alternatives.

Function

Once this option is selected, the information for the active image is displayed on the corners of all of the image planes (sagittal, coronal and transversal) and also on the MIP.

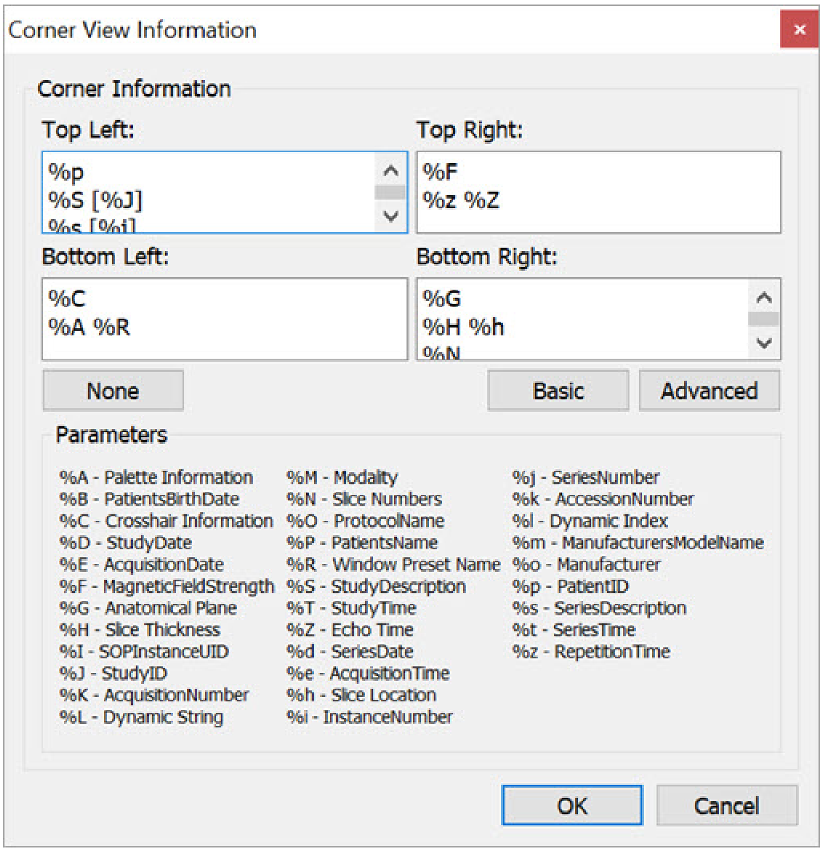


Info Displayed

Configuration

You can configure what type of information to be displayed on each corner of the image viewports by going to **Tools** > **Configuration**.

On the **Display** tab, click on the Corner Info button and use the patterns shown in the window to select what information you want to display on each corner of the image viewports.



Top Left:
%p
%S [%J]
%s [%i]

Top Right:
%F
%z %Z

Bottom Left:
%C
%A %R

Bottom Right:
%G
%H %h
%N

%A - Palette Information
%B - PatientsBirthDate
%C - Crosshair Information
%D - StudyDate
%E - AcquisitionDate
%F - MagneticFieldStrength
%G - Anatomical Plane
%H - Slice Thickness
%I - SOPInstanceUID
%J - StudyID
%K - AcquisitionNumber
%L - Dynamic String
%M - Modality
%N - Slice Numbers
%O - ProtocolName
%P - PatientsName
%R - Window Preset Name
%S - StudyDescription
%T - StudyTime
%Z - Echo Time
%d - SeriesDate
%e - AcquisitionTime
%h - Slice Location
%i - InstanceNumber
%j - SeriesNumber
%k - AccessionNumber
%l - Dynamic Index
%m - ManufacturersModelName
%o - Manufacturer
%p - PatientID
%s - SeriesDescription
%t - SeriesTime
%z - RepetitionTime

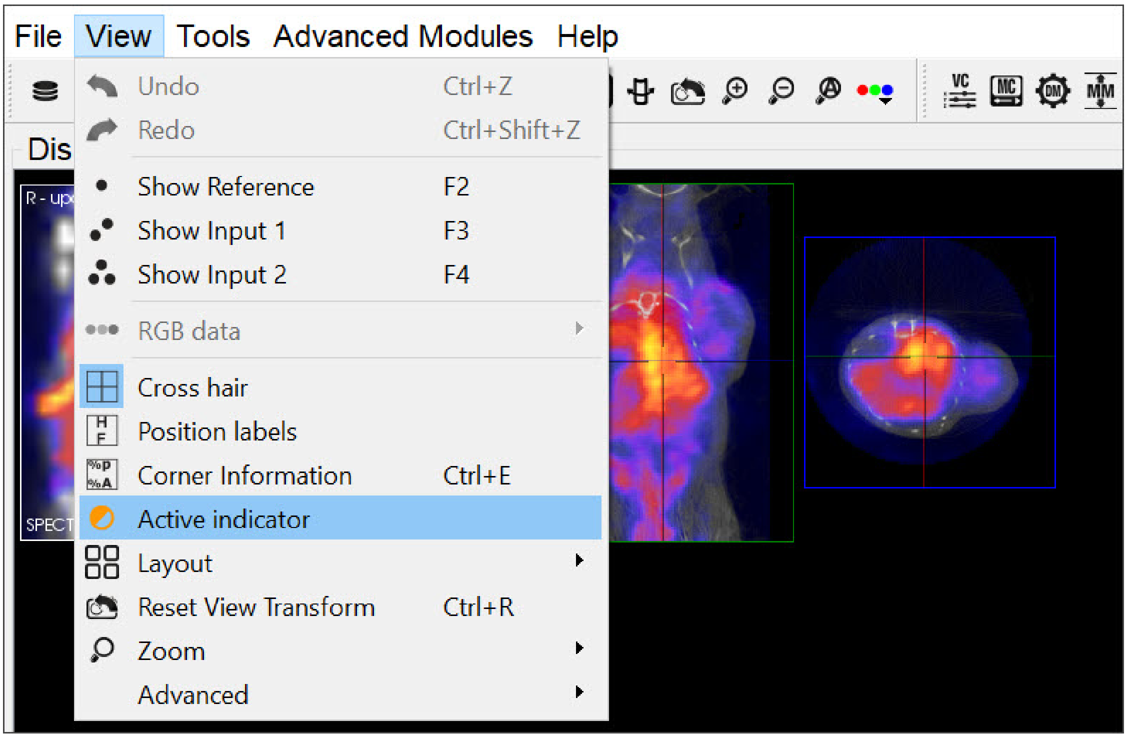
Configure Corner Information

Active Indicator

The **Active Indicator** option places icons in the viewports that indicate which datasets are currently active in the **Display**.

Getting There

To turn on this option, go to the **View** menu and select **Active Indicator**.

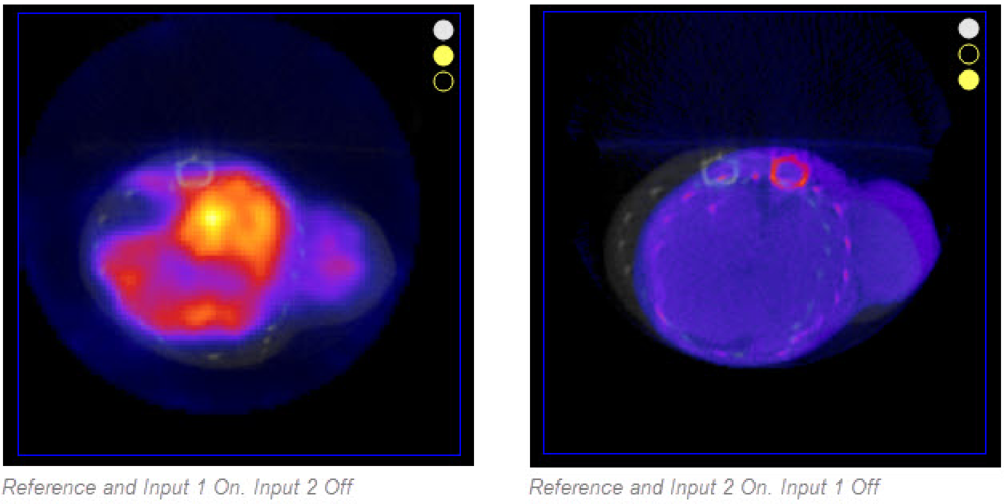


Active Indicator

Function

The **Active Indicators** appear in the upper right corner of the viewports.

The top, middle and bottom indicators correspond to the **Reference**, **Input 1** and **Input 2**, respectively. If the indicator is a solid circle, the corresponding input is on. If the indicator is a hollow circle, the corresponding input is off.



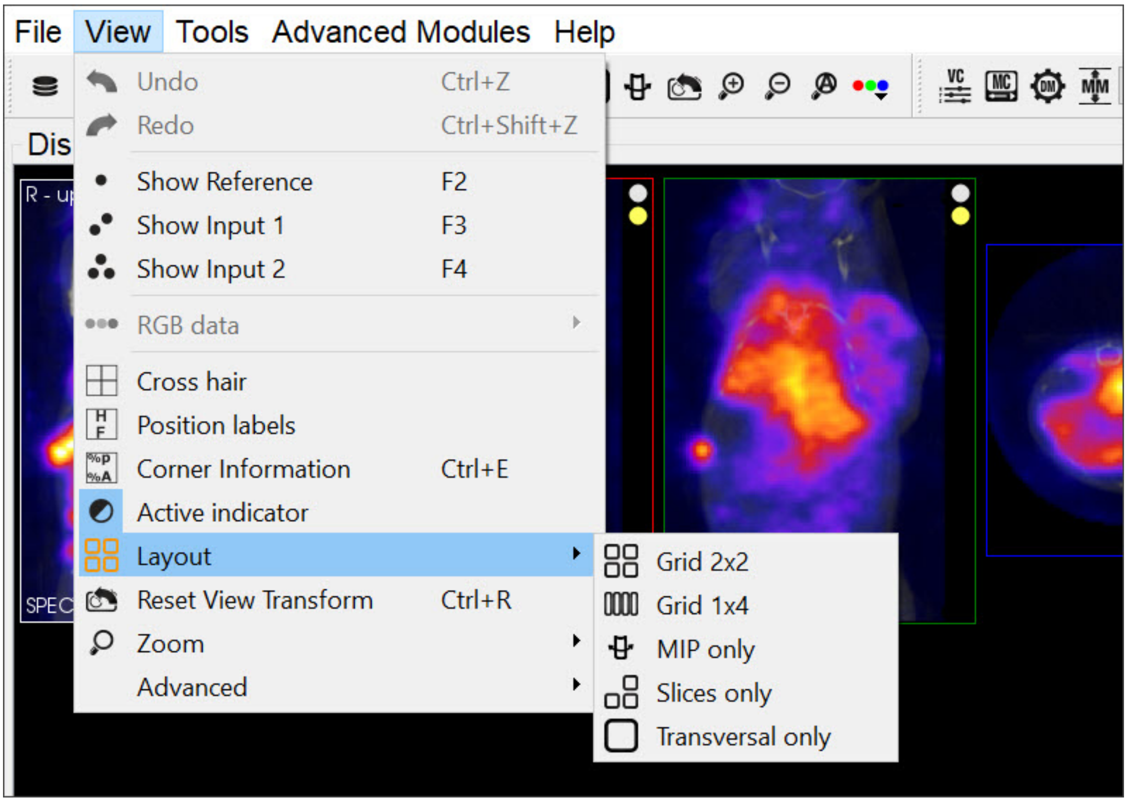
Active and Inactive Data

Layout

This feature offers a variety of layouts for viewing studies. You can view all the slices and the MIP together simultaneously or each study individually.

Getting There

To select a layout option for the images, go to the **View** menu and click **Layout**.



Layout

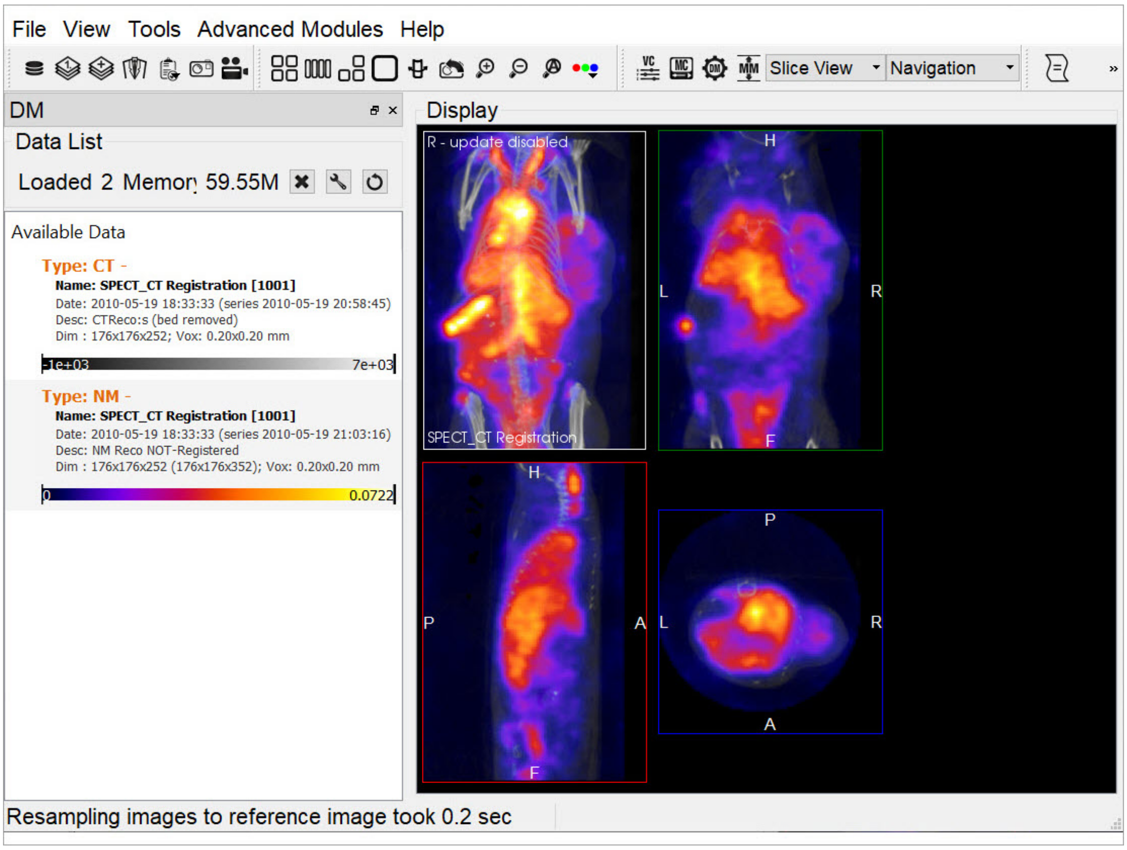
Alternatively, the different layouts can be activated by clicking on the **Layout** thumbnails in the Main Window.

Thumbnail	Description
⊞	Grid 2x2
▥	Grid 1x4
⊕	MIP only
⊞	Slices only
▢	Transversal only

Layout Options

Grid 2x2

In the **Grid 2x2** layout, the MIP and the coronal slice are located on the upper half of the screen, and the sagittal and transversal slices are located on the bottom half of the screen.



Loaded 2 Memor 59.55M

Available Data

Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)
Desc: CTReco:s (bed removed)
Dim : 176x176x252; Vox: 0.20x0.20 mm
-1e+03 7e+03

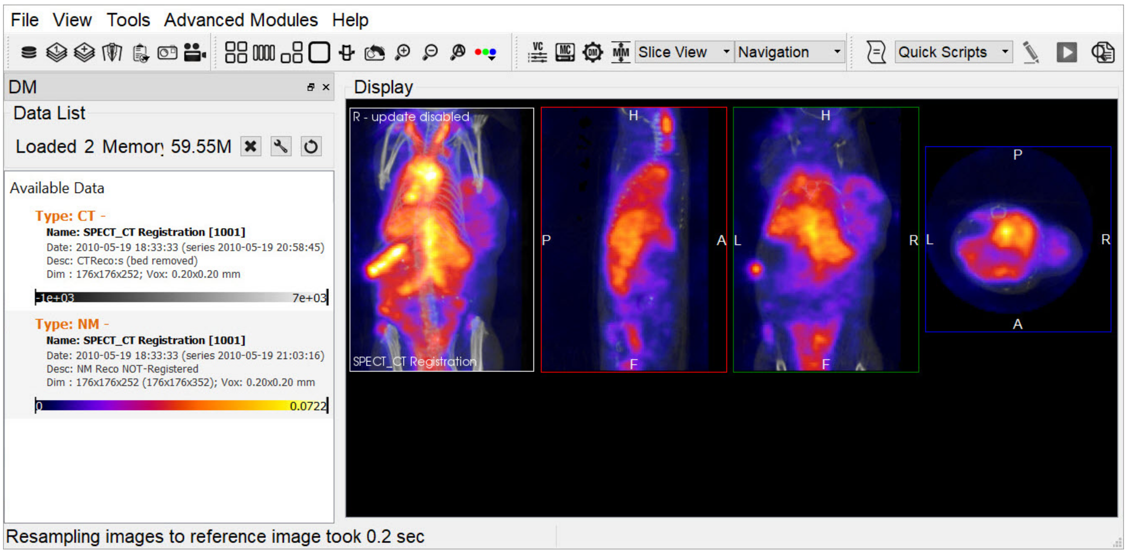
Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)
Desc: NM Reco NOT-Registered
Dim : 176x176x252 (176x176x352); Vox: 0.20x0.20 mm
0 0.0722

Resampling images to reference image took 0.2 sec

Grid 2x2

Grid 1x4

In the **Grid 1x4** layout, the MIP and all three slices are laid out in a single row.



Loaded 2 Memor 59.55M

Available Data

Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)
Desc: CTReco:s (bed removed)
Dim : 176x176x252; Vox: 0.20x0.20 mm
-1e+03 7e+03

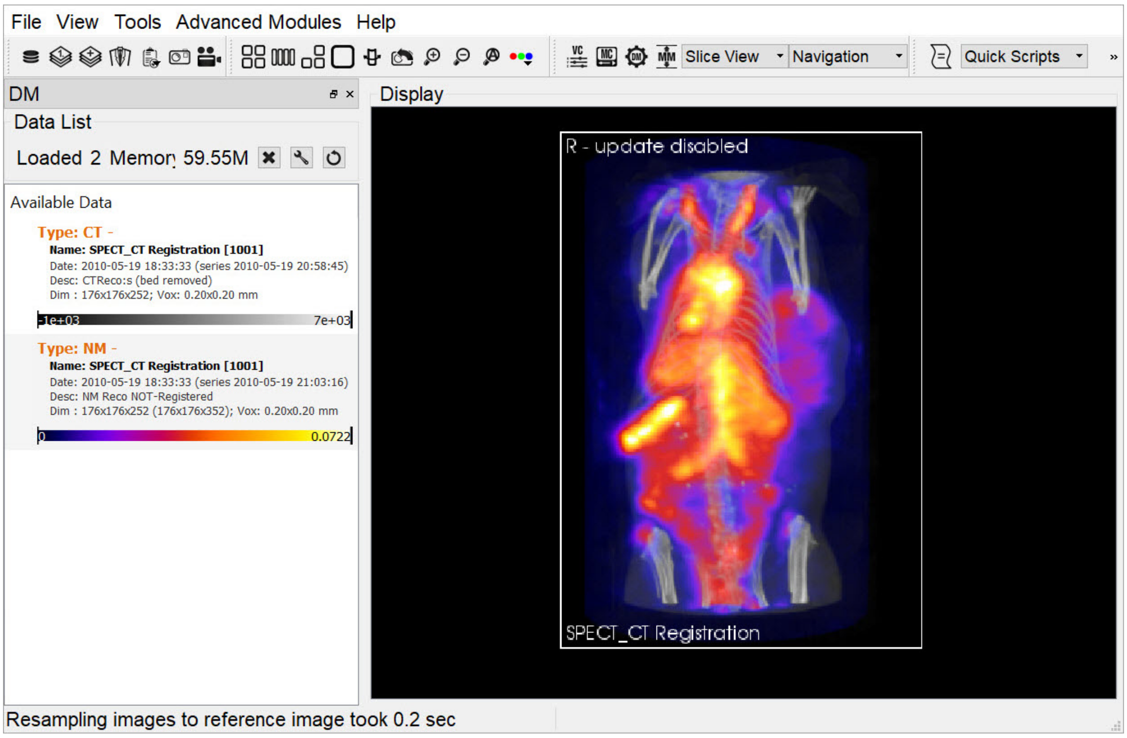
Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)
Desc: NM Reco NOT-Registered
Dim : 176x176x252 (176x176x352); Vox: 0.20x0.20 mm
0 0.0722

Resampling images to reference image took 0.2 sec

Grid 1x4

MIP only

In the **MIP only** layout, only the MIP is visible. The slices are not in view.



Loaded 2 Memory 59.55M

Available Data

Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)
Desc: CTReco:s (bed removed)
Dim : 176x176x252; Vox: 0.20x0.20 mm
-1e+03 7e+03

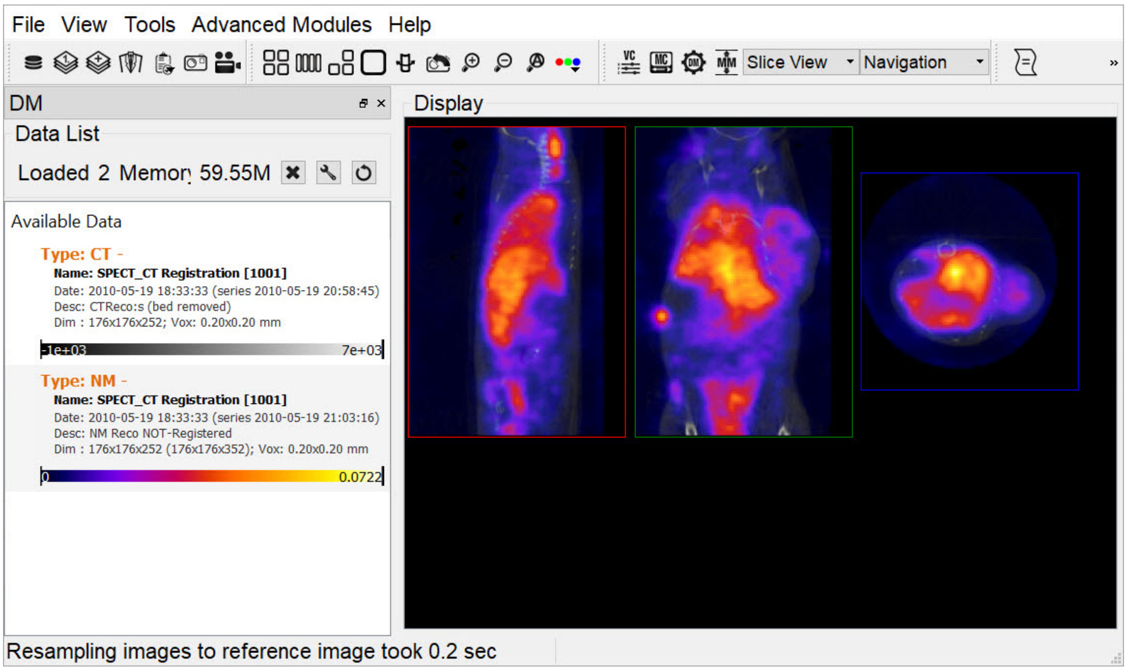
Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)
Desc: NM Reco NOT-Registered
Dim : 176x176x252 (176x176x352); Vox: 0.20x0.20 mm
0 0.0722

Resampling images to reference image took 0.2 sec

MIP only

Slices only

In the **Slices only** layout, only the slices are visible. The MIP is not in view.



Loaded 2 Memory 59.55M

Available Data

Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)
Desc: CTReco:s (bed removed)
Dim : 176x176x252; Vox: 0.20x0.20 mm
-1e+03 7e+03

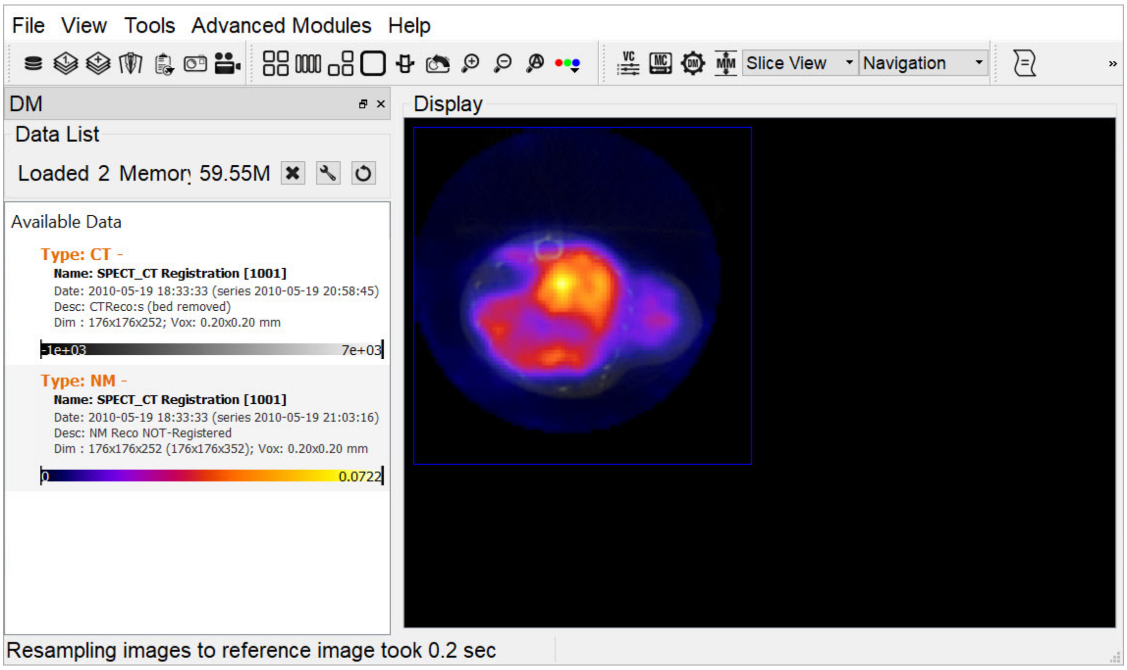
Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)
Desc: NM Reco NOT-Registered
Dim : 176x176x252 (176x176x352); Vox: 0.20x0.20 mm
0 0.0722

Resampling images to reference image took 0.2 sec

Slices only

Transverse only

In the **Transverse only** layout, only the transverse slice is in view.



Loaded 2 Memory 59.55M

Available Data

Type: CT -

Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)
Desc: CTReco:s (bed removed)
Dim : 176x176x252; Vox: 0.20x0.20 mm

-1e+03 7e+03

Type: NM -

Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)
Desc: NM Reco NOT-Registered
Dim : 176x176x252 (176x176x352); Vox: 0.20x0.20 mm

0 0.0722

Resampling images to reference image took 0.2 sec

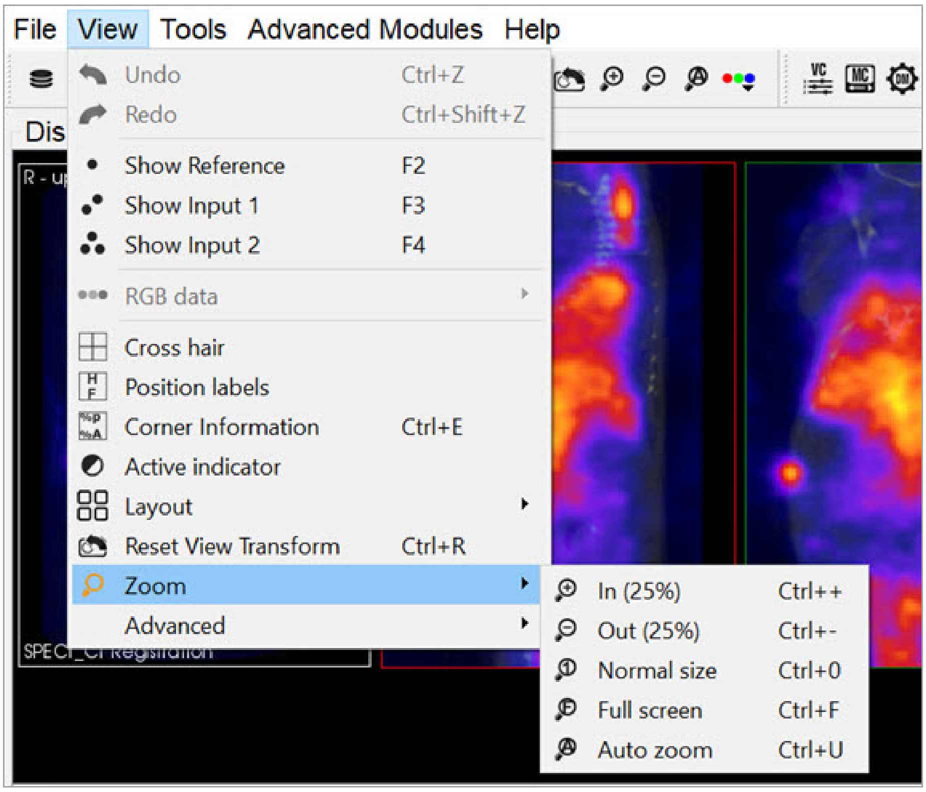
Transverse only

Zoom

The **Zoom** function allows for altering the viewpoint of the images by zooming in and out, and also provides the option of a full screen view.

Getting There

There are three different methods for operating the **Zoom** function. The first method is to go to the **View** menu and select **Zoom**.



Zoom

The second method is to use the following keyboard shortcuts:

Function	Shortcut
Zoom in (25%)	Ctrl + +
Zoom out (25%)	Ctrl + -
Normal size	Ctrl + 0
Full screen	Ctrl + F
Auto zoom	Ctrl+ Z

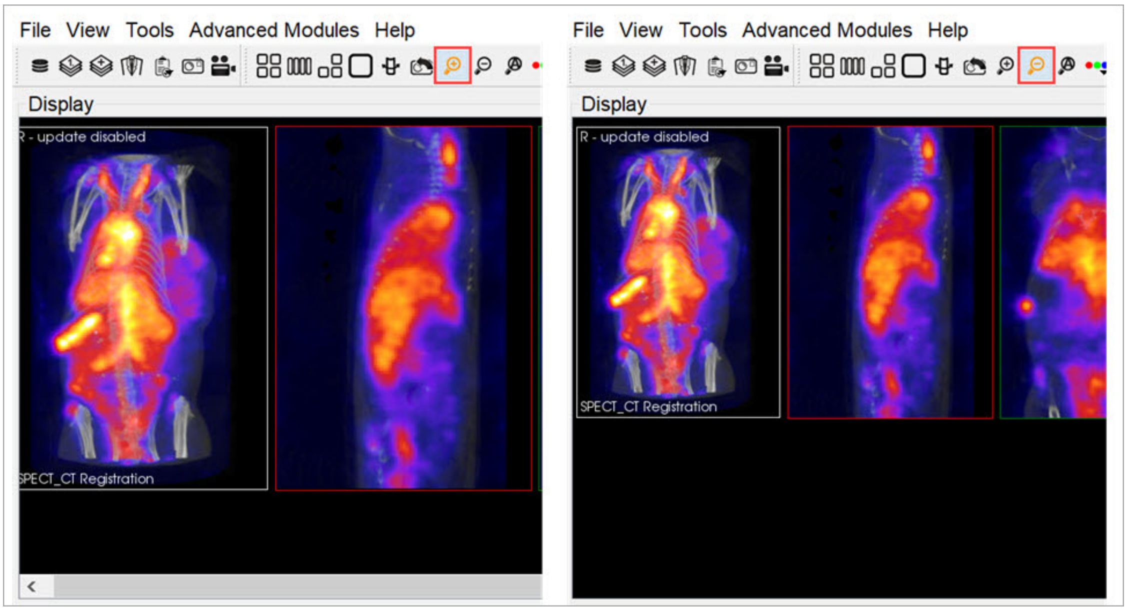
For more information on keyboard shortcuts, see the Keyboard Shortcuts page.

The third method is to click on the **Zoom In** and **Zoom Out** thumbnails in the Main Window.

Function

The **Zoom In** option allows for to zooming in by 25% increments. The **Zoom Out** option allows for zooming out by 25%

increments.



Zoom In and Out

The **Normal Size** is the default angle. Selecting this option will bring the images back to their original viewing angle.

The **Full Screen** options displays VivoQuant in full screen mode. To enable and disable this mode, hit the keyboard shortcut Ctrl + F.

The **Auto Zoom** option automatically increases the viewing angle of the images if the size of VivoQuant's window is increased. To access this option, click on the **Auto Zoom** thumbnail on the top bar.

ℹ **Note:** If the **Auto Zoom** function is not selected and the size of VivoQuant's window is increased, the image slices will stay in the same viewing angle and will not automatically fit the larger window size.

VQScript

VQScript, or **VivoScript**, is an implementation of **ECMAScript** (JavaScript) that allows users to access large parts of **VivoQuant**.

JavaScript structures

VQScript syntax is identical to JavaScript syntax.

Loop

```
for (var i=0; i&lt;10; ++i) {
        ...
}
```

Function

```
function blub() { ... }
function bar(p1, p2, p3) { return p1+p2+p2; }
var res = bar(1,2,3);
```

Array

```
var array  = new Array();
array[0]   = 'foo';
array[1]   = 'bar';
var array2 = new Array('foo', 'bar');
var array3 = [ 'foo', 'bar' ];
var last   = array2.pop();      // remove and get last element
array2.push('burp');          // add element
```

Other array functions are, for instance, concat, join, reverse, sort, unshift, shift.

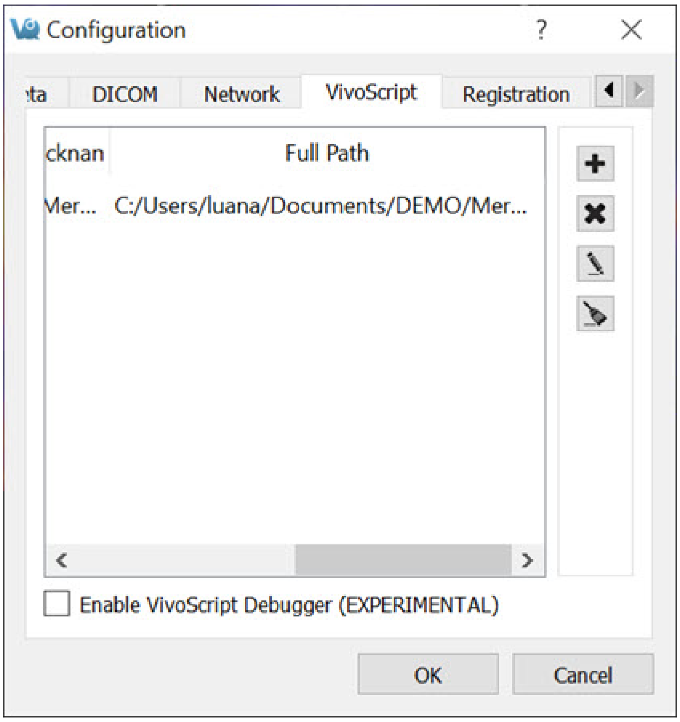
The VQScript Toolbar

Adding Script Shortcuts to the Toolbar

Shortcuts for commonly executed **VQScripts** can be added to the **Quick Scripts** menu on the **VQScript** toolbar

To add a **Quick Script** shortcut:

1. Go to **Tools->Configuration** and click on the **VivoScript** tab.

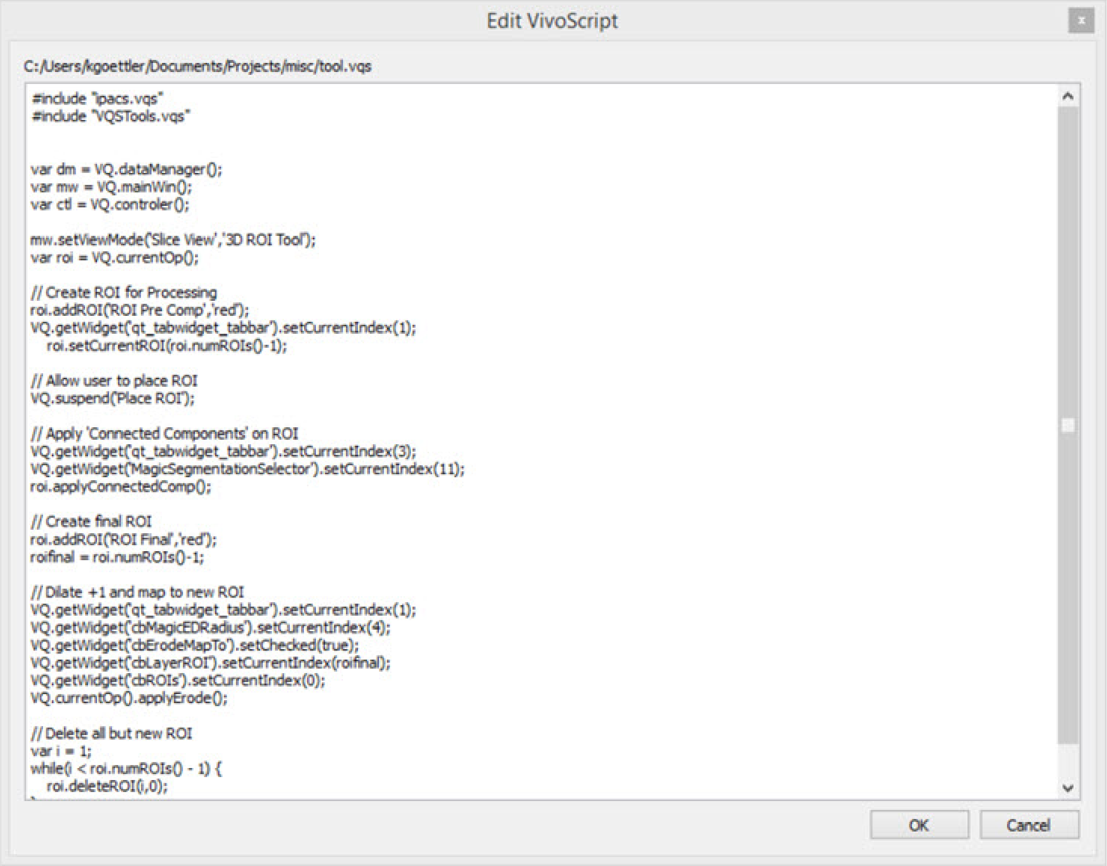


cknan	Full Path
Mer...	C:/Users/luana/Documents/DEMO/Mer...

☐ Enable VivoScript Debugger (EXPERIMENTAL)

2. Select a script for which quick access is desired by clicking the **Add Quick Script** button and navigating to the directory where the script is saved.
3. Add a nickname for the script in the dialog box that appears.
4. The script will now appear in the configuration window as well as in the **Quick Scripts** menu on the **VQScript** toolbar.

Quick Scripts can be edited directly from the **VQScript** toolbar by clicking on the **Edit VivoScript** button . A window will appear in which the user can edit the script.



C:/Users/kgoettler/Documents/Projects/misc/tool.vqs

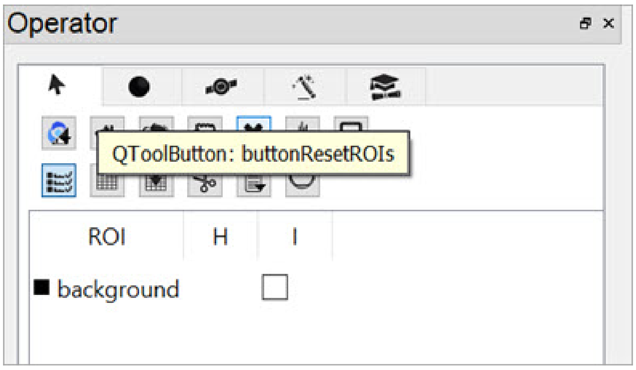
```
#include "ipacs.vqs"
#include "VQSTools.vqs"


var dm = VQ.dataManager();
var mw = VQ.mainWin();
var ctl = VQ.controler();

mw.setViewMode('Slice View','3D ROI Tool');
var roi = VQ.currentOp();

// Create ROI for Processing
roi.addROI('ROI Pre Comp','red');
VQ.getWidget('qt_tabwidget_tabbar').setCurrentIndex(1);
   roi.setCurrentROI(roi.numROIs()-1);

// Allow user to place ROI
VQ.suspend('Place ROI');

// Apply 'Connected Components' on ROI
VQ.getWidget('qt_tabwidget_tabbar').setCurrentIndex(3);
VQ.getWidget('MagicSegmentationSelector').setCurrentIndex(11);
roi.applyConnectedComp();

// Create final ROI
roi.addROI('ROI Final','red');
roifinal = roi.numROIs()-1;

// Dilate +1 and map to new ROI
VQ.getWidget('qt_tabwidget_tabbar').setCurrentIndex(1);
VQ.getWidget('cbMagicEDRadius').setCurrentIndex(4);
VQ.getWidget('cbErodeMapTo').setChecked(true);
VQ.getWidget('cbLayerROI').setCurrentIndex(roifinal);
VQ.getWidget('cbROIs').setCurrentIndex(0);
VQ.currentOp().applyErode();

// Delete all but new ROI
var i = 1;
while(i < roi.numROIs() - 1) {
   roi.deleteROI(i,0);
```

Edit Quick Script

Using the Peek Tool

The **Peek Tool** is used to reveal the names of elements (called widgets) in the operator GUIs for use in scripts. The command VQ.getWidget("widgetName") can then be used to interact with these elements.

For example, to determine the name of the button in the **3D ROI Tool** that resets all ROIs, click on the **Peek** button on **VivoQuant's** top bar, and then click on the desired button in the **3D ROI Tool** operator box. A yellow box containing the class and name of the selected button will be displayed.



Using the Peek Tool

Then, the command VQ.getWidget("buttonResetROIs").click() ca be used to click the button and reset all ROIs.

VQScript Examples

Included with VivoQuant are 30 VQScript example scripts to help you get started working with VQScript. These scripts illustrate some of the many ways VQScript may be used to streamline workflows in VivoQuant. To learn more about each files, see the VQScript Example Scripts page.

VQScript Classes

Click here to see the list of VivoScript Classes.

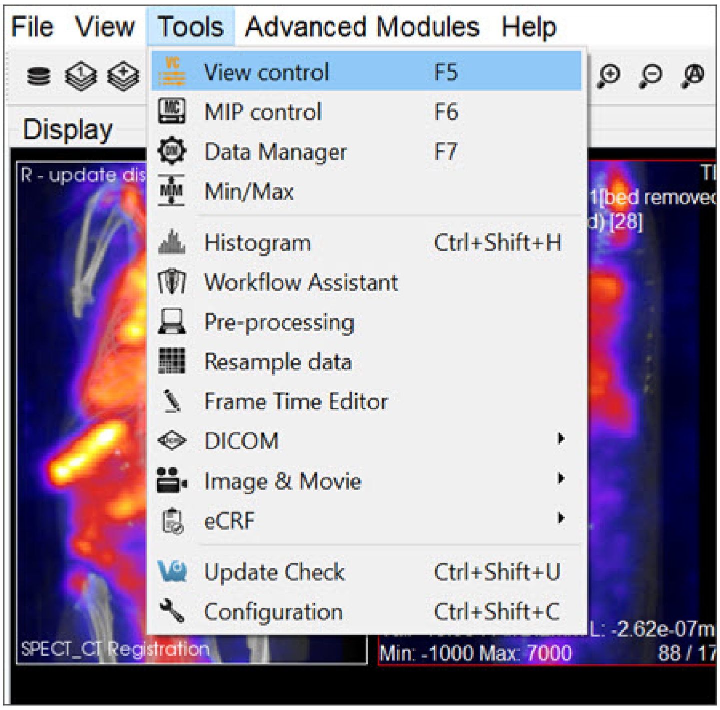
View Control

The **View Control** palette is a powerful tool for manipulating image appearance in the **Main Window**.

Getting There

There are three different methods for reaching the **View Control** tool. The first method is to use the **View Control** thumbnail in the Main Window.

The second method is to go to **View Control** under the **Tools** menu.

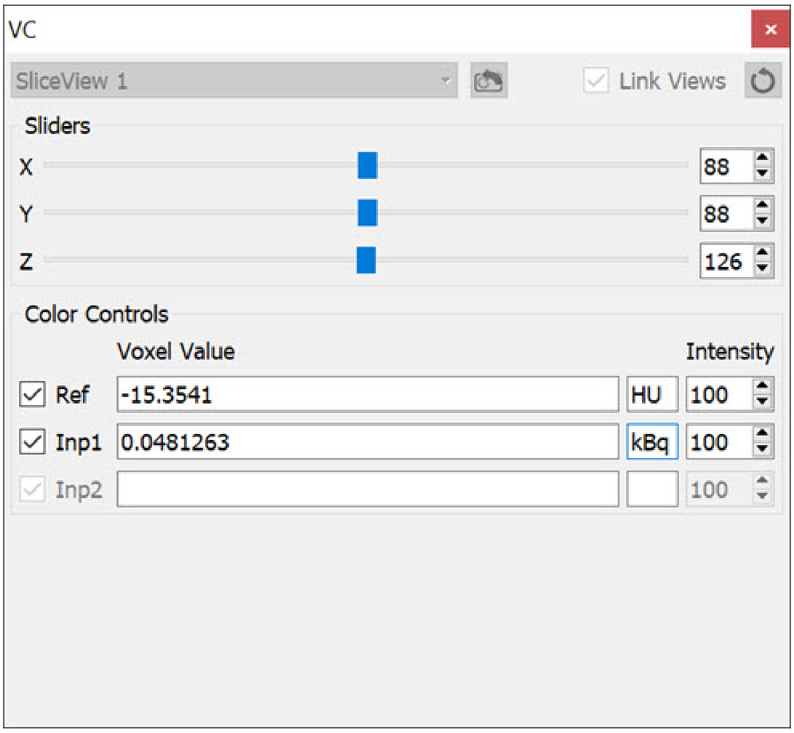


View Control

The third method is to use the keyboard shortcut F5. For more on keyboard shortcuts, please see Keyboard Shortcuts.

Function

The **View Control** window provides a variety of options for manipulating the appearance of open data sets in the main window. Options include Sliders for slice selection, Color Controls and **Voxel Values**.



X 88
Y 88
Z 126

☑ Ref -15.3541 HU 100
☑ Inp1 0.0481263 kBq 100
☑ Inp2 100

View Control Operator

Sliders

Adjusting the x, y, and z sliders in the **Sliders** section changes the sagittal, coronal, and transverse slices, respectively, that are shown in the **Display**. The cross hairs displayed on the main window also reflect the x, y, and z slider values.

Color Controls

The **Color Controls** display information about the datasets loaded at the **Reference**, **Input 1** and **Input 2** positions.

The checkboxes on the left toggle the visibility of the datasets in the Display. Next to these, the **Voxel Values** of each dataset at the current slice are displayed along with their respective units.

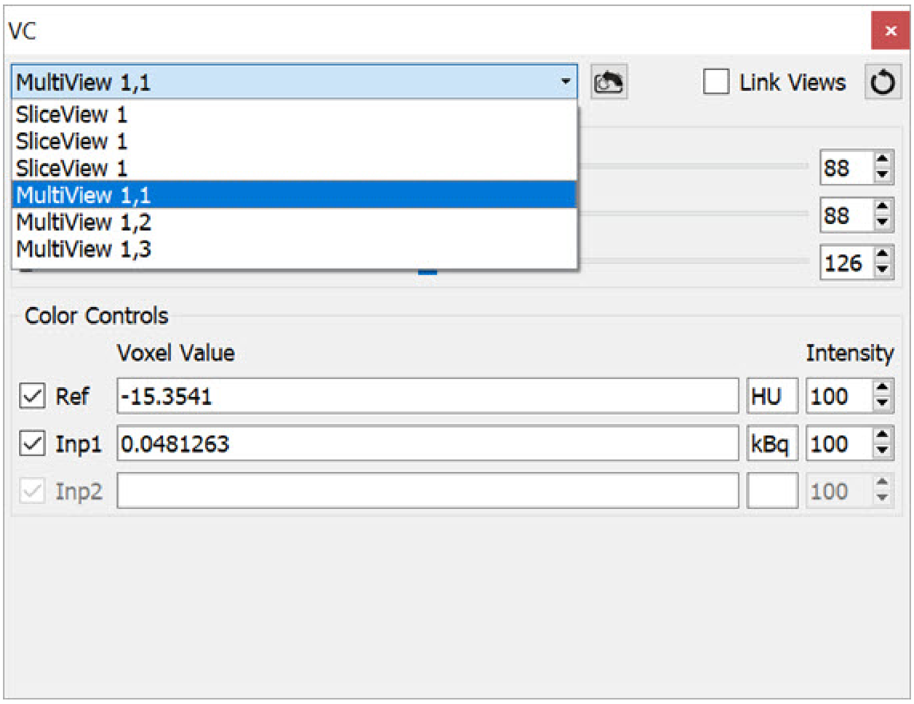
ℹ **Note:** If given proper Hounsfield or quantification calibration, the voxel values will be given in Hounsfield units or MBq.

The **Intensity** pinboxes control the relative transparency of the dataset. Decreasing the intensity value increases the transparency of the image.

View Control in Multi-View

The **Multi View** mode enables users to customize the layout of viewports in the Display. When in Multi View, additional controls become available, extending the in the **View Control** normal functionality to the **Multi View Display**. Users may also select whether navigation is linked across viewports, or if viewports may be navigated independently of one another. For more information on setting up the Display in this view mode, see the Multi View page.

In **Multi View**, the information in the **Sliders** and **Color Controls** is automatically updated to reflect information from the viewport through which the user is navigating. To update these with information from another viewport, use the drop down menu in the upper left hand corner and select the desired viewport. Alternatively, click on or navigate through another viewport in the Display to update the **Viewer Control**.



88
88
126

Color Controls

Voxel Value | Intensity

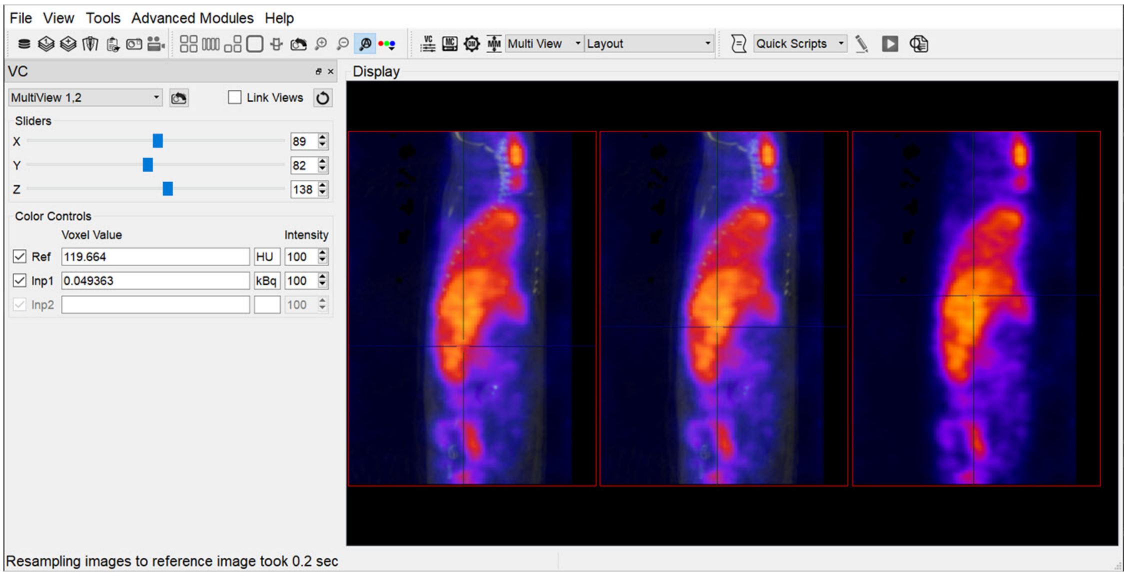
☑ Ref -15.3541 HU 100

☑ Inp1 0.0481263 kBq 100

☑ Inp2 100

Update Dataset Information

By default, the **Viewer Control** links all viewports in **Multi View** together. This means that any navigation through the slices in one viewport is reflected in all other viewports automatically. Viewports may be unlinked by unchecking the **Link Views** checkbox in the upper right corner of the **Viewer Control**. This will allow users to navigate through each viewport independently.



X 89
Y 82
Z 138

Color Controls

Voxel Value | Intensity

☑ Ref 119.664 HU 100

☑ Inp1 0.049363 kBq 100

☑ Inp2 100

Resampling images to reference image took 0.2 sec

Navigate Viewports

To reset all viewports to the same slice, click on the **Sync Viewport Settings** button located next to the **Link Views** checkbox.

Note: The **Link Views** functionality only affects the slice-by-slice navigation between viewports. Zooming and panning within each viewport will remain independent.

To reset the **Zoom** and **Pan** in a specific viewport, select the desired viewport (either by selecting it from the drop down menu or by clicking on the viewport) and click the **Reset** button in the **Viewer Control**. This will reset only the selected viewport. To reset all viewports at once, click the **Reset** button on the toolbar.

MIP Control

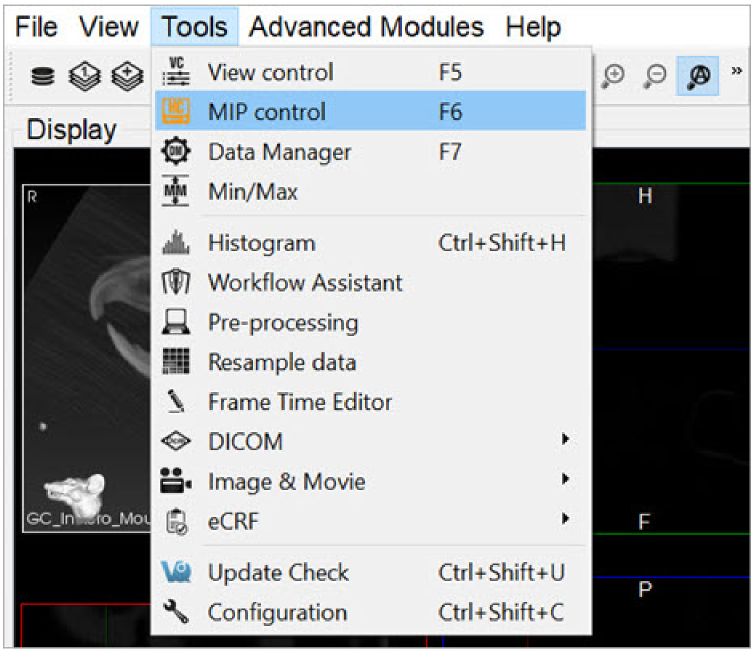
The MIP (Maximum Intensity Projection) control can be used to manipulate the active 3D rendered volume. See MIP Explained for a more detailed description of how the MIP is generated.

This tool also allows to automatically rotate the **3D volume** and create custom movements that can be exported as videos or gifs.

Getting There

There are three different methods for reaching the **MIP Control** window. The first method is to use the **MIP Control** thumbnail in the Main Window.

The second method is to go to **MIP Control** under the **Tools** menu.

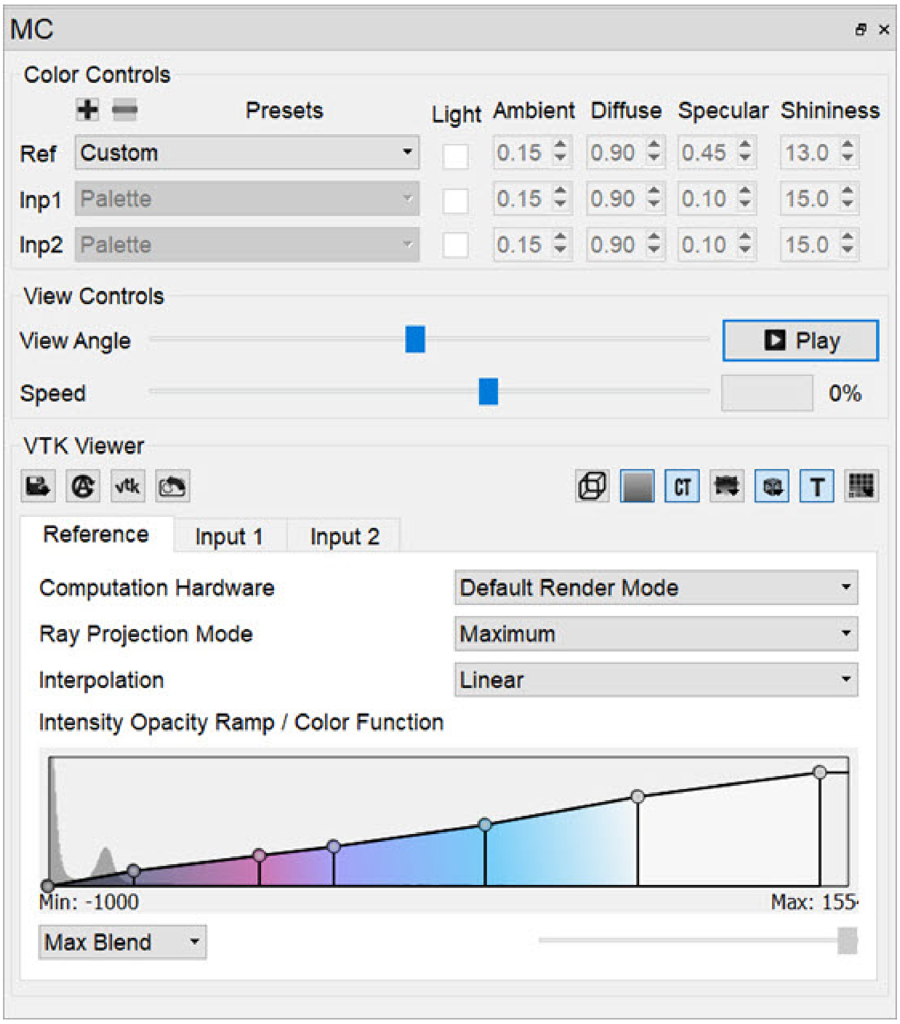


MIP Controls

The third method is to use the keyboard shortcut **F6**. For a complete list of keyboard shortcuts, see Keyboard Shortcuts.

Function

The MIP Control window provides a variety of options for manipulating the MIP and the appearance of open data sets in VivoQuant's main window. Options include Playing a MIP Movie, Color Controls, View Controls, VTK Viewer, Transfer Function, and MPR View.


MC

Color Controls

	Presets	Light	Ambient	Diffuse	Specular	Shininess
Ref	Custom	☐	0.15	0.90	0.45	13.0
Inp1	Palette	☐	0.15	0.90	0.10	15.0
Inp2	Palette	☐	0.15	0.90	0.10	15.0

View Controls

View Angle

Speed

0%

VTK Viewer

Reference | Input 1 | Input 2

Computation Hardware: Default Render Mode

Ray Projection Mode: Maximum

Interpolation: Linear

Intensity Opacity Ramp / Color Function

Min: -1000

Max: 155

Max Blend

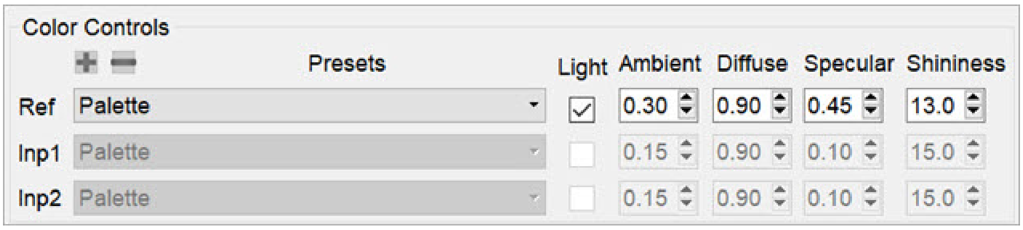
MIP Controls Function

Playing a MIP Movie

The MIP movie is automatically generated upon the loading of a data set. Using the mouse, it can be manually rotated in the main window. Hitting Play in the MIP Control enables automatic rotation of the MIP movie. The slider bar marks the rotation progress of the MIP movie. For large data sets, it can sometimes take several moments for the MIP movie to be generated. The progress bar in the MIP Control indicates how much of the MIP movie has been successfully calculated.

Color Controls

The **Color Controls** section provides users with the ability to define tissues and their corresponding coloring properties (opacity and RGB), for volume rendering.

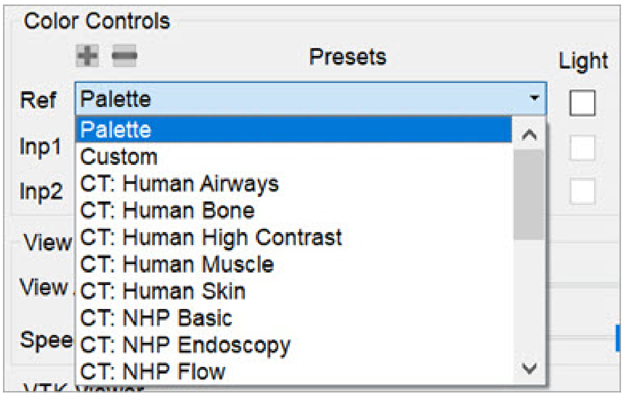

Color Controls

	Presets	Light	Ambient	Diffuse	Specular	Shininess
Ref	Palette	☑	0.30	0.90	0.45	13.0
Inp1	Palette	☐	0.15	0.90	0.10	15.0
Inp2	Palette	☐	0.15	0.90	0.10	15.0

Color Controls

VivoQuant volume renderer allows for manipulating 3 data sets at the same time: Reference, Input 1 and Input 2. Users can select canned tissue presets, as well as creating and saving custom tissue properties, and editing existing tissue opacity and color functions.

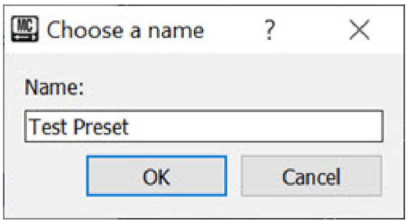
Tissue properties can be selected from the **Presets** combo box.



Select Presets

Users can select any of the following preset options:

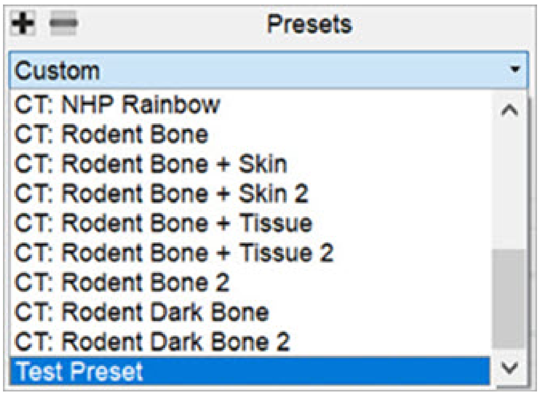
- **Palette:** Syncs with the palette selected in the Data Manager and reacts to min/max changes. This option does not allow custom coloring for the function. New presets cannot be added based on this option. Therefore the **Add Preset** and **Remove Preset** buttons are disabled.
- **Custom:** Allows for coloring from the current function. The default colors will be those of the palette option if no presets were selected beforehand. This is the only option that allows for adding new presets. To add a new custom preset, click on the **Add Preset** button ➕. A popup window opens prompting the user to enter a name for the new custom preset.



Name: Test Preset

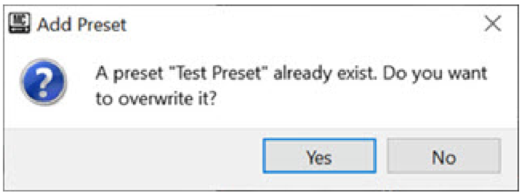
Create Preset

The newly created preset will then appear on the list of presets in the **Presets** combo box.



Newly Created Presets

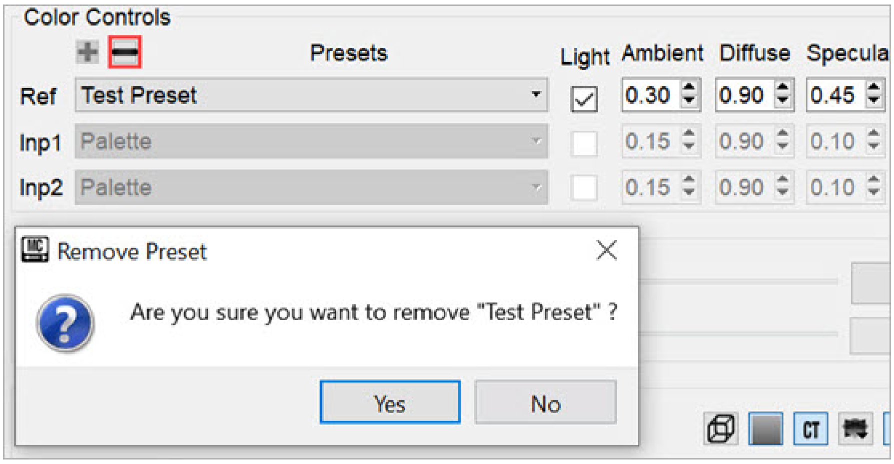
⚠ **Important:** When adding preset with a name that already exist, a popup window appears asking the user to confirm whether they would like to overwrite the previous preset or not.



A preset "Test Preset" already exist. Do you want to overwrite it?

Overwrite Preset

To remove a custom preset, click on the **Remove Preset** button ⊟. A popup window opens asking the user to confirm deletion of the custom preset.



	Presets	Light	Ambient	Diffuse	Specula
Ref	Test Preset	☑	0.30	0.90	0.45
Inp1	Palette	☐	0.15	0.90	0.10
Inp2	Palette	☐	0.15	0.90	0.10

Are you sure you want to remove "Test Preset" ?

Remove Preset

- **CT Tissue Types and Species:** These are presets that present CT property configurations that are specific to different tissue types and species. Some examples include: CT: Human Bone; CT: Human Muscle; CT: NHP Basics; CT: NHP PET; CT: Rodent Bone + Skin; CT: Rodent Dark Bone; among others.

Users can edit the shading settings by enabling the **Light** checkbox under **Color Controls**. The available shading and lighting settings are as follows:

Ambient	Ambient light is the light that is scattered by the environment. It is a simple approximation of global illumination that is independent from the light position, object orientation, observer's position or orientation. That is, ambient light has no direction.
Diffuse	Diffuse light is the illumination that a surface receives from a light source and reflects equally in all directions.
Specular	Specular light is a light that retains its reflective qualities. When this light hits a surface, reflection bounces back into the camera. Specular light is a bright spot on an object. It is the result of total reflection of incident light in a concentrate region.
Shininess	Shininess is a material property that determines the size and sharpness of specular highlights.

View Controls

Upon loading a data set, an MIP movie showing the image rotation is automatically generated. By using the mouse, the image can be manually rotated in the main window. Clicking on the **Play** button ▶ in the **View Controls** enables automatic rotation of the MIP movie. The **View Angle** slider bar shows the rotation progress. It also allows for fine control of the camera position. By default, the camera rotates around the Z-axis, and each step is a 3-degree rotation.

For large data sets, the MIP movie may take several minutes to be generated. The progress bar in the under the **Play** button indicates how much of the MIP movie has been successfully calculated. The **Speed** slider allows for fine control of the MIP rotation speed.

View Controls

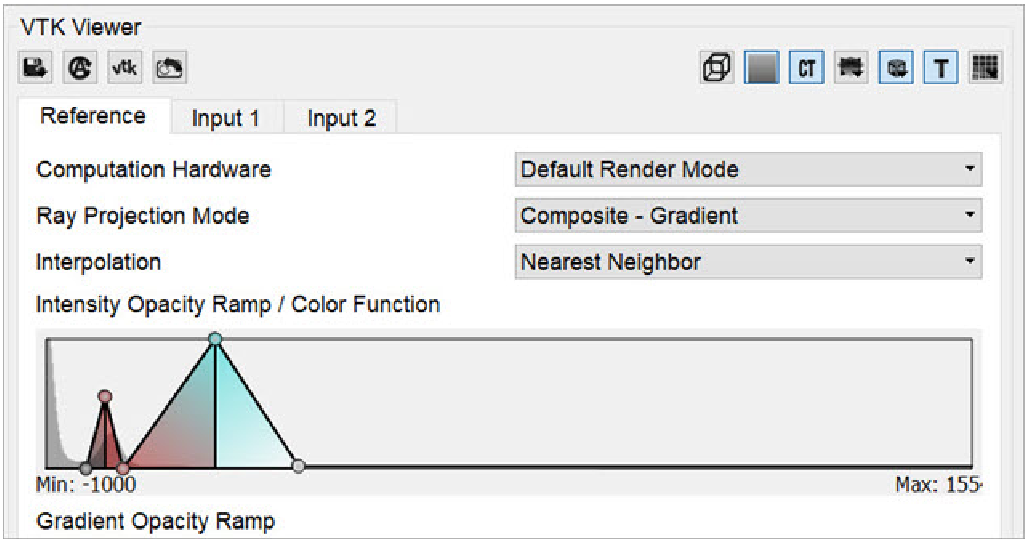
VTK Viewer

The **Visualization Toolkit (VTK)** is open source software used for manipulating and displaying scientific data. VivoQuant uses the VTK library to generate the 3D Volume (MIP).

Each operator has default **VTK Viewer** settings which are refreshed upon opening an operator window.

The MIP Projection **VTK Viewer** allows for fine tuning of some of the parameters offered by the VTK renderer. Some functions include:

- Opacity and color transfer editing function by means of image histograms.
- CPU and GPU based volume rendering pipelines.
- Interpolation mode selector to change the quality of the VTK rendering.
- Ability to save settings to disk and load previously saved VTK settings.



Computation Hardware: Default Render Mode
Ray Projection Mode: Composite - Gradient
Interpolation: Nearest Neighbor

VTK Viewer

The following table describes the options that are available for adjusting the VTK viewer:

Icon	Function	Description
	Save / Load Settings	Provides an option to save the current settings or load previously saved VTK settings.
	Auto Update	Provides an option to enable or disable automatic settings update.
vtk	**Force Refresh**	Forces re-rendering of the VTK viewer.
	Reset Camera	Resets the camera of the VTK viewer to its initial position.
	Bounding Box	Enables VTK bounding box and clipping.
■	**Gradient Box**	If enabled, replaces black background with VTK gradient grey background.
CT	**Toggle MIP**	Toggles the classic MIP in the VTK viewer.
	Toggle MPR	Toggles Multi-planar reconstruction (MPR) view in VTK viewer. Hold down to toggle background transparency.
	Orientation Cube	Toggles orientation cube in the VTK viewer. Hold down to select the orientation model: Default, Human, Human Head, Rodent or Rodent Head.
T	**Annotation**	Toggles visible annotations in the VTK viewer.
	Quality	Changes performance of VTK viewer by optionally down-sampling the VTK image. Hold this button down to specify the resolution of the image: Fine, Standard, or Fast.

Transfer Function

Transfer functions are tools for assigning optical properties to scalar volume data sets. For direct volume rendering, for example, opacity can be set depending on the gray value at a given voxel position.

VivoQuant's **VTK Viewer** allows for editing opacity and color transfer functions by using image histograms and other volume rendering options.

- **Computation hardware:** This option allows users to choose the desired processing platform for image rendering. Options are: Default Render Mode; CPU Render Mode; or GPU Render Mode.

  ☑ **Tip: GPU** processes data faster than **CPU**, but usually has smaller memory.

  Depending on the available hardware, use GPU for rendering images smaller than 1 GB, and CPU for rendering images bigger than 1GB.

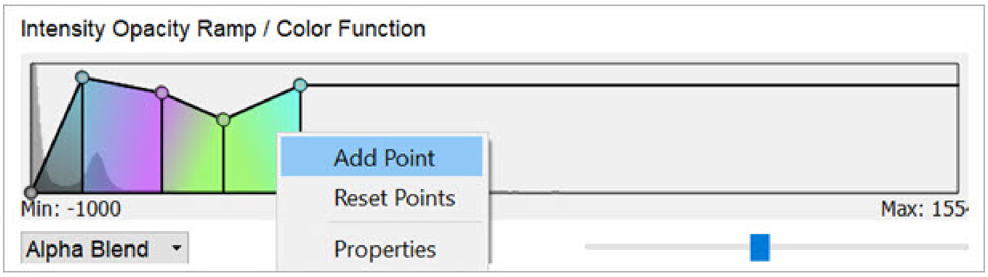
- **Ray Projection Mode:** This option allows users to choose the desired ray projection method. Options are: Maximum; Minimum; Average; Surface; Composite-Gradient; and Composite-Feature Detection.

- **Interpolation:** This option allows users to change the quality of the VTK rendering by changing the smoothing applied to the texture mapping when sampling between two voxels. Options are: Linear; or Nearest neighbor.

- **Histogram:** For Intensity Transfer Function, the X-Axis represents pixel intensity. For Gradient Transfer Function, the X-Axis represents gradient intensity. For both of the previous modes, the Y-Axis represents the weight factor between 0-1.

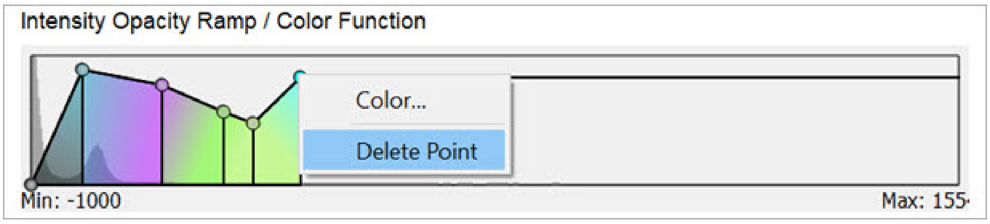
  You can add a point to the transfer function in the histogram. To do so, right-click on the position you would like the new point to be added to within the histogram, and select **Add new point**. You can also reset the point to their original value by right-clicking the histogram and selecting **Reset**.

To manually edit the X axis values of the histogram, right click and select **Properties**. A window opens with editable fields to enter the Minimum and Maximum values. You can return the X axis to its original minimum and maximum values by clicking the **Reset** button.



Add Point

When adding a new point to the function, a color picker window opens which by default assigns interpolated color between the two surrounding points. Users are allowed to change this color. Also, the color of any of the function points can be changed by right-clicking it and selecting **Color**. To remove a point from the histogram, right-click on the point to be deleted and select **Delete Point**.

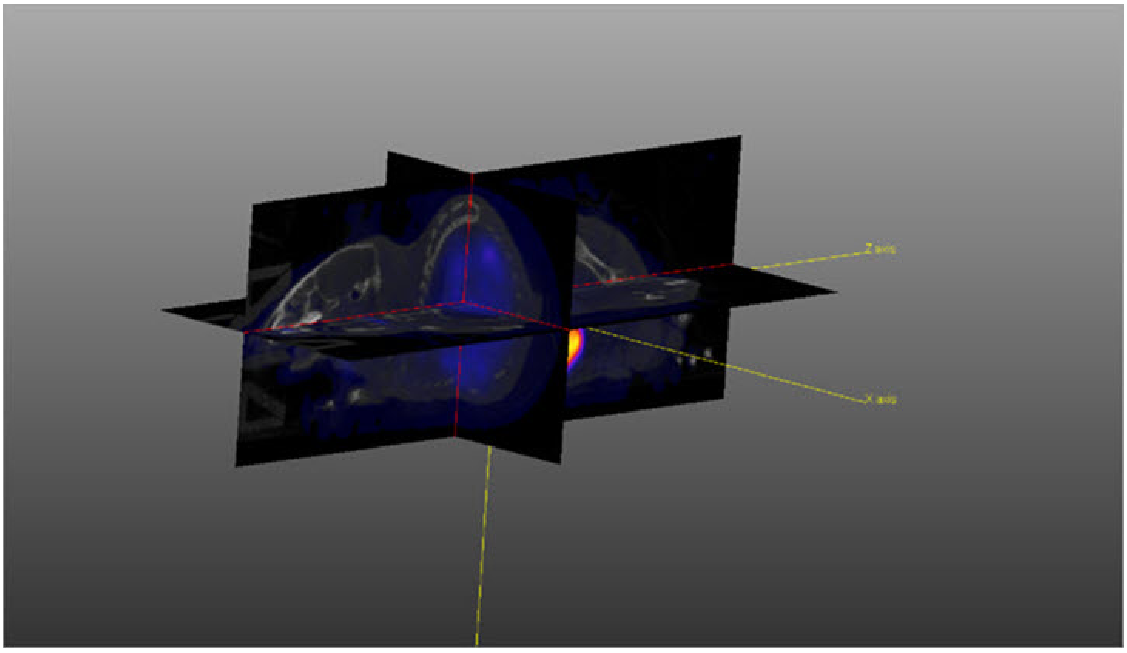


Delete Point

- **Blending:** Controls how volume blend together. Options are: Max or Alpha.

MPR View

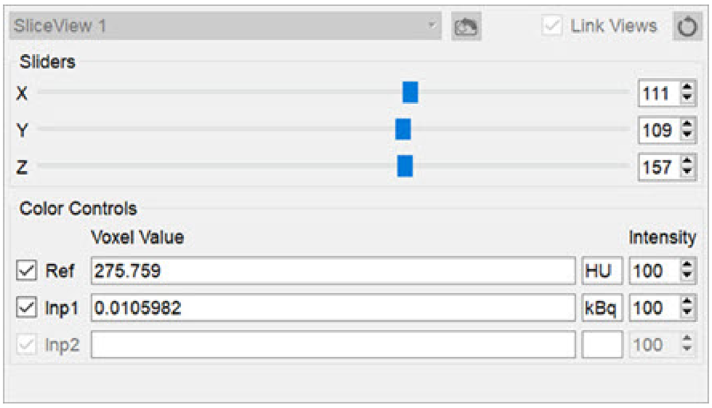
The **Multi-Planar Reconstruction View (MPR)** simultaneously displays a sagittal, coronal, and transversal slice of the reconstruction. The View Control is used to change the active planes while the sliders and checkboxes across the top of the window may be used to rotate the view, display the bounding box, reset the view, and turn on/off individual planes.



MPR View

The image in **MPR View** may be rotated by using a left-click and dragging the mouse. Similarly, panning may be controlled by holding the Shift key, using a left-click, and dragging the mouse. The zoom may be changed by using the mouse's scroll wheel.

To change the active planes in the MPR View, use the (X,Y,Z) sliders in the View Control.



SliceView 1

☑ Link Views

Sliders

X 111

Y 109

Z 157

Color Controls

		Voxel Value		Intensity
☑	Ref	275.759	HU	100
☑	Inp1	0.0105982	kBq	100
☑	Inp2			100

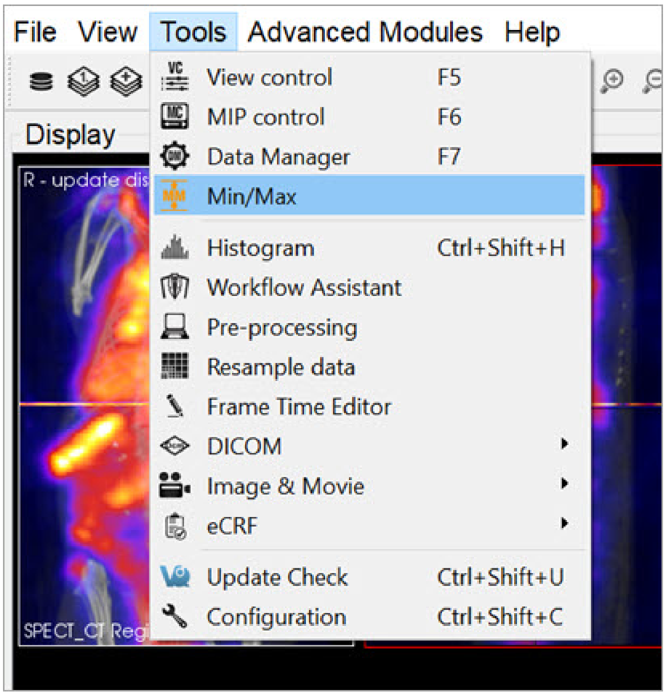
Sliders

Min/Max Tool

The **Min/Max Tool** allows you to adjust the windowing of visible voxels for the first three Inputs.

Getting There

The **Min/Max Tool** is available via the **Tools** menu.

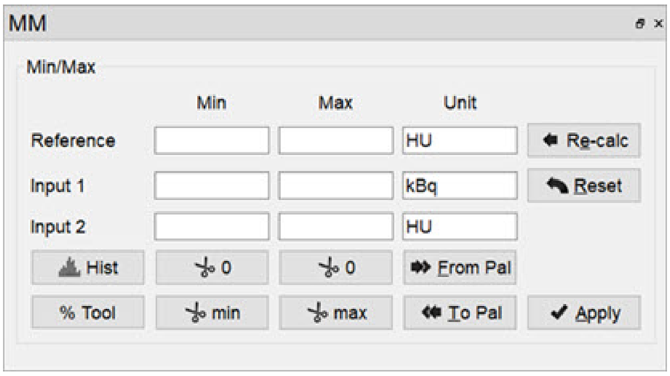


Min/Max Tool

You can also access the **Min/Max Tool** by clicking on the **Min/Max Tool** thumbnail MM in the Main Window.

Function

The **Min/Max Tool** displays the windowing values with units for the **Reference**, **Input 1** and **Input 2**. The Display Configuration determines whether the windowing is displayed based on **Minimum/Maximum** or **Level/Width**.



Min/Max Tool Operator

The windowing values allows you to calculate the colors for each voxel in the **Display**, via a mapping from voxel values to the colors in the color palette. Any values below the minimum will return the *lowest* color (e.g. black in the gray palette), while any values above the maximum will return the *highest* color (e.g. white in the gray palette).

The **Min/Max Tool** uses a *cache* feature, whereby minimum and maximum values for inputs are stored in a *cache* and used by the color mapping until the user forces the tool to recalculate them. This enables you to keep the color scale consistent when working with multiple datasets.

Option	Description
Re-calc	Recalculates the min/max values for all data sets from the original data. Min/max value will be min/max voxel values in dataset.
Reset	Resets the min/max values to the values stored in the cache.
Apply	Stores min/max values in cache and applies values to the datasets.
From Pal	Copies the current palette window as set in the Data Manager to the Min/Max Tool fields.
To Pal	Copies the current Min/Max Tool fields to the palette window settings in the Data Manager.

The buttons with the **Cut** icon ✂ will clip the data based on values in the tool. This can be useful when trying to clip dense bone from a **CT** scan, for instance, or background noise from a PT scan.

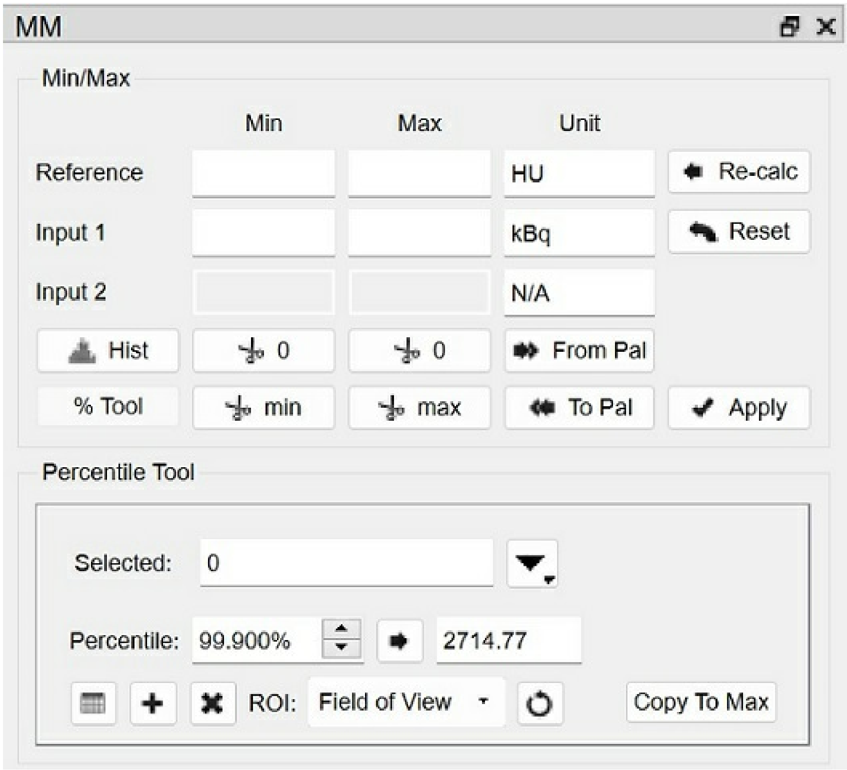
Option	Description
✂ 0 (Min)	Sets all values below the minimum to 0.
✂ 0 (Max)	Sets all values above the maximum to 0.
✂ min	Sets all values below the minimum to the minimum.
✂ max	Sets all values above the maximum to the maximum.

Histogram

The **Histogram** button Hist opens the **Histogram Tool**. This tool generates a histogram of voxel values in the loaded datasets. For more on this, visit the Histogram Tool page.

Percentile Tool

The **Percentile** button % Tool brings up the **Percentile Tool**, which calculates the pixel value associated with the X^{th} percentile from the histogram of the image.



Reference: Unit HU

Input 1: Unit kBq

Input 2: Unit N/A

Selected: 0

Percentile: 99.900% ➡ 2714.77

ROI: Field of View

Percentile Tool

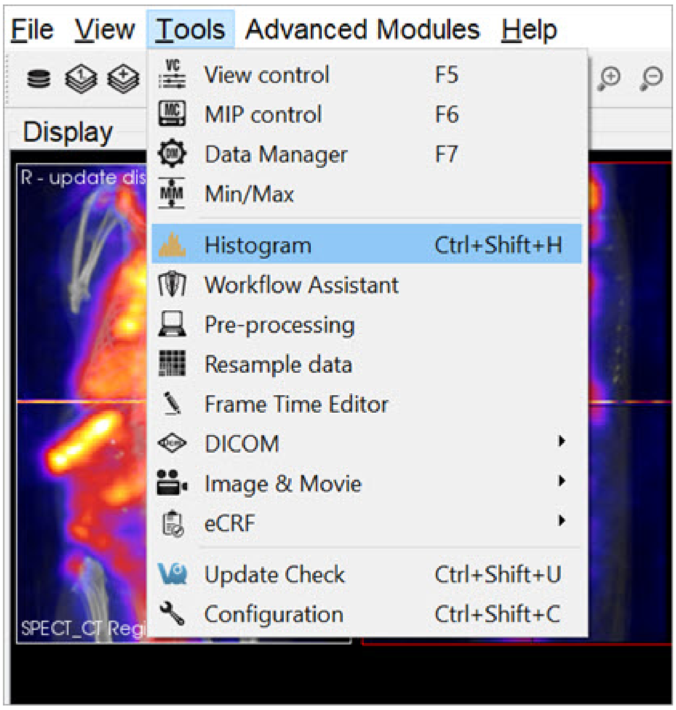
Option	Description
➡	Calculates the percentile value for selected image in the drop down list to the right.
▦	Shows percentile value with Patient Name, Patient ID, Acquisition Time, Percentile, Cutoff Value, and Units information from image metadata.
✚	Loads calculated percentile value into table.
✖	Deletes the selected row from the percentiles table.
↻	Resets the value in the **ROI** field to **Field of View**.
Copy To Max	Copies computed pecentile value to the Max value above.

Histogram

The **Histogram** tool is used to plot a histogram of the voxel values in a loaded data set.

Getting There

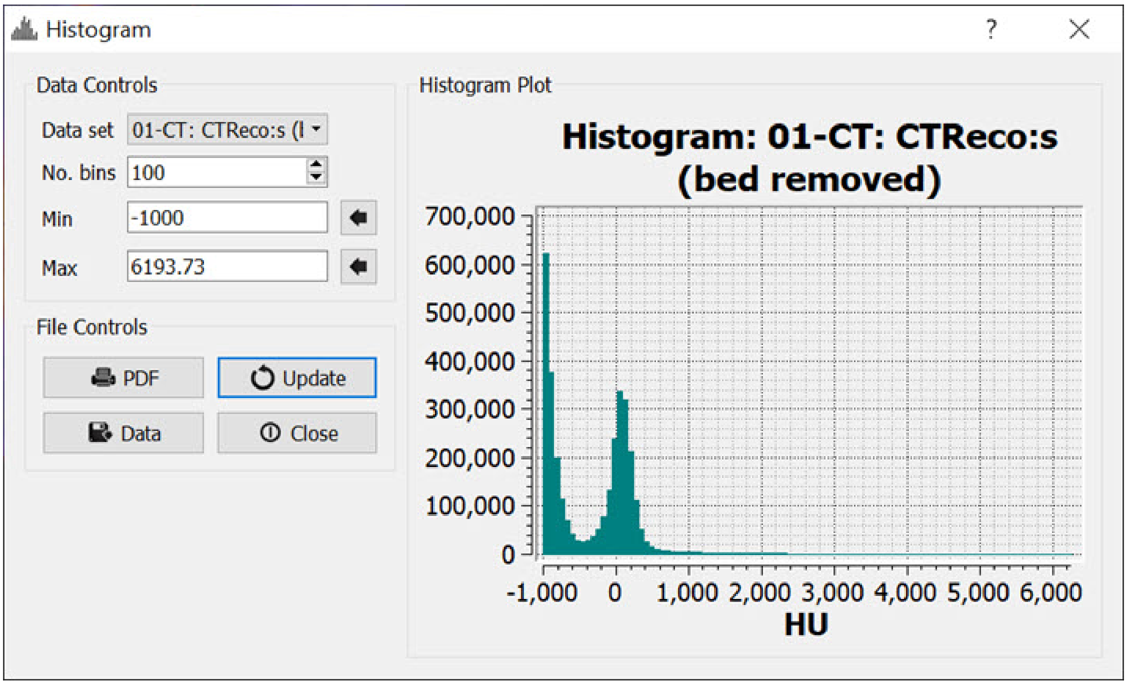
The **Histogram** tool may be reached via the **Tools Menu** or by using the keyboard shortcut Ctrl+ Shift+H.



Histogram

Function

The **Histogram** tool is operated via two control panels: **Data Controls** and **File Controls**.



Data set 01-CT: CTReco:s (l

No. bins 100

Min -1000

Max 6193.73

Histogram Panels

Data Controls

Option	Description
Data Set	This pulldown menu allows the selection of the data set to be histogrammed.
No. bins	Sets the number of bins into which to divide the data.
Min	Sets the minimum value for which data will be displayed. The Set button, ⬅, automatically loads this field with the minimum value in the object.
Max	Sets the maximum value for which data will be displayed. The Set button, ⬅, automatically loads this field with the maximum value in the object.

File Controls

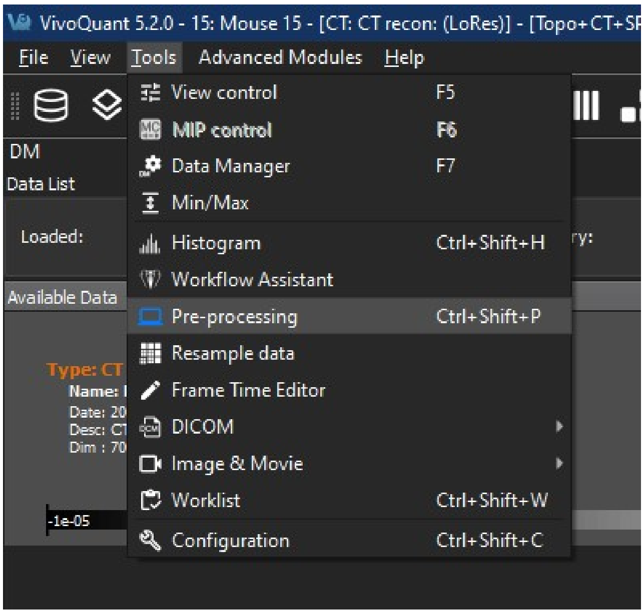
Option	Description
PDF	Saves the existing plot into a PDF file.
Data	Writes the data into a text file. The format is in two columns with the first column representing bin center points (x-axis values) and the second column representing the number of voxels in each bin (y-axis values).
Update	Refreshes the histogram plot. Use this button after changing the No. bins, Min., or Max. values.
Close	Exits the Histogram Tool.

Preprocessing Tool

The **Preprocessing Tool** lets you specify a unique pre-processing protocol and execute it in one step. There are many preprocessing operations included in the **Preprocessing** tool that may be added to the protocol.

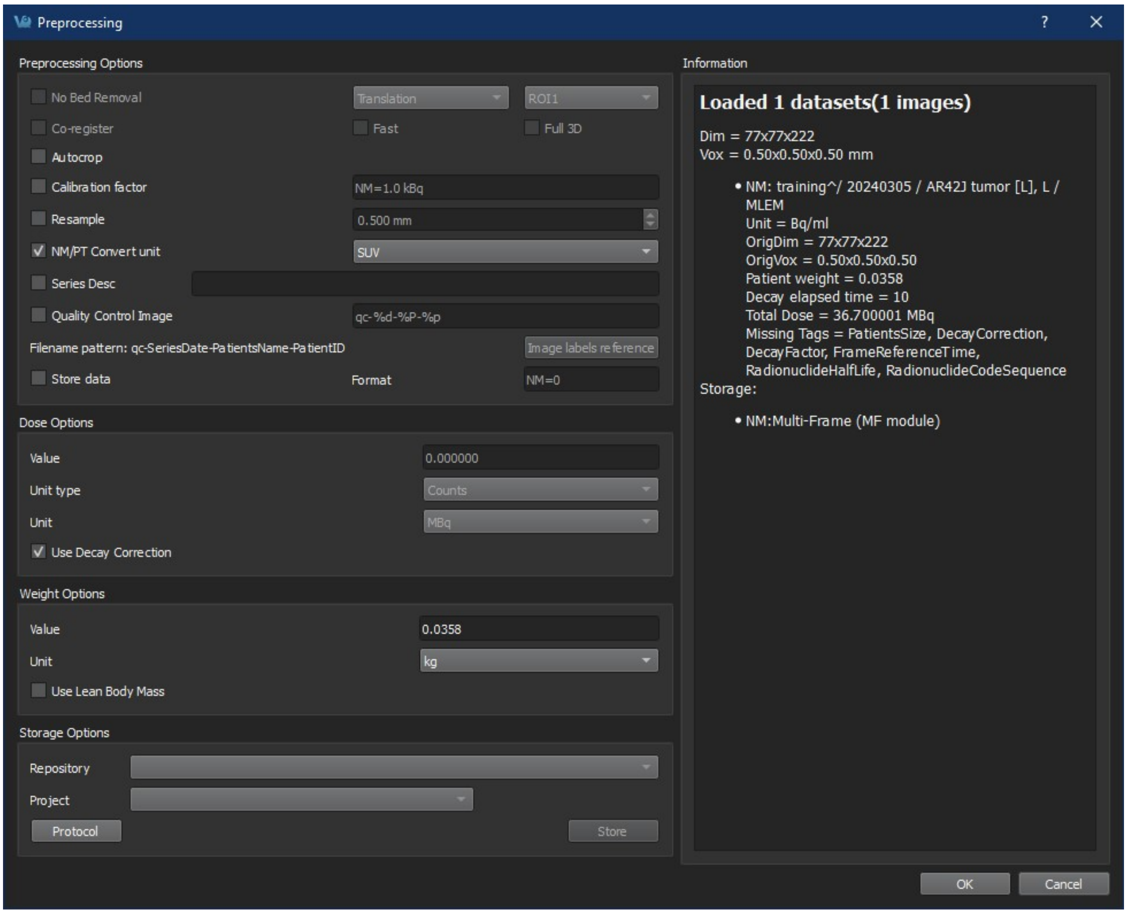
Getting There

The **Preprocessing Tool** is available via the **Tools Menu**.



Preprocessing Tool

Function



Preprocessing Options

☐ No Bed Removal — Translation — ROI1
☐ Co-register — ☐ Fast — ☐ Full 3D
☐ Autocrop
☐ Calibration factor — NM=1.0 kBq
☐ Resample — 0.500 mm
☑ NM/PT Convert unit — SUV
☐ Series Desc
☐ Quality Control Image — qc-%d-%P-%p
Filename pattern: qc-SeriesDate-PatientsName-PatientID — Image labels reference
☐ Store data — Format — NM=0

Dose Options

Value — 0.000000
Unit type — Counts
Unit — MBq
☑ Use Decay Correction

Weight Options

Value — 0.0358
Unit — kg
☐ Use Lean Body Mass

Storage Options

Repository
Project

Information

Loaded 1 datasets(1 images)

Dim = 77x77x222
Vox = 0.50x0.50x0.50 mm

- NM: training^/ 20240305 / AR42J tumor [L], L / MLEM
  Unit = Bq/ml
  OrigDim = 77x77x222
  OrigVox = 0.50x0.50x0.50
  Patient weight = 0.0358
  Decay elapsed time = 10
  Total Dose = 36.700001 MBq
  Missing Tags = PatientsSize, DecayCorrection, DecayFactor, FrameReferenceTime, RadionuclideHalfLife, RadionuclideCodeSequence

Storage:

- NM:Multi-Frame (MF module)

Preprocessing Tool Panel

The **Preprocessing Tool** panel is divided into four sections. The first section is the **Preprocessing Options** section, which includes the preprocessing operations that may be included in the protocol.

CT Bed Removal	Automatically detects the bed position within the image and removes the CT voxels which constitute the animal bed. (Only supports Minerve beds).
Co-register	Performs automatic image co-registration of all inputs to the Reference. If **Fast** or **Full 3D** are not checked, then **Standard** and **Translation** are used respectively.
Autocrop	Performs automatic cropping. Search for boundaries starts at the end slices of the image and moves towards the center of the image until a non-background voxel is detected from all 6 faces.
Calibration Factor	Applies a scalar multiplication to NM data (PET/SPECT). It is important to pay attention to the formatting of the input cell. Calibration factors per modality [comma separated] in format - **"Mod=1.0 Unit"**. Example: *"PT=13456.7 BQML"*. The case of the unit should match what is listed in the **Information window.**
Resample	Up/Downsamples voxels to the specified pixel dimensions.
NM/PT Convert unit	Converts to supported uptake and concentration units. If converting to SUV, please make sure the **Weight** and **Injected Dose** options are accurate, including their units.
Series Description	Appends text to end of series description for all datasets.
Quality Control Image	Generates and stores quality control image of preprocessed image. Results stored in the project webdisk of the repository specified below.
Store Data	Saves image data being preprocessed to specified iPACS repository below.
Format	Specifies formats in which the data will be saved. The numbers 0, 1, and 2 correspond to multi-frame (MF module), multi-frame (MF function groups), and single frames (one Z slice per file) formats, respectively. For multiple data sets, formats are separated by a comma. The current formats of the loaded data sets will be displayed in this section upon opening the tool as well as in the Information section.

The second and third sections are the **Dose** and **Weight** options for image unit calculations. The dose options are not relevant for conversions to units other than SUV or Percent Injection Dose and will be hidden otherwise. The weight options are not relevant for conversions to units other than SUV and will be hidden otherwise.

The default unit for the dose depends on the modality and SOPClass of the image. The weight and dose fields will automatically populate with values from the DICOM header, or can be set manually or from an iPACS datapoint using the VQS function setUptakeParameter.

If **Use Decay Correction** is checked, the dose will be decay corrected using information about the half-life and scan times obtained either from the DICOM header or from values set using the **setUptakeParameter** function.

If **Use Lean Body Mass** is checked, the weight will be corrected using the James or Janmahasatian formulas, where the Janmahasatian formula is used for BMI greater than 43 for men and 37 for women. The **Information** section of the Preprocessing Tool shows the DICOM tags that are used for decay correction and their values in each loaded image, including for each frame of a dynamic dataset.

The fourth section is **Storage Options**, where users may designate the iPACS repository and Project folder where preprocessed datasets will be saved (note: Store data must be checked).

Repository	Specifies the repository. Repositories can be configured in the **DICOM** tab of the **Configuration** window. See the DICOM settings page for more information.
Project	Specifies the sub-project (iPACS) or sub-folder (local path) to which data will be saved.
Protocol	Copies and/or pastes preprocessing protocol settings to be used at a later time. Modifications can be made directly within the **Protocol** window.
Store	Store Image data to the specified location.

The **Information** section displays information about the current state of datasets loaded in **VivoQuant**. Included in this information is the image dimensions and voxel size for the datasets as a whole, as well as basic header metadata about each dataset specifically.

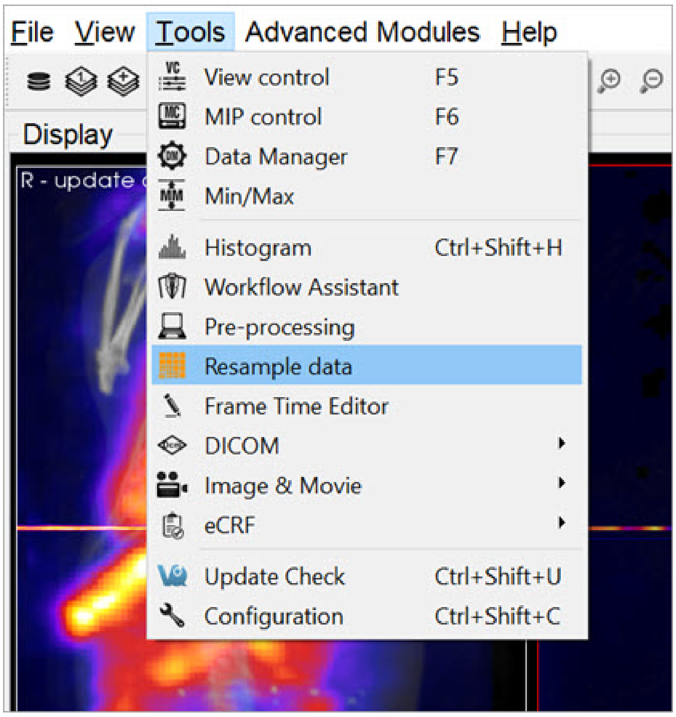
To execute the pre-processing protocol, click **OK**.

Resample Data

The **Resample Data** tool allows for rebinning of reconstructed data into an arbitrary voxel size. This tool may be useful when attempting to fuse multiple large data sets, especially when dealing with high-resolution modalities like MRI and CT.

Getting There

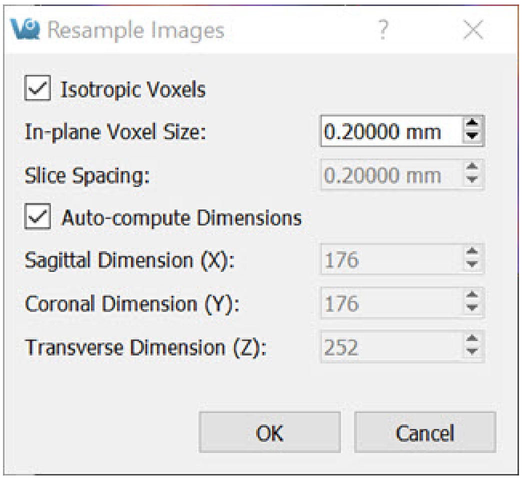
The **Resample Data** option is available within the **Reorientation/Registration Tool** via **Operations** -> **Resample**, or by navigating to **Tools** -> **Resample Data**.



Resample Data

Using the Tool

Upon selecting **Resample Data**, a small dialog box appears, displaying the current voxel size and dimensions of the image. Uncheck the **Isotropic Voxels** box to adjust the slice spacing. Similarly, uncheck the **Auto-compute Dimensions** box to adjust the dimensions of the image. Enter a new voxel size into **In-plane Voxel Size** and hit **OK** to resample the data to have voxels at the new size.



Resample Images

☑ Isotropic Voxels

In-plane Voxel Size: 0.20000 mm

Slice Spacing: 0.20000 mm

☑ Auto-compute Dimensions

Sagittal Dimension (X): 176

Coronal Dimension (Y): 176

Transverse Dimension (Z): 252

Resample Data Options

DICOM Tools

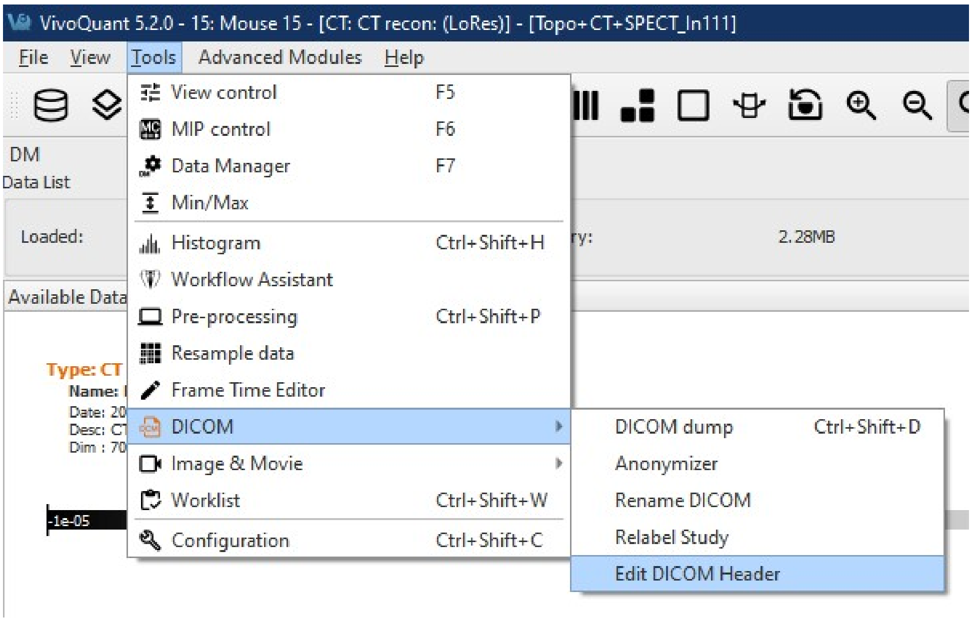
The **DICOM** Tools submenu contains features to aid in the management of DICOM data.

DICOM Dump

The **DICOM Dump** tool provides the information contained in the DICOM headers for images files currently loaded in the **Main Window**. Images loaded from other file types (such as NIFTI) have DICOM headers generated from their contents.

Getting There

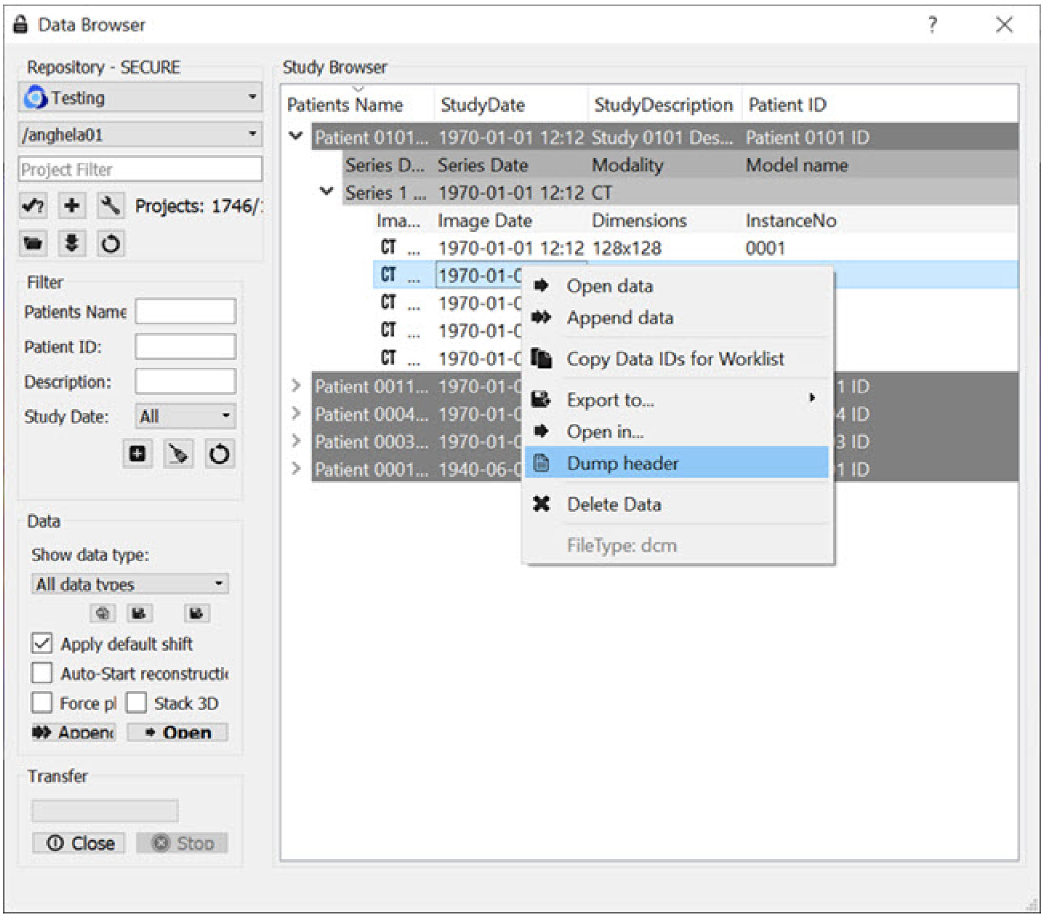
There are several ways to access the **DICOM Dump**. The first method is via the **Tools Menu** in the Main Window.



DICOM Dump

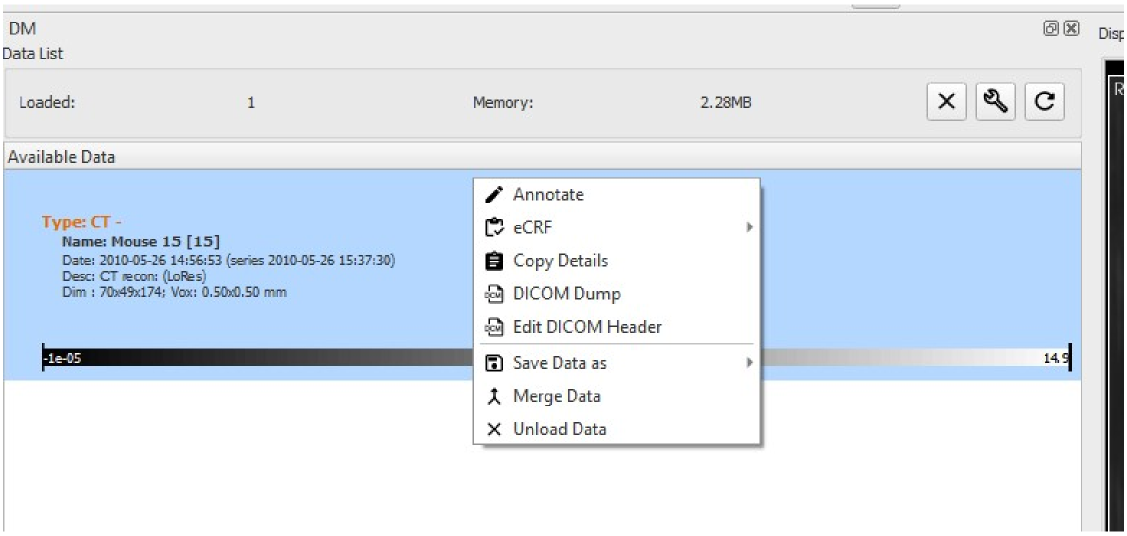
The second method for reaching the **DICOM Dump** is to use the keyboard shortcut Ctrl+Shift+D.

The third method is via the Data Browser. Right click on a dataset and click **Dump Header**.



Access via Data Browser

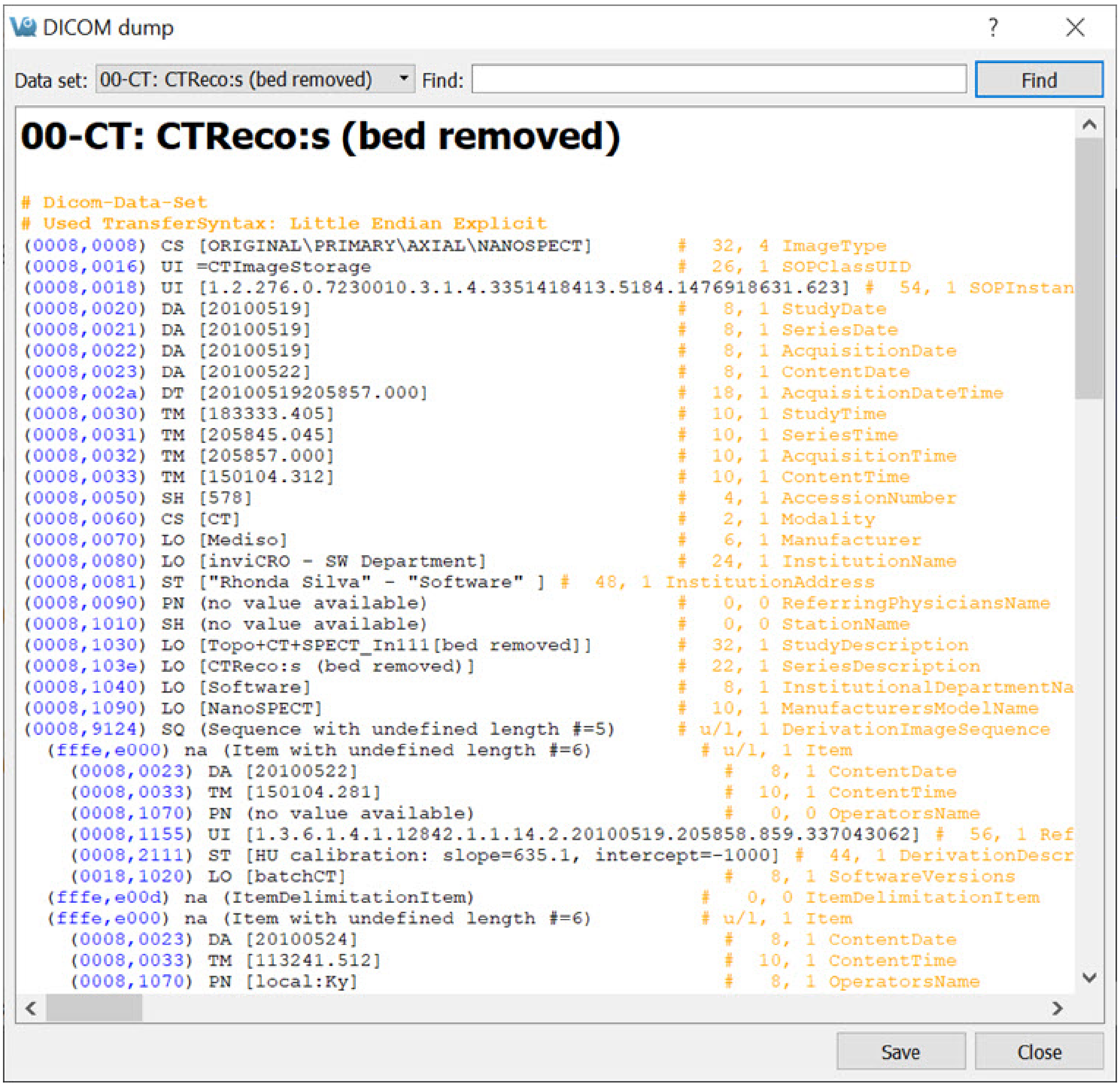
The fourth method is via the [Data Manager](). Right click on a dataset and click **DICOM Dump**.



Access via Data Manager

Function

Upon activating the tool, a new **DICOM dump** window opens, showing information from the DICOM headers for any active datasets. Use the **Data set** pull-down menu, in the top-left corner, to choose which set of DICOM header information to display.



```
# Dicom-Data-Set
# Used TransferSyntax: Little Endian Explicit
(0008,0008) CS [ORIGINAL\PRIMARY\AXIAL\NANOSPECT]       #  32, 4 ImageType
(0008,0016) UI =CTImageStorage                          #  26, 1 SOPClassUID
(0008,0018) UI [1.2.276.0.7230010.3.1.4.3351418413.5184.1476918631.623] #  54, 1 SOPInstan
(0008,0020) DA [20100519]                               #   8, 1 StudyDate
(0008,0021) DA [20100519]                               #   8, 1 SeriesDate
(0008,0022) DA [20100519]                               #   8, 1 AcquisitionDate
(0008,0023) DA [20100522]                               #   8, 1 ContentDate
(0008,002a) DT [20100519205857.000]                     #  18, 1 AcquisitionDateTime
(0008,0030) TM [183333.405]                             #  10, 1 StudyTime
(0008,0031) TM [205845.045]                             #  10, 1 SeriesTime
(0008,0032) TM [205857.000]                             #  10, 1 AcquisitionTime
(0008,0033) TM [150104.312]                             #  10, 1 ContentTime
(0008,0050) SH [578]                                    #   4, 1 AccessionNumber
(0008,0060) CS [CT]                                     #   2, 1 Modality
(0008,0070) LO [Mediso]                                 #   6, 1 Manufacturer
(0008,0080) LO [inviCRO - SW Department]                #  24, 1 InstitutionName
(0008,0081) ST ["Rhonda Silva" - "Software" ] #  48, 1 InstitutionAddress
(0008,0090) PN (no value available)                     #   0, 0 ReferringPhysiciansName
(0008,1010) SH (no value available)                     #   0, 0 StationName
(0008,1030) LO [Topo+CT+SPECT_In111[bed removed]]       #  32, 1 StudyDescription
(0008,103e) LO [CTReco:s (bed removed)]                 #  22, 1 SeriesDescription
(0008,1040) LO [Software]                               #   8, 1 InstitutionalDepartmentNa
(0008,1090) LO [NanoSPECT]                              #  10, 1 ManufacturersModelName
(0008,9124) SQ (Sequence with undefined length #=5)     # u/l, 1 DerivationImageSequence
  (fffe,e000) na (Item with undefined length #=6)         # u/l, 1 Item
    (0008,0023) DA [20100522]                               #   8, 1 ContentDate
    (0008,0033) TM [150104.281]                             #  10, 1 ContentTime
    (0008,1070) PN (no value available)                     #   0, 0 OperatorsName
    (0008,1155) UI [1.3.6.1.4.1.12842.1.1.14.2.20100519.205858.859.337043062] #  56, 1 Ref
    (0008,2111) ST [HU calibration: slope=635.1, intercept=-1000] #  44, 1 DerivationDescr
    (0018,1020) LO [batchCT]                                #   8, 1 SoftwareVersions
  (fffe,e00d) na (ItemDelimitationItem)                   #   0, 0 ItemDelimitationItem
  (fffe,e000) na (Item with undefined length #=6)         # u/l, 1 Item
    (0008,0023) DA [20100524]                               #   8, 1 ContentDate
    (0008,0033) TM [113241.512]                             #  10, 1 ContentTime
    (0008,1070) PN [local:Ky]                               #   8, 1 OperatorsName
```

DICOM Dump Window

Enter a search string into the **Find** field, in the upper right portion of the DICOM dump window. The **DICOM Dump** tool uses the DICOM dictionary listed in the DICOM Configuration to read the DICOM header. Each row in the **DICOM Dump** represents a DICOM header data entry.

See the dummy DICOM entry below that illustrates the meaning of each field in the **DICOM Dump**:

(0000,FFFF)	**AZ**	[12\18]	# 4,2	VQ DICOM Example

- (0000,FFFF) is a hexadecimal DICOM address where 0000 represents the group number for that data entry. Even group numbers correspond to DICOM defined groups, while odd numbers are reserved for private groups. The FFFF half of the address specifies the element number for that particular entry in the group indicated by the first half of the address.
- A two-character item of the form **AZ** identifies the **Value Representation** (VR) for that data entry. Several VR types are specified in the DICOM standard. For example, a **Value Representation** of **US** indicates that the data entry will be in the form *"Unsigned Short"*.
- The actual data values for the data entry (12,18) are displayed next in the **Value Field** (VF). The values are shown inside square brackets.
- After the hash mark (#), the **Value Length** (VL) for the data entry is displayed. The VL depends on the VR type and the number of values in the data entry.
- Some data entries contain multiple subsets as indicated by the **Value Multiplicity** (VM). Subsets are indicated by the backslash character in the data value field. In the example shown above, there are two subsets: 12 and 18.
- The final element of the DICOM entry is the description of the data entry. For DICOM-defined tags, this field will display relevant information regarding the content of the data entry (i.e., VQ DICOM Example). For private tags, this field will display Unknown Tag and Data.

Anonymizer

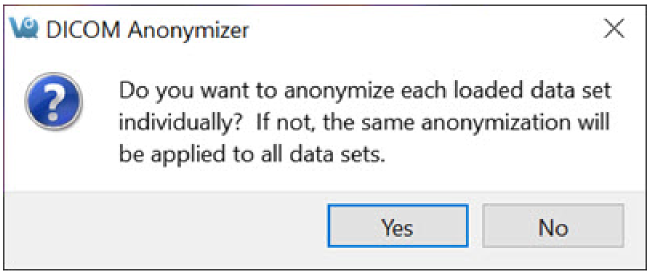
The **Anonymizer** anonymizes the data to the user.

Getting There

This function can be found under the **Tools** -> **DICOM** menu, or the **DCM** button in the Main Window.

Function

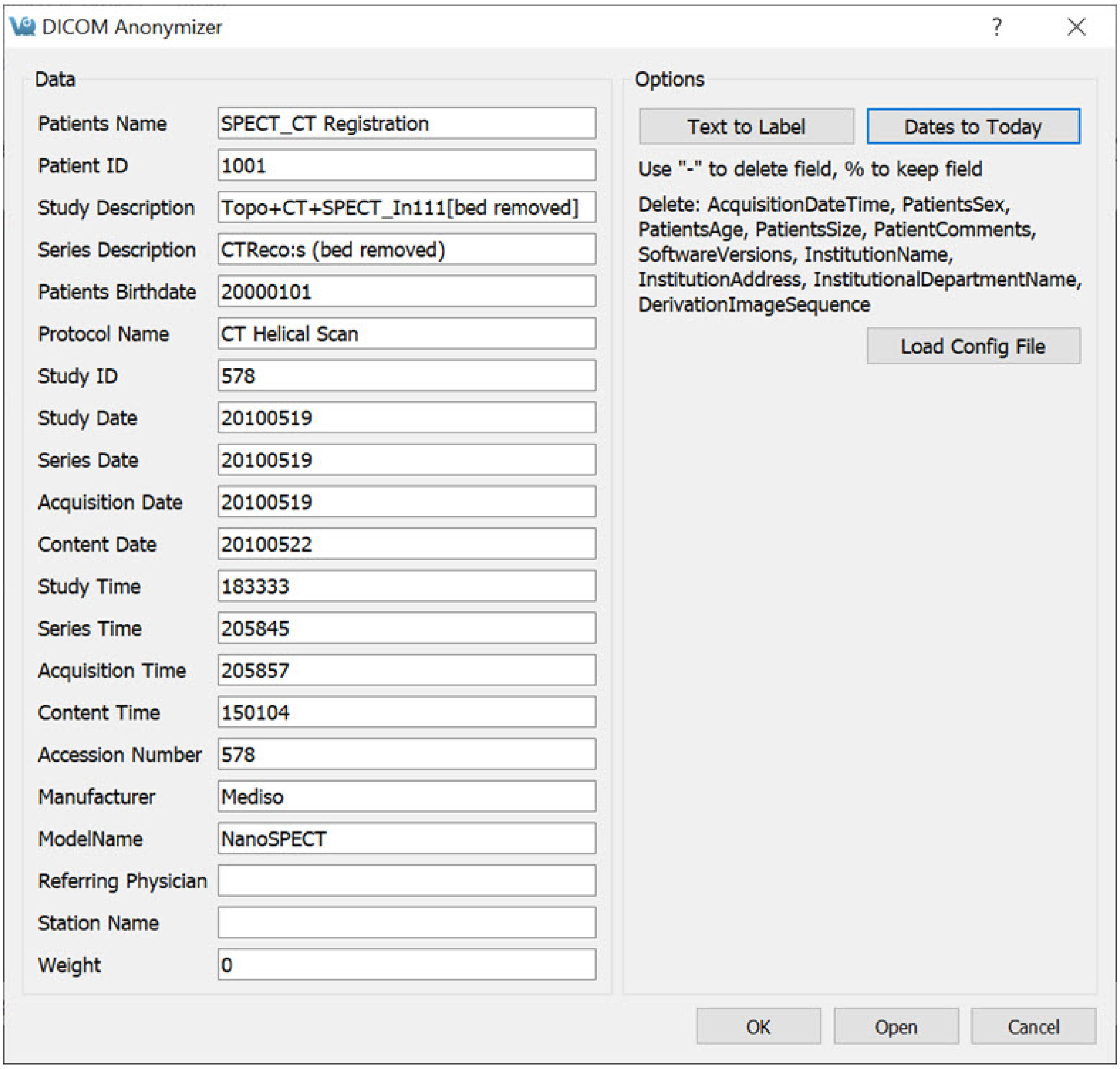
Upon selecting the **Anonymizer**, a dialog box appears prompting the user to decide whether to anonymize each loaded dataset individually (Yes) or anonymize them all together (No).



Do you want to anonymize each loaded data set individually? If not, the same anonymization will be applied to all data sets.

Anonymize Dataset

In the **Anonymizer**, header fields can be edited to remove sensitive information, such as the imaging dates, or identifying text fields. The fields can be edited manually or by setting the text to the label of the field and the dates to a new date. The buttons **Text to Label** and **Dates to Today** will fill in these sections as described. Use the **Load Config File** button to upload a configuration file. Selecting **OK** will apply the changes.



Patients Name: SPECT_CT Registration
Patient ID: 1001
Study Description: Topo+CT+SPECT_In111[bed removed]
Series Description: CTReco:s (bed removed)
Patients Birthdate: 20000101
Protocol Name: CT Helical Scan
Study ID: 578
Study Date: 20100519
Series Date: 20100519
Acquisition Date: 20100519
Content Date: 20100522
Study Time: 183333
Series Time: 205845
Acquisition Time: 205857
Content Time: 150104
Accession Number: 578
Manufacturer: Mediso
ModelName: NanoSPECT
Referring Physician:
Station Name:
Weight: 0

Use "-" to delete field, % to keep field

Delete: AcquisitionDateTime, PatientsSex, PatientsAge, PatientsSize, PatientComments, SoftwareVersions, InstitutionName, InstitutionAddress, InstitutionalDepartmentName, DerivationImageSequence

Edit Header Fields

Rename DICOM Files

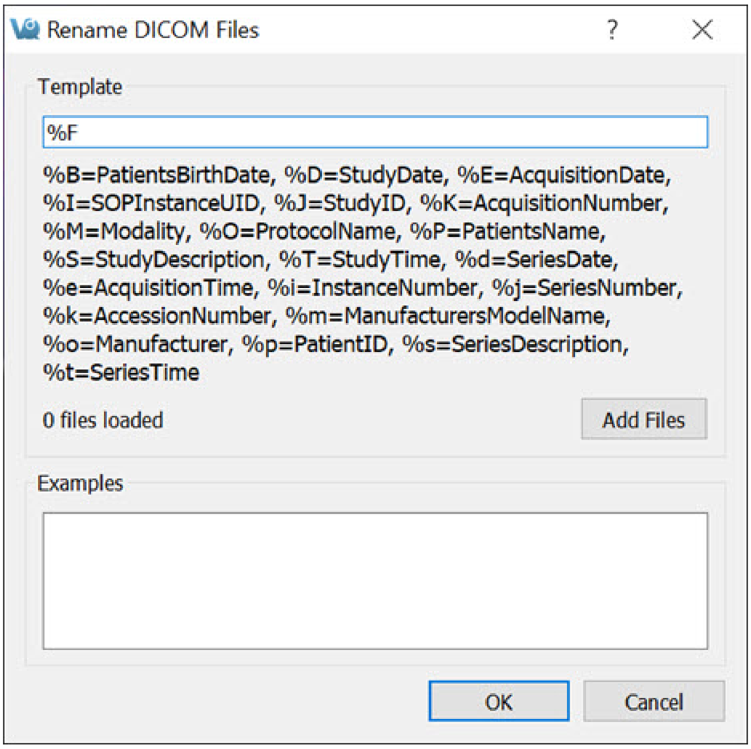
Use the **Rename DICOM** function to rename locally stored DICOM files according to information from selected fields of the headers.

Getting There

This function can be found under the **Tools** -> **DICOM** menu, or the **DCM** button in the Main Window.

Function

Choose which files to rename by using the **Add Files** button. Construct new image names by typing into the **Template** text box, using the key beneath the text box for reference. Each token represents a particular field of the DICOM header. The new names of the selected files will be displayed in the **Examples** window as they are entered. Names must be unique for the renaming operation to be successful. Renaming will also fail if illegal characters, such as backwards or forwards slashes, are used. To execute renaming, click **OK**.



%F

%B=PatientsBirthDate, %D=StudyDate, %E=AcquisitionDate, %I=SOPInstanceUID, %J=StudyID, %K=AcquisitionNumber, %M=Modality, %O=ProtocolName, %P=PatientsName, %S=StudyDescription, %T=StudyTime, %d=SeriesDate, %e=AcquisitionTime, %i=InstanceNumber, %j=SeriesNumber, %k=AccessionNumber, %m=ManufacturersModelName, %o=Manufacturer, %p=PatientID, %s=SeriesDescription, %t=SeriesTime

0 files loaded

Rename DICOM

Relabel Study

The **Relabel Study** tool allows for the following fields to be edited or renamed:

- Patient Name
- Patient ID
- Study Description
- Series Description
- Patients Birthday
- Protocol Name

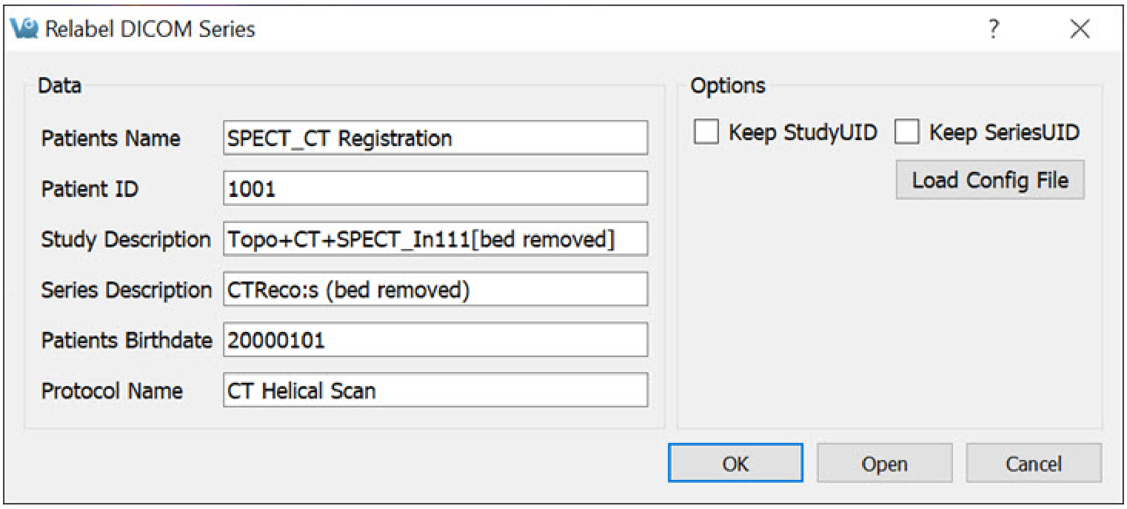
Getting There

This function can be found under the **Tools** -> **DICOM** menu, or the **DCM** button in the Main Window.

Function

Upon selecting the **Relabel Study** option, a dialog box appears prompting the user to decide whether to relabel each loaded dataset individually (Yes) or relabel them all together (No).

Enter the desired **Data** fields to change. Select the desired **Repository** and **Project** to store in the **Storage** section and click **OK**, or click **Open** if no data are already loaded.



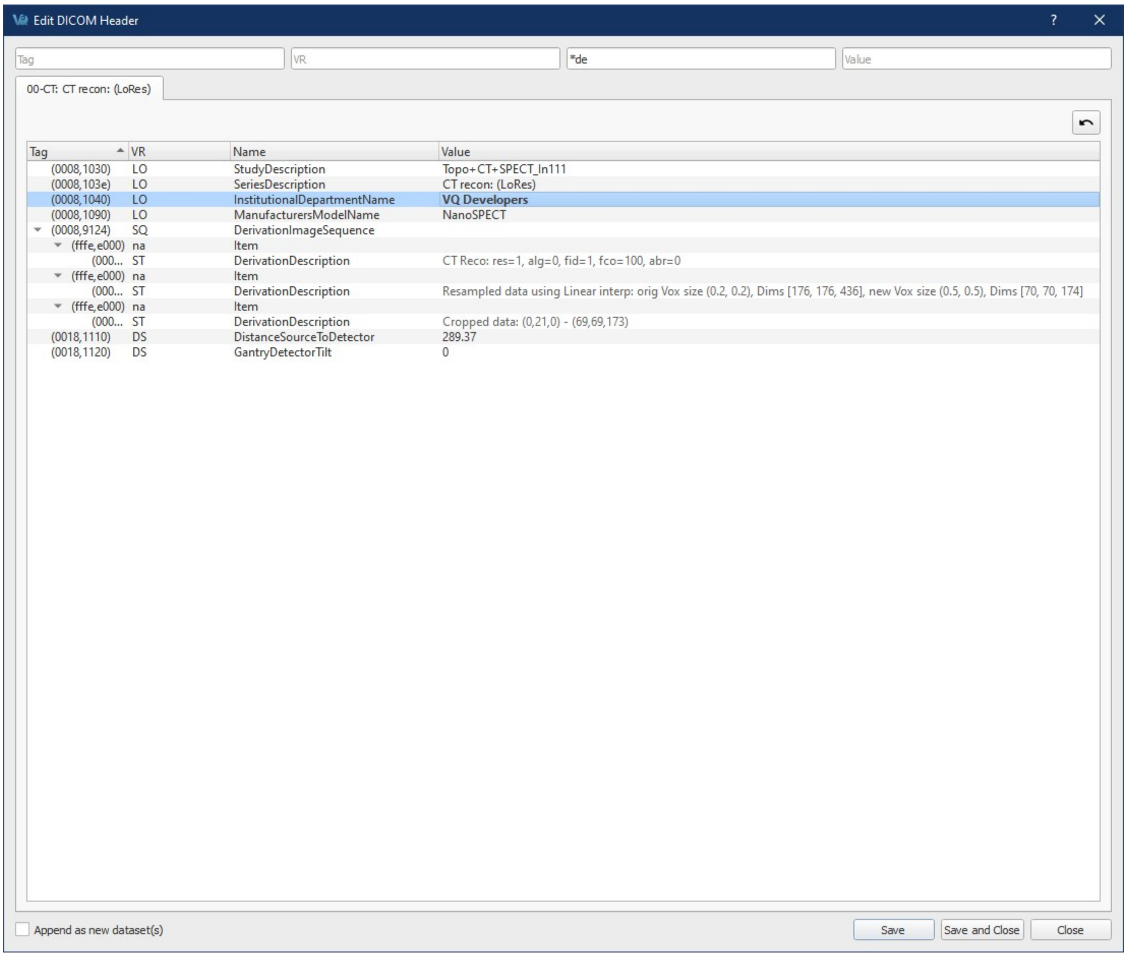
Patients Name	SPECT_CT Registration
Patient ID	1001
Study Description	Topo+CT+SPECT_In111[bed removed]
Series Description	CTReco:s (bed removed)
Patients Birthdate	20000101
Protocol Name	CT Helical Scan

☐ Keep StudyUID ☐ Keep SeriesUID

Relabel Study

DICOM Editor

The DICOM editor tool allows users to modify DICOM headers.



Tag | VR | *de | Value

Tag	VR	Name	Value
(0008,1030)	LO	StudyDescription	Topo+CT+SPECT_In111
(0008,103e)	LO	SeriesDescription	CT recon: (LoRes)
(0008,1040)	LO	InstitutionalDepartmentName	VQ Developers
(0008,1090)	LO	ManufacturersModelName	NanoSPECT
(0008,9124)	SQ	DerivationImageSequence	
(fffe,e000)	na	Item	
(000...	ST	DerivationDescription	CT Reco: res=1, alg=0, fid=1, fco=100, abr=0
(fffe,e000)	na	Item	
(000...	ST	DerivationDescription	Resampled data using Linear interp: orig Vox size (0.2, 0.2), Dims [176, 176, 436], new Vox size (0.5, 0.5), Dims [70, 70, 174]
(fffe,e000)	na	Item	
(000...	ST	DerivationDescription	Cropped data: (0,21,0) - (69,69,173)
(0018,1110)	DS	DistanceSourceToDetector	289.37
(0018,1120)	DS	GantryDetectorTilt	0

☐ Append as new dataset(s)

DICOM Editor Window

Note: See the restricted_tags page for instructions to control editing of DICOM tags.

Getting There

This function can be found under the **Tools** -> **DICOM** menu, the **DCM** button, or by right-clicking on an image in the Data Manager.

Function

The DICOM headers are presented in an expandable tree format for each image loaded into the editor. Columns can be sorted independently between images by clicking on the column headers.

Editing

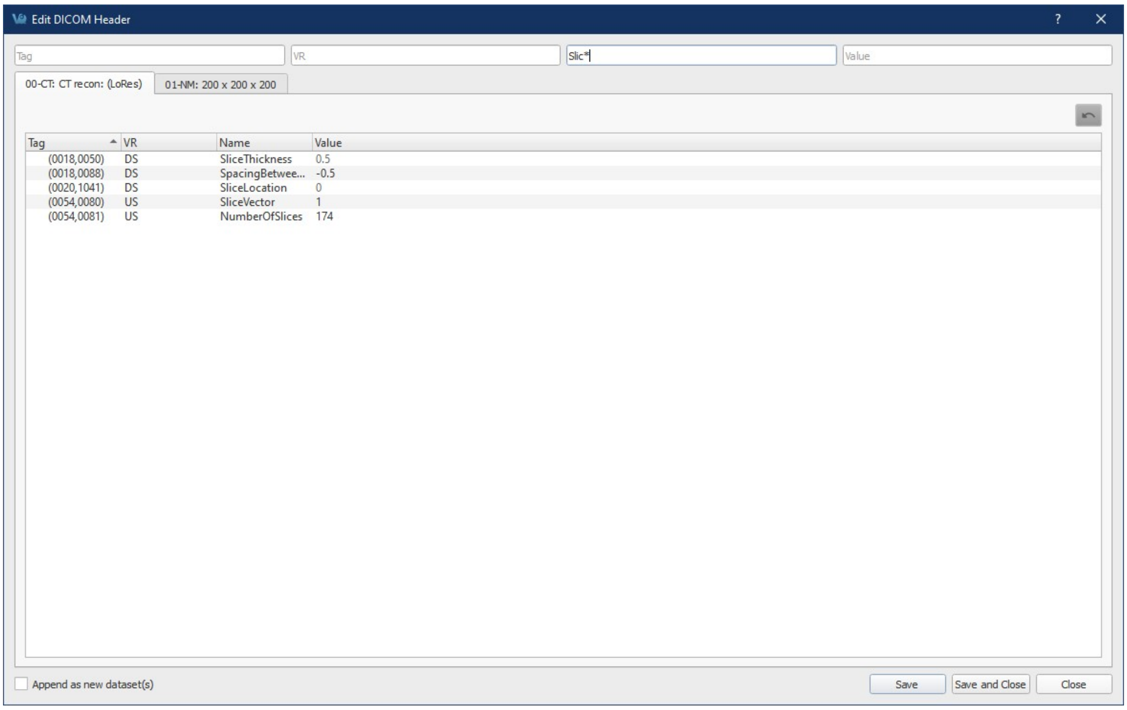
Simply change the text in the value column to the desired value. When a value is changed, it will be shown in **bold text**. Values restricted from editing will be shown in gray text.

To revert all edits on one of the image headers, click the Revert ↶ button.

Filtering

The user can filter by DICOM tag, tag names, Value Representation (VR), or value. Non-matching header entries in each image will be filtered out.

Filtering is case-insensitive and supports wildcards. The filter will automatically surround the text with the* character when interpreting the query so that fields like NumberOfValues or NameOfPatient can be found by just entering of. To filter to subwords within text, include the * character surrounded by parts of the subword.



Slic*

Tag	VR	Name	Value
(0018,0050)	DS	SliceThickness	0.5
(0018,0088)	DS	SpacingBetwee...	-0.5
(0020,1041)	DS	SliceLocation	0
(0054,0080)	US	SliceVector	1
(0054,0081)	US	NumberOfSlices	174

DICOM Editor filter

Saving changes

The checkbox option Append as new dataset(s) allows the user to create and load a new image with the updated header upon save. When this option is unchecked, the currently loaded image will be updated instead.

If multiple images' headers are changed, clicking one of the Save options will update each image (or create new ones if the append option is checked).

ℹ **Note:** Users should save their images to disk or iPACS after editing the DICOM header.

Autoradiography Calibration

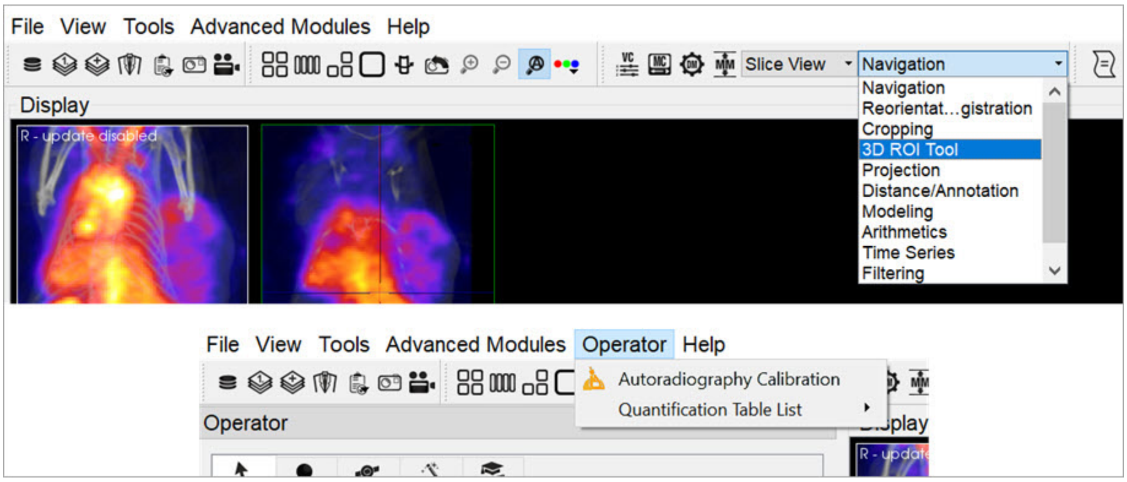
You can load, view, analyze and save **Autoradiography** data using the same tools VivoQuant uses for *in vivo* image data. Once loaded into **VivoQuant**, data can be reoriented, cropped, rescaled, and quantified.

The **Autoradiography Calibration** tool allows you to calibrate autoradiography data based on known calibration standards in the image.

ℹ **Note:** This tool is available only with a **CiQuant Module** license. For more information, contact support@invicro.com.

Getting There

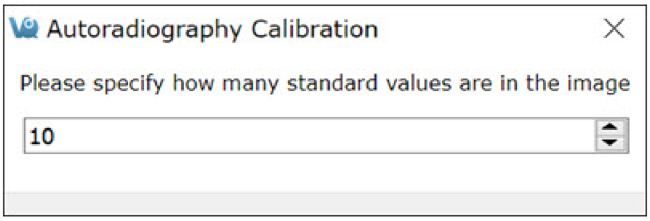
To access the tool, activate to the **3D ROI Tool** operator, then go to the **Operator** tab in the main menu and select **Autoradiography Calibration**.



DICOM Dump

Function

Once the you start the tool, it asks several questions to establish how it will be used. The first prompt asks for the number of calibration standards being used. This determines the number of ROIs that populate the **3D ROI Tool**.



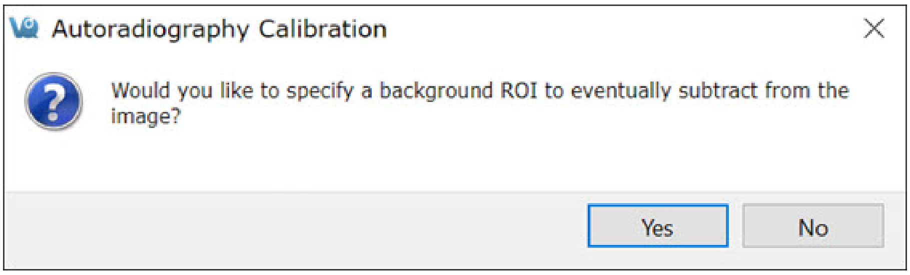
Autoradiography Calibration

Please specify how many standard values are in the image

10

Calibration Standards Prompt

The second prompt asks if there will be a background ROI used. This influences the calibration curve. In most cases, a background ROI is recommended.

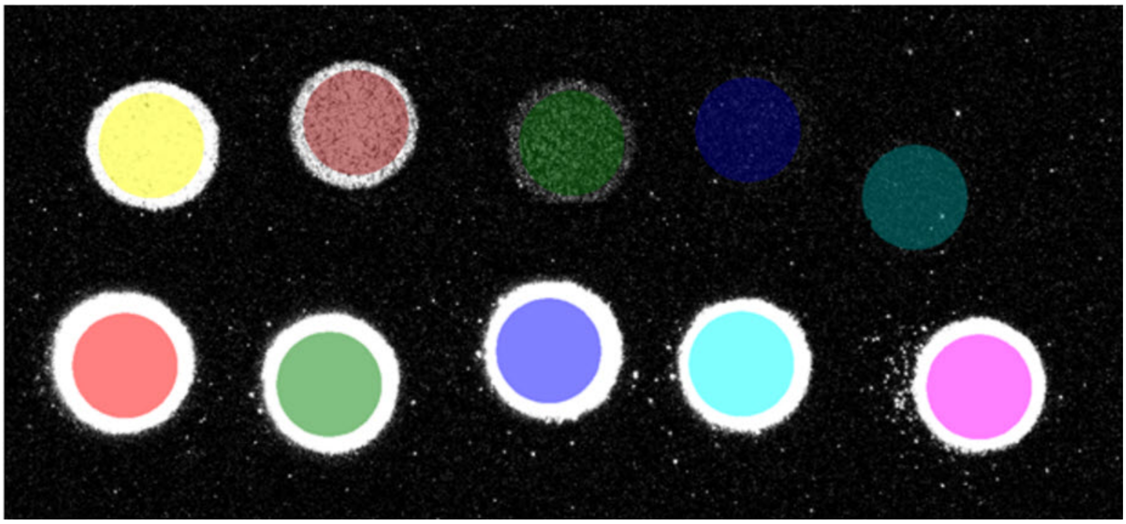


Autoradiography Calibration

Would you like to specify a background ROI to eventually subtract from the image?

Background ROI Prompt

The ROIs are populated based on the answers to these questions. You then need manually place them in the correct locations in the image. Use the **3D Paint Mode** tools to perform this task. Regions should appear similar to the image below.



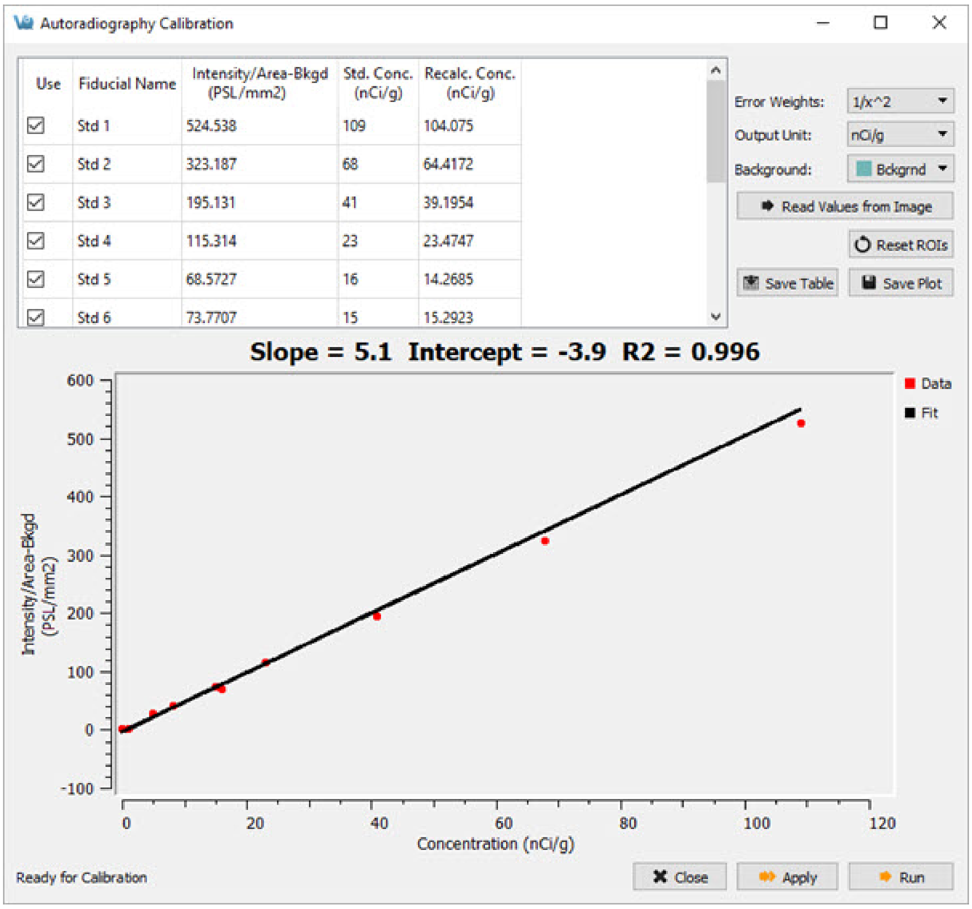
3D Paint Mode

Image Calibration

After segmenting the calibration standards, click **Read Values from Image**. The table displays the mean value of each region. Provide the true value of each standard as well as the correct output unit. Also, choose from the available **Error Weight** techniques.

After you have established the settings, click **Run**. The plot populates with the values of the standards and provided values along with the calculated fit line. Changing the settings, particularly the **Error Weights**, will change the output calibration curve.

To see how the curve changes with different settings, change them and click **Run**. Once the curve fits as desired, click **Apply** to apply the calibration to the data.



Autoradiography Calibration

Use	Fiducial Name	Intensity/Area-Bkgd (PSL/mm2)	Std. Conc. (nCi/g)	Recalc. Conc. (nCi/g)
☑	Std 1	524.538	109	104.075
☑	Std 2	323.187	68	64.4172
☑	Std 3	195.131	41	39.1954
☑	Std 4	115.314	23	23.4747
☑	Std 5	68.5727	16	14.2685
☑	Std 6	73.7707	15	15.2923

Error Weights: 1/x^2

Output Unit: nCi/g

Background: Bckgrnd

Slope = 5.1 Intercept = -3.9 R2 = 0.996

Ready for Calibration

Image Calibration

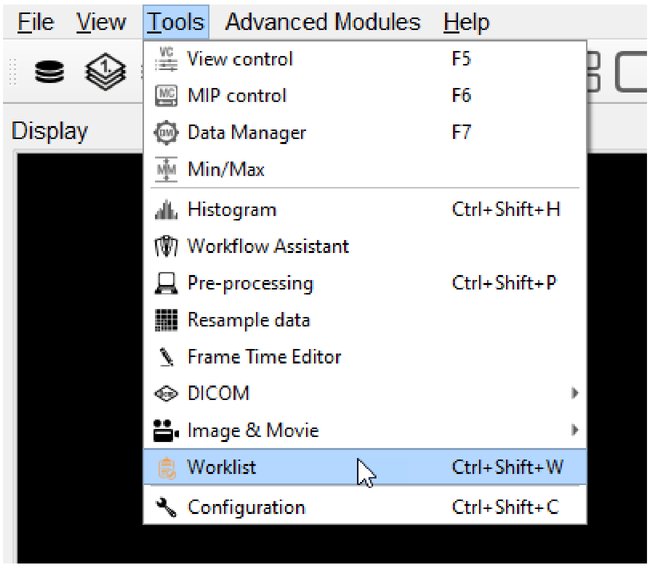
Worklist Tool

The **Worklist** provides an interface for viewing tasks created from iPACS Workflows, completing electronic case report forms (eCRF) and opening data associated with the tasks.

Getting There

There are three methods to open this tool. The first method is using the **Worklist** thumbnail in the Main Window.

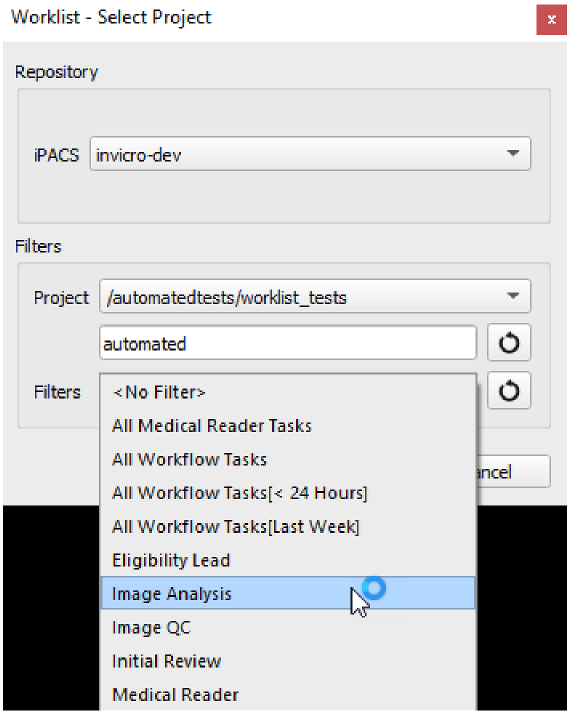
The second method is to go to **Worklist** under the **Tools** menu.



Worklist

Finally, the **Worklist** is also available by using the keyboard shortcut Ctrl+Shift+W.

Select Project



iPACS: invicro-dev

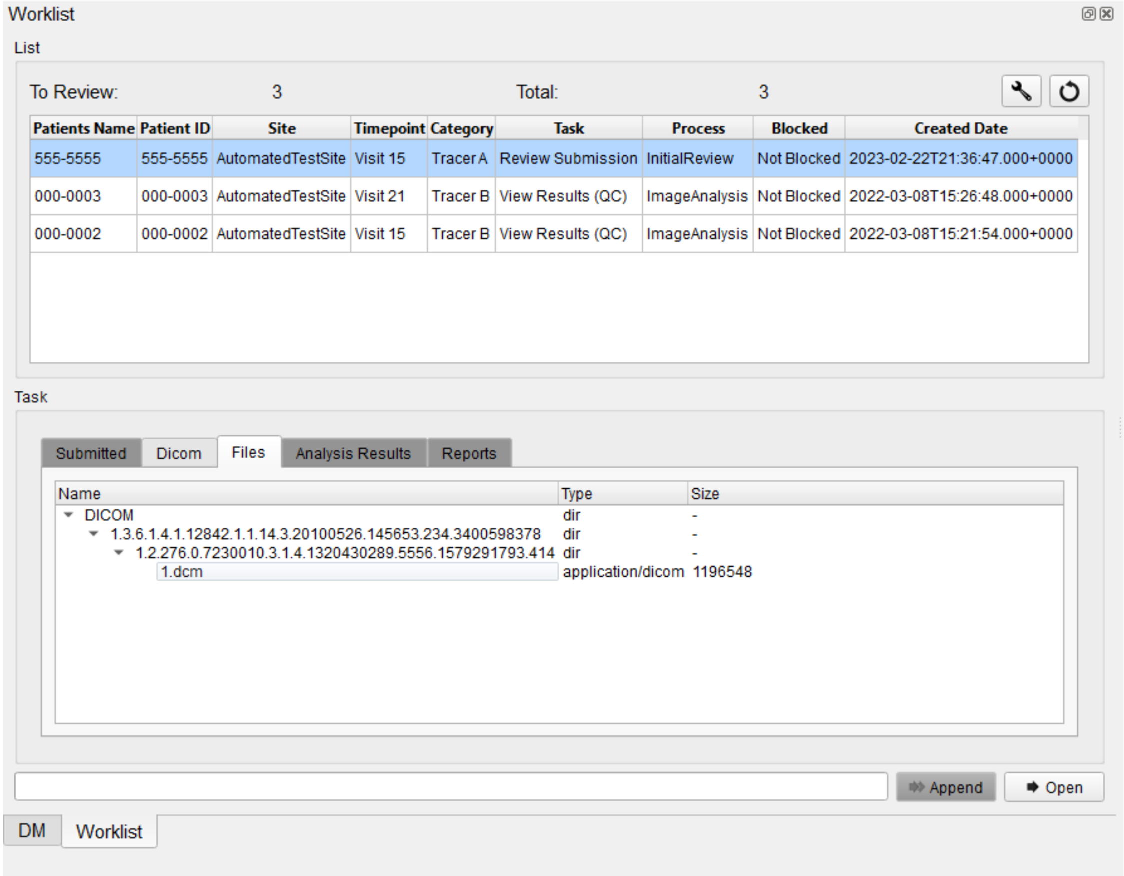
Project: /automatedtests/worklist_tests

automated

Select Project

The first step in using the **Worklist** is to select an iPACS project. Any of the iPACS repositories that have been added in the **Data Browser** are available to use for the worklist in the **iPACS** dropdown. The project can be selected using the **Project** dropdown, which can be filtered the same way as in the Data Browser. The **Filters** dropdown allows the user to filter the worklist results by task type, using the same options available in the **Task List** on the iPACS.

Once a project and task filter have been selected, the tasks assigned to the current user will appear in the task list panel. The current user is the user whose credentials were used to login to the iPACS in the **Data Browser**. The task list can be refreshed at any time using the refresh button, and the current project and filter can be changed using the settings button. Clicking on a task opens the **Task** panel, which displays images and files associated with the task organized in tabs based on their type.



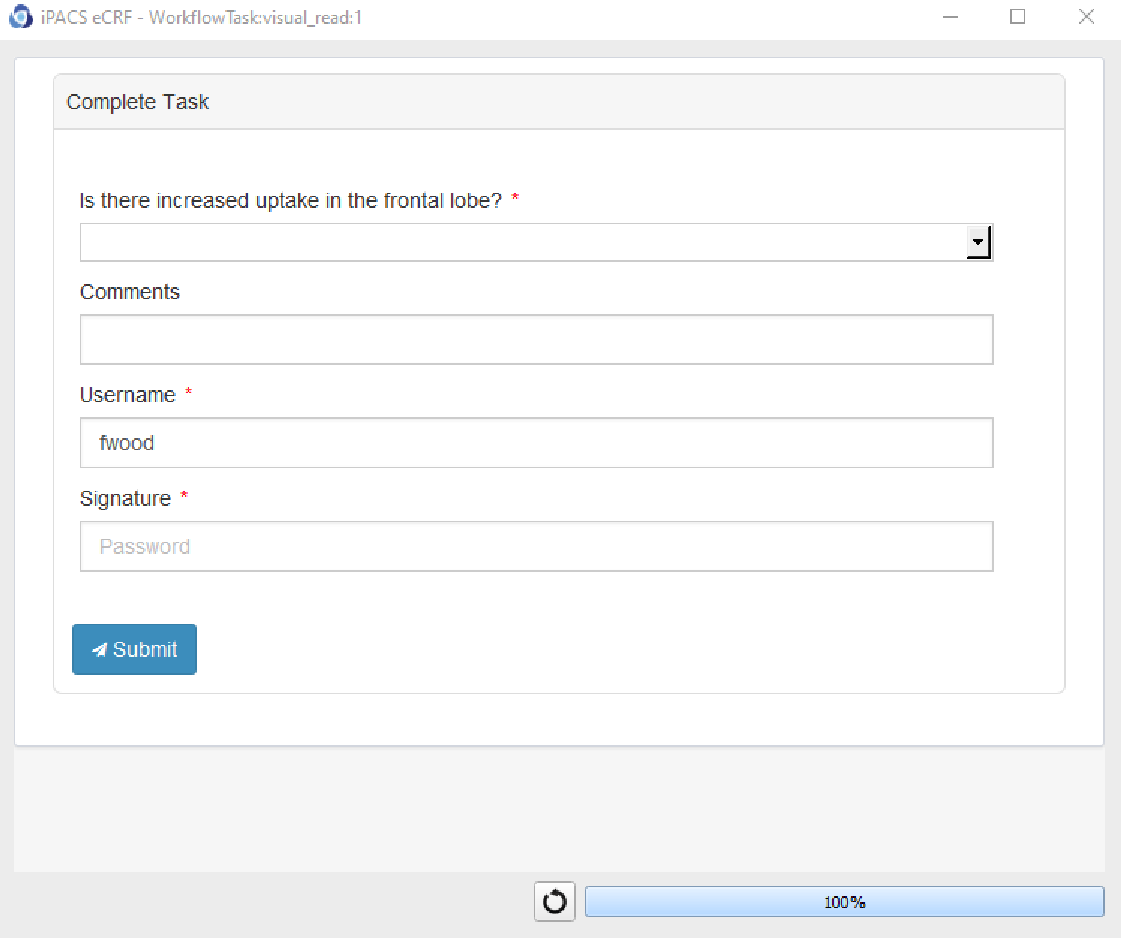
To Review: 3 Total: 3

Patients Name	Patient ID	Site	Timepoint	Category	Task	Process	Blocked	Created Date
555-5555	555-5555	AutomatedTestSite	Visit 15	Tracer A	Review Submission	InitialReview	Not Blocked	2023-02-22T21:36:47.000+0000
000-0003	000-0003	AutomatedTestSite	Visit 21	Tracer B	View Results (QC)	ImageAnalysis	Not Blocked	2022-03-08T15:26:48.000+0000
000-0002	000-0002	AutomatedTestSite	Visit 15	Tracer B	View Results (QC)	ImageAnalysis	Not Blocked	2022-03-08T15:21:54.000+0000

Name	Type	Size
DICOM	dir	-
1.3.6.1.4.1.12842.1.1.14.3.20100526.145653.234.3400598378	dir	-
1.2.276.0.7230010.3.1.4.1320430289.5556.1579291793.414	dir	-
1.dcm	application/dicom	1196548

Task Viewer

The **Append** and **Open** buttons open or append the data associated with the task in the data list and open the task's associated eCRF form. The user can view and interact with the data in VQ and complete the form in the eCRF window. After the form is submitted, a popup window indicates whether the submission was successful and a refresh of the task list will show that the task is no longer assigned to the user.


iPACS eCRF - WorkflowTask:visual_read:1

Complete Task

Is there increased uptake in the frontal lobe? *

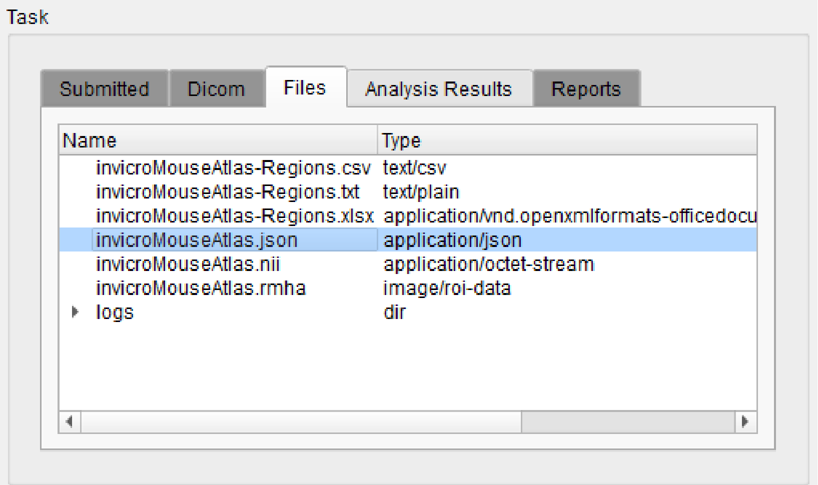
Comments

Username *
fwood

Signature *
Password

eCRF Viewer

Depending on the type of task, different tabs will be enabled in the **Task** panel. For submission tasks, the data appears in the **Submitted** tab. Once a submission task is completed and a task has data indexed in the browser, its data appears in the **Dicom** tab. For tasks that have files associated with them, which will appear in the **Files** tab of the task viewer, the right-click menu provides the “Open Externally” option for opening files using the system’s default application for that file type.

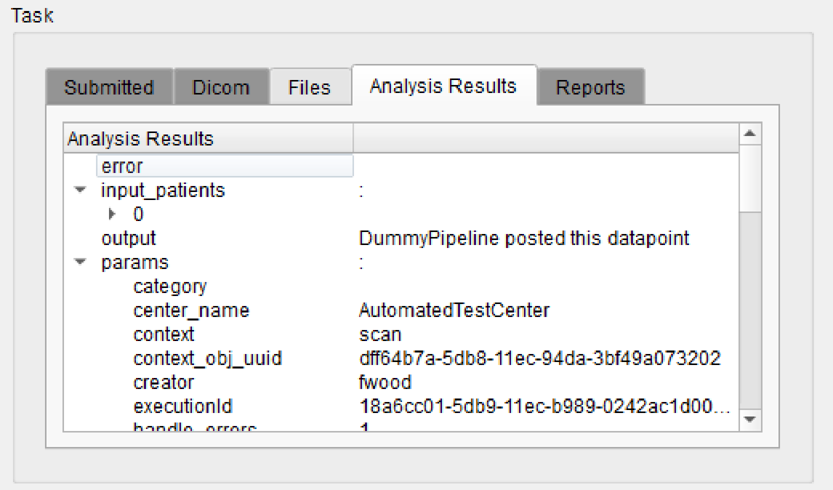


Name	Type
invicroMouseAtlas-Regions.csv	text/csv
invicroMouseAtlas-Regions.txt	text/plain
invicroMouseAtlas-Regions.xlsx	application/vnd.openxmlformats-officedocu
invicroMouseAtlas.json	application/json
invicroMouseAtlas.nii	application/octet-stream
invicroMouseAtlas.rmha	image/roi-data
logs	dir

Files Tab

Files that appear in the Files tab that can be opened in VivoQuant, such as images and RMHAs, can also be opened in VivoQuant using the Open and Append buttons and the Open and Append options in the right-click menu. Choosing this option for an RMHA will open the 3D ROI Operator and load the RMHA file.

For tasks that are the output or result of an iPACS pipeline, the **Analysis Results** tab will be available. The Analysis Results tab shows the JSON output of the pipeline in an expandable tree format. The JSON can be downloaded as a file or copied to the clipboard using the right-click menu.



Analysis Results	
error	
input_patients	:
0	
output	DummyPipeline posted this datapoint
params	:
category	
center_name	AutomatedTestCenter
context	scan
context_obj_uuid	dff64b7a-5db8-11ec-94da-3bf49a073202
creator	fwood
executionId	18a6cc01-5db9-11ec-b989-0242ac1d00...
handle_errors	1

Analysis Results

The **Reports** tab contains PDF file reports which can be opened using the right-click tab similarly to the Files tab.

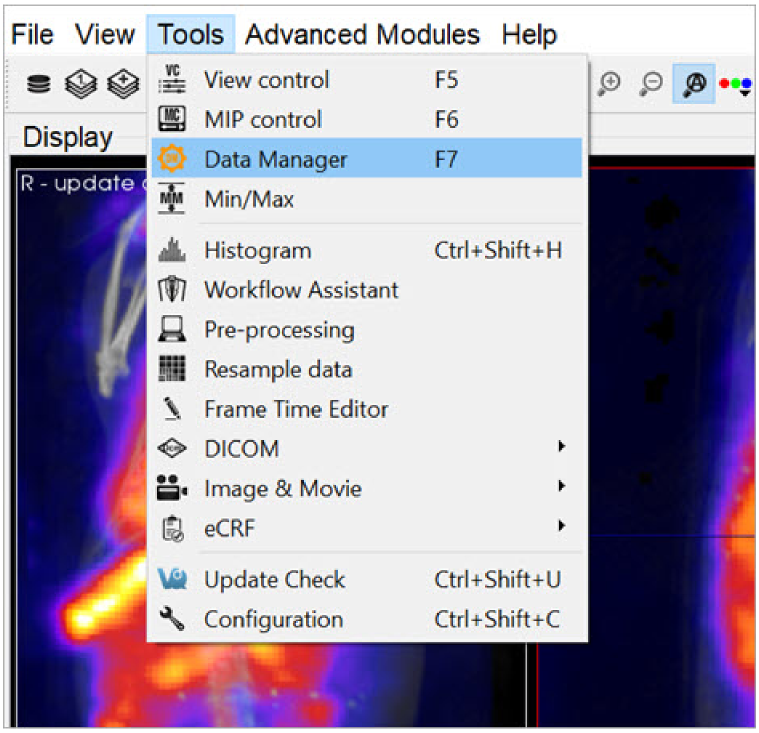
Data Manager

The **Data Manager** presents information about the datasets loaded into VivoQuant. While VivoQuant only displays up to three datasets in the **Display** at a time, post-processing operations may be performed on any number of datasets in the **Data Manager**. The only limiting factor in the number of simultaneously loaded dataset is the system memory.

Getting There

There are three methods to open this tool. The first method is using the **Data Manager** thumbnail in the Main Window.

The second method is to go to **Data Manager** under the **Tools** menu.



Data Manager

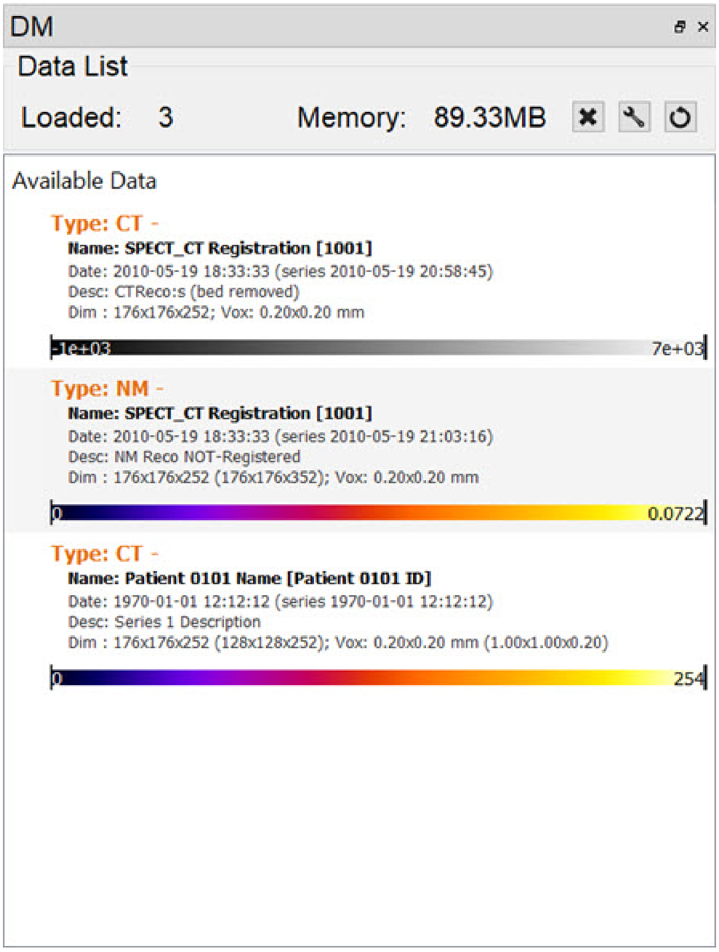
Finally, the **Data Manager** is also available by using the keyboard shortcut F7.

Using the Data Manager

The **Data Manager** displays a list of all datasets loaded into **VivoQuant**, along with information about each of them. This tool can hold as many datasets as the system memory allows; however, the first, second and third datasets in the **Data Manager** are the only three that appear in the Display. These datasets are the **Reference**, **Input 1**, and **Input 2**, respectively.

The information displayed by the **Data Manager** includes the image type, name, dimensions and voxel size. For DICOM data, the **Study Date**, **Series Date**, and **Series Description** will also be included when available. The information that is shown can also be customized with the Data Manager Text Configuration.

Below this information is a color bar specific to each dataset. The color bar defines the colors that will be used to represent the dataset in the **Display**. The colors can be changed by right-clicking the color bar and selecting the desired color palette. **VivoQuant** selects color palettes for datasets by default based on modality (CT, PT, MR, etc.). Default color palette options may be changed in the Display tab of the Configuration window. These changes do not affect the minimum and maximum values stored in the **Min/Max Tool**. For more information on changing the minimum and maximum values, see the Min/Max Tool page.



Loaded: 3

Memory: 89.33MB

Type: CT -

Name: SPECT_CT Registration [1001]

Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)

Desc: CTReco:s (bed removed)

Dim : 176x176x252; Vox: 0.20x0.20 mm

Type: NM -

Name: SPECT_CT Registration [1001]

Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)

Desc: NM Reco NOT-Registered

Dim : 176x176x252 (176x176x352); Vox: 0.20x0.20 mm

Type: CT -

Name: Patient 0101 Name [Patient 0101 ID]

Date: 1970-01-01 12:12:12 (series 1970-01-01 12:12:12)

Desc: Series 1 Description

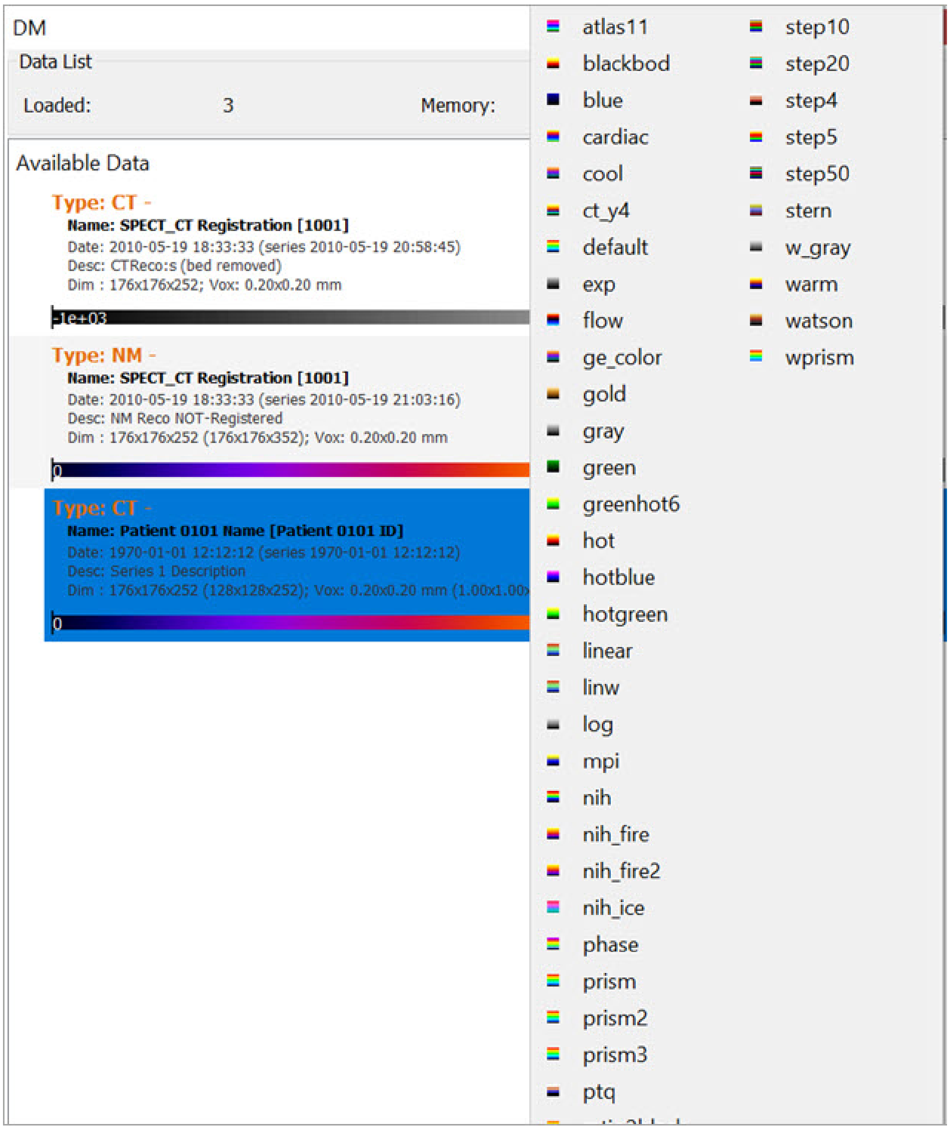
Dim : 176x176x252 (128x128x252); Vox: 0.20x0.20 mm (1.00x1.00x0.20)

Data Manager Window

If the windowing is using the **Min/Max** option, the palette can be adjusted by clicking on the black bars at the far left or right of the palette to adjust the window min or max, respectively. If the windowing is using the **Level/Width** option, the width of the window is adjusted by clicking and dragging the ends, while the center is adjusted by clicking and dragging the middle of the palette display. The **Level/Width** palette can be also adjusted similarly to the **Min/Max** by holding the Shift key while dragging the ends.

The windowing can be adjusted within the image as well, by holding a right-click and dragging the mouse. In the **Min/Max** setting, dragging left/right will adjust the min while up/down will adjust the max. In the **Level/Width** setting, dragging left/right will adjust the level, while up/down will adjust the width. This function works within any of the operators and does not require that the **Data Manager** is active.

The color palettes for a single frame of data can be edited in the **Data Manager** by right-clicking on the color palette.



DM

Data List

Loaded: 3 Memory:

Available Data

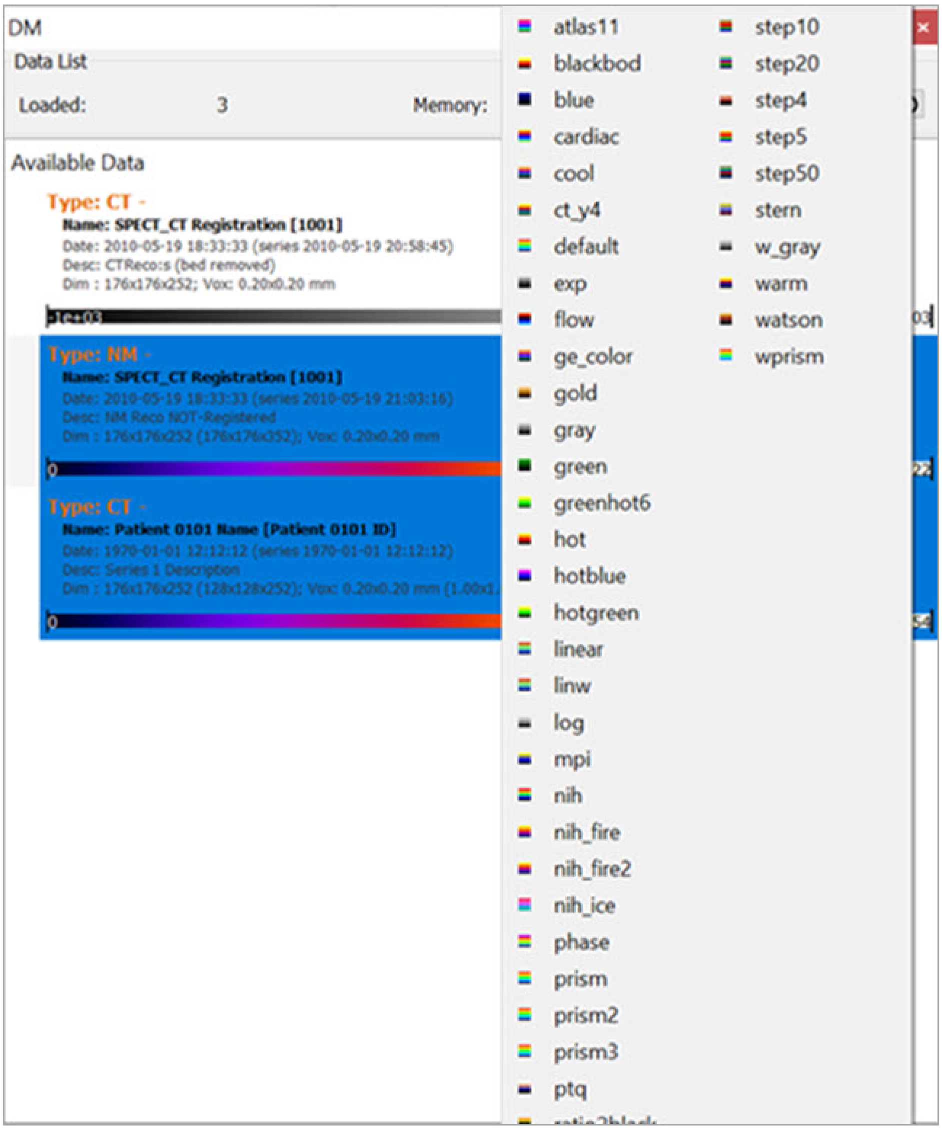
Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)
Desc: CTReco:s (bed removed)
Dim : 176x176x252; Vox: 0.20x0.20 mm

Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)
Desc: NM Reco NOT-Registered
Dim : 176x176x252 (176x176x352); Vox: 0.20x0.20 mm

Type: CT -
Name: Patient 0101 Name [Patient 0101 ID]
Date: 1970-01-01 12:12:12 (series 1970-01-01 12:12:12)
Desc: Series 1 Description
Dim : 176x176x252 (128x128x252); Vox: 0.20x0.20 mm (1.00x1.00

Edit Single Frame

To edit multiple frames at once, use Ctrl or Shift to select multiple frames, then right-click on one of the palettes, and all frames will be edited together. This technique can also be used for editing the **Min/Max** for the palettes of multiple frames at once.



Loaded: 3 Memory:

Available Data

Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)
Desc: CTReco:s (bed removed)
Dim : 176x176x252; Vox: 0.20x0.20 mm

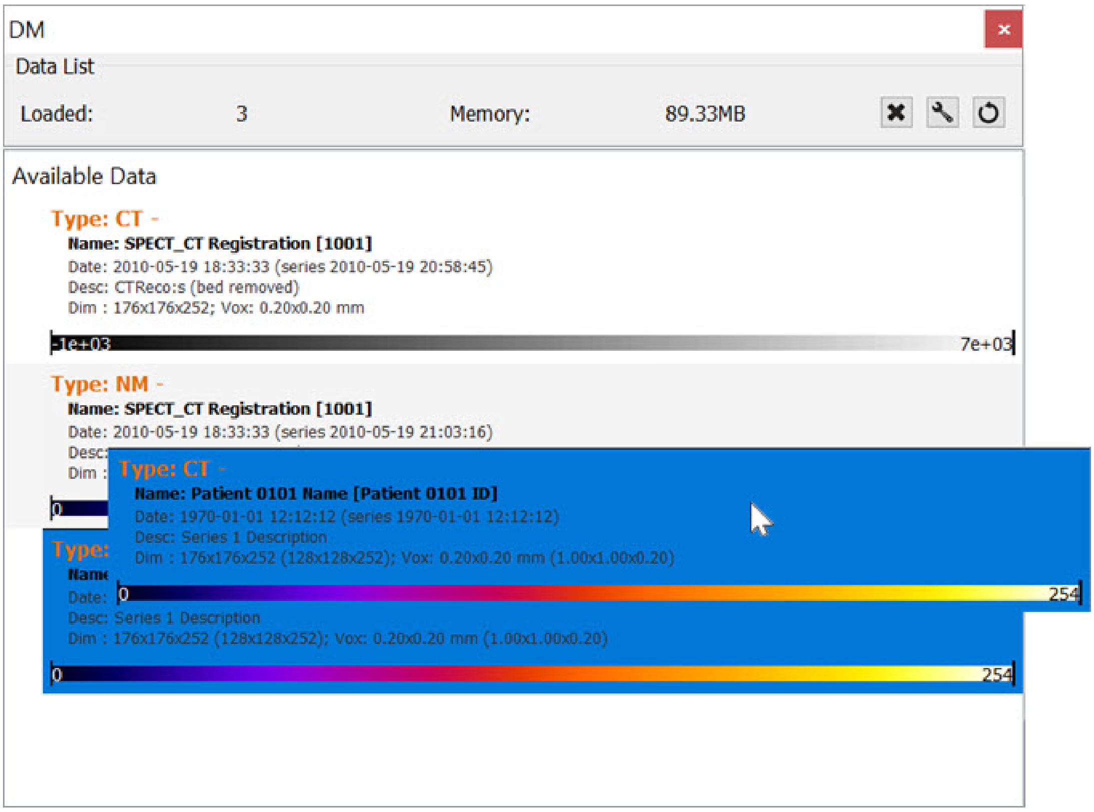
Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)
Desc: NM Reco NOT-Registered
Dim : 176x176x252 (176x176x352); Vox: 0.20x0.20 mm

Type: CT -
Name: Patient 0101 Name [Patient 0101 ID]
Date: 1970-01-01 12:12:12 (series 1970-01-01 12:12:12)
Desc: Series 1 Description
Dim : 176x176x252 (128x128x252); Vox: 0.20x0.20 mm (1.00x1.

Edit Multiple Frames

Ordering Data

Data may be rearranged into any order in the **Data Manager** by dragging a dataset and dropping it to the desired position. Alternatively, data can be moved into the **Reference**, **Input 1** or **Input 2** location by right-clicking and selecting **Move to Reference/Input 1/Input 2**.



Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)
Desc: CTReco:s (bed removed)
Dim : 176x176x252; Vox: 0.20x0.20 mm

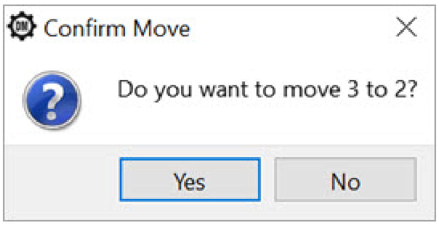
Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)

Type: CT -
Name: Patient 0101 Name [Patient 0101 ID]
Date: 1970-01-01 12:12:12 (series 1970-01-01 12:12:12)
Desc: Series 1 Description
Dim : 176x176x252 (128x128x252); Vox: 0.20x0.20 mm (1.00x1.00x0.20)

Desc: Series 1 Description
Dim : 176x176x252 (128x128x252); Vox: 0.20x0.20 mm (1.00x1.00x0.20)

Move to Reference

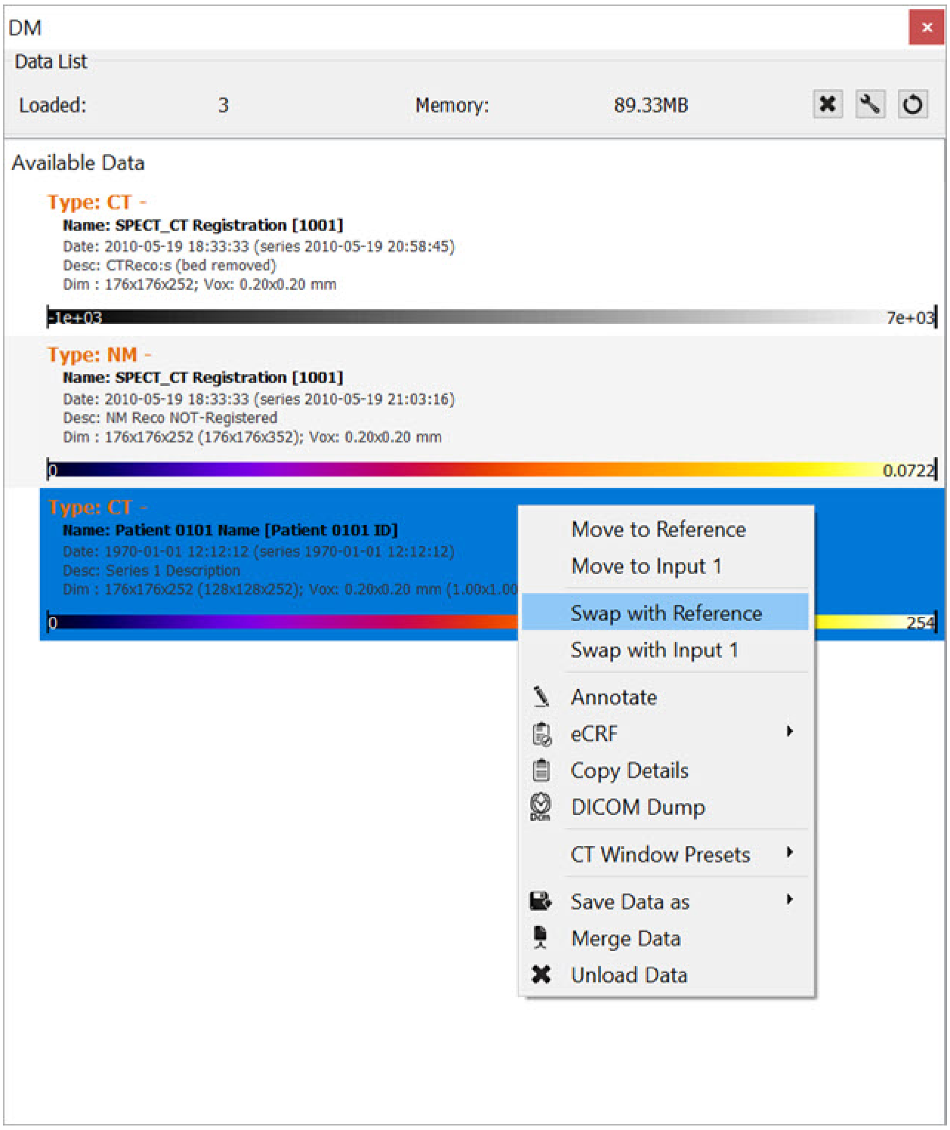
A prompt will appear confirming the move. Click **OK** to complete the move.



Do you want to move 3 to 2?

Confirm Move

A dataset can also be quickly swapped with the dataset in the **Reference**, **Input 1**, or **Input 2** positions by right-clicking on a dataset and selecting **Swap with Reference /Input 1 /Input 2** .



Loaded: 3
Memory: 89.33MB

Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)
Desc: CTReco:s (bed removed)
Dim : 176x176x252; Vox: 0.20x0.20 mm

Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)
Desc: NM Reco NOT-Registered
Dim : 176x176x252 (176x176x352); Vox: 0.20x0.20 mm

Type: CT -
Name: Patient 0101 Name [Patient 0101 ID]
Date: 1970-01-01 12:12:12 (series 1970-01-01 12:12:12)
Desc: Series 1 Description
Dim : 176x176x252 (128x128x252); Vox: 0.20x0.20 mm (1.00x1.00

Swap with Reference

Options

Right clicking on a dataset brings up a menu with several data manipulation options.

Option	Description
Move to Reference/Input 1/Input 2	Moves the selected data set to either the Reference/Input 1/Input 2.
Annotate	Allows an annotation to be added to the data details.
Copy Details	Copies data set details to the clipboard, from where they may be pasted into other files.
DICOM Dump	Opens the DICOM header information for the selected data sets.
Save Data as	Allows data to be saved as DICOM, TRaster, Raw, 4D or ITK image file.
Merge Data	Merges two or more selected data sets into one.
Unload Data	Unloads data from **VivoQuant**.

More Information

Many of the functions in **VivoQuant** are directed to specific images loaded in the **Data Manager**, so it is important to pay attention to the order in which data has been loaded into it.

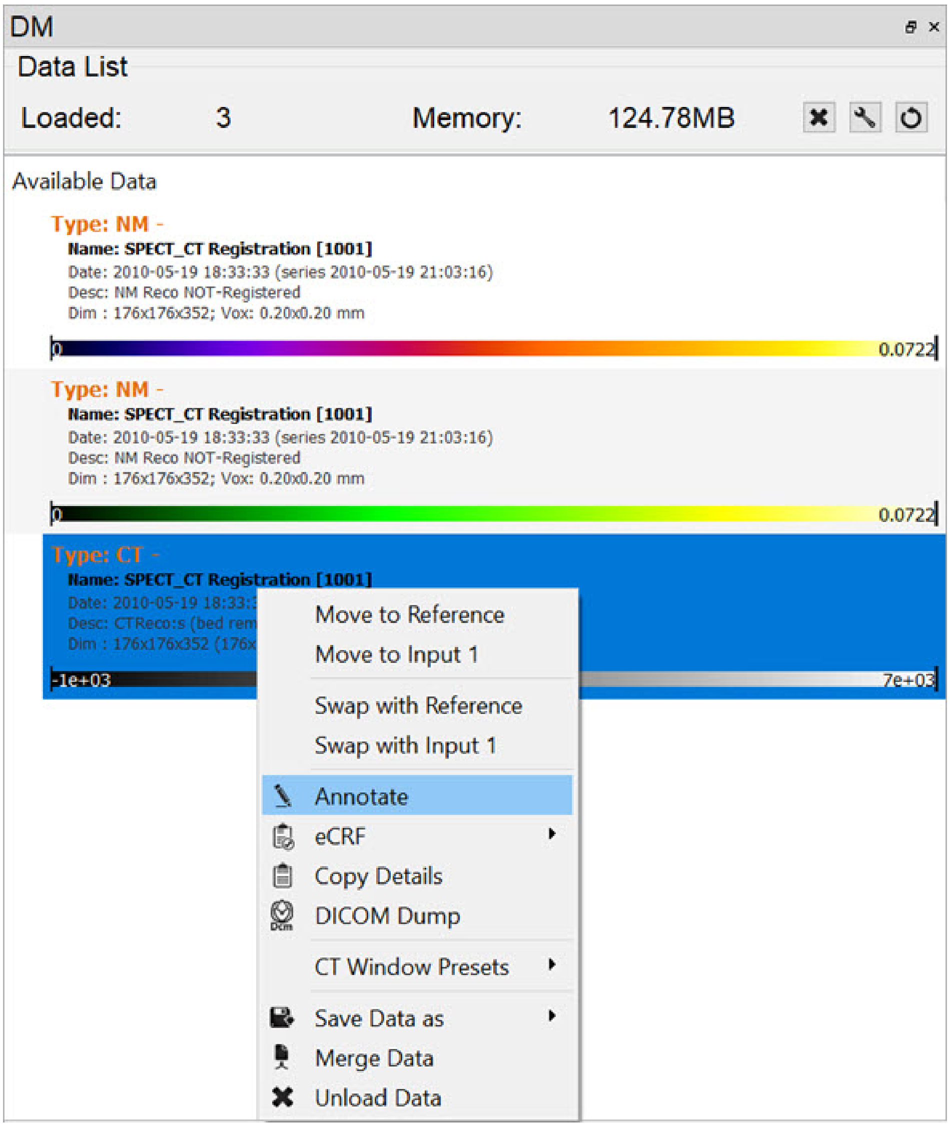
See How To Make a Dynamic Movie for a practical example that makes use of the **Data Manager**.

Annotation

The Annotation tool allows you to write and save a comment on any of the files currently loaded in the Data Manager

Adding An Annotation

Right click on the data in the DM you want to edit and select Annotate.



Loaded: 3

Memory: 124.78MB

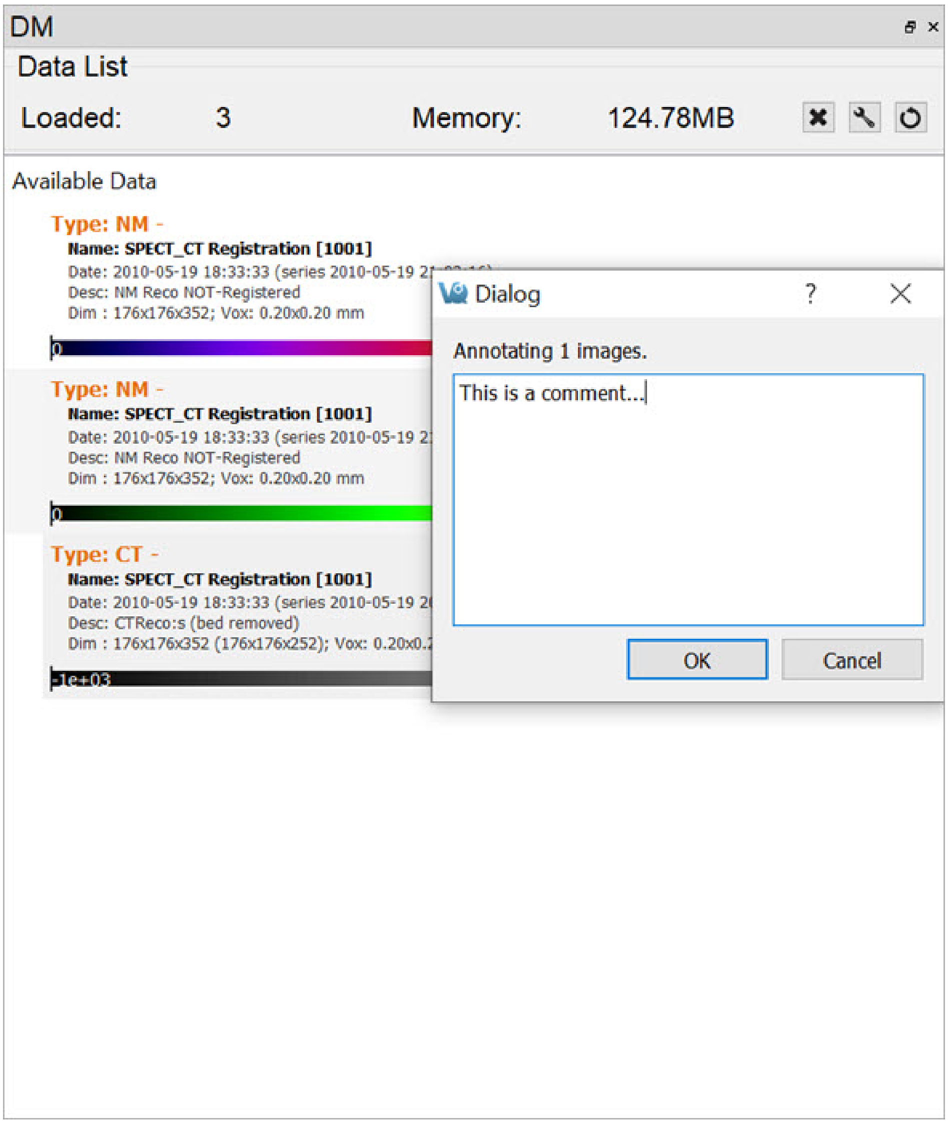
Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)
Desc: NM Reco NOT-Registered
Dim : 176x176x352; Vox: 0.20x0.20 mm

Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)
Desc: NM Reco NOT-Registered
Dim : 176x176x352; Vox: 0.20x0.20 mm

Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:3
Desc: CTReco:s (bed rem
Dim : 176x176x352 (176x

Add Annotation

Write your comment and select OK.



Available Data

Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 2
Desc: NM Reco NOT-Registered
Dim : 176x176x352; Vox: 0.20x0.20 mm

Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 2
Desc: NM Reco NOT-Registered
Dim : 176x176x352; Vox: 0.20x0.20 mm

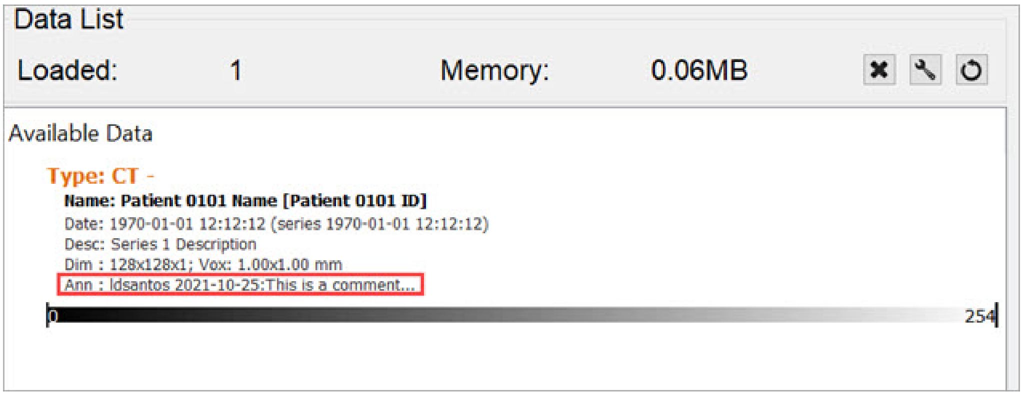
Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 2
Desc: CTReco:s (bed removed)
Dim : 176x176x352 (176x176x252); Vox: 0.20x0.

Annotating 1 images.

This is a comment...

Write Comment

Your annotation will appear in the data as Ann. It will read Ann: [user] [date]:[annotation]

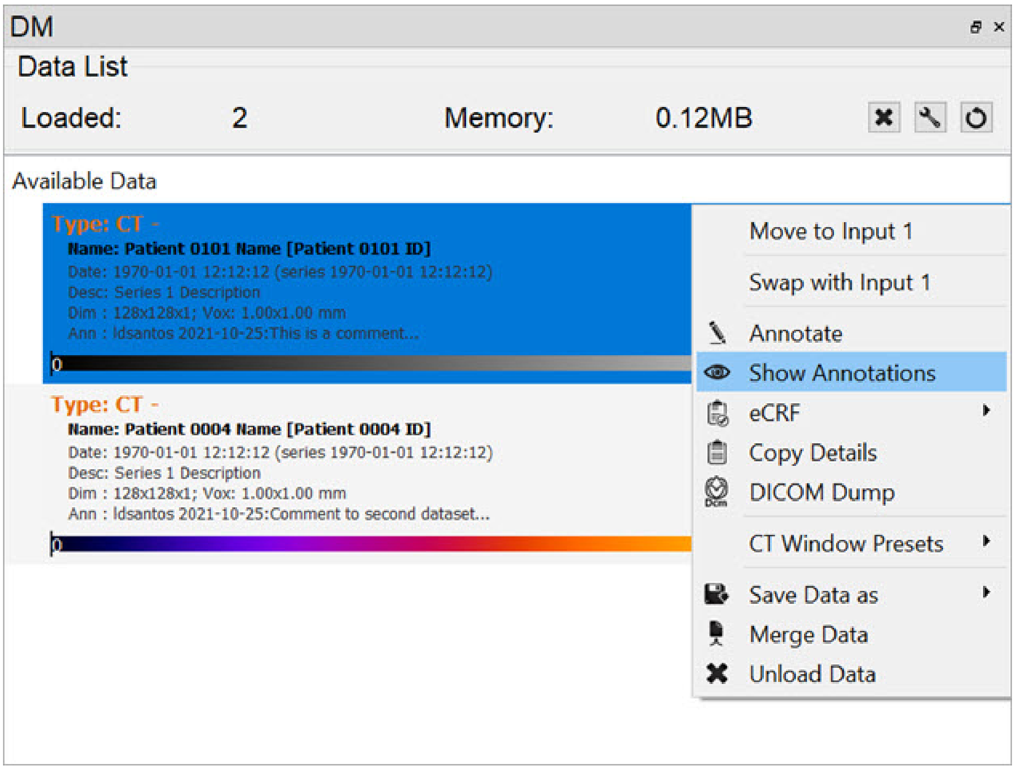


Available Data

Type: CT -
Name: Patient 0101 Name [Patient 0101 ID]
Date: 1970-01-01 12:12:12 (series 1970-01-01 12:12:12)
Desc: Series 1 Description
Dim : 128x128x1; Vox: 1.00x1.00 mm
Ann : ldsantos 2021-10-25:This is a comment...

Annotated Data

You can add as many annotations as needed following the same steps as above. To view all your annotations in full, right click on the data and select **Show Annotations**.



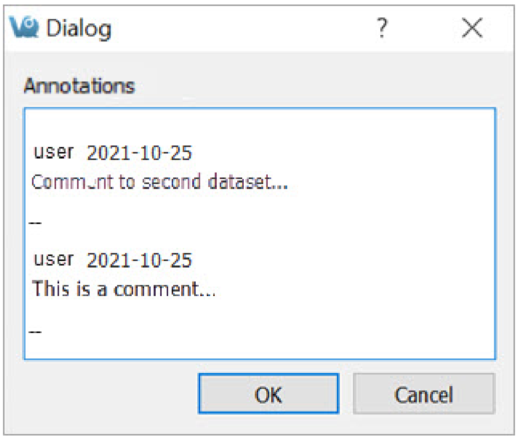
Loaded: 2

Memory: 0.12MB

Type: CT -
Name: Patient 0101 Name [Patient 0101 ID]
Date: 1970-01-01 12:12:12 (series 1970-01-01 12:12:12)
Desc: Series 1 Description
Dim : 128x128x1; Vox: 1.00x1.00 mm
Ann : ldsantos 2021-10-25:This is a comment...

Type: CT -
Name: Patient 0004 Name [Patient 0004 ID]
Date: 1970-01-01 12:12:12 (series 1970-01-01 12:12:12)
Desc: Series 1 Description
Dim : 128x128x1; Vox: 1.00x1.00 mm
Ann : ldsantos 2021-10-25:Comment to second dataset...

Show Annotations



user 2021-10-25
Comment to second dataset...
--
user 2021-10-25
This is a comment...
--

Annotations Panel

You can also check, edit, and delete your annotations in **iPACS**. Just log in, locate the file you annotated, click on its number of data points (DP) and a chart will appear with your annotation and options to edit or delete.

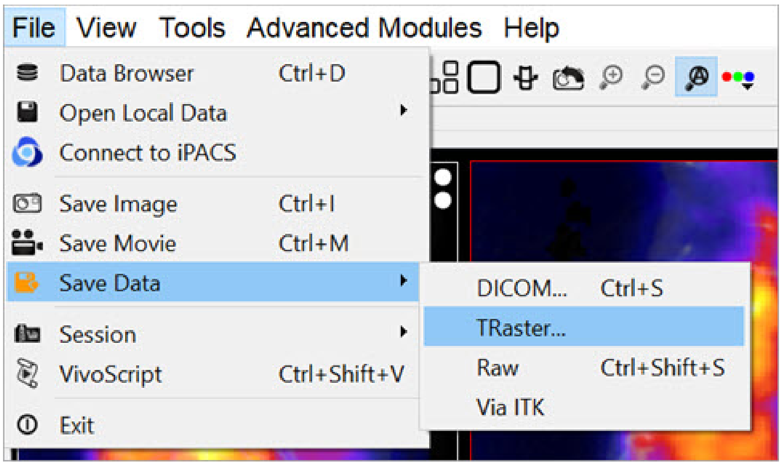
Annotations can only be deleted in iPACS. You have to refresh your iPACS browser or update VivoQuant in order for your annotation edits to appear in either.

Save Data

The data can be saved in four different formats. It can be saved as DICOM, TRaster, Raw data files, or Via ITK. The data can be saved as a DICOM file after post-processing and then be reopened in VivoQuant in its new format for further processing. Saving the data in different formats enables it to be opened in different programs at a later stage.

Getting There

The data can be saved by selecting **Save data** under the **File** menu after data has been loaded.



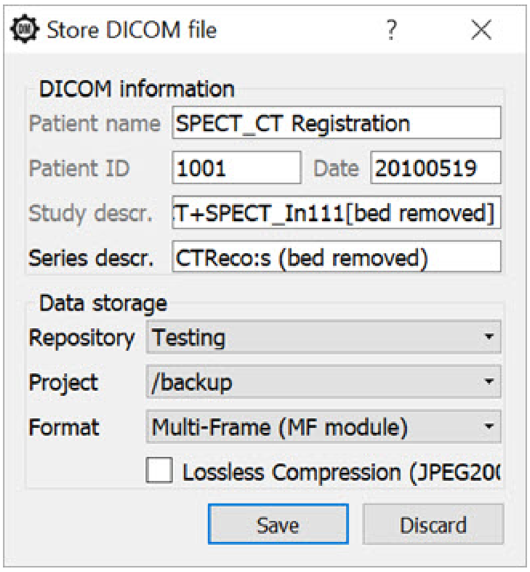
Save Data As

Function

Once the **Save Data** option has been selected, there is an option to save the data in four different formats.

- DICOM
- TRaster
- Raw
- Via ITK

DICOM	If the data is to be saved as a DICOM file, a Store DICOM file window is displayed. Any relevant information or description of the study can be entered into the **DICOM information** section of the window. Under the **Data Storage** section, the repository and the format of the saved DICOM files can be specified. The DICOM files are saved by clicking on **Save** or it can be canceled by clicking **Discard**.



Patient name: SPECT_CT Registration
Patient ID: 1001
Date: 20100519
Study descr.: T+SPECT_In111[bed removed]
Series descr.: CTReco:s (bed removed)
Repository: Testing
Project: /backup
Format: Multi-Frame (MF module)
☐ Lossless Compression (JPEG20

Save as DICOM

TRaster	If the data is to be saved as a Raster file, a **Save Data as Raster** window will be displayed and here the data can be saved to an appropriate location.
Raw	If the data is to be saved as a raw file, a **Save Data as Raw** window will be displayed and here the data can be saved to an appropriate location.
Via ITK	If the data is to be saved via ITK, a **Save Data via ITK** window will be displayed and here the data can be saved to an appropriate location.

Image Magick

Use the **Image Magick** suite to manipulate frames and movies within **VivoQuant**. These options are useful for generating appealing and informative dynamic movies.

Getting There

Select the **Image and Movie** option of the **Tools** menu.

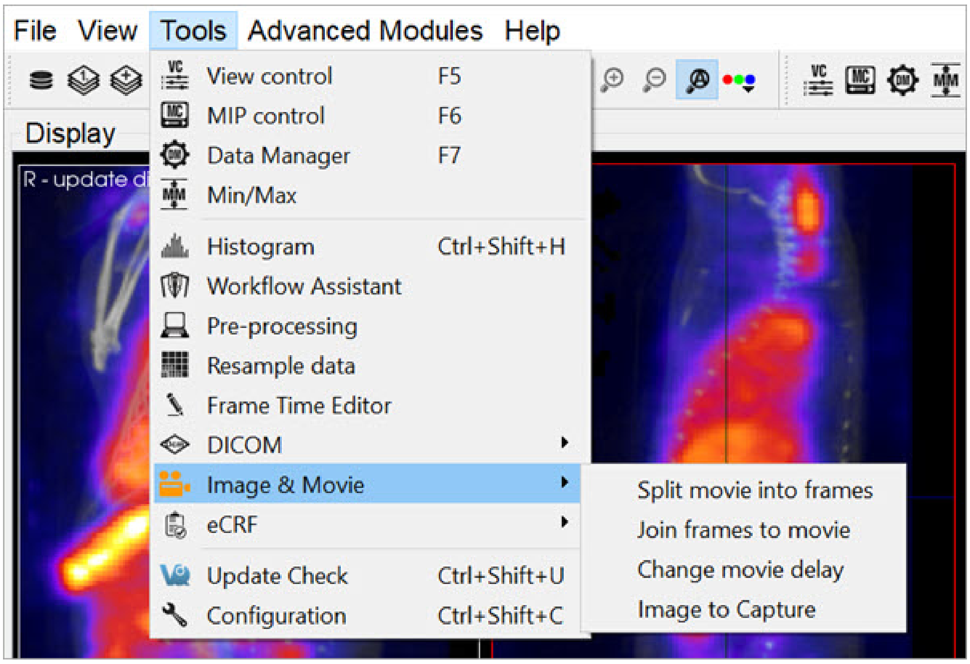


Image Magick

Function

The **Image Magick** options available in **VivoQuant** provide an excellent tool for generating informative movies for dynamic and gated data acquisitions. These tools allow you to combine datasets in meaningful ways to reflect the dynamic nature of the physiological processes taking place.

The **Image Magick** suite provides four options:

- Split Movie into Frames
- Join Frames to Movie
- Change Movie Delay
- Image to Capture

Split Movie Into Frames

This option takes a movie file (options include .gif, .mpg, .mng, and .mpeg) and splits it into individual frames (options include .png, .bmp, .jpeg, .jpg, and .tif).

Join Frames to Movie

This tool allows you to take individual images (options include .png, .bmp, .jpeg, .jpg, and .tif) and combine them into a movie file (options include .gif, .mng, .mpg, and .mpeg).

Change Delay

Depending on the size and style of the movie taken, the default frame time may be too fast or too slow. This tools allows you to select a pre-existing movie and change the frame time (in milliseconds).

Image to Capture

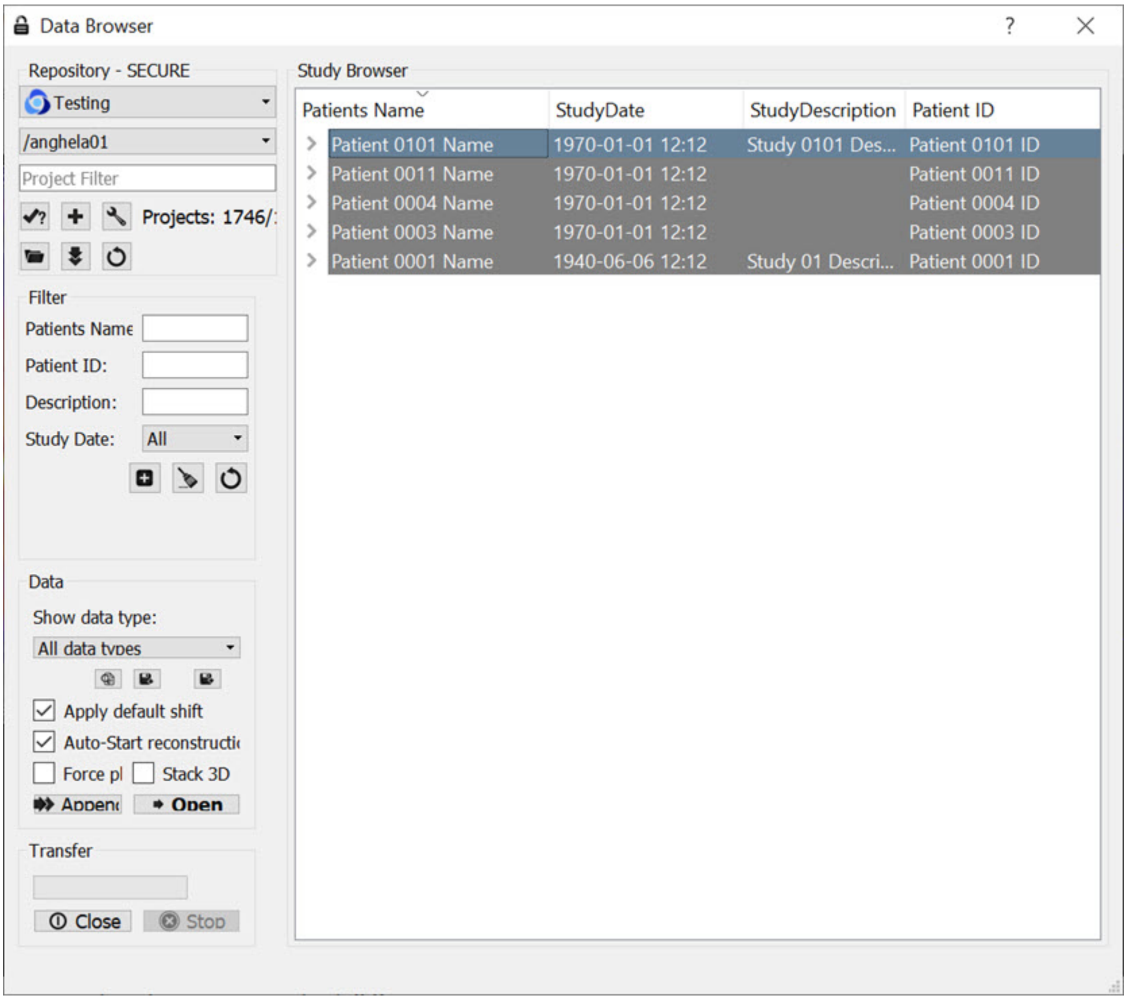
The **Image to Capture** feature allows you to load an image or movie from a file on the local machine, edit it, and then re-save it. The **Capture Viewer** also supports importation of the image/movie into a DICOM/iPACS repository by using the **Save Capture** button.

How to make dynamic movies

Dynamic and cardiac-gated images and movies are useful for illustrating the changing distribution of radioactivity governed by a dynamic physiological process. This guide provides step-by-step instructions on the proper generation of such files. Use the links to visit the **VivoQuant** Manual for more details on any particular feature.

Before using this guide, it is important to understand how to process images so that they are color-comparable across multiple frames. Matching color scales between two images is not enough to ensure that they are directly color-comparable. Instead, it is necessary to ensure that the colors in each loaded correspond to the same physical voxel values. You can achieve this relationship using the **Min/Max** tool to define the range of voxel values spanned across the color bar.

Load all relevant data sets. These data sets may be only SPECT images (as in this example) or a reference CT in addition to multiple SPECT images.



Repository - SECURE: Testing

/anghela01

Projects: 1746/

Study Date: All

Show data type: All data types

☑ Apply default shift

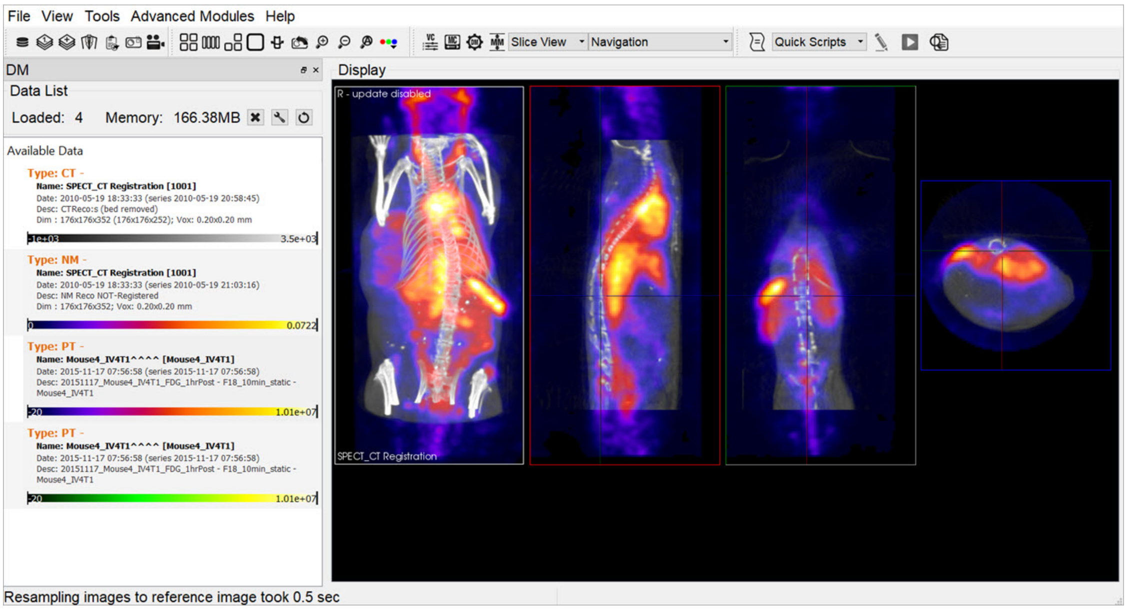
☑ Auto-Start reconstructi

☐ Force pl ☐ Stack 3D

Patients Name	StudyDate	StudyDescription	Patient ID
Patient 0101 Name	1970-01-01 12:12	Study 0101 Des...	Patient 0101 ID
Patient 0011 Name	1970-01-01 12:12		Patient 0011 ID
Patient 0004 Name	1970-01-01 12:12		Patient 0004 ID
Patient 0003 Name	1970-01-01 12:12		Patient 0003 ID
Patient 0001 Name	1940-06-06 12:12	Study 01 Descri...	Patient 0001 ID

Load Relevant Datasets

Adjust the Zoom and Color Palettes to your liking.



Data List

Loaded: 4 Memory: 166.38MB

Available Data

Type: CT -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 20:58:45)
Desc: CTReco:s (bed removed)
Dim : 176x176x352 (176x176x252); Vox: 0.20x0.20 mm
-1e+03 3.5e+03

Type: NM -
Name: SPECT_CT Registration [1001]
Date: 2010-05-19 18:33:33 (series 2010-05-19 21:03:16)
Desc: NM Reco NOT-Registered
Dim : 176x176x352; Vox: 0.20x0.20 mm
0 0.0722

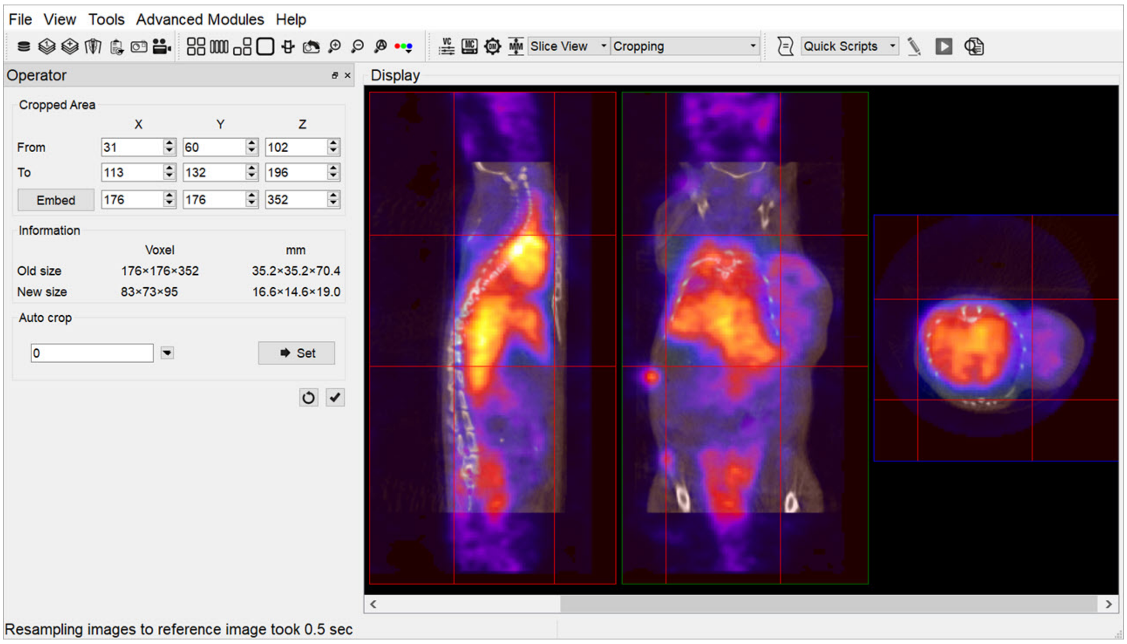
Type: PT -
Name: Mouse4_IV4T1^^^^ [Mouse4_IV4T1]
Date: 2015-11-17 07:56:58 (series 2015-11-17 07:56:58)
Desc: 20151117_Mouse4_IV4T1_FDG_1hrPost - F18_10min_static - Mouse4_IV4T1
-20 1.01e+07

Type: PT -
Name: Mouse4_IV4T1^^^^ [Mouse4_IV4T1]
Date: 2015-11-17 07:56:58 (series 2015-11-17 07:56:58)
Desc: 20151117_Mouse4_IV4T1_FDG_1hrPost - F18_10min_static - Mouse4_IV4T1
-20 1.01e+07

Resampling images to reference image took 0.5 sec

Adjust Zoom and Color

Use the Cropping Tool to select the region of interest.



Cropped Area

	X	Y	Z
From	31	60	102
To	113	132	196
Embed	176	176	352

Information

	Voxel	mm
Old size	176×176×352	35.2×35.2×70.4
New size	83×73×95	16.6×14.6×19.0

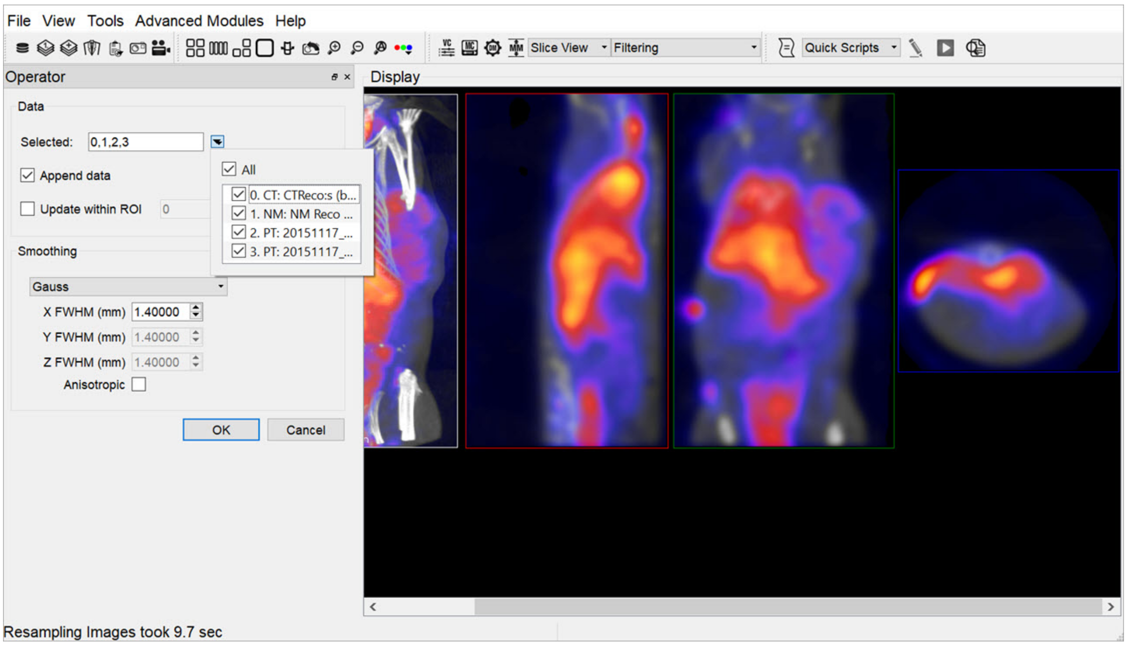
Auto crop

0

Resampling images to reference image took 0.5 sec

Cropping

If desired, use the Filtering Operator. Note that if you check Input 3 and higher in the **Select** pull-down menu of the **Filtering** operator, then smoothing will be applied to loaded data sets not displayed in the Main Window, but visible in the Data Manager.



Selected: 0,1,2,3

☑ Append data

☐ Update within ROI 0

☑ All
☑ 0. CT: CTReco:s (b...
☑ 1. NM: NM Reco ...
☑ 2. PT: 20151117_...
☑ 3. PT: 20151117_...

Gauss

X FWHM (mm) 1.40000

Y FWHM (mm) 1.40000

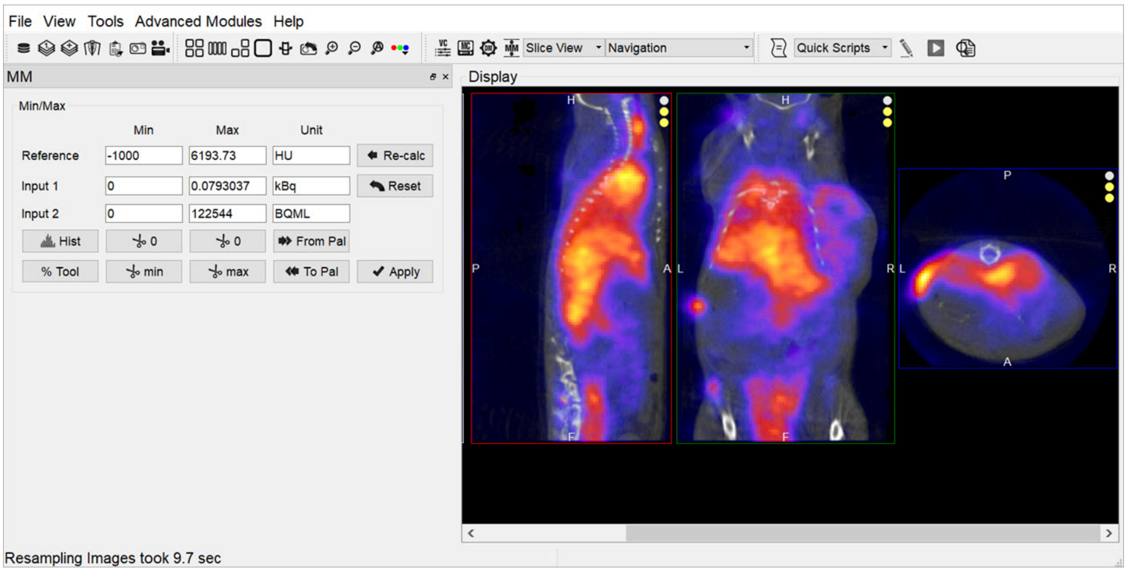
Z FWHM (mm) 1.40000

Anisotropic ☐

Resampling Images took 9.7 sec

Filtering

One of the most critical steps is the application of the Min/Max Tool. First, use the **Re-Calc** button to display the current minimum and maximum values used for color scaling. Choose common **Min/Max** values across all three data sets. Use the **Apply** button to adjust the color scaling accordingly. The three visible data sets are now color-consistent: the same colors represent the same voxel values across each data set.

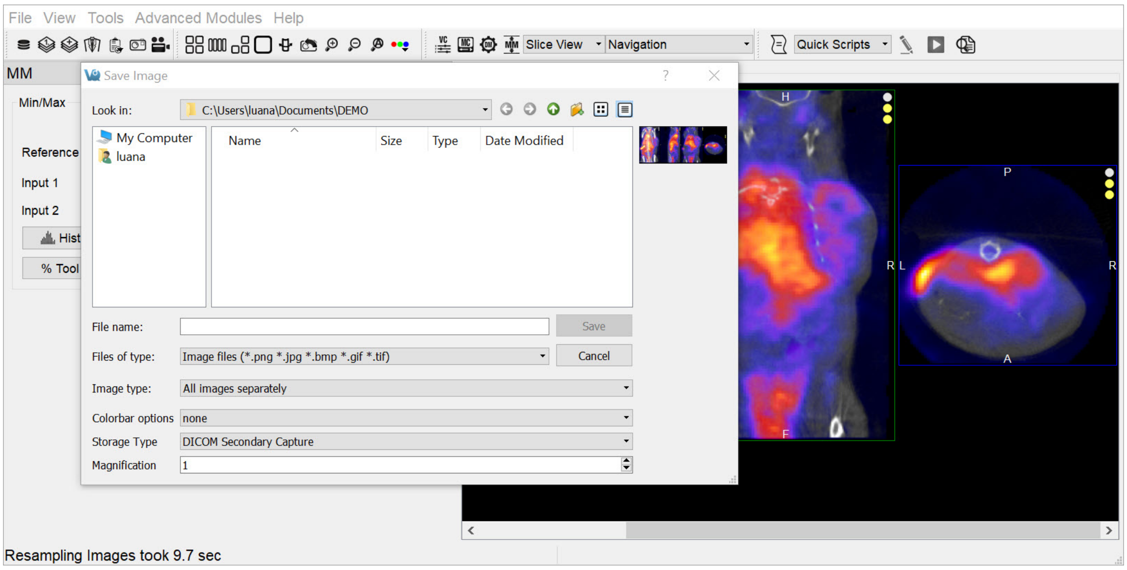


	Min	Max	Unit
Reference	-1000	6193.73	HU
Input 1	0	0.0793037	kBq
Input 2	0	122544	BQML

Resampling Images took 9.7 sec

Min/Max Tool

Save images for each data set using the Save Image option. The **All s separately** option in the **Storage Type** pull-down automatically saves five images (sagittal, coronal, transverse, MIP, all-in-one) simultaneously.



Look in: C:\Users\luana\Documents\DEMO

File name:

Files of type: Image files (*.png *.jpg *.bmp *.gif *.tif)

Image type: All images separately

Colorbar options: none

Storage Type: DICOM Secondary Capture

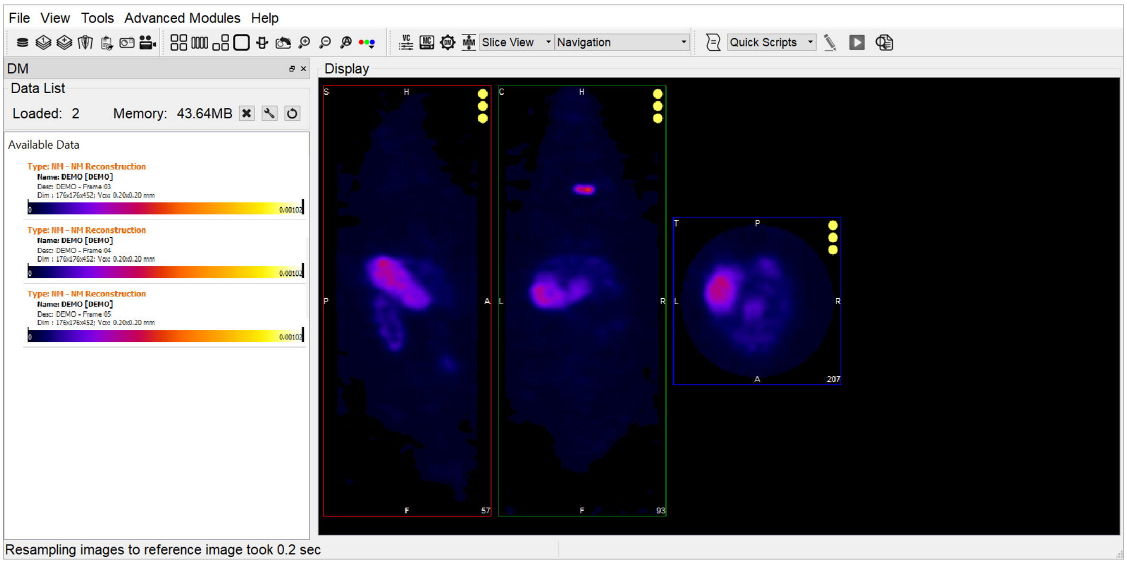
Magnification: 1

Resampling Images took 9.7 sec

All Images Separately

Use the **Slice Control** or appropriate Keyboard Shortcuts to toggle between visible data sets and save the appropriate images.

After collecting the images for the first three frames, use the **Data Manager** to save these processed frames (if desired) and then unload these data sets so that the next three frames in the queue become visible data sets. All operations (such as Cropping, Projection, and Smoothing) applied to the original three data sets are also been applied to the queued data sets, with the exception of the **Min/Max** tool.



Data List

Loaded: 2 Memory: 43.64MB

Available Data

Type: NM - NM Reconstruction
Name: DEMO [DEMO]
Desc: DEMO - Frame 03
Dim : 176x176x452; Vox: 0.20x0.20 mm

Type: NM - NM Reconstruction
Name: DEMO [DEMO]
Desc: DEMO - Frame 04
Dim : 176x176x452; Vox: 0.20x0.20 mm

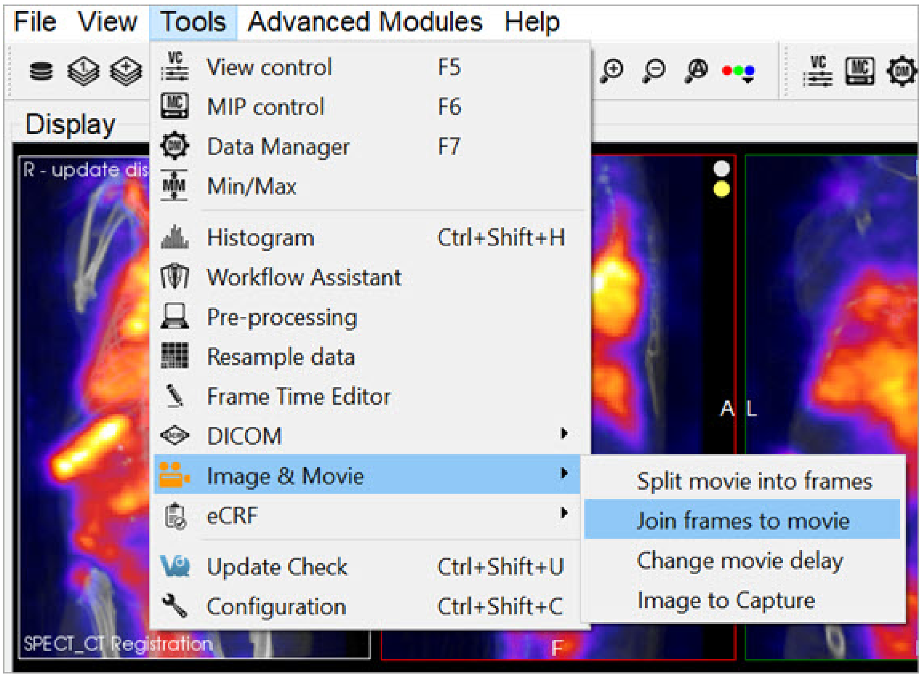
Type: NM - NM Reconstruction
Name: DEMO [DEMO]
Desc: DEMO - Frame 05
Dim : 176x176x452; Vox: 0.20x0.20 mm

Resampling images to reference image took 0.2 sec

Slice Control

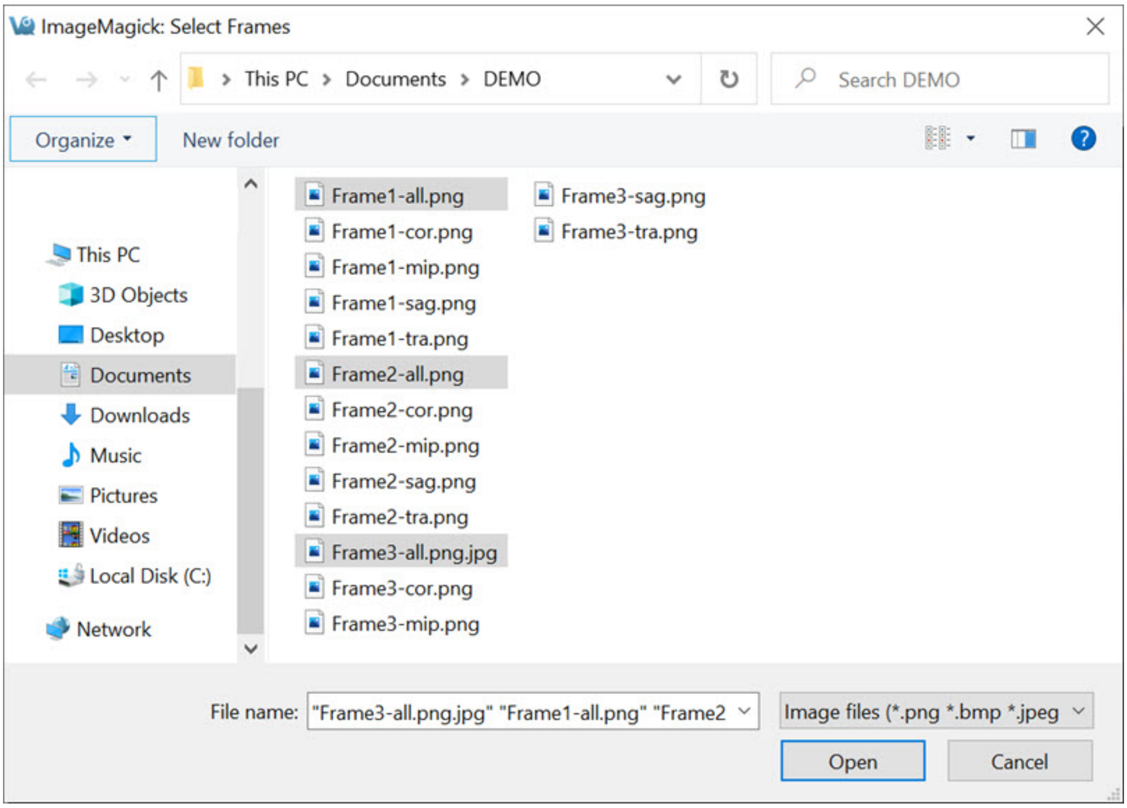
Ensure again that the minimum and maximum values are consistent across datasets, so that the newly loaded data sets are properly prepared. Save the images and data as described above.

After saving all desired images, generate the dynamic movie using the Join Frames to Movie option.



Join Frames to Movie

Select the images you wish to include in the movie.



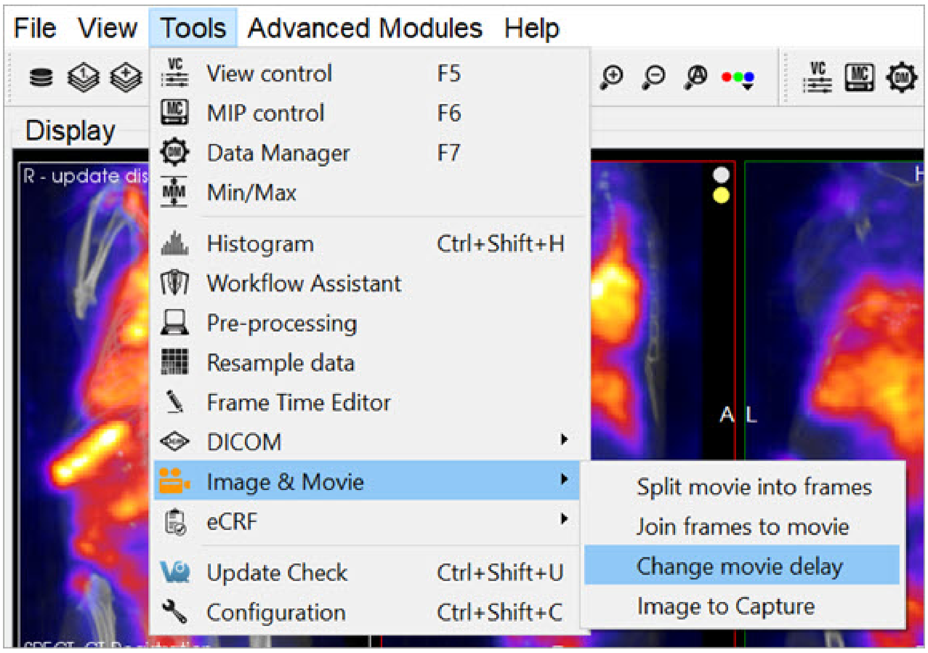
File name: "Frame3-all.png.jpg" "Frame1-all.png" "Frame2

Image files (*.png *.bmp *.jpeg

Select s

Type in a name and choose a format type for the movie file. The default file format is .gif.

Finally, use the Change Movie Delay option to speed up or slow down the movie frame rate.



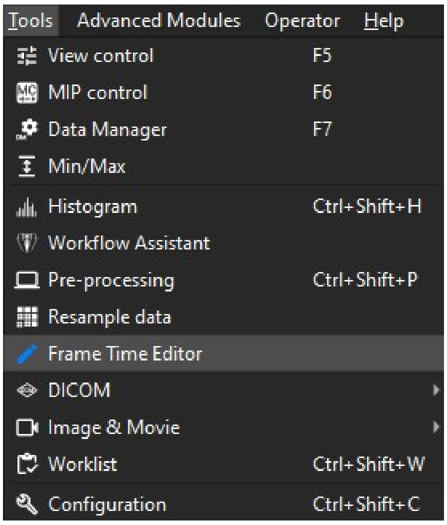
Change Movie Delay

Frame Time Editor

The **Frame Time Editor** tool allows you to change the frame duration in the DICOM Header

Getting There

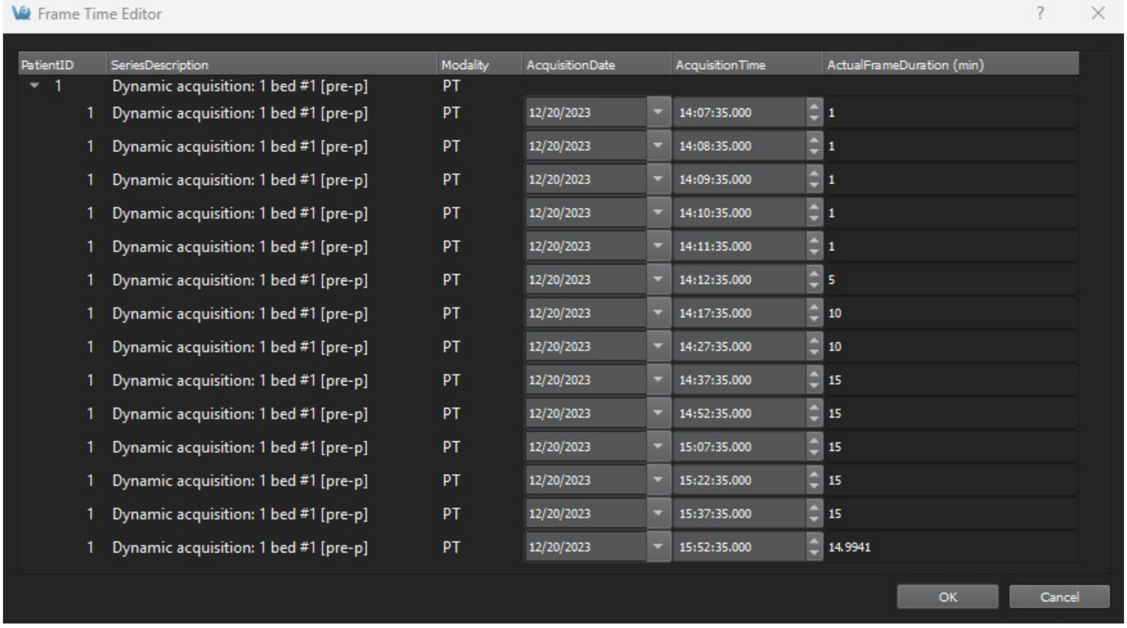
The **Frame Time Editor** is available via the **Tools** menu.



Frame Time Editor

Function

Here you can change the **AcquisitionDate**, **AcquisitionTime** and **ActualFrameDuration**.



PatientID	SeriesDescription	Modality	AcquisitionDate	AcquisitionTime	ActualFrameDuration (min)
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT			
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	14:07:35.000	1
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	14:08:35.000	1
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	14:09:35.000	1
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	14:10:35.000	1
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	14:11:35.000	1
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	14:12:35.000	5
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	14:17:35.000	10
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	14:27:35.000	10
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	14:37:35.000	15
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	14:52:35.000	15
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	15:07:35.000	15
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	15:22:35.000	15
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	15:37:35.000	15
1	Dynamic acquisition: 1 bed #1 [pre-p]	PT	12/20/2023	15:52:35.000	14.9941

Frame Time Editor

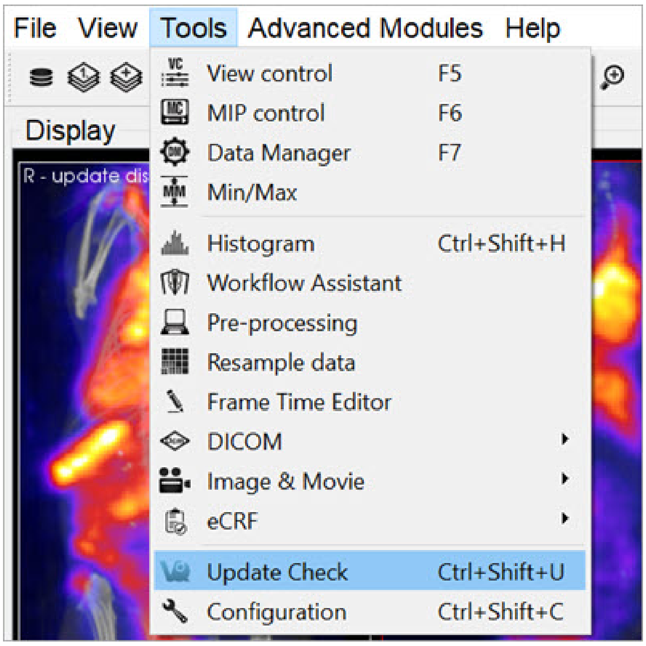
Note: It uses the DICOM tags **FrameAcquisitionDuration** if it's dynamic data; otherwise, it uses **ActualFrameDuration**.

Update Check

VivoQuant is frequently updated to provide more and better tools for all post-processing needs. Therefore, periodic **Update Checks** are recommended to ensure that you have the latest software available.

Getting There

There are two methods to access the **Update Check** function. The first method is through the **Tools** menu.

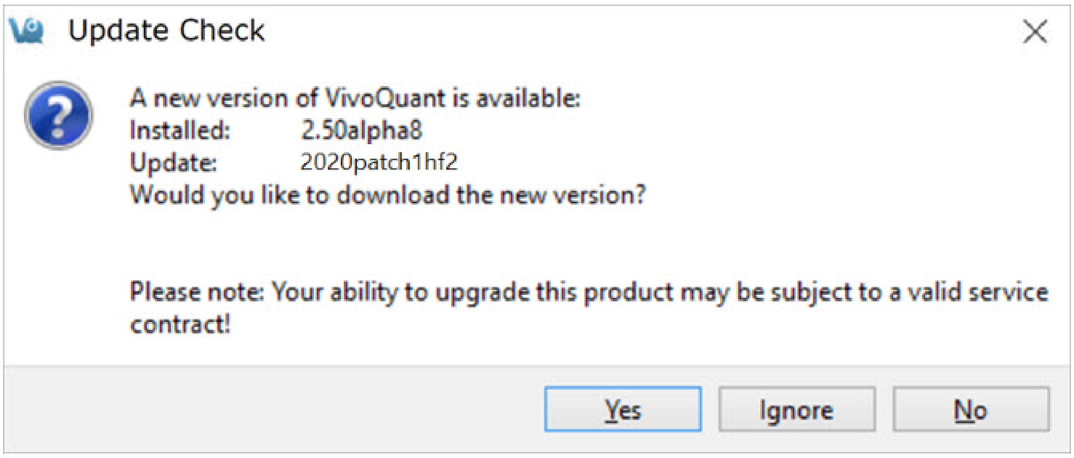


Update Check

The second method is to use the keyboard shortcut Ctrl+Shift+u.

Function

If an update is available, the **Update Check** will present a window providing an option for downloading the new version. You may either choose to download, by clicking on Yes; not to download, by clicking on No; or to ignore entirely, by clicking on Ignore.



A new version of VivoQuant is available:
Installed: 2.50alpha8
Update: 2020patch1hf2
Would you like to download the new version?

Please note: Your ability to upgrade this product may be subject to a valid service contract!

Update Options

If you download the new version, you will be prompted to follow several straightforward installation steps. For more information on installation, see the Installation section of this manual.

Advanced Modules

The **Advanced Modules** Menu contains a wide range of tools available for a variety of post-processing applications.

- Plug-In Modules
    - Multi-Atlas Segmentation Tool
    - 3D Brain Atlas Tool
    - Pharmacokinetic Modeling
- NanoSPECT
    - QuantiCalc
    - Specific Activity Calculator
    - SUV Calculator
    - Crosstalk Removal
    - Biodistribution Visualization
    - Split Projections
- Calibration
    - CT Geometrical Calibration
    - MMP SPECT Calibration
    - Near-Field Uniformity QC
- Dosimetry Calc

Plug-In Modules

VivoQuant™ offers a variety of additional **Plug-in Modules** in addition to the base license. These are accessed through the Advanced Modules Menu.

- Multi-Atlas Segmentation Tool
- 3D Brain Atlas Tool
- Pharmacokinetic Modeling

For more information on the **inviCRO's Advanced Segmentation Tool Kit**, please contact your **inviCRO** representative or email support@invicro.com.

You can also access a helpful **How To** illustrating the main features of the **3D Brain Atlas Tool** by going to **Tools** -> **Workflow Assistant** and selecting the **3D Brain Atlas Analysis Tool** workflow.

Multi-Atlas Segmentation Tool

Overview

The **Multi-Atlas Segmentation Tool** generates ROIs by registering a series of images in a Reference Library to the image that has been loaded in the Data Manager. The **Reference Images** must each have a corresponding ROI. The tool registers the images in the **Reference Library** to the loaded data, and applies the same transformation to the corresponding ROI. The tool then works on a voxel-by-voxel basis, classifying a voxel to the new ROI if a greater percentage of the reference sets classified that voxel as within the ROI than the threshold percentage set by the user. Important factors that influence performance include image contrast, animal positioning consistency, and the size of the reference library.

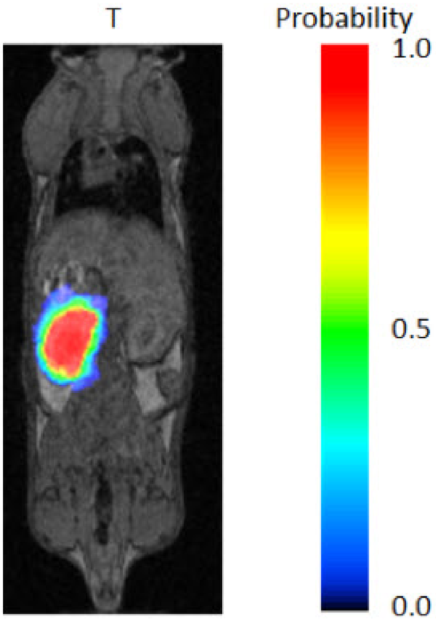
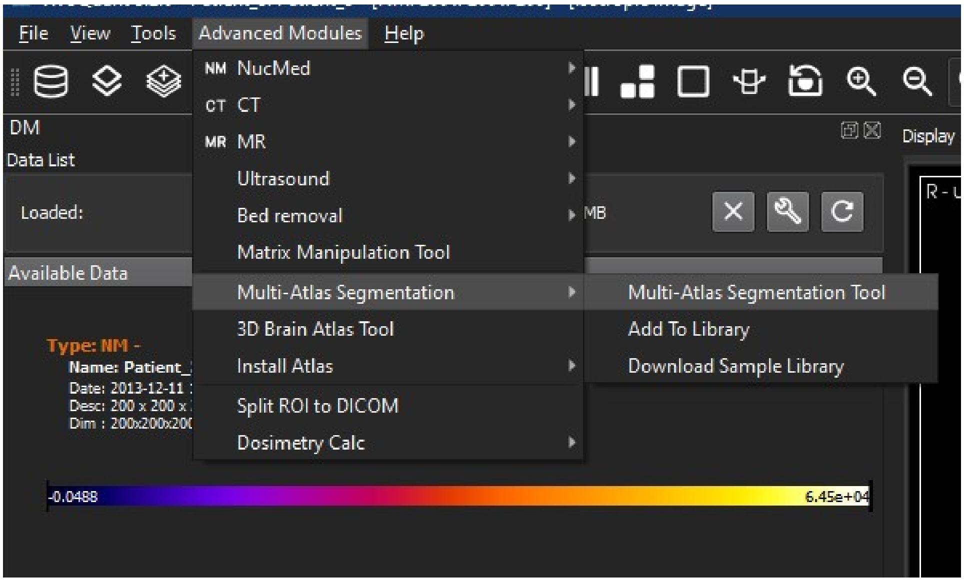


Image ROI

Getting There

You can access the **Multi-Atlas Segmentation Tool** by navigating to **Advanced Modules** -> **Multi-Atlas Segmentation**. Here, there are three options: Multi-Atlas Segmentation, Add to Library, and Download Sample Library.



Multi-Atlas Segmentation

Adding to Reference Library

The **Reference Library** is the basis of the efficacy of the **Multi-Atlas Segmentation Tool**. The **Reference Library** is stored locally, and is built in one data set at a time.

The first step in adding a data set to the **Reference Library** is to open the data and ROI. In order to add to the **Library**, there must be an active ROI in the **3D ROI Tool**. There can be multiple ROIs, but it is important, when building the **Reference Library**, to keep the naming of ROIs consistent; that is, if the organ of interest is the left kidney, always call it exactly Left Kidney, otherwise, it will not be recognized as all the same organ (however, capitalization does not have an effect).

With the data and ROI loaded simply navigate to and click **Add to Library** as described above. The GUI will appear.

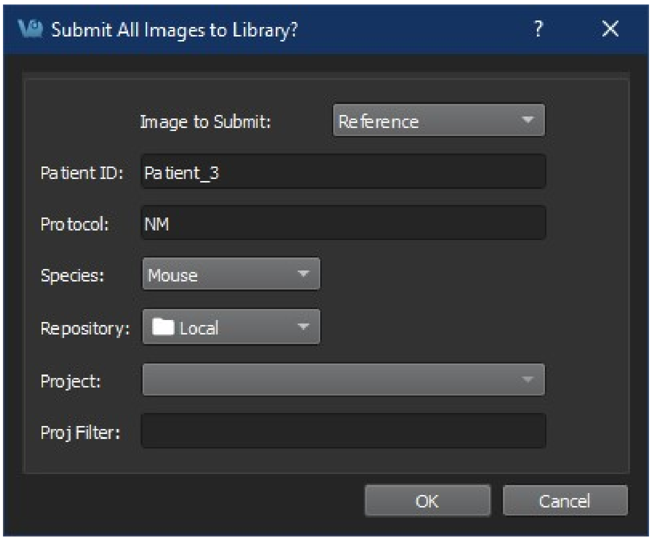

Submit All Images to Library?

Image to Submit: Reference
Patient ID: Patient_3
Protocol: NM
Species: Mouse
Repository: Local
Project:
Proj Filter:

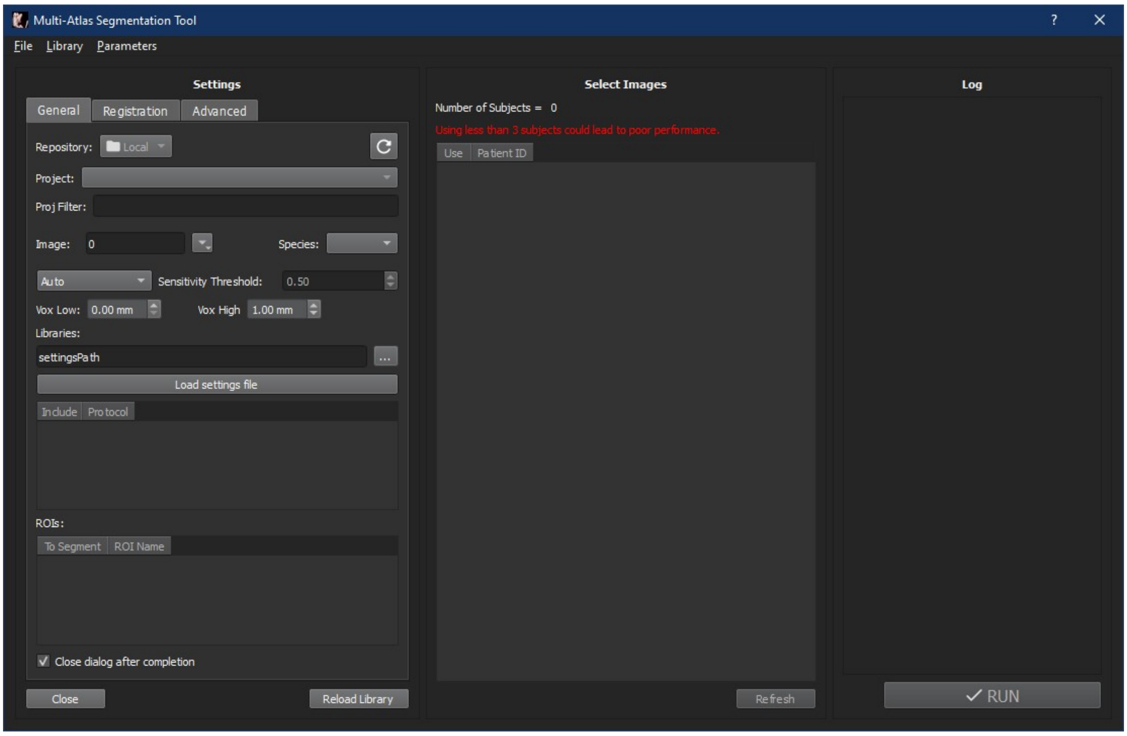
Add Reference to Library

The GUI offers four editable fields:

Image to Submit	This option allows you to select which of the loaded images to submit to the Reference Library.
Patient ID	The Patient ID can be anything that is unique and will help you identify this data set when selecting which scans to use from your Reference Library.
Protocol	The Protocol should include information as to how the image was acquired, the field of view, modality, etc. This will be used as a filter to determine which scans from the Reference Library will be used by the tool.
Species	The Species dropdown list contains frequently imaged species. If you wish to have additions made to the options provided please contact your Account Manager or support@invicro.com.

Segmenting With The Tool

With the image on which the new ROI is to be drawn loaded in the Data Manager, open the **Multi-Atlas Segmentation Tool**. You can apply the segmentation settings and perform other tasks from the tool's GUI.



Repository: Local

Project:

Proj Filter:

Image: 0

Species:

Auto

Sensitivity Threshold: 0.50

Vox Low: 0.00 mm

Vox High 1.00 mm

Libraries: settingsPath

☑ Close dialog after completion

Number of Subjects = 0

Using less than 3 subjects could lead to poor performance.

Segmentation Tool

Settings

The tool relies on the settings you select. There are two levels of settings, the **Basic Settings**, explained below, and the **Advanced Settings**, which should not need to be modified.

Basic Settings

The **Basic Settings** tab contains most of the settings that will need to be changed. Here, you can select the appropriate **Reference Images**, the appropriate **Test Image**, **ROIs** to segment, and **Probability Threshold** to use.

ℹ **Note:** To reload the settings from a previous run, click Load settings file and browse to the output path to find the generated settings.txt file.

Reference List Selection

Selecting the proper **Reference** scan is imperative to the proper functionality of the tool. The settings you select that factor into the images used are outlined in the table below:

Image	The image in the Data Manager that will be the basis of the ROIs generated.
Species	The species of the animal being segmented. This is based on the available options in the Reference Library.
Voxel Size	The Low and High parameters for the voxel size of the **Reference Images** available. The default low is 0.00mm and the default high is the voxel size of the data loaded. Using **Reference Data** with a lower resolution than the data that has been loaded will compromise the quality of the Reference ROI.
Protocols	A list displaying the protocols present in the **Reference Library**. Changing the protocols included will narrow the **Reference List**. Only include **Reference Images** with the same protocol as the image loaded in the Data Manager.
ROIs	A list displaying the possible ROIs to generate based on those present in the **Reference Library**. Only those selected will be generated by the Tool.

Other Basic Settings

You can also edit the **Probability Threshold**. Following the registration of each **Reference Image** to the image in the **Data Manager**, each voxel is assigned a probability that it belongs in the ROI. Only voxels with a probability greater than the threshold you set will be mapped to the ROI. The default for this setting is 0.5; and, typically, the ROI will become larger as the threshold is lowered.

Select Images

The middle pane of the GUI allows you to select which images to use for the final **Reference List**. These should already have been narrowed down by your previous selections in the **Settings** pane. It is up to you how many **Reference Images** to use. However, the time the tool takes to run is largely influenced by how many **Reference Images** are selected.

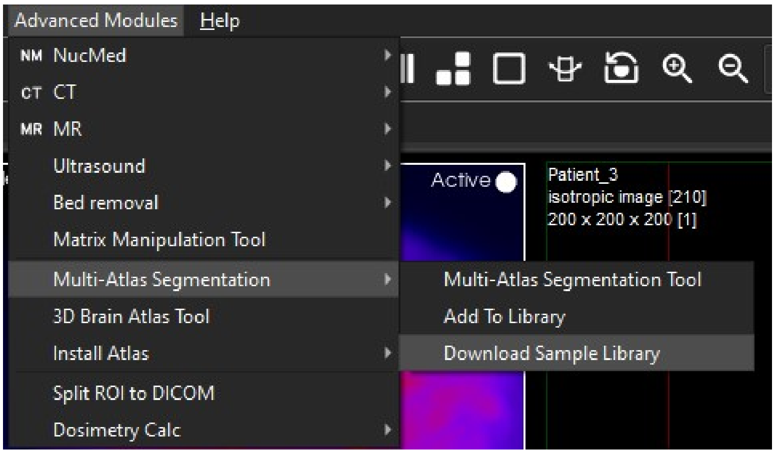
Run Tool and View Log

Once the **Settings** and the **Reference Images** have been selected, click **Run** in the lower right corner of the GUI to run the tool. The **Log** outlines the steps taken by the tool. At its completion, the tool remains open, but **VivoQuant** navigates to the **3D ROI Tool**, where the new ROIs can be viewed and modified.

ℹ **Note:** Uncheck the option Close dialog after completion to keep the tool open in order to inspect the log.

Downloading Sample Library

A sample **Reference Library** is available depending on the **VivoQuant** license. This option is used for testing and learning how to operate the tool. To download it, navigate to **Advanced Modules->Multi-Atlas Segmentation->Download Sample Library**.



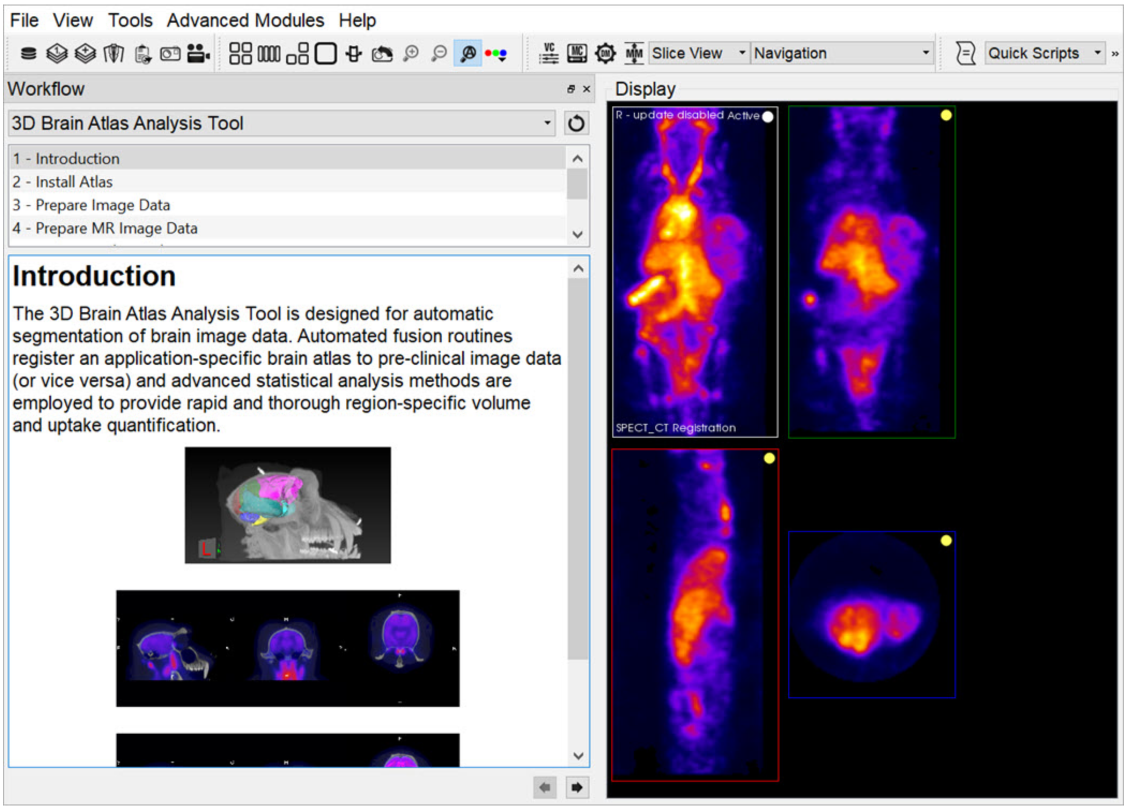
Download Sample Library

3D Brain Atlas Tool

Overview

Use the **3D Brain Atlas Tool** to perform brain region analysis. The tool can handle **CT** or **MR** data as the input and **MR**, **PET**, or **SPECT** for the input functional data.

Instructions for the use of the tool are available through the **Workflow Assistant**, which can be accessed via the **Tools** menu.



Introduction

The 3D Brain Atlas Analysis Tool is designed for automatic segmentation of brain image data. Automated fusion routines register an application-specific brain atlas to pre-clinical image data (or vice versa) and advanced statistical analysis methods are employed to provide rapid and thorough region-specific volume and uptake quantification.

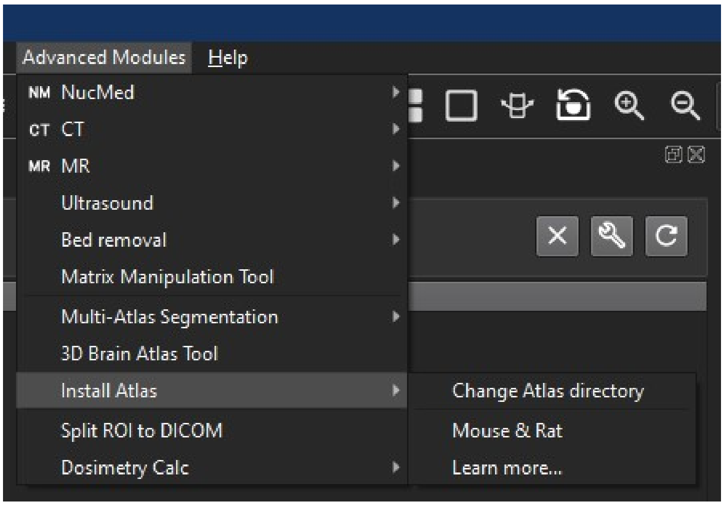
Workflow Assistant

❗ **Warning:** Please use caution when scaling data in this tool, as this can lead to errors in quantitation. For more information, refer to the Treatment of Quantitative Data page.

The brain atlas path location

The brain atlas path can be set via the Advanced Modules > Install Atlas > Change Atlas directory option. Typically the default path is located next to the VivoQuant cache:

Platform	Default path
macOS	~/Library/VivoQuant/atlas
Ubuntu	~/.VivoQuant/atlas
Windows	%appdata%/inviCRO/VivoQuant/atlas



Customizing the atlas path

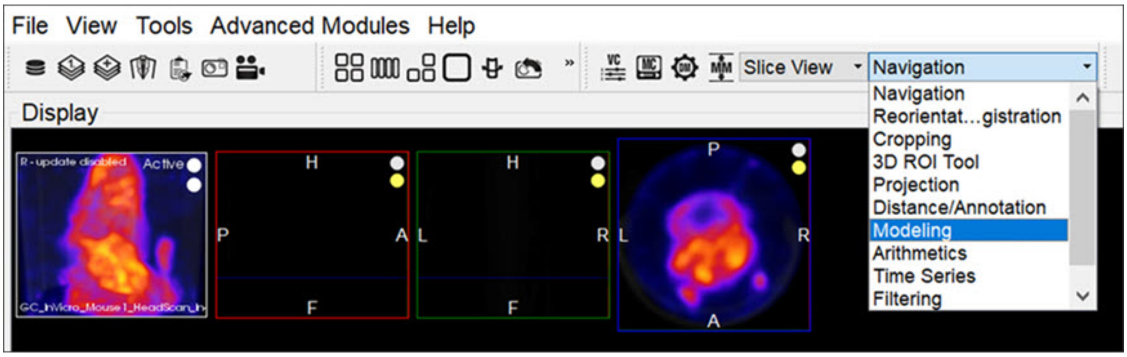
ℹ **Note:** Users can also download a sample Mouse and Rat atlas from this menu.

Pharmacokinetic Modeling

> Pharmacokinetic modeling is available in **VivoQuant** as a plug-in for the **Modeling** operator. Access to the plug-in depends on your **VivoQuant** license. For information on your license, please contact your account manager or email support@invicro.com

Getting There

The **Modeling** operator can be accessed via the tool pull-down menu on **VivoQuant's** front panel.



Modeling Operator

Function

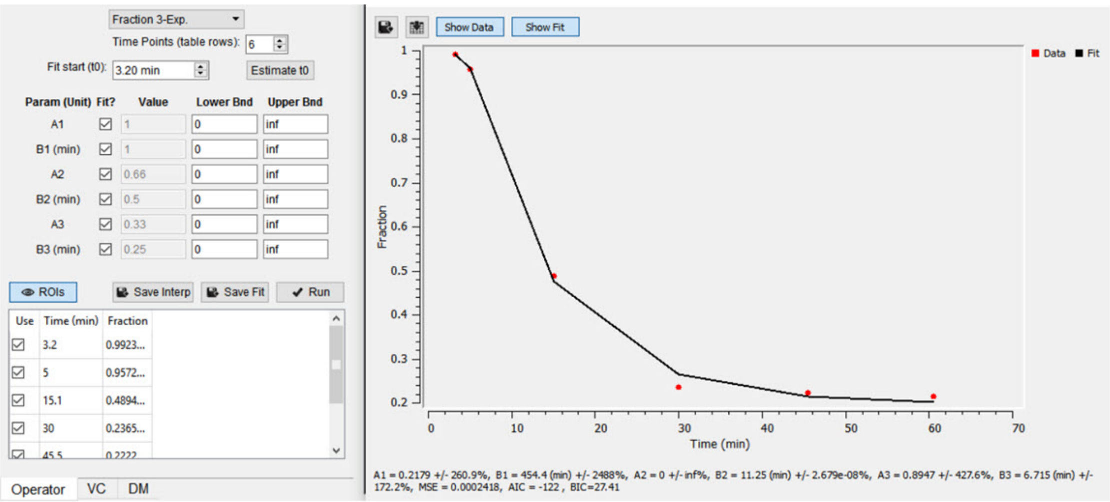
For more on the function of the Modeling operator, see the Modeling operator page.

Input/Reference Function

Every tissue model requires the input of an additional temporal curve, either as an arterial input function or concentration of a reference tissue. These temporal data may be derived from image data directly or from acquired samples. The operator supports input and computation of parent fraction samples, plasma fraction samples, whole blood concentration, and plasma concentration. In addition, these data can be stored and retrieved from disk and from an iPACS.

Parent/Plasma Fraction

The experimentalist may have acquired blood samples throughout the subject's scanning session. From these samples, the ratio of unmetabolized tracer to the sum of unmetabolized tracer and its derivative metabolites can be measured and used to account for the dynamic nature of *available* tracer. This is also known as the *parent fraction* or *plasma free fraction*. Without it, the tissue model must assume that metabolism of the tracer is negligible. Whether measured, simulated, or estimated, the parent fraction can play an important role in accurate estimation of tissue kinetics downstream. Similarly, the fraction of plasma to whole blood (including red blood cells) has been shown to be an important factor in the estimation of an appropriate arterial input function [1]. The fraction modeling can be selected from the dropdown of models or from the **Operator** menu.



Time Points (table rows): 6

Fit start (t0): 3.20 min

Param (Unit)	Fit?	Value	Lower Bnd	Upper Bnd
A1	☑	1	0	inf
B1 (min)	☑	1	0	inf
A2	☑	0.66	0	inf
B2 (min)	☑	0.5	0	inf
A3	☑	0.33	0	inf
B3 (min)	☑	0.25	0	inf

Use	Time (min)	Fraction
☑	3.2	0.9923...
☑	5	0.9572...
☑	15.1	0.4894...
☑	30	0.2365...
☑	45.5	0.2222

A1 = 0.2179 +/- 260.9%, B1 = 454.4 (min) +/- 2488%, A2 = 0 +/- inf%, B2 = 11.25 (min) +/- 2.679e-08%, A3 = 0.8947 +/- 427.6%, B3 = 6.715 (min) +/- 172.2%, MSE = 0.0002418, AIC = -122 , BIC=27.41

Fraction Modeling

Both plasma and parent fraction data can be input using the same tool. Towards the bottom of the operator, space is provided for a table of fraction data. There are 3 columns. The first one can be used to exclude specific time points from the table. The second column contains the time of each sample in units of minutes. The last column contains *free fraction* values, assumed to have a value between zero and one. Users can choose to use a linear interpolation of the points or fit a sum of exponentials to the provided points. The **Save Interp** button can be used to save the points as is, at which point the tool will prompt the user for a name to give the saved curve. If this option is chosen, the operator will prepend a value to time=zero, assuming that the fraction is equal to one at that time. After the last provided time point, the value is assumed to remain constant equal to the last fraction value.

Users may want to *smooth* the fraction points with a sum of exponentials. Up to 3 exponentials can be used to fit the curve. If less exponentials are desired, users can fix model parameters for one or more of the exponentials (i.e. fix A3=0 and B3=0) [2]. To do so, use the **Run** button to estimate model parameters under the input conditions provided by the user.

⚠ **Important:** Use the Estimate t_0 button to estimate the start point for the model.

Once you are satisfied with the model estimates, click on **Save Fit** while the estimate plots are open to save the current model-estimated fraction curve to the list.

$$f(t, A_1, B_1, A_2, B_2, A_3, B_3) = A_1 e^{-B_1 t} + A_2 e^{-B_2 t} + A_3 e^{-B_3 t}$$

$$\text{Where:}$$

$$f(t < t_0) = \min(1, 1 + \frac{f_0 - 1}{t_0} t)$$

$$f(t \geq t_0) = \text{full model}$$

Model Assumptions

This model makes the following assumptions:

- The exponential decay begins at user-provided t0
- Provided fraction measurements lie between zero and one

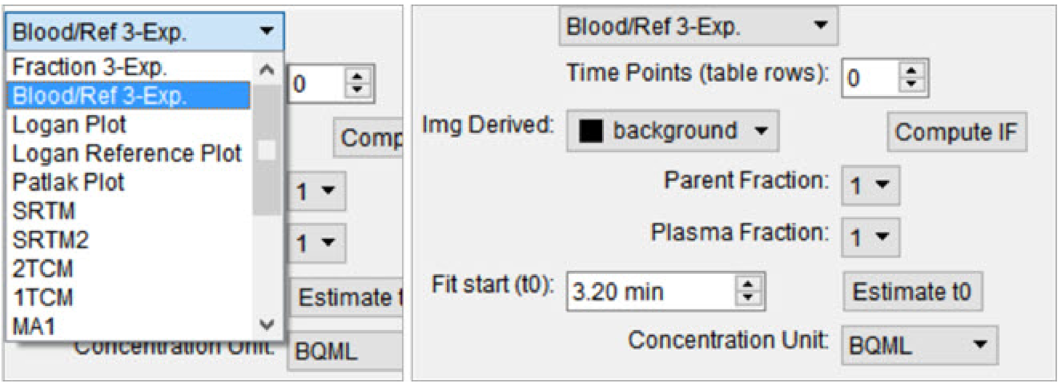
References

[1] “Red blood cells: a neglected compartment in pharmacokinetics and pharmacodynamics”. *Hinderling. Pharmacol Rev, 1997*. Link .

[2] “Optimal Metabolite Curve Fitting for Kinetic Modeling of 11C-WAY-100635”. *Wu, et al. JNM, 2007*. Link .

Arterial Input Function

An **Arterial Input Function** (**AIF**) is required for Logan, Patlak, 1- and 2-tissue compartment, and MA1 analysis. To add time points to an **AIF**, begin by selecting Blood/Ref 3-Exp from the list of models.



Blood/Ref 3-Exp.
Time Points (table rows): 0
Img Derived: background
Parent Fraction: 1
Plasma Fraction: 1
Fit start (t0): 3.20 min
Concentration Unit: BQML

Arterial Input Function

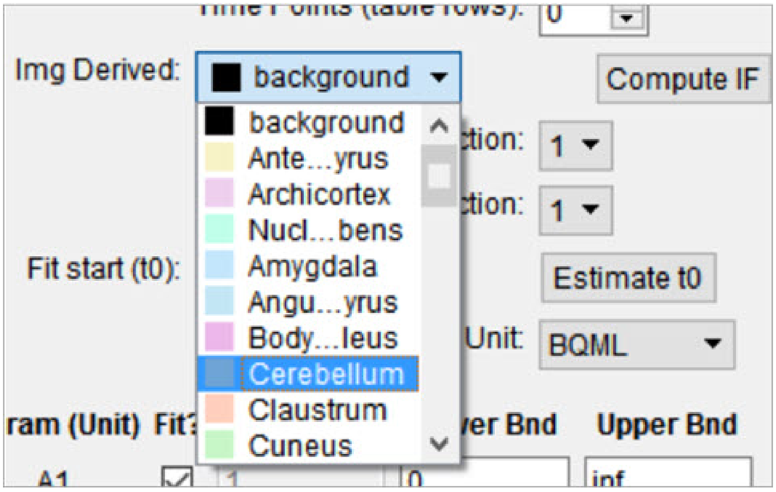
Similar to the parent fraction, users can select to save a linear interpolation of points or a smooth model estimate of **AIF** samples. Either way, samples should be input into the table of values as a first step. This may be done with a copy/paste from an external spreadsheet program or by incrementing the **Time Points** (table rows) number and manually editing the table. The table assumes a structure with the number of rows equal to the number of samples. Each sample has three columns. The first column indicates whether that sample should be excluded or not. The second column contains the time (in minutes) at which sample was measured. Times should be consistently relative to the same reference start time as the final modeled time activity curves. The third column contains the measured concentration value at that time. If parent or plasma fraction data are available and applicable to the provided samples, select them from the dropdown. If none is selected, the fraction is assumed to be one for the entirety of the time activity curve. If image derived samples are desired, the user may also compute the samples directly from the average concentration values with ROIs in the loaded image. To do this, select the appropriate region from the dropdown and click on the *Compute IF* button. For more information on segmenting regions of interest from an image, see the 3D ROI tool.

⚠ **Important:** Select a unit of concentration for the samples. By default, this dropdown will be set to the unit of the loaded image data.

If a sum of exponentials model for the samples is desired for *smoothing* the data, click on **Run** to estimate exponential parameters for the data. Before doing so, it may be important to select an appropriate t_0 value. This is best estimated from the samples themselves with the **Estimate t_0**, which will set t_0 to the time point where the maximum concentration occurs in the samples. The linearly interpolated samples or model fit may be saved for use in tissue modeling with the **Save Interp** or **Save Fit** buttons, respectively.

Reference Tissue Compartment

The reference tissue compartment concentrations can be readily computed similar to the **Arterial Input Function** (**AIF**). Like the **AIF**, you may input the concentrations from a spreadsheet or by manual input; however, it is more likely you will want to derive the concentration values from a reference region segmented on the loaded images. For more information on segmentation techniques in **VivoQuant**, see the 3D ROI Tool page. Begin by navigating to the Blood/Ref 3-Exp. model in the operator. Next, select the appropriate region of interest in the **Img Derived** dropdown.

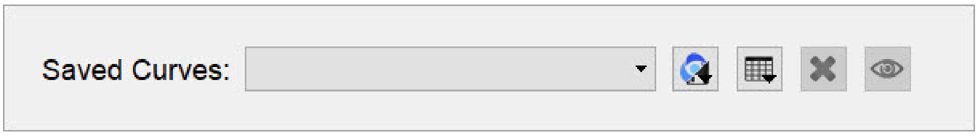


Reference Tissue Compartment

The **Compute IF** button will compute the average concentration in the selected region and populate the table, one row for each volume loaded. The time points are computed from the image acquisition times and frame durations, set to the midpoint of each frame, and relative to the start of the dynamic scan. Should the temporal information be missing from the image data, this can be added using the **Frame Time Editor**, found in the **Tools** menu. A sum of exponentials model can also be estimated from the table data. Ensure that the parent/plasma fraction inputs are disabled by setting their respective dropdown setting to 1. To save a linear interpolation of the concentrations, click on the **Save Interp** button. Should you want to fit a sum of exponentials, begin by specifying an appropriate t_0 parameter, which can typically be estimated using the **Estimate t_0** button. Fitting the sum of exponentials model can be done with the **Run** button, at which point you will be able to save the fit using the **Save Fit** button.

Saving and Loading of Fraction, AIF, and Reference Region Data

All temporal curves can be saved with the **Save Interp** or **Save Fit** buttons. When they are saved, their user-provided name appears in the dropdown of **Saved Curves**.



Saved Curves

Controls next to the dropdown are available for saving, loading, and viewing the curves. The 🌐 menu provides options for storing the temporal data to/from the iPACS or as a spreadsheet on your local hard drive. This is particularly useful to avoid re-entry of the information should you want to re-run analysis at a later date. The ▦ menu is an additional tool for the user to store the current linearly interpolated samples or modeled data into the list of saved curves. The ✖ button clears the currently selected temporal curve from the list. Lastly, the 👁 button opens a new dialog window showing a plot of the temporal curve which can be saved as a local image for quality control.

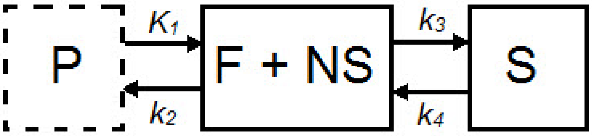
Additional Resources

- “Emission Tomography: The Fundamentals of PET and SPECT”, *Miles Wernick & John Aarsvold. Elsevier, 2004.* Print.
- “Fractions of unchanged tracer in plasma”, *Vesa Oikonen. Turku PET Center website.* Link
- “Converting blood TAC to plasma TAC”, *Vesa Oikonen. Turku PET Center website.* Link
- “Blood sampling in PET studies”, *Vesa Oikonen. Turku PET Center website.* Link
- “Arterial input function from PET image”, *Vesa Oikonen. Turku PET Center website*. Link

Models

Two-Tissue Compartment Model (2TCM)

The 2TCM is a three-compartment model that includes two tissue compartments: one tissue compartment represents free and nonspecifically bound tracer within the tissue (referred to as *nondisplaceable*), and the other tissue compartment represents specifically bound tracer within the tissue. The third compartment represents tracer within the arterial plasma.



Parameter	Description
$C_{ND}(t)$	Concentration in F + NS compartment, nodisplaceable tracer.
$C_S(t)$	Concentration in specifically bound (S) compartment.
$C_p(t)$	Concentration in plasma (P) compartment.
K_1(mL*cm^3*min^{-1})	Transfer of ligand from arterial plasma to tissue.
k_2 (min^{-1})	Transfer of ligand from tissue to arterial plasma.
k_3(min^{-1})	Transfer of ligand into specifically bound compartment.
k_4 (min^{-1})	Transfer of ligand out of specifically bound compartment.

For those tracers for which a compartmental model is appropriate, estimation of the rate constants provides valuable information about tracer uptake and binding [1]. Due to the difficulty of reliably estimating all four parameters of the **2TCM**, lumped or macroparameters are often employed. Macroparameters are rate constants which are functions of individual microparameters (e.g. K_1, k_2, k_3 and k_4). One such macroparameter that is estimated by the **2TCM** is the total volume of distribution, V_T.

When the **2TCM** is applied to image data with a reference region, the distribution volume ratio (DVR) can be calculated: DVR = V_T/V_{ND}, where V_{ND} is the estimated distribution volume in a region that is devoid of the target site or receptor (often called the reference region or nondisplaceable region). Binding potential (BP_{ND}) can then be calculated by BP_{ND} = DVR - 1.

Model Assumptions

This model makes the following assumptions:

- The tracer binds reversibly.
- Nonspecifically bound ligand equilibrates rapidly with free tissue ligand.
- Compartmental model assumptions:
    - The tracer kinetics or behavior can be represented by a compartmental model.
    - Tracer concentration within each compartment is well-mixed and does not vary spatially.
    - First-order kinetics can describe exchange of ligand between compartments.

ℹ **Note:** Violation of any of these assumptions may produce biased parameter estimates. While the model will still run in **VivoQuant**, the estimated parameters may not accurately reflect the true tracer kinetics.

The **2TCM** is currently implemented in **VivoQuant** using a basis function method approach [2] and unweighted fitting in this basis function method,

$$\alpha_{1,2} = \frac{(k_2 + k_3 + k_4) \mp \sqrt{(k_2 + k_3 k_4)^2 - 4k_2 k_4}}{2}$$

Required Inputs

This model requires the following inputs:

- Metabolite-corrected arterial plasma input curve.
- ROI(s) or voxels.

Outputs

Region-level analysis:

- Plot of data from each ROI with 2TCM fit.
- V_T, K_1, k_2, k_3, k_4, mean-squared error (MSE) of fit, Θ_1, and Θ_2 are shown when the cursor is hovered over the model fit plot.
- V_T, K_1, k_2, k_3, k_4, mean-squared error (MSE), data and **2TCM** fit for each ROI can be saved out to .csv

References

[1] “A quantitative model for the in vivo assessment of drug binding sites with positron emission tomography”. *Mintun, et al. Ann Neurol, 1984.* Link .

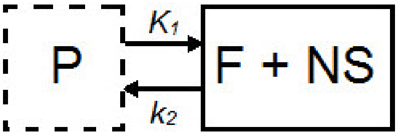
[2] “Kinetic modelling using basis functions derived from two-tissue compartmental models with a plasma input function: general principle and application to [18F]fluorodeoxyglucose positron emission tomography”. *Hong, et al. NeuroImage, 2010.* Link .

Additional Resources

“Compartmental Models”, *Vesa Oikonen. Turku PET Center website.* Link .

One-Tissue Compartment Model (1TCM)

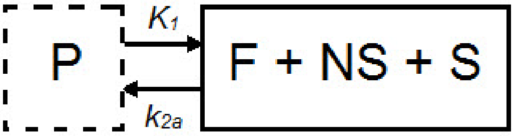
The **1TCM** is a two-compartment model that includes one compartment representing tracer within the tissue (free and nonspecifically bound tracer which together are referred to as *nondisplaceable* tracer) and one compartment representing tracer within the arterial plasma [1].



Parameter	Description
$C_{ND}(t)$	Concentration in F + NS compartment, nondisplaceable tracer.
$C_p(t)$	Concentration in plasma (P) compartment.
K_1 (mL*cm^3*min^{-1})	Transfer of ligand from arterial plasma to tissue.
k_2 (min^{-1})	Transfer of ligand from tissue to arterial plasma.
$V_T = K_1/k_2$	Total volume of distribution.

For tracers for which a compartmental model is appropriate, estimation of the rate constants provides valuable information about tracer uptake [2]. The **1TCM** is generally easier and less computationally intensive to solve than the **2TCM**, because it is a simpler model and has fewer parameters. Additionally, the **1TCM** model parameters can generally be estimated with better identifiability than the **2TCM** model parameters.

In some cases, the exchange of tracer between the nondisplaceable and bound tissue is sufficiently fast, so the two cannot be distinguished kinetically. In these cases, the nondisplaceable and bound tissue compartments may be collapsed into one compartment that represents both the nondisplaceable and specifically bound tracer within the tissue [3]. In these cases, apparent transfer of ligand from tissue to arterial plasma is represented by the parameter k_{2a} and $V_T = K_1/k_{2a}$.



When a tracer that specifically binds to a target can be represented by a **1TCM** as above, and has a reference region the distribution volume ratio (*DVR*) can be calculated: $DVR = V_T/V_{ND}$, where V_{ND} is the estimated distribution volume in the reference region. Binding potential (BP_{ND}) can then be calculated by $BP_{ND} = DVR - 1$.

Model Assumptions

This model makes the following assumptions:

- The tracer binds reversibly.
- Nonspecifically bound ligand equilibrates rapidly with free tissue ligand.
- Compartmental model assumptions:
    - The tracer kinetics or behavior can be represented by a compartmental model.
    - Tracer concentration within each compartment is well-mixed and does not vary spatially.
    - First-order kinetics may be used to describe exchange of ligand between compartments

ℹ **Note:** Violation of any of these assumptions may produce biased parameter estimates. While the model will still run in **VivoQuant**, the estimated parameters may not accurately reflect the true tracer kinetics..

Required Inputs

This model requires the following inputs:

- Metabolite-corrected arterial plasma input curve
- ROI(s) or voxels

Outputs

Region-level analysis:

- Plot of data from each ROI with **1TCM** fit.
- V_T, K_1, k_2, and mean-squared error (MSE) of fit are shown when the cursor is hovered over the model fit plot.
- V_T, K_1, k_2, and mean-squared error (MSE) of fit, data, and 1TCM fit for each ROI can be saved out to .csv.

Voxel-level analysis

- Plot of data for each voxel with **1TCM** fit. Select the voxel for which you would like to see the model fit by clicking on it with the image viewer.
- V_T, K_1, k_2, and mean-squared error (MSE) of fit are shown when the cursor is hovered over the model fit plot.
- Parameter maps for V_T, K_1, k_2, and mean-squared error (MSE).

References

[1] "Kinetic modeling in positron emission tomography". *Morris, et al. In: Emission Tomography: The Fundamentals of PET and SPECT* (Eds: wermick MN, Aarsvold JN). 2004.

[2] "Comparison of methods for analysis of clinical [11C]raclopride studies". *Lammerstsma, et al. JCBFM,* 1996. Link

[3] "Kinetic modelling using basis functions derived from two-tissue compartmental models with a plasma input function: general principle and application to [18F]fluorodeoxyglucose positron emission tomography". *Hong, et al. NeuroImage,* 2010. Link .

Additional Resources

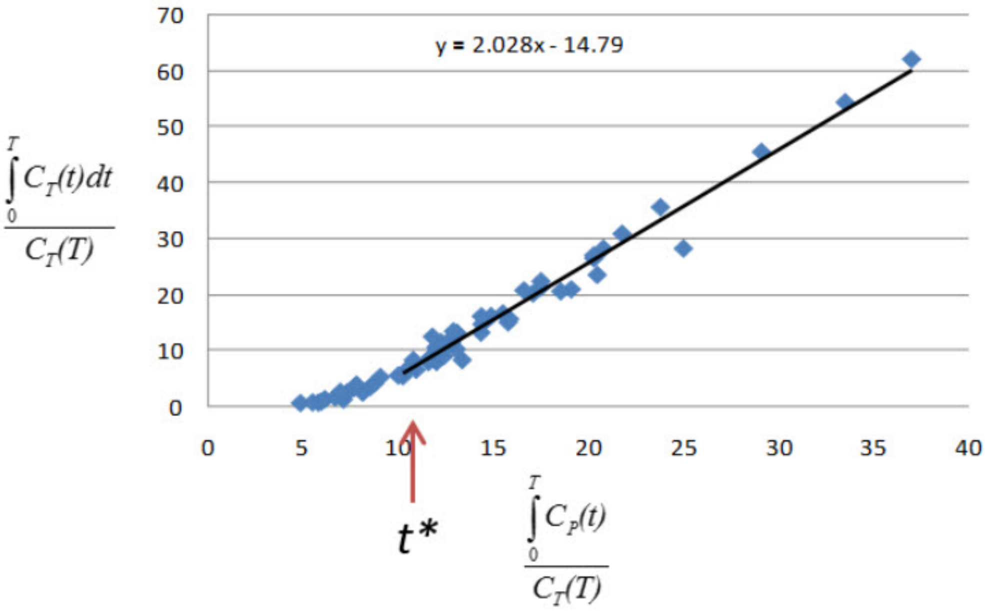
"Compartmental Models", Vesa Oikonen. Turku PET Center website. Link

Logan Graphical Method (Logan Plot)

The **Logan Graphical Method** [1] was developed for reversibly bound tracers based on the *Patlak* method for irreversibly bound tracers [2]. The Logan method proposes that after some time *t**, the plot of

$$\frac{\int_0^T C_T(t)dt}{C_T} \quad \text{vs.} \quad \frac{\int_0^T C_p(t)dt}{C_T}$$

where C_T is the concentration of the tracer in the tissue and C_P is the concentration of the tracer in the metabolite-corrected arterial plasma, becomes linear with slope equal to the total volume of distribution, V_T.



When the **Logan Plot** is applied to image data with a reference region, the distribution volume ratio (*DVR*) can be calculated: DVR = V_T/V_{ND}, where V_{ND} is the estimated distribution volume in the reference region. BP_{ND} is related to *DVR* by BP_{ND} = *DVR - 1*

The **Logan Plot** is a rearrangement of tracer kinetic equations to yield a useful linear equation. However, the mapping of transformed variables is nonlinear in C_T(t), and this results in an underestimation of V_T which becomes more pronounced with larger true V_T and increased noise [1,3]. Therefore, the **Logan graphical method** may not be the best method to use when data are noisy, and other methods should be considered.

Model Assumptions

This model makes the following assumptions:

- The tracer binds reversibly
- After some time *t** the slope of the plot of $\frac{\int_0^T C_T(t)dt}{C_T}$ vs. $\frac{\int_0^T C_p(t)dt}{C_T}$ approaches linearity.

ℹ **Note:** Violation of any of these assumptions may produce biased parameter estimates. While the model will still run in **VivoQuant**, the estimated parameters may not accurately reflect the true tracer kinetics.

Required Inputs

This model requires the following inputs:

- Metabolite-corrected arterial plasma input curve
- ROI(s) or voxels
- *t** (in scan time)
    - *Selection of t**: The **Logan plot** as implemented in **VivoQuant** requires that the user inputs the *t**, which defines the time at which the plotted data become linear. In **VivoQuant** the default *t** value is 0. This is likely not the appropriate value for your experiment. *t** values are tracer dependent. For characterized tracers, we suggest reviewing the literature to see which *t** values have been used in **Logan method**. The simplest way to select a reasonable *t** value for your data is to run the model once with the default *t** value, review the **Logan plots** to find the point at which they become linear (*t**), then re-run the model with the appropriate *t** (in scan time) value.

Outputs

Region-level analysis

- Logan plot with line fit for each voxel. Select the voxel for which you would like to see the Logan plot by clicking on it within the image viewer.
- V_T, fitted line intercept, and mean-squared error (MSE) of fit are shown when the cursor is hovered over the Logan plot.
- Parameter maps for VT, fitted line intercept, and MSE.

References

[1] "Kinetic modeling in positron emission tomography". Morris, et al. In: *Emission Tomography: The Fundamentals of PET and SPECT* (Eds: wermick MN, Aarsvold JN). 2004.

[2] "Comparison of methods for analysis of clinical [11C]raclopride studies". *Lammerstsma, et al. JCBFM*, 1996. Link

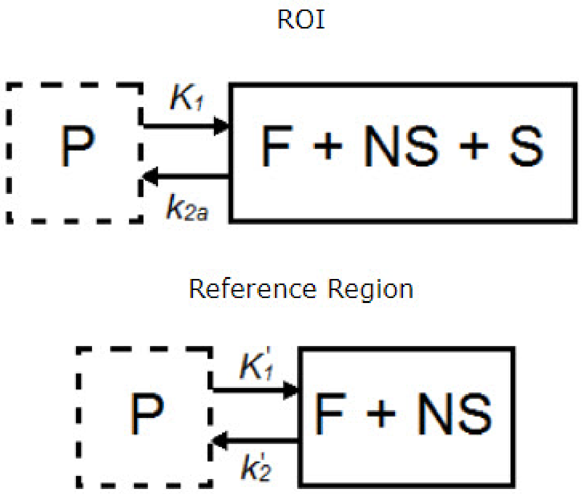
[3] "Effects of Statistical Noise on Graphic Analysis of PET Neuroreceptor Studies". *Slifstein and Laruelle. JNM, 2000*. Link

Additional Resources

"Multiple Time Graphical Analysis (MTGA)", Vesa Oikonen. Turku PET Center website. Link

Simplified Reference Tissue Model (SRTM)

The **simplified reference tissue model** (SRTM) [1] allows for quantification of tracer kinetics without requiring an arterial input function. **SRTM** is a numerically robust model which assumes that the tracer can be represented by 1-tissue compartment models in both the ROIs and the reference region.



Parameter	Description
$C_T(t)$	Concentration in F + NS + S compartment.
$C_{ND}(t)$	Concentration in F + NS compartment, nondisplaceable tracer.
$C_P(t)$	Concentration in plasma (P) compartment.
K_1 (mL*cm^3*min^{-1})	Transfer of ligand from arterial plasma to tissue.
k_{2a} (min^{-1})	Apparent transfer of ligand from tissue to arterial plasma.
K_1' (mL*cm^3*min^{-1})	Transfer of ligand from arterial plasma to reference tissue.
k_2' (min^{-1})	Transfer of ligand from reference tissue to arterial plasma.

$$R_1 = \frac{K_1}{K_1'}$$

$$BP_{ND} = \frac{k_2}{k_{2a}} - 1$$

$$k_2 = k_2' R_1$$

Model Assumptions

This model makes the following assumptions:

- The tracer binds reversibly.
- Tracer concentration in all regions or voxels-of-interest as well as the reference region (see below) can be represented by a 1-tissue compartment model.
- A region/tissue exists which is devoid of the target site/receptor. We call this region the reference region. It represents the concentration of the tracer which is free in tissue and/or bound to off-target sites (non-specific binding). An ideal reference region is a) devoid of the target site/receptor, and b) has the same concentration of tracer free in tissue and nonspecifically bound as the ROI.

ℹ **Note:** Violation of any of these assumptions may produce biased parameter estimates. While the model will still run in **VivoQuant**, the estimated parameters may not accurately reflect the true tracer kinetics [2]. SRTM is currently implement in VivoQuant using a basis function method approach and unweighted fitting [3].

Required Inputs

This model requires the following inputs:

- Reference tissue curve.
- ROI(s) or voxels.

Outputs

Region-level analysis

- Plot of data from each ROI with SRTM fit.
- BP_{ND}, R_1,k_2,k_2’, and mean-squared error (MSE) of fit are shown when the cursor is hovered over the model fit plot.
- BP_{ND}, R_1,k_2,k_2’, and mean-squared error (MSE), data and SRTM fit for each ROI can be saved out to .csv.

Voxel-level analysis

- Plot of data for each voxel with SRTM fit. Select the voxel for which you’d like to see the model fit by clicking on it with the image viewer.
- BP_{ND}, R_1,k_2,k_2’, and mean-squared error (MSE) of fit are shown when the cursor is hovered over the model fit plot.
- Parameter maps for BP_{ND}, R_1,k_2,k_2’ and MSE.

References

[1] “Simplified reference tissue model for PET receptor studies”, *Lammerstma and Hume. NeuroImage, 1996.* Link

[2] “The simplified reference tissue model: model assumption violations and their impact on binding potential”, *Salinas, et al. JCBFM, 2015.* Link

[3] “Parametric imaging of ligand-receptor binding in PET using a simplified reference region model”. *Gunn, et al. NeuroImage, 1997.* Link

Additional Resources

"Reference region input compartmental models", *Vesa Oikonen. Turku PET Center website*. Link .

Simplified Reference Tissue Model 2 (SRTM2)

SRTM2 is a two-pass version of SRTM that attempts to reduce noise in parametric images by fitting all voxels with a fixed, global k_2' [1]. In practice, SRTM estimates k_2' for every voxel or region, but since there is only one reference region, in principle there is only one true k_2' value [1]. Fixing k_2' reduces the number of parameters estimated and thus reduces noise in parametric images [1]. However, this improvement in precision may come at the price of an increase in bias [1].

ℹ **Note:** SRTM2 can be used on both the region- and voxel-level but generally shows greatest advantage over SRTM when used at the voxel-level.

Model Assumptions

This model makes the following assumptions:

- The tracer binds reversibly
- Tracer concentration in all regions or voxels-of-interest as well as the reference region (see below) can be represented by a 1-tissue compartment model.
- A region/tissue exists which is devoid of the target site/receptor. We call this region the reference region. It represents the concentration of the tracer which is free in tissue and/or bound to off-target sites (non-specific binding). An ideal reference region is a) devoid of the target site/receptor, and b) has the same concentration of tracer free in tissue and nonspecifically bound as the ROI.
- There is only one true k_2' value. k_2' is the rate of tracer efflux from the reference region to the plasma.

ℹ **Note:** Violation of any of these assumptions will invalidate the model and may produce biased parameter estimates. While the model will still run in **VivoQuant**, the estimated parameters may not accurately reflect the true tracer kinetics. SRTM2 is currently implemented in **VivoQuant* using a basis function method approach and unweighted fitting [2].

Required Inputs

This model requires the following inputs:

- Reference tissue curve.
- ROI(s) or voxels.
- A fixed k_2'
- *Selection of a fixed* k_2'*: The value to which to fix k_2' should be selected based on the tracer and the experiment. For characterized tracers, we suggest reviewing the literature to see how the fixed k_2' has been selected in different studies and the effect of the method to fix k_2' on SRTM2 parameter estimates. Generally, k_2' can be fixed to the median value estimated by a first-pass of SRTM from all voxels with a BPND value > a set minimum [3,4] or all voxels with a BPND value within a given range [5]. The idea behind using BPND values to select voxels for inclusion in the median is to exclude voxels which maybe represent noise or have poor SRTM fit. For most tracers there is a range of physiologically-relevant BPND values. Values outside of that range may be non-physiological. Other studies have fixed k_2' to the population average value estimated from a 1-tissue compartment model fit to the reference region [3] or estimated k_2' for each subject by a simultaneous SRTM fit including all target regions with coupled k_2' [3,6]. SRTM fit with coupled k_2' is not currently available in **VivoQuant**.

Outputs

Region-level analysis

- Plot of data from each ROI with SRTM2 fit.
- BP_{ND}, R_1,k_2a, and mean-squared error (MSE) of fit are shown when the cursor is hovered over the model fit plot.
- BP_{ND}, R_1,k_{2a}, and mean-squared error (MSE), data and SRTM2 fit for each ROI can be saved out to .csv.

Voxel-level analysis

- Plot of data for each voxel with SRTM2 fit. Select the voxel for which you'd like to see the model fit by clicking on it with the image viewer.
- BP_{ND}, R_1, k_{2a}, and mean-squared error (MSE) of fit are shown when the cursor is hovered over the model fit plot.
- Parameter maps for BP_{ND}, R_1, k_{2a}, and MSE.

References

[1] "Noise reduction in the simplified reference tissue model for neuroreceptor functional imaging.", *Wu and Carson. JCBFM, 2002*. Link

[2] "Parametric imaging of ligand-receptor binding in PET using a simplified reference region model". *Gunn, et al. NeuroImage, 1997.* Link

[3] "Tracer kinetic modeling of [(11)C]AFM, a new PET imaging agent for the serotonin transporter". *Naganawa, et al. JCBFM, 2013.* Link

[4] "Parametric Imaging and Test-Retest Variability of 11C-(+)-PHNO Binding to D2/D3 Dopamine Receptors in Humans on the High-Resolution Research Tomograph PET Scanner", *Gallezot, et al. JNM, 2014*. Link

[5] "Kinetic modeling of the serotonin 5-HT1B receptor radioligand [11C]P943 in humans". Gallezot, et al. JCBFM, 2010 Link

[6] "Assessment of striatal dopamine D2/D3 receptor availability with PET and 18F-desmethoxyfallypride: comparison of imaging protocols suited for clinical routine". *Amtage, et al. JNM, 2012*. ¨Link

Additional Resources

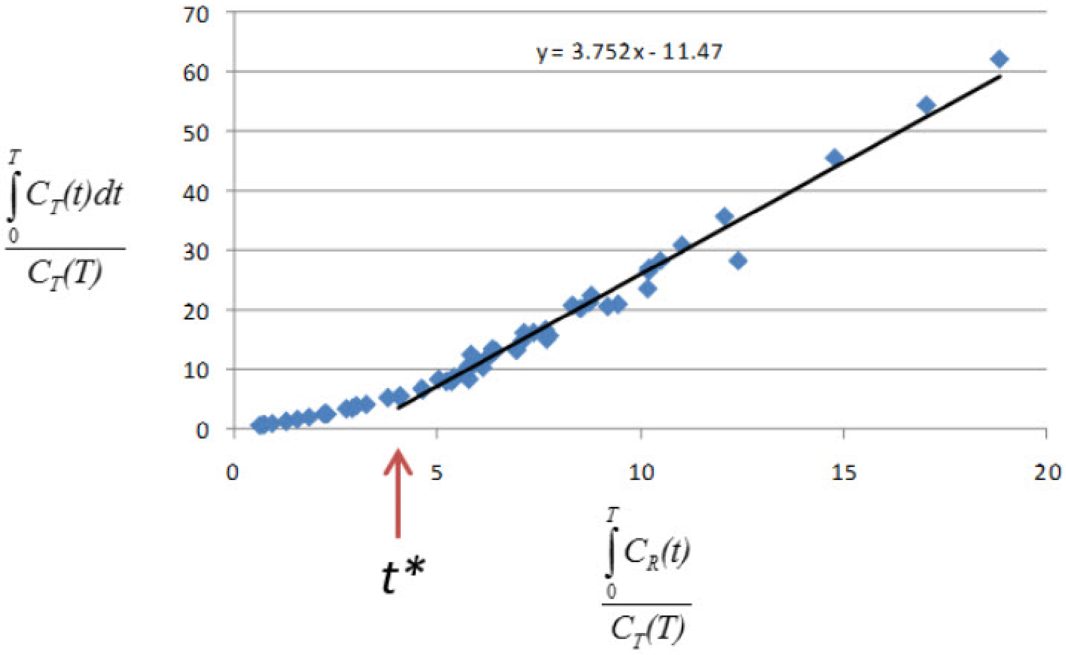
"Reference region input compartmental models", *Vesa Oikonen. Turku PET Center website*. Link.

Logan Non-Invasive Graphical Method (Logan reference plot)

The **Logan non-invasive graphical method** [1] was developed for reversibly bound tracers based on the Logan graphical method and *Patlak* method for irreversibly bound tracers [2,3]. The Logan reference method proposes that after some time *t**, the plot of

$$\frac{\int_0^T C_T(t)dt}{C_T} \quad \text{vs.} \quad \frac{\int_0^T C_R(t)dt}{C_T}$$

(where C_T is the concentration of the tracer in the tissue and C_R is the concentration of the tracer in the reference region) becomes linear with slope equal to the distribution volume ratio (*DVR*). Binding potential (BP_{ND}) is related to *DVR* by $BP_{ND} = DVR - 1$.



The **Logan plot** is a rearrangement of tracer kinetic equations to yield a useful linear equation. However, the mapping of transformed variables is nonlinear in $C_T(t)$, and this results in an underestimation of *DVR* which becomes more pronounced with larger true *DVR* and increased noise [1,4]. Therefore, the **Logan graphical method** may not be the best method to use when data are noisy, and other methods should be considered.

Method Assumptions

This model makes the following assumptions:

- The tracer binds reversibly.
- A region/tissue exists which is devoid of the target site/receptor. We call this region the reference region. It represents the concentration of the tracer which is free in tissue and/or bound to off-target sites (non-specific binding). An ideal reference region is a) devoid of the target site/receptor, and b) has the same concentration of tracer free in tissue and nonspecifically bound as the ROI.
- After some time t* the slope of the plot of $\frac{\int_0^T C_T(t)dt}{C_T}$ vs. $\frac{\int_0^T C_R(t)dt}{C_T}$ approaches linearity.

Note: Violation of any of these assumptions may produce biased parameter estimates. While the model will still run in **VivoQuant**, the estimated parameters may not accurately reflect the true tracer kinetics.

Required Inputs

This model requires the following inputs:

- Reference tissue curve.
- ROI(s) or voxels.
- *t** (in scan time)
  - *Selection of t**: The Logan reference plot as implemented in **VivoQuant** requires that the user inputs the *t** which defines the time at which the plotted data become linear. In **VivoQuant**, the default *t** value is 0. This is likely not be the appropriate value for your experiment. *t** values are tracer dependent. For characterized tracers, we suggest reviewing the literature to see which *t** values have been used in Logan reference method. The simplest way to select a reasonable *t** value for your data is to run the model once with the default *t** value, review the Logan reference plots to find the point at which they become linear (*t*/), *then re-run the model with the appropriate* *t/* (in scan time) value.

Outputs

Region-level analysis

- Logan plot with line fit for each ROI.
- *DVR*, fitted line intercept, and mean-squared error (MSE) of fit are shown when the cursor is hovered over the Logan plot.
- *DVR*, fitted line intercept, and transformed Logan space data for each ROI can be saved out to .csv.

Voxel-level analysis

- Logan plot with line fit for each voxel. Select the voxel for which you would like to see the Logan plot by clicking on it within the image viewer.
- *DVR*, fitted line intercept, and MSE of fit are shown when the cursor is hovered over the Logan plot.
- Parameter maps for *DVR*, fitted line intercept, and MSE.

References

[1] “Distribution volume ratios without blood sampling from graphical analysis of PET data”. *Logan, et al. JCBFM, 1996*. Link

[2] “Graphical analysis of reversible radioligand binding from time-activity measurements applied to [N-11C-methyl]-(-)-cocaine PET studies in human subjects”. *Logan, et al. JCBFM, 1990*. Link

[3] “Graphical evaluation of blood-to-brain transfer constants from multiple-time uptake data”. *Patlak, et al. JCBFM, 1983*. Link

[4] “Effects of Statistical Noise on Graphic Analysis of PET Neuroreceptor Studies”. *Slifstein and Laruelle. JNM, 2000*. Link

Additional Resources

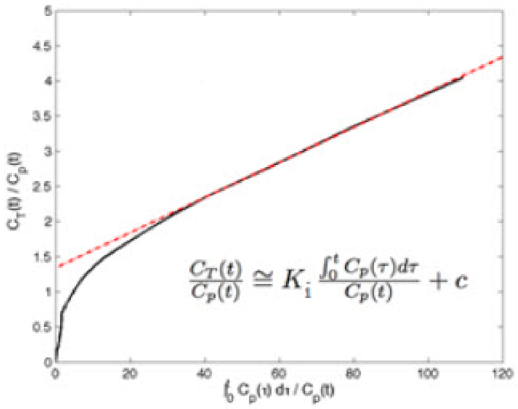
“Multiple Time Graphical Analysis (MTGA)”, *Vesa Oikonen. Turku PET Center website*. Link

Patlak Analysis (Patlak Plot)

Patlak analysis is rearrangement of tracer kinetic equations to yield a useful linear equation [1]. Patlak analysis proposes that after some time *t**, the plot of

$$\frac{C_T(t)}{C_P(t)} \text{ vs. } \frac{\int_0^T C_P(t)dt}{C_P(T)}$$

where C_T is the concentration of the tracer in the tissue and C_P is the concentration of the tracer in the metabolite-corrected arterial plasma, becomes linear with slope equal to the net influx rate constant, K_i. The rate constant K_i represents influx and trapping of the tracer into the tissue [1,2].



In terms of a two-tissue compartment model where $k_4 = 0$ because the tracer is irreversibly trapped, $K_i = \frac{K_1 k_3}{k_2 + k_3}$

Model Assumptions

This model makes the following assumptions:

- The tracer binds irreversibly
- After some time *t**, the slope of the plot of $\frac{C_T(t)}{C_P(t)}$ vs. $\frac{\int_0^T C_P(t)dt}{C_P(T)}$ approaches linearity.

ℹ **Note:** Violation of any of these assumptions may produce biased parameter estimates. While the model will still run in **VivoQuant**, the estimated parameters may not accurately reflect the true tracer kinetics.

Required Inputs

This model requires the following inputs:

- Metabolite-corrected arterial plasma input curve.
- ROI(s) or voxels
- *t** (in scan time)
    - *Selection of t**: The **Patlak plot** as implemented in **VivoQuant** requires that the user inputs the *t** which defines the time at which the plotted data become linear. In **VivoQuant** the default *t** value is 0. This is likely not be the appropriate value for your experiment. *t** values are tracer dependent. For characterized tracers, we suggest reviewing the literature to see which *t** values have been used in Patlak analysis. The simplest way to select a reasonable *t** value for your data is to run the model once with the default *t** value, review the Patlak plots to find the point at which they become linear (*t**), then re-run the model with the appropriate *t** (in scan time) value.

Outputs

Region-level analysis

- Patlak plot with line fit for each ROI.
- K_i, fitted line intercept (*V*), and mean-squared error (MSE) of fit are shown when the cursor is hovered over the **Patlak plot**.
- K_i and transformed Patlak space data for each ROI can be saved out to .csv.

Voxel-level analysis

- **Patlak plot** with line fit for each voxel. Select the voxel for which you would like to see the **Patlak plot** by clicking on it within the image viewer.
- K_i, fitted line intercept (*V*), and mean-squared error (MSE) of fit are shown when the cursor is hovered over the **Patlak plot**.
- Parameter maps for K_i, fitted line intercept (*V*), and MSE.

References

[1] “Graphical evaluation of blood-to-brain transfer constants from multiple-time uptake data”. *Patlak, et al. JCBFM, 1983*. Link.

[2] “Net Influx Rate, (Ki)”, *Vesa Oikonen. Turku PET Center website*. Link.

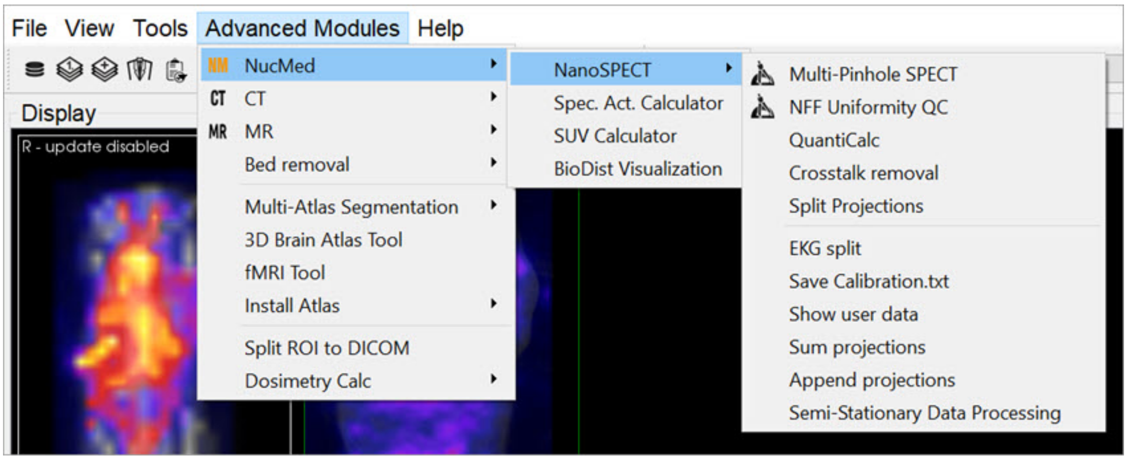
Additional Resources

“Multiple Time Graphical Analysis (MTGA)”, *Vesa Oikonen. Turku PET Center website*. Link.

NanoSPECT Tools

The NanoSPECT Tools sub-menu contains features primarily associated with improving SPECT quantification.

- QuantiCalc
- Specific Activity Calculator
- SUV Calculator
- Crosstalk Removal
- Biodist. Visualization
- Split Projections



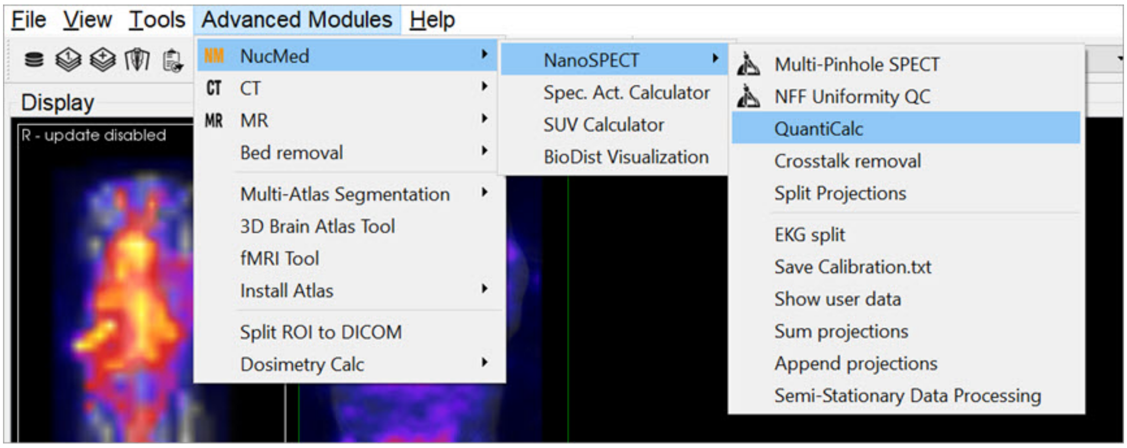
NanoSPECT Tools

QuantiCalc

The **Quantification Calculator** enables a feature unique to the NanoSPECT/CT imaging system: the ability to perform absolute quantification in small-animal SPECT imaging.

Getting There

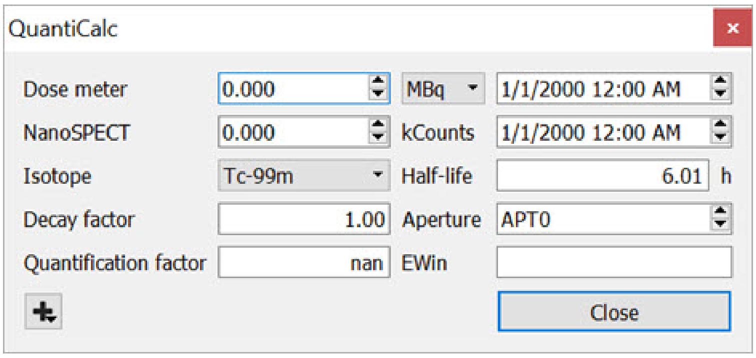
The **QuantiCalc** tool is available going to **Advanced Modules** > **NucMed** > **NanoSPECT**.



QuantiCalc Tool

Function

The **Quantification Calculator** is used to calculate a **Quantification Factor**. To perform absolute quantification, Quantification Factors must be calculated for each isotope and aperture combination used in the NanoSPECT/CT. The Quantification Factors are stored in the Quantification Database. For information on collecting the data necessary to calculate Quantification Factors, see the NanoSPECT/CT documentation.



Dose meter 0.000 MBq 1/1/2000 12:00 AM
NanoSPECT 0.000 kCounts 1/1/2000 12:00 AM
Isotope Tc-99m Half-life 6.01 h
Decay factor 1.00 Aperture APT0
Quantification factor nan EWin

QuantiCalc Data

The procedure for collecting **Quantification Factor** data involves performing a highly-specified SPECT measurement on a syringe filled with isotope. The fields of the QuantiCalc window may then be filled according to:

Dose Meter	Record the amount of activity in the syringe in MBq,kBq, mCi or uCi as measured by a dose calibrator. Include the time of the measurement.
NanoSPECT	Record the activity value measured by the **NanoSPECT** from reconstructed data. Include the time of data collection.
Isotope	Select the isotope present in the syringe. Isotopes offered include Ga-67, I-123, I-125, Lu-177, Tc-99, Tl-201, In-111, and Xe-133. The half-life of the selected isotope will be automatically populated in units of hours.
Decay Factor	The information from the **Dose Meter**, **NanoSPECT**, and **Isotope** fields will be used to calculate a decay factor between the time of **Dose Meter** measurement and data collection.
Quantification Factor	The information from the above fields is all combined to determine a **Quantification Factor** for that particular isotope and aperture. This **Quantification Factor** can then be entered in the **Quantification Database.**

Quantification Database

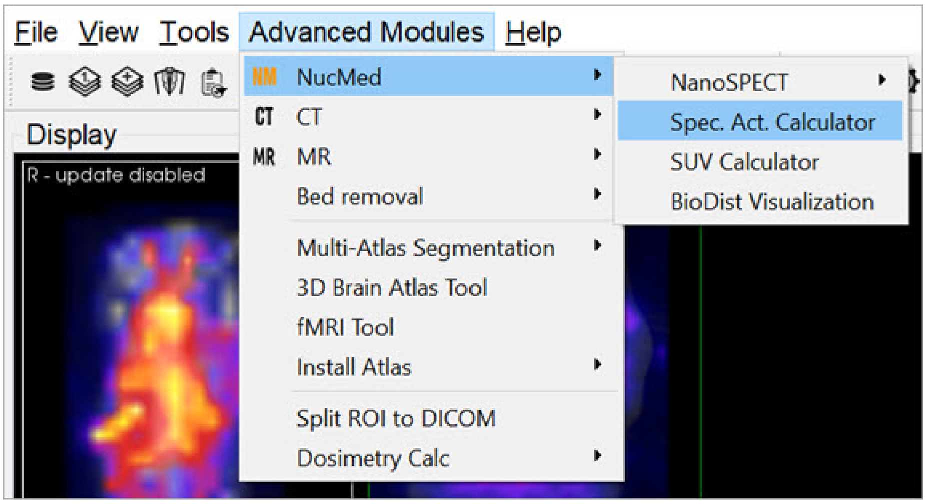
The **Quantification Database** stores all of the **Quantification Factors** calculated for any isotope and aperture combination measured with the **NanoSPECT/CT**.

Specific Activity Calculator

The **Specific Activity Calculator** accepts an input volume, activity, specific activity for a given isotope and calculates the amount of isotope present in the sample both in moles and moles/volume.

Getting There

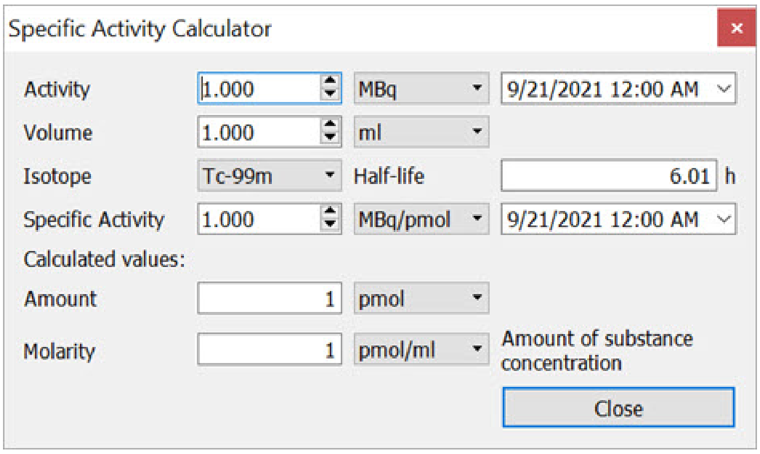
Access the **Specific Activity Calculator** by going to **NucMed** > **Apect. Act. Calculator**.



Specific Activity Calculator

Function

The **Specific Activity Calculator** requires several values to make its calculations. An activity, volume, isotope, and specific activity are used to calculate the number of excited molecules and molarity of a given sample.


Specific Activity Calculator

Activity: 1.000 MBq 9/21/2021 12:00 AM

Volume: 1.000 ml

Isotope: Tc-99m Half-life 6.01 h

Specific Activity: 1.000 MBq/pmol 9/21/2021 12:00 AM

Calculated values:

Amount: 1 pmol

Molarity: 1 pmol/ml Amount of substance concentration

QuantiCalc Tool

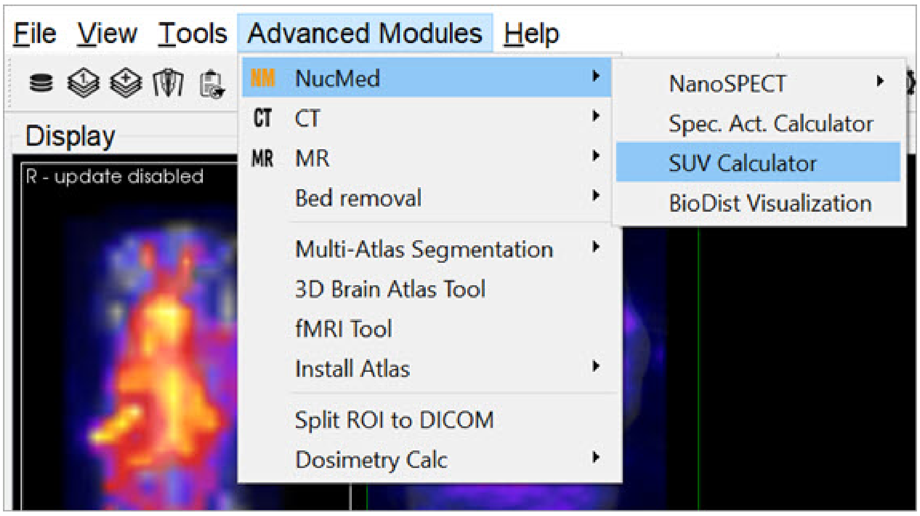
Value	Units	Description
Activity	MBq, kBq, mCi, or µCi and measurement time.	Amount of isotope as measured in a dosimeter or with the NanoSPECT.
Volume	cm3, mm3, ml, µl	The volume containing the activity.
Isotope	Hours	The isotope of interest and its associated half-life. Several pre-defined options are available.
Specific Activity	MBq/pmol, kBq/pmol and measurement time.	The specific activity of the isotope being used as measured by a specific activity calibration. Specific activity describes the number of excited atoms out of the total atoms present in a given sample, i.e., the amount of the activity that has not yet decayed to a ground state.
Amount	pmol, nmol, or #	The calculated amount, or number, of excited molecules in the sample.
Molarity	pmol/ml, nmol/ml	The calculated molarity, or concentration, of excited molecules in a sample of activity.

SUV Calculator

Use the **SUV Calculator** to calculate a specific uptake value (SUV), given the appropriate entries of injected dose, subject weight, and activity concentration.

Getting There

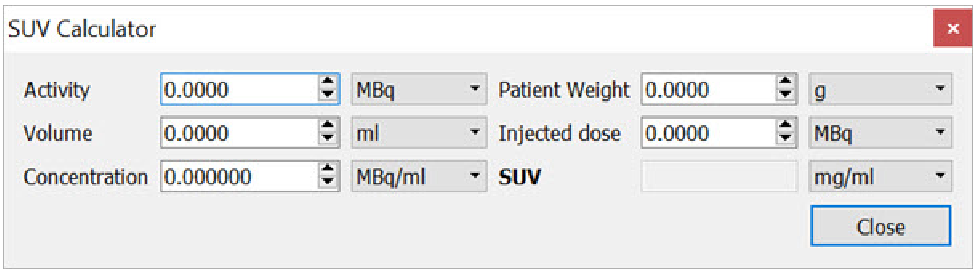
Access the SUV Calculator by going to **Advanced Modules** > **NucMed** > **SUV Calculator**.



SUV Calculator

Function

The **SUV Calculator** requires several values to make its calculations. An activity and volume are used to calculate an activity concentration. The subject weight and injected dose are used in conjunction with the activity concentration to calculate the SUV. Units for these entries are user-selectable.



SUV Calculator

Activity	0.0000	MBq	Patient Weight	0.0000	g
Volume	0.0000	ml	Injected dose	0.0000	MBq
Concentration	0.000000	MBq/ml	**SUV**		mg/ml

SUV Calculator - Values

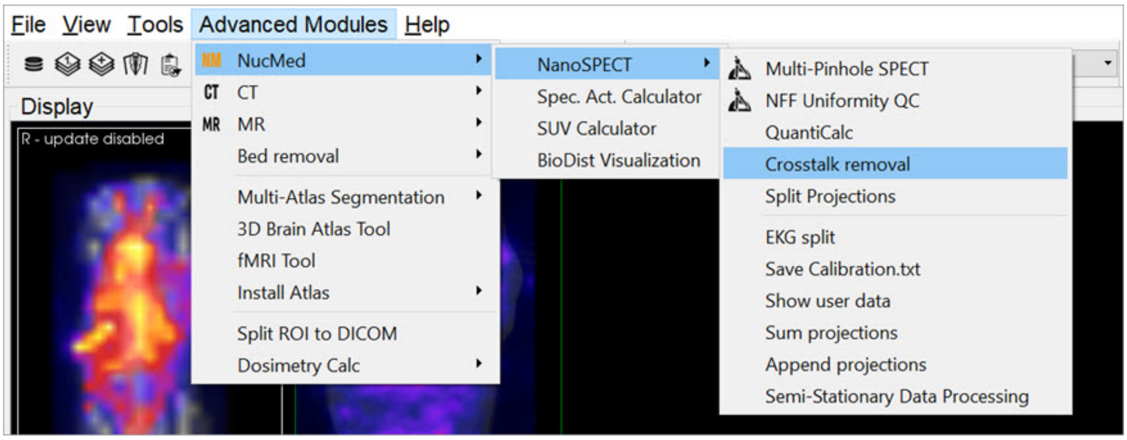
Value	Units	Description
Activity	MBq, kBq, mCi, or μCi	Amount of isotope as measured in a dosimeter or with the NanoSPECT.
Volume	cm3, mm3, ml, μl	The volume containing the activity.
Concentration	kBq/ml, MBq/ml, mCi/ml, kBq/mm3, MBq/mm3	The ratio of activity to volume.
Patient Weight	g, kg	The weight of the animal or object of interest.
Injected Dose	MBq, kBq, mCi, or μCi	The amount of isotope successfully injected into the subject.
SUV	mg/ml, g/ml, kg/ml, g/l, g/mm3, kg/mm3	The specific uptake value (SUV) given the patient weight, activity concentration, and injected dose specified in the other fields.

Crosstalk Removal

Use the **Crosstalk Removal** tool to remove crosstalk photons in dual-isotope SPECT images. The limits in energy resolution inherent to SPECT imaging result in some overlap between the energy spectra of isotopes with relatively similar peak energies. For example, in dual-isotope I-123 and Tc-99m imaging, some I-123 photons will spill over into the Tc-99m window and vice versa. The **Crosstalk Removal** tool is applied to projection data to remove these “spill over” photons or crosstalk.

Getting There

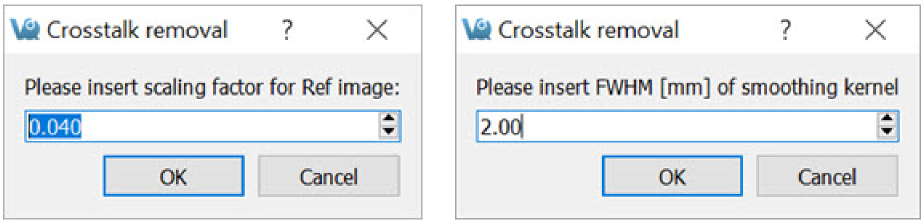
Access the **Crosstalk Removal** tool by going to **Advanced Modules**>**NucMed**>**NanoSPECT**.



Crosstalk Removal

Function

The **Crosstalk Removal** tool requires you to enter the scaling factor of both the Input and Reference images, as well as the Full-Width Half-Maximum (FWHM) of the smoothing kernel in order to remove crosstalk photons.



Please insert scaling factor for Ref image: 0.040

Please insert FWHM [mm] of smoothing kernel 2.00

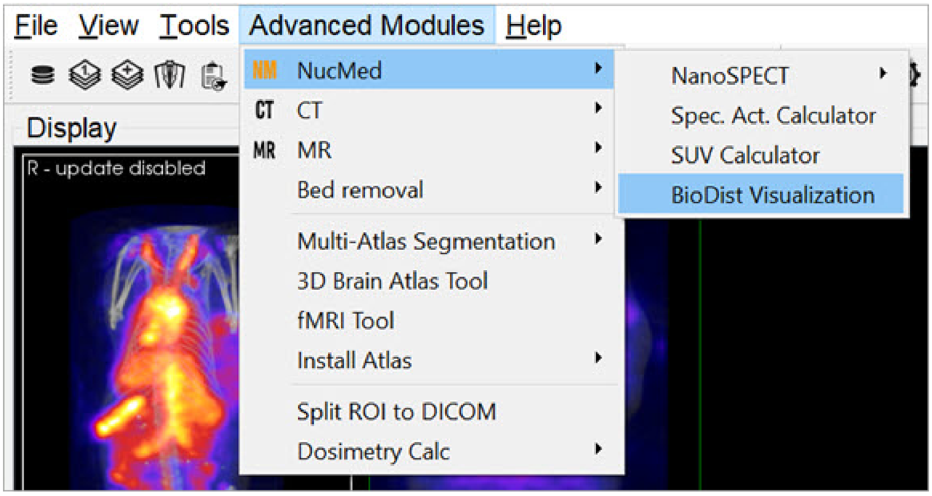
Crosstalk Removal

Biodistribution Visualization

The **Biodistribution Visualization** tool creates an atlas representation of measured mouse biodistribution values.

Getting There

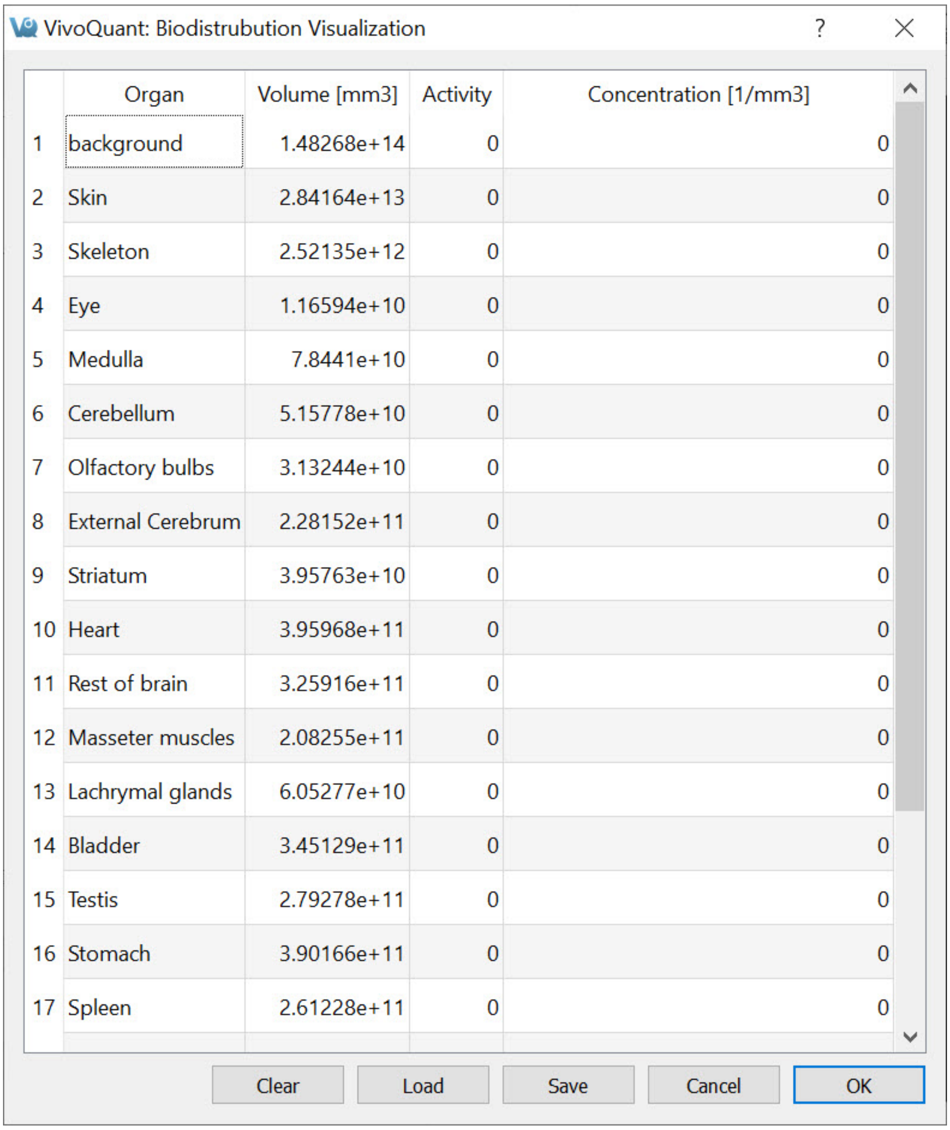
Biodistribution Visualization is accessible by going to **Advanced Modules**>**NucMed**>**BioDist Visualization** .



Biodistribution Visualization

Function

To use the **Biodistribution Visualization** function, enter the total measured activity for each region-of-interest available in the atlas list.



	Organ	Volume [mm3]	Activity	Concentration [1/mm3]
1	background	1.48268e+14	0	0
2	Skin	2.84164e+13	0	0
3	Skeleton	2.52135e+12	0	0
4	Eye	1.16594e+10	0	0
5	Medulla	7.8441e+10	0	0
6	Cerebellum	5.15778e+10	0	0
7	Olfactory bulbs	3.13244e+10	0	0
8	External Cerebrum	2.28152e+11	0	0
9	Striatum	3.95763e+10	0	0
10	Heart	3.95968e+11	0	0
11	Rest of brain	3.25916e+11	0	0
12	Masseter muscles	2.08255e+11	0	0
13	Lachrymal glands	6.05277e+10	0	0
14	Bladder	3.45129e+11	0	0
15	Testis	2.79278e+11	0	0
16	Stomach	3.90166e+11	0	0
17	Spleen	2.61228e+11	0	0

ROI Measured Activity List

After entering the appropriate values, select one of the buttons at the end of the list.

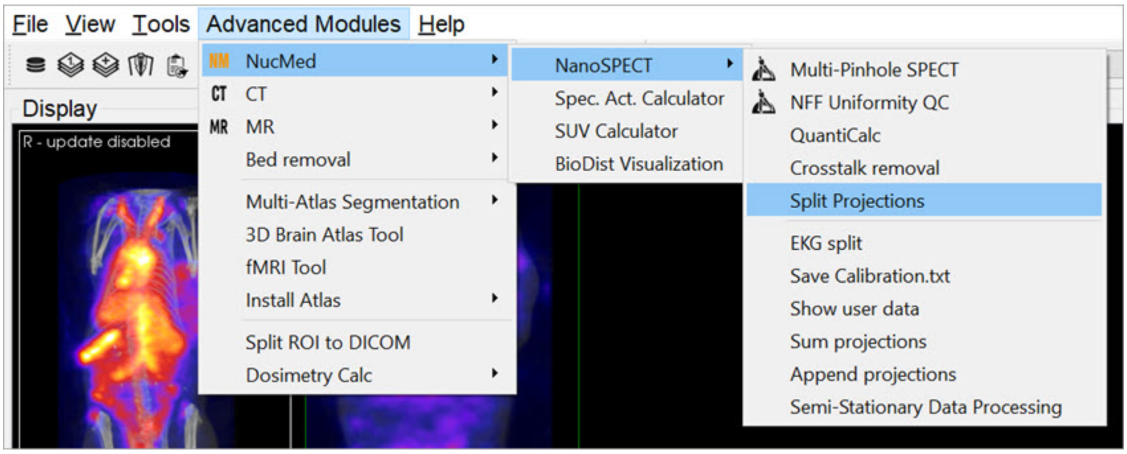
Button	Description
Clear	Clears all fields
Load	Loads a previously saved biodistribution text file.
Save	Saves the current biodistribution data into a text file.
Cancel	Closes the Biodistribution Visualization window.
OK	Prepares the atlas with the entered biodistribution information.

Split Projections

Use the **Split Projections** tool to split a single SPECT projection data DICOM file into multiple projection data files along one of several DICOM fields.

Getting There

Access the **Split Projections** tool by going to **Advanced Modules** > **NucMed** > **NanoSPECT**>**Split Projections**.



Split Projections

Function

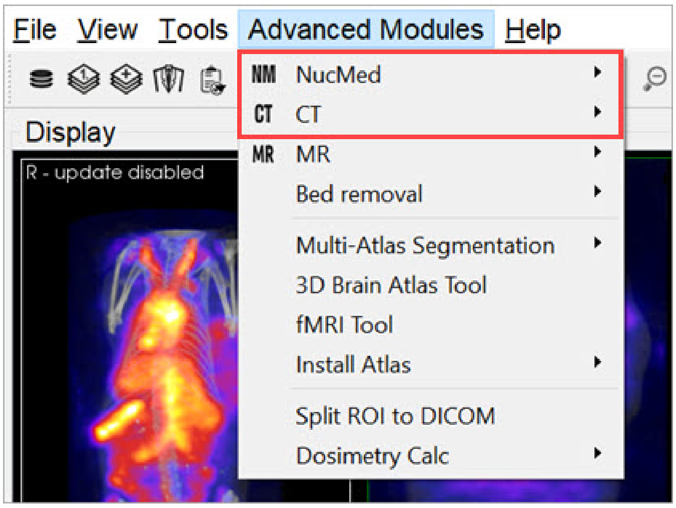
Upon selecting the **Split Projections** tool, the **Data Browser** opens. Select an appropriate SPECT projection data set. A pulldown menu of split options is presented. After splitting, a confirmation message is presented to verify successful saving of the new data sets.

Calibration

Use this tool to evaluate data from several different **NanoSPECT** calibration measurements, including CT Geometrical, Multi-Pinhole SPECT, and Near Field Flood.

Getting There

The **Calibration** menu is available in the **Advanced Modules** menu.



Advanced Modules Calibration

Function

To calibrate and maintain the **NanoSPECT/CT** imaging system, several calibration measurements are required. The **Calibration** menu provides options for analyzing:

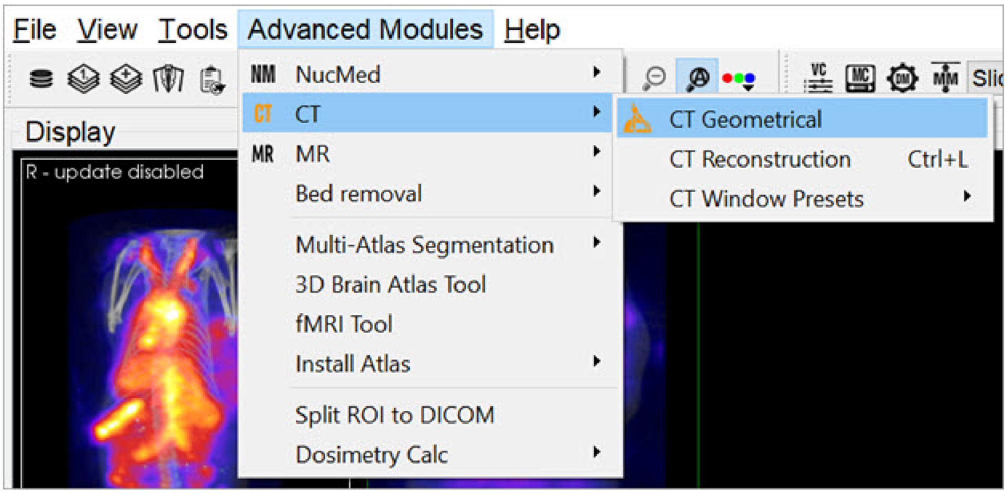
- CT Geometrical Calibrations
- Multi-Pinhole SPECT Calibrations
- Near Field Flood QC Measurements

CT Geometrical Calibration

Use this tool to evaluate **CT Geometrical Calibration** data.

Getting There

Access the **CT Geometrical Calibration** tool by going to **Adanced Modules**>**CT**>**GT Geometrical**.



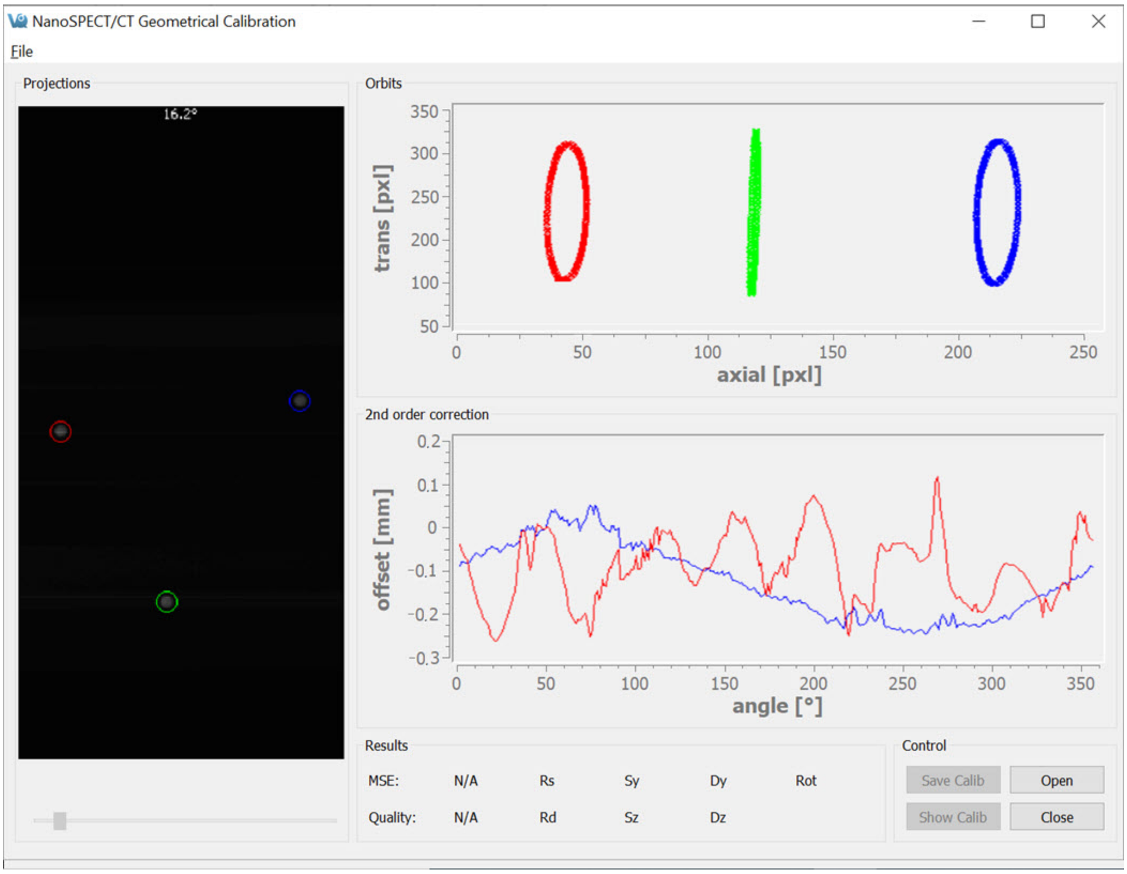
CT Geometrical Calibration

Function

The gantry of the **NanoSPECT** has a reproducible wobble as it rotates around its axis. The **CT Geometrical** calibration measures this wobble and generates a file that is used to correct for the wobble in the reconstruction.

The calibration data is also used to assess the severity of the wobble and to insure that it does not exceed +/-0.5mm.

A CT Geometrical measurement consists of a set of projection data collected in a circular CT measurement of the Geometrical CT phantom. The orbits of the three metal balls embedded in the *Plexiglas* of the phantom are used to assess the wobble in the gantry. Example settings for this measurement include 55kVp, 360 projections, 1000ms. The protocol needed to run this measurement is called CT Geometrical and can be found in the **Service Protocols** section of the **Nucline**. After collecting the measurement data, it may be loaded into the **CT Geometrical** calibration panel using the **Open** button described below.



MSE: N/A

Quality: N/A

CT Geometrical Calibration Panel

The **CT Geometrical Calibration** panel is divided into five sections: **Projections**, **Orbits**, **2nd Order Corrections**, **Results**, and **Control**.

The **Projections** panel displays the projections collected in the calibration measurement as they are being analyzed. Each of the three metal fiducials is marked by a red, green, or blue circle. The progress of the measurement is also noted in this panel.

The **Orbits** panel displays the trajectory of the three metal fiducials as the projections are analyzed. The trajectories appear flat in the primary view; however, by drawing a box around a given trajectory it may be expanded to fill the entire panel, providing a more illustrative view.

To zoom in on a particular orbit, draw a box by holding down the left mouse button and dragging.

Upon release of the button, the display will show only the selected orbit. To return to the full view, just right-click.

The 2nd Order Corrections panel displays an important result of the calibration. This panel plots the axial and transaxial wobble of the gantry as it rotates. It is critical that these values be less than +/-0.5mm to enable successful correction of the gantry motion in the CT reconstruction.

The **Results** panel provides further calibration results, including a mean-square error (MSE) value that represents the deviation of the fiducials from their ideal trajectories. A one-word Quality assessment is provided as well as numerical values for other parameters including the radius of the source (Rs), radius of the detector (Rd), offsets of the source axially (Sz) and transaxially (Sy), and offsets of the detector axially (Dz) and transaxially (Dy).

The **Control** panel houses four buttons, including:

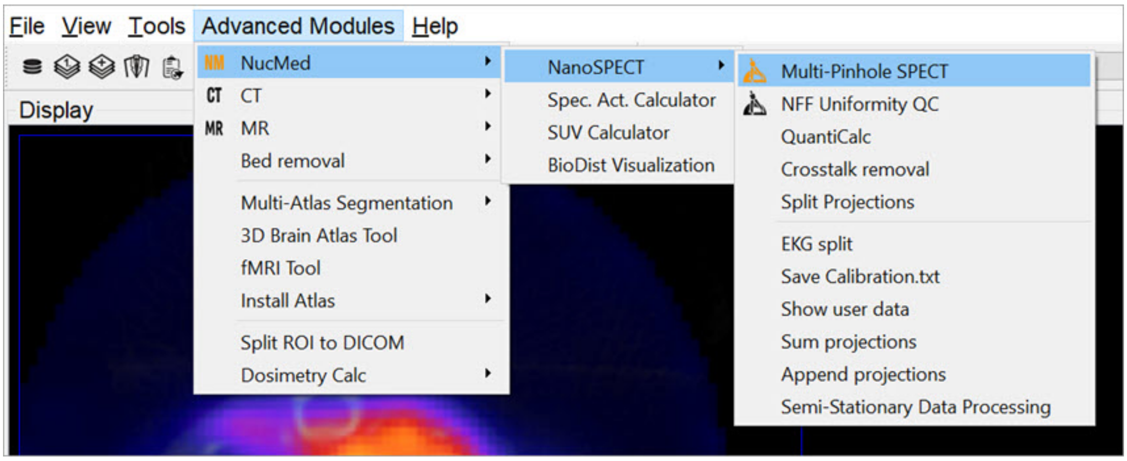
Button	Function
Open	Opens the **Data Browser** where a **CT Geometrical** dataset may be selected for analysis.
Close	Closes the **CT Geometrical** panel.
Save Calib	Saves the existing calibration in the format used by the **NanoSPECT/CT**.
Show Calib	Shows the existing calibration in the format used by the **NanoSPECT/CT**.

MMP SPECT Calibration

Use this tool to evaluate SPECT geometrical calibration data.

Getting There

The **MMP SPECT Calibration** tool is available in the **Advanced Modules** Menu.

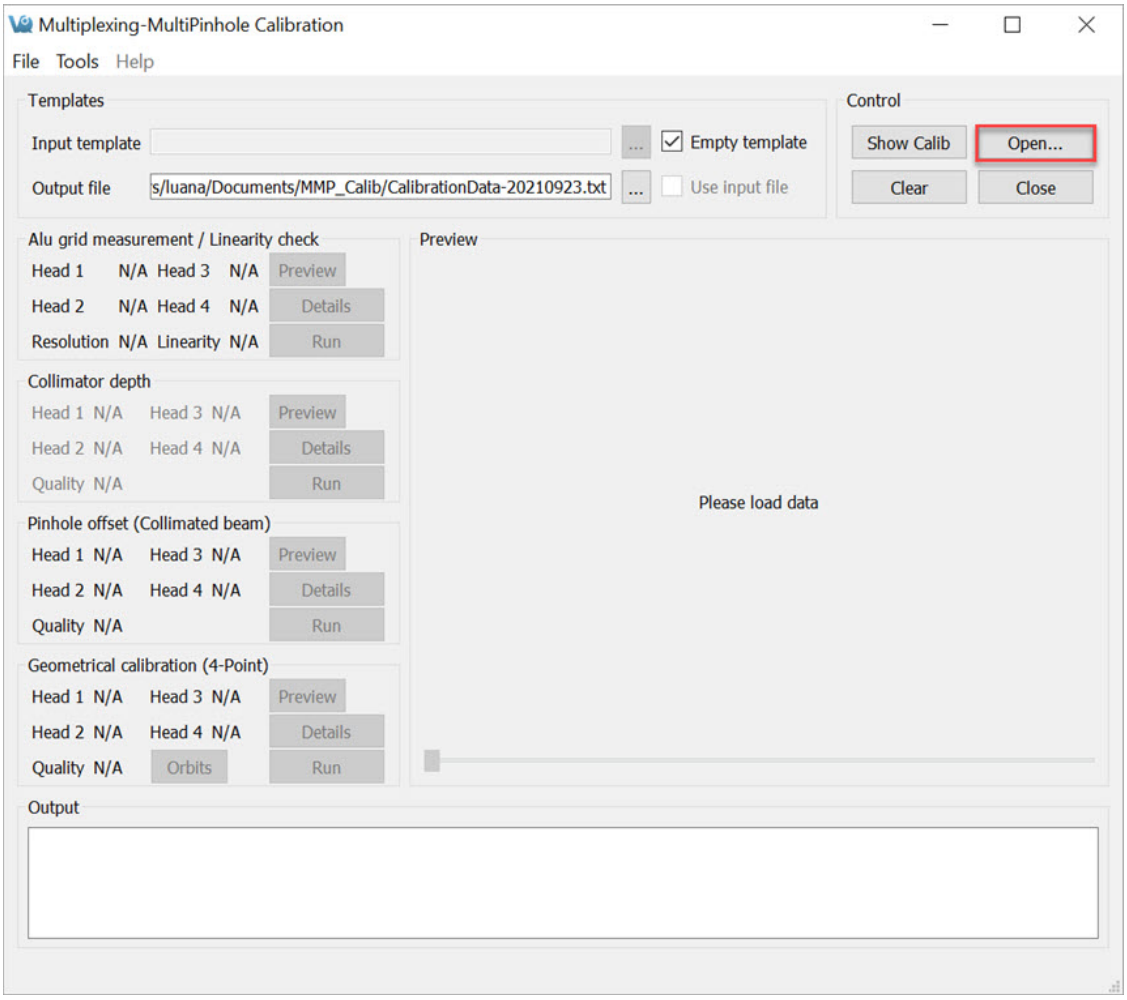


MMP SPECT Calibration

Function

To successfully implement multiplexed multiple-pinhole methods in small-animal SPECT, several calibrations are necessary. You can use the **MMP SPECT** panel to analyze four different small-animal SPECT calibrations, including linearity, collimator depth, pinhole offset, and geometrical. The panel is split into eight sections: Templates, Control, Preview, Output, and a section for each of the four calibrations. There are also several helpful tools in the MMP Menus.

To run the tool, hit the **Open** button and select all of the relevant data (should be titled Service^SPECT_0*_CalibName and consist of 64 Intrinsic Resolution data sets, 4 Collimated Beam data sets, and 1 4-point data set) from the **Data Browser**. The **MMP Tool** reads in the calibration data and recognizes which data corresponds to which calibration. The panels for the individual calibrations display the completeness of the data. Once all necessary data is present, use the **Run** buttons in succession from the top calibration (**Aluminum Grid**) to the bottom calibration (**Four-Point**). Results for each calibration are presented in their respective panels; a description of possible errors is listed in Calibration Failures.

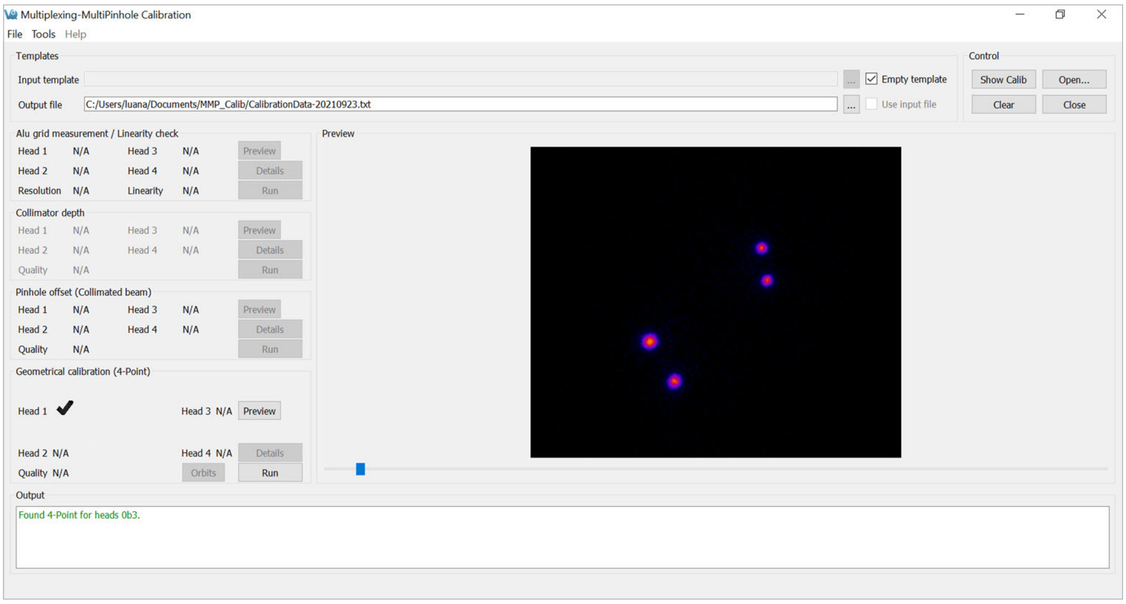


☑ Empty template

Output file: s/luana/Documents/MMP_Calib/CalibrationData-20210923.txt

Open Data

After successfully completing the analysis, the result CalibrationData_YYYYMMDD.txt file can be copied into C:\Nucline\Calibrations\CalibrationData.txt to update the calibration information used by the NanoSPECT.



☑ Empty template

Output file: C:/Users/luana/Documents/MMP_Calib/CalibrationData-20210923.txt

```
Found 4-Point for heads 0b3.
```

MMP SPECT Calibration Panel

Templates

The **Templates** section controls the input and output files used/generated by the calibration analysis.

Input Template	You can use a previously-generated CalibrationData.txt file as an input template for the data. This feature is particularly useful if partial calibrations (i.e., only a 4-point measurement) have been performed.
Empty Template	As a default, an empty template, designed for use with the Nucline software, is used to generate the CalibrationData.txt file.
Output File	You may specifiy any name for the Output file of the calibration analysis. The default name is CalibrationData_YYYYMMDD.txt.

Control

The **Control** panel has four buttons for manipulating the MMP Calibration window.

Button	Description
Show Calib	Opens the current CalibrationData_YYYYMMDD.txt file for viewing.
Open...	Opens a browser that is to be used for loading MMP Calibration data (DICOM format).
Clear	Clears the **Output** panel of the **MMP Calibration** window.
Close	Closes the **MMP Calibration** window.

The Calibrations

Four different MMP calibrations may be analyzed with this tool. For each calibration, **Preview**, **Details**, and **Run** buttons are provided.

Button	Description
Preview	allows the user to view the images for that particular calibration in the Preview panel.
Details	provides information about each calibration.
Run	performs the analysis of that measurement. Additionally, the orbits from the 4-point calibration may be displayed using the Orbits button.

Aluminum Grid Measurement / Linearity Check

Data for the **Aluminum Grid Measurement** is collected with a device containing 16 carefully-positioned holes. The collimated beam source holder is placed in each hole. The resulting 16 point images are used to analyze the linearity of the detector.

Collimator Depth

The collimator depth phantom is used to collect data for the collimator depth calibration. This calibration was once used to determine the distance from the detector plane to the pinhole plane, however, it is now out-of-date and is turned off by default. It may be turned back on using the “Enable ColDepth” option found in the MMP Menus.

Pinhole Offset (Collimated Beam)

The **Pinhole Offset** calibration evaluates the deviation between the center of the pinhole plane and the center of the detector plane.

Geometrical Calibration (4-point)

The 4-point calibration provides a wealth of geometrical information for the NanoSPECT/CT. This geometrical information is then used by special algorithms to determine the forward model necessary for successful SPECT reconstruction.

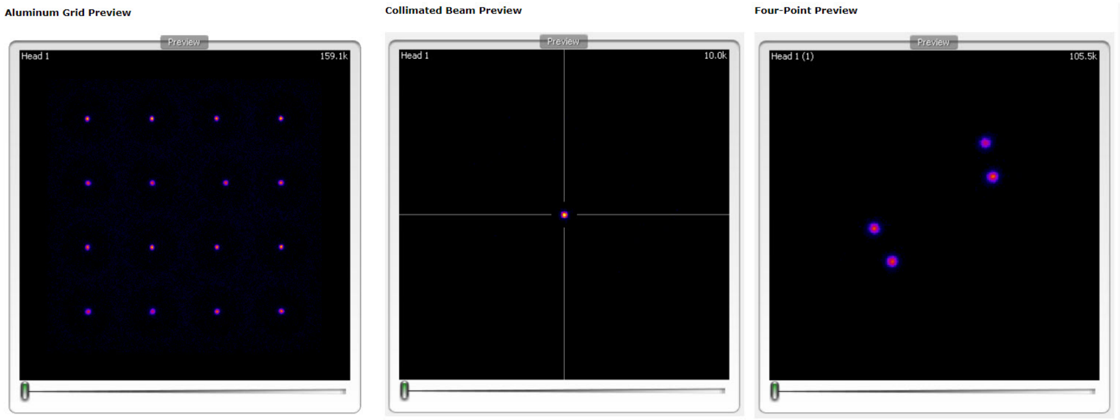
Calibration Failures

In each calibration panel, there are also fields relaying information about the completeness of the data for each head and some quality measure (either **Resolution**, **Linearity**, or **Quality**). The table below includes information about the limits for passing a particular calibration and how to interpret error messages. In each case, x designates a head number. For example, in the 4-point calibration, a R1 (as shown in the screen shot) would indicate that the Radius of Rotation for Head 1 was outside the acceptable limits.

Calibration	Error	Message	Interpretation Limits
Intrinsic Resolution	Rx	Intrinsic detector resolution	>2.4 mm
Intrinsic Resolution	Px	Pixel Size	<0.97mm or >1.03mm
Intrinsic Resolution	Lx	Quality of linearity	>30 (A.U.)
Collimator Depth	Hx	Detector plane to aperture plane distance	>130.1mm or <134.1mm
Collimated Beam	Hx	Absolute distance between aperture center and detector center (y or z)	>1.5mm
4-Point	Ax	Absolute aperture offset (transaxial or axial)	>1.0mm
4-Point	Dx	Absolute detector offset (transaxial or axial)	>1.5mm
4-Point	Rx	Radius of rotation	>45.9mm or <43.9mm
4-Point	Q	Overall quality of the calibration	>3.0 (A.U.)
4-Point	B	Horizontal bed offset	>3.0mm

Preview

The **Preview** panel displays calibration data for a particular calibration (selected using that calibration's Preview button). This panel is useful for checking head order in the 4-point calibration or determining a missing point in the **Linearity Check** calibration. The slider bar at the bottom allows movement between heads.



Preview Types

Output

The **Output** panel provides a log of the steps being performed. For example, the **Output** section will inform the user that files have been found, provide the numerical results from the analysis, and help identify potential errors.

MMP Menus

Several useful fixes and features may be found in the **MMP Menus** of **File**, **Tools**, and **Help**.

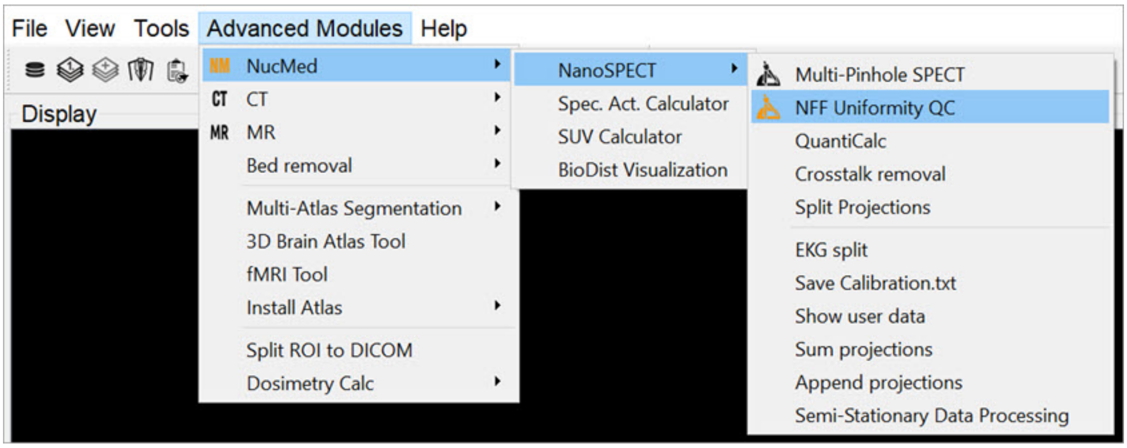
MMP Menu	Item	Function	Keyboard Shortcut
File	Open Data...	Identical to the **Open** button in the Control panel, this opens a browser to allow the loading of calibration data files.	Ctrl-O
File	Basic Configuration	The ID of the **NanoSPECT** and # of heads (typically 2 or 4) are set in this panel, pictured below.	Ctrl-B
File	Enable ColDepth	By default, the collimator depth phantom is not used in the MMP Calibration analysis. However, it may be enabled with this checkbox.	
File	Exit	Used to exit the MMP Calibration tool.	Ctrl+Q
File	Enable ColDepth	By default, the collimator depth phantom is not used in the MMP Calibration analysis. However, it may be enabled with this checkbox.	
Tools	Merge 4-point files	In the presence of only one single-pinhole aperture, 4-point data are collected one head at a time. This tool merges those data into a single file.	
Tools	Convert Calib File	On some Nucline versions, a slightly modified version of the calibration data is needed. This tool converts the calibration file accordingly.	

Near-Field Uniformity

The **Near-Field Flood Uniformity** (**NFF QC**) is a quality control procedure for monitoring the stability of the PMT gains for each head in the NanoSPECT/CT. To collect NFF QC data, please run the **QC SPECT Near-Field** Flood (NFF) protocol in the **Configuration/QC Protocols** panel of the **Nucline** software.

Getting There

To gget to the **Near-Field Uniformity** analysis panel, go to **Advanced Modules** > **NucMed** > **NanoSPECT**.

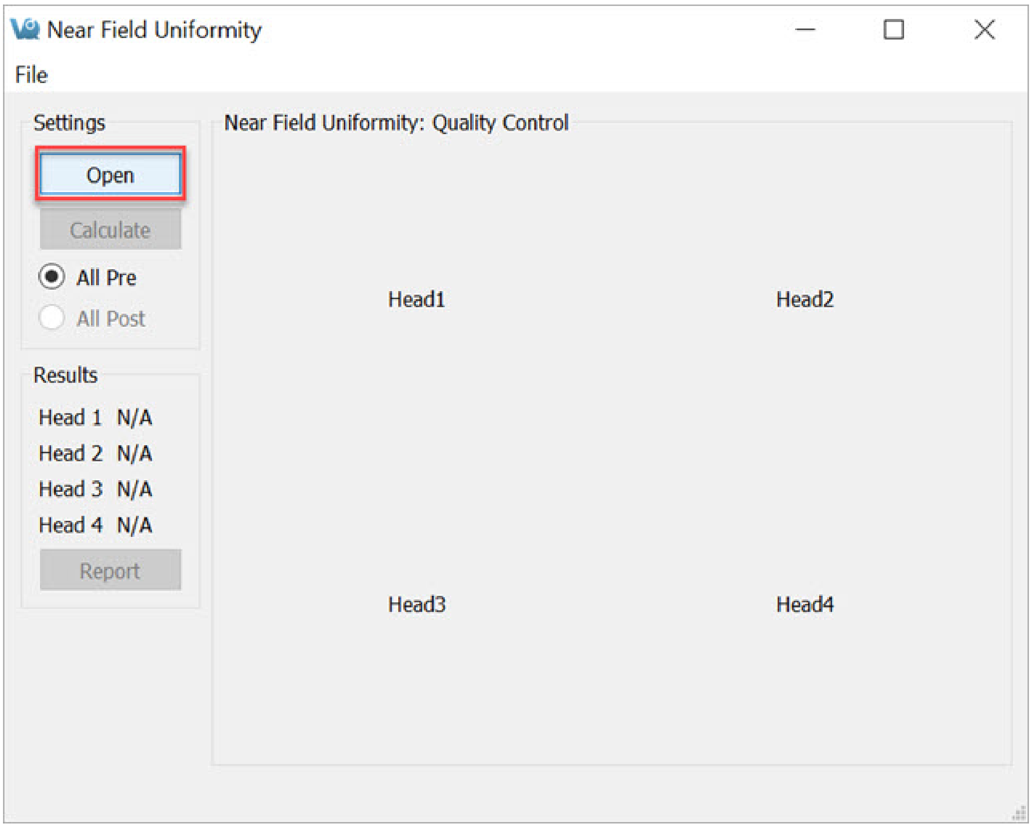


NF Uniformity Calibration

Function

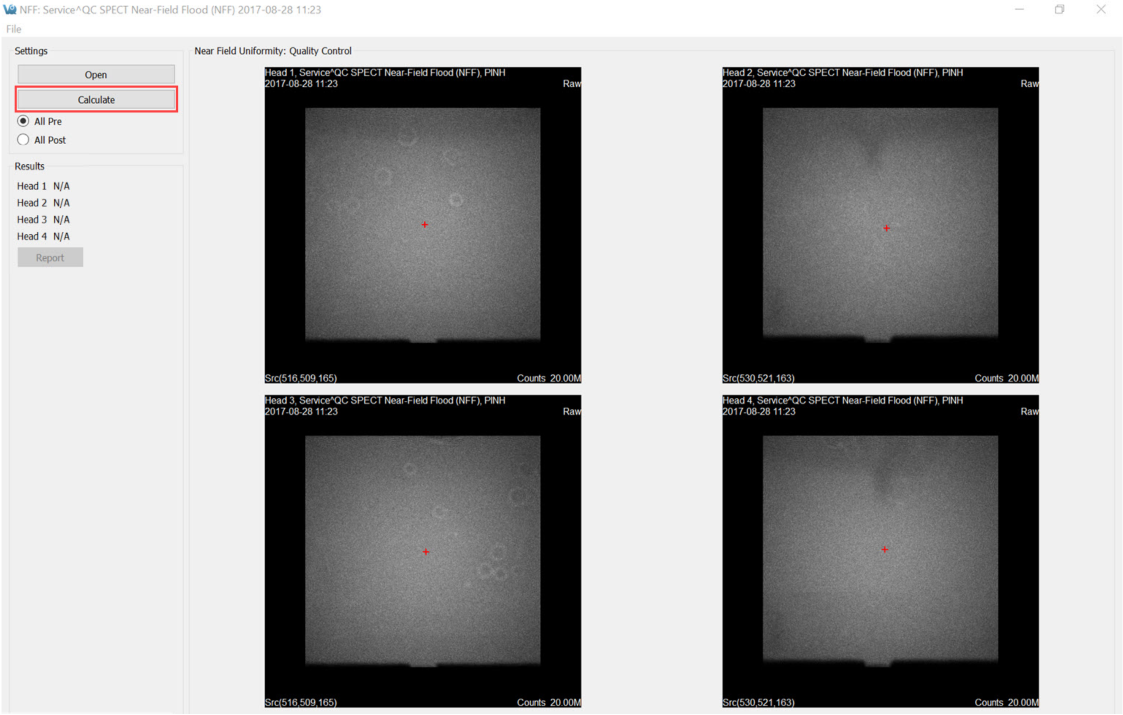
The **Near-Field Uniformity** tool analyzes NFF QC data for monitoring detector uniformity. To begin the procedure, use the **QC SPECT Near-Field Flood (NFF)** protocol to collect NFF QC data. Place ~0.5MBq of Tc-99m in as small a volume as possible in a PCR (Eppendorf) tube. Place this tube in the NFF phantom, a specially-designed holder for the Minerve bed. Center the point source in the object space as well as possible (using the images and countrates as a guide). Run the NFF Protocol, rotate 90-degrees, and run the **NFF Protocol** a 2nd time. Now that data are collected, they may be analyzed using the **Near-Field Uniformity** tool.

The initial NFF panel shows gray areas for each head and an array of buttons. To load the data, press the **Open** button.



NFF Panel

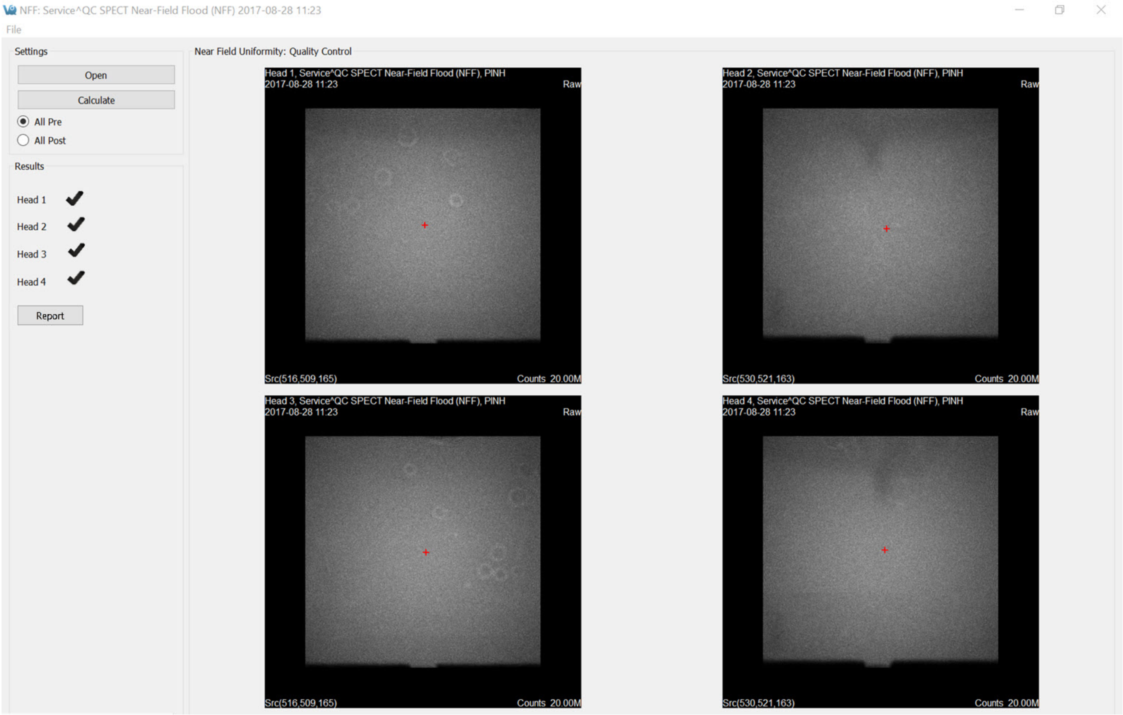
The data for each head will appear in the appropriate box. To run the analysis, press **Calculate**.



Calculate

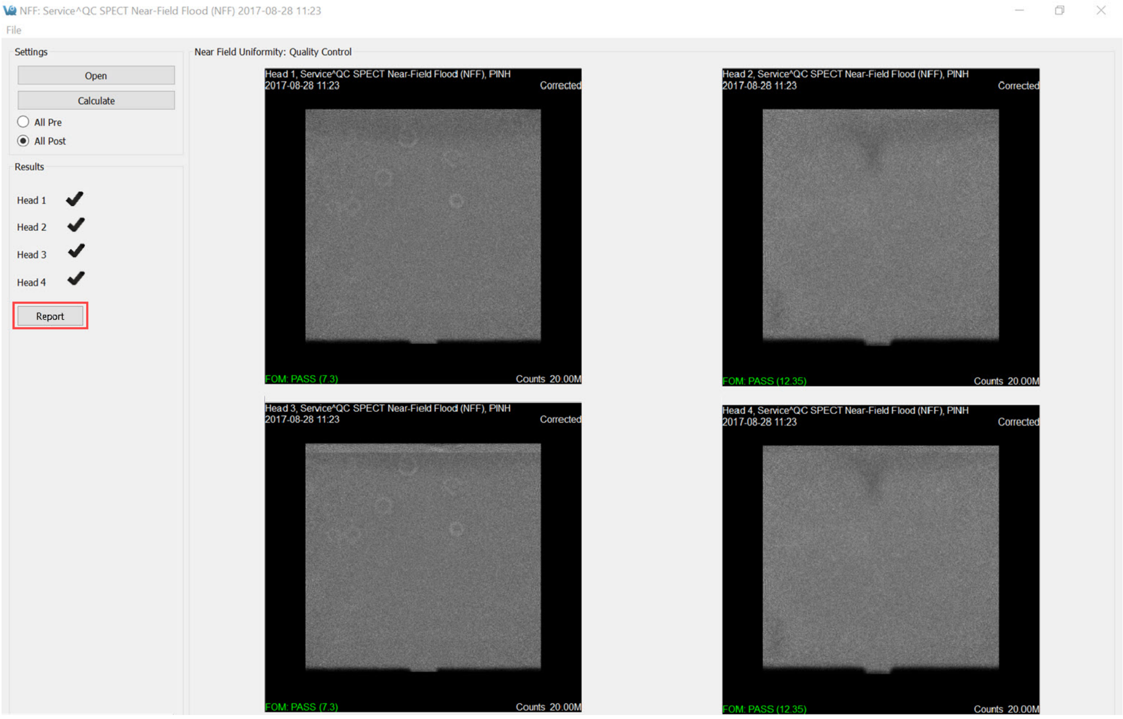
As the data are analyzed, the screen is grayed out. Progress can be monitored in the **Results** panel shown on the left.

Once the data are analyzed, the (x,y,z) calculated source position will be displayed in the lower-left corner of each **Raw** image. These images are indicated by the appearance of the word **Raw** in the upper-right corner. Also, the raw images are displayed when the **All Pre** push-button is selected. The red plus sign on each image indicates the source position with respect to the detector.



Results

Viewed the corrected images by clicking the **All-Post** button. Use Ctrl+T to toggle between the two sets of images. The FOM for each data set is displayed in the lower left corner. A green checkmark in the **Results** section indicates that the head passed the calibration. A red FOM in the **Results** section means that the data are questionable and should be sent to a service engineer for further analysis. Finally, to create a PDF containing the pre- and post-correction images, press **Report**.



FOM Data

Dosimetry Calc

Use the using **VivoQuant's Dosimetry Calc** tool, in conjunction with the third party application **OLINDA** (Organ Level INternal Dose Assessment), to estimate whole body dosimetry data. The **Dosimetry Calc** tool calculates the cumulative activity per unit activity administered (units in uCi-hr/uCi) which is the required input to the OLINDA application for dosimetry calculations.

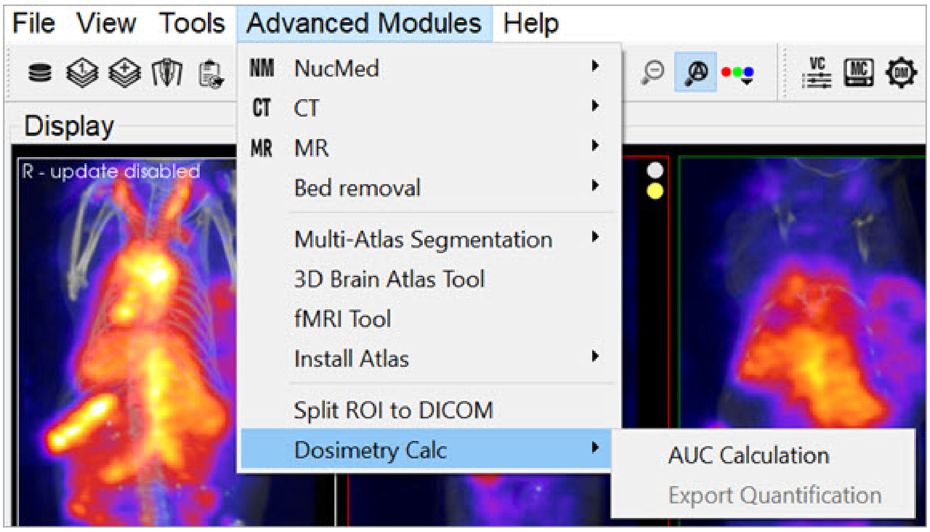
The cumulative activity per unit activity administered is estimated using the following area under the curve (AUC) method. The tool uses a curve fitting algorithm which fits the experimental isotope's exponential decay curve to the percent injected dose per gram (% ID/g) vs time curve of the experimental data. The AUC is calculated using trapezoidal approximations for experimental measurements, and the remaining AUC is calculated using the analytical solution to the definite integral.

The data is then stored in a .CSV file that can be copied into the **OLINDA** application.

ℹ **Note:** Before continuing ensure that a **Remainder Body ROI** has been created. This is a required data point for the **OLINDA** application.

Getting There

To access the **Dosimetry Calc** tool, the **3D ROI Tool** must be active. Go to the **Advanced Modules** tab, then move down to **Dosimetry Calc**.

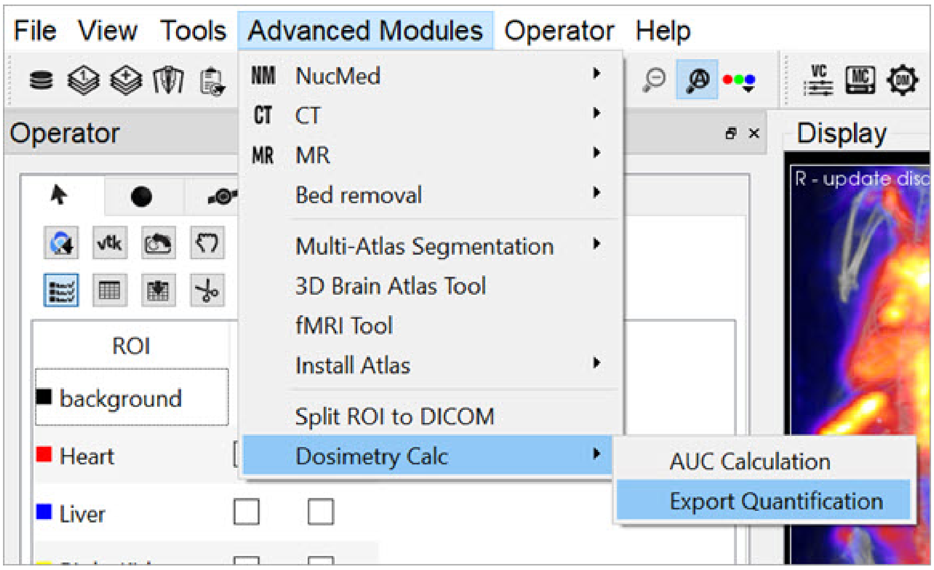


Dosimetry Calculation Tools

Function

Getting Started

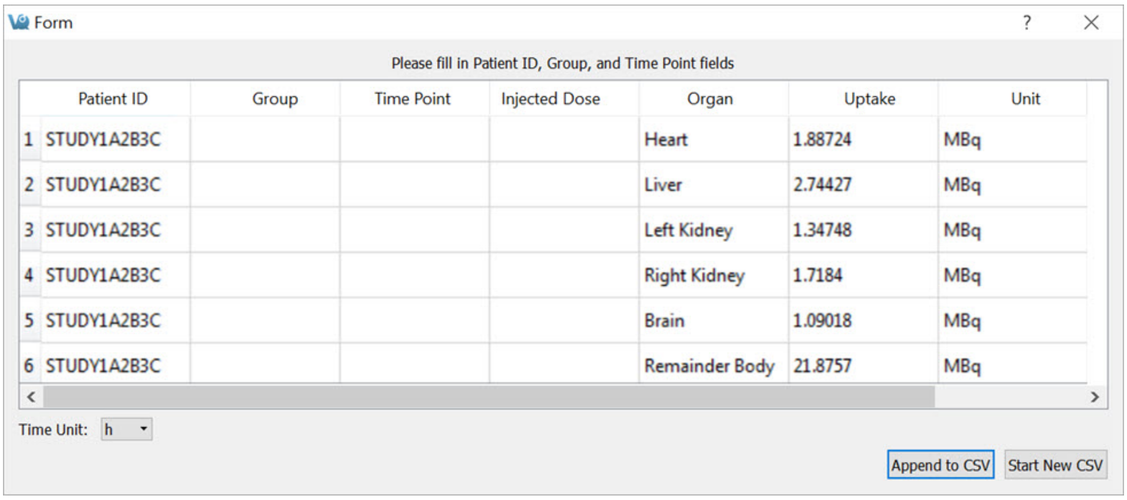
Start the tool by selecting **Export Quantification**.



Export Quantification

Once the tool starts, a spreadsheet appears and requests you to fill in missing information from the study. You can do this either in **VivoQuant** or in another spreadsheet software.

☑ **Tip:** It is likely easier to make changes in batch in a spreadsheet software.



Please fill in Patient ID, Group, and Time Point fields

	Patient ID	Group	Time Point	Injected Dose	Organ	Uptake	Unit
1	STUDY1A2B3C				Heart	1.88724	MBq
2	STUDY1A2B3C				Liver	2.74427	MBq
3	STUDY1A2B3C				Left Kidney	1.34748	MBq
4	STUDY1A2B3C				Right Kidney	1.7184	MBq
5	STUDY1A2B3C				Brain	1.09018	MBq
6	STUDY1A2B3C				Remainder Body	21.8757	MBq

Time Unit: h

Data Spreadsheet

Column	Info
Group	Group number. This allows for multiple groups to be used at once.
Time Point	Time point of the study for each frame. The time units can be manipulated using the drop down menu on the bottom left of the window or manually in another spreadsheet software.
Injected Dose	Initial injected dose.

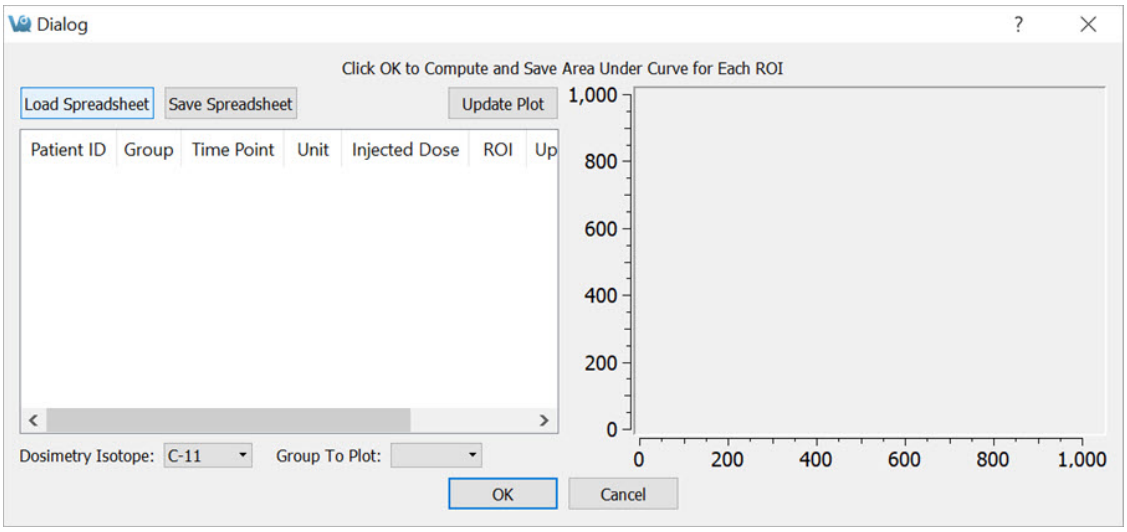
Once the spreadsheet is complete, save the information as an easily accessible .CSV file. In VivoQuant you may append an existing .CSV file or start a new one.

Using the AUC Calculation

Go to **Advanced Modules**, then select **Dosimetry Calc** > **AUC Calculation**.

Click **Load Spreadsheet** in the top left corner of the dialog box, and call the spreadsheet you created in the last section. In the **Dosimetry Isotope** drop down menu, select the isotope that was used in the experiment. If the isotope used is not listed, open the file isotopes.txt located in the **VivoQuant** install directory (default is C:\Program Files\inviCRO\VivoQuant) and add the isotope information.

Ensure that you select the correct isotope, because the **Dosimetry Calc** tool uses a curve fit algorithm and extrapolates using only isotope-specific radioactive decay information.



Click OK to Compute and Save Area Under Curve for Each ROI

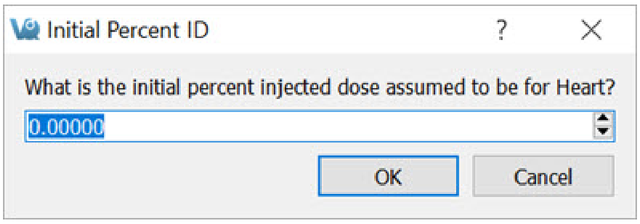
Patient ID	Group	Time Point	Unit	Injected Dose	ROI	Up

Dosimetry Isotope: C-11

Group To Plot:

Load Spreadsheet

Next, click **Update Plot** and enter the initial percent injected doses assumed for each of the ROIs.

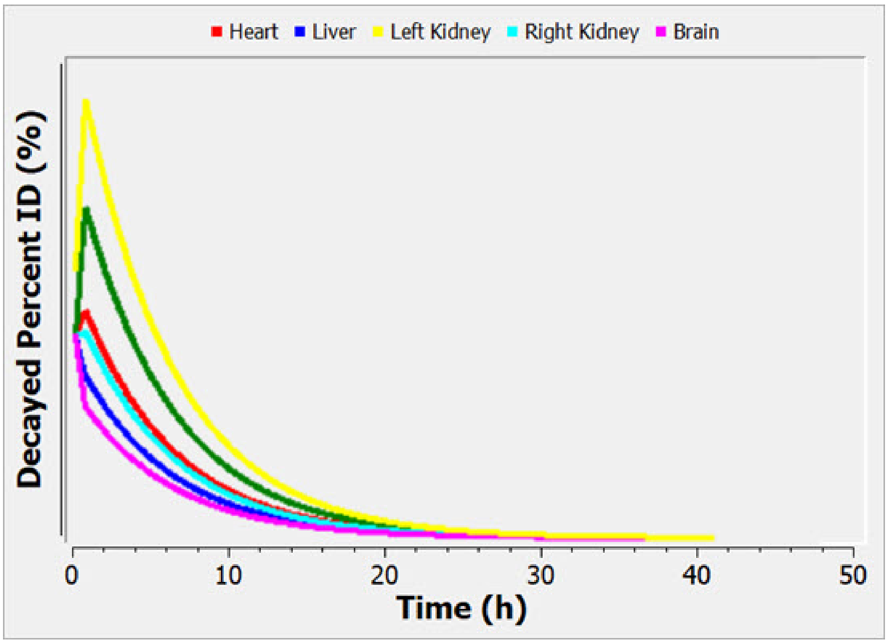


What is the initial percent injected dose assumed to be for Heart?

0.00000

Update Plot

The **Plot** should now appear next to the table in the window.



Decay Percent ID

Click **OK** and save as another .CSV file. This data is now ready to be used in the **OLINDA** software.

Treatment of Quantitative Data

Overview

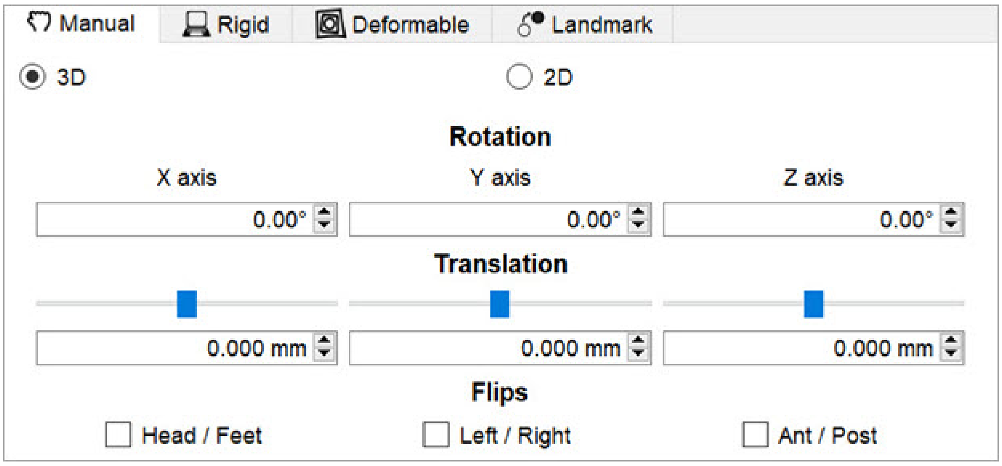
Image data can be quantitative, therefore care must be given to preserving data integrity when modifying it in **VivoQuant**. Regardless of whether data is reported in units of uptake (uCi, Bq, etc.) or concentration (uCi/cc, %Id/g, etc.), the data itself is representative of uptake measured within a given region. As such, the relationship between the uptake (U), the volume (V) and concentration (C) of uptake of a region must be preserved through any transformations if the data is to remain accurate.

That is to say, the relationship given by $C = \frac{U}{V}$ must be preserved.

VivoQuant is meticulous about preserving this relationship whenever data is resampled such that all three metric can be measured accurately within a region before and after resampling. Workflows that involve scaling the raw data, however, require specific attention from the user. When data is scaled, the volume of regions change. From the equation above, it is clear this needs a proportional change in either the uptake or the concentration of regions, but not both. Consequently, either the sums of data across regions is preserved (uptake) or the averages of data across regions is preserved (concentration), but not both. Therefore, once the resampling has been performed with scaling, the user should not convert between units of concentration (or equivalents, such as %ID/g and SUV) and uptake. Doing so would result in systematically biased numbers.

Reorientation/Registration Tool

The **Reorientation/Registration** operator may scale data.



● 3D ○ 2D

Rotation: X axis 0.00° | Y axis 0.00° | Z axis 0.00°

Translation: 0.000 mm | 0.000 mm | 0.000 mm

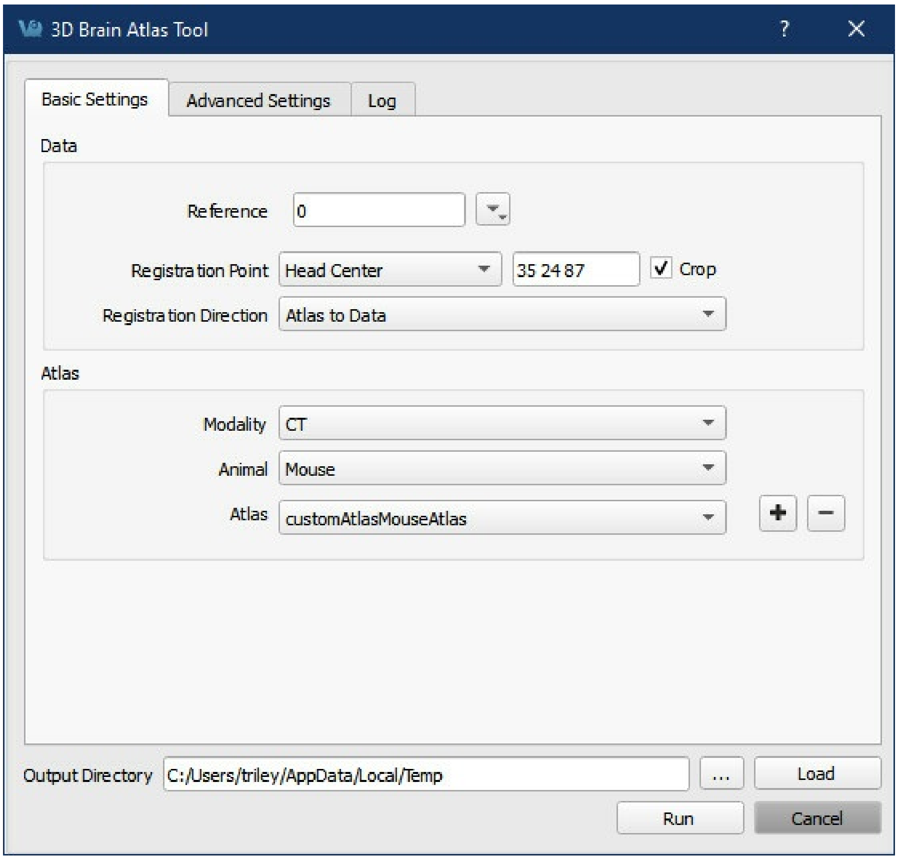
Flips: ☐ Head / Feet ☐ Left / Right ☐ Ant / Post

Reorientation/Registration Tool

Manual scaling can be enabled in the **Operator** menu. Non-linear and affine registrations may also scale the data, and can be accessed through the other tabs in the Operator window.

⚠ **Important:** Do not convert units after an image has been rescaled. Converting units will compromise the accuracy of the data.

3D Brain Atlas Tool



Reference: 0

Registration Point: Head Center 35 24 87 ☑ Crop

Registration Direction: Atlas to Data

Modality: CT

Animal: Mouse

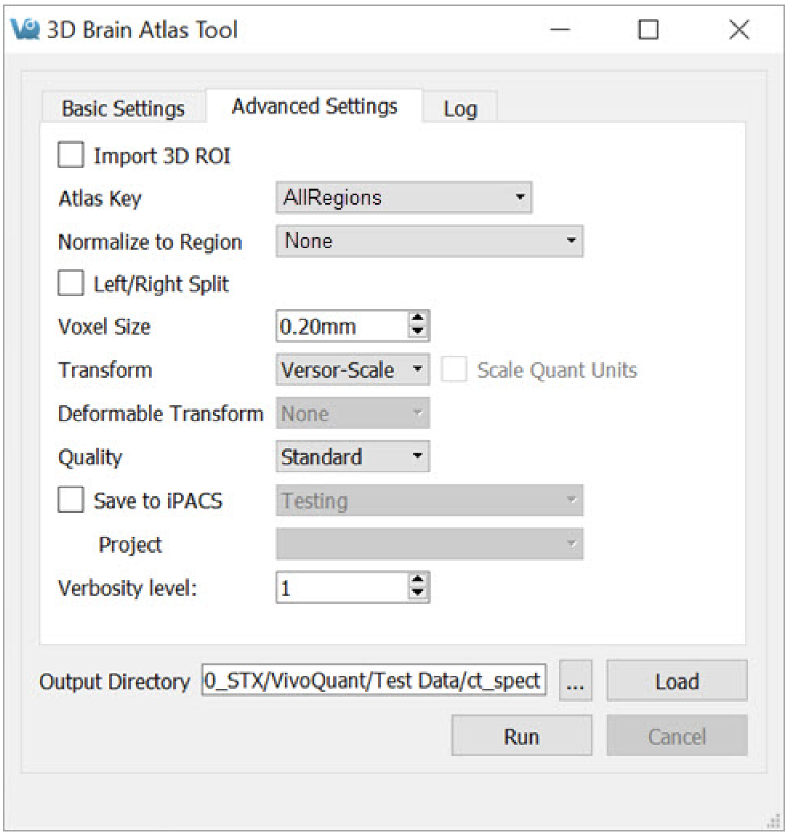
Atlas: customAtlasMouseAtlas

Output Directory: C:/Users/triley/AppData/Local/Temp

3D Brain Atlas Tool

The tool gives the next options:

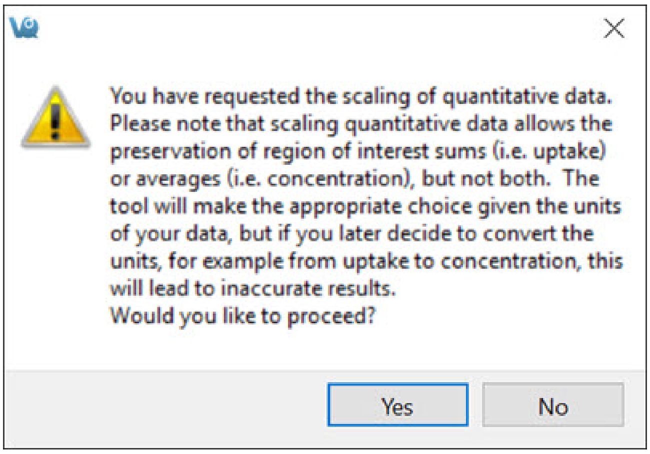
- **Registration Point**: option to determine the technique to perform the transformation.
  - **Head Center**: will center the reference's head and do all the operations to present the brain atlas, it is the best method for cropped output. Options **Registration Direction** and **Crop** are enabled for this technique.
  - **Cursor Seed Point**: will seed the operation with the crosshair point in order to present the brain atlas, it is the best method for non-cropped output. In this technique **Registration Direction** is "Atlas to Data" and **Crop** is unchecked, both always fixed.
- **Registration Direction**:
  - **Atlas to Data**, the default choice, will simply transform the brain atlas ROIs to fit the data and will avoid scaling and resampling the data altogether.
  - **Data to Atlas** will, however, resample the images and may scale the data depending on the type of transformation used. The type of transformation used is found in the Transform drop-down menu in the **Advanced Settings** tab.
- **Crop**: when is enabled will crop the output.



☐ Import 3D ROI
Atlas Key: AllRegions
Normalize to Region: None
☐ Left/Right Split
Voxel Size: 0.20mm
Transform: Versor-Scale ☐ Scale Quant Units
Deformable Transform: None
Quality: Standard
☐ Save to iPACS: Testing
Project:
Verbosity level: 1
Output Directory: 0_STX/VivoQuant/Test Data/ct_spect ...

Advanced Settings

If using a transformation that could rescale the data, the option to **Scale Quant Units** will be available. If checked, a box will appear to warn of the effect of scaling quantitative data.



You have requested the scaling of quantitative data. Please note that scaling quantitative data allows the preservation of region of interest sums (i.e. uptake) or averages (i.e. concentration), but not both. The tool will make the appropriate choice given the units of your data, but if you later decide to convert the units, for example from uptake to concentration, this will lead to inaccurate results.
Would you like to proceed?

Scale Quant Units Warning

Clicking **Yes** will check the box and allow **VivoQuant** to rescale the data. No transform will scale data unless this box is checked. If the box is checked, a **Versor** transform will still not scale the data, but **Versor-Scale** or **Versor-Affine** transforms will.

This is only applicable to quantitative data. Non-quantitative data that is loaded will be scaled regardless of the settings here.

⚠ **Important:** Do not convert units after an image has been rescaled. Converting units will compromise the accuracy of the data.

How do I Know if my Data is Quantitative or Not?

VivoQuant detects quantification based on the units provided by the image data's meta-information. Units of activity (Bq, kBq, MBq, GBq, Ci, mCi, uCi, nCi, COUNTS, PSL), concentration (activity per mm3, m3, cc, L, ml, uL), %ID, %ID/g and SUV should all be considered quantitative and are recognized as such by **VivoQuant**.

Logging

Log file

VivoQuant will always write a log file that is unique per-session. You can find this log in the temp folder, its name contains the following pattern vivoquant_[datetime]_session-[random id].log.

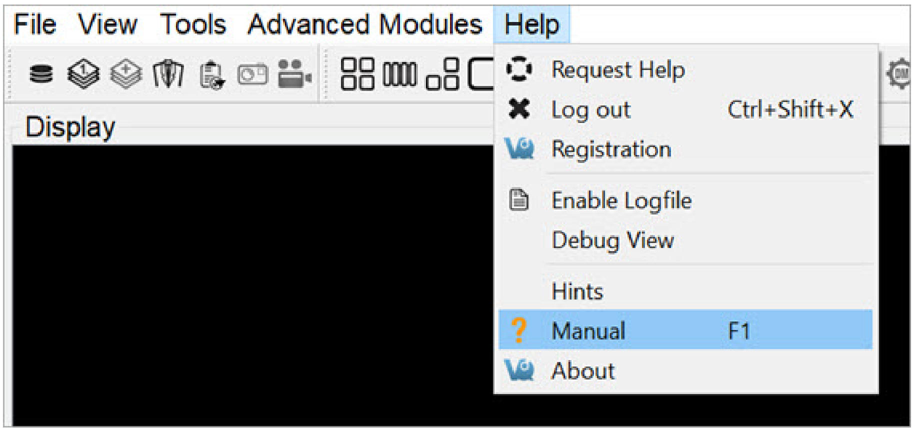
This will be automatically added to the report when you create a Help Report

Manual

A **VivoQuant** manual has been created to guide the user through all the post-processing functions in a clear and step-by-step manner.

Getting There

To open the manual go to **Manual** under the **Help** menu.



VivoQuant User Manual

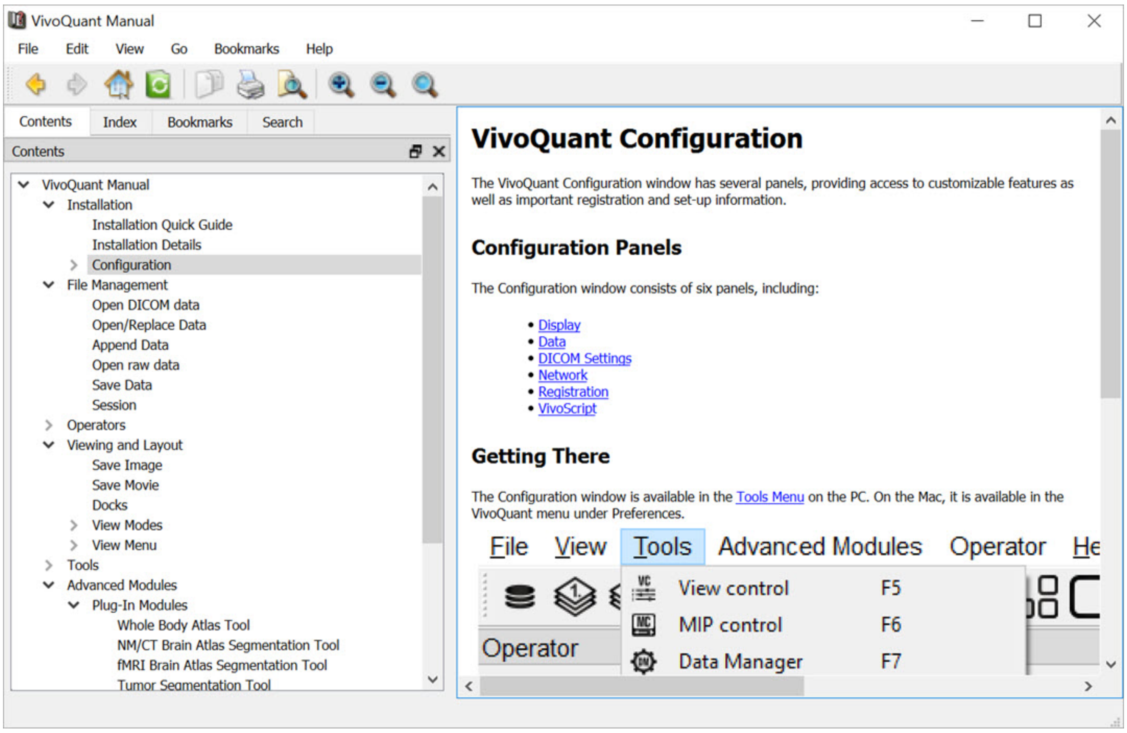
The keyboard shortcut F1 can also be used to open the manual.

Function

Users can browse through the different chapters of the **Manual** to read an in depth explanation of all of the post-processing functions and instructions on their use.

The different sections covered in the manual are as follows:

- Installation
- File Management
- View
- Post-Processing
- Tools
- Help
- Keyboard Shortcuts



VivoQuant Configuration

The VivoQuant Configuration window has several panels, providing access to customizable features as well as important registration and set-up information.

Configuration Panels

The Configuration window consists of six panels, including:

- Display
- Data
- DICOM Settings
- Network
- Registration
- VivoScript

Getting There

The Configuration window is available in the Tools Menu on the PC. On the Mac, it is available in the VivoQuant menu under Preferences.

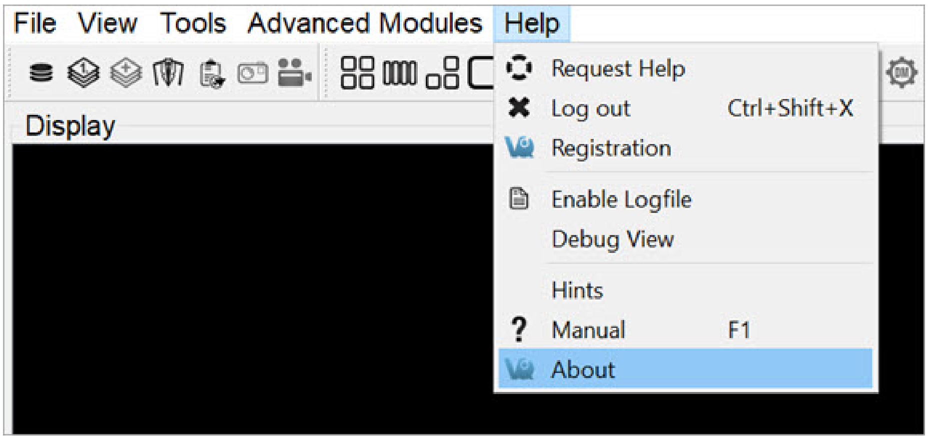
Manual Sections

The sections on the left can be viewed in detail by left-clicking on them. This will open up sub sections which can be viewed on the right.

About

Getting There

To open the About section go to **About** under the **Help** menu.



About VivoQuant

Function

The **About** feature provides information about **VivoQuant**. It informs the user what version of VivoQuant is installed, and provides the contact information for the creator of **VivoQuant**. It also displays who the **VivoQuant** program is registered to.

It also supplies the web links to the DICOM toolkit and the Qwt project used to help make this program.

VivoQuant® 2021 [64bit] (Build vq-2021-0-g70645b283)
Web page: http://www.VivoQuant.com/
© 2002-2008 Christian Lackas, <lackas@spect-ct.com>
© 2008-2021 Invicro, LLC <info@invicro.com>

This copy is registered to:
Demo Licenses
Imaging
"Luana Dos Santos" - "SW" <ldossantos@invicro.com>

All licenses can be found in credits.
This product uses the OFFIS DICOM Toolkit DCMTK, © 1994-2017, OFFIS e.V.
This product is based in part on the work of the Qwt project.
The Insight Segmentation and Registration Toolkit (ITK): © Insight Software Consortium.
Visualization Toolkit (VTK): © 1993-2008 Ken Martin, Will Schroeder, Bill Lorensen
ImageMagick: © 1999-2016 ImageMagick Studio LLC
Qt: © 2016 The Qt Company Ltd.
ANTs: © 2009-2013 ConsortiumOfANTS
Ceres Solver: © 2016 Google Inc.
ECAT 7 Loading library: © 2003-2010 Turku PET Centre

About Info

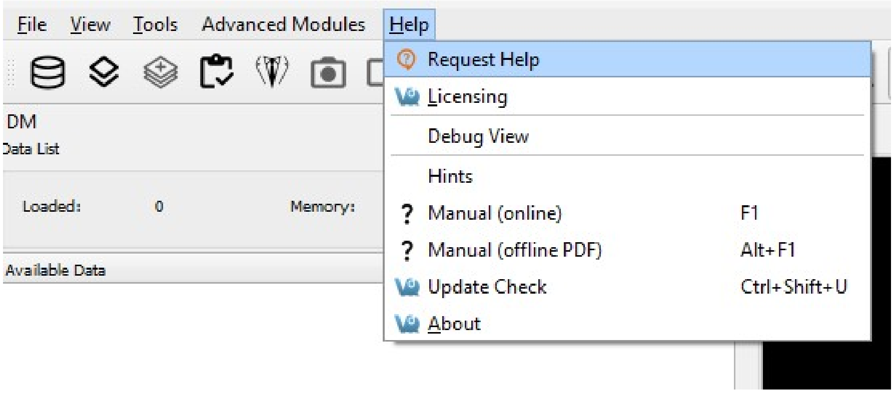
Help Reporter

VivoQuant's Reporter Tool assists users in submitting service and applications reports for review by the **inviCRO** service team. The tool offers a variety of pre-defined report sequences as well as an option for a manual report. Reports are bundled into .zip files that you can then submit during service request creation.

Note: Only information visible in the **Reporter** window is uploaded when a report is submitted. No personal, confidential, or otherwise hidden information is collected.

How to use the VQ Reporter Tool

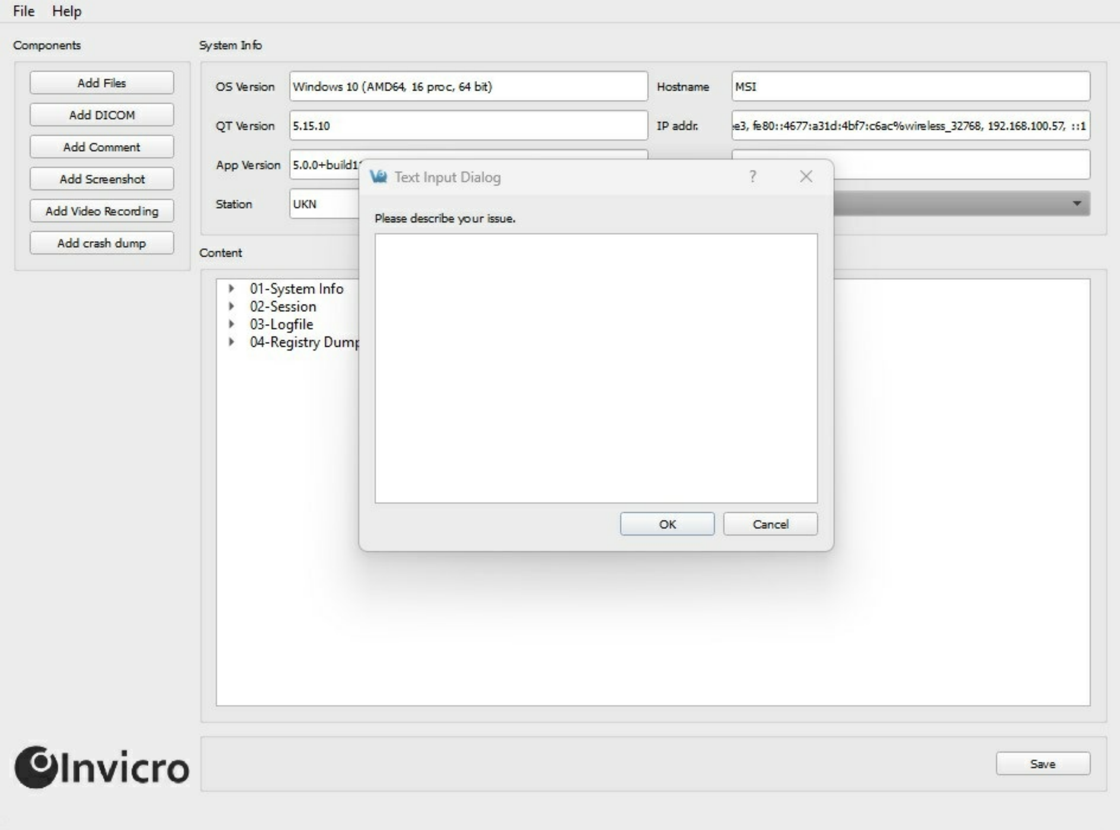
To get to the **Help Reporter** tool, go to **Help** > **Request Help**.



Reporter Tool

Initializing the **Help Reporter** will save a copy of the session currently in-progress.

Most reports will first request a written description of the problem to be included in a text file attached to the report.



OS Version: Windows 10 (AMD64, 16 proc, 64 bit)
Hostname: MSI
QT Version: 5.15.10
IP addr.: e3, fe80::4677:a31d:4bf7:c6ac%wireless_32768, 192.168.100.57, ::1
App Version: 5.0.0+build1
Station: UKN

Please describe your issue.

Reporter Input Dialog

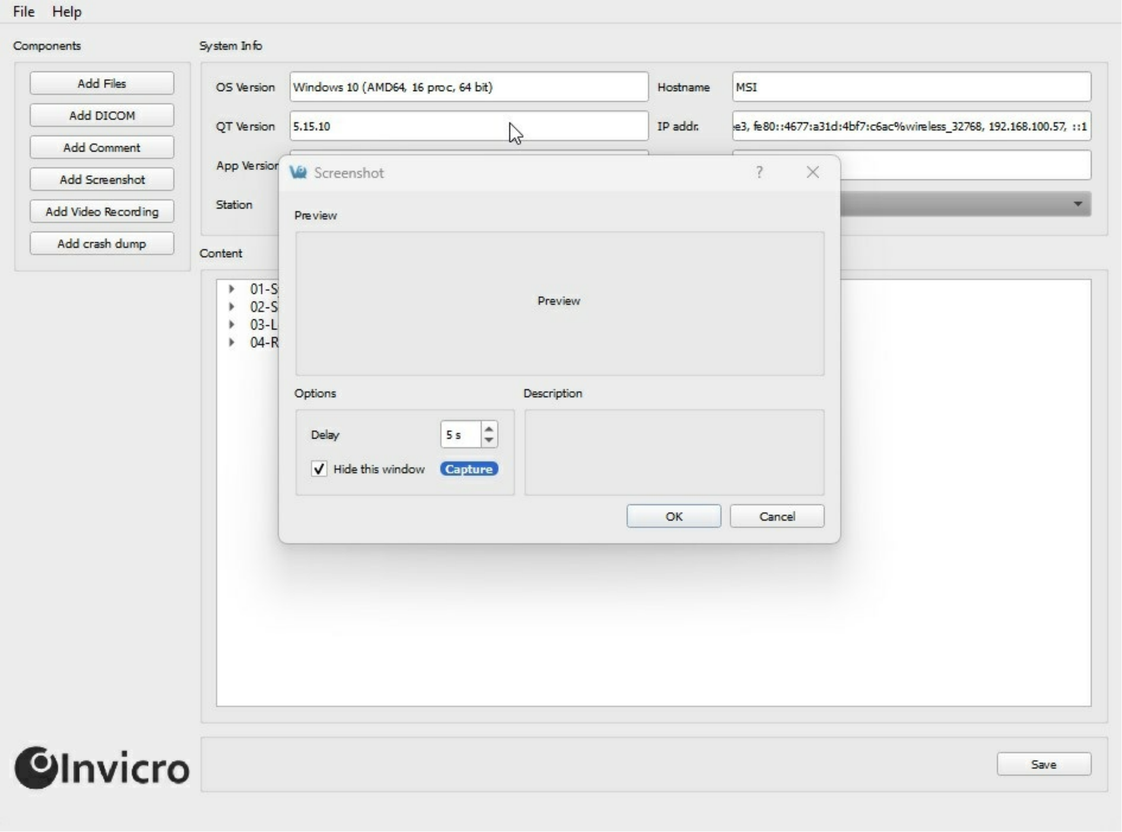
For all reports, it is possible to add additional files and images using the **Add** buttons arrayed across the left-hand side of the tool.

The **Add Files** button opens a window that can be used to manually select files. Multiple files may be selected simultaneously for inclusion in the report.

The **Add DICOM** button opens the Data browser where files may be selected. To load into the Reporter, either press the **Open** button or right-click and choose **Load into Reporter**.

The **Add Comment** button opens the Text Dialog Input window, which may be used to add additional written comments to the report.

The **Add Screenshot** button opens a screenshot acquisition dialogue. The dialogue has a capture delay to allow files to be opened or procedures begun prior to acquisition of the screenshot.

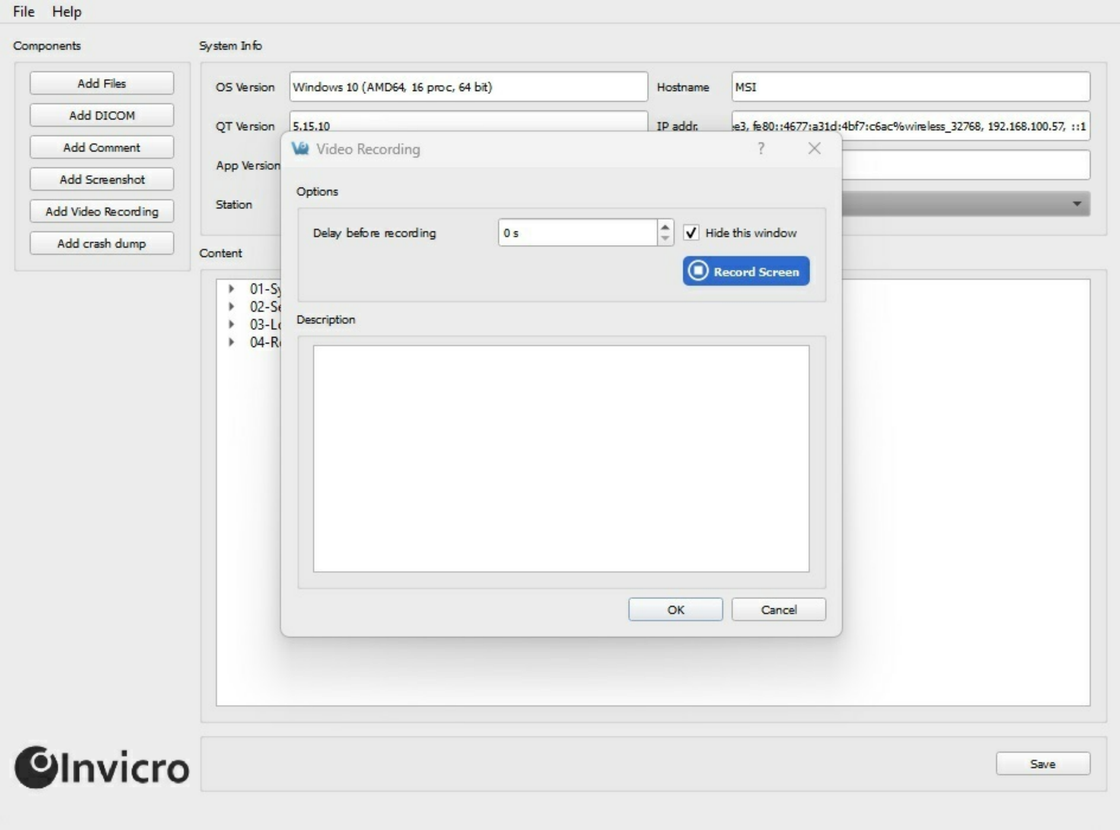


OS Version: Windows 10 (AMD64, 16 proc, 64 bit)
Hostname: MSI
QT Version: 5.15.10
IP addr: e3, fe80::4677:a31d:4bf7:c6ac%wireless_32768, 192.168.100.57, ::1
Delay: 5 s
☑ Hide this window

Add Screenshot

The **Add Video Recording** button opens a video acquisition dialogue. The dialogue has also a capture delay option. You can record a video of up to 2 minutes. The VivoQuant application can be captured when it is located on the primary monitor.

⚠ **Important:** This records the entire screen where **VivoQuant** is open, including other apps visible on that same screen



OS Version: Windows 10 (AMD64, 16 proc, 64 bit)

Hostname: MSI

QT Version: 5.15.10

IP addr: e3, fe80::4677:a31d:4bf7:c6ac%wireless_32768, 192.168.100.57, ::1

Options

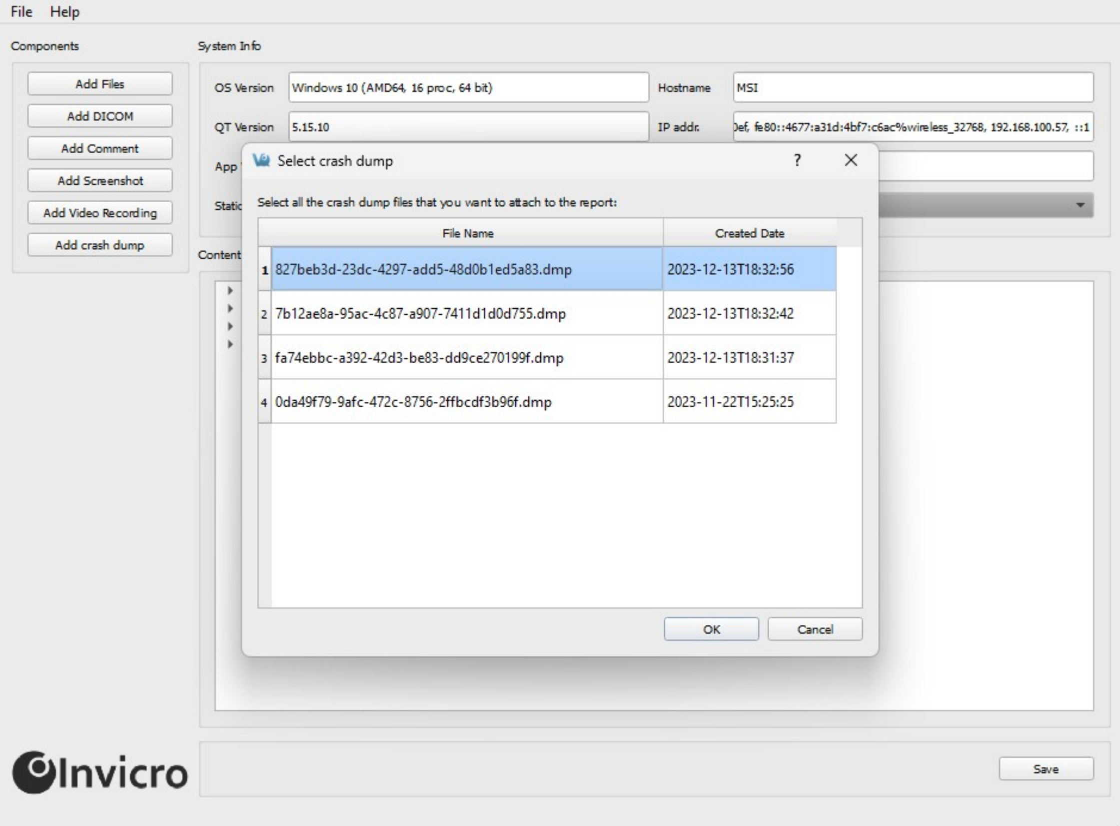
Delay before recording: 0 s

☑ Hide this window

Description

Add Video Recording

The **Add crash dump** button opens a dialogue to select a **VivoQuant** crash dump files.



OS Version: Windows 10 (AMD64, 16 proc, 64 bit)

Hostname: MSI

QT Version: 5.15.10

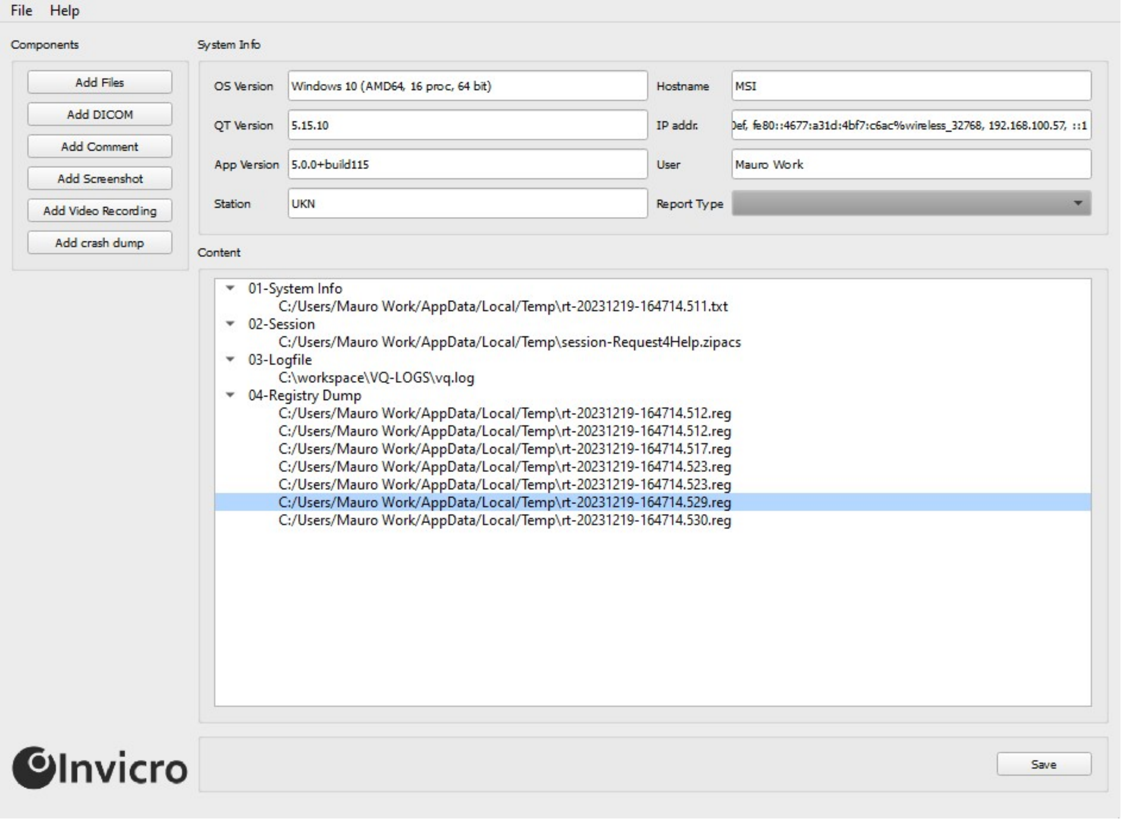
IP addr:)ef, fe80::4677:a31d:4bf7:c6ac%wireless_32768, 192.168.100.57, ::1

Select all the crash dump files that you want to attach to the report:

	File Name	Created Date
1	827beb3d-23dc-4297-add5-48d0b1ed5a83.dmp	2023-12-13T18:32:56
2	7b12ae8a-95ac-4c87-a907-7411d1d0d755.dmp	2023-12-13T18:32:42
3	fa74ebbc-a392-42d3-be83-dd9ce270199f.dmp	2023-12-13T18:31:37
4	0da49f79-9afc-472c-8756-2ffbcdf3b96f.dmp	2023-11-22T15:25:25

Add crash dump

In addition to the manual **Add** button options, the pre-defined report options will automatically gather certain files and add them to the report. Users can review some low-level items in the Content section by double-clicking on them.

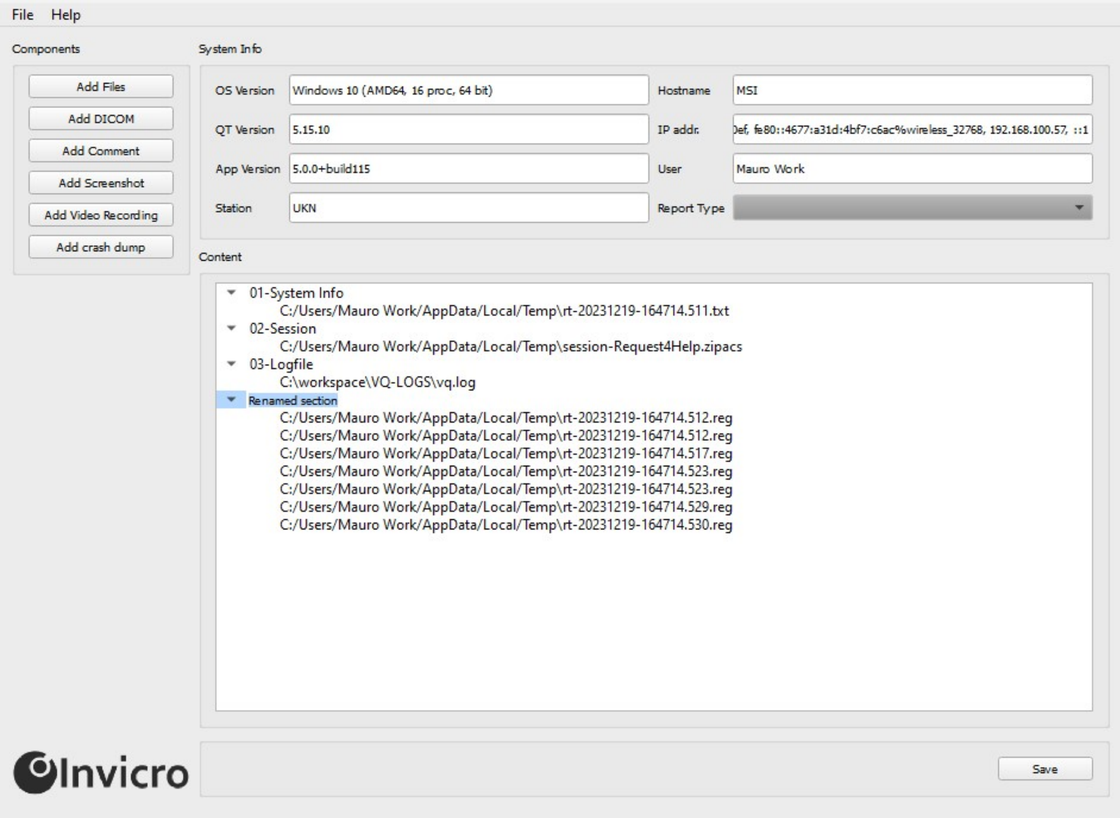


OS Version: Windows 10 (AMD64, 16 proc, 64 bit)
Hostname: MSI
QT Version: 5.15.10
IP addr.: ef, fe80::4677:a31d:4bf7:c6ac%wireless_32768, 192.168.100.57, ::1
App Version: 5.0.0+build115
User: Mauro Work
Station: UKN
Report Type:

```
▾ 01-System Info
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.511.txt
▾ 02-Session
      C:/Users/Mauro Work/AppData/Local/Temp\session-Request4Help.zipacs
▾ 03-Logfile
      C:\workspace\VQ-LOGS\vq.log
▾ 04-Registry Dump
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.512.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.512.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.517.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.523.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.523.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.529.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.530.reg
```

Content Panel

It is also possible to rename entries in the **Content** section by double-clicking on the top-level element.



OS Version: Windows 10 (AMD64, 16 proc, 64 bit)
Hostname: MSI
QT Version: 5.15.10
IP addr.: ef, fe80::4677:a31d:4bf7:c6ac%wireless_32768, 192.168.100.57, ::1
App Version: 5.0.0+build115
User: Mauro Work
Station: UKN
Report Type:

```
▾ 01-System Info
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.511.txt
▾ 02-Session
      C:/Users/Mauro Work/AppData/Local/Temp\session-Request4Help.zipacs
▾ 03-Logfile
      C:\workspace\VQ-LOGS\vq.log
▾ Renamed section
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.512.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.512.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.517.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.523.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.523.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.529.reg
      C:/Users/Mauro Work/AppData/Local/Temp\rt-20231219-164714.530.reg
```

Rename Content

Once all relevant files have been included in the report, click save and choose a filename. The zip file that is generated can be included in issue reports to **Invicro** support support@invicro.com to help the investigation of the issue.

Standalone Help Reporter

Another way to use **Help Reporter** is through its own application allowing you to create a report in case you are unable to start **VivoQuant**. It is located in the start menu with the name **Service Reporter**.

Overview

The **iPACS Sync** application is designed for batch, two-way data transfers between the **WebDisk** of a specific iPACS project and a local storage location. Directories and files are synchronized between the source and destination locations, and data transfers are authorized by an iPACS user's account permissions.

Batch Transfer Data to and from the iPACS

Browse the following links to learn more about using **iPACS Sync** to batch transfer data.

- Download latest iPACS Sync Application
- Configure a Sync Job
- Run a Sync Job
- Sync Specific Files from an iPACS

Configure a Sync Job

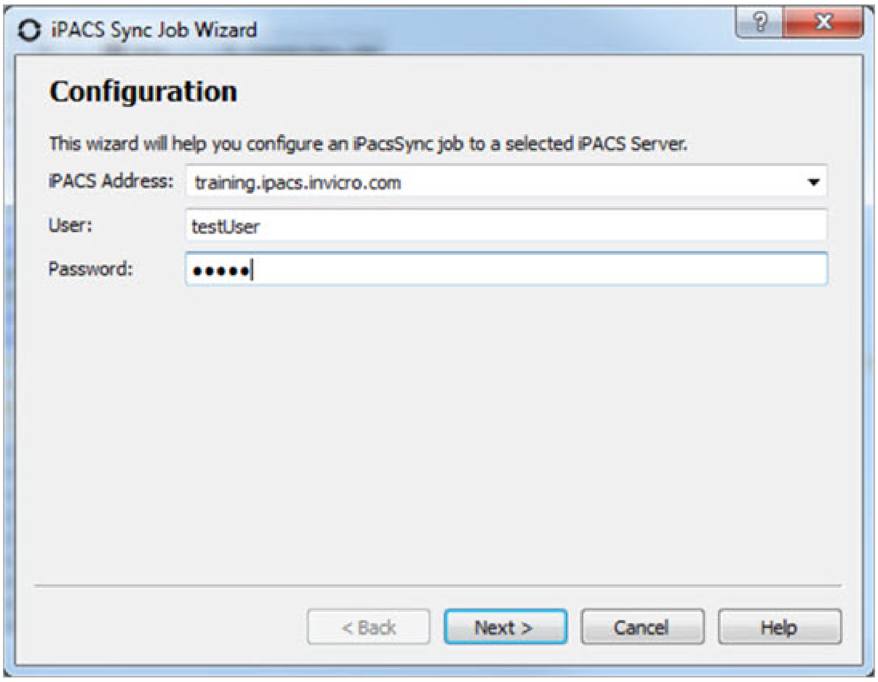
Create a Sync Job using the Wizard

To create a new job, click **Create New Job** at the top of the **iPACS Sync** application window. This will launch the **iPACS Sync Job Wizard**, which will guide you through the process of setting up a Sync job.

Job: test

Open Sync Job Wizard

1. Specify the iPACS URL or IP address in the **iPACS Address** field. Previously used addresses are available by clicking the arrow at the right of the text field.
2. Enter the username and password to use for the Sync. Data transfers adhere to the roles associated with an iPACS user's account.
3. After entering the required information, click **Next**.



iPACS Sync Job Wizard

Configuration

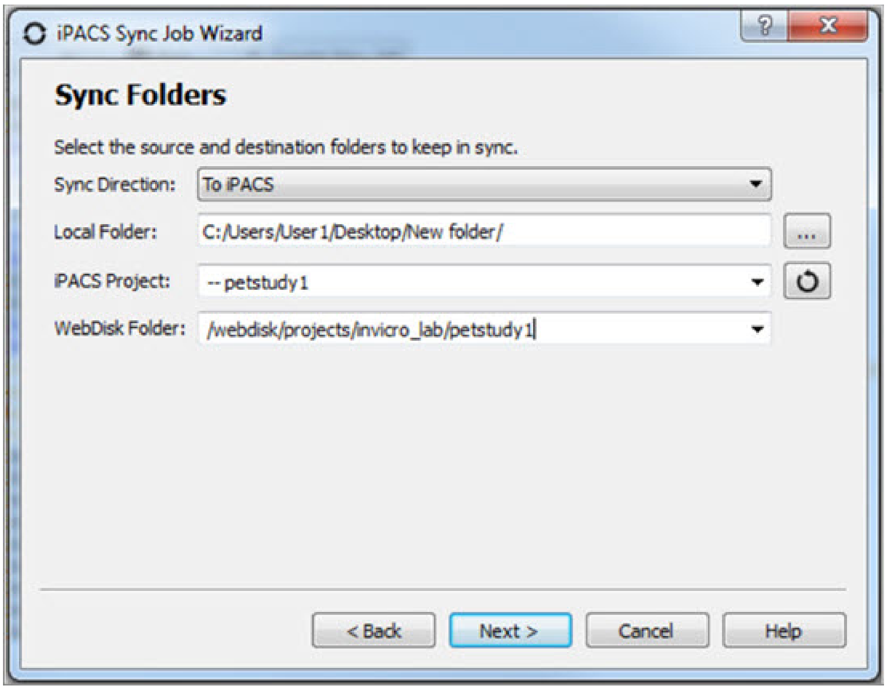
This wizard will help you configure an iPacsSync job to a selected iPACS Server.

iPACS Address: training.ipacs.invicro.com

User: testUser

Password: •••••

4. The wizard will attempt to download and install the sync key file for the specified iPACS. Alternatively, you can access the wizard via a web browser on the home admin page. The admin page is only available to users with the admin role.
5. Once the Sync Key is installed, click **Next**.
6. Specify the direction of the Sync.
7. Provide the complete path to the local directory to use in the Sync.
8. Select the project on the iPACS to use for the Sync.
    - The ↻ button will retrieve a list of projects on the iPACS, which can be selected by clicking the arrow to the right of the text field.
    - The path of the iPACS project can also be manually entered in the **iPACS Project field**.
9. The **WebDisk** folder for the selected project will automatically populate into the **WebDisk Folder** field. You can select subfolders via the drop-down menu to the right of the text field.
10. After entering the required information, click **Next**.



Sync Folders

Select the source and destination folders to keep in sync.

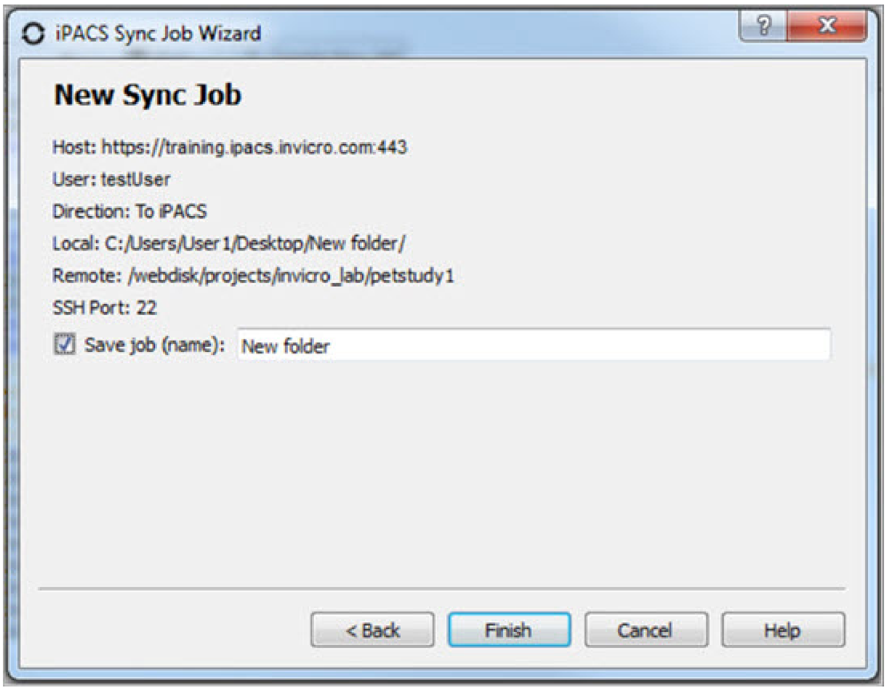
Sync Direction: To iPACS

Local Folder: C:/Users/User1/Desktop/New folder/

iPACS Project: -- petstudy1

WebDisk Folder: /webdisk/projects/invicro_lab/petstudy1

11. A summary page shows all the selected settings for the new Sync job.
12. Enter a name for the Sync job, then click **Finish**.



New Sync Job

Host: https://training.ipacs.invicro.com:443

User: testUser

Direction: To iPACS

Local: C:/Users/User1/Desktop/New folder/

Remote: /webdisk/projects/invicro_lab/petstudy1

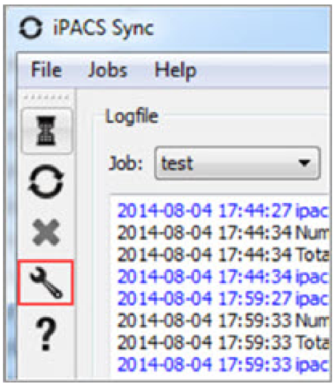
SSH Port: 22

☑ Save job (name): New folder

The Sync job is now created, and will be run immediately. Further settings can be configured, as described in the following sections.

Configuring Additional Settings

The **iPACS Sync Config** window allows you to manually create new Sync jobs and edit the configuration settings of existing jobs. To access the **iPACS Sync Config** window, click on the wrench icon 🔧 on the left side of the main window.

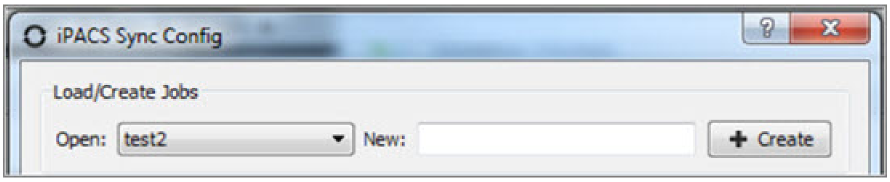


Job: test

```
2014-08-04 17:44:27 ipac
2014-08-04 17:44:34 Num
2014-08-04 17:44:34 Tota
2014-08-04 17:44:34 ipac
2014-08-04 17:59:27 ipac
2014-08-04 17:59:33 Num
2014-08-04 17:59:33 Tota
2014-08-04 17:59:33 ipac
```

Configuring Additional Settings

Select the job to configure from the **Open** drop-down, or enter a name and click **Create** to create a new Sync job.

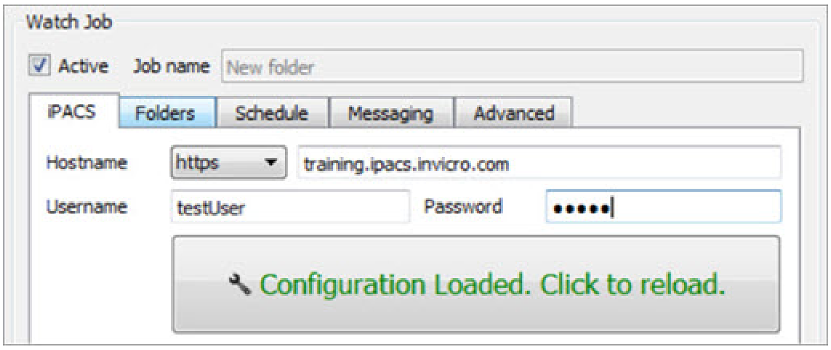


Open: test2

Create New Sync Job

iPACS Setup

Make a job active or inactive. Specify the iPACS URL or IP address in the **Hostname** field. Data transfers adhere to the roles associated with an iPACS user's account. If the **Username** and **Password** information are not provided here, the application will prompt for it before every data transfer iteration. Click the **Configuration** button to automatically obtain the sync key file from the iPACS if necessary.



☑ Active

Hostname: https training.ipacs.invicro.com

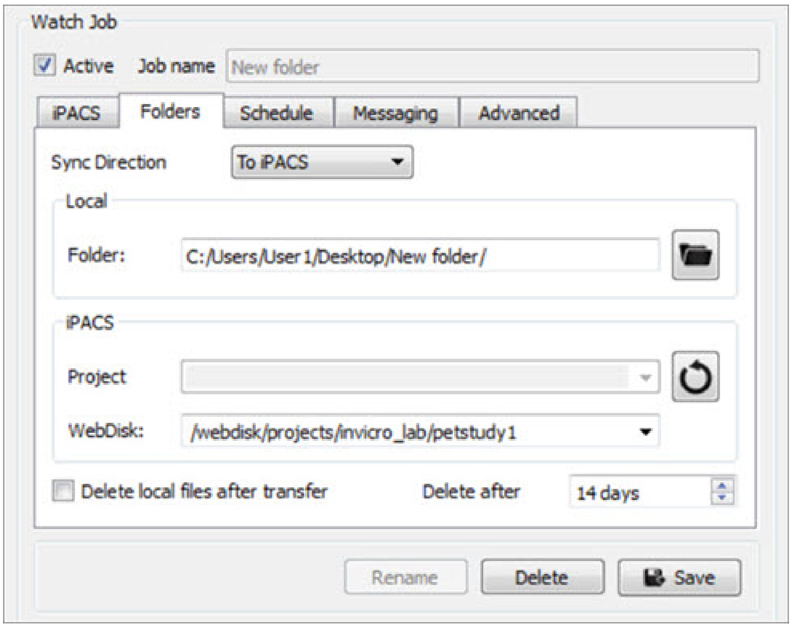
Username: testUser

Password: •••••

iPACS Setup

Directory Setup

Specify the direction of the Sync. Provide the complete path to the local directory to use in the Sync. Select the project on the iPACS to use for the Sync; the ↻ button will retrieve a list of projects on the iPACS, which can be selected by clicking the arrow to the right of the text field. The **WebDisk** folder for the selected project will automatically be entered into the **WebDisk** field. Subfolders can be selected by clicking the arrow to the right of the text field.



☑ Active Job name: New folder

Sync Direction: To iPACS

Folder: C:/Users/User1/Desktop/New folder/

Project:

WebDisk: /webdisk/projects/invicro_lab/petstudy1

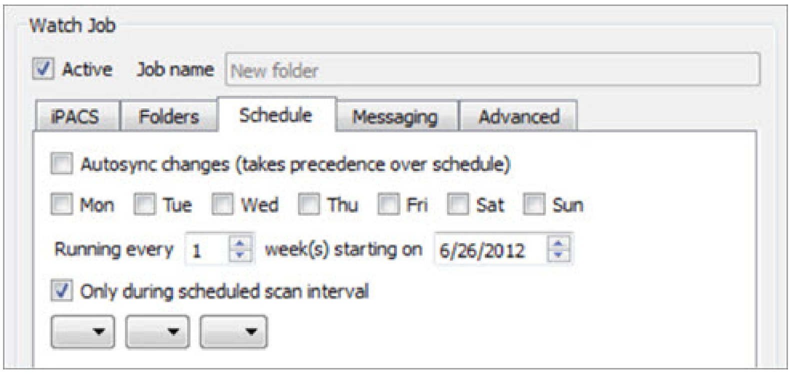
☐ Delete local files after transfer Delete after: 14 days

Directory Setup

Setting	Description
Delete local files after transfer	Files that were successfully transferred to the server are deleted locally. This feature is potentially dangerous and could lead to loss of data if not used properly.
Delete after	Schedule when files are removed from source location.

Scheduler

Create a schedule for when a Sync job will run.



☑ Active Job name: New folder

☐ Autosync changes (takes precedence over schedule)

☐ Mon ☐ Tue ☐ Wed ☐ Thu ☐ Fri ☐ Sat ☐ Sun

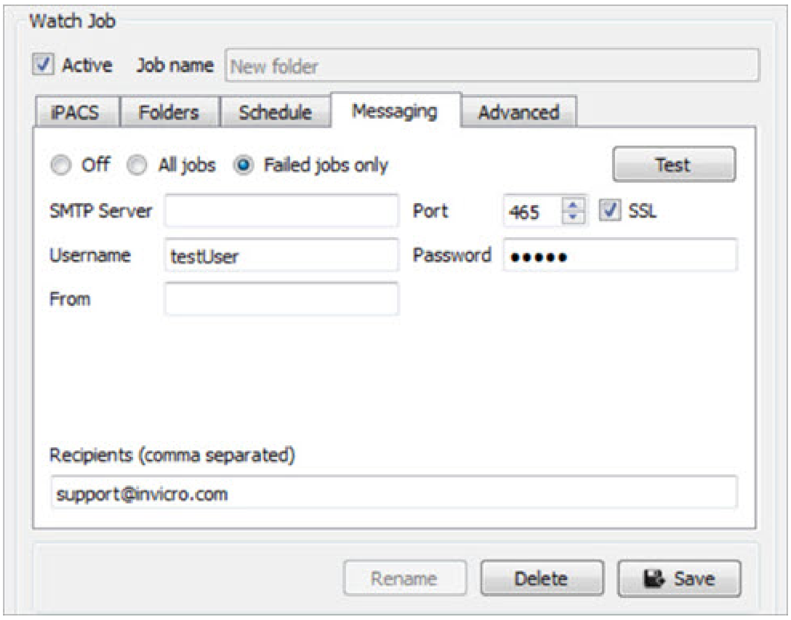
Running every 1 week(s) starting on 6/26/2012

☑ Only during scheduled scan interval

Scheduler

Setting	Description
Scan interval	Specify how often a Sync job runs while the application is open.
Autosync changes	A Sync job will automatically start whenever a new folder is added to the top level folder.
Only during scheduled scan interval	A Sync job will automatically start at the time specified on the days selected.

Notifications



☑ Active Job name New folder

○ Off ○ All jobs ● Failed jobs only

SMTP Server

Port 465 ☑ SSL

Username testUser

Password •••••

From

Recipients (comma separated)

support@invicro.com

Notifications

Setting	Description
Message Notifications	Turn on **Message Notifications** and specify what type of messages are sent.
SMTP Server	Contact your IT department for the server address. Normally can be found in the settings tab of your Email Client.
Port	Contact your IT department for the server address. Normally can be found in the settings tab of your Email Client.
Username	Username used associate with your email account.
Password	Authorization to access your email account.
From	Email account from which the notification will be sent.
Recipients	Notifications will be sent to the provided email addresses.

Advanced

Include or exclude files by specifying their extension. (e.g. *.dcm *.img *.hdr *.txt *.png). Filter is applied recursively through the subfolders of the top-level folder. The user can also provide files containing which file names, file extensions, and/or folders to include or exclude. Example text files would include the following:

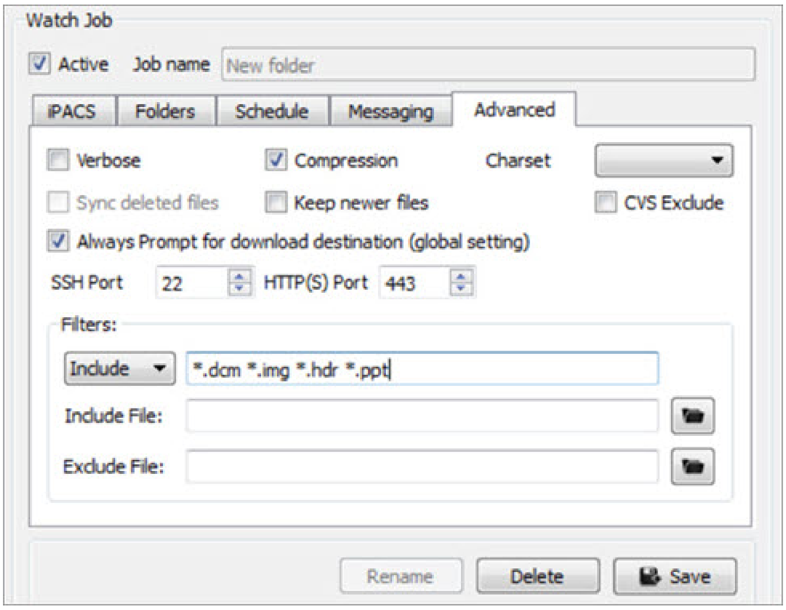
Include:

+ 2009*/ + *.csv

Exclude:

- *

In this example, all folders beginning with 2009 and all .csv files within those folders would be included in the transfer. All other files would be excluded.



☑ Active Job name New folder

☐ Verbose
☑ Compression
Charset
☐ Sync deleted files
☐ Keep newer files
☐ CVS Exclude
☑ Always Prompt for download destination (global setting)
SSH Port 22
HTTP(S) Port 443

Filters:
Include *.dcm *.img *.hdr *.ppt
Include File:
Exclude File:

Exclude

Setting	Description
Verbose	Print more detailed log messages.
Compression	Data is compressed before sending.
Filename charset	Specify as US-ASCII, ISO-8859-1, UTF-8 or disable this feature.
Sync deleted files	Remove remote files that are no longer available locally. This feature is potential dangerous and could lead to loss of data if not used properly.
Keep newer files	Modified files at destination end will not be overwritten.
CVS Exclude	Ignore all version control hidden files (.svn folder) when restoring files via iPACS sync.
Always Prompt for download destination (global setting)	Prompt user to specify download destination for each file downloaded via iPACS sync from the iPACS.

Store Job

Click **Save** at the bottom of the window to save any changes to the Sync configuration. Click **Cancel** to discard all changes since the last time the configuration was saved.

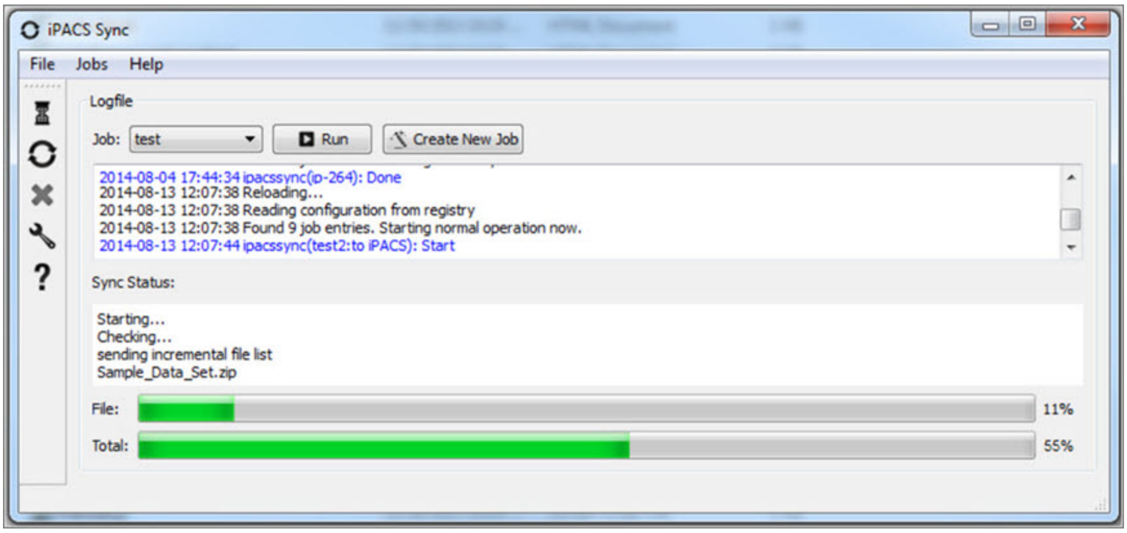
Store Job

Syncing data to iPACS

The following sections describe how to run an iPACS Sync job:

Run a Sync Job

Sync jobs are created/modified in the configuration window. To run a job, select the appropriate job and click **Run**.



```
2014-08-04 17:44:34 ipacssync(ip-264): Done
2014-08-13 12:07:38 Reloading...
2014-08-13 12:07:38 Reading configuration from registry
2014-08-13 12:07:38 Found 9 job entries. Starting normal operation now.
2014-08-13 12:07:44 ipacssync(test2:to iPACS): Start
```

```
Starting...
Checking...
sending incremental file list
Sample_Data_Set.zip
```

Run a Job

Icon Descriptions

Icon	Description
⌛	Pause a Sync Job
⟳	Run all active Sync Jobs
✖	Stop a Sync Job
🔧	Open the configuration page
?	Open the help guide

Quick Sync

This feature is a simple way to quickly download all files from a WebDisk folder, or it can facilitate the transfer of large amounts of data from the iPACS to a local location.

To download all files and folders in a WebDisk folder, follow these steps:

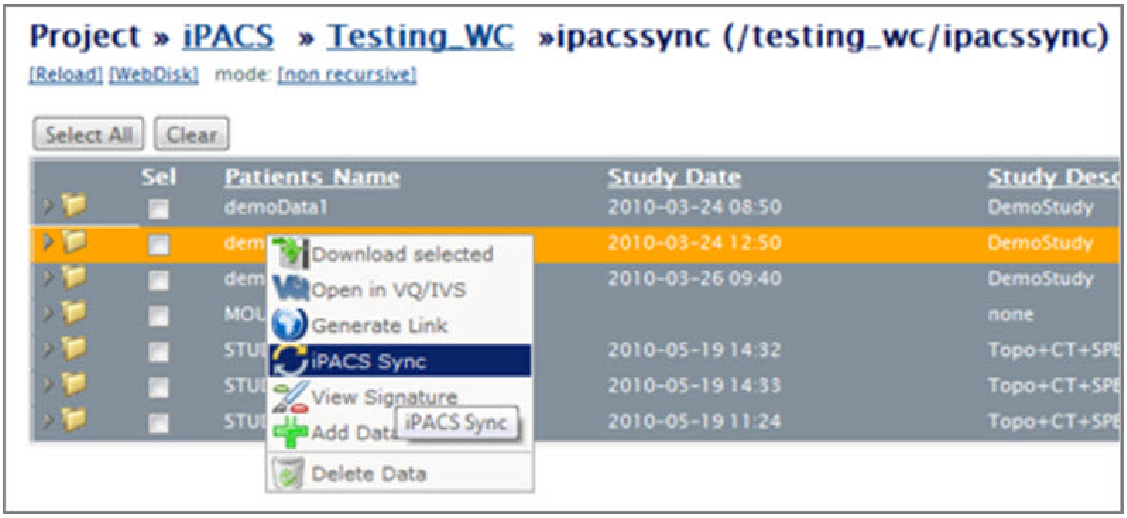
1. Navigate to the desired WebDisk folder on the iPACS.
2. Click **iPACS Sync URL** under **Other Links** on the right side of the page.
3. Copy the URL to the clipboard.

4. In the iPACS Sync client, go to **Jobs** -> **Quick Sync**, then paste the URL.
5. Select a folder where the iPACS files will be saved.
6. The iPACS Sync client will run a job to transfer all files and folders from that WebDisk folder to the specified location.

Quick Sync

To download selected files from iPACS, follow these steps:

1. Select the desired files from the Browser or WebDisk, then right-click one of them and select **iPACS Sync.**
2. A browser.irsync file will be downloaded.
3. In the iPACS Sync client, open the browser.irsync file by going to **Jobs** -> **Quick Sync File**, then selecting the file.
4. Select a folder where the iPACS files will be saved.
5. The iPACS Sync client will run a job to transfer the selected files to the specified lo cation.



Sel	Patients Name	Study Date	Study Desc
☐	demoData1	2010-03-24 08:50	DemoStudy
☐	dem	2010-03-24 12:50	DemoStudy
☐	dem	2010-03-26 09:40	DemoStudy
☐	MOU		none
☐	STU	2010-05-19 14:32	Topo+CT+SPE
☐	STU	2010-05-19 14:33	Topo+CT+SPE
☐	STU	2010-05-19 11:24	Topo+CT+SPE

Download from iPACS

Create a custom Brain Atlas

How to create a Custom Brain Atlas

A custom brain atlas can allow the user to perform other registrations based on your own ROIs, and on images of other animal species. This can be done with the provided wizard in VivoQuant.

The following files comprise an atlas:

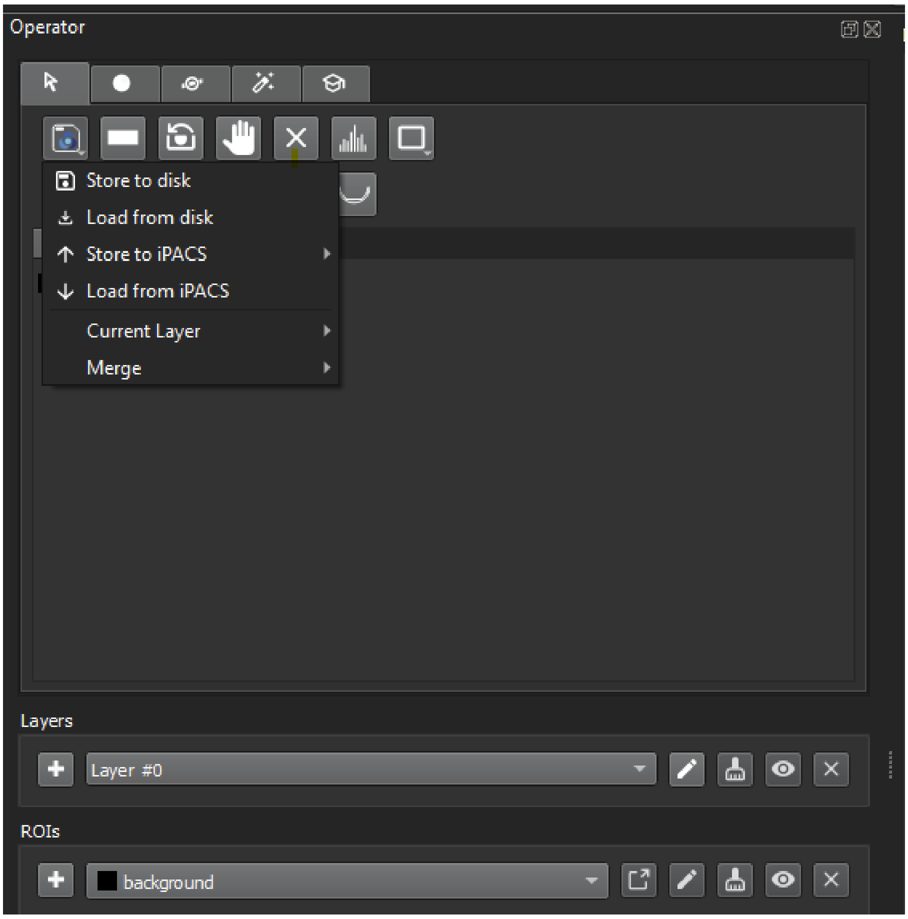
Item	Format	Description
Reference image	.raw	The reference image data on which your ROI atlas has been segmented
Reference Image Header	.mhd	The header corresponding to the raw reference image
ROI Atlas	.rmha	The segmented regions of your reference image in which you'd like to use as an atlas
ROI Key	.csv	A CSV file of the region names in the order that they appear in the rmha file

Note: These files will be located in the configured atlas path.

Note: The tool can handle CT or MR data as the input and MR, PET, or SPECT for the input functional data.

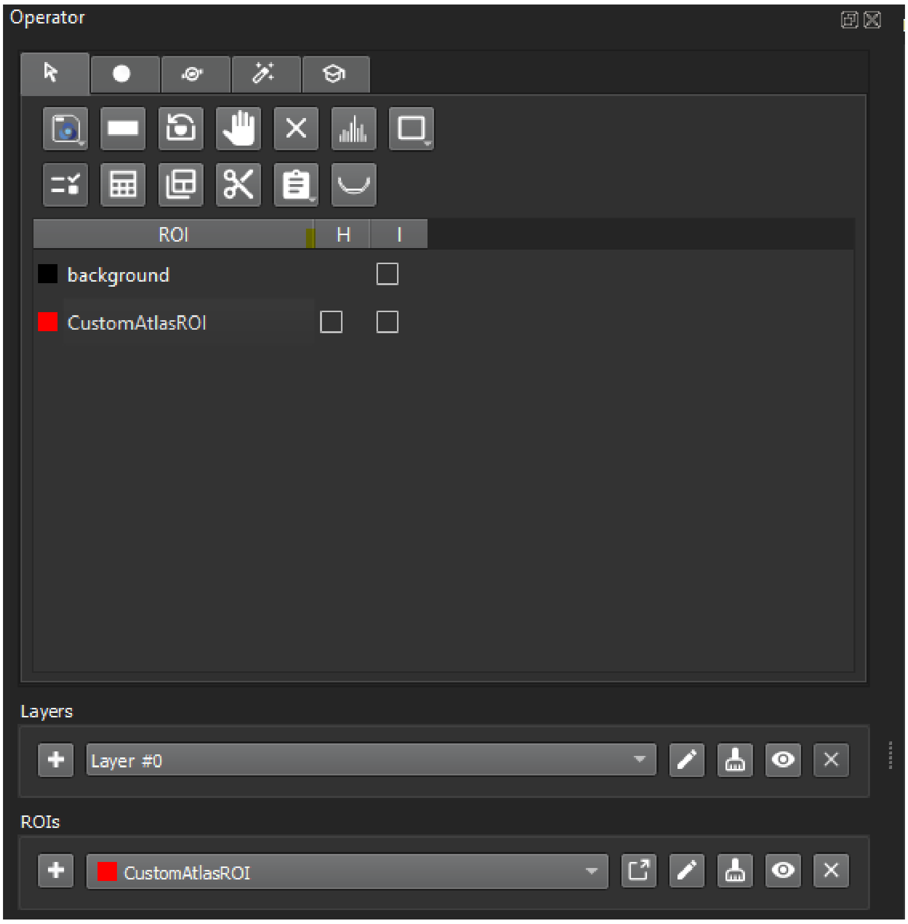
Creating a custom atlas with the wizard

1. Open your data then go to the 3D ROI Tool. Load in the ROI(s) (stored either locally or on iPACS):



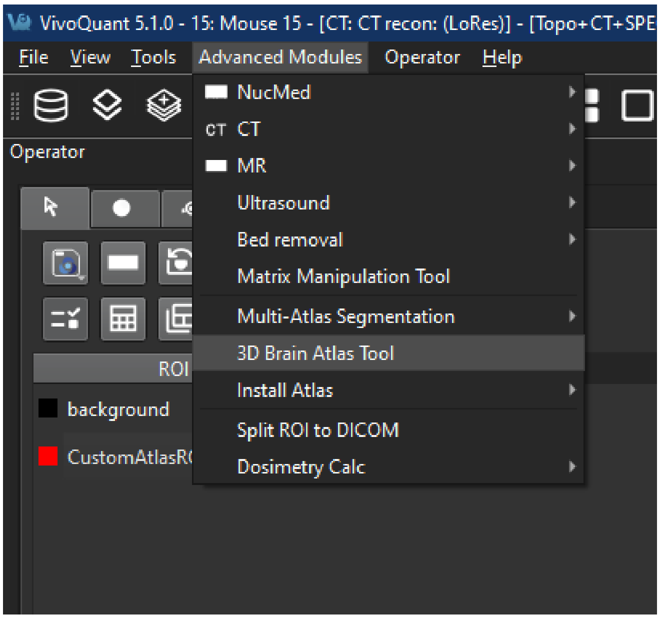
Load ROI

2. The ROI(s) should be available in the ROI selector and should also appear on the ROI table:

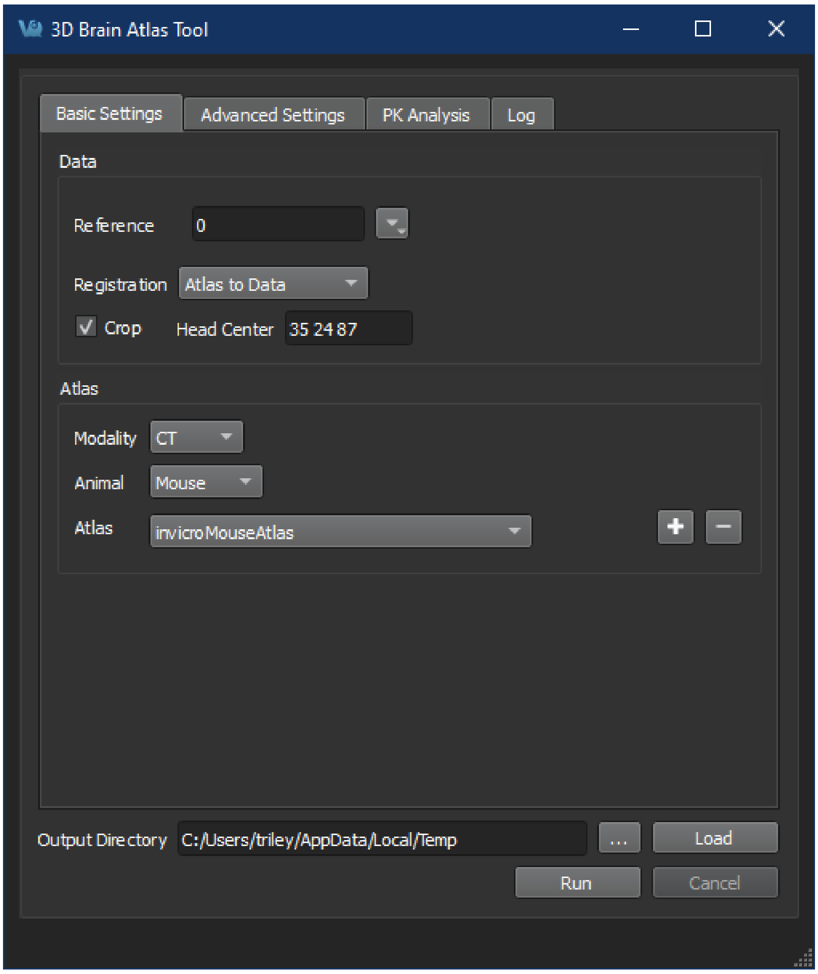


Loaded ROI

3. Navigate to Advanced Modules > 3D Brain Atlas tool, then select the + button:



Brain Atlas Tool menu



Reference 0

Registration Atlas to Data

☑ Crop Head Center 35 24 87

Modality CT

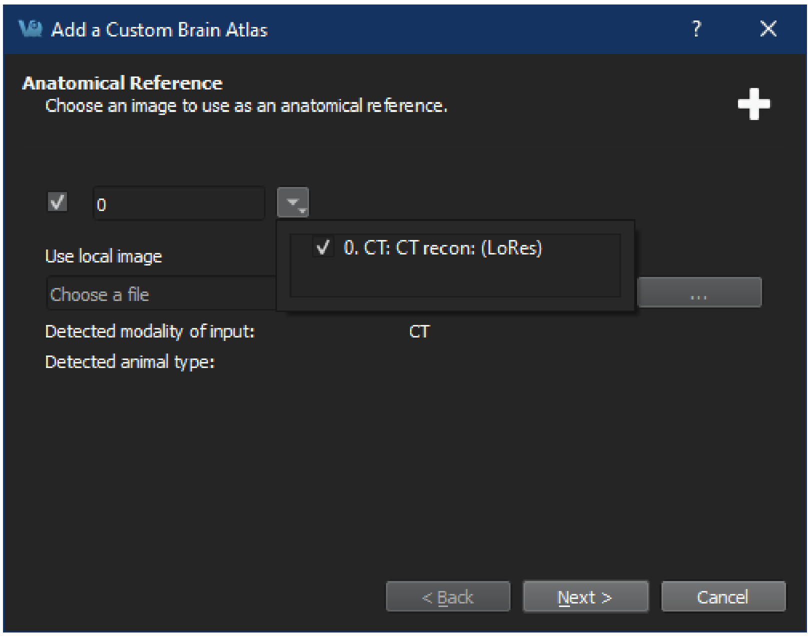
Animal Mouse

Atlas invicroMouseAtlas

Output Directory C:/Users/triley/AppData/Local/Temp

Add new atlas

4. Follow the steps prompted by the Brain Atlas Tool Wizard to select reference images and ROIs.



Anatomical Reference

Choose an image to use as an anatomical reference.

☑ 0

✓ 0. CT: CT recon: (LoRes)

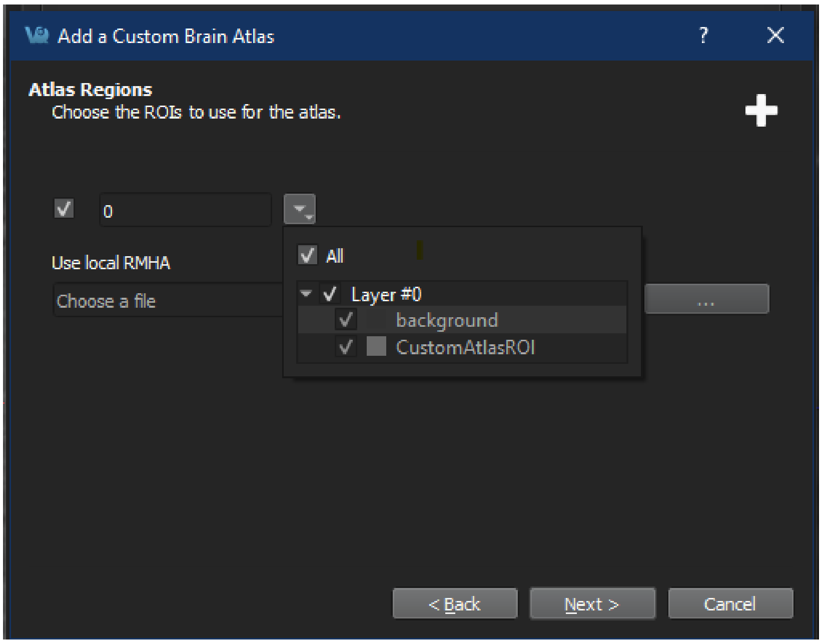
Use local image

Choose a file

Detected modality of input: CT

Detected animal type:

Selected loaded ROIs



Add a Custom Brain Atlas

Atlas Regions
Choose the ROIs to use for the atlas.

☑ 0

Use local RMHA

Choose a file

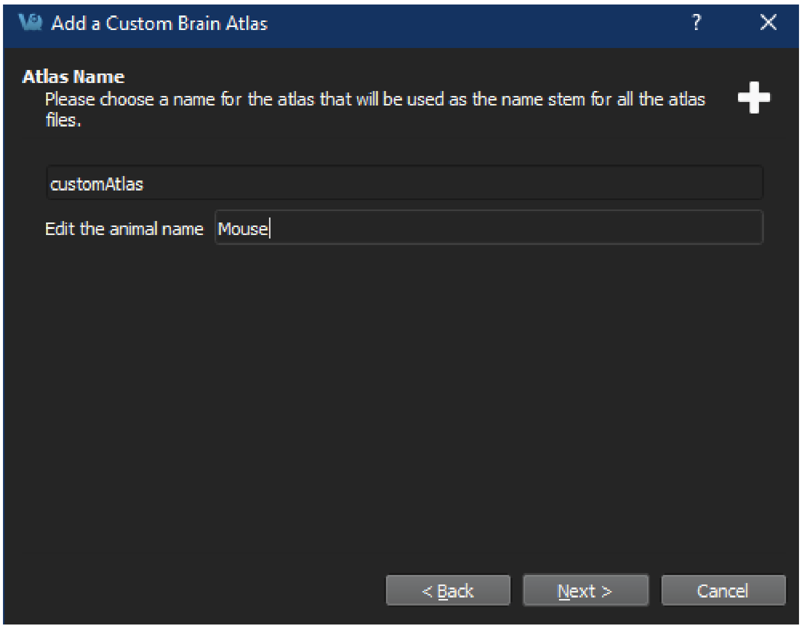
☑ All

✓ Layer #0

✓ background

✓ CustomAtlasROI

Selected loaded ROIs



Add a Custom Brain Atlas

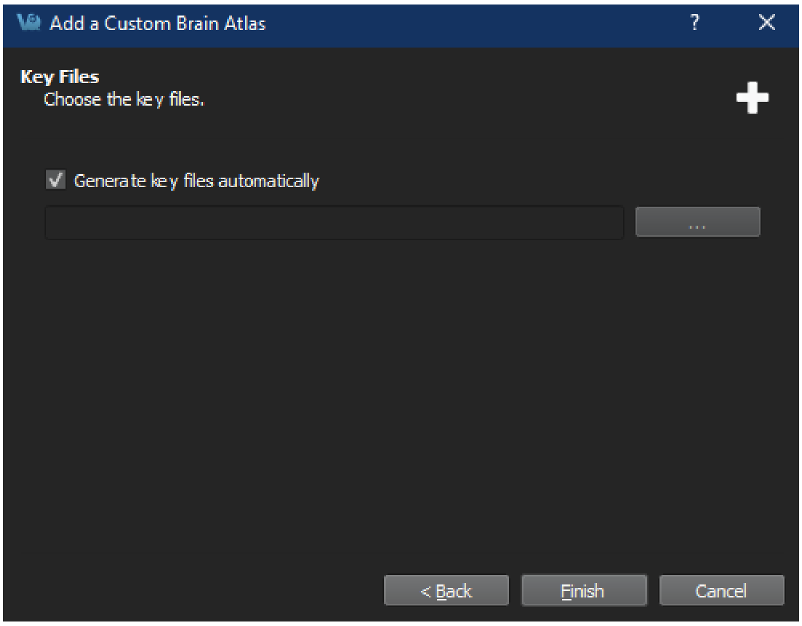
Atlas Name
Please choose a name for the atlas that will be used as the name stem for all the atlas files.

customAtlas

Edit the animal name: Mouse

Set atlas name

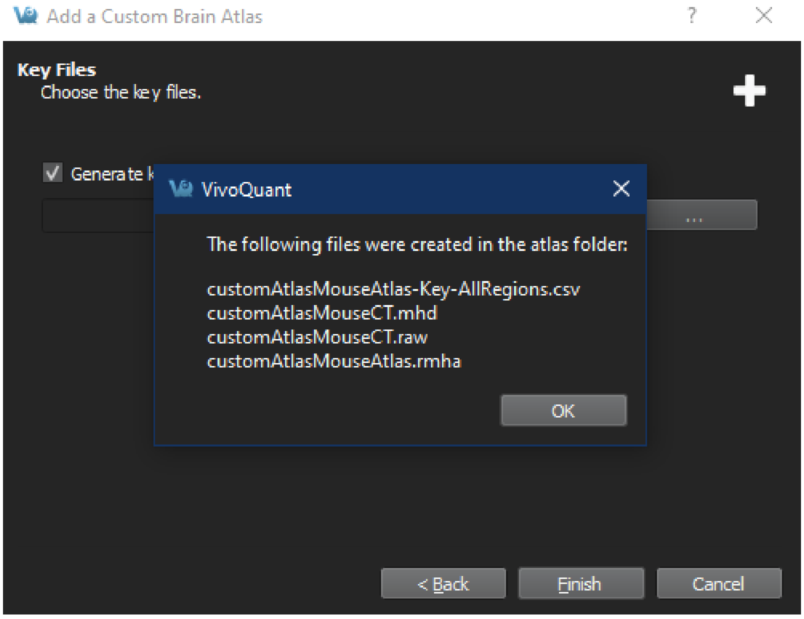
⚠ **Important:** When choosing the animal name, ensure that there is a corresponding entry in the specieslist.txt file, or the atlas will not appear 3D Brain Atlas Tool dialog.



☑ Generate key files automatically

Add key files

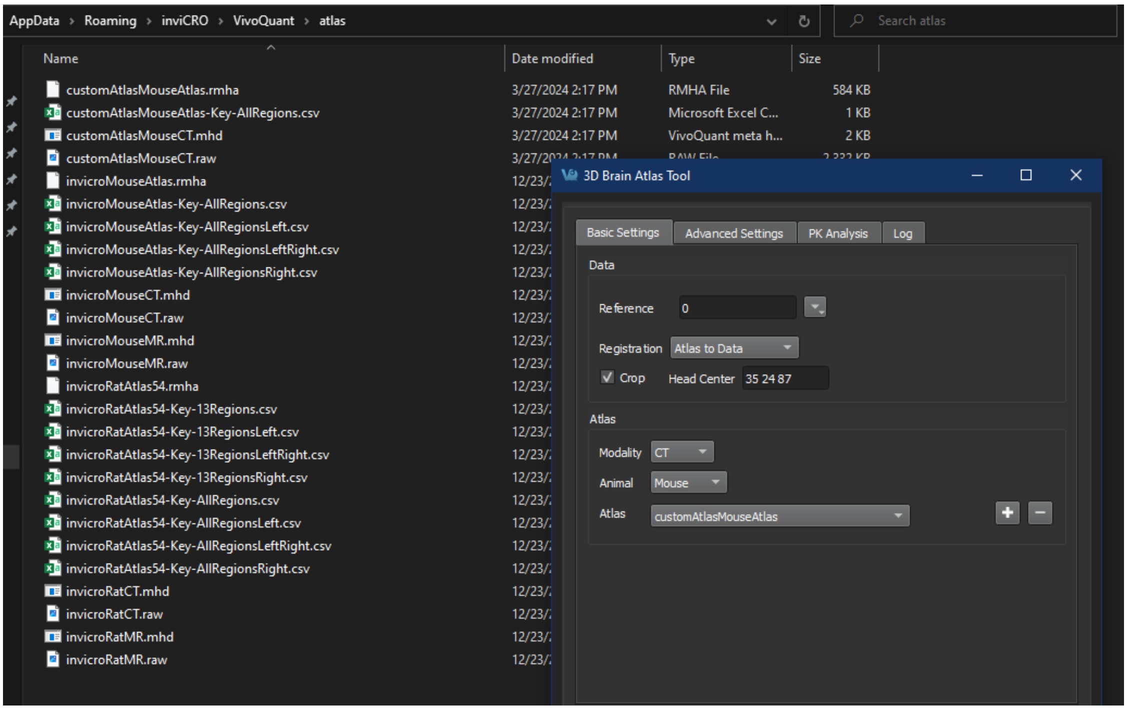
⚠ **Important:** If selecting manually generated keyfiles, at least two must be selected in the file dialog (one left and one right) with CTRL+select (as appropriate for your platform). The filenames must match the either atlasName-Left.csv or atlasName-Right.csv



The following files were created in the atlas folder:

```
customAtlasMouseAtlas-Key-AllRegions.csv
customAtlasMouseCT.mhd
customAtlasMouseCT.raw
customAtlasMouseAtlas.rmha
```

Saved documents



Name	Date modified	Type	Size
customAtlasMouseAtlas.rmha	3/27/2024 2:17 PM	RMHA File	584 KB
customAtlasMouseAtlas-Key-AllRegions.csv	3/27/2024 2:17 PM	Microsoft Excel C...	1 KB
customAtlasMouseCT.mhd	3/27/2024 2:17 PM	VivoQuant meta h...	2 KB
customAtlasMouseCT.raw	3/27/2024 2:17 PM	RAW File	2,332 KB
invicroMouseAtlas.rmha	12/23/		
invicroMouseAtlas-Key-AllRegions.csv	12/23/		
invicroMouseAtlas-Key-AllRegionsLeft.csv	12/23/		
invicroMouseAtlas-Key-AllRegionsLeftRight.csv	12/23/		
invicroMouseAtlas-Key-AllRegionsRight.csv	12/23/		
invicroMouseCT.mhd	12/23/		
invicroMouseCT.raw	12/23/		
invicroMouseMR.mhd	12/23/		
invicroMouseMR.raw	12/23/		
invicroRatAtlas54.rmha	12/23/		
invicroRatAtlas54-Key-13Regions.csv	12/23/		
invicroRatAtlas54-Key-13RegionsLeft.csv	12/23/		
invicroRatAtlas54-Key-13RegionsLeftRight.csv	12/23/		
invicroRatAtlas54-Key-13RegionsRight.csv	12/23/		
invicroRatAtlas54-Key-AllRegions.csv	12/23/		
invicroRatAtlas54-Key-AllRegionsLeft.csv	12/23/		
invicroRatAtlas54-Key-AllRegionsLeftRight.csv	12/23/		
invicroRatAtlas54-Key-AllRegionsRight.csv	12/23/		
invicroRatCT.mhd	12/23/		
invicroRatCT.raw	12/23/		
invicroRatMR.mhd	12/23/		
invicroRatMR.raw	12/23/		

Reference 0

Registration Atlas to Data

☑ Crop Head Center 35 24 87

Modality CT

Animal Mouse

Atlas customAtlasMouseAtlas

Saved output

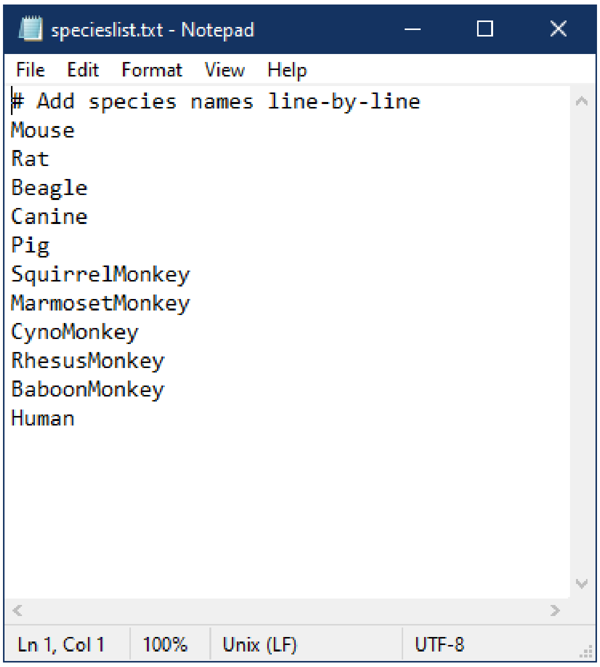
The custom atlas should be ready to use.

The specieslist.txt file

If you should need to create an atlas for another species, you can do so by editing the specieslist.txt file that's located next to the VivoQuant application. Typically, this file can be found at the following locations:

Windows: C:\Program Files\inviCRO\VivoQuant\specieslist.txt

macOS: /Applications/VivoQuant/Contents/MacOS/specieslist.txt



```
# Add species names line-by-line
Mouse
Rat
Beagle
Canine
Pig
SquirrelMonkey
MarmosetMonkey
CynoMonkey
RhesusMonkey
BaboonMonkey
Human
```

Species list file

⚠ **Important:** On some platforms, you may need administrator access to modify this file.

☑ **Tip:** Users can make variations on species' names if an atlas is needed on a specific data type. For example, a PlanarMouse and VolumetricMouse species name could be created.

Key file format

Content

The key file is a comma separated text file without a header row. Empty lines, or lines starting with # or $ are ignored.

The line format is:

input index of the ROI in the .rmha file,output ROI index in the resulting segmentation,ROI name

For example, the keyfile below corresponds to an .rmha ROI file which has 28 disjointed ROIs, which will map to 14 regions in the resulting output segmentation:

```
1,1,Medulla
2,2,Cerebellum
3,3,Midbrain
4,4,Pons
5,5,Cortex
6,6,Hippocampus
7,7,Thalamus
8,8,Hypothalamus
9,9,Striatum
10,10,Pallidum
11,11,Olfactory
12,12,Corpus Call
13,13,White Matter
14,14,Ventricles
15,1,Medulla
16,2,Cerebellum
17,3,Midbrain
18,4,Pons
19,5,Cortex
20,6,Hippocampus
21,7,Thalamus
22,8,Hypothalamus
23,9,Striatum
24,10,Pallidum
25,11,Olfactory
26,12,Corpus Call
27,13,White Matter
28,14,Ventricles
```

Keyfile format

Filename

The wizard will generate a key file with the following name format:

atlasName-Key-nRegionsRegionsdirection.csv

The atlasName is entered by the user in the wizard process.

The nRegions value will be either All if all ROIs in the current layer were selected to be used, or the number of ROIs.

The direction value could be one of Left, Right or LeftRight if the user has ROIs with the text left or right (case insensitive) in the ROI names. It will be empty if none of the selected ROIs were named this way.

This pattern could be used to create segmentations for left cerebellum and right cerebellum separately, or cerebellum combined.

Hardware Requirements

The following table outlines the minimum and recommended hardware requirements needed to install VivoQuant in your computer:

	Minimum	Recommended
Operating System	64-bit Windows (10 or 11)	
	10.9 Mac OS or later	
	Ubuntu 20.04	
RAM	8 to 12 GB	12+ GB
Processor	64 bit (For MacOS, x86 support required)	
GPU	OpenGL 2.0+	OpenGL 3.0

Corrupted Data

Data files used in VivoQuant, such as VQ sessions, images and movies, might become corrupted after being processed. For example, a VQ session zipacs file might get corrupted during the unzipping process. On these occasions, we recommend clearing the cache before attempting to open the corrupted file again.

VivoQuant Cache Files

VivoQuant cache stores data files such as images or VQ sessions that are frequently accessed or were used recently in a local repository to improve load time.

If you are using **Windows OS**, you can find the VivoQuant cache at the following location:

C:\Users\<username>\AppData\Roaming\inviCRO\VivoQuant\cache

- Cache files can also be quickly accessed by typing the following path in Windows navigation bar:

  %appdata%/inviCRO/VivoQuant/cache

In **MAC**, the caches files are located here:

~/Library/VivoQuant

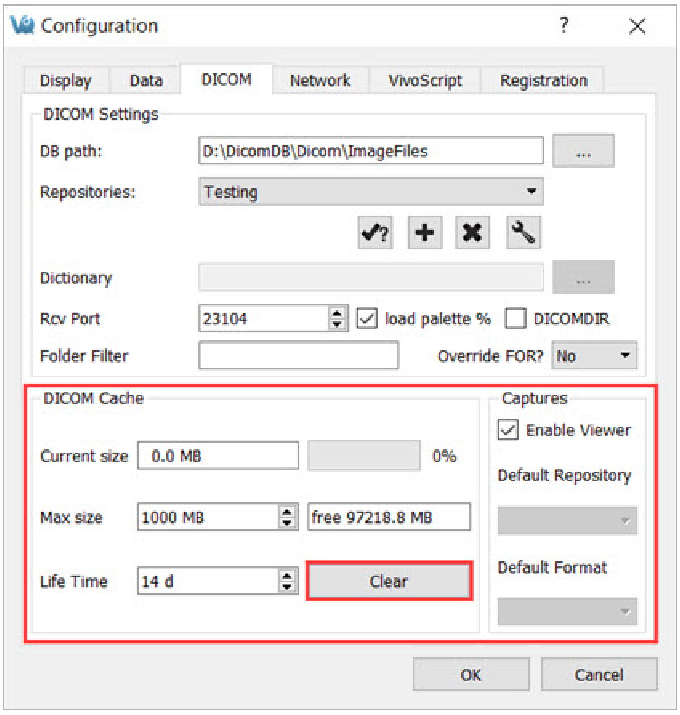
If you are using **Linux**, you can find the VivoQuant cache here:

~/.VivoQuant

Clear VivoQuant Cache

To clear the cache, you can navigate to the above location and manually delete the stored data.

Alternatively, you can clear the cache directly on VivoQuant by navigating to **Tools** → **Configuration** → **DICOM**, and hitting the **Clear** button in the **DICOM Cache** section.



DB path: D:\DicomDB\Dicom\ImageFiles

Repositories: Testing

Rcv Port: 23104 ☑ load palette % ☐ DICOMDIR

Override FOR? No

Current size: 0.0 MB 0%

Max size: 1000 MB free 97218.8 MB

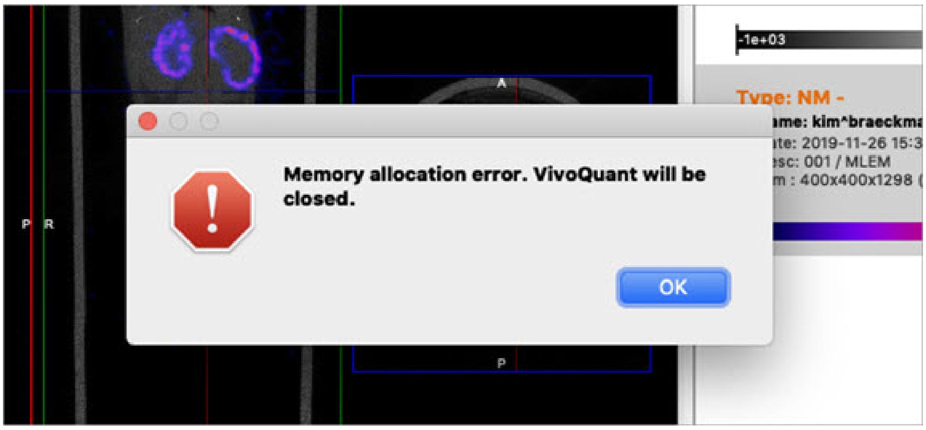
Life Time: 14 d

☑ Enable Viewer

Clear VivoQuant Cache

Memory Allocation Error

While loading, coregistering, or cropping images, you might receive a **Memory Allocation** error message followed by a VivoQuant crash. This error may occur when manipulating large datasets.



Memory allocation error. VivoQuant will be closed.

Memory Allocation Error

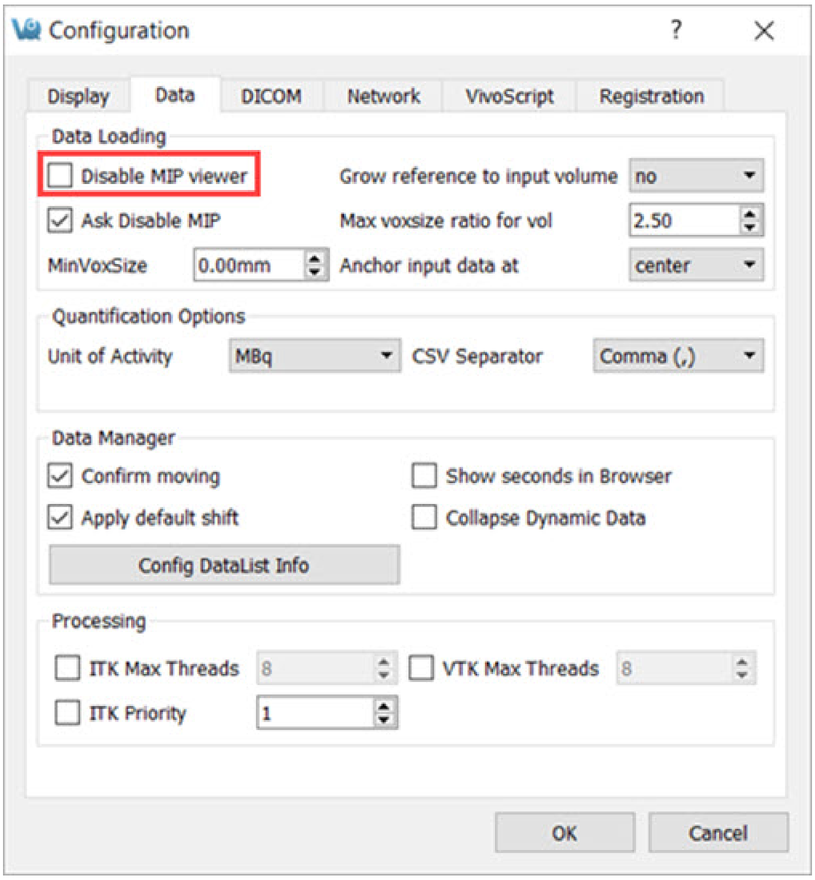
Troubleshooting the Memory Allocation Error

Follow these steps to avoid memory allocation errors:

1. Disable the MIP viewer to lower resource consumption.
2. Downsample your data via the Preprocessing tool
3. Crop your data to remove unnecessary empty space around the subject and decrease the data size.
4. Load in the NM image prior to the CT, so that the CT downsamples to the same voxel size as the NM.
5. Work on a computer that meets or exceeds the hardware recommendations.

Disabled MIP

If you can't see the MIP view or 3D rendering of your data, make sure that **MIP Viewer** is enabled the in your VivoQuant instance. To do this, navigate to **Tools** → **Configuration** → **Data**, and uncheck the **Disable MIP viewer** check box.



Data Loading

☐ Disable MIP viewer

Grow reference to input volume: no

☑ Ask Disable MIP

Max voxsize ratio for vol: 2.50

MinVoxSize: 0.00mm

Anchor input data at: center

Quantification Options

Unit of Activity: MBq

CSV Separator: Comma (,)

Data Manager

☑ Confirm moving

☐ Show seconds in Browser

☑ Apply default shift

☐ Collapse Dynamic Data

Processing

☐ ITK Max Threads: 8

☐ VTK Max Threads: 8

☐ ITK Priority: 1

Enable MIP Viewer

Further Troubleshooting

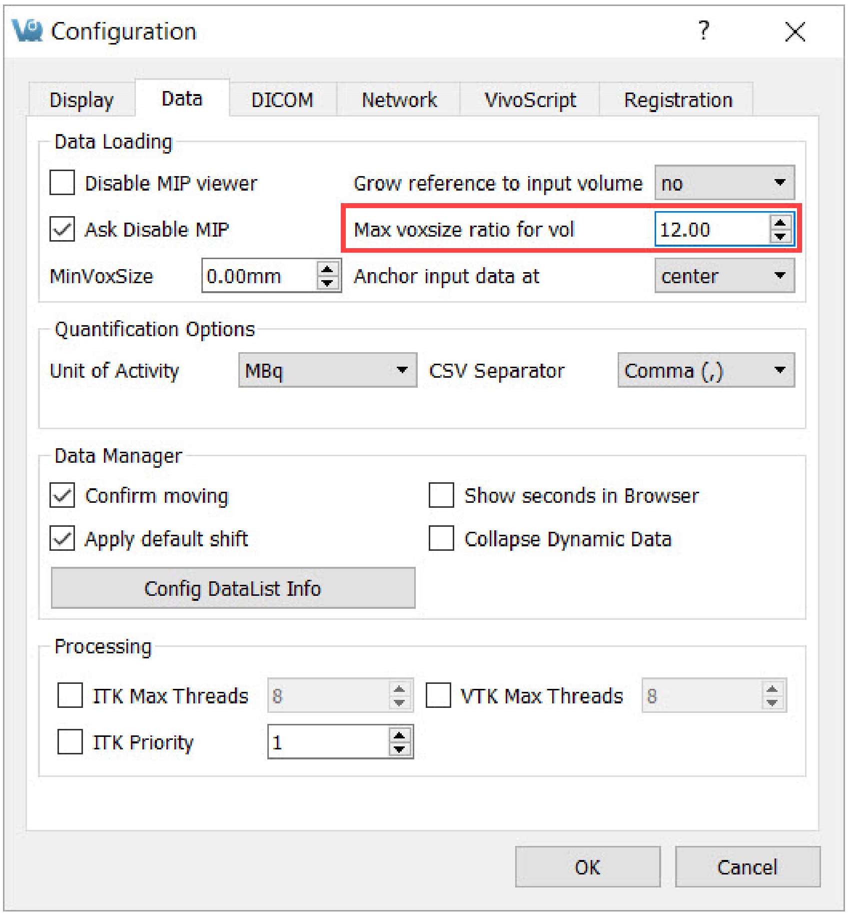
If, after enabling the **MIP Viewer** via VivoQuant's configuration, it still doesn't appear, or if the **Disable MIP viewer** checkbox is greyed out, try the following possible solutions:

Install OpenGL

OpenGL 2.0 is the minimum requirement for MIP to work, but 3.0+ is preferred. Make sure one of these versions is installed on your computer. For more information on minimum hardware requirements for VivoQuant, see Hardware Recommendations.

Check for Planar Data

A MIP cannot be generated with planar data. Note that, even if your data is not planar, VivoQuant might interpret it as such if the Max Voxsize Ratio is less than that of your image. You can increase the ratio by navigating to **Tools** → **Configuration** → **Data**, and increasing the number for the field **Max voxsize ratio for vol**.



☐ Disable MIP viewer

Grow reference to input volume: no

☑ Ask Disable MIP

Max voxsize ratio for vol: 12.00

MinVoxSize: 0.00mm

Anchor input data at: center

Unit of Activity: MBq

CSV Separator: Comma (,)

☑ Confirm moving

☐ Show seconds in Browser

☑ Apply default shift

☐ Collapse Dynamic Data

☐ ITK Max Threads: 8

☐ VTK Max Threads: 8

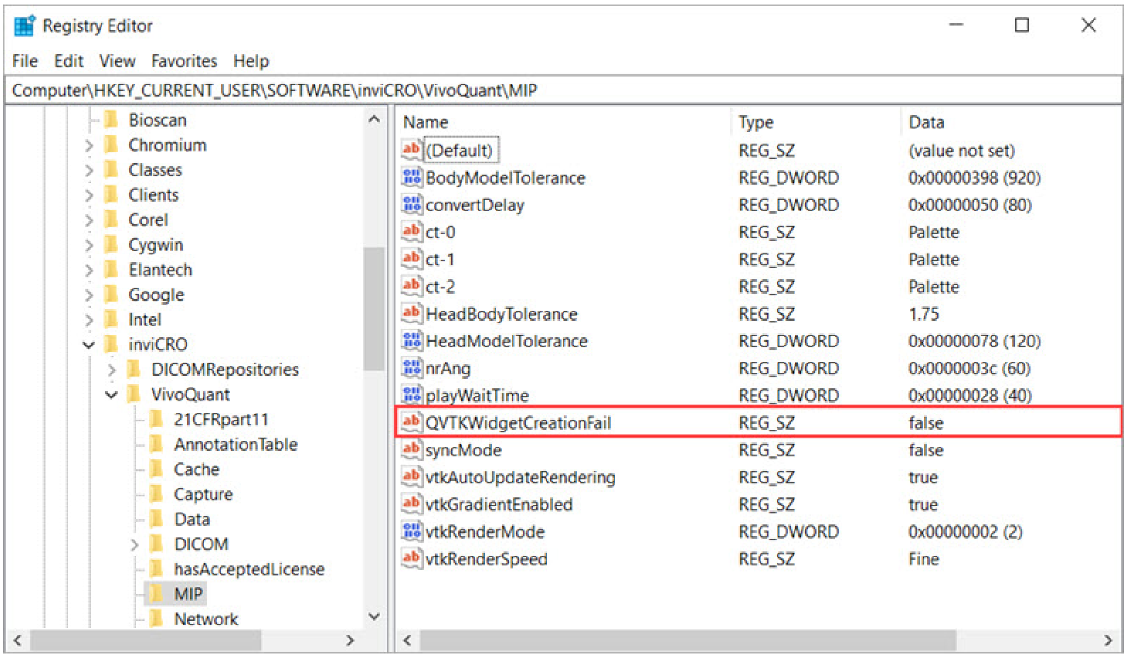
☐ ITK Priority: 1

Change Max Voxsize Ratio

Check Internal Settings

If a previous run of VQ failed to set up the MIP, a setting might be preventing further attempts to create it. To reset this setting, follow the below steps:

- **On Windows**: Open the **Registry Editor** and navigate to: Computer\HKEY_CURRENT_USER\Software\inviCRO\VivoQuant\MIP. Check that the QVTKWidgetCreationFail is set to false.

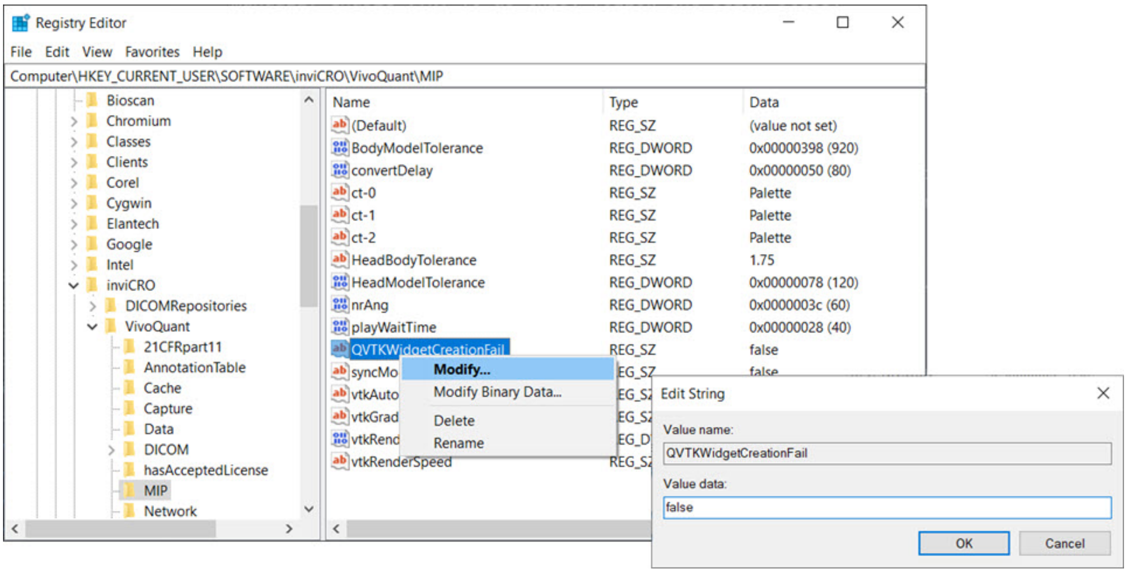


Computer\HKEY_CURRENT_USER\SOFTWARE\inviCRO\VivoQuant\MIP

Name	Type	Data
(Default)	REG_SZ	(value not set)
BodyModelTolerance	REG_DWORD	0x00000398 (920)
convertDelay	REG_DWORD	0x00000050 (80)
ct-0	REG_SZ	Palette
ct-1	REG_SZ	Palette
ct-2	REG_SZ	Palette
HeadBodyTolerance	REG_SZ	1.75
HeadModelTolerance	REG_DWORD	0x00000078 (120)
nrAng	REG_DWORD	0x0000003c (60)
playWaitTime	REG_DWORD	0x00000028 (40)
QVTKWidgetCreationFail	REG_SZ	false
syncMode	REG_SZ	false
vtkAutoUpdateRendering	REG_SZ	true
vtkGradientEnabled	REG_SZ	true
vtkRenderMode	REG_DWORD	0x00000002 (2)
vtkRenderSpeed	REG_SZ	Fine

Windows Registry Editor

If you need to set the correct key value, right-click the key, select **Modify** and type false in the **Value data** field. You will need to restart VivoQuant for the change to take effect.



Computer\HKEY_CURRENT_USER\SOFTWARE\inviCRO\VivoQuant\MIP

Name	Type	Data
(Default)	REG_SZ	(value not set)
BodyModelTolerance	REG_DWORD	0x00000398 (920)
convertDelay	REG_DWORD	0x00000050 (80)
ct-0	REG_SZ	Palette
ct-1	REG_SZ	Palette
ct-2	REG_SZ	Palette
HeadBodyTolerance	REG_SZ	1.75
HeadModelTolerance	REG_DWORD	0x00000078 (120)
nrAng	REG_DWORD	0x0000003c (60)
playWaitTime	REG_DWORD	0x00000028 (40)
QVTKWidgetCreationFail	REG_SZ	false
syncMo	EG_SZ	false
vtkAuto	EG_SZ	
vtkGrad	EG_SZ	
vtkRend	EG_D	
vtkRenderSpeed	REG_SZ	

Value name: QVTKWidgetCreationFail

Value data: false

Set Key Value

- **On Mac:** open the Terminal and run the following command: defaults write com.invicro.VivoQuant "MIP.QVTKWidgetCreationFail" 0

> For further support, please contact support@invicro.com.

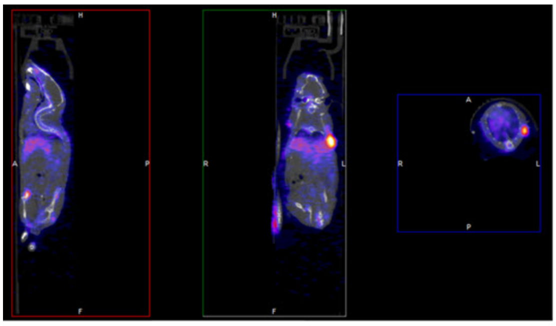
Image Distortion and Mirroring

When loading data into VivoQuant, you might notice that the images appear upside-down or squished in the Display.

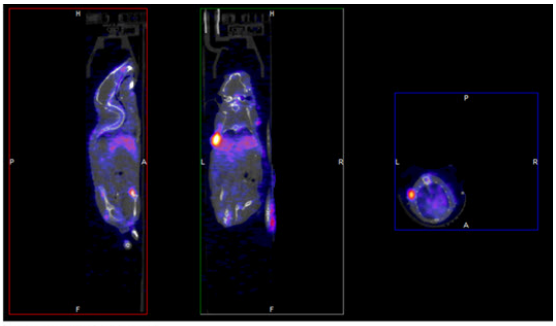
Mirroring

Left/Right Mirroring

VivoQuant allows you to choose between two **Left**/**Right** orientation options: **Neurologist** (**LR**) and **Radiologist** (**RL**).



Radiologist Mode (RL)



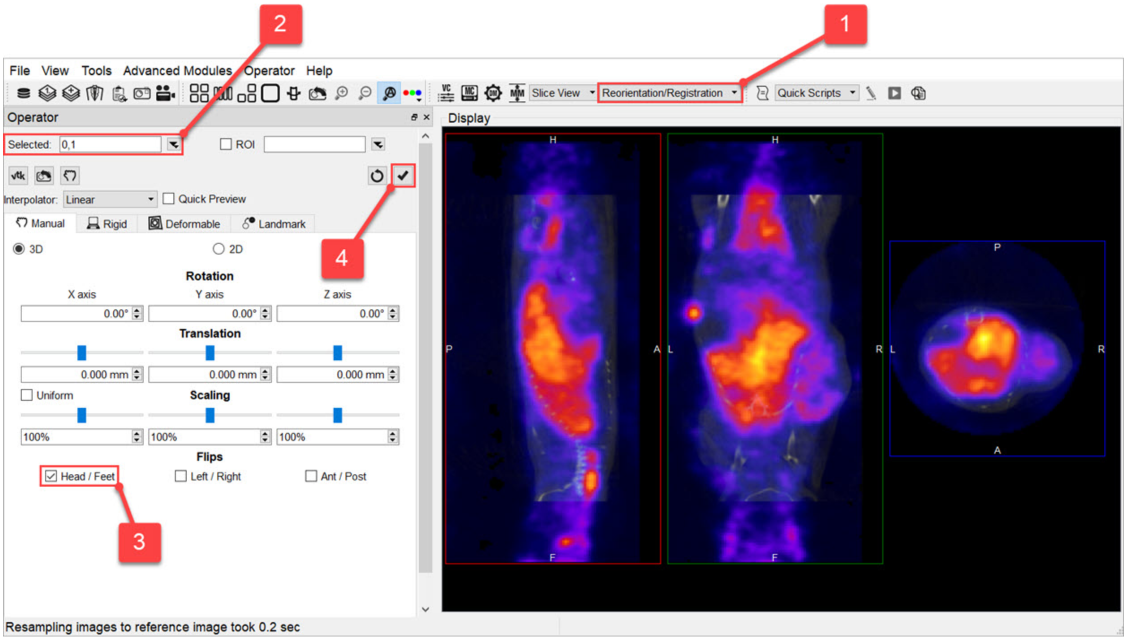
Neurologist Mode (LR)

To select an orientation mode, navigate to **Tools** → **Configuration** → **Display**, and use the **Orientation** drop-down menu to choose the desire orientation option.

Head/Feet Mirroring

If you notice that your images appear upside down, you can change the **Head**/**Feet** orientation by following these steps:

1. Navigate to the **Reorientation/Registration** operator.
2. Select all the images in your dataset.
3. Check the **Head/Feet** checkbox.
4. Click the checkmark ✓ button to apply your changes.



Selected: 0,1

☐ ROI

Interpolator: Linear

☐ Quick Preview

● 3D ○ 2D

Rotation

X axis 0.00° Y axis 0.00° Z axis 0.00°

Translation

0.000 mm 0.000 mm 0.000 mm

☐ Uniform

Scaling

100% 100% 100%

Flips

☑ Head / Feet ☐ Left / Right ☐ Ant / Post

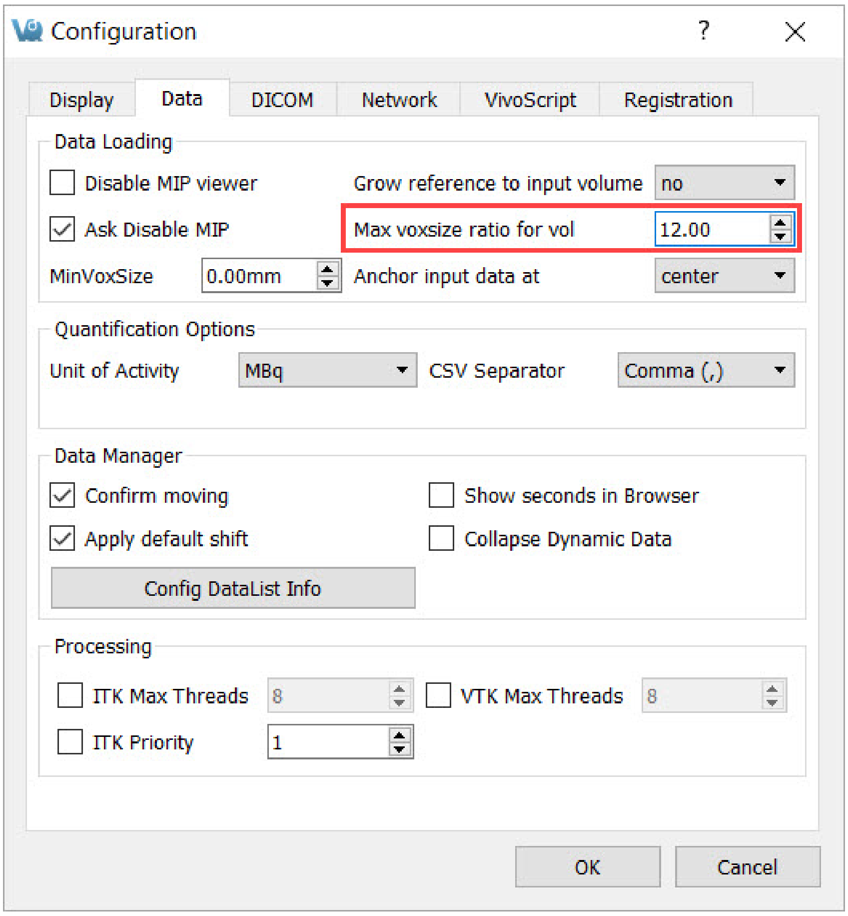
Resampling images to reference image took 0.2 sec

Change Head/Feet Orientation

Distortion

If you notice that your images appear distorted, they might be loading as planar images. If the voxel size ratio for a non-planar image is greater than your configured maximum ratio, VivoQuant forces the image to load as a planar image. Increasing this maximum value will prevent this distortion.

To do this, navigate to **Tools** → **Configuration** → **Data**, and increase the number for the **Max voxsize ratio for vol** field.



Data Loading

☐ Disable MIP viewer

Grow reference to input volume: no

☑ Ask Disable MIP

Max voxsize ratio for vol: 12.00

MinVoxSize: 0.00mm

Anchor input data at: center

Quantification Options

Unit of Activity: MBq

CSV Separator: Comma (,)

Data Manager

☑ Confirm moving

☐ Show seconds in Browser

☑ Apply default shift

☐ Collapse Dynamic Data

Processing

☐ ITK Max Threads: 8

☐ VTK Max Threads: 8

☐ ITK Priority: 1

Change Max Voxsize Ratio