Regulatory Information

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Caution: US Federal law and other national laws restrict this medical device to sale to, or use by, or on the order of a physician.

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Indications for Use

These indications apply to MIM in its entirety. Depending on your specific licenses and functionality, some indications may not apply to your use of the software.

MIM software is used by trained medical professionals as a tool to aid in evaluation and information management of digital medical images. The medical image modalities include, but are not limited to, CT, MR, CR, DX, MG, US, SPECT, PET, and XA as supported by ACR/NEMA DICOM 3.0. MIM assists in the following indications:

- Receive, transmit, store, retrieve, display, print, and process medical images and DICOM objects.
- Create, display, and print reports from medical images.
- Registration, fusion display, and review of medical images for diagnosis, treatment evaluation, and treatment planning.
- Evaluation of cardiac left ventricular function and perfusion, including left ventricular end-diastolic volume, end-systolic volume, and ejection fraction.
- Localization and definition of objects such as tumors and normal tissues in medical images.
- Creation, transformation, and modification of contours for applications including, but not limited to, quantitative analysis, aiding adaptive therapy, transferring contours to radiation therapy treatment planning systems, and archiving contours for patient follow-up and management.
- Quantitative and statistical analysis of PET/SPECT brain scans by comparing to other registered PET/SPECT brain scans.
- Planning and evaluation of permanent implant brachytherapy procedures (not including radioactive microspheres).
- Calculating absorbed radiation dose as a result of administering a radionuclide.
- Assist with the planning and evaluation of ablation procedures by providing visualization and analysis, including energy zone visualization through the placement of virtual ablation devices validated for inclusion in MIM-Ablation. The software is not intended to predict specific ablation zone volumes or predict ablation success.

Caution: When using this device clinically within the United States, the user should only use FDA-approved radiopharmaceuticals. If used with unapproved ones, this device should only be used for research purposes.

When used for diagnostic purposes, the mobile thin client is not intended to replace a full workstation and should only be used when there is no access to a workstation.

Lossy compressed mammographic images and digitized film screen images must not be reviewed for primary image interpretations. Images that are printed to film must be printed using a FDA-approved printer for the diagnosis of digital mammography images. Mammographic images must be viewed on a display system that has been cleared by the FDA for the diagnosis of digital mammography images. The software is not to be used for mammography CAD.

Caution: All treatment plan reports shall be approved by a qualified person before the information in them is used for radiotherapy treatment purposes. The responsible organization shall ensure that individuals authorized to perform treatment planning functions are appropriately trained for the functions they perform, and the operator shall always be aware that the quality of the output depends critically on the quality of the input data. Any irregularities or uncertainties about input data units, identification, or quality of any other nature shall be thoroughly investigated before the data are used.

Caution: Any health professional having a complaint or grounds for dissatisfaction relating to the identity, quality, durability, reliability, safety, effectiveness, or performance of a device should notify MIM Software. Moreover, if a device has malfunctioned, MIM Software or its representative must be informed immediately. If a MIM Software product could have caused or contributed to the death or serious injury of a patient, MIM Software or its representative must be informed immediately. These serious incidents must also be reported to the Competent Authority of the European Member State or, when applicable, the equivalent regulatory authority, where the user and/or patient is established.

Caution: Users must perform validation when developing their own extensions or workflows and when modifying any default extensions or workflows that MIM Software provides. For extensions and workflows developed or modified by the user or provided by a third-party, MIM Software (i) does not endorse, control, monitor, or verify the contents, (ii) does not provide any warranty; and (iii) is not liable for any loss, damage, or injury sustained resulting from downloading, installing, accessing, integrating, supporting, or using the extension or workflow.

Caution: Due to the inherent nature of medical images, with their variable characteristics (e.g., level of noise and artifacts), the degree of accuracy may be variable as well. These limitations must be considered before making any decision based on images and quantitative values. It is recommended that acceptance testing be performed prior to use. This testing should include, at a minimum, all representative data sets (images) intended for transfer, all types of transfers desired for a type of data set, and clinical evaluation of each representative data set on the receiving end after each desired type of transfer.

For more information on accuracy details, see appendix or white paper information.

Use of MIM on Mobile Devices

MIM Software Inc. has previously worked with board certified radiologists to evaluate mobile devices for diagnostic reading. Devices tested included Apple iPad, Kindle Fire HDX, Samsung Galaxy Note Pro, and Microsoft Surface. In these cases, testers affirmed that the devices they evaluated were capable of displaying images at diagnostic quality.

Due to the number of available mobile devices, and the frequency with which new mobile devices are released, MIM cannot evaluate all available mobile devices for diagnostic reading. However, displays have dramatically increased in quality (e.g., resolution, contrast) since these earlier devices were tested. It is at the discretion of the user and their employer to determine which mobile devices are acceptable for diagnostic reading, and to ensure that these devices are properly calibrated.

Intended Use

MIM software is intended for trained medical professionals including, but not limited to, radiologists, oncologists, physicians, medical technologists, dosimetrists, and physicists.

MIM is a medical image and information management system that is intended to receive, transmit, store, retrieve, display, print, and process digital medical images, as well as create, display, and print reports from those images. The medical modalities of these medical imaging systems include, but are not limited to, CT, MR, CR, DX, MG, US, SPECT, PET, and XA as supported by ACR/NEMA DICOM 3.0.

MIM provides the user with the means to display, register, and fuse medical images from multiple modalities. Additionally, it evaluates cardiac left ventricular function and perfusion, including left ventricular end-diastolic volume, end-systolic volume, and ejection fraction. The Region of Interest (ROI) feature reduces the time necessary for the user to define objects in medical image volumes by providing an initial definition of object contours. The objects include, but are not limited to, tumors and normal tissues.

MIM provides tools to quickly create, transform, and modify contours for applications including, but not limited to, quantitative analysis, aiding adaptive therapy, transferring contours to radiation therapy treatment planning systems, and archiving contours for patient follow-up and management.

MIM aids in the assessment of PET/SPECT brain scans. It provides automated quantitative and statistical analysis by automatically registering PET/SPECT brain scans to a standard template and comparing intensity values to a reference database or to other PET/SPECT scans on a voxel by voxel basis, within stereotactic surface projections or standardized regions of interest.

MIM allows the dose distribution of an implant to be individually shaped for each patient and is a general purpose brachytherapy planning system used for prospective and confirmation dose calculations for patients undergoing a course of brachytherapy using permanent implants of various radioisotopes (not including radioactive microspheres).

MIM allows voxel-based dose calculations for patients who have been administered radioisotopes or radioactive microspheres.

MIM assists with the planning and evaluation of ablation procedures by allowing the energy zone that comprises the ablation zone to be visualized on medical imaging through the placement of virtual ablation devices for the purpose of confirming ablation zone placement.

Contents

Getting Started

MIM Encore® Workflows and Nuclear Medicine Processing: Introduction

MIM® comes with workflows built to handle common processing requests. Workflows let you automate image display, use Nuclear Medicine processing, and more. There are two types:

- Default workflows are universal and can be used immediately with patient data by any user.
- Template workflows typically require testing with your site's individual patient data to ensure functionality. Please contact MIM Software® Support if you would like to test a template workflow.

MIM also comes with built-in Nuclear Medicine processing capabilities. These can be used for colonic transit, liver-lung shunt, lung quantification, and more. See Default Nuclear Medicine Processing for more information.

Note: This guide serves as a reference to workflows included with MIM. For details on how to import, launch, and manage signatures for workflows, please see the *MIM Encore for Radiology and Nuclear Medicine User Guide*.

Default PET, CT, and MR Workflows

Default Workflow: Universal PET/CT Review

Processing

This workflow automatically organizes images for viewing, based on the inputs selected. The PET swapping feature lets you easily change the fusion you are looking at.

Workflow Inputs

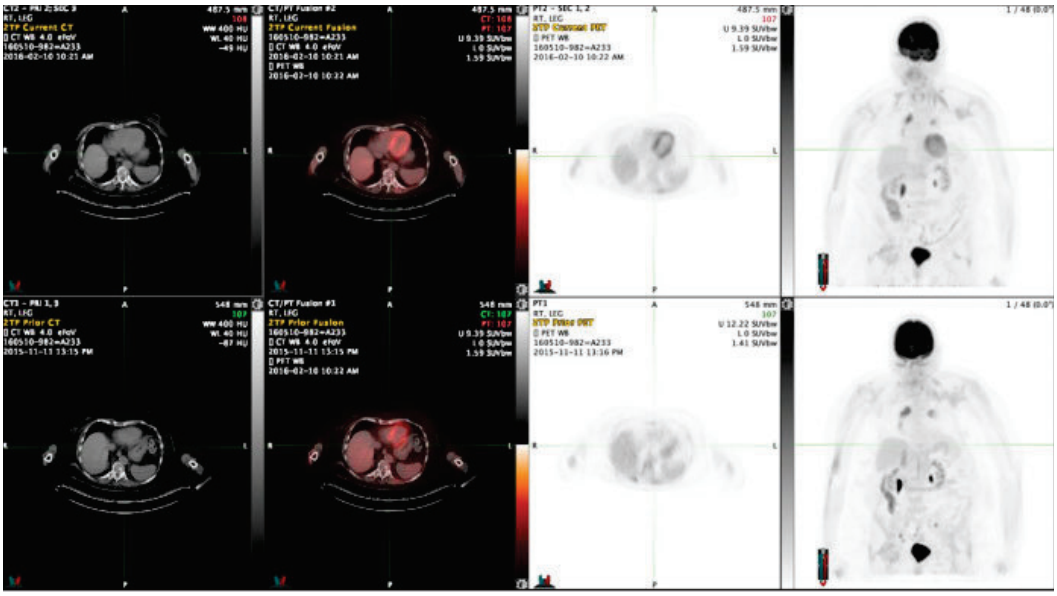
Important: At least one whole-body image is required for this workflow to run successfully.

- Up to six whole-body PET/CT time points
  - The workflow adapts to the number of time points selected.
  - PET NAC images are optional.
- Up to four whole-body PET/CTs with additional bed positions (head/neck or legs)
  - The workflow assumes each study will include whole-body images as well as the additional bed positions.
  - The workflow does not account for scenarios with three bed positions.
- Additional diagnostic CTs (the two most recent time points)
  - If one diagnostic CT is present, the CT will be displayed alongside the PET/CT.
  - If multiple diagnostic CTs are present, the CTs will be displayed on separate pages.
- MRs
  - If an MRAC PET is available along with a whole-body PET/CT, PET/MR fusions will be generated and displayed on individual pages.
  - If multiple MR sequences are present, they will be displayed on separate pages.

Tip: If your series do not match the inputs for the Universal PET/CT Review workflow, try running the **PET/CT or SPECT/CT - Quad** workflow or the **PET/CT or SPECT/CT - Compare** workflow instead. These workflows provide a basic viewing display for one or two series.

Workflow Outputs

Commonly-used viewing pages for whole body and applicable spot images. Pages are dependent on the number of time points and additional bed positions loaded.



Example of a page display that is output by the Universal PET/CT Review workflow.

Default Workflow: Hybrid PET/MR - Standard

Processing

This workflow automatically organizes up to two time points of PET/MR images for viewing, based on the inputs selected. The MR swapping feature lets you easily change the fusion you are looking at.

Workflow Inputs

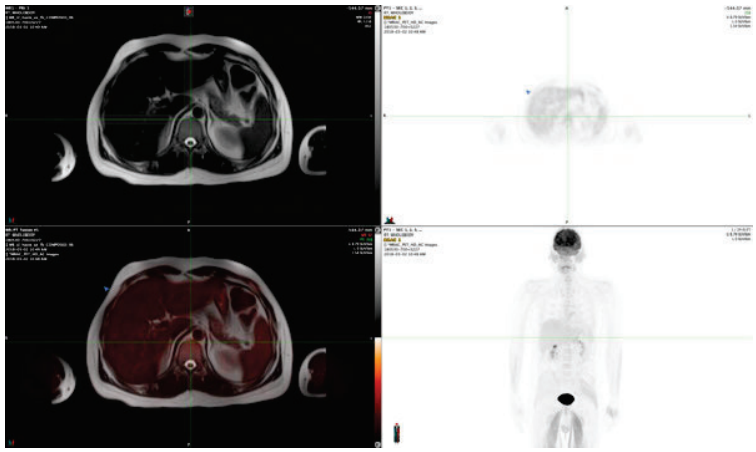
- Any number of MR sequences
- Prior PET/CTs

Additional Information

- The workflow can display a MRAC PET fused to any number of MR sequences.
- The logic will fuse the designated MRAC PET to all MR sequences that are loaded in the workflow.
- The number of rows and columns that will be shown in each hanging protocol can be adjusted in the workflow before it is launched.

Workflow Outputs

Commonly-used viewing pages for whole body and applicable spot images. Pages are dependent on the number of time points and additional bed positions loaded.



Example of a page display that is output by the Hybrid PET/MR - Standard workflow.

Default Workflow: Universal SPECT/CT Review

Processing

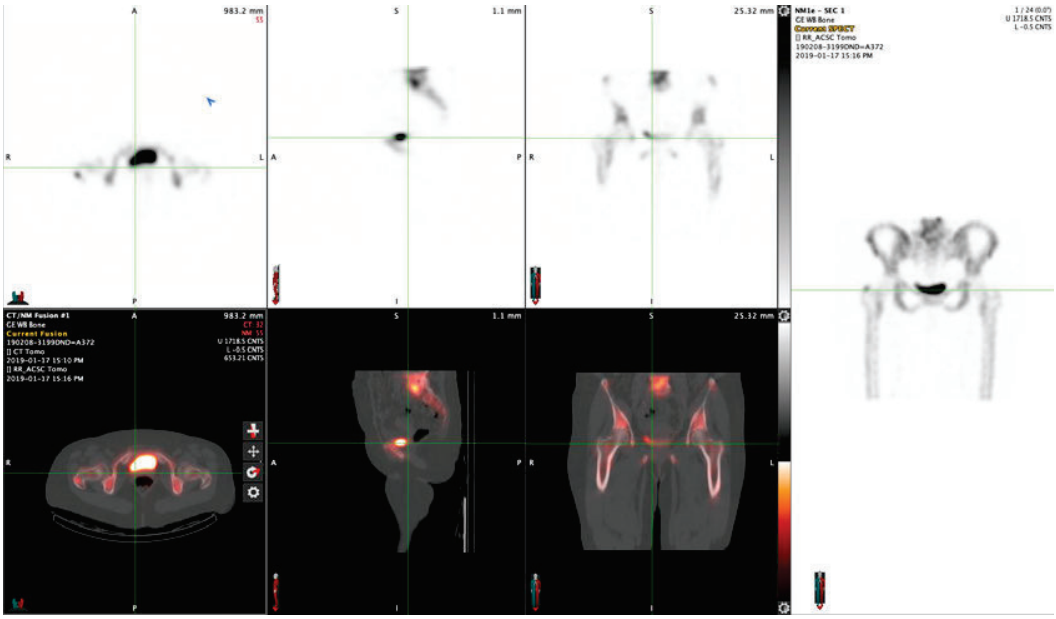
This workflow automatically organizes images for viewing, based on the inputs selected.

Workflow Inputs

- Up to two SPECT/CT time points
- NAC SPECT images (optional)
- Single and dual bed positions
- Planar NM images if present

Workflow Outputs

Commonly-used viewing pages for whole body and applicable spot images. Pages are dependent on the number of time points and additional bed positions loaded.



Example of a page display that is output by the Universal SPECT/CT Review workflow.

Default Workflow: CT Bone Contouring

Processing

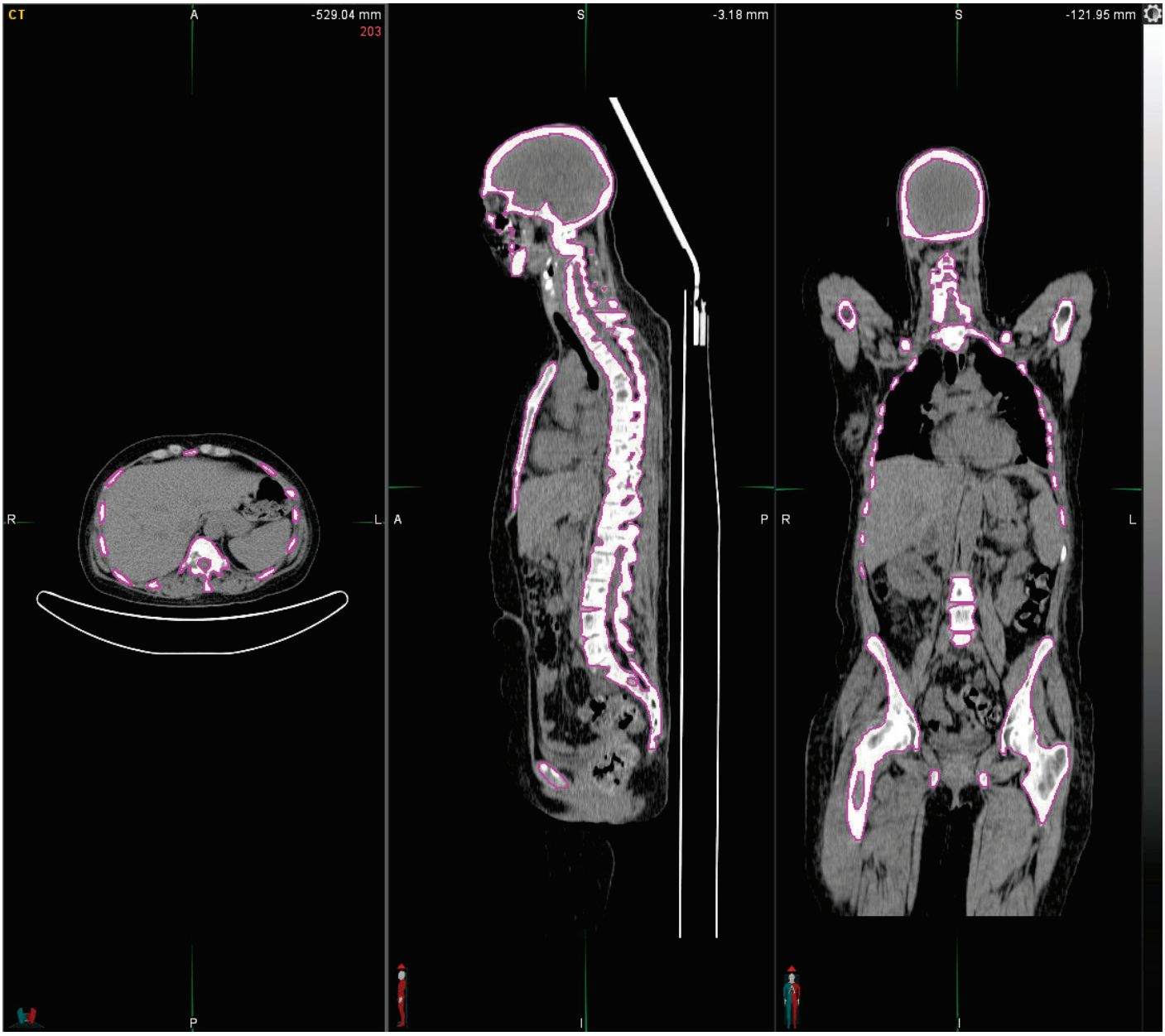
1. You are prompted to rename the bone contour.
2. You are prompted to review and edit the generated bone contour.

Workflow Inputs

One CT image

Workflow Outputs

A single contour for all bone structures.


CT
A
-529.04 mm
203
R
L
P
S
-3.18 mm
A
P
I
S
-121.95 mm
R
L
I

Default Workflow: WB Bone and Planar Viewing

Processing

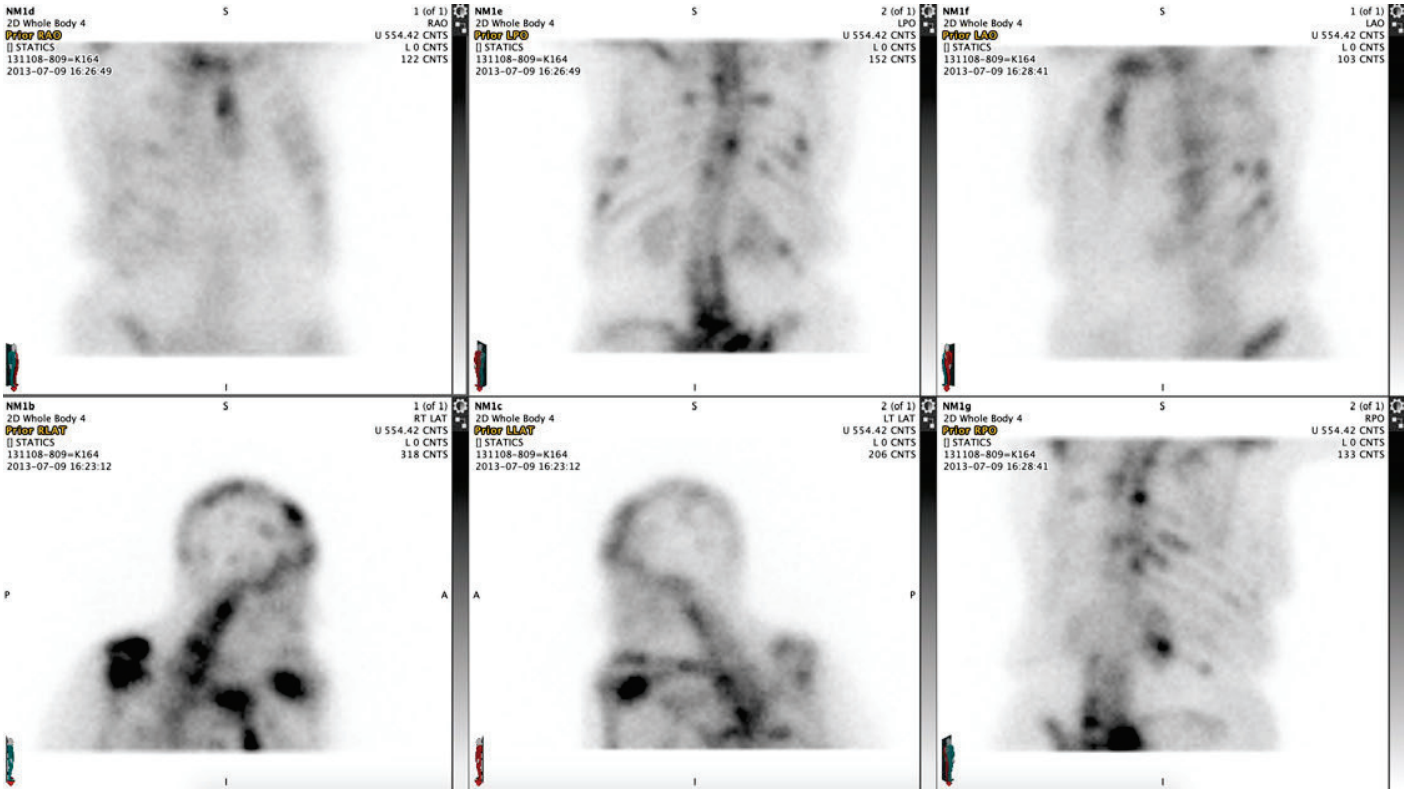
- The workflow uses built-in logic to display the images and accommodate various monitor setups.
- Up to two time points are supported.

Workflow Inputs

Planar acquisitions

Workflow Outputs

Page displays that account for all selected images.



Default Workflow: Combine Lumbar MR

Note: The combined series is intended only for treatment planning and **not** diagnostic applications.

Processing

1. You are prompted to select a primary MR series.
    - When the workflow is finished, the reconstructed series shares the same patient orientation as the specified primary, so it is recommended to choose a series without significant rotation.
2. You are prompted to select a z resolution in millimeters to resample the primary series.
    - The default resolution is 1 millimeter.
    - A smaller resolution smooths step artifacts, but significantly increases the size of the series.
3. The workflow resamples the MR at the specified resolution and combines all slices into a single series.

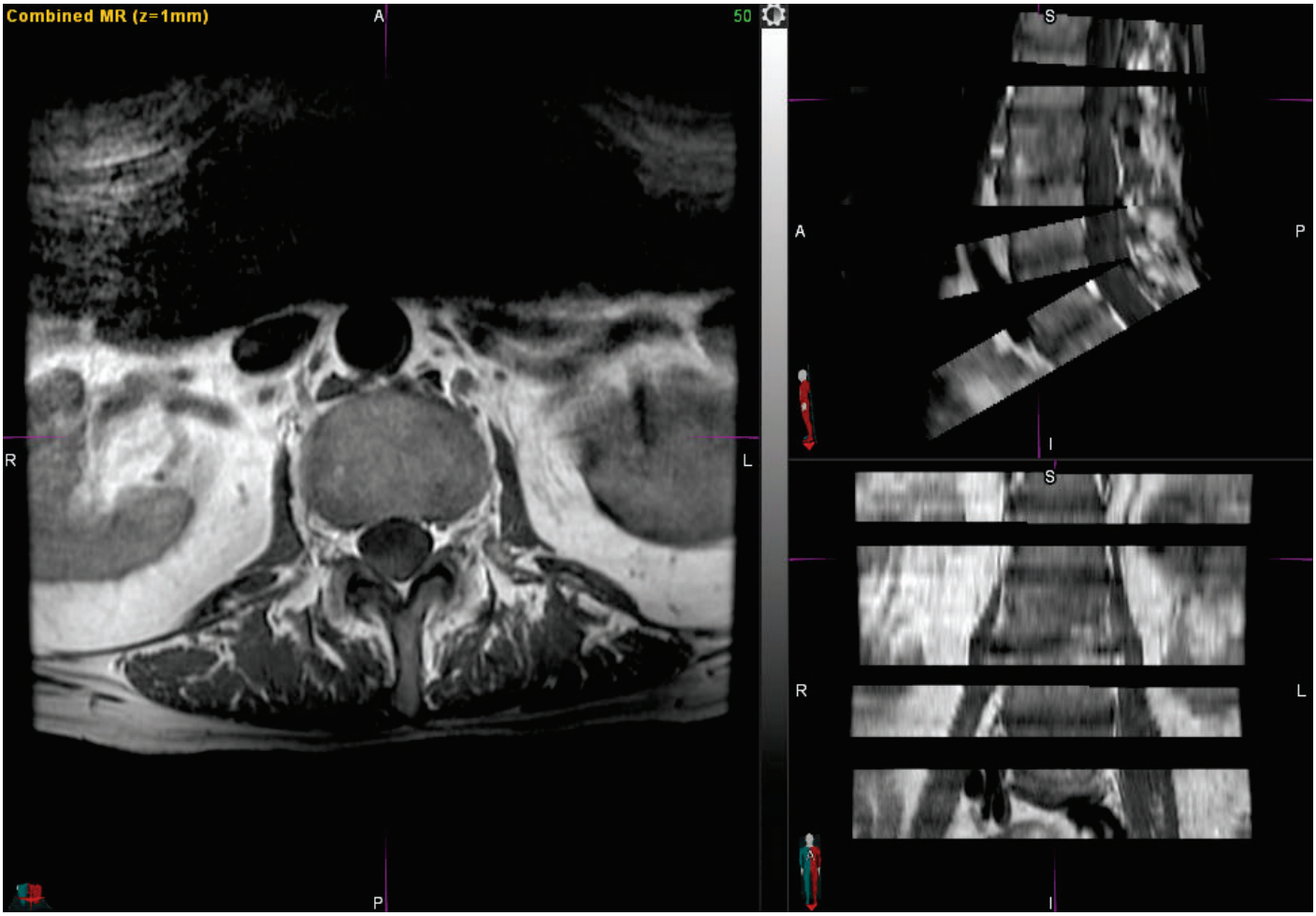
Workflow Inputs

- Multiple 3D regions
- Multiple 2D slices
- A combination of 3D regions and 2D slices

Note: At least five slices at a given angle are required to load the series as a 3D volume.

Workflow Outputs

A single MR series.


Combined MR (z=1mm)
A
50
R
L
P
S
A
P
I
S
R
L
I

Default Nuclear Medicine Workflows

Default Workflow: Brain Autocontouring

Processing

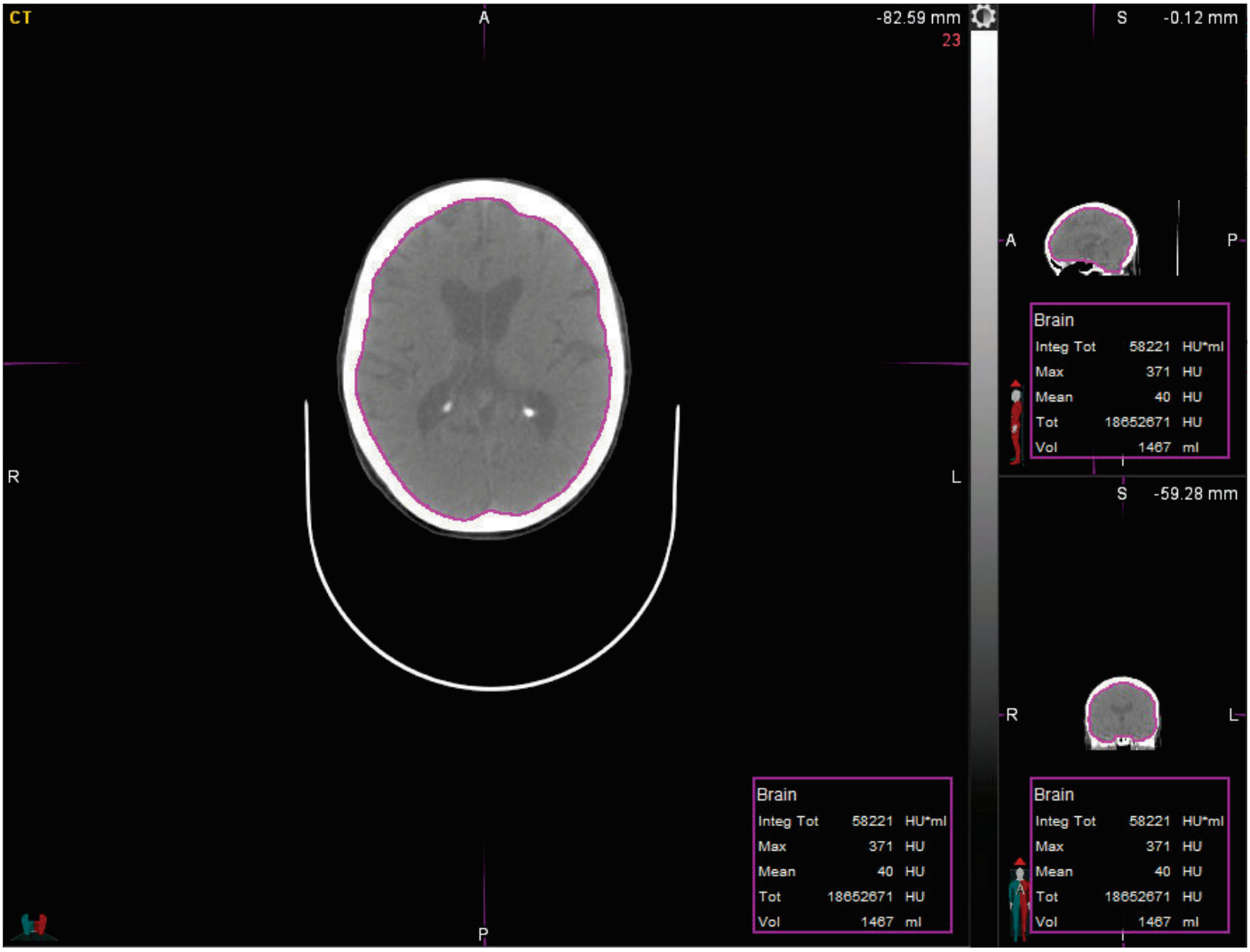
1. You are prompted to review and edit the generated brain contour.
2. You are prompted to save the brain contour.

Workflow Inputs

One CT image

Workflow Outputs

A single brain contour.


CT
A
-82.59 mm
23
S
-0.12 mm
A
P
Brain
Integ Tot 58221 HU*ml
Max 371 HU
Mean 40 HU
Tot 18652671 HU
Vol 1467 ml
R
L
S
-59.28 mm
R
L
P
Brain
Integ Tot 58221 HU*ml
Max 371 HU
Mean 40 HU
Tot 18652671 HU
Vol 1467 ml
Brain
Integ Tot 58221 HU*ml
Max 371 HU
Mean 40 HU
Tot 18652671 HU
Vol 1467 ml

Default Workflow: Cardiac Amyloidosis PYP

Processing

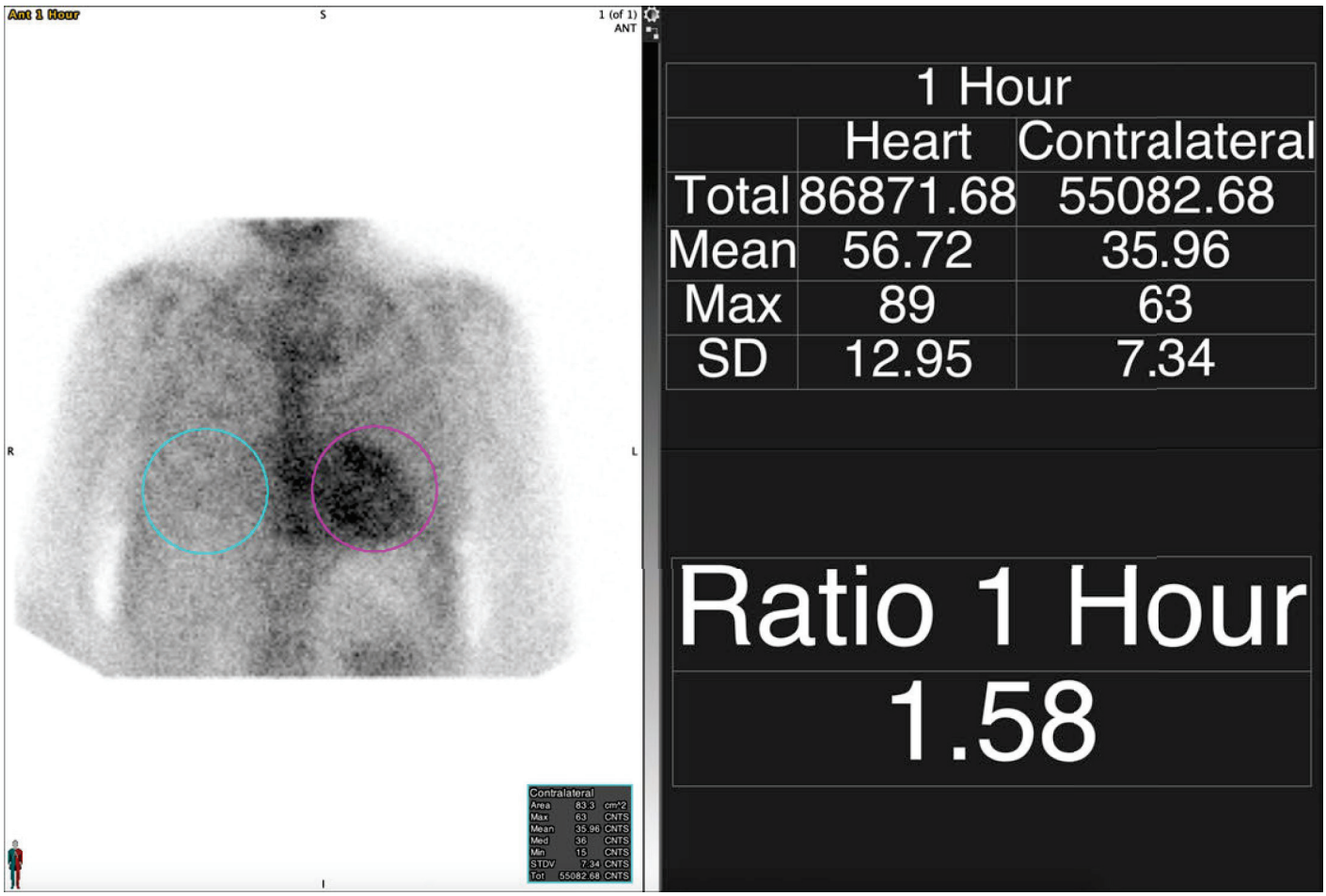
1. You are prompted to create an ROI around the heart.
2. The workflow mirrors the heart ROI across the image to form a background region.
3. You are prompted to adjust the ROIs if needed.

Workflow Inputs

- Planar anterior image
- Optional lateral images and SPECT/CT

Workflow Outputs

PYP Analysis statistics (including heart to contralateral ratio)


Ant 1 Hour
S
1 (of 1)
ANT
R
L
I
Contralateral
Area 83.3 cm^2
Max 63 CNTS
Mean 35.96 CNTS
Med 36 CNTS
Min 15 CNTS
STDV 7.34 CNTS
Tot 55082.68 CNTS
1 Hour
Heart
Contralateral
Total 86871.68 55082.68
Mean 56.72 35.96
Max 89 63
SD 12.95 7.34
Ratio 1 Hour
1.58

Default Workflow: Create Total Tumor Burden Stat Table

Processing

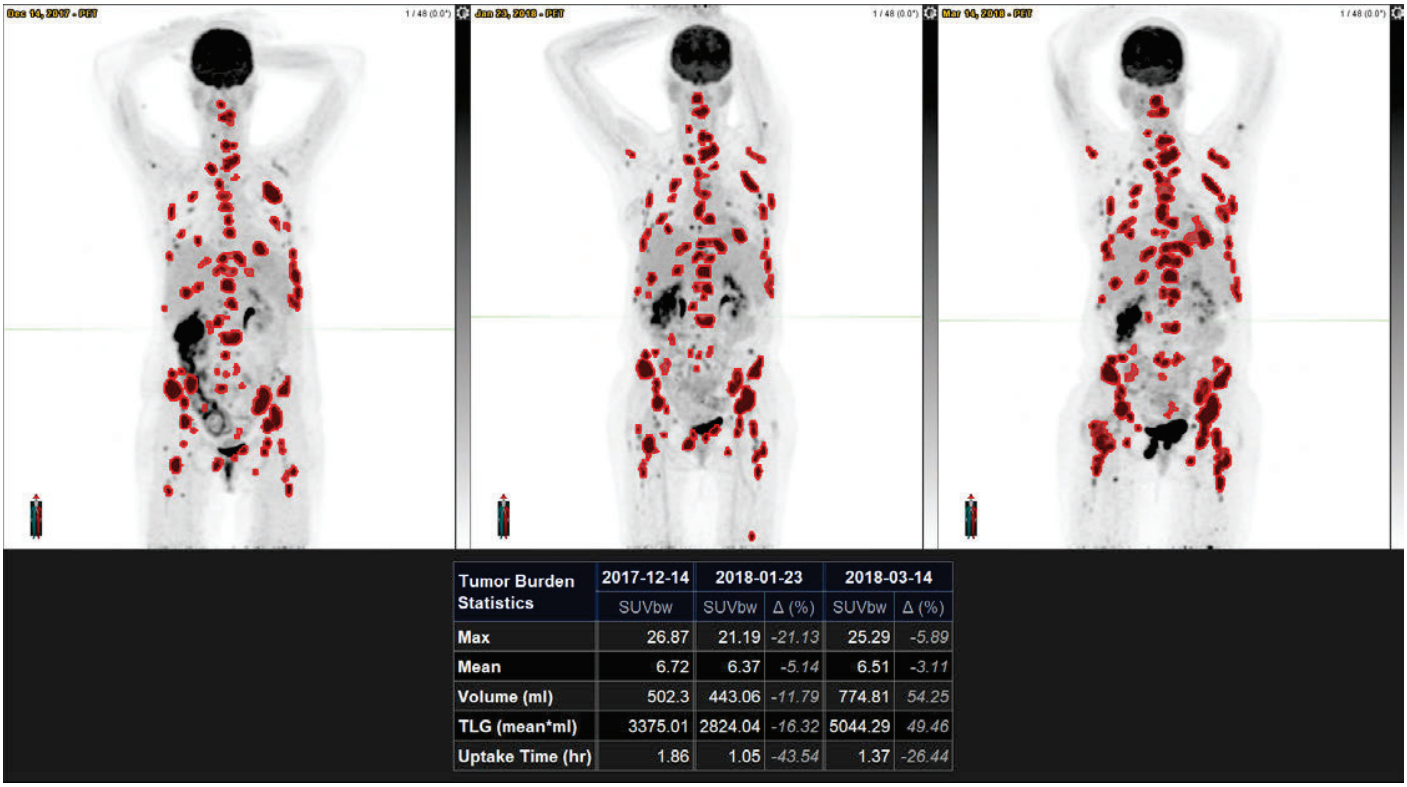
1. If multiple series are selected as inputs, you are prompted to select which series to evaluate.
2. The workflow sums all VOIs on the specified series into a Total Tumor Burden VOI and produces a Tumor Burden Statistics table.

Inputs

Single or multiple PET and/or SPECT series with contours.

Outputs

The specified series to evaluate with a tumor burden statistics table. The table shows the percent change relative to the baseline visit.



Tumor Burden Statistics	2017-12-14	2018-01-23		2018-03-14	
	SUVbw	SUVbw	Δ (%)	SUVbw	Δ (%)
Max	26.87	21.19	-21.13	25.29	-5.89
Mean	6.72	6.37	-5.14	6.51	-3.11
Volume (ml)	502.3	443.06	-11.79	774.81	54.25
TLG (mean*ml)	3375.01	2824.04	-16.32	5044.29	49.46
Uptake Time (hr)	1.86	1.05	-43.54	1.37	-26.44

Default Workflow: Dynamic Flow Processing

Processing

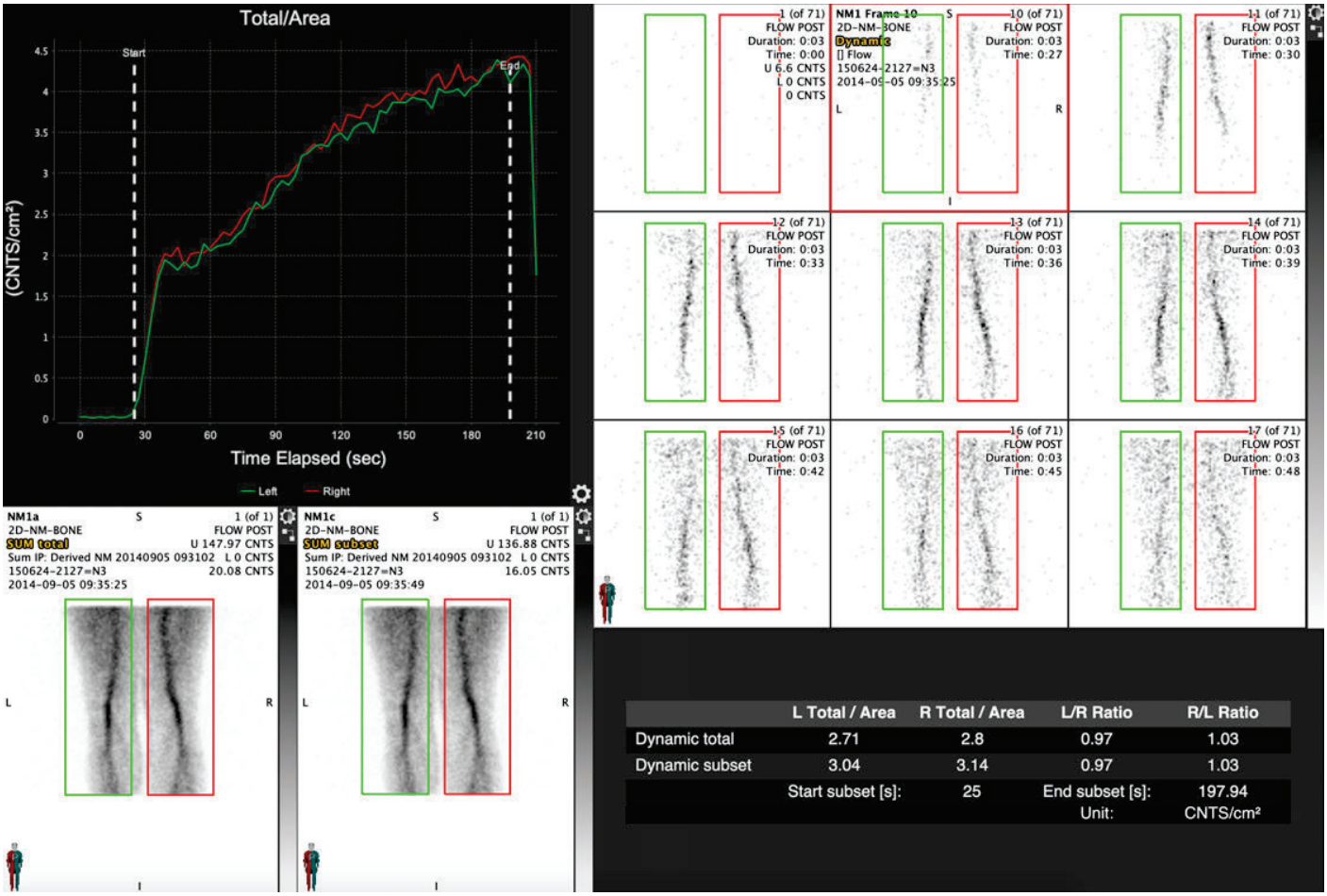
1. You are prompted to draw the Right contour.
2. The workflow automatically mirrors the contour.
3. You are prompted to move the mirrored contour to the desired position.
4. You are prompted to specify the start and end of the desired time period.
5. The workflow automatically compares the counts between the two contours for the specified time period.

Workflow Inputs

Dynamic planar acquisition

Workflow Outputs

- A graph showing the ratio between total counts in the ROI and the area.
- A dynamic image view with the left and right contours visible.
- A total summed image (summed from the entire image).
- A subset summed image (summed from the start/end annotations set in the graph).
- A results table showing the ratios between the area and total per ROI as well as between the two ROIs.


Total/Area
Start
End
(CNTS/cm²)
Time Elapsed (sec)
Left
Right
NM1a
2D-NM-BONE
SUM total
Sum IP: Derived NM 20140905 093102
150624-2127=N3
2014-09-05 09:35:25
NM1c
2D-NM-BONE
SUM subset
Sum IP: Derived NM 20140905 093102
150624-2127=N3
2014-09-05 09:35:49
NM1 Frame 10
2D-NM-BONE
Dynamic
150624-2127=N3
2014-09-05 09:35:25
FLOW POST
L Total / Area
R Total / Area
L/R Ratio
R/L Ratio
Dynamic total
2.71
2.8
0.97
1.03
Dynamic subset
3.04
3.14
0.97
1.03
Start subset [s]:
25
End subset [s]:
197.94
Unit:
CNTS/cm²

Default Workflow: Gallbladder Ejection Fraction (EF)

Processing

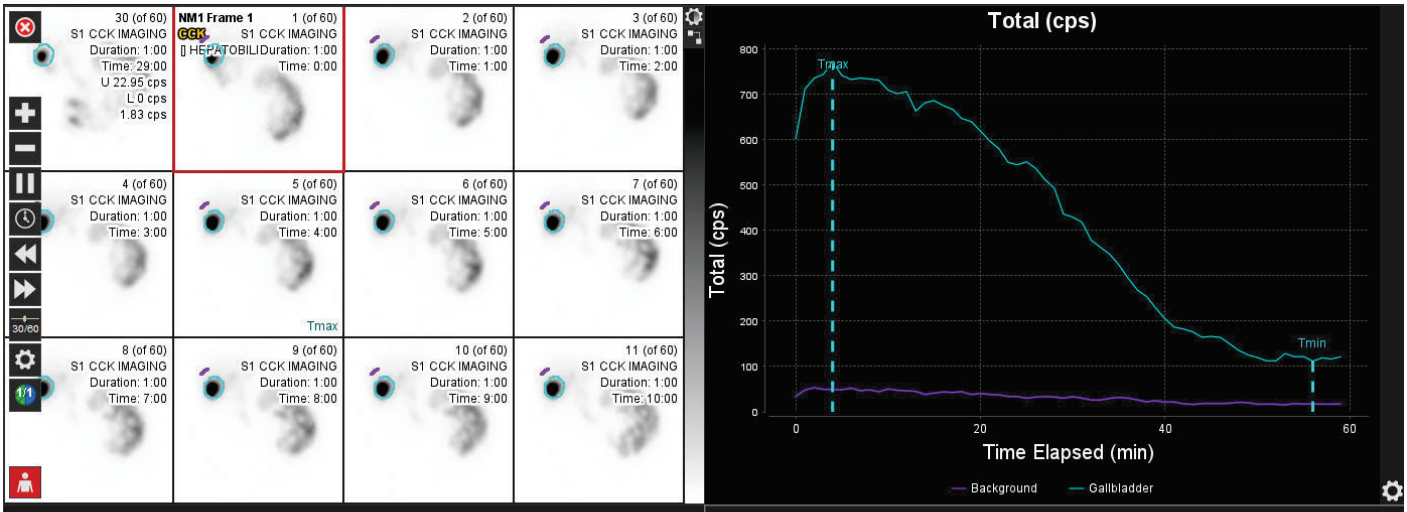
1. The workflow automatically contours the following regions:
    - Gallbladder
    - Background
2. You are prompted to edit the auto-generated contours as needed, or delete the contours and draw them manually.
3. You are prompted to modify the contours per frame if necessary.
4. The workflow calculates the ejection fraction of the gallbladder along with Tmax and Tmin.[1]

Workflow Inputs

- One dynamic ejection series
- Any dynamic flow series
- Any static series

[1]Tulchinsky M, Ciak BW, Delbeke D, et al. SNM Practice Guideline for Hepatobiliary Scintigraphy 4.0. JNM 2010; 38(4):210-218.

Workflow Outputs



Normal Values

Infusion Duration	Time of calculation (min)	Fifth Percentile	50th Percentile
60	15	0	28
60	30	22	69
60	45	38	83
60	60	49	90

Ziessman HA, Tulchinsky M, Lavely WC, et al. Sincalide-stimulated choles-cintigraphy: a multicenter investigation to determine optimal infusion method-ology and gallbladder ejection fraction normal values. J Nucl Med. 2010; 51:277–281.

Hepatobiliary Results

Tmax	4	min
Tmin	56	min
Ejection Fraction:	85.51	%
Ejection Period:	52	min

☑ Perform decay correction

Decay Correction Isotope: ^99m^Technetium

Default Workflow: Gastric Emptying

Processing

1. You are prompted to contour the following regions:
    - Stomach
    - Background
2. MIM® calculates the gastric percent retention or percent emptying over time.[1]

Workflow Inputs

Dynamic acquisition or static anterior/posterior images

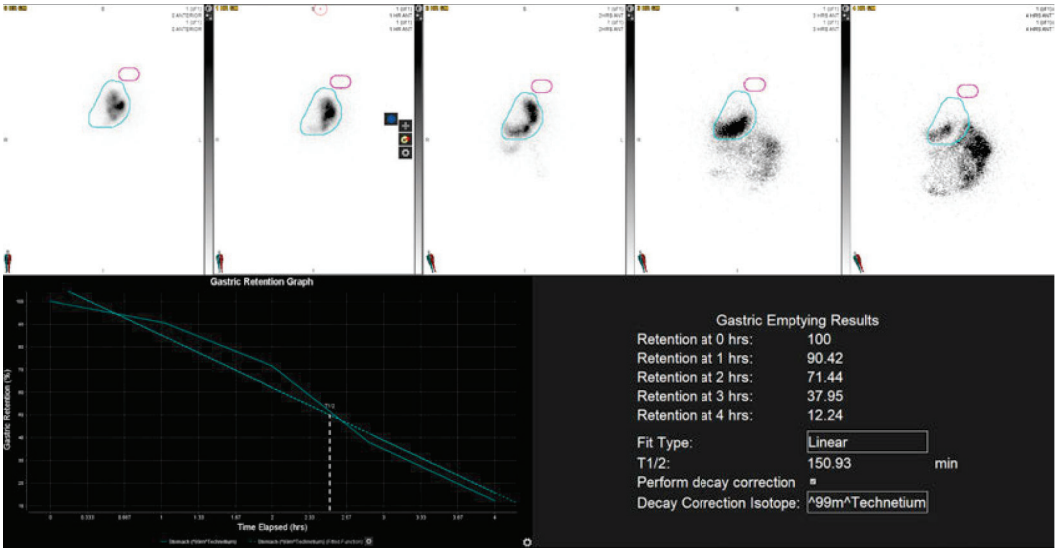
Workflow Outputs

- A graph showing retention.
- A graph and a table showing retention over time.

By default, the graph shows a linear fit curve. Click the **Fit Type** field below the graph if you want to change the type of curve displayed. For example, you could change the fit type to exponential for a liquid gastric emptying exam, such as for ^{99}Tc DTPA or ^{111}In DTPA.

Related: Refer to Fit Type Calculations: Technical Details for more information about fit curve calculation.

[1] Abell, Camilleri, Donohoe, Hasler, Lin, Maurer, McCallum, Nowak, Nusynowitz, Parkman, Shreve, Szarka, Snape, & Ziessman: Consensus Recommendations for Gastric Emptying Scintigraphy: A Joint Report of the American Neurogastroenterology and Motility Society and the Society of Nuclear Medicine. Am J Gastroenterol. 2008; 103:753- 763.



A graph of counts over time and a table with results.

Notes

- Processing can be performed on single and/or dual isotope exams.
- Decay correction is available for the following isotopes: ^{99m}Tc, ^{111}In, ^{67}Ga, ^{201}Tl, ^{123}I, ^{131}I, and ^{177}Lu.
- You can configure various parameters for gastric processing via **Settings** >> **General Preferences** >> **Imaging** >> **NM Processing** >> **Gastric Emptying**.
    - MIM calculates gastric retention by default. To calculate gastric emptying instead, check **Show as Percent Emptied**.
    - If desired, display additional statistics by checking **Enable Lag Time** and **Enable Emptying Rate**.
    - If desired, check **Use Tmax to determine 100% retention**.
- Compatibility with the Swedish National Protocol[1] for gastric emptying is provided.

[1]Grybäck P, Hermansson G, Lyrenäs E, Beckman KW, Jacobsson H, Hellström PM. Nationwide standardisation and evaluation of scintigraphic gastric emptying: reference values and comparisons between subgroups in a multicentre trial. Eur J Nucl Med. 2000 Jun;27(6):647-55.

Default Workflow: LesionID®

Use LesionID to quantify areas of increased uptake across any number of time points. For more information and detailed instructions, see the *MIM Encore for Radiology and Nuclear Medicine User Guide*.

Tip: Use LesionID Pro for segmentation powered by Contour ProtégéAI+™ and for additional quantification options. Please contact MIM Software Support at support.mimsoftware.com for more information about licensing for LesionID Pro.

Processing

1. You are prompted to define segmentation settings and create contours for each time point:
    - Whether to segment areas of uptake in the whole body or in a specific area.
    - Whether to define your own activity-cutoff value or use PERCIST criteria to calculate an activity-cutoff value.
    - Define lower and upper volume limits to prevent unwanted regions from being contoured.
2. You are presented options to redefine existing contours:
    - Whether to redefine all contours or selected contours.
    - Choose the method to use to redefine contours.
3. You are presented options to sort Lesions, calculate total tumor burden, and save contours.

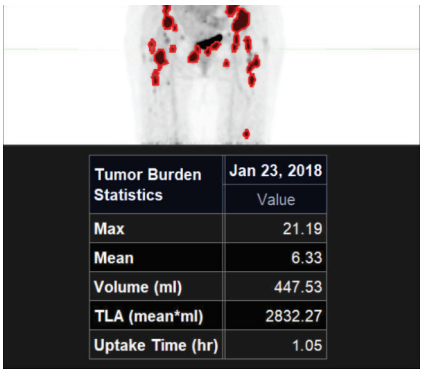
Workflow Inputs

- At least one PET/CT or SPECT/CT
- RTstruct files (optional)

Workflow Outputs

- A contour set containing all segmented lesions and a combined tumor burden.

- A tumor burden page with a statistics table.



Tumor Burden Statistics	Jan 23, 2018
	Value
Max	21.19
Mean	6.33
Volume (ml)	447.53
TLA (mean*ml)	2832.27
Uptake Time (hr)	1.05

Default Workflow: Liver Functional Analysis

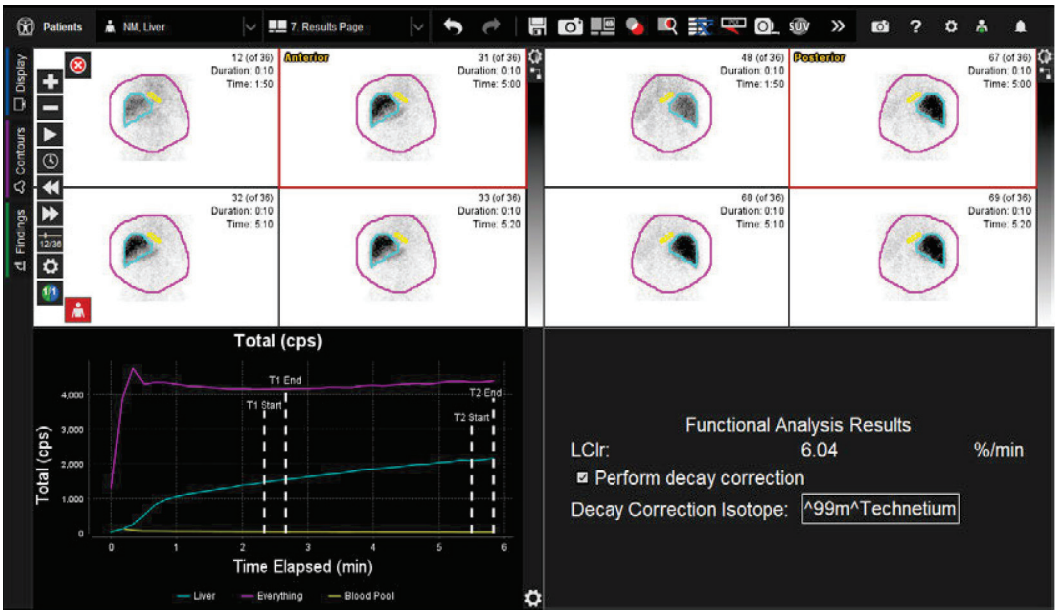
Processing

1. You are prompted to contour the following regions:
    - Everything
    - Liver
    - Blood Pool
2. The workflow calculates the Liver Clearance Rate (LCLr) in percent/minute using the Ekman Formula.[1]

Workflow Inputs

Dynamic planar anterior/posterior images

Workflow Outputs



A graph showing uptake over time.

[1]Ekman M, Fjalling M, Friman S, et al. Liver uptake function measured by IODIDA clearance rate in liver transplant patients and healthy volunteers. Nucl Med Comm 1996; 17:235-242.

Default Workflow: Lung Autocontouring

Processing

1. You are prompted to review and edit the generated lung contours.
2. You are prompted to save the lung contours.

Workflow Inputs

A single CT series

Workflow Outputs

- A left lung contour
- A right lung contour

Default Workflow: Lung Processing

Processing

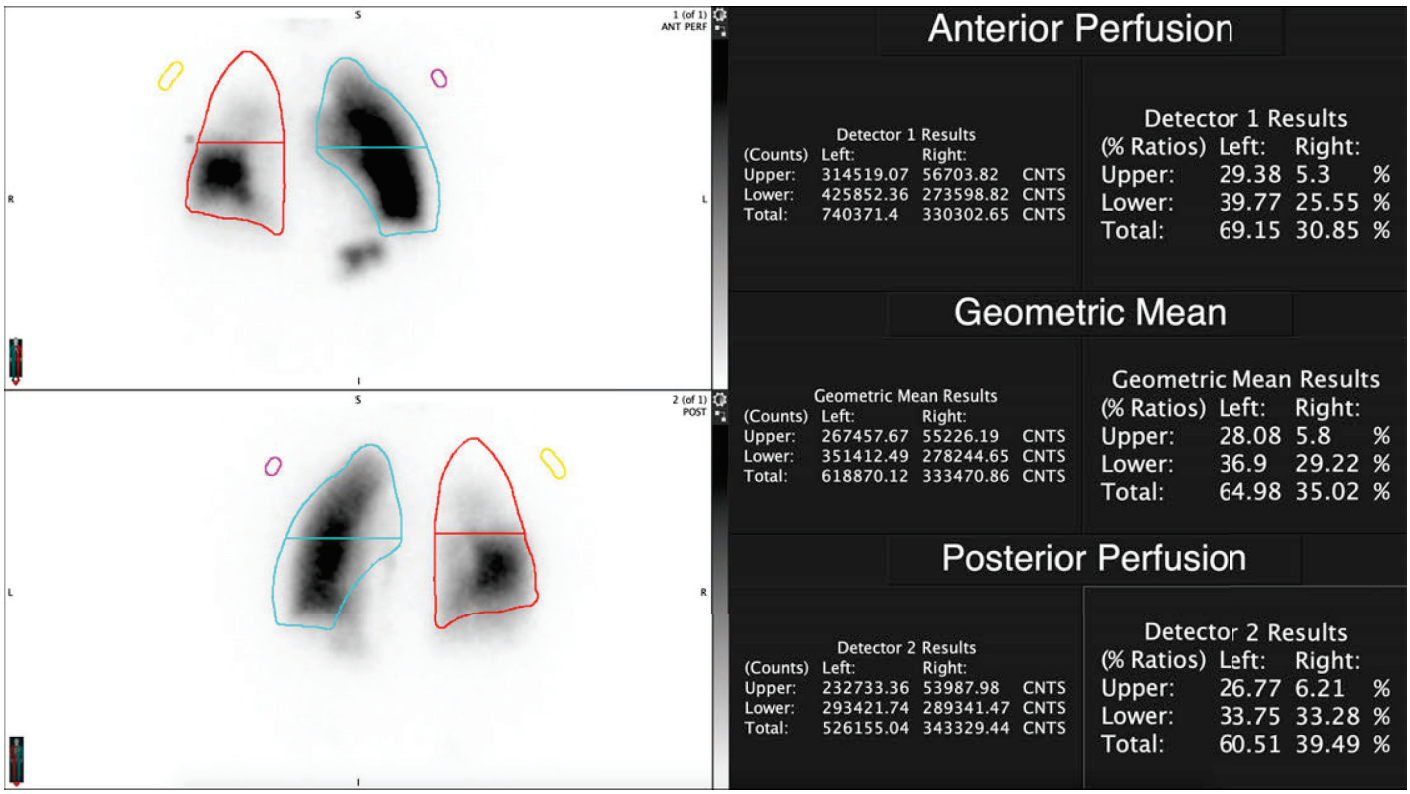
1. You are prompted to select desired quantification based on images selected.
2. You are prompted to contour the lungs and optional background regions.
3. The workflow automatically segments the lungs into different regions (the number of regions can be adjusted in General Preferences).
4. The workflow calculates the regional uptake in the lungs.

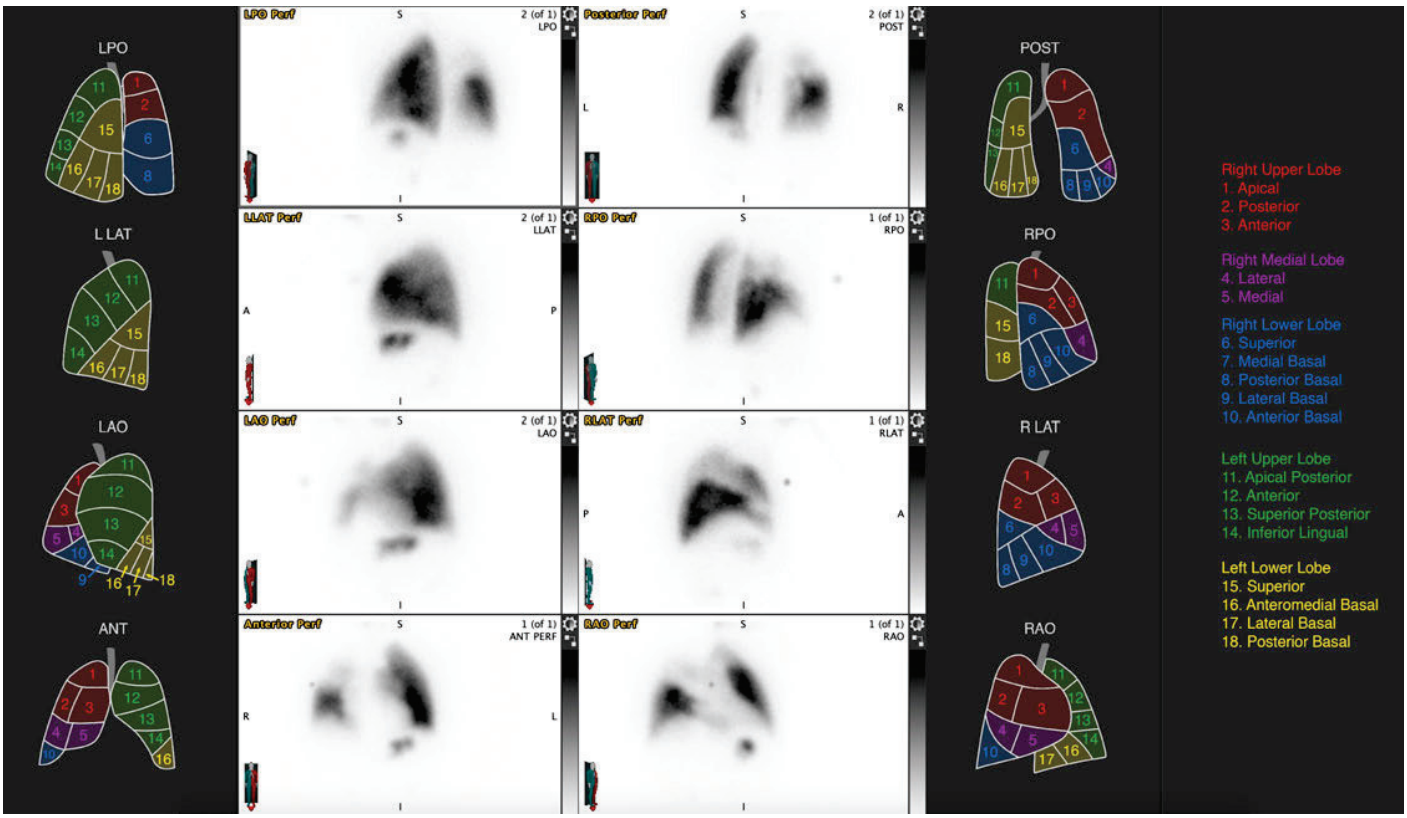
Workflow Inputs

- Planar NM images
- SPECT Perfusion and/or Ventilation
- Optional: CT image

Workflow Outputs

- Lobe segmentation diagrams
- Lung Quant statistics


Anterior Perfusion
Detector 1 Results
(Counts) Left: Right:
Upper: 314519.07 56703.82 CNTS
Lower: 425852.36 273598.82 CNTS
Total: 740371.4 330302.65 CNTS
Detector 1 Results
(% Ratios) Left: Right:
Upper: 29.38 5.3 %
Lower: 39.77 25.55 %
Total: 69.15 30.85 %
Geometric Mean
Geometric Mean Results
(Counts) Left: Right:
Upper: 267457.67 55226.19 CNTS
Lower: 351412.49 278244.65 CNTS
Total: 618870.12 333470.86 CNTS
Geometric Mean Results
(% Ratios) Left: Right:
Upper: 28.08 5.8 %
Lower: 36.9 29.22 %
Total: 64.98 35.02 %
Posterior Perfusion
Detector 2 Results
(Counts) Left: Right:
Upper: 232733.36 53987.98 CNTS
Lower: 293421.74 289341.47 CNTS
Total: 526155.04 343329.44 CNTS
Detector 2 Results
(% Ratios) Left: Right:
Upper: 26.77 6.21 %
Lower: 33.75 33.28 %
Total: 60.51 39.49 %


LPO
L LAT
LAO
ANT
POST
RPO
R LAT
RAO
Right Upper Lobe
1. Apical
2. Posterior
3. Anterior
Right Medial Lobe
4. Lateral
5. Medial
Right Lower Lobe
6. Superior
7. Medial Basal
8. Posterior Basal
9. Lateral Basal
10. Anterior Basal
Left Upper Lobe
11. Apical Posterior
12. Anterior
13. Superior Posterior
14. Inferior Lingual
Left Lower Lobe
15. Superior
16. Anteromedial Basal
17. Lateral Basal
18. Posterior Basal

Default Workflow: 3D Lung Quant

Processing

1. You are prompted to select desired quantitation settings using a table in the workflow.
2. You are prompted to manually or automatically contour the lungs.

Workflow Inputs

SPECT/CT (CT optional) Ventilation and Perfusion

Workflow Outputs

- Lung Quant statistics
- Optional: RTstruct

Default Workflow: 3D Lung Quant with Projected Images

Processing

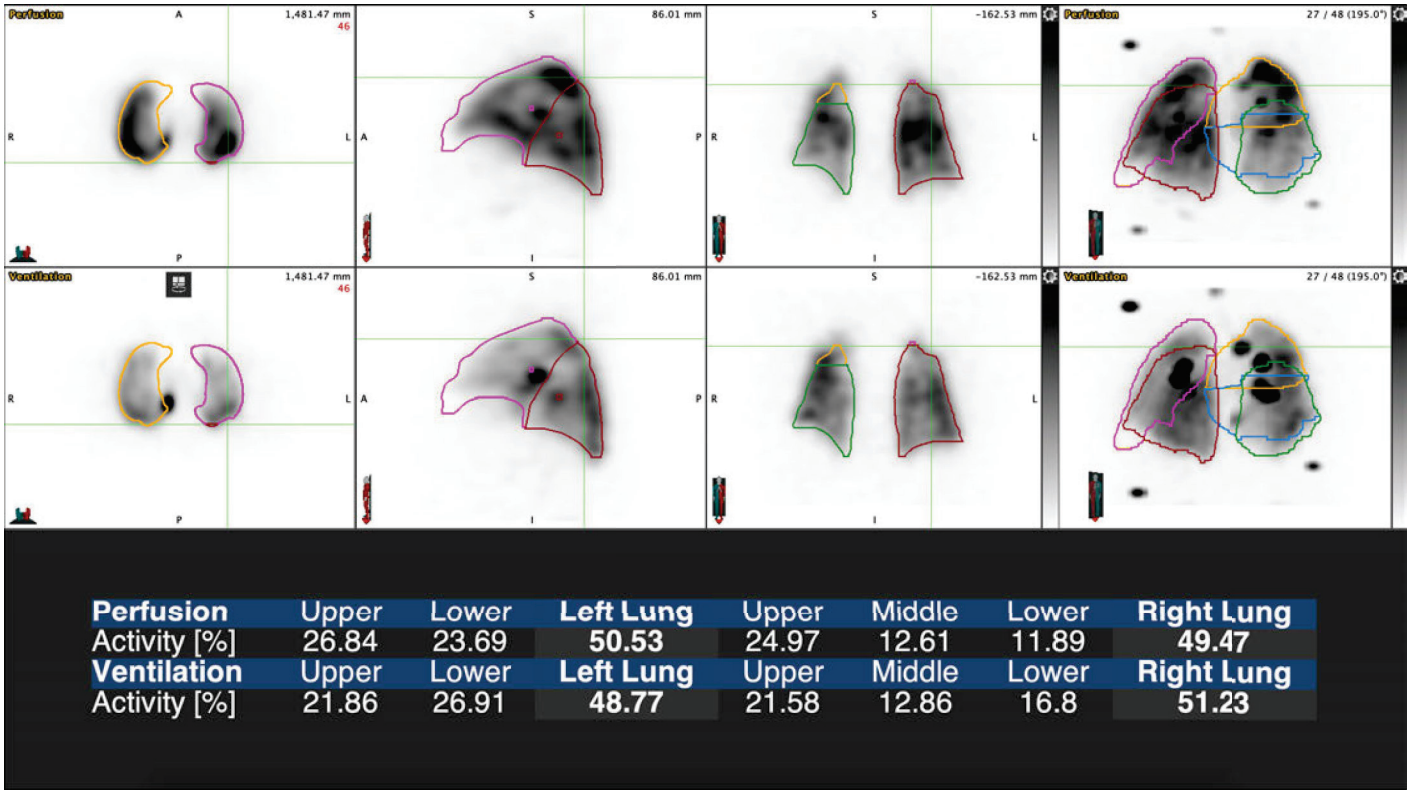
1. You are prompted to select desired quantitation settings.
2. You are prompted to manually or automatically contour the lungs.

Workflow Inputs

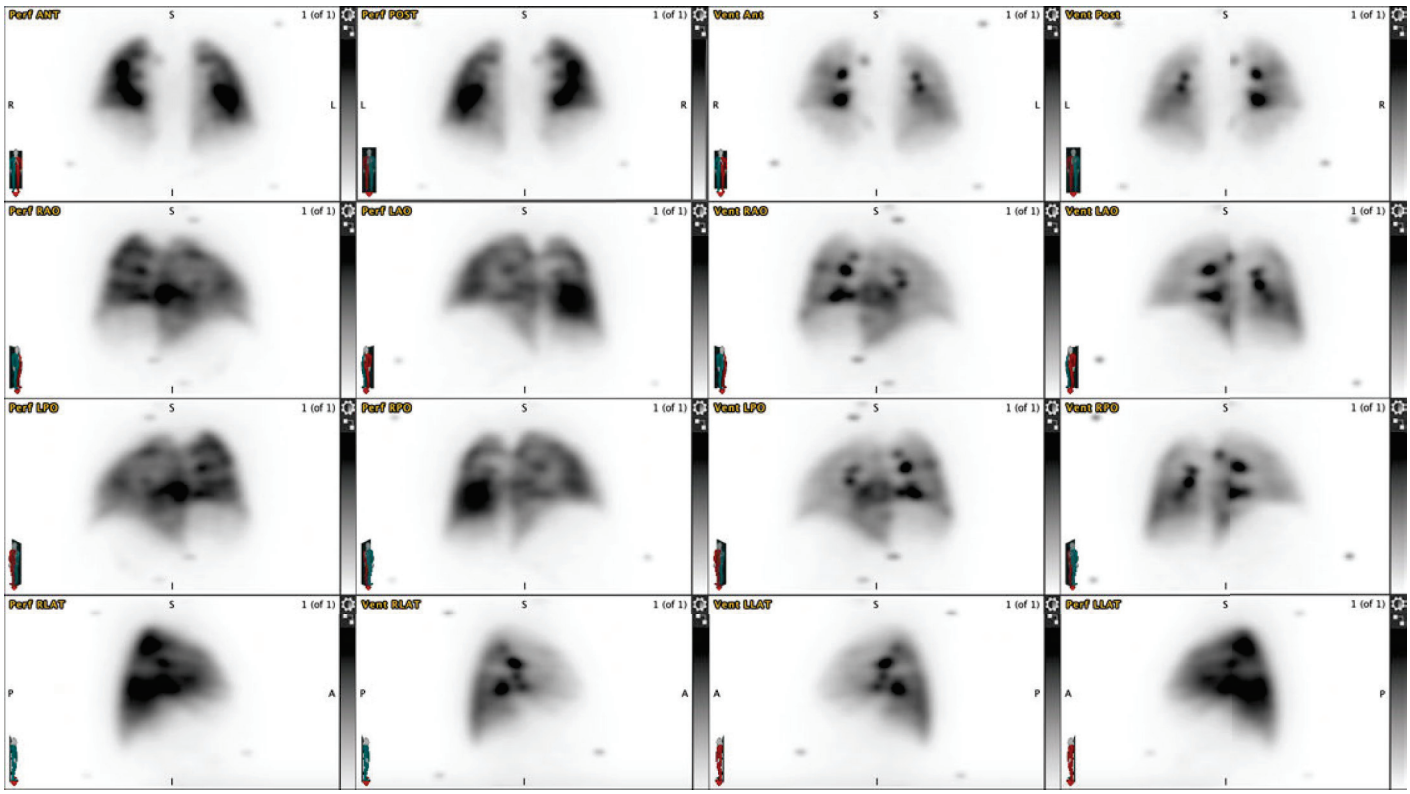
- SPECT/CT (CT optional) Ventilation and Perfusion
- Raw Tomo Images

Workflow Outputs

- Lung quant statistics
- Projected planar images (attenuated correction based on reconstruction setup)
- Optional: RTstruct



Perfusion	Upper	Lower	Left Lung	Upper	Middle	Lower	Right Lung
Activity [%]	26.84	23.69	50.53	24.97	12.61	11.89	49.47
Ventilation	**Upper**	**Lower**	**Left Lung**	**Upper**	**Middle**	**Lower**	**Right Lung**
Activity [%]	21.86	26.91	48.77	21.58	12.86	16.8	51.23


Perf ANT
Perf POST
Vent Ant
Vent Post
Perf RAO
Perf LAO
Vent RAO
Vent LAO
Perf LPO
Perf RPO
Vent LPO
Vent RPO
Perf RLAT
Vent RLAT
Vent LLAT
Perf LLAT

Default Workflow: Lung Ratio

Processing

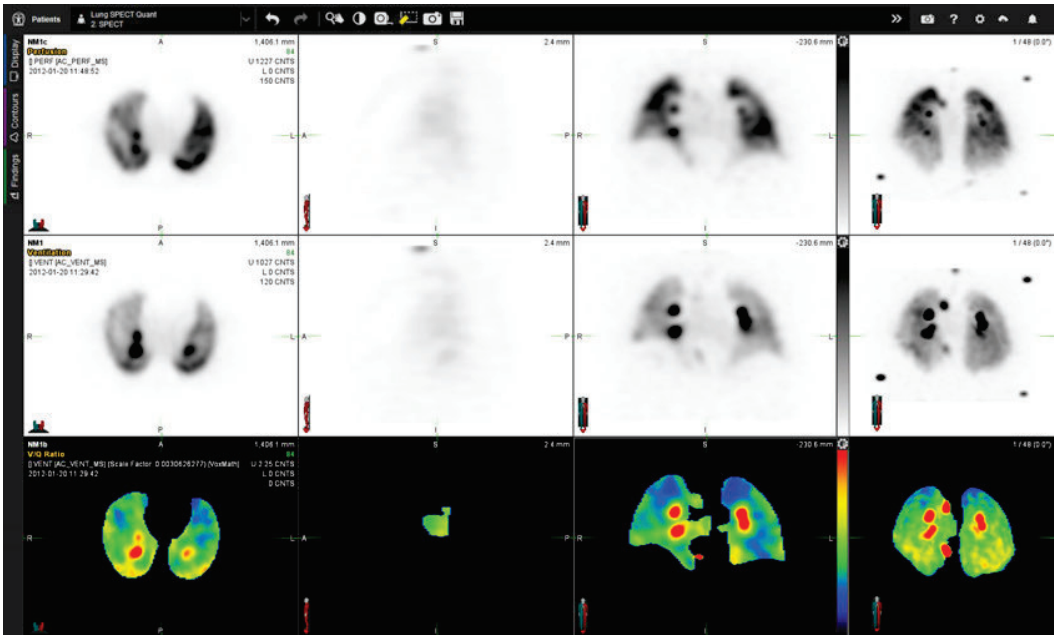
1. You are prompted review fusion alignment.
2. The workflow automatically detects where ventilation is higher than perfusion.
3. If a CT is present, the results are fused to the CT.

Workflow Inputs

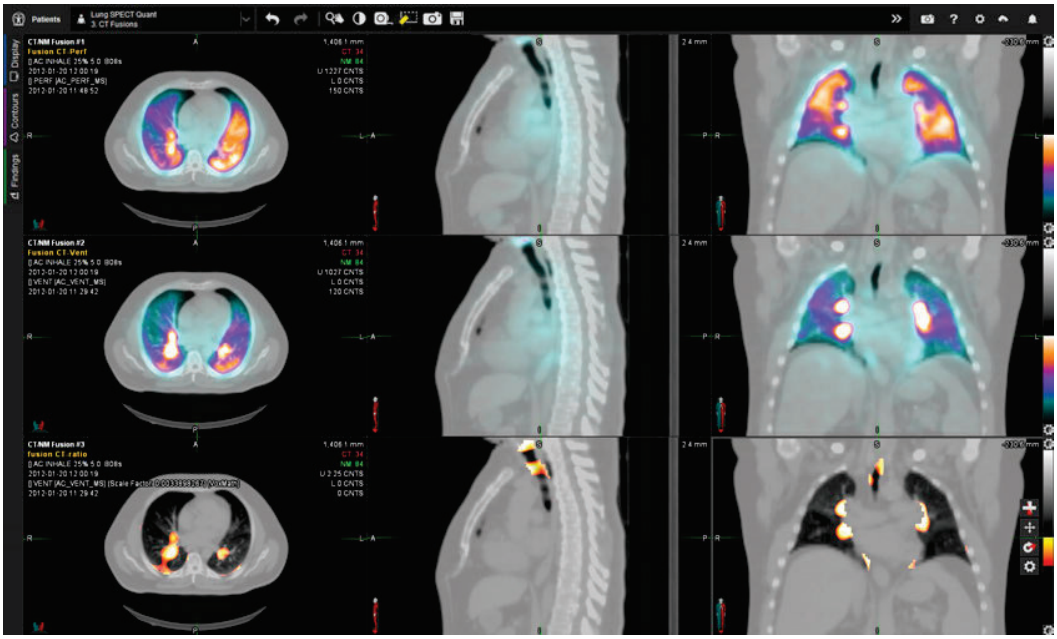
- Planar or SPECT perfusion and ventilation images
- CT (optional)

Workflow Outputs

Results page showing where ventilation is higher than perfusion.



Final results with no CT present.



Final results with a CT present.

Default Workflow: Lung SPECT CT Viewing

Processing

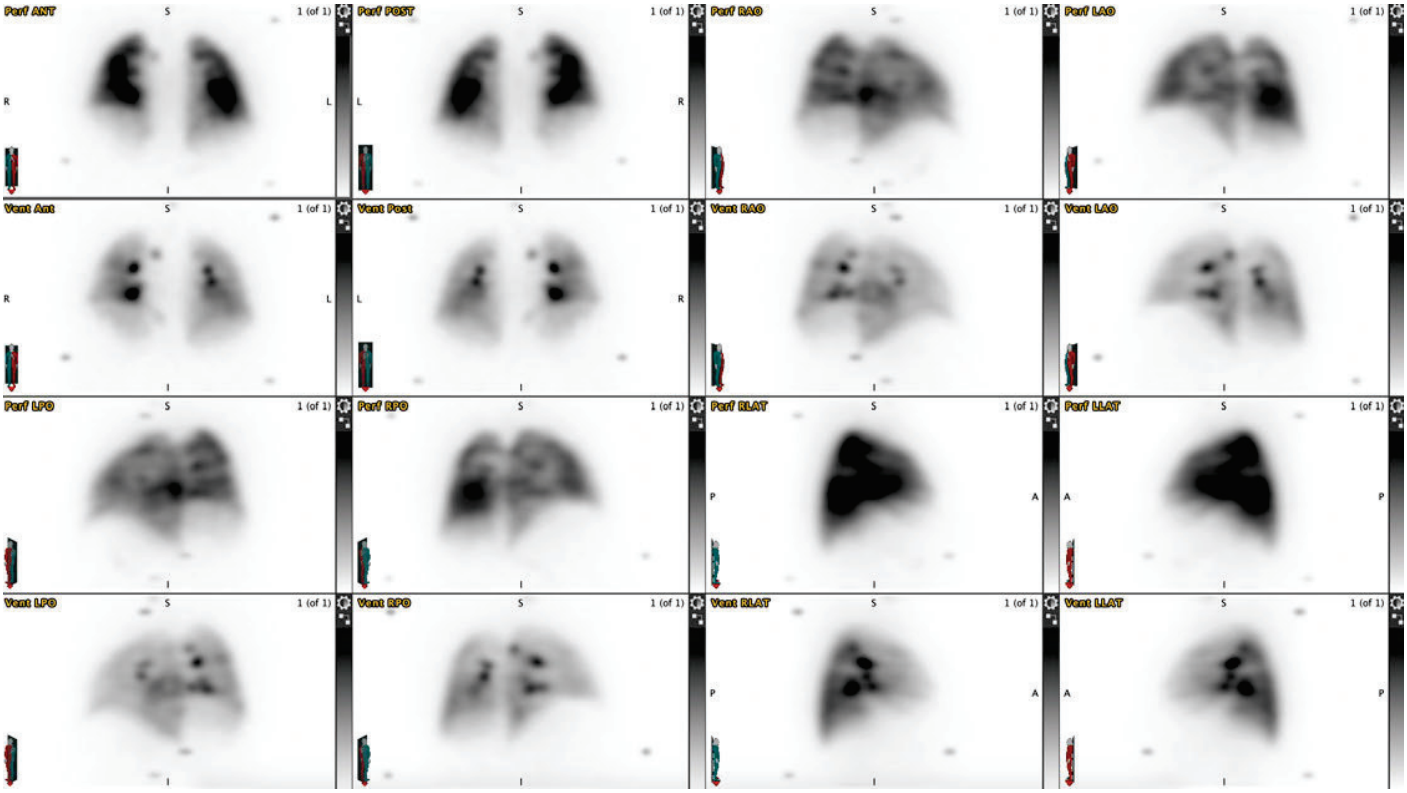
The workflow uses built-in logic to display the images and accommodate various monitor setups.

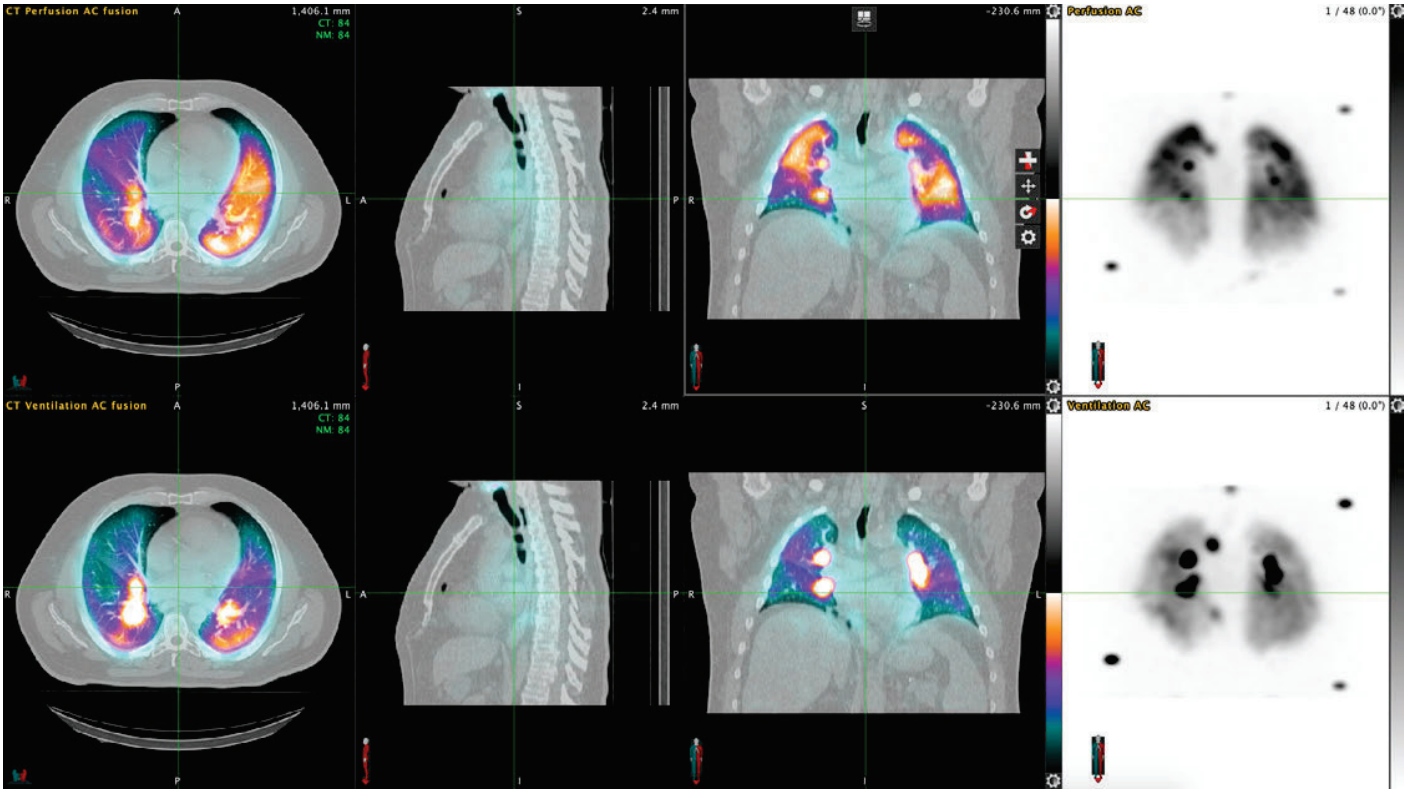
Workflow Inputs

- Corrected SPECT Perfusion and/or Ventilation
- Non-corrected SPECT Perfusion and/or Ventilation
- CT
- Planar NM images

Workflow Outputs

Page displays that account for all selected images.




CT Perfusion AC fusion
1,406.1 mm
CT: 84
NM: 84
2.4 mm
-230.6 mm
Perfusion AC
1 / 48 (0.0°)
CT Ventilation AC fusion
1,406.1 mm
CT: 84
NM: 84
2.4 mm
-230.6 mm
Ventilation AC
1 / 48 (0.0°)

Default Workflow: MUGA

Processing

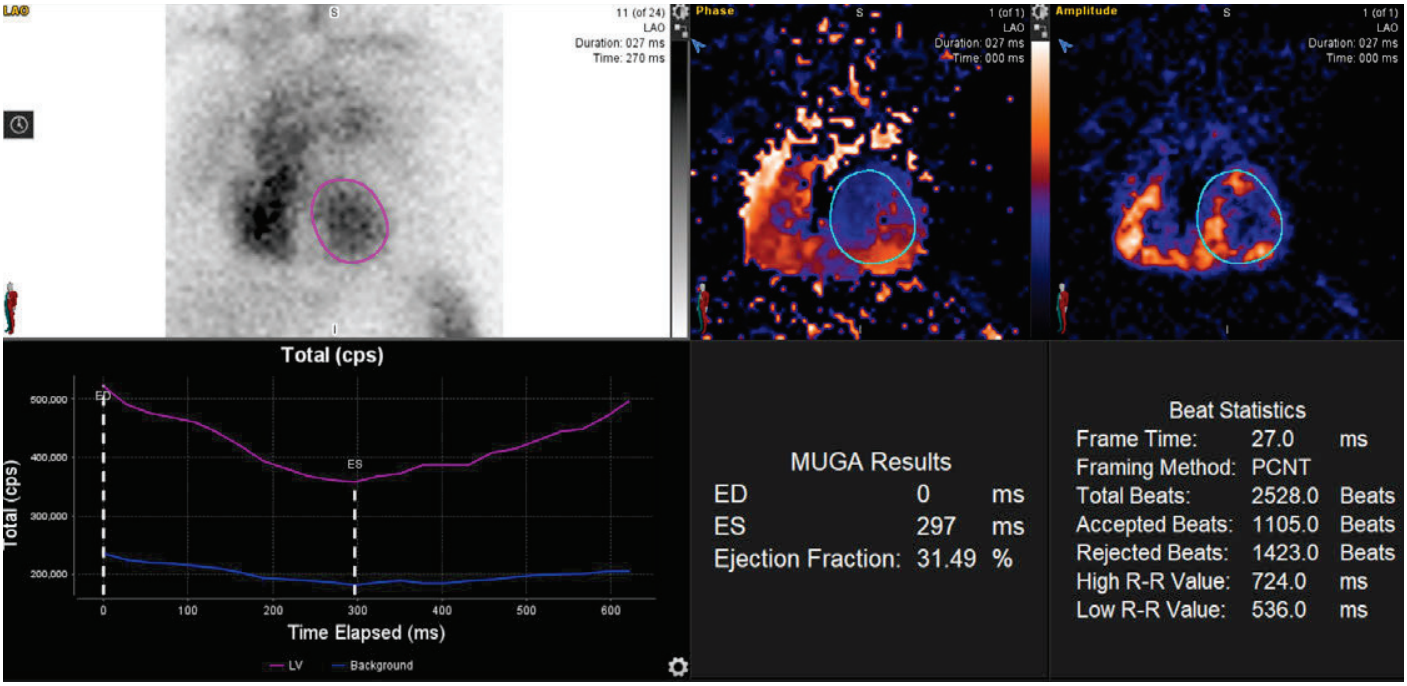
1. You are prompted to localize to the center of the left ventricle.
2. The workflow automatically segments the left ventricle.
3. The workflow automatically generates a background region.
4. The workflow calculates the frames where End Diastolic (ED) and End Systolic (ES) occur, and then reports the time of those frames.
5. The workflow calculates the Ejection Fraction percentage.

Workflow Inputs

- MUGA scan with LAO image
- Optional: Anterior and LLAT acquisitions

Workflow Outputs

- A graph showing ES and ED over time
- ED, ES, and Ejection Fraction values
- Phase and Amplitude images
- Phase histogram



Notes:

- The background mean activity is the same across all frames, and is derived from the mean of the background region on the ES frame. The blue background curve is the total background activity present in LV across all the frames.
- See the MUGA section of the Appendix for additional details.

Workflow Options

Set Parameters for Auto-Generating the Background Contour

The workflow automatically generates a background contour to use as a reference range when processing. Follow these steps to determine the size and/or position of the background contour.

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"auto-generation"**. Select **MUGA** on the left side.
3. Update the Background Auto-Generation Parameters as needed:
    - To set the size, configure the **Region Width** and **Region Thickness** fields.
    - To set the position:
        i. Deselect **Set region position automatically** and enter a **Region Position**.
        ii. Deselect **Set distance to LV automatically** and enter a **Distance from LV**.

4. Click **OK** to save the changes and close the window.

Set Segmentation Parameters (MIM 7.2 and Later)

MIM 7.1 and earlier: These options are not configurable.

Follow these steps if you do not want to use the 4D Gaussian smoothing filter or if you want to tighten the LV segmentation.

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"auto-generation"**. Select **MUGA** on the left side.
3. Update the MUGA Segmentation Parameters as needed:
    - Set the **Image Filter** if you do not want to use the Gaussian filter.
    - Adjust the **LV Tightness** slider if you want to make the internal intensity drop looser or tighter. By default, a value of 0.55 is used.
4. Click **OK** to save the changes and close the window.

Determine Phase Histogram Settings

By default, the workflow output includes a phase histogram. Follow these steps if you do not want the phase histogram or to configure how it appears.

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for **"auto-generation"**. Select **MUGA** on the left side.
3. Scroll down to the Phase Histogram section:
    - Deselect **Include phase histogram in MUGA processing** if you do not want a phase histogram to be produced.
    - Deselect **Weight by amplitude** if you do not want the pixel counts to be weighted by the corresponding pixels in the amplitude image.
    - Update the **Bin Width (Degrees)** if desired.
4. Click **OK** to save the changes and close the window.

Default Workflow: NM Viewing

Processing

- The workflow uses built-in logic to display the images and accommodate various monitor setups.
- Choosing whether to group images by time point (e.g., current and prior images) or image type (e.g., whole-body images vs. spot images) can be adjusted in the workflow before it is launched.

Workflow Inputs

- 2D images
- 3D SPECT images
- CTs
- PTs
- OTs

Workflow Outputs

Page displays that account for all selected images.

Default Workflow: Parathyroid Subtraction

Processing

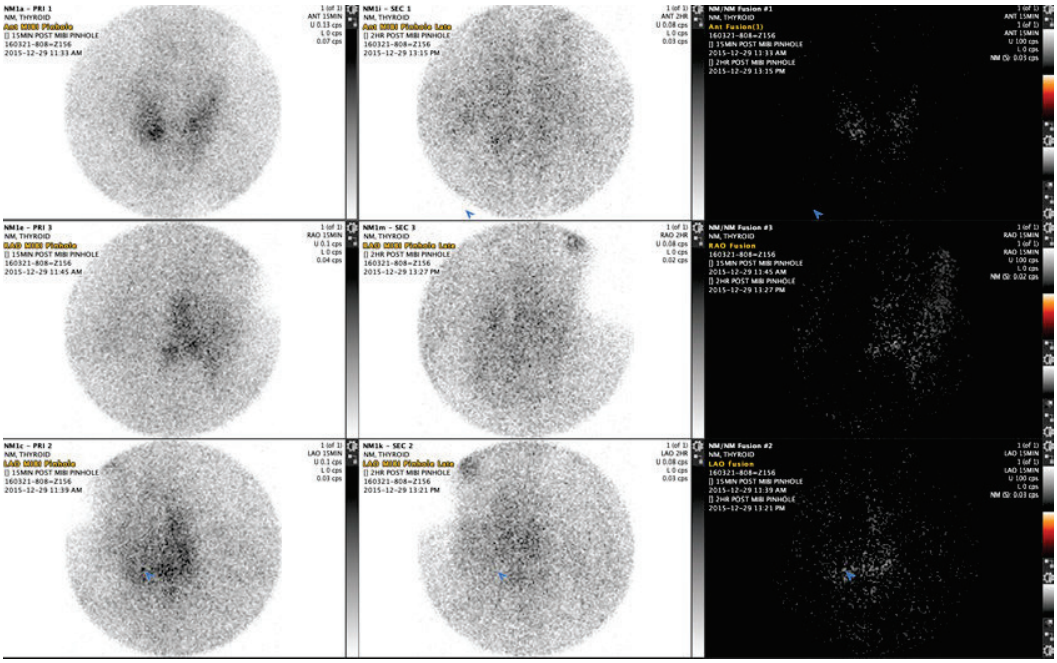
The workflow creates subtraction images for parathyroid viewing. Subtraction images can be created the following imaging protocols:

- Dual isotope planar or SPECT/CT acquisitions
- Early/late planar or SPECT/CT acquisitions

Workflow Inputs

- Planar images
- SPECT/CT

Workflow Outputs



Displays showing the planar or SPECT/CT acquisitions and subtraction images.

Default Workflow: Renal DMSA

Processing

If you are using a SPECT image:

1. You are prompted to localize to the center of the left and right kidney (if present) to auto-generate contours.
2. You are prompted to review the kidney contours.
3. The workflow calculates the split function of the kidneys for two detectors as well as the geometric mean of the image.

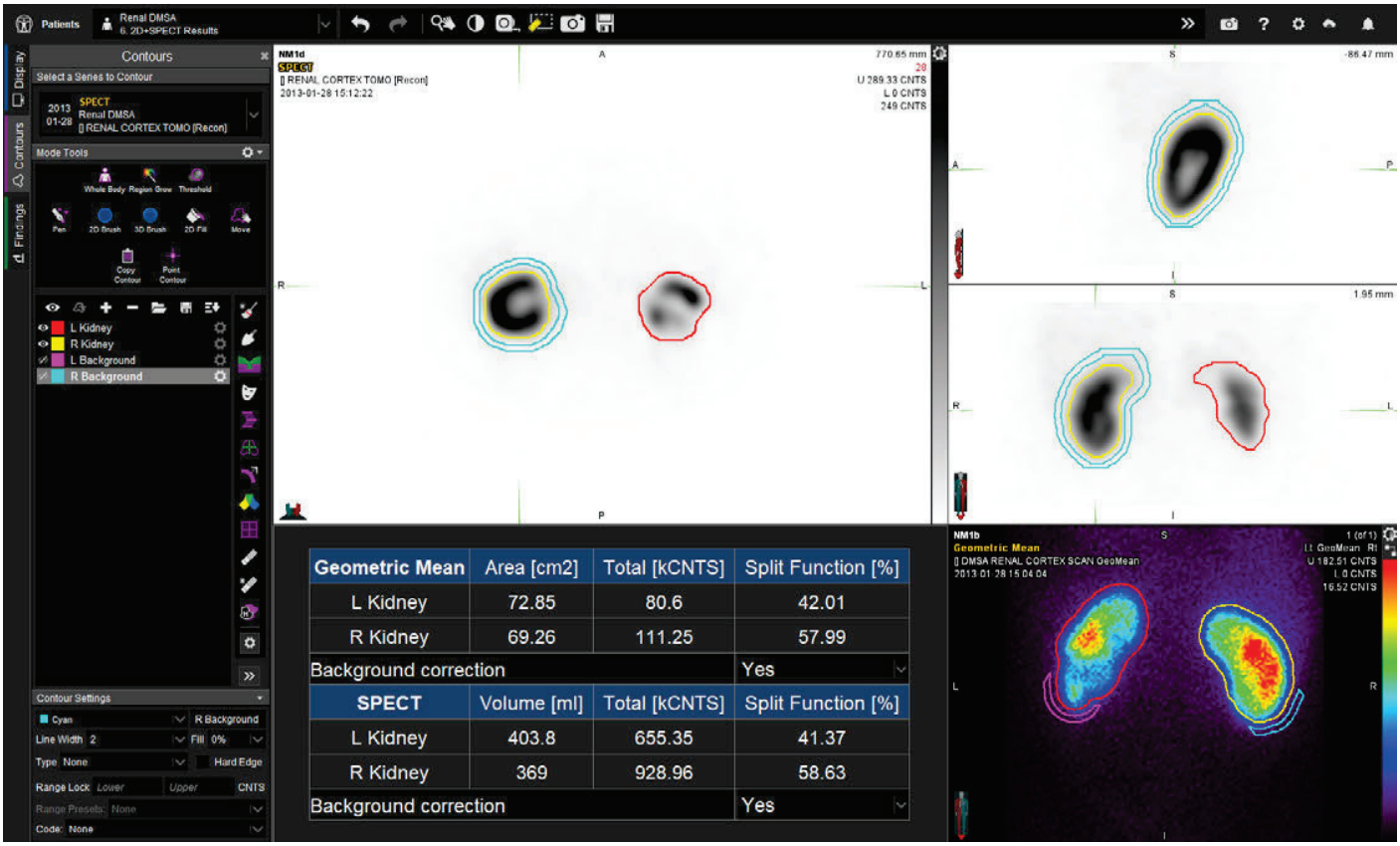
If you are not using a SPECT image:

1. You are prompted to confirm if both kidneys are present or if one is missing.
2. The workflow automatically contours the kidneys specified in Step 1.
3. You are prompted to review the kidney contours.
4. You are prompted to localize to the center of the left and right kidney (if present) to auto-generate contours.
5. You are prompted to review the kidney contours.
6. The workflow calculates the split function of the kidneys for two detectors as well as the geometric mean of the image.

Workflow Inputs

Planar images

Workflow Outputs



Geometric Mean	Area [cm2]	Total [kCNTS]	Split Function [%]
L Kidney	72.85	80.6	42.01
R Kidney	69.26	111.25	57.99
Background correction			Yes

SPECT	Volume [ml]	Total [kCNTS]	Split Function [%]
L Kidney	403.8	655.35	41.37
R Kidney	369	928.96	58.63
Background correction			Yes

Default Workflows: Renal MAG3 (Single and Dual Acquisitions)

Processing

1. You are prompted to confirm if both kidneys are present or if one is missing.
2. The workflow automatically contours the kidneys specified in Step 1.
3. You are prompted to contour the aorta if desired, and to review the kidney contours.
4. The workflow automatically generates the Left Background and Right Background.
5. You are prompted to edit contours by frame if necessary.
6. If the study includes Lasix®, you are also prompted to enter the diuretic injection time.
7. The workflow calculates the following statistics:
    - Split Function
    - Counts
    - Tmax
    - T1/2
    - T2/3
    - Tmax to T1/2
    - Tmax to T2/3
    - Tdiuretic
    - T1/2 (Diuretic)
    - Tdiuretic to T1/2
    - Excretion Index (T20/Tmax)
    - Renal Retention (T19-20/T2-3 minutes)

Workflow Inputs

Single dynamic acquisition or pre- and post- Lasix dynamic acquisition.

Workflow Outputs

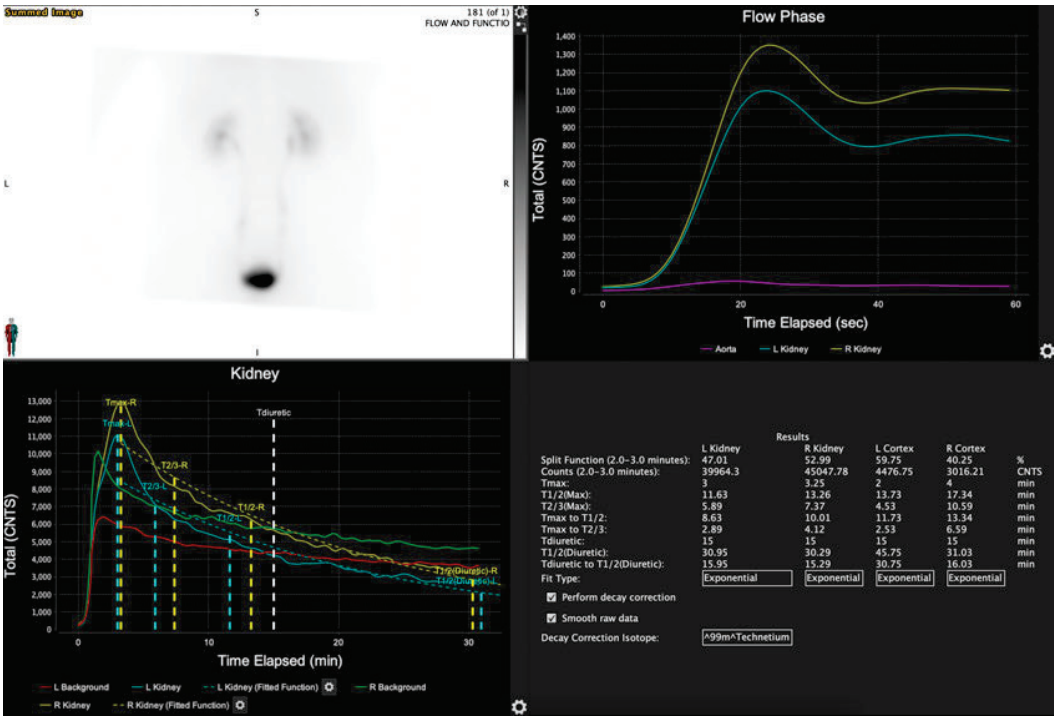
- A graph showing the flow phase.
- A graph and a table showing counts per second for different regions over time.

By default, the graph shows:

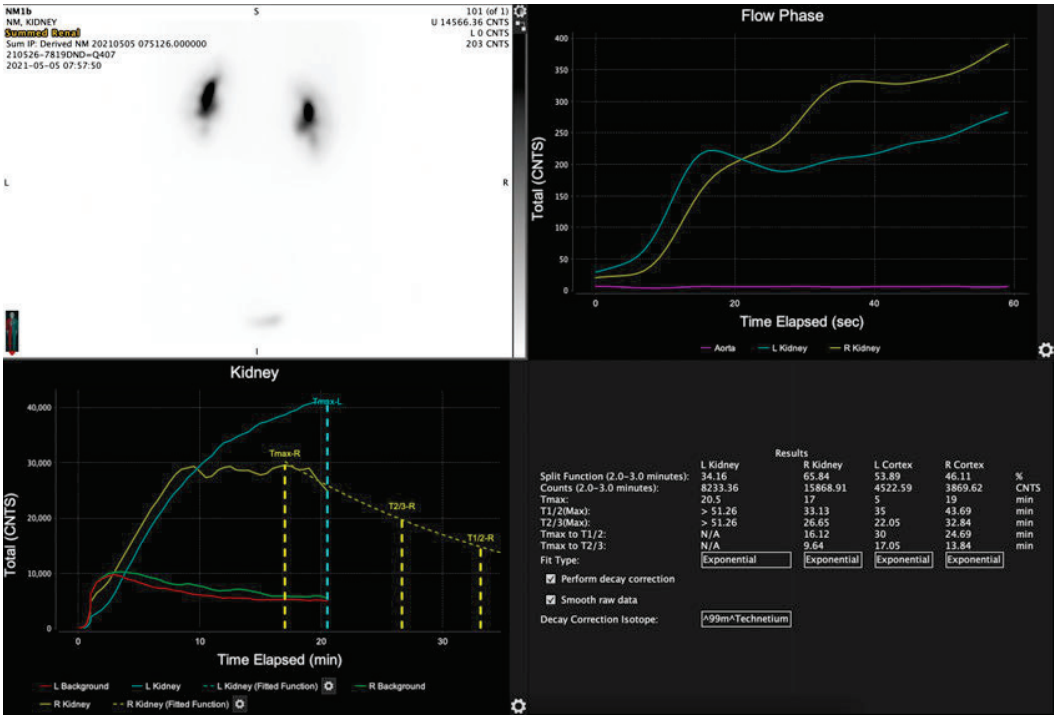
- An exponential fit curve when T1/2 is not reached during the acquisition.
- A hexic fit curve when T1/2 is reached during the acquisition.

Click the **Fit Type** field below the graph if you want to change the type of curve displayed.

Related: Refer to Fit Type Calculations: Technical Details for more information about fit curve calculation.



An example of single acquisition results.



Examples of dual acquisition results.

Note: MIM® uses the Integral Method[1] to calculate absolute counts for split function calculation. See the Split Function and Renal Retention equations in the Appendix.

[1]Prigent A, Cosgriff P, Gates GF, et al: Consensus report on quality control of quantitative measurements of renal function obtained from the renogram: International consensus committee from the scientific committee of radionuclides in nephrourology. Sem Nucl Med 29:146-159, 1999.

Default Workflow: Salivary Processing

Processing

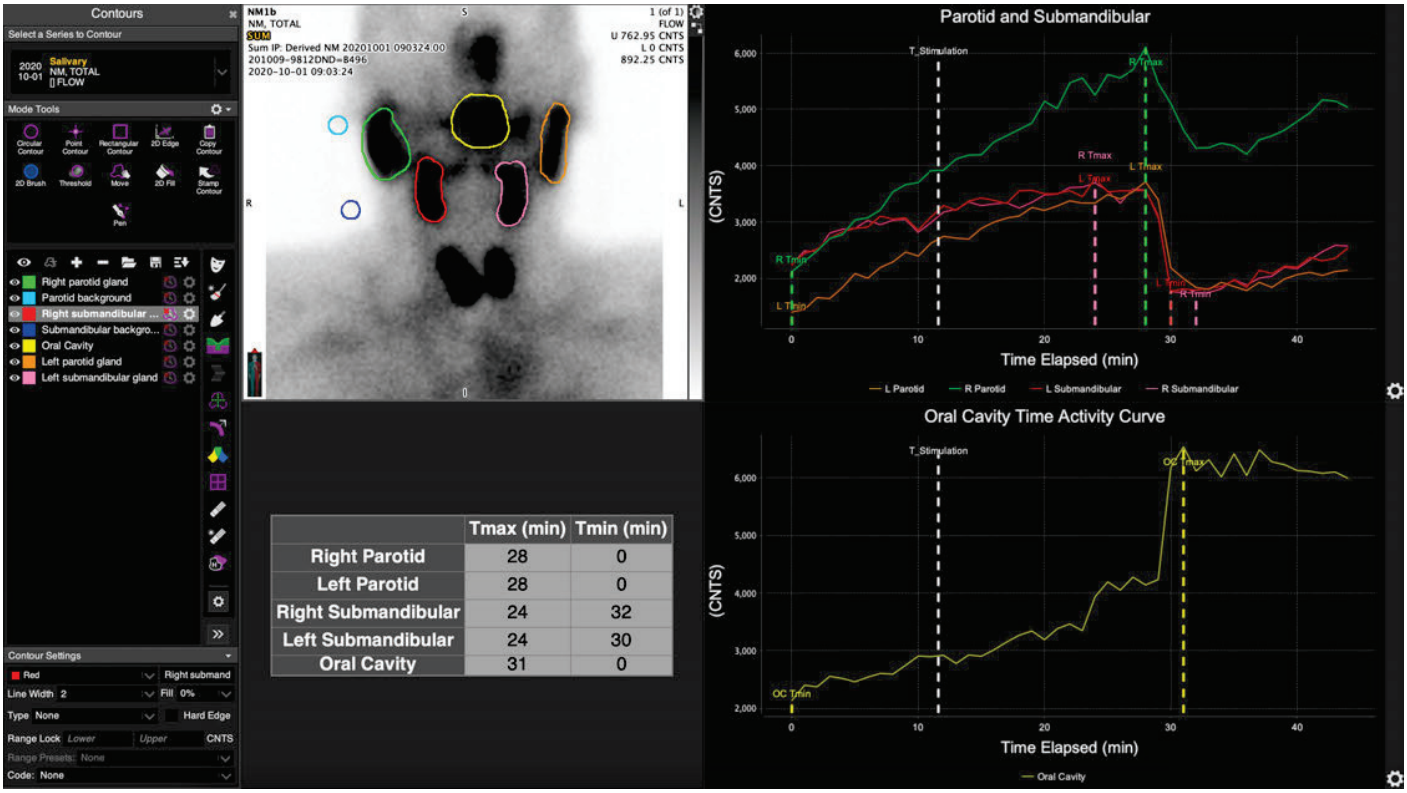
1. You are prompted to create the following contours on a derived summed image:
    - Right Parotid
    - Parotid Background
    - Right Submandibular
    - Submandibular Background
    - Oral Cavity
2. The workflow automatically mirrors the contours.
3. You are prompted to adjust the mirrored contours as needed.
4. You are prompted to enter the time of stimulation.

Workflow Inputs

Dynamic planar acquisition

Workflow Outputs

- A table showing Tmax and Tmin for all regions of interest.
- A time activity curve for the parotid and submandibular glands.
- A time activity curve for the oral cavity.



	Tmax (min)	Tmin (min)
Right Parotid	28	0
Left Parotid	28	0
Right Submandibular	24	32
Left Submandibular	24	30
Oral Cavity	31	0

Default Workflow: Sort Lesions by Stat

Note: This workflow can only be launched within an open session.

Processing

1. You are prompted to select which statistic to sort lesions by:
    - Head-to-Toe
    - Volume
    - SUVmax
    - Total Lesion Activity
2. You are prompted to ensure that your settings are configured to display contours alphabetically.

Workflow Inputs

A list of contours.

Workflow Outputs

A reordered contour list based on the selected sorting method.

Default Workflow: Thyroid Uptake

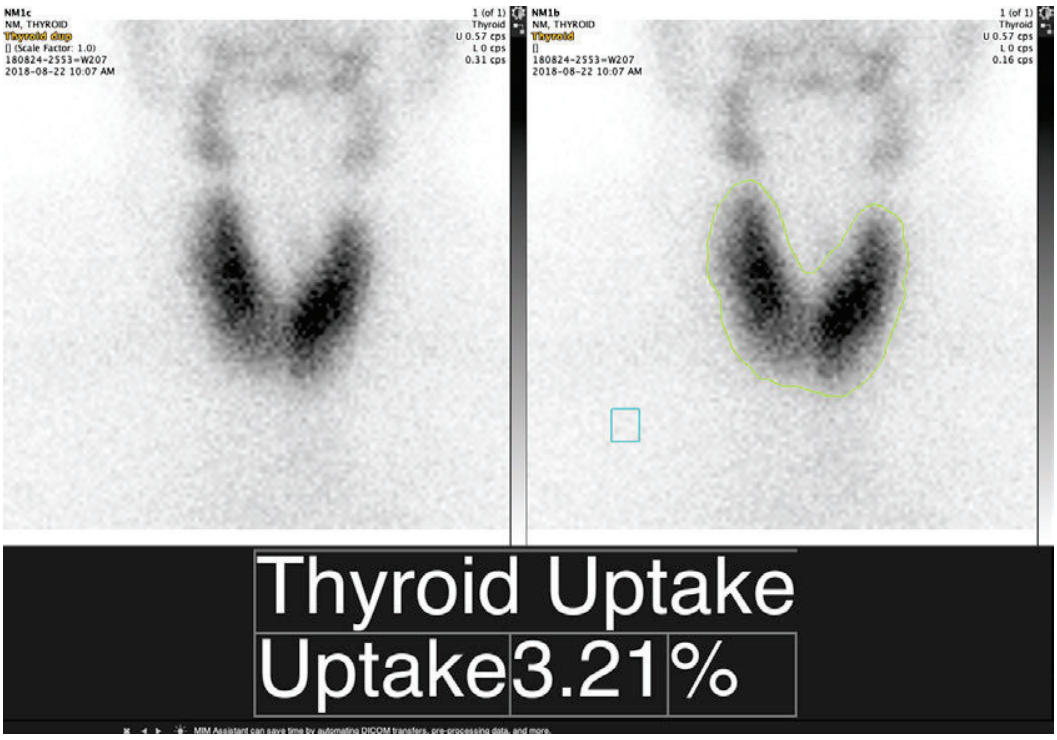
Processing

1. You are prompted to contour the following regions:
    - Thyroid
    - Background
2. The workflow calculates thyroid uptake for either ^{99m}Tc or ^{123}I for up to three different time points.

Workflow Inputs

- Pre- and post-syringe images
- Pre-administration capsule image

Workflow Outputs



The uptake percentage of the thyroid.

Notes

- Pre- and post-syringe images are required for this workflow. Both images are used to determine the total injected activity that is used for calculations. Thyroid images are decay corrected.
- Results are background corrected.

Default Nuclear Medicine Processing

Default NM Processing: Colonic Transit

Processing

1. You are prompted to contour the following regions:
    - Background (Optional)
    - Small Bowel
    - Ascending Colon
    - Transverse Colon
    - Descending Colon
    - Rectosigmoid
2. MIM® calculates the percent retention and geometric center of the isotope in the colon.[1]

Inputs

0 to 48HR static anterior/posterior images

Outputs

- Results are automatically decay-corrected for the corresponding isotope, and geometric mean calculations are used for emptying percentages.
- The results are reported in terms of percent retention from baseline for each region of the colon at certain times.
- Background correction is applied if the background region is drawn.

Notes

- The workflow uses MIM's built-in NM Processing tool, which follows the SNNMI/EANM charcoal delayed capsule 5 ROI guideline.[2]
- Decay correction is available for the following isotopes:
    - ^{99m}Tc
    - ^{111}In
    - ^{67}Ga

[1]Charles F, Camilleri M, Phillips SF et al. Scintigraphy of the Whole Gut: Clinical Evaluation of Transit Disorders. Mayo Clin Proc. 1995; 70:113-118.
[2]Maurer AH, Camilleri M, Donohoe K, et al. The SNMMI and EANM Practice Guideline for Small-Bowel and Colon Transit 1.0. J Nucl Med. 2011; 54(11): 7.

- ^{201}Tl
- ^{123}I
- ^{131}I
- ^{177}Lu

Default NM Processing: Liver-Lung Shunt

Processing

1. You are prompted to contour the following regions:
    - Liver
    - Lungs
2. MIM® calculates the tracer shunting from the liver to the lungs.[1]

Inputs

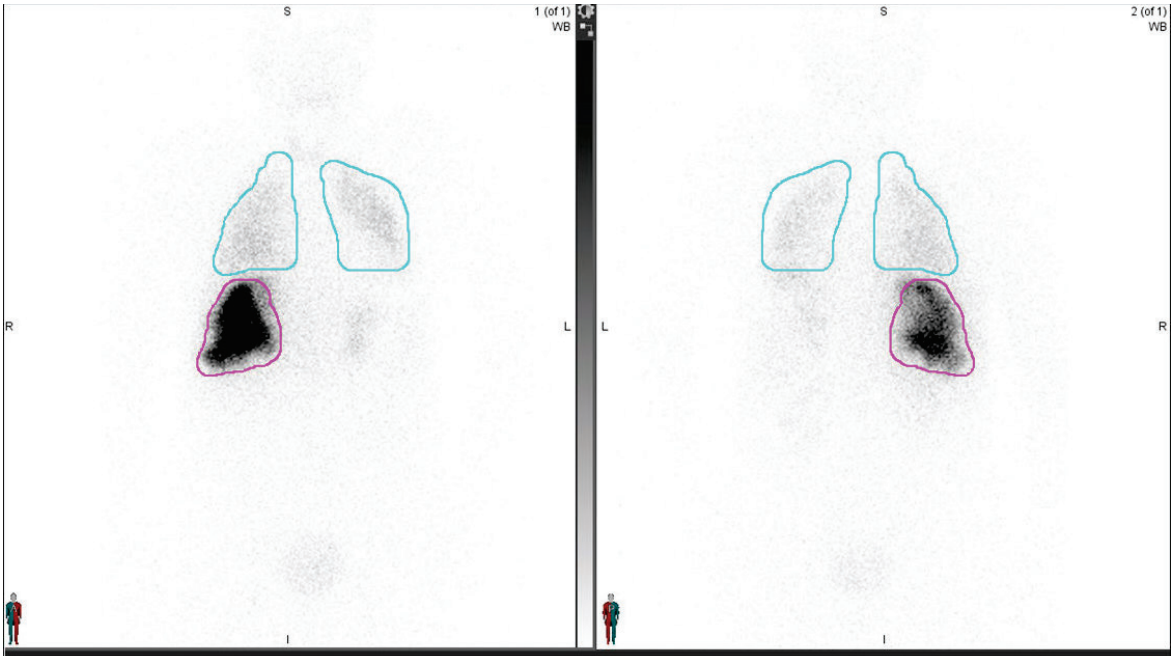
Planar anterior or posterior images, or SPECT/CT acquisition

Note: For planar anterior and posterior images, the liver and lung total counts are calculated from a derived geometric mean image.

Outputs

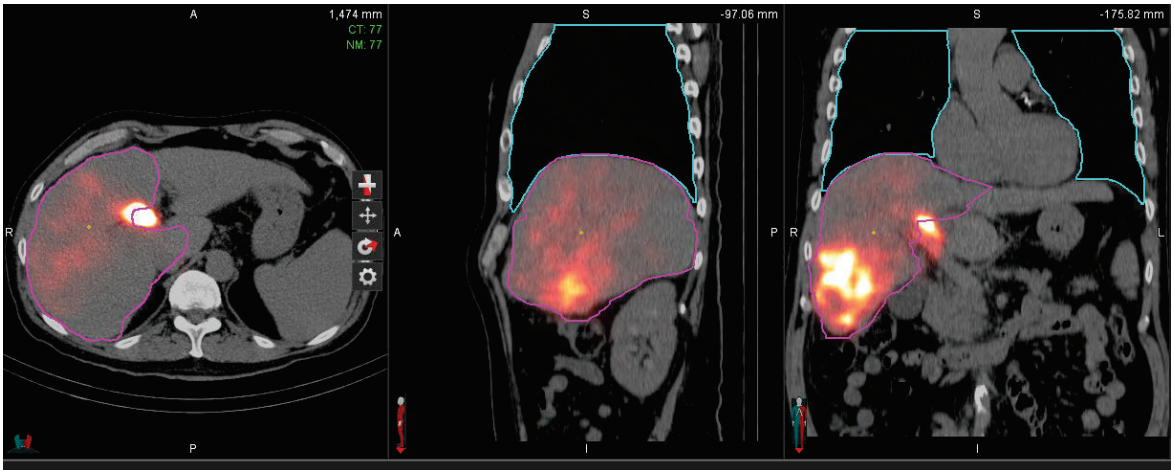
- Total counts of the liver and lungs
- The liver-lung shunt percentage

[1]Dezarn WA, Cessna JT, DeWerd LA, Feng W, Gates VL, Halama J, Kennedy AS, Nag S, Sarfaraz M, Sehgal V, Selwyn R, Stabin MG, Thomadsen BR, Williams LE, Salem R; American Association of Physicists in Medicine. Recommendations of the American Association of Physicists in Medicine on dosimetry, imaging, and quality assurance procedures for 90Y microsphere brachytherapy in the treatment of hepatic malignancies. Med Phys. 2011 Aug; 38(8):4830.



Liver-Lung Shunt Results

Liver Total:	55.98	cps
Lung Total:	16.35	cps
Liver-Lung Shunt:	22.6	%



Liver-Lung Shunt Results

Liver Total:	120178512	CNTS
Lung Total:	10506203	CNTS
Liver-Lung Shunt:	8.04	%

Default NM Processing: Lung Quantification

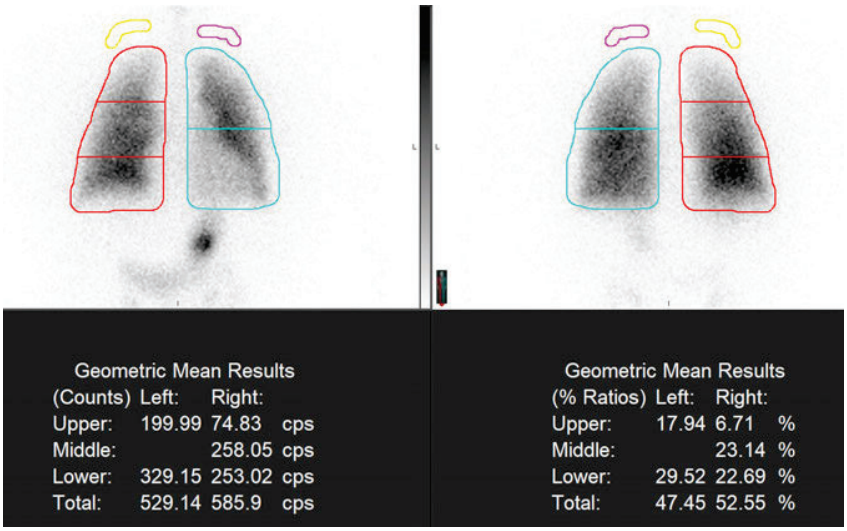
Processing

1. You are prompted to segment the lungs into different segments:
    - Left lung segmentation options:
        - Upper and lower segments
        - Upper, middle, and lower segments
    - Right lung segmentation option:
        - Upper, middle, and lower segments
2. Optionally, you are prompted to draw a background.
3. MIM® calculates the regional uptake in the lungs.

Inputs

Planar or SPECT lung images

Outputs



A table showing counts and percent ratios for each segment per lung.

Default NM Processing: Small Bowel Transit

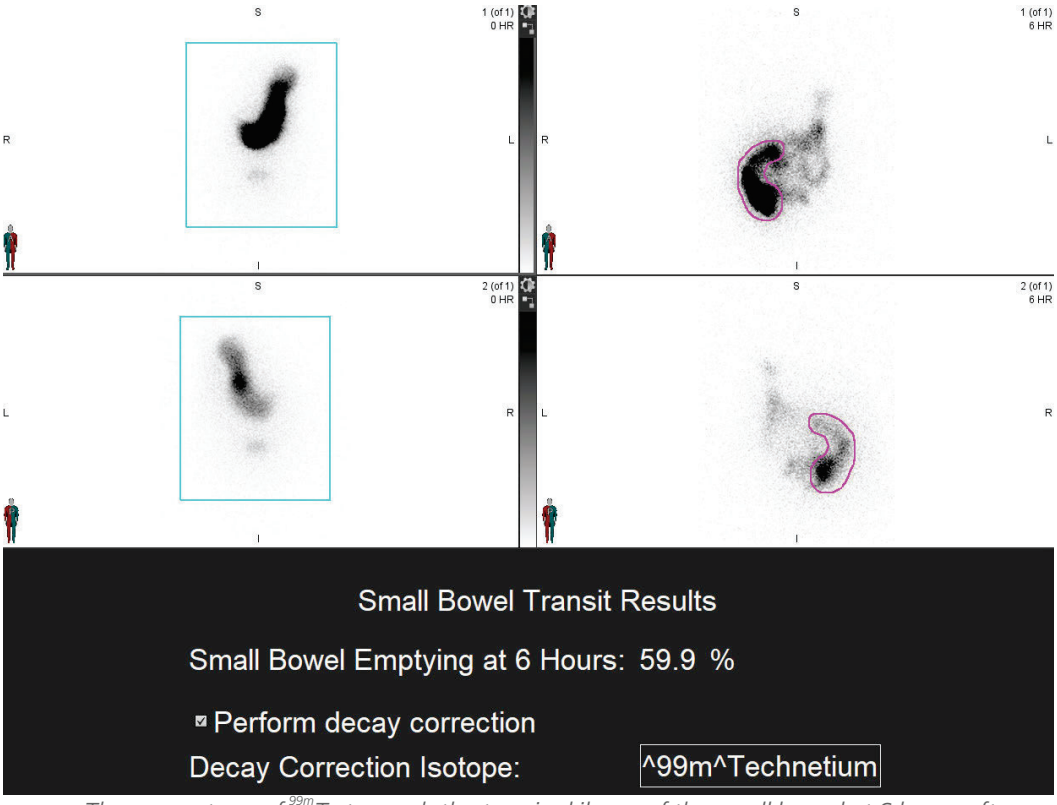
Processing

1. You are prompted to contour the following regions:
    - Total Abdominal
    - Terminal Ileum
2. MIM® calculates the percentage of ^{99m}Tc to reach the terminal ileum of the small bowel at 6 hours after administration of the tracer.

Inputs

Planar images

Output



The percentage of ^{99m}Tc to reach the terminal ileum of the small bowel at 6 hours after administration of the tracer.

Template Nuclear Medicine Workflows

Template Workflow: Esophageal Transit

Processing

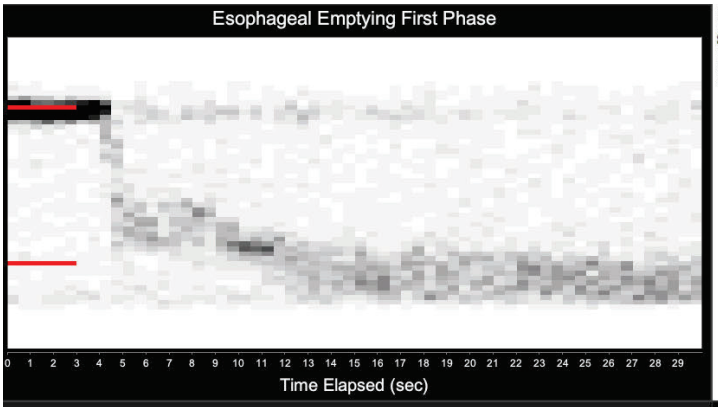
1. You are prompted to create a transit contour on the dynamic image.
2. The workflow automatically segments the transit contour into upper, mid, and lower regions.

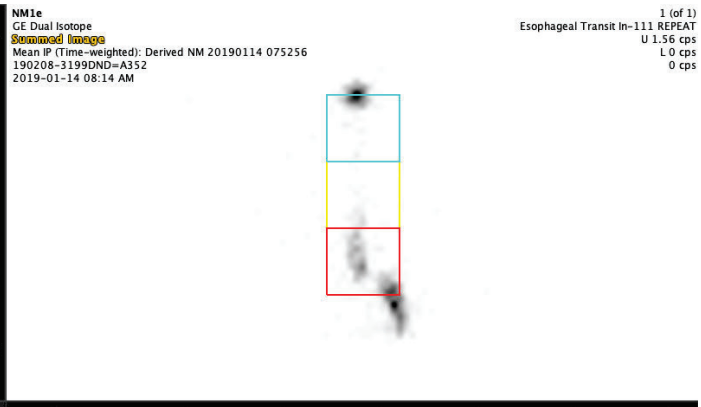
Workflow Inputs

Dynamic planar acquisition

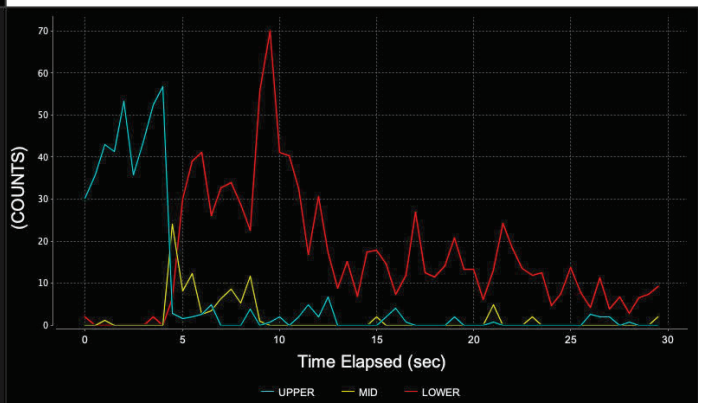
Workflow Outputs

- Choosing whether an esophageal emptying graph is generated for the first phase of the study or the entire exam can be adjusted in the workflow before it is launched.
- A time-activity curve with the activity in the upper, mid, and lower regions.
- Transit percentages for the upper, mid, and lower regions.





	Upper	Mid	Lower
50% Transit Time (sec)	4.26	5.56	10.93
90% Transit Time (sec)	4.46	8.93	20.41
Residual at End(%)	0	8.31	13.09



Template Workflow: Renal Processing (GFR or ERPF)

Processing

1. The workflow automatically determines the amount of injected activity based on the pre- and post-syringe images.
2. If the information is not available in the DICOM, you are prompted to enter the patient's height, weight, and age.
3. You are prompted to confirm if both kidneys are present or if one is missing.
4. You are prompted to review the auto-generated kidney contours.
5. You are prompted to draw the aorta.
6. If the study includes Lasix®, you are also prompted to enter the diuretic injection time.
7. The workflow processes the case using a combination of custom statistics and the NM Processing tool (i.e., the processing is separate from the Renal MAG3 processing).

Workflow Inputs

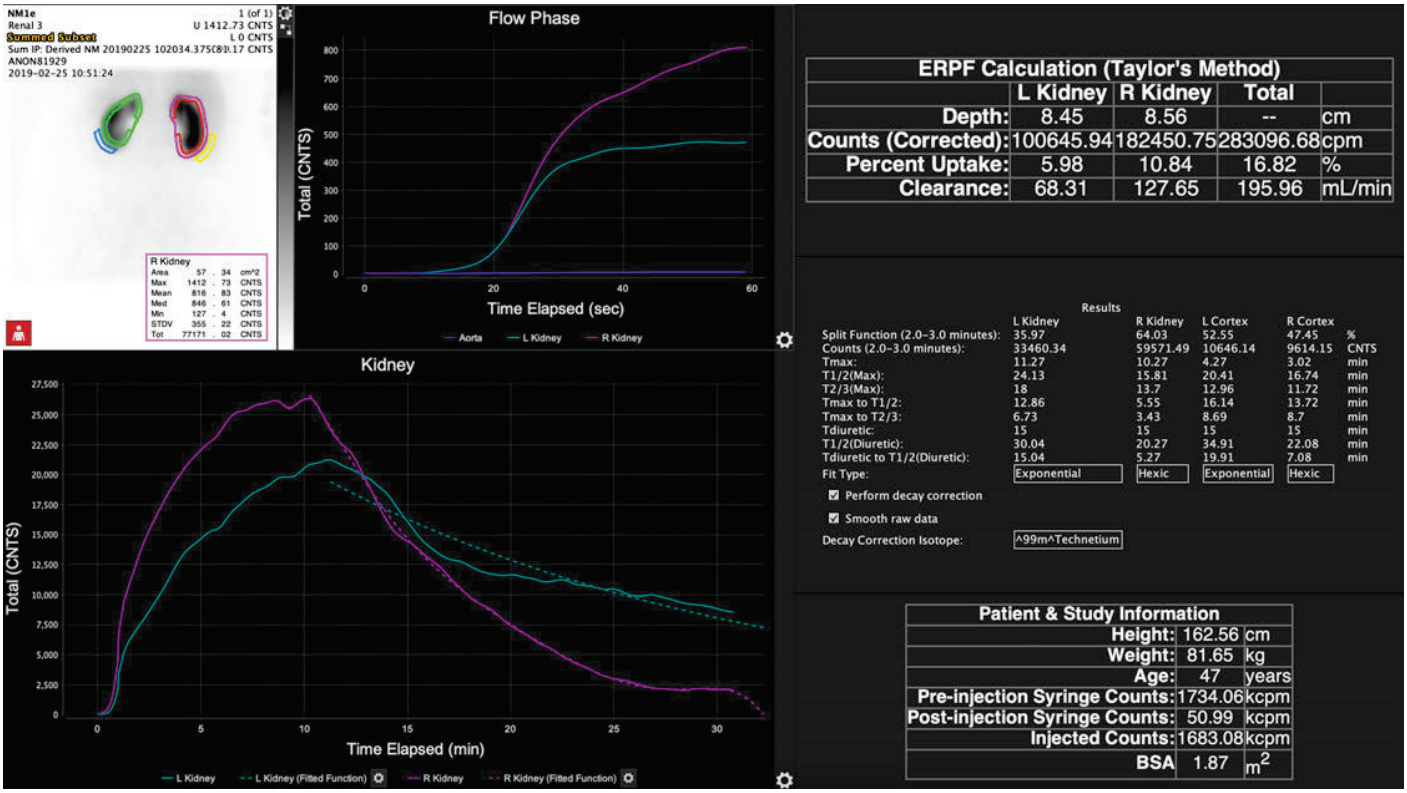
- Dynamic planar renal image
- Pre- and post-syringe images

Workflow Outputs

- A table with patient information, including injected activity and BSA
- A table with GFR results (Gates method[1]) or ERPF results (Taylor method[2])
- A table with kidney results, plus Lasix® results if administered

[1]Gates G. Computation of Glomerular Filtration Rate with Tc-99m DTPA: An In-House Computer Program. JNM 1984;613-168.

[2]Taylor A, Corrigan P, Ernest G, et al. Measuring Technetium-99m Clearance with an Improved Camera Based Method. JNM 1995;36:1689-1695.



ERPF Calculation (Taylor's Method)				
	L Kidney	R Kidney	Total	
Depth:	8.45	8.56	--	cm
Counts (Corrected):	100645.94	182450.75	283096.68	cpm
Percent Uptake:	5.98	10.84	16.82	%
Clearance:	68.31	127.65	195.96	mL/min

Results

	L Kidney	R Kidney	L Cortex	R Cortex	
Split Function (2.0–3.0 minutes):	35.97	64.03	52.55	47.45	%
Counts (2.0–3.0 minutes):	33460.34	59571.49	10646.14	9614.15	CNTS
Tmax:	11.27	10.27	4.27	3.02	min
T1/2(Max):	24.13	15.81	20.41	16.74	min
T2/3(Max):	18	13.7	12.96	11.72	min
Tmax to T1/2:	12.86	5.55	16.14	13.72	min
Tmax to T2/3:	6.73	3.43	8.69	8.7	min
Tdiuretic:	15	15	15	15	min
T1/2(Diuretic):	30.04	20.27	34.91	22.08	min
Tdiuretic to T1/2(Diuretic):	15.04	5.27	19.91	7.08	min
Fit Type:	Exponential	Hexic	Exponential	Hexic	

Perform decay correction

Smooth raw data

Decay Correction Isotope: ^99m^Technetium

Patient & Study Information		
Height:	162.56	cm
Weight:	81.65	kg
Age:	47	years
Pre-injection Syringe Counts:	1734.06	kcpm
Post-injection Syringe Counts:	50.99	kcpm
Injected Counts:	1683.08	kcpm
BSA	1.87	m^2

Template Workflow: SPECTRA Recon® and SPECTRA Quant®

Processing

SPECTRA Recon includes Filtered Backprojection and OSEM[1] reconstruction methods, including CT-based or Chang's attenuation correction, triple energy window scatter correction, and resolution recovery.

SPECTRA Quant includes OSEM reconstruction methods, attenuation correction using the patient's CT, scatter correction, depth-dependent resolution recovery, and Bq/ml conversion.

SPECTRA Recon and SPECTRA Quant should always be run via a customized workflow. This workflow is built by MIM Software® as part of a special setup and implementation process. For more information on the implementation process and fee, please contact MIM Software Support at 866-421-2536 or email support@mimsoftware.com.

Notes

- SPECTRA Recon and SPECTRA Quant may not yet be commercially available in some countries. Please contact your local MIM Software representative for further details.
- For more information, see the *SPECTRA Recon User Guide* and *SPECTRA Quant User Guide*. You can also view relevant white papers at mimsoftware.com/training, under the Radiology and Nuclear Medicine section.

[1]Hudson, HM, Larkin RS. Accelerated image reconstruction using ordered subsets of projection data. IEEE Trans Med Imaging 1994; 13: 601-609.

Appendix

MIM Encore Processing and Workflows: Technical Details

Equations

$$Geometric\ Mean = \sqrt{anterior \times posterior}$$

$$Background\ Correction = total\ ROI\ counts - (ROI\ pixels \times background\ mean\ counts)$$

$$Ejection\ Fraction = 100 \times \frac{total\ counts\ T_{max} - total\ counts\ T_{min}}{total\ counts\ T_{max}}$$

$$Uptake/Filling\ Percentage = \frac{ROI\ counts}{total\ counts}$$

$$Retention = (1 - percent\ change) \times 100$$

$$Percent\ Change = \left|\frac{late - early}{early}\right| \times 100$$

Percent changes equals the change in counts from time 0.

$$Split\ Function\ (Renal\ DMSA)\ \% =$$

$$100 \times \frac{left\ or\ right\ kidney\ geometric\ mean\ background\ corrected\ counts}{right + left\ kidney\ geometric\ mean\ background\ corrected\ counts}$$

$$Split\ Function\ (Renal\ MAG3)\ \% = 100 \times \frac{left\ or\ right\ kidney\ background\ corrected\ counts}{right + left\ kidney\ background\ corrected\ counts}$$

By default, MIM determines the split function percentage across the 2-3 minute range. If desired, change this range by going to Settings >> **General Preferences** >> **Imaging** >> **NM Processing** >> **Renal MAG3 (Lasix®)** and change the **Uptake Phase Start** and **Uptake Phase End** fields.

$$Glomular\ Filtration\ Rate\ (GFR)$$

$$GFR = 100 \times \frac{\frac{background\ corrected\ right\ kidney\ counts}{e^{-uX}} + \frac{background\ corrected\ left\ kidney\ counts}{e^{-uX}}}{pre\text{-}injection\ counts - post\text{-}injection\ counts}$$

$$Effective\ Renal\ Plasma\ Flow\ (ERPF)$$

$$ERPF = 100 \times \frac{(right\ kidney\ counts - background) + (left\ kidney\ counts - background)}{pre\text{-}injection\ counts - post\text{-}injection\ counts}$$

$$Liver\ Clearance\ Rate\ (LClr) = \frac{L(t_2) - L(t_1)}{A(t_1) \int_{t_1}^{t_2} C_{norm}{}^{t}\ dt}$$

See Footnote[1] for additional details regarding this LClr equation.

$$Lag\ Time = T_{\frac{9}{10}}$$

The lag time indicates when a contour is at 90% full.

$$Emptying\ Rate = The\ slope\ of\ the\ emptying\ or\ retention\ curve\ (reported\ in\ \frac{\%}{min})$$

$$Excretion\ Index = \frac{counts\ from\ 19-20\ minute\ frame}{counts\ at\ T_{max}}$$

Excretion Index is the ratio above for the background-subtracted right and left whole kidney and cortical counts.[2]

Adjust the location of the Tdiuretic time point by going to Settings >> **General Preferences** >> **Imaging** >> **NM Processing** >> **Renal MAG3 (Lasix®)** and changing the **Default Diuretic Injection Time** setting. Diuretic injection times prior to the start of imaging (e.g., T-15min) can also be selected.

By default, MIM determines the excretion index using the 19-20 minute time frame. If desired, change this by going to Settings >> **General Preferences** >> **Imaging** >> **NM Processing** >> **Renal MAG3 (Lasix®)** and change the **Excretion Index Numerator Start** and **Excretion Index Numerator End** fields.

$$Renal\ Retention = \frac{counts\ from\ 19-20\ minute\ frame}{counts\ from\ 2-3\ minute\ frame}$$

By default, MIM determines renal retention using the frames in the equation above.[3] If desired, change this by going to Settings >> **General Preferences** >> **Imaging** >> **NM Processing** >> **Renal MAG3 (Lasix®)** and change the **Renal Retention Numerator Start**, **Renal Retention Numerator End**, **Renal Retention Denominator Start**, and **Renal Retention Denominator End** fields.

$$Emptying\ Percentage = \left| \frac{late - early}{early} \right| \times 100$$

$$Lung\ Shunt\ Fraction = 100 \times \frac{lung\ total\ counts}{lung + liver\ total\ counts}$$

$$Lung\ Percent\ Ratio = \frac{lung\ lobe\ count}{left + right\ lung\ total\ counts}$$

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[1]Ekman M, Fjalling M, Friman S, et al. Liver uptake function measured by IODIDA clearance rate in liver transplant patients and healthy volunteers. Nucl Med Comm 1996; 17:235-242.
[2]Taylor, A., Blaufox, M., Dubovsky, E. et al. Society of Nuclear Medicine procedure guideline for the diagnosis of renovascular hypertension 3.0 procedure guidelines. Policy Pract. 2003; www.snm.org.
[3]Li Y, Russell CD, Palmer-Lawrence J, Dubovsky EV. Quantitation of renal parenchymal retention of technetium-99mMAG3 in renal transplants. J Nucl Med. 1994 May;35(5):846-50.

$$MUGA\ Ejection\ Fraction\ Percent = 100 \times \frac{1 - ES\ BG\ corrected}{ED\ BG\ corrected}$$

$$Percent\ Retention\ (Colonic) = \frac{total\ counts\ in\ region\ X\ at\ 24\ or\ 48\ hours}{total\ counts\ in\ 'Total\ Abdomen'\ region\ at\ (baseline\ time)}$$

$$Geometric\ Center\ (Colonic) = \frac{(AC\%\times 1)+(TC\%\times 2)+(DC\%\times 3)+(RS\%\times 4)+(ST\%\times 5)}{100}$$

In the Geometric Center (Colonic) equation, AC=ascending colon, TC=transverse colon, DC=descending colon, RS=rectosigmoid, and ST=stool. Geometric Center is calculated for each time point.

$$Filling\ \%\ at\ 6\ Hours\ (Small\ Bowel\ Transit) = \frac{total\ counts\ in\ terminal\ ileum\ ROI\ at\ 6\ hours}{total\ counts\ in\ abdominal\ ROI\ at\ 0\ hours}$$

See Footnote[1] for the reference for the Small Bowel Transit equation.

Decay Correction

MIM will attempt to perform decay correction by default on the processing types listed below. Note that MIM may not be able to perform decay correction on some data sets, even if decay correction is enabled.

- Colonic Transit
- Gallbladder EF
- Gastric Emptying
- Liver Functional Analysis
- Post-Void
- Renal MAG3 (Lasix)
- Small Bowel Transit

If desired, disable decay correcting by going to Settings >> **General Preferences** >> **Imaging** >> **NM Processing** and unchecking any options.

Perform Motion Correction

MIM uses a projection/reprojection fitting approach iteratively to correct motion during SPECT reconstruction.

In the first iteration, MIM reconstructs a 3D volume from the raw projection data using the user-specified reconstruction algorithm and parameters. MIM then reprojects the volume to generate reprojection data. During the reconstruction and reprojection procedure, most of the motion in the raw projection data should be averaged over all the projection views, so the reprojection data can be treated as motion-free

[1]Maurer AH, Camilleri M, Donohoe K, et al. The SNMMI and EANM Practice Guideline for Small-Bowel and Colon Transit 1.0. J Nucl Med. 2011; 54(11): 7.

data. MIM then aligns the raw projection data to the reprojection data to extract the motion in the raw data view-by-view. The raw projection data is then motion corrected.

In the second iteration, MIM uses the motion-corrected raw data from the first iteration to run reconstruction again. The reconstructed 3D volume from this iteration should eliminate most — if not all — of the motion in the original raw data.

Liver Segmentation

This processing method can be used with SPECT or planar images and calculates regional uptake in the liver using eight user-defined segments (Couinaud Classification).

MUGA

This processing method automatically contours the left ventricle of a MUGA scan and generates a background region. Prior to the Ejection Fraction calculation, the user has the option to edit the Left Ventricle ROI and propagate it automatically to all other frames. The equation used for the Left Ventricle Ejection Fraction is as follows: EF (%) = 100% x (1-ES BG corrected/ED BG corrected).

MIM's left ventricular edge detection method on a MUGA scan is based on a radial coordinate system with 36 radii and the origin at the centroid of the left ventricular region. When a MUGA series is processed (via a workflow or with the NM Processing tool), MIM first applies a pre-processing step which includes resampling the image and applying 4D Gaussian smoothing. This is to compensate for images with large voxel size and minimize the influence of image noise on the edge detection algorithm.

User input is required to identify the center of the left ventricle on the first image frame. From this input, the approximate centroid of the LV is identified. From that origin, MIM searches along the 36 radial vectors and finds the true edge point for each one based on the gradient-based method. Some post-processing (e.g., smoothing) is applied to these edge points, and they are then connected to create the LV contour on the first frame.

LV segmentation on the following frames is accomplished by sequentially propagating the contour from the previous frame. MIM determines approximately where the LV centroid is using the LV contour from the previous frame. From that centroid, MIM searches along the 36 radial vectors as before, however, this time the processing considers where the edge points are for the previous frame, which should not be too far from those of the current frame. Using the similar gradient-based edge detection algorithm, along with the previous frame's edge as both a guidance and restriction, MIM detects the true edge on the current frame.

Then, the automatically generated background region is selected from 18 regions of equal arc at various angles and distances from the lateral border. The region with the minimum mean counts is chosen for background correction. The mean counts/pixel in this frame are multiplied by the number of pixels in the Left Ventricle contour for each frame and then subtracted from the total counts in that contour.

Placement of the Background ROI affects the EF results and can be configured in the General Preferences if you prefer not to use the automatic region generation. Go to Settings  >> **General Preferences** >> **Imaging** >> **NM Processing** >> **MUGA**. Uncheck **Set region position automatically** to set the Region Position, Region Width, and Region Thickness you would like to use for Background ROI generation.

Renal MAG3 (with and without Lasix)

This processing method uses user-defined contours to calculate multiple statistics including split function, T1/2, T2/3, Tmax, Tdiuretic, Tmax to T1/2, Tmax to T2/3, Tdiuretic to T1/2, Excretion Index (T20/Tmax), and Renal Retention (T20/3).

Tmax to T1/2 = The time from max counts until 1/2 of the counts remain.

Tmax to T2/3 = The time from max counts until 2/3 of the counts remain.

Tdiuretic to T1/2 = The time from diuretic injection until 1/2 of the counts from that time remain.

Tdiuretic to T2/3 = The time from diuretic injection until 2/3 of the counts from that time remain.

Some dependent ROIs can be auto-generated while running this method. After drawing the left and/or right kidney ROI(s), the auto-ROI buttons for cortex and background ROIs will become active. Left-clicking on these buttons will generate a new ROI for R/L cortex or R/L background. The size and position of these auto-generated regions are configurable. For more information on configuring auto-ROIs, see the Auto-ROI section below.

This processing method also supports the presence of 1, 2, or more kidneys. To add or remove a kidney from the processing, simply use the **Add Kidney** and **Remove Kidney** buttons during the ROI drawing step.

Auto-ROI

Several dependent ROIs can be generated automatically from the kidney while running the NM processing tool. For Renal MAG3, these ROIs include Right and Left Cortex as well as Right and Left Background ROIs. After drawing the kidney ROIs, the Auto-ROI button will become active for the corresponding dependent regions.

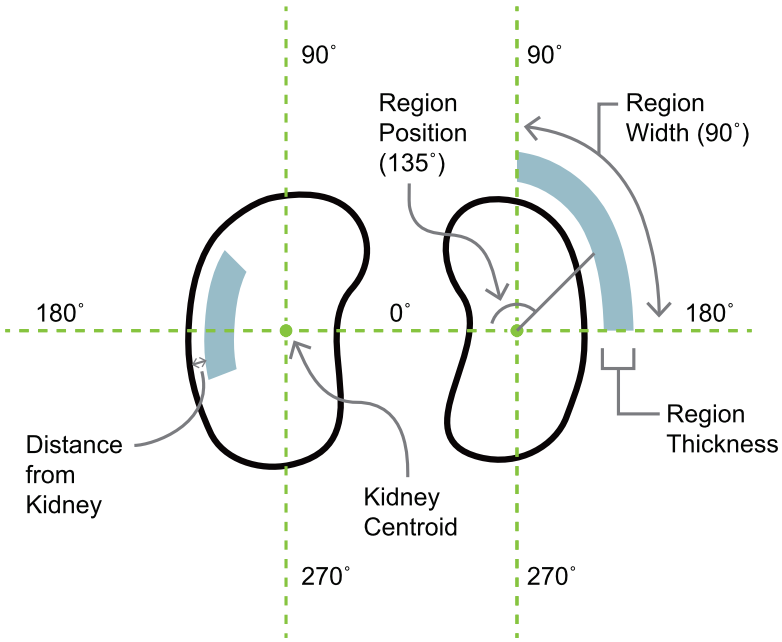
The parameters for each set of Auto-ROIs are configurable. Settings are located at Settings >> **General Preferences** >> **Imaging** >> **NM Processing** >> **Renal MAG3 (Lasix®)**.

The setting for region position, region width, region thickness, and distance from the kidney can be set for background and cortical regions. The "Region position" parameter sets the angle at which the center of the new region will lie with respect to 0° (medial direction). The "Region width" defines the angular width of the new region. The "Region thickness" refers to the thickness of the region in mm, and the "Distance from kidney" refers to the distance in mm from the outer edge of the kidney ROI.

The "Generate region inside kidney" option inverts the "Distance from kidney" parameter so the region is generated inside the outer edge of the kidney ROI.

The "Invert region" option inverts the "Region width" parameter so the region is generated everywhere except the position specified by the region position and width.

The "Widen region base" option edits the base edges of the region so they are not angled toward the centroid of the kidney.


90˚
90˚
Region
Position
(135˚)
Region
Width (90˚)
180˚
0˚
180˚
Region
Thickness
Distance
from
Kidney
Kidney
Centroid
270˚
270˚

PET Edge® & PET Edge®+ Tools: Technical Details

MIMTD-656 • 24 Oct 2023

MIM Software's PET Edge tool is based on finding object edges with spatial derivatives.[1] A point inside the object of interest and six points near the edge of the object are defined by the user by left-clicking near the center of the object and dragging to a point near the edge of the object. Five additional edge points are automatically determined at equal angular increments from the user-defined edge point. The software uses this initial edge definition to define a contiguous 3D set of edge points.

MIM Software's PET Edge+ tool requires a single, user-generated point inside of the lesion. An active contour algorithm is used to find the region of elevated activity corresponding to the lesion. Then, spatial derivatives are used to refine the boundaries and find the edges. PET Edge+ produces better and more consistent results than PET Edge. The active contour algorithm allows it to better segment lesions with complex shapes, such as non-ellipsoid lesions and lesions with a necrotic center. Additionally, this tool requires only a single user-generated point, instead of an ellipsoid, which reduces inter-user variability.

Both PET Edge and PET Edge+ are provided with MIM Encore®, MIM Maestro®, and MIM SurePlan™ licenses.

[1]Spatial derivatives are the change in image count levels as a function of location in the image. Assuming the object has different intensity than the background, there is a change in count level at the edge of the object.

SUV: Technical Details

MIMTD-696 • 18 Sep 2023

Contents

SUV Formulas

SUVbw

Standardized uptake value (SUV) is the ratio of the actual µCi/cc in a voxel to the expected µCi/cc in a voxel at that time, assuming that the radioactivity is uniformly distributed in the body and that the total radioactivity in the body decays only due to the physical half-life of the isotope. The density of body tissues is assumed to be equal to that of water so that expected µCi/cc equals (mCi of isotope injected * physical isotope decay at that time) / (kg weight of patient). Therefore,

$$SUV_{bw} = \frac{\mu Ci}{cc} \div \frac{mCi \times PD}{kg}$$

where µCi/cc is the measured µCi/cc, mCi is the amount of isotope injected, PD is the physical radioisotope decay from injection to scanning time, and kg is the patient weight in kilograms.

SUVlbm and SUVbsa

In addition to body-weight SUV (SUVbw), MIM can calculate lean-body-mass SUV (SUVlbm) and body-surface-area SUV (SUVbsa). The below formulas for calculating LBM and BSA are from Sugawara et al.[1] To Calculate SUVlbm or SUVbsa, MIM replaces the patient weight in kilograms in the SUVbw formula above with the LBM or BSA value:

$$LBM(female) = 1.07kg - 148(kg/cm)^2$$

[1] Y. Sugawara, K. R. Zasadny, A. W. Neuhoff, and R. L. Wahl. Reevaluation of the Standardized Uptake Value for FDG: Variations with Body Weight and Methods for Correction. Radiology. 1999 Nov;213(2):521-5.

$$LBM(male) = 1.1kg - coefficient(kg/cm)^2$$

$$BSA = 0.007184 \times kg^{.425} \times cm^{.725}$$

In these formulas, kg is the patient weight in kilograms, cm is the patient height in centimeters, and the coefficient is either 120 or 128. See LBM(male) Coefficient of 120 vs. 128 for more information.

Note: If the sex of the patient is "O," MIM uses the formula for LBM(male).

Additional Information

LBM(male) Coefficient of 120 vs. 128

By default, MIM uses a coefficient of 120 in calculations of SUVlbm for males. In MIM 6.8 and later, you can switch the SUVlbm coefficient for males to 128 instead of 120. To switch the coefficient, go to Settings >> **General Preferences** and search for "lean body". Select **SUV** on the left side, and deselect **Use legacy lean body mass coefficient (120) for SUVlbm**.

The formula that uses a coefficient of 120 can be traced to an article by Morgan and Bray, in which the original LBM(male) formula is misquoted as using a coefficient of 120 instead of 128. Sugawara et al first incorporated LBM into SUV and cited the Morgan and Bray paper that contains the misquote. The version of the formula with 120 as the coefficient has been subsequently quoted in the PET literature. For more details, see *QIBA PET Profile Appendix H*.[2]

Note on SUV Activity Calculation

PET calculates the activity in a voxel as Bq/ml, which is emissions/sec/ml. To calculate SUV, MIM adjusts decay correction to be relative to the injection time. The uniform distribution of activity is calculated as Bq injected divided by the weight of the patient in g (Bq/g). Therefore, the ratio of SUV activity in a voxel relative to activity with uniform distribution is g/ml.

SUV Peak 6.1.6

SUVpeak is calculated using the method defined in the PERCIST 1.0 guidelines.[3] The value of the spherical region is found by convolving a spherical kernel with the image data at the user's preferred resolution (either the volume's native resolution or 1x1x1 mm resolution). The value of each element in the kernel represents what percentage of the kernel's element is inside the sphere to account for partial voxels along the edge of the sphere. We consider the sphere to be outside of the contour if one of the kernel's elements is both partially in the sphere and its corresponding sample location on the volume is outside of the contour.

Note: To set SUV Peak resolution, go to Settings >> **General Preferences** and search for **"peak"**. Select **Advanced** on the left side to access this setting.

---

[2]FDG-PET/CT Technical Committee. FDG-PET/CT as an Imaging Biomarker Measuring Response to Cancer Therapy, Quantitative Imaging Biomarkers Alliance, Version 1.05, Publicly Reviewed Version. QIBA, December 11, 2013. Available from: RSNA.ORG/QIBA.
[3]Wahl RL, Jacene H, Kasamon Y, Lodge MA. From RECIST to PERCIST: evolving considerations for PET response criteria in solid tumors. J Nucl Med. 2009;50:122S–150S.

SUV Total

SUVtotal is the sum of all activity over all voxels in an image:

$$SUV_{total} = SUV_{mean} \times number\ of\ voxels$$

Total Glycolytic Activity (TGA), Total Lesion Glycolysis (TLG), Total Metabolic Index (TMI)

The Total Glycolytic Activity (also known as the Total Lesion Glycolysis or Total Metabolic Index) of a region is calculated as the product of the region's volume and mean SUV.

Relevant DICOM Attributes

MIM uses the following DICOM tags for SUV calculation:

- Series Time or Acquisition Time
- Series Date or Acquisition Date
- Units
- Decay Correction
- Patient Weight
- Radionuclide Total Dose
- Acquisition Date/Time
- Radiopharmaceutical Start Date/Time
- Radionuclide Half Life

MIM uses these additional DICOM tags for SUVlbm and SUVbsa calculation:

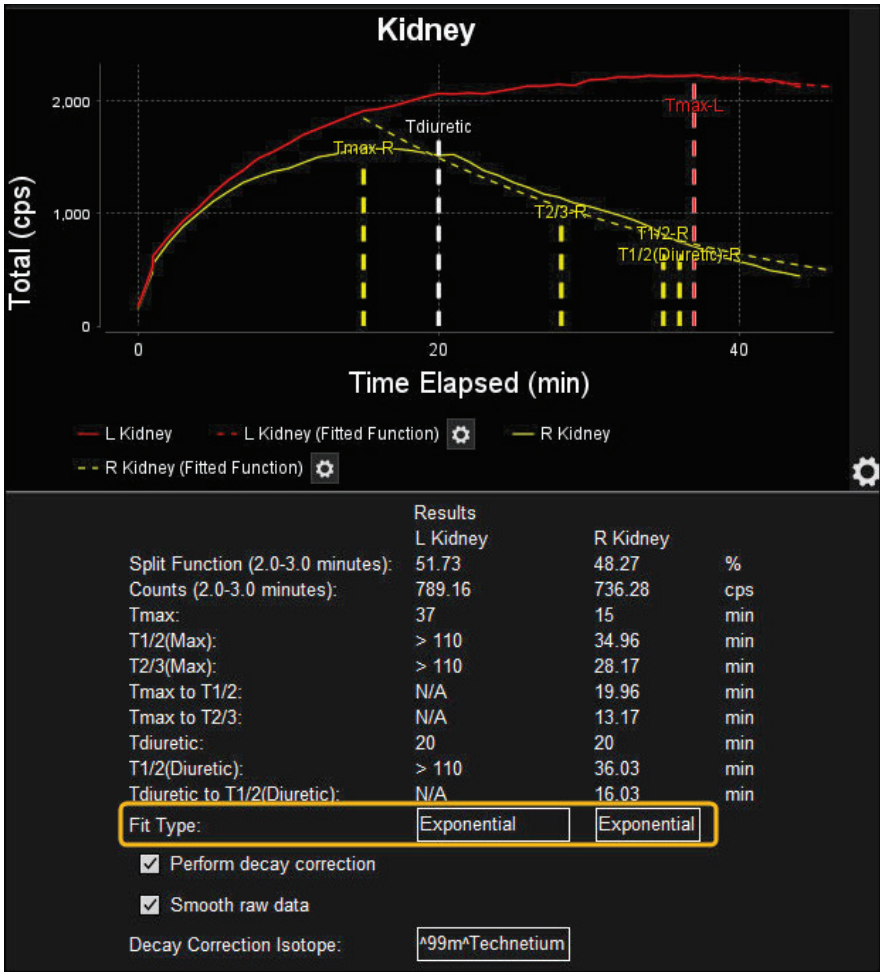
- Patient Sex
- Patient Size (height)

Fit Type Calculations: Technical Details

MIMTD-1794 • 10 Jan 2024

Overview

Some workflows produce a graph display and apply a fit curve to the graph. For applicable workflows, you can use the **Fit Type** field below the graph to change the fit type.



In this example, the Renal MAG3 workflow shows a graph using an exponential fit type.

Tip: Click the gear in the lower-right corner of the image and select **Emphasize Fit Curves** to dim the other lines on the graph. Or, select **Hide Fit Curves** if you don't want to see the fit curves.

Available Fit Types

Exponential

Extends the rate of change proportional to the initial amount of the quantity.

Hexic

A least-squares fit of a sextic polynomial to six points.

Linear

Provides a connect-the-dots fit between the data points provided. For values outside the domain of the points, it returns the Y value of the closest datapoint.

Quadratic

A least-squares fit of a cubic polynomial to four points.

Cubic

A least-squares fit of a cubic polynomial to three points.

Polynomial Spline

Fits spline functions between the points and interpolates between them.

Gaussian

Fits a peak (bell curve) to the data.

Harmonic

Fits a cosine function to the given data points. This fit type is unlikely to be useful for processed data.

Power

Custom function. This fit type is unlikely to be useful for processed data.

Version 7.4

Have questions about MIM Software?
Contact MIM Software Support for technical assistance:
support.mimsoftware.com

MIMneuro®
User Guide

Version 7.1 - 7.4

Important: View the most up-to-date versions of MIM documentation at www.mimsoftware.com/training. Downloaded or printed content may be supplanted or superseded by updated versions. You may obtain the most current documentation from the MIM Software Knowledge Center.

Symbols Used in Documentation

Caution: Indicates potential hazards or restrictions on use that are critical for safe use of the product or for compliance with legal or regulatory standards.

Important: Indicates information that must be read and understood to successfully complete a task. Failure to review and act on important information may result in unexpected system behavior.

Tip: A helpful hint related to system behavior or usability. Tips are not required for task completion.

Related: Introduces a link to additional optional information that may be relevant or helpful when learning about a topic or completing a task.

Regulatory Information

MIMTD-759 • 21 Apr 2025

Caution: Federal law restricts this device to sale by or on the order of a physician.

Important: This product may not yet be commercially available in some countries. Please contact your local MIM Software representative for further details.

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Caution: The following intended uses and indications apply to MIM in its entirety. Depending on your specific licenses and functionality, and the region where you use the software, some indications may not apply to your use of MIM.

Intended Use

MIM software is intended for trained medical professionals including, but not limited to, radiologists, oncologists, physicians, medical technologists, dosimetrists, and physicists.

MIM is a medical image and information management system that is intended to receive, transmit, store, retrieve, display, print, and process digital medical images, as well as create, display, and print reports from those images. The medical modalities of these medical imaging systems include, but are not limited to, CT, MR, CR, DX, MG, US, SPECT, PET, and XA as supported by ACR/NEMA DICOM 3.0.

MIM provides the user with the means to display, register, and fuse medical images from multiple modalities. Additionally, it evaluates cardiac left ventricular function and perfusion, including left ventricular end-diastolic volume, end-systolic volume, and ejection fraction. The Region of Interest (ROI) feature reduces the time necessary for the user to define objects in medical image volumes by providing an initial definition of object contours. The objects include, but are not limited to, tumors and normal tissues.

MIM provides tools to quickly create, transform, and modify contours for applications including, but not limited to, quantitative analysis, aiding adaptive therapy, transferring contours to radiation therapy treatment planning systems, and archiving contours for patient follow-up and management.

MIM aids in the assessment of PET/SPECT brain scans. It provides automated quantitative and statistical analysis by automatically registering PET/SPECT brain scans to a standard template and comparing intensity values to a reference database or to other PET/SPECT scans on a voxel by voxel basis, within stereotactic surface projections or standardized regions of interest.

MIM allows the dose distribution of an implant to be individually shaped for each patient and is a general purpose brachytherapy planning system used for prospective and confirmation dose calculations for patients undergoing a course of brachytherapy using permanent implants of various radioisotopes (not including radioactive microspheres).

MIM allows voxel-based dose calculations for patients who have been administered radioisotopes or radioactive microspheres.

MIM assists with the planning and evaluation of ablation procedures by allowing the energy zone that comprises the ablation zone to be visualized on medical imaging through the placement of virtual ablation devices for the purpose of confirming ablation zone placement.

Indications for Use

MIM software is used by trained medical professionals as a tool to aid in evaluation and information management of digital medical images. The medical image modalities include, but are not limited to, CT, MR, CR, DX, MG, US, SPECT, PET, and XA as supported by ACR/NEMA DICOM 3.0. MIM assists in the following indications:

- Receive, transmit, store, retrieve, display, print, and process medical images and DICOM objects.
- Create, display, and print reports from medical images.
- Registration, fusion display, and review of medical images for diagnosis, treatment evaluation, and treatment planning.
- Evaluation of cardiac left ventricular function and perfusion, including left ventricular end-diastolic volume, end-systolic volume, and ejection fraction.
- Localization and definition of objects such as tumors and normal tissues in medical images.
- Creation, transformation, and modification of contours for applications including, but not limited to, quantitative analysis, aiding adaptive therapy, transferring contours to radiation therapy treatment planning systems, and archiving contours for patient follow-up and management.
- Quantitative and statistical analysis of PET/SPECT brain scans by comparing to other registered PET/SPECT brain scans.
- Planning and evaluation of permanent implant brachytherapy procedures (not including radioactive microspheres).
- Calculating absorbed radiation dose as a result of administering a radionuclide.
- Assist with the planning and evaluation of ablation procedures by providing visualization and analysis, including energy zone visualization through the placement of virtual ablation devices validated for inclusion in MIM-Ablation. The software is not intended to predict specific ablation zone volumes or predict ablation success.

When using the device clinically within the United States, the user should only use FDA-approved radiopharmaceuticals. If used with unapproved ones, this device should only be used for research purposes.

Lossy compressed mammographic images and digitized film screen images must not be reviewed for primary image interpretations. Images that are printed to film must be printed using a FDA-approved printer for the diagnosis of digital mammography images. Mammographic images must be viewed on a display system that has been cleared by the FDA for the diagnosis of digital mammography images. The software is not to be used for mammography CAD.

When used for diagnostic purposes, the mobile thin client is not intended to replace a full workstation and should only be used when there is no access to a workstation.

Use of MIM on Mobile Devices

MIM Software Inc. has previously worked with board certified radiologists to evaluate mobile devices for diagnostic reading. Devices tested included Apple iPad, Kindle Fire HDX, Samsung Galaxy Note Pro, and Microsoft Surface. In these cases, testers affirmed that the devices they evaluated were capable of displaying images at diagnostic quality.

Due to the number of available mobile devices, and the frequency with which new mobile devices are released, MIM cannot evaluate all available mobile devices for diagnostic reading. However, displays have dramatically increased in quality (e.g., resolution, contrast) since these earlier devices were tested. It is at the discretion of the user and their employer to determine which mobile devices are acceptable for diagnostic reading, and to ensure that these devices are properly calibrated.

Caution: All treatment plan reports shall be approved by a qualified person before the information in them is used for radiotherapy treatment purposes. The responsible organization shall ensure that individuals authorized to perform treatment planning functions are appropriately trained for the functions they perform, and the operator shall always be aware that the quality of the output depends critically on the quality of the input data. Any irregularities or uncertainties about input data units, identification, or quality of any other nature shall be thoroughly investigated before the data are used.

Caution: Any health professional having a complaint or grounds for dissatisfaction relating to the identity, quality, durability, reliability, safety, effectiveness, or performance of a device should notify MIM Software. Moreover, if a device has malfunctioned, MIM Software or its representative must be informed immediately. If a MIM Software product could have caused or contributed to the death or serious injury of a patient, MIM Software or its representative must be informed immediately. These serious incidents must also be reported to the Competent Authority of the European Member State or, when applicable, the equivalent regulatory authority, where the user and/or patient is established.

Caution: Users must perform validation when developing their own extensions or workflows and when modifying any default extensions or workflows that MIM Software provides. For extensions and workflows developed or modified by the user or provided by a third-party, MIM Software (i) does not endorse, control, monitor, or verify the contents, (ii) does not provide any warranty; and (iii) is not liable for any loss, damage, or injury sustained resulting from downloading, installing, accessing, integrating, supporting, or using the extension or workflow.

Caution: Due to the inherent nature of medical images, with their variable characteristics (e.g., level of noise and artifacts), the degree of accuracy may be variable as well. These limitations must be considered before making any decision based on images and quantitative values. It is recommended that acceptance testing be performed prior to use. This testing should include, at a minimum, all representative data sets (images) intended for transfer, all types of transfers desired for a type of data set, and clinical evaluation of each representative data set on the receiving end after each desired type of transfer.

For more information on accuracy details, see appendix or white paper information.

Contents

Getting Started

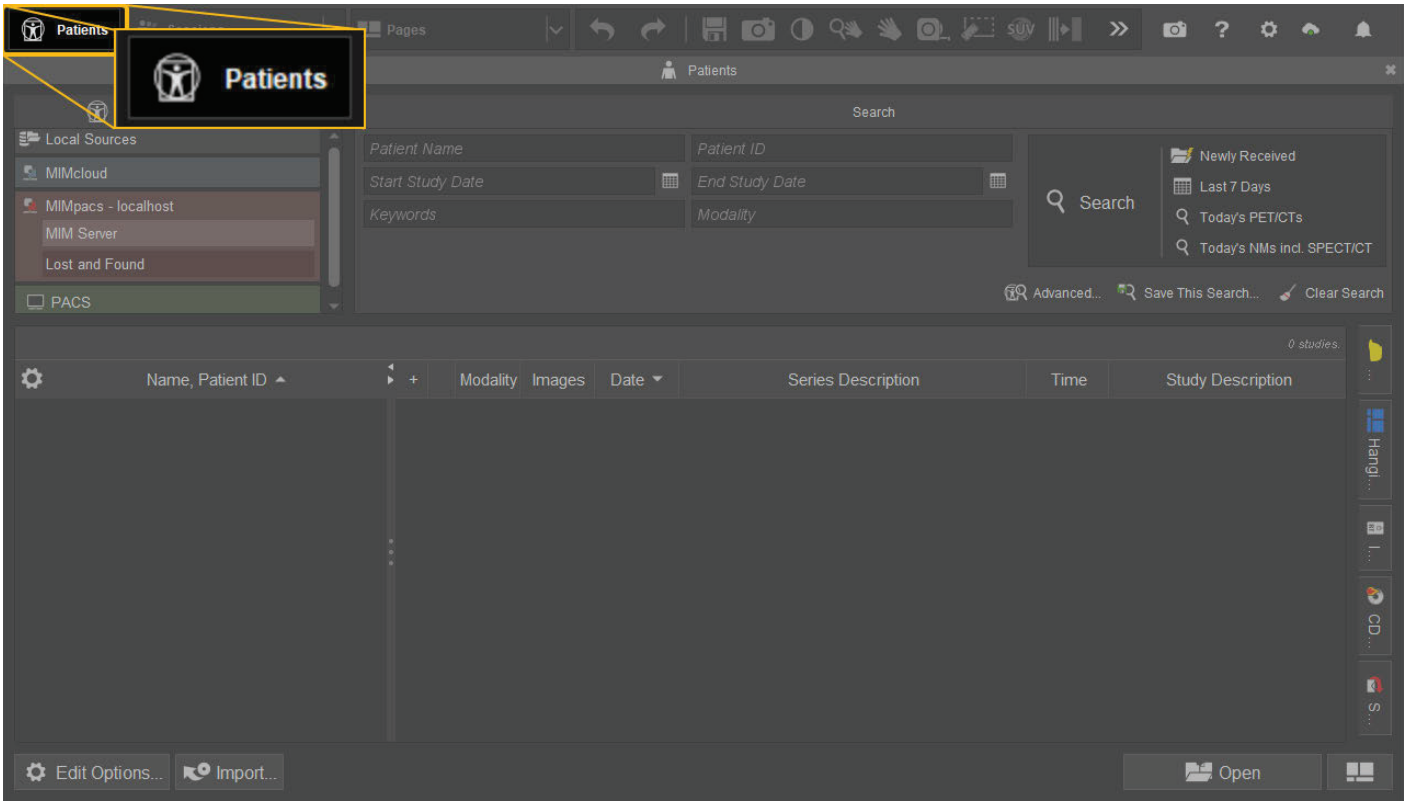
Find and Open Patient Data

MIMTD-1642 • 07 Sep 2023

Overview

Use the patient list to find and open patient data. When you launch MIM®, the patient list appears by default.

To return to the patient list anytime, click the **Patients** button in the upper-left corner.

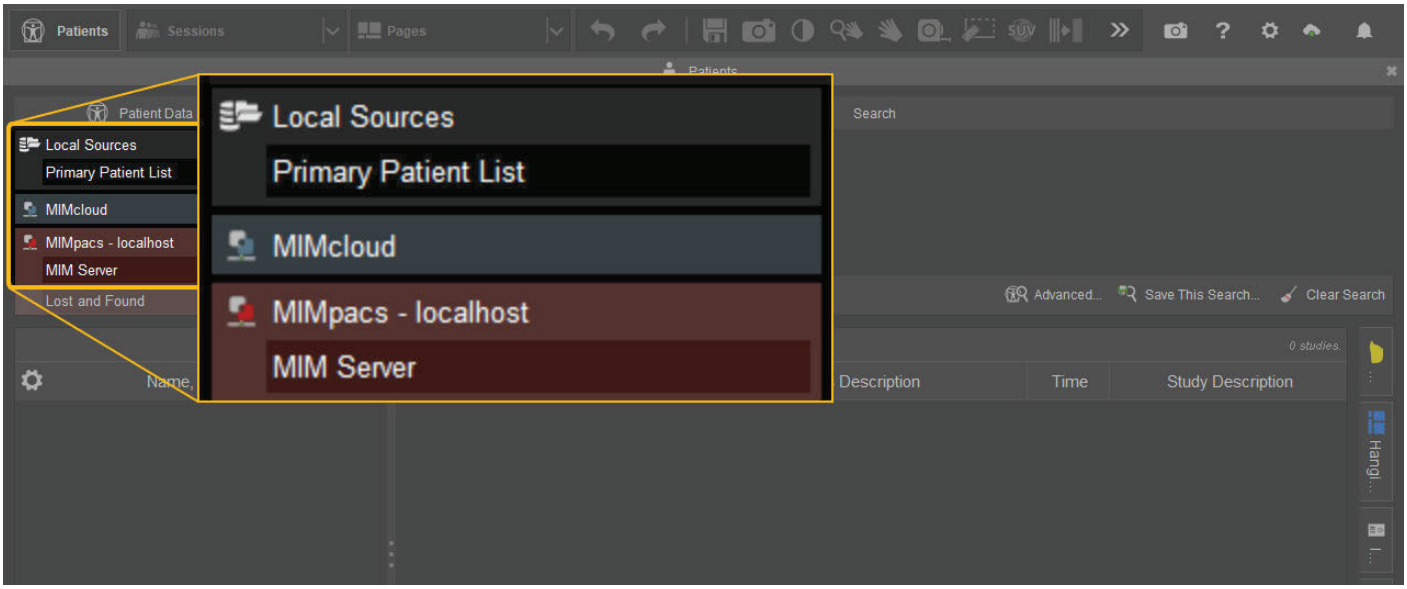


Contents

Find and Open Data

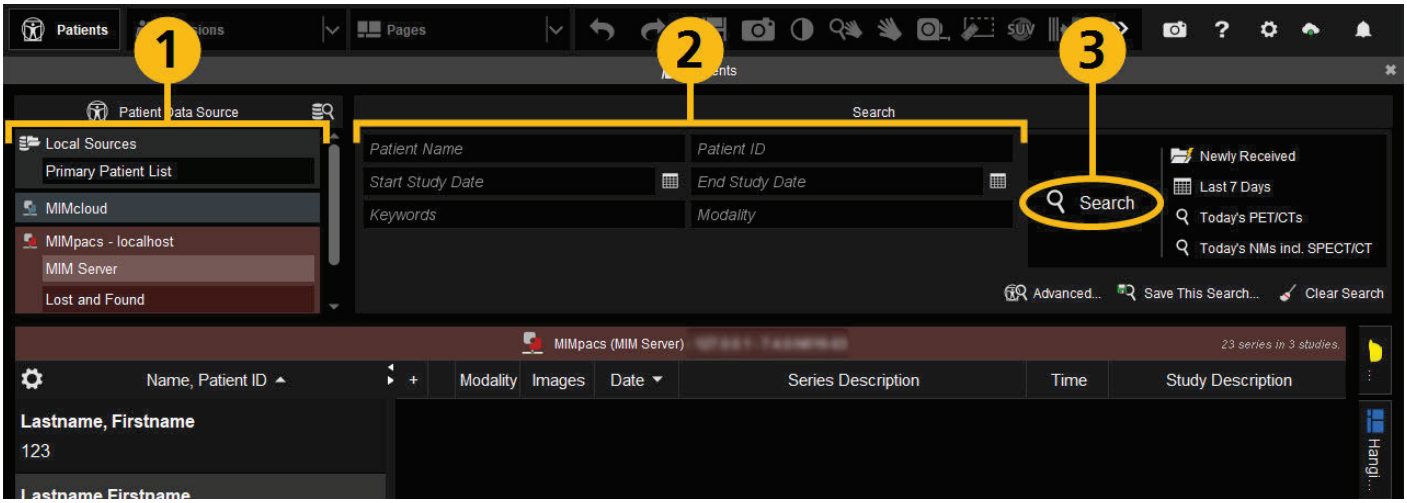
Patient data sources are in the upper-left corner. Search for patient data and open it directly from any of the following patient data sources:

- **Local Sources** (Gray) — Data in these sources is stored on your computer.
- **MIMcloud® Sources** (Blue) — Data in these sources is stored in MIMcloud. For more information about MIMcloud, go to mimcloud.com.
- **MIMpacs™ Sources** (Red) — Data in these sources is stored on your organization's MIM server.



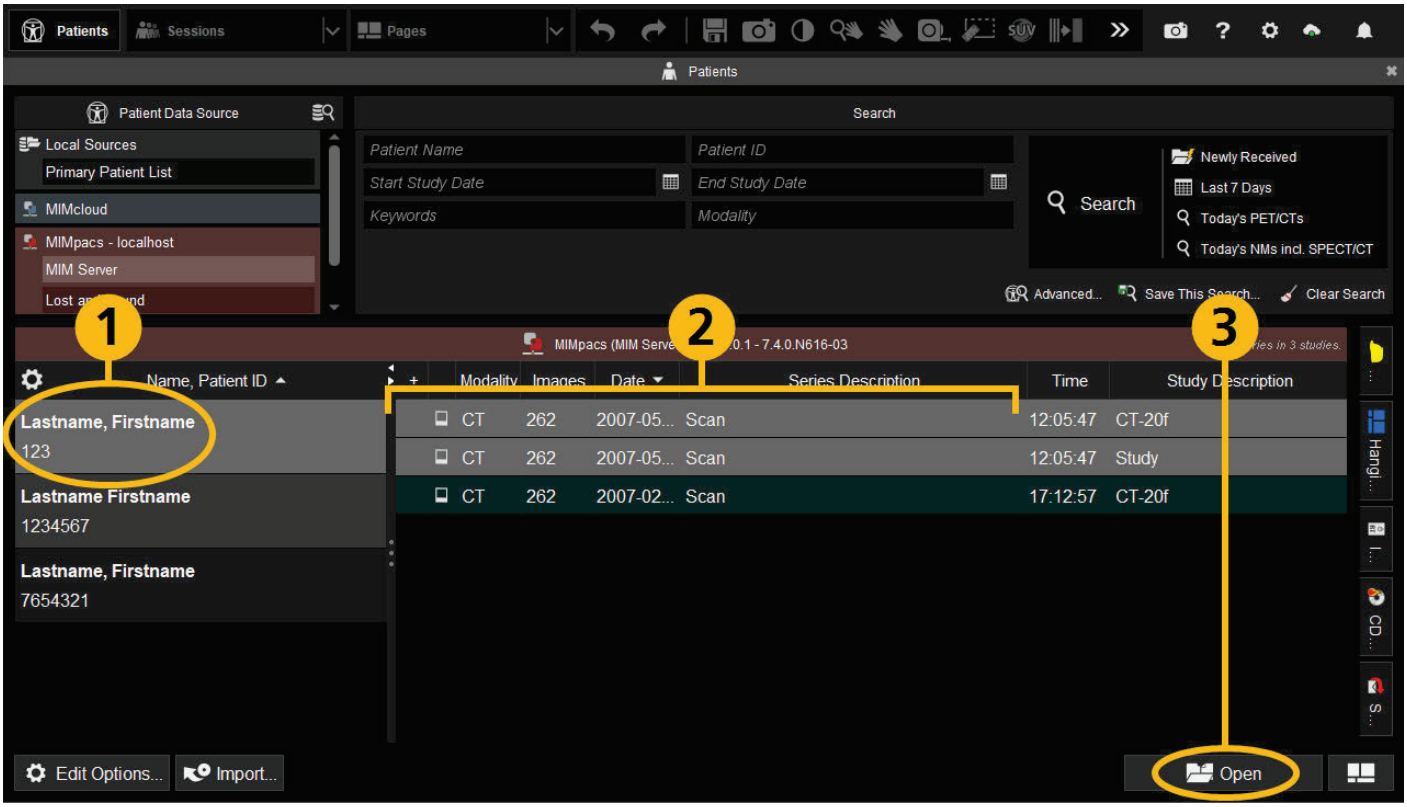
Important: If the data that you want to open is not in local sources, MIMcloud sources, or MIMpacs sources, you must first retrieve or import the data. Refer to Query and Retrieve from PACS or Import Data from a Local File, Folder, or CD below.

Find Data



1. Select the desired patient data source.
2. Enter search criteria as necessary. All search fields are optional.
3. Click the **Search** button. Search results appear below the data sources, in the column on the left side.

Open Data



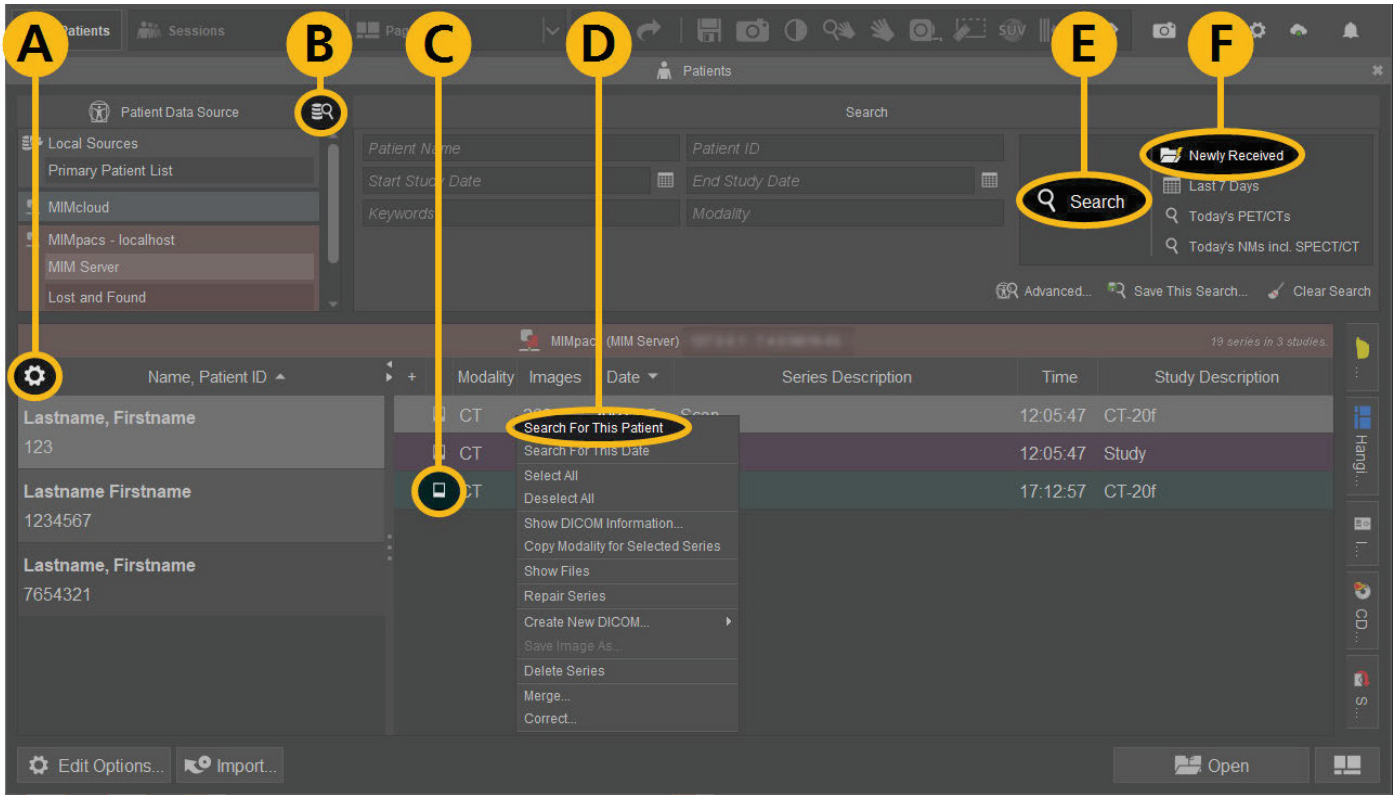
1. Select the desired patient from the column on the left side. Individual series appear in the center of the screen.
2. If you want to open only certain series, select one or more individual series. If you do not select individual series, all series for the patient will open.

> **Tip:** To select multiple patients or series at a time, hold the Ctrl key while clicking, or left-click drag over multiple items.

3. To open the data into a MIM session, click the **Open** button. Or, to automate processing, launch a MIM Workflow™.

> **Related:** For more information about workflows, refer to Launch MIM Workflows™.

Tips for Searching



A. To change how the search results are sorted, click the settings button above the search results on the left side.

B. *MIM 7.2 and later:* To search for a specific patient data source, click the button and start typing the name of the source. This is useful if one of your data sources has many individual patient lists.
MIM 7.1 and earlier: This functionality is not available.

C. To preview an image before you open it, hover over the thumbnail symbol on the left side of the series information.

D. To see all series for a patient, instead of only those returned by the search criteria, right-click a search result and select **Search for This Patient**.

> **Related:** For instructions on using the other options in this right-click menu, refer to Manage Patient Data.

E. To clear all search criteria, right-click the **Search** button.

F. To show only newly received data, click **Newly Received** next to the **Search** button.

Related: To set up other one-click search buttons that bundle a set of search criteria, refer to Search Quickly with Saved Searches.

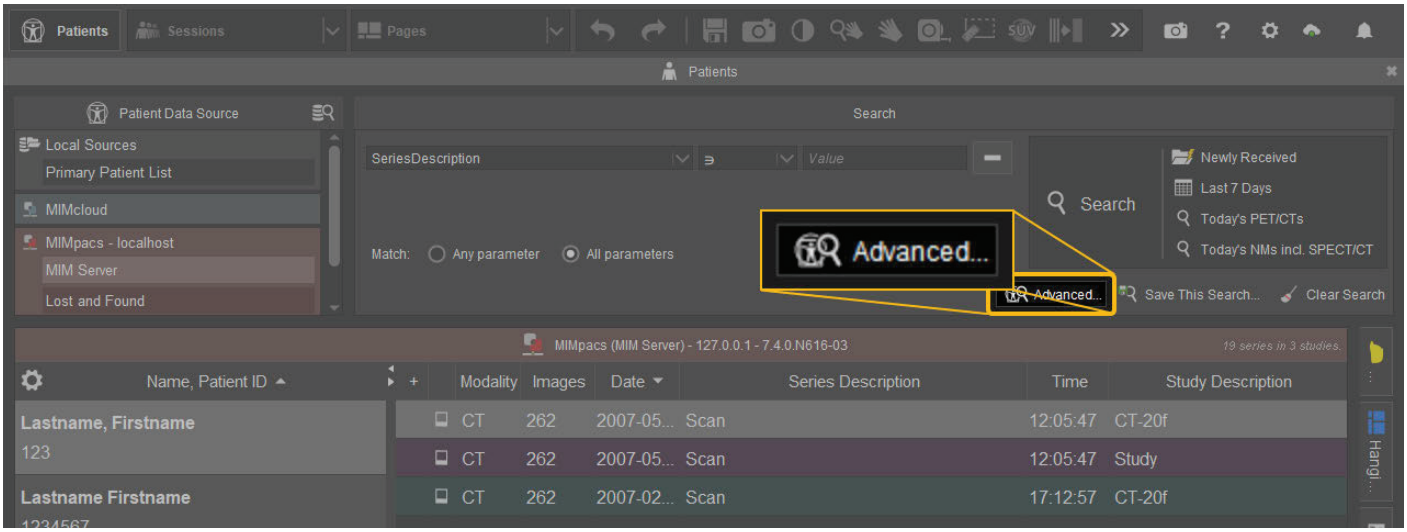
Adjust Patient List Options

To personalize a variety of patient list functions, go to Settings in the upper-right corner of MIM and choose **Patient List Options**. Adjustments that you can make include the following:

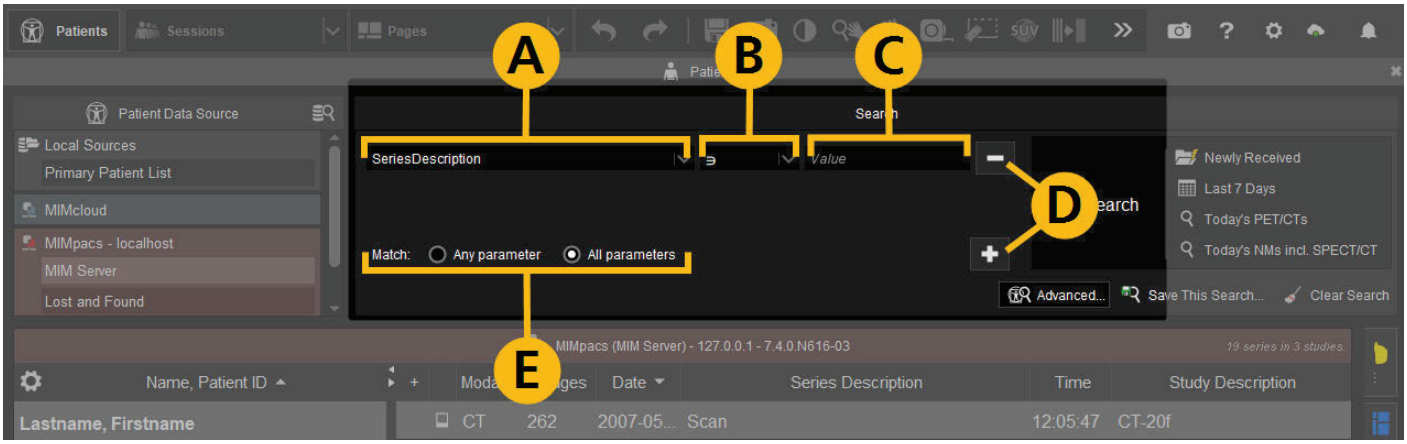
- Choose which series columns (e.g., Modality, Series Description, Time) are shown and in which order.
- Set the patient list view to show newly received series by default.
- Change the default sorting method for search results.

Do Advanced Searches

If desired, click the **Advanced...** button in the middle of the search panel to find data using DICOM tag-based search filters.



Follow these tips to use the advanced search options:



A. Select a DICOM tag (e.g., SeriesDescription). Scroll through the menu to see common tags, or start typing to find other tags.

B. Select an operator (e.g., =). To see an explanation of what the operator does, select the operator and hover over the field.

C. Enter a value (e.g., WB AC).

D. To add a search filter, click the ✚ button. To remove a search filter, click the ▬ button.

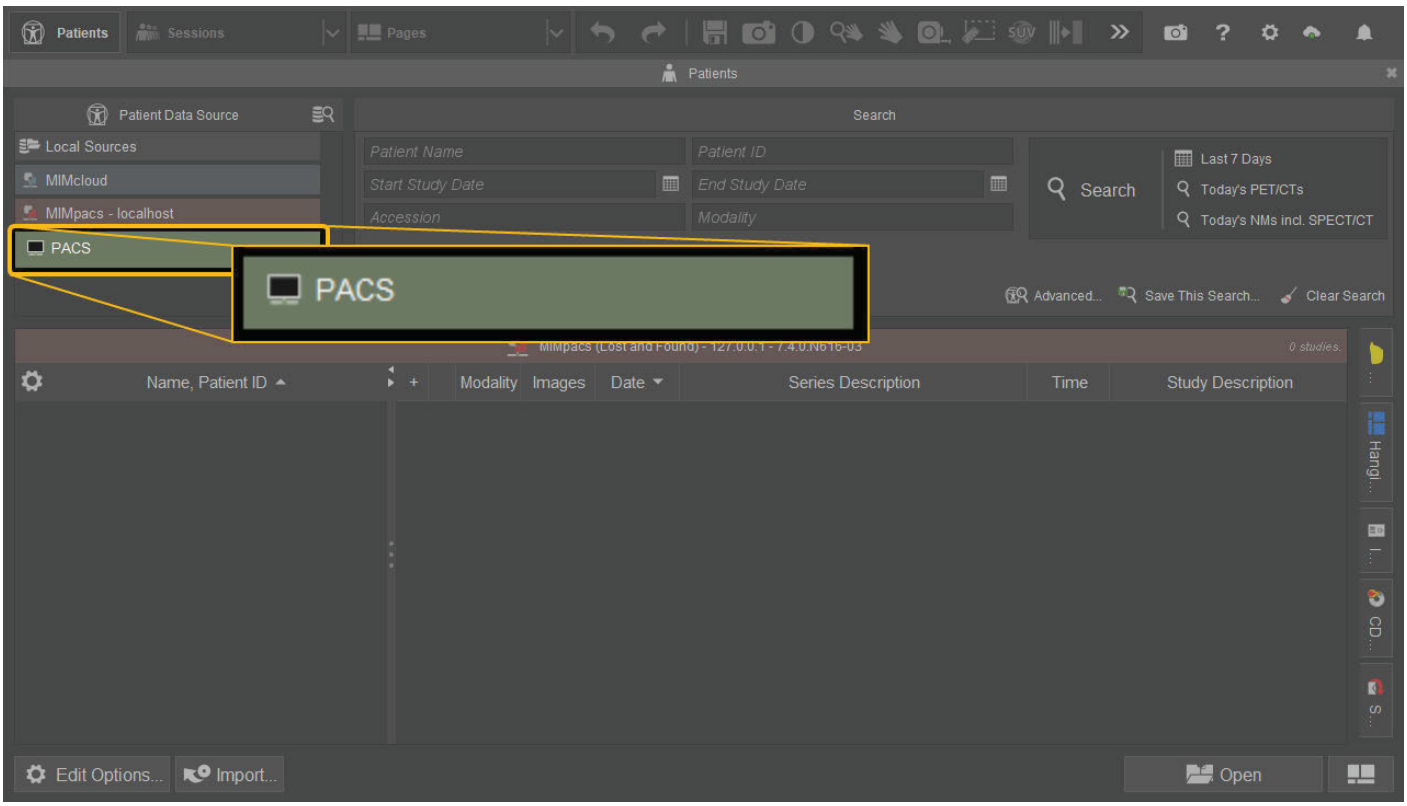
E. Select whether the search should return results that match any or all of the filters that you configure.

Related: To save advanced searches as one-click search buttons, refer to Search Quickly with Saved Searches.

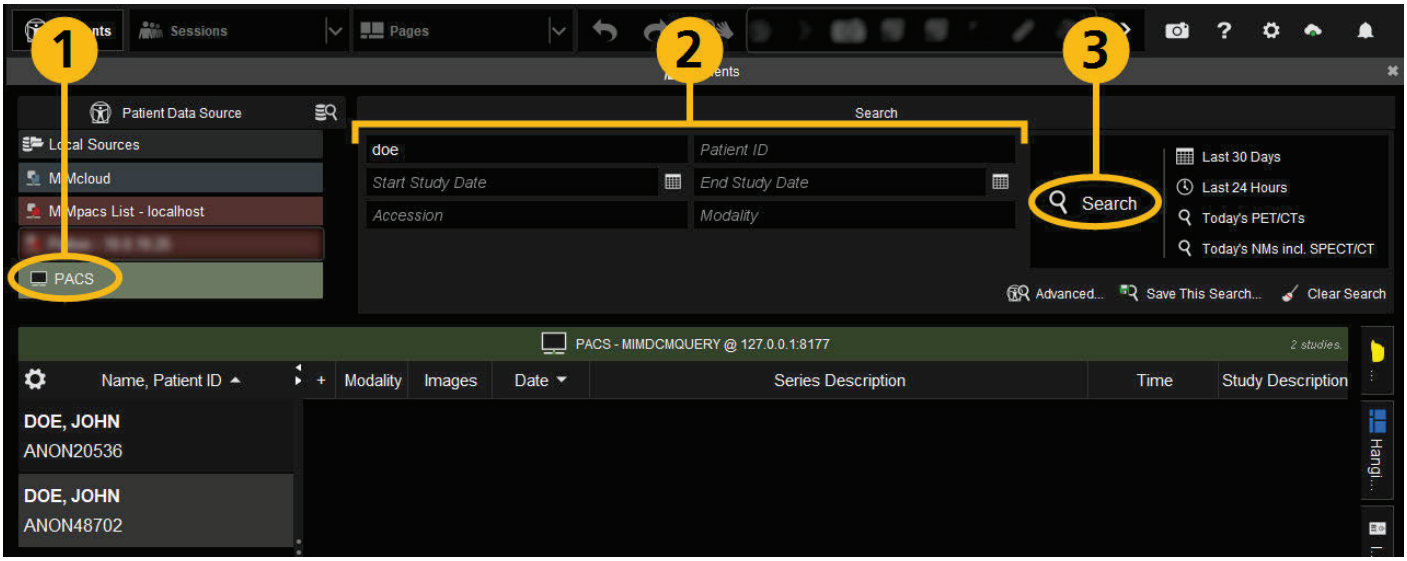
Query and Retrieve from PACS

PACS lists, or third-party DICOM locations, are highlighted in green and located under MIM patient lists. You can search for patient data in these data sources. To open the data, you must send it to a MIM patient

list.


Patients
Sessions
Pages
Patients
Patient Data Source
Local Sources
MIMcloud
MIMpacs - localhost
PACS
Search
Patient Name
Patient ID
Start Study Date
End Study Date
Accession
Modality
Search
Last 7 Days
Today's PET/CTs
Today's NMs incl. SPECT/CT
Advanced...
Save This Search...
Clear Search
PACS
MIMpacs (Lost and Found) - 127.0.0.1 - 7.4.0.N616-03
0 studies.
Name, Patient ID
Modality
Images
Date
Series Description
Time
Study Description
Edit Options...
Import...
Open

Search a PACS List



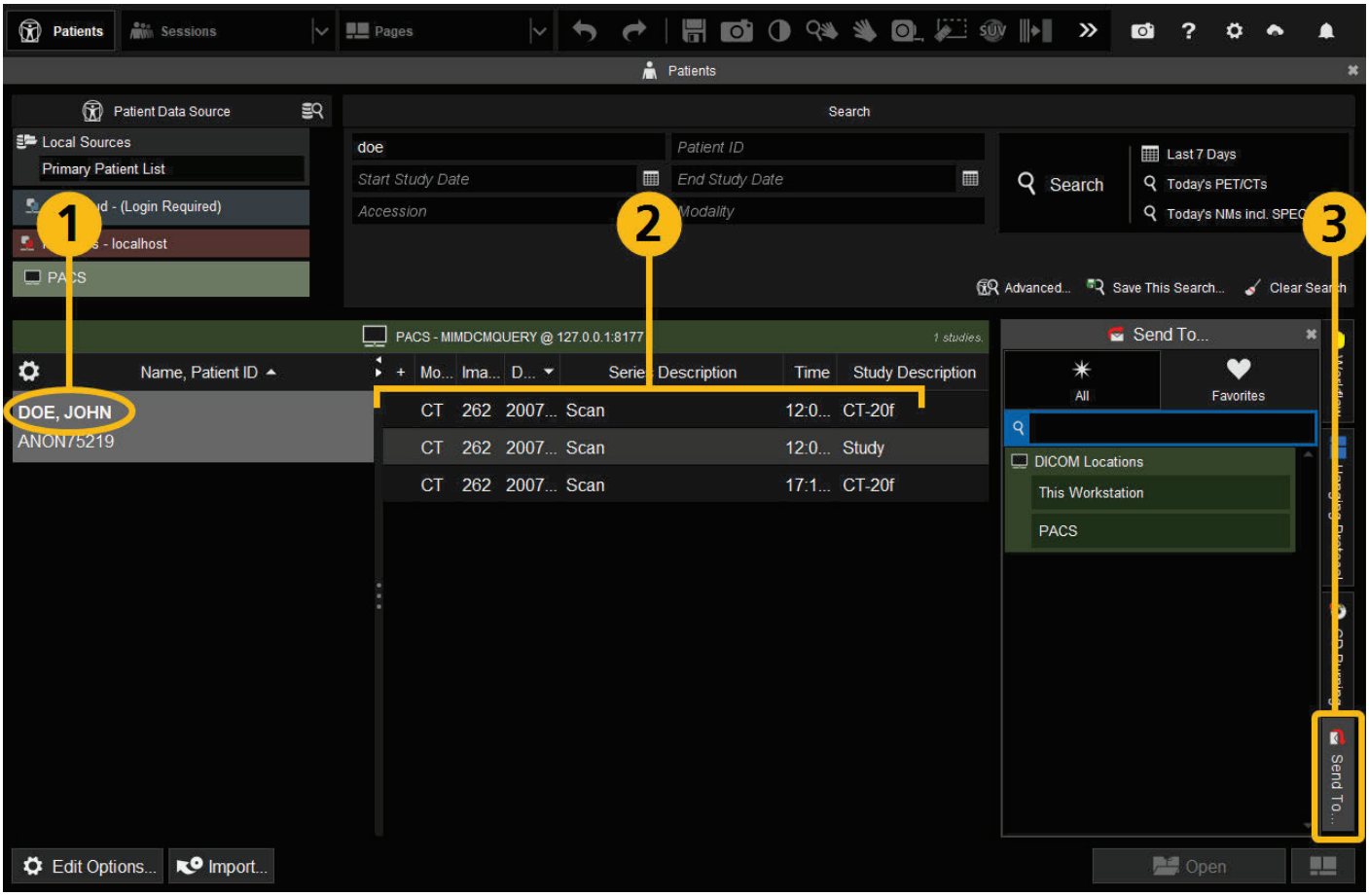
1. Select the desired PACS list.
2. Enter search criteria as necessary. All fields are optional.

> **Important:** Each PACS supports different search criteria when queried by another system such as MIM. Some search criteria may not return results.

3. Click the **Search** button. Search results appear below the data sources, in the column on the left side.

> **Tip:** For more details about search options, refer to Tips for Searching and Do Advanced Searches above.

Send Data from PACS to a MIM Patient List



1. Select the desired patient from the column on the left side.
2. If you want to send only certain series, select one or more individual series. If you do not select individual series, all series for the patient are sent.

> **Tip:** To select multiple patients or series at a time, hold the Ctrl key while clicking, or left-click drag over multiple items.

3. Click the **Send To...** tab in the lower-right corner, then click the desired destination. The data is sent to the selected location.

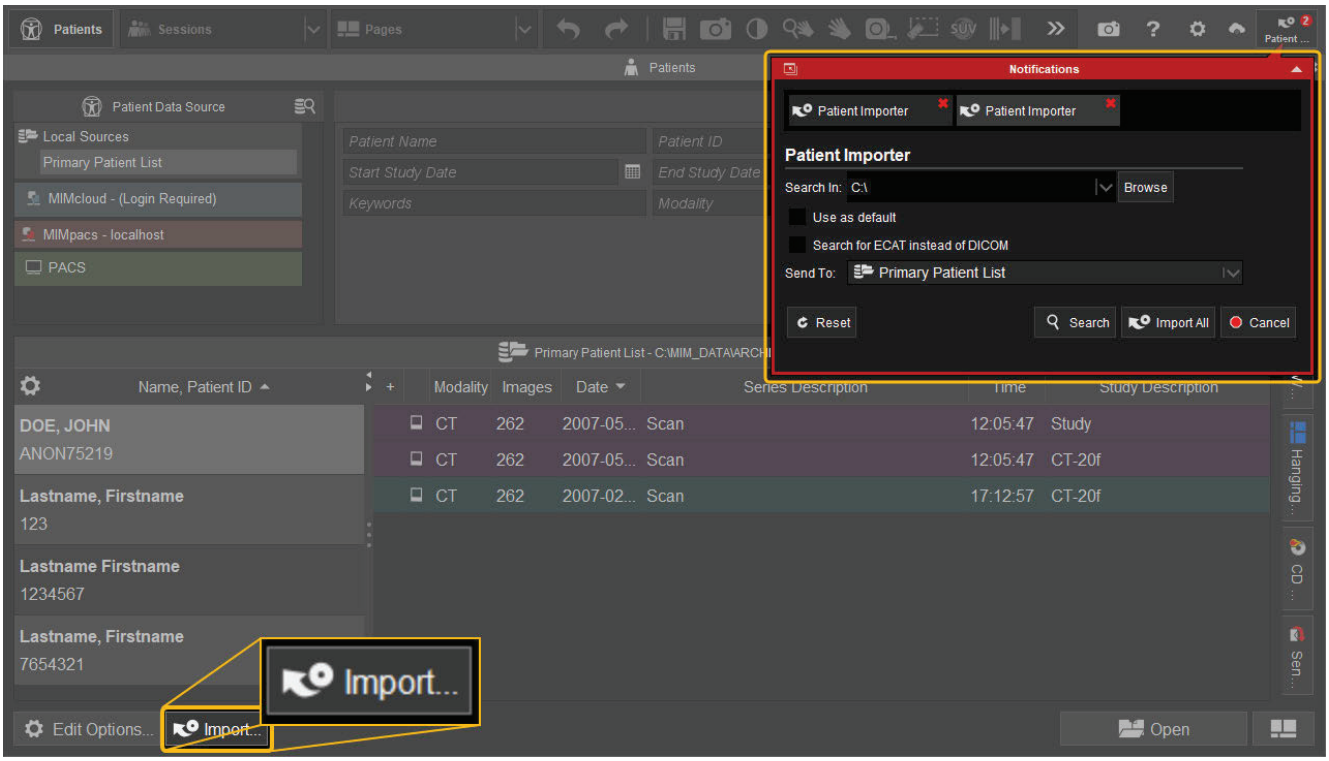
> **Tip:** The **This Workstation** destination sends data to the MIMpacs patient list set up in Settings ⚙ >> **Network Services** >> **DICOM Store**.

To open the data, go to the patient list that you sent the data to. Follow the steps in Find and Open Data above.

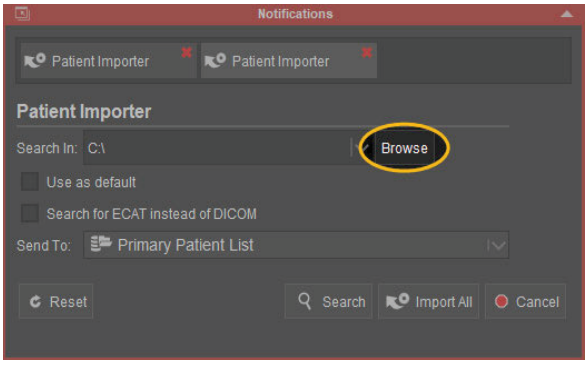
Import Data from a Local File, Folder, or CD

To import data from a local file, folder, or CD into a MIM patient list, follow these steps:

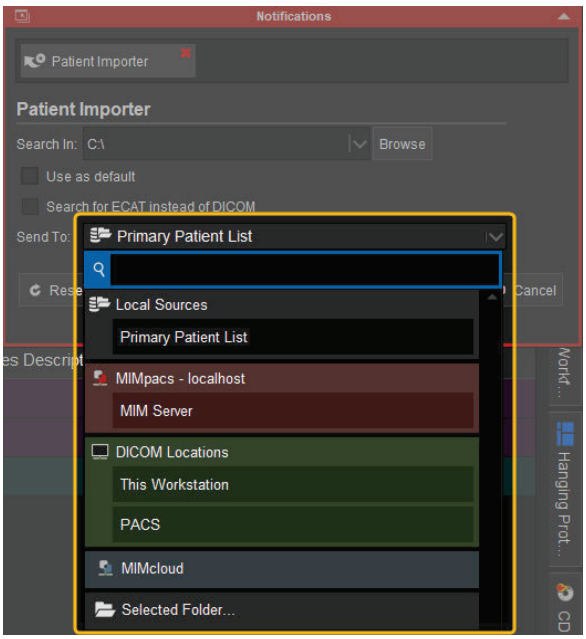
1. Click the **Import...** button in the lower-left corner. A Notifications window appears.



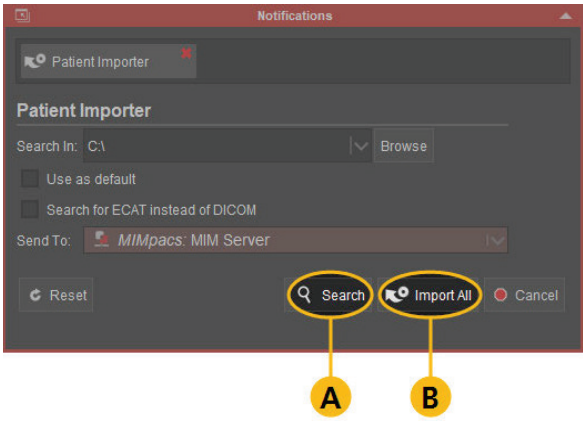
2. Click the **Browse** button in the Notifications window to find the filepath or drive where data is stored.



3. Choose a **Send To** location in the Notifications window dropdown.



4. Click **Search** or **Import All**:



   A. To select only some of the data to import, click the **Search** button.
      i. In the **Patient Search** window that appears, check the individual series that you want to send to a MIM patient list.
      ii. Click the **Import** button in the lower-right corner of the window.
   B. To import all of the data from the filepath or drive that you browsed to, click the **Import All...** button.

To open the data, go to the patient list that you imported the data into. Follow the steps in Find and Open Data above.

View and Process Data in MIM® Sessions

MIMTD-605 • 09 Nov 2023

Overview

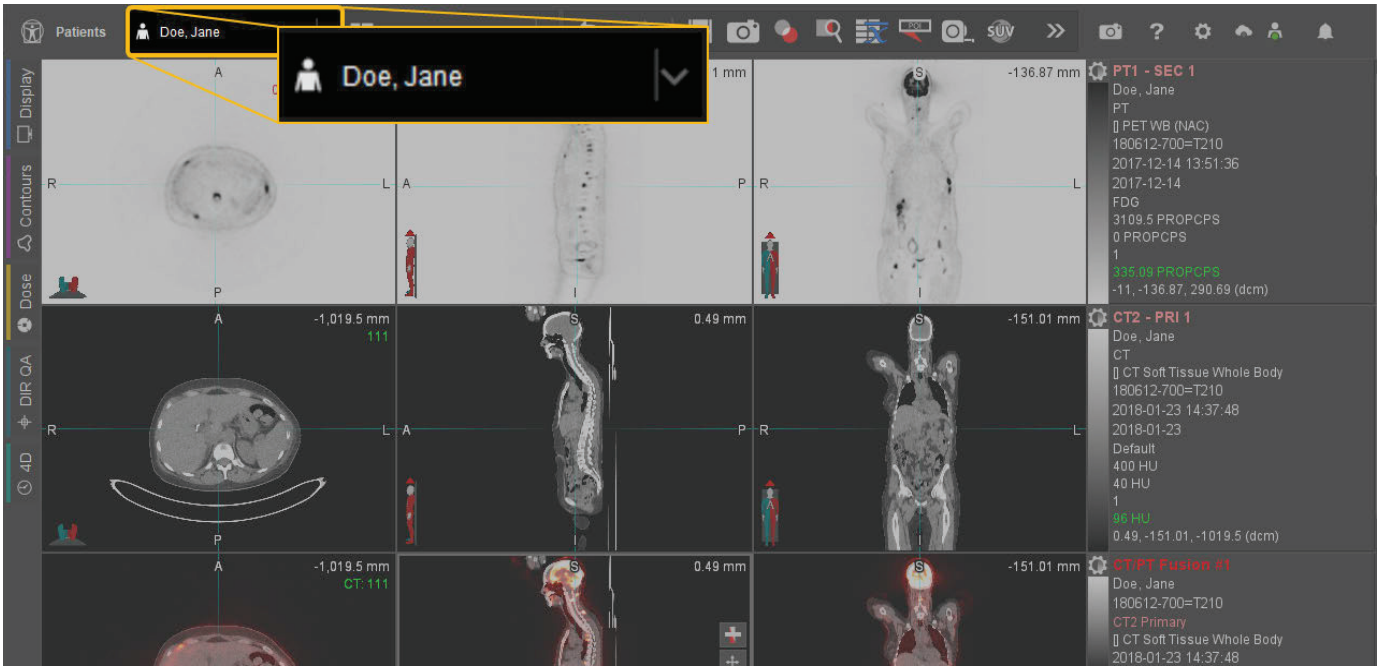
MIM opens patient data into a workspace called a **session**.

- You can open multiple sessions at once to keep your work separated and organized.
- You can save sessions. Saving a session preserves your work, including all images, displays, and registrations. When you save a session, it can be reopened at any time.

Contents

Session Basics

When patient data is open in a session, the patient name is displayed in the session dropdown menu. This menu is located in the upper-left corner of MIM.

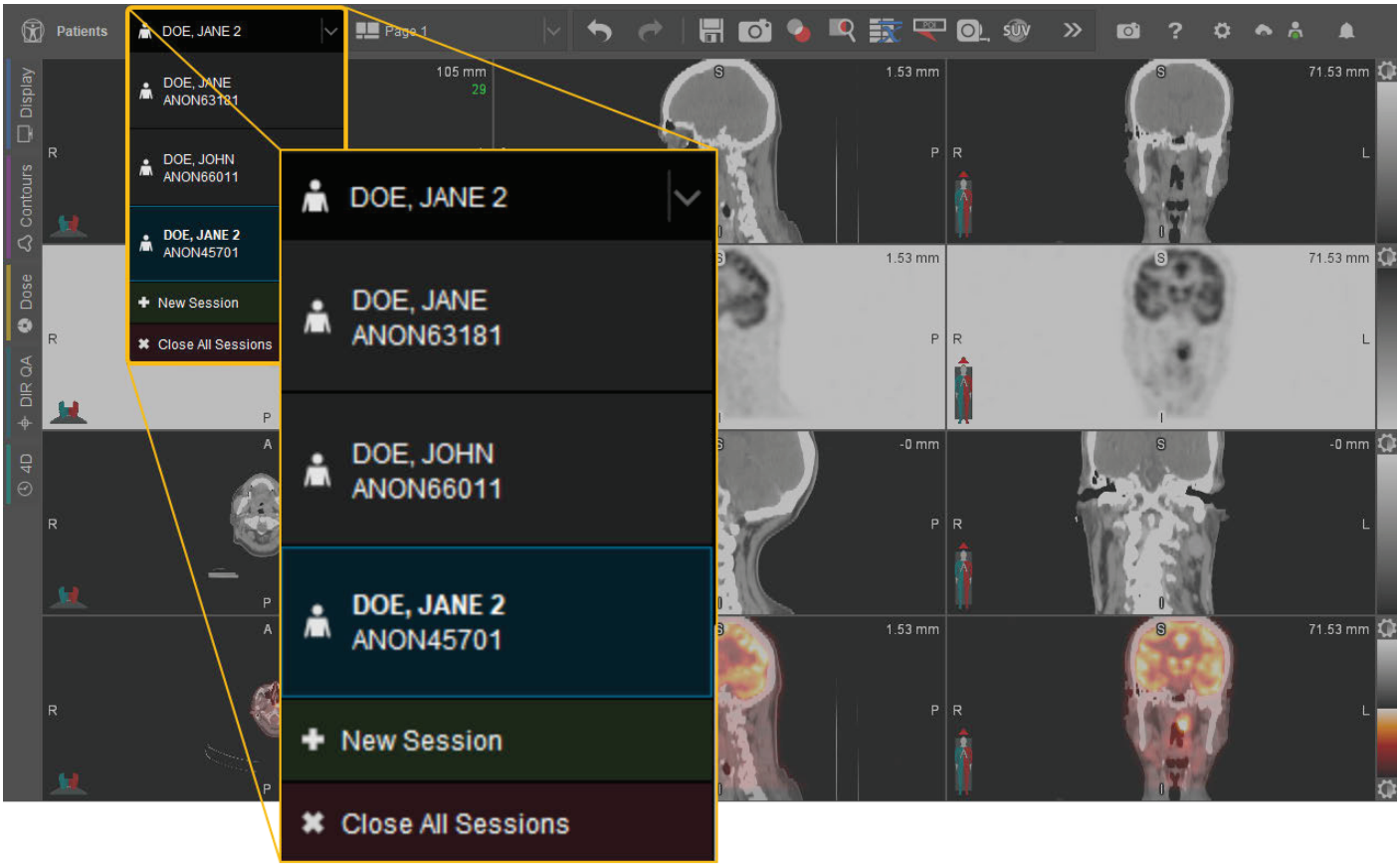


Important: *MIM 7.3 and later*: There is a separate pages dropdown menu to the right of the session dropdown menu. *MIM 7.2 and earlier*: The session dropdown menu also contains information about the pages in the session.

For more information, see Pages below.

Use the dropdown menu to:

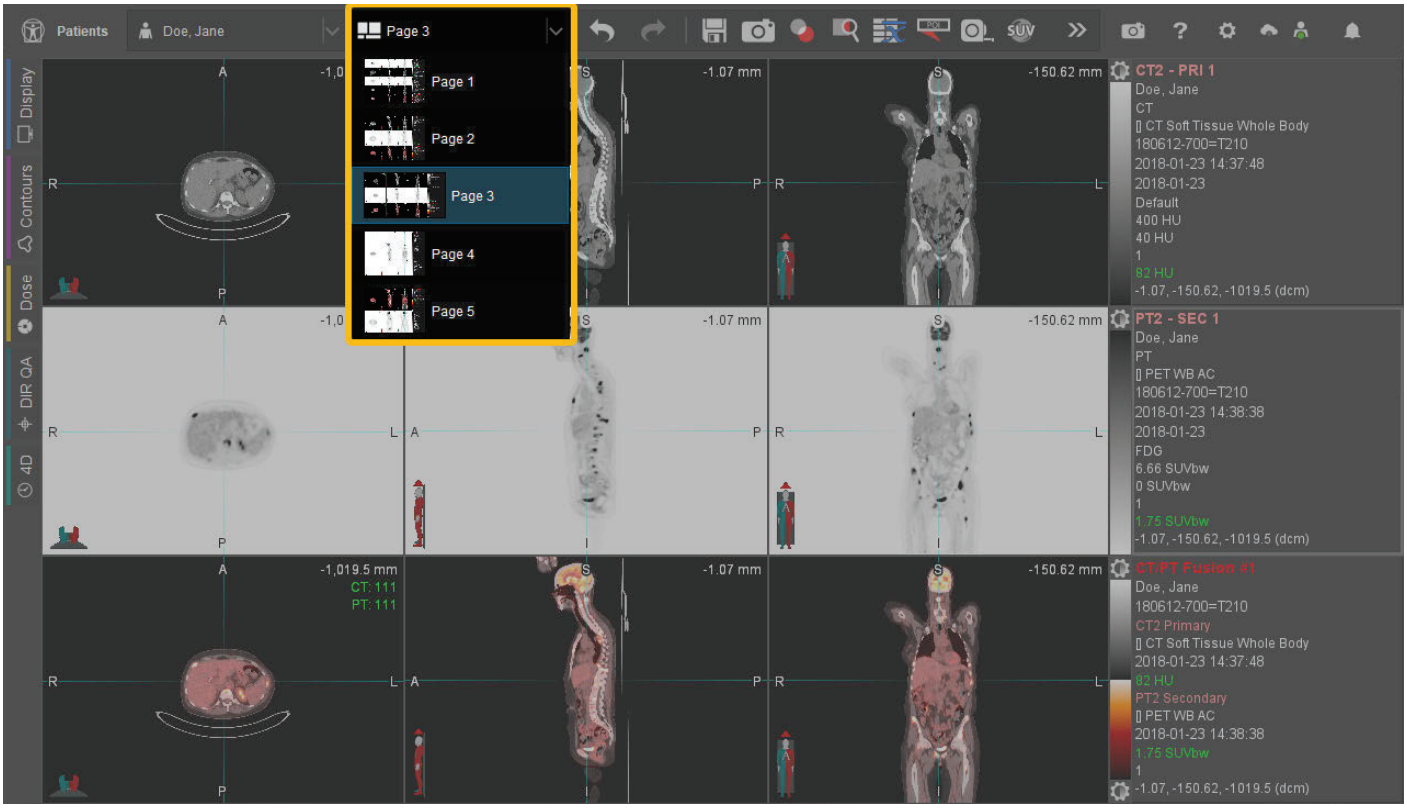
- Switch from one session to another — Select the session you would like to switch to.
- Start a new session — Click **New Session**. You are returned to the patient list. Select and open data to start a new session.
- Close a session — Hover the mouse over the session name and click the ✖ button. Or, click **Close All Sessions** to close all sessions.



Pages

Each session can have multiple pages. Pages display images, and sometimes tables or graphs of additional information. Move from page to page using the left and right arrow keys.

To see a list of all pages and switch to any page, click the dropdown menu in the upper-left corner of MIM.



Rename a Page

1. Open the dropdown in the upper-left corner of MIM and hover over the page you want to rename.
2. Click the button to rename the page. The Notifications window opens.
3. Enter a name for the page in the **Page name** field.
4. Click the **OK** button.

Close a Page

1. Open the dropdown menu in the upper-left corner of MIM and hover over the page you want to close.
2. Click the button for the page.

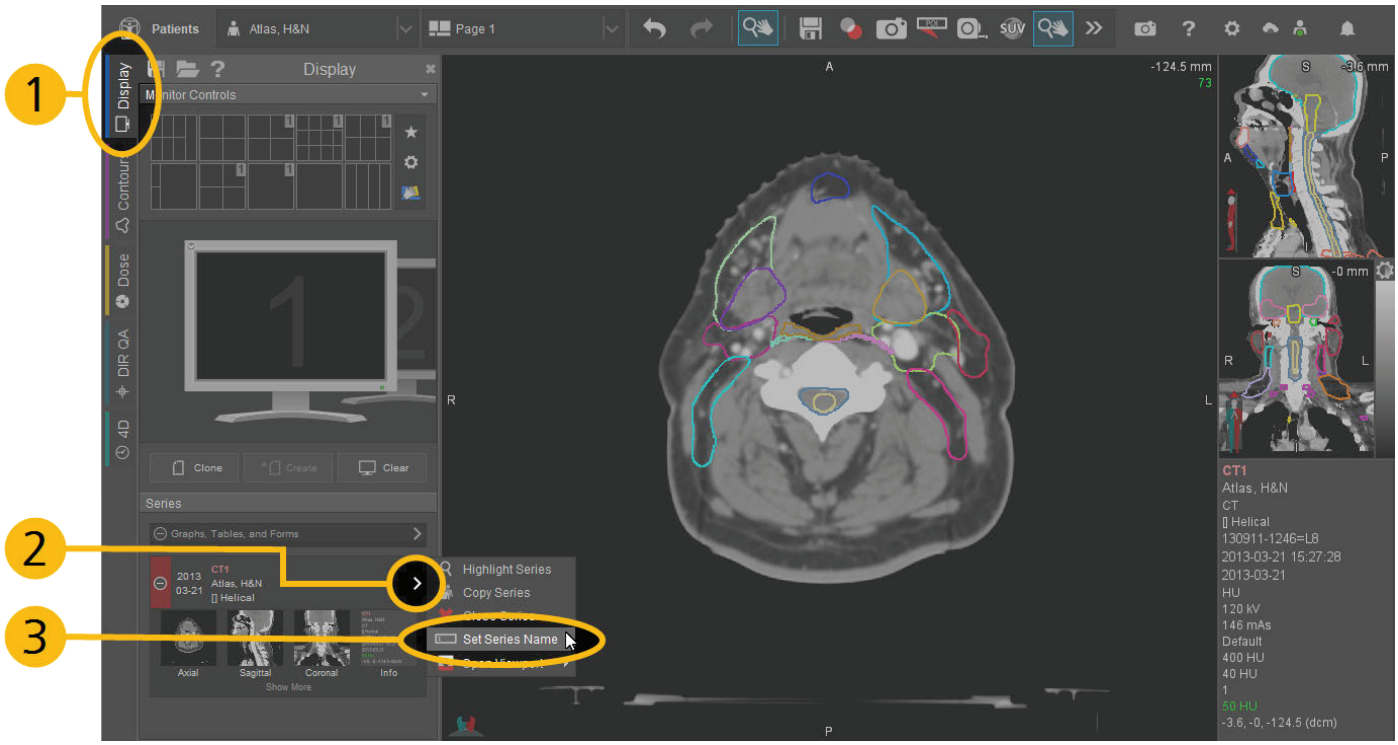
Session Tools

After patient data is open in a session, use the following options to adjust the view, process the data, and more:

- **MIM toolbar** — The toolbar is found near the top of MIM.It can be configured to include the tools you use most. See Access Tools: The Toolbar and the Radial Menu.
- **Radial menu** — Right-click to access the radial menu. Configure the tools found in your radial menu by going to Settings >> **General Preferences** and searching for "**radial menu**". See Access Tools: The Toolbar and the Radial Menu for more information.
- **Sidebars** — The sidebars you see on the left side of MIM depend on your license. Each sidebar contains various processing options.
- **Keyboard shortcuts** — Keyboard shortcuts can be mapped to many of MIM's tools and let you navigate sessions more quickly. See Set Keyboard Shortcuts for more information.
- **Workflows** — You can launch a workflow after patient data is already open in a session, just like you would from the patient list. Use the button in the upper-right corner of MIM and search for the **Launch Workflow** tool.

Rename a Series in a Session

When you rename a series in a session, the name is displayed in the upper-left corner of each viewport the series appears in. Assigning names is often easier than trying to differentiate series based on their default names (CT1, CT2, PT1, etc.). Applying a name in this way does not change the series description or any other metadata. The name only serves as a label in the session.



1. With images open in a session, click the **Display** tab to expand the Display sidebar.
2. In the lower half of the Display sidebar, click the arrow button next to the series you want to rename.
3. Select **Set Series Name**. The Notifications window opens.
4. Enter a name for the series, then click **OK**.

Localize and Scroll

MIMTD-606 • 25 Jul 2023

Overview

MIM's many settings let you configure localizing and scrolling behaviors to suit your individual preferences.

Contents

Localize

- Click within an image to localize on an area of interest in all planes.
- Left-click drag to gradually move the point of localization.
- Double-click in any plane to maximize the viewport. Double-click again to restore the viewport's original size.

Change the Appearance of the Crosshairs and Cursor

Use the following default keyboard shortcuts to quickly change the appearance of the crosshairs:

Crosshair Change	Keyboard Shortcut
Change Crosshair Style	=
Change Crosshair Color	Shift+=
Toggle Crosshair Visibility	Ctrl+=

To change the style, color, and other crosshair settings, go to Settings >> **General Preferences** and search for "**crosshairs**".

To change the style and color of the cursor, go to Settings >> **General Preferences** and search for "**cursors**".

Scroll

To manually scroll through an image slice by slice, use any of the following methods:

- Right-click drag up or down.
- Scroll your mouse wheel up or down, or use two fingers on your trackpad.
- Press the up and down keys on your keyboard.

Tip: If you prefer to scroll through an image by left-click dragging, adjust the mouse behavior via Settings >> **General Preferences** and searching for "**mouse behaviors**". See Configure Mouse Behaviors for more information.

Fast Scroll (MIM 7.2 and Later)

If scrolling seems too fast or too slow, you can adjust your fast scroll preference to control whether MIM skips slices when scrolling. Slices will not be skipped when you scroll the mouse wheel at a steady pace, or when you right-click drag.

Follow these steps to enable fast scrolling:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fast scroll**".
3. Select **Enable skipping of slices with fast scroll**.

Toggle Fast Scrolling in a Session with a Keyboard Shortcut (MIM 7.2 and Later)

Use a keyboard shortcut command to toggle fast scrolling on and off during a session. This command enables or disables fast scrolling in your current MIM session. The preference toggled in this command does not carry over after session is closed, and it does not change your fast scrolling preference (see Fast Scroll (MIM 7.2 and Later) above).

Follow these steps to assign a keyboard shortcut to toggle fast scrolling:

1. Click the Settings button in the upper-right corner of MIM, and go to **Keyboard Shortcuts...**.
2. Search for "Toggle fast scrolling" in the empty field below the Category dropdown menu.
3. Double-click **Toggle Fast Scrolling (Current Session)** and assign the desired key binding.

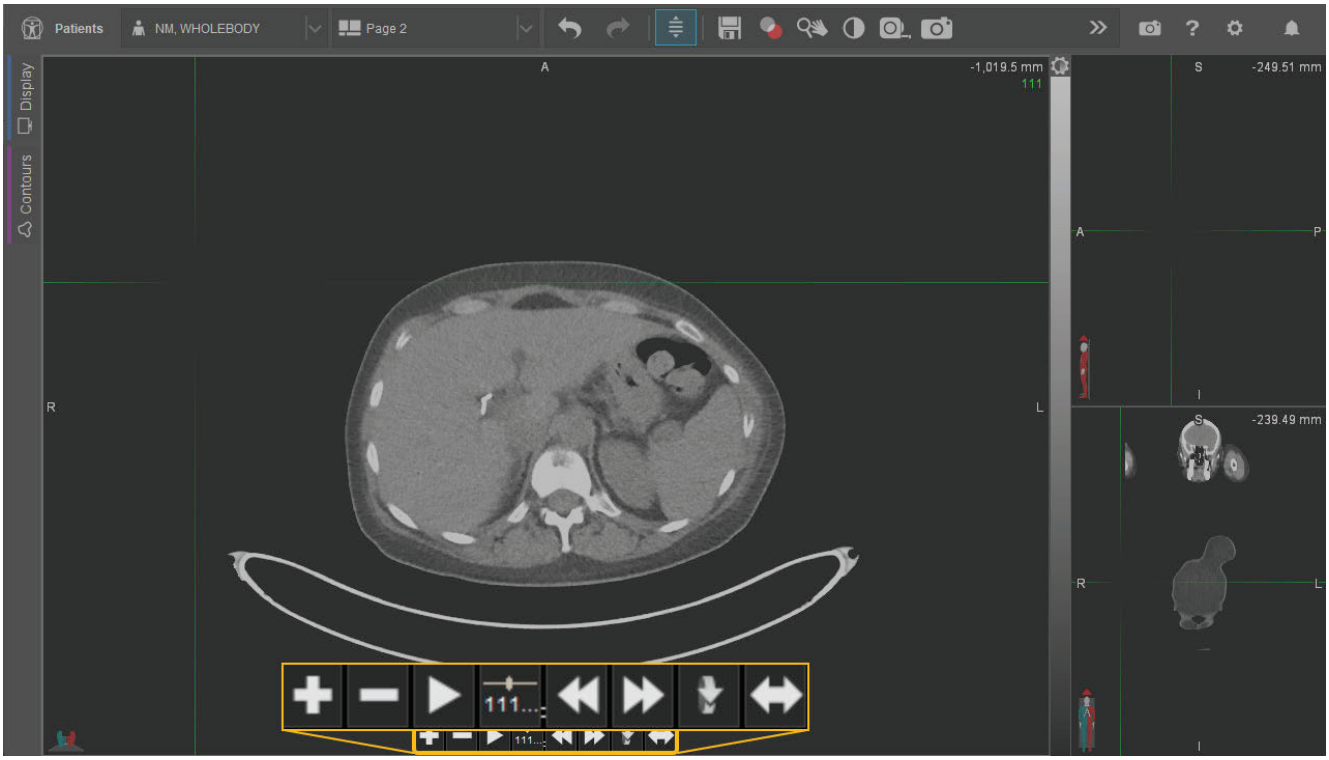
Related: For detailed instructions on using keyboard shortcuts, see Set Keyboard Shortcuts.

Autoscroll (MIM 7.2 and Later)

Use the Autoscroll tool to scroll automatically through an image in any plane. The tool lets you click a button, or press a key, to start playing through the axial, sagittal, or coronal plane slice by slice. Controls are available to adjust the speed, play/pause, step forward, step backward, play from the top, and reverse direction.

Activate Autoscroll

1. Activate the **Autoscroll** tool from the MIM toolbar or radial menu. You may need to click the button at the top of MIM to search for this tool.
2. Hover in any viewport. The autoscroll control buttons appear at the bottom of the viewport.
3. Use the buttons to control autoscrolling. Hover over each button for a short description of the functionality.



Tip: When you move the cursor to a different viewport, autoscrolling pauses.

Use Autoscroll with Keyboard Shortcuts

You can assign keyboard shortcuts for the following commands:

- Activate Autoscroll
- Play or pause Autoscroll
- Reverse direction
- Scroll from the top

Follow these steps to assign Autoscroll keyboard shortcuts:

1. Click the Settings button in the upper-right corner of MIM, and go to **Keyboard Shortcuts...**.
2. Search for "Autoscroll" in the empty field below the Category dropdown menu to see the relevant keyboard shortcuts.
3. Double-click each shortcut name and assign the desired key binding.

Related: For detailed instructions on using keyboard shortcuts, see Set Keyboard Shortcuts.

Autoscroll General Preferences

To adjust autoscroll general preferences, click the Settings button in the upper-right corner of MIM. Go to **General Preferences** >> **Viewing**.

The following preferences can be adjusted:

- **Start Autoscroll from the current localization** — Enable this preference to start autoscrolling from the slice that you are currently localized on. Disable this preference to start autoscrolling from the first slice in the series.
- **Autoscroll Delay (ms)** — Change the length of the delay between each slice. When you click the plus or minus button in the Autoscroll controls, the delay that is set in the general preferences decreases or increases by 50 ms with each click.

Zoom and Pan

MIMTD-607 • 05 Oct 2023

Overview

Interactively zoom and pan to inspect specific areas of an image.

Contents

Zoom

Access the **Zoom** tool from the toolbar or radial menu.

> **Related:** For more information, see Access Tools: The Toolbar and the Radial Menu.

- Left-click drag up and down to zoom.
- Right-click drag to pan the image while in the zoom mode.

You can also use keyboard shortcuts for zooming. By default, the following shortcuts are set in MIM®:

1: Reset Zoom

2: Zoom In

3: Zoom In More

4: Zoom Out

Related: *MIM 7.3 and later*: You can configure MIM to zoom when you click or drag with a set mouse button. For more information, refer to Configure Mouse Behaviors. *MIM 7.2 and earlier*: This functionality is not available.

Pan

Access the **Pan** tool from the toolbar or radial menu.

Related: For more information, see Access Tools: The Toolbar and the Radial Menu.

- Left-click drag to pan the image.
- Right-click drag up and down to move through slices in the current plane (this behavior is the same when no tool is selected.)

Tip: You can also pan via right-click using the Zoom tool. Refer to Zoom above. If you prefer to pan via left-click, use the Pan tool.

Related: *MIM 7.3 and later*: You can configure MIM to pan when you click or drag with a set mouse button. For more information, refer to Configure Mouse Behaviors. *MIM 7.2 and earlier*: This functionality is not available.

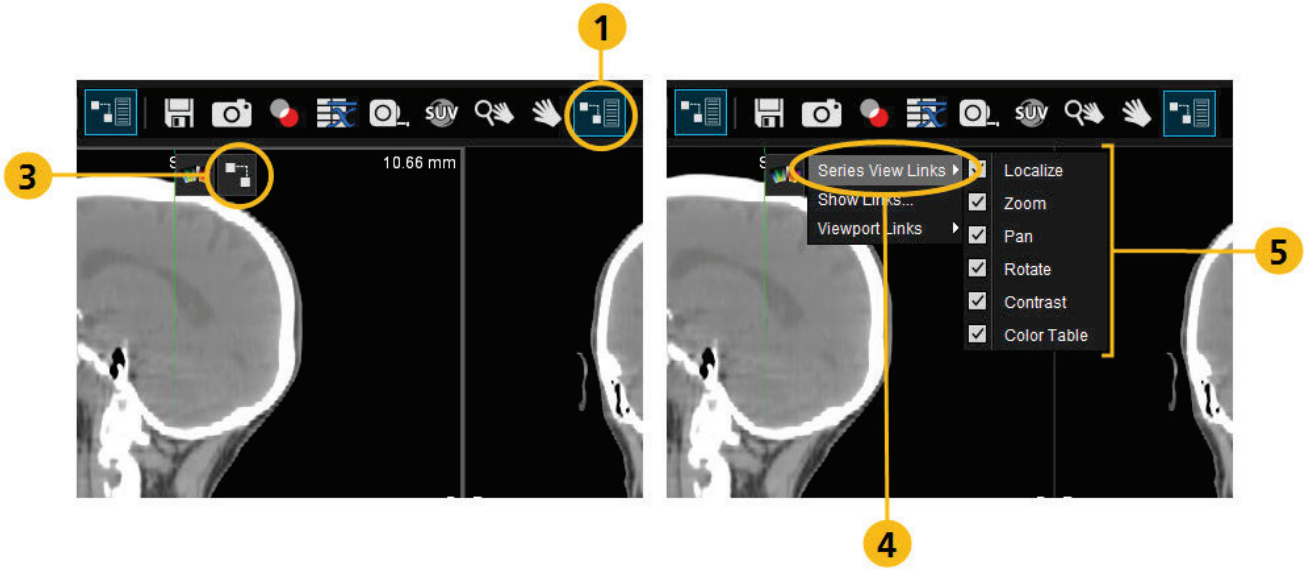
Scroll, Zoom, Pan, or Rotate a Series Independently

To scroll, zoom, pan, or rotate a series independently from all of the other series in the session, follow these steps:

1. Activate the **Link Manager** tool.

Related: If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

2. Hover over the series that you want to scroll, zoom, pan, or rotate independently. The Link Manager button appears in the center at the top of the viewport.
3. Click the **Link Manager** button in the viewport.
4. Hover over **Series View Links**.



5. Toggle any of the settings to enable or disable the links:
   - To scroll the series separately, deselect **Localize**.
   - To zoom the series separately, deselect **Zoom**.
   - To pan the series separately, deselect **Pan**.
   - To rotate the series separately, deselect **Rotate**.

Important: If the series is part of a fusion, the fusion continues to localize, zoom, pan, or rotate with the primary image.

Access Tools: The Toolbar and the Radial Menu

MIMTD-1683 • 01 Nov 2023

Overview

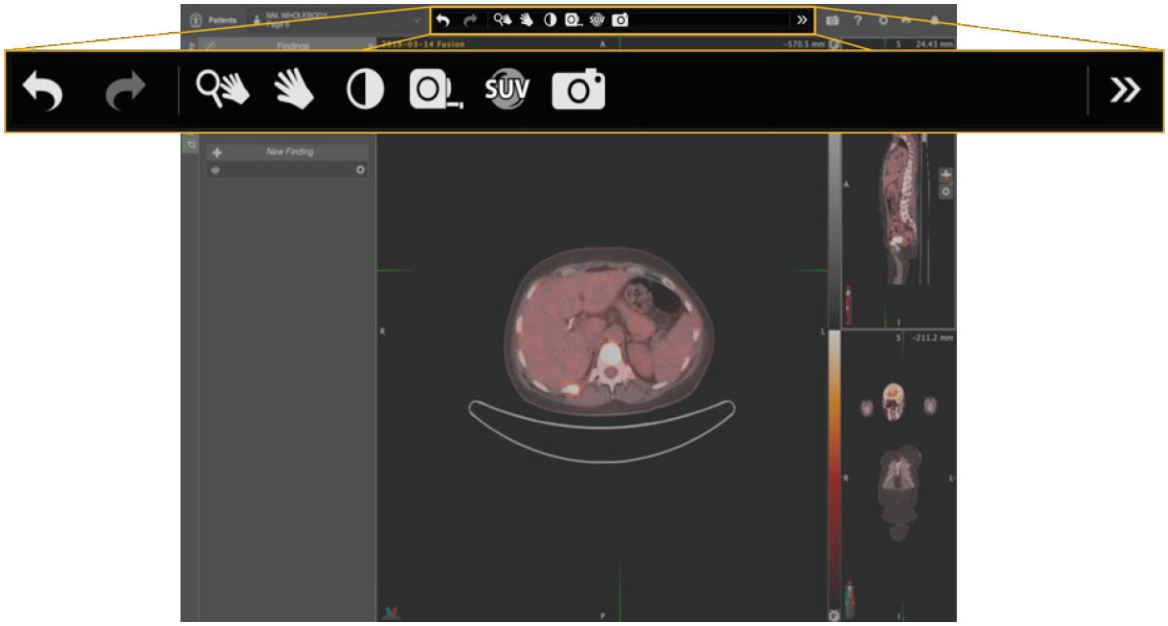
Access frequently used MIM® tools through the toolbar and the radial menu. You can add or remove tools so that your favorites are easy to find.

> **Tip**: To share and standardize these settings across your organization, a MIM administrative user should make the additions or updates while logged in to the **Edit Site Defaults** login mode. See Update Default Settings for Users for prerequisites and instructions.

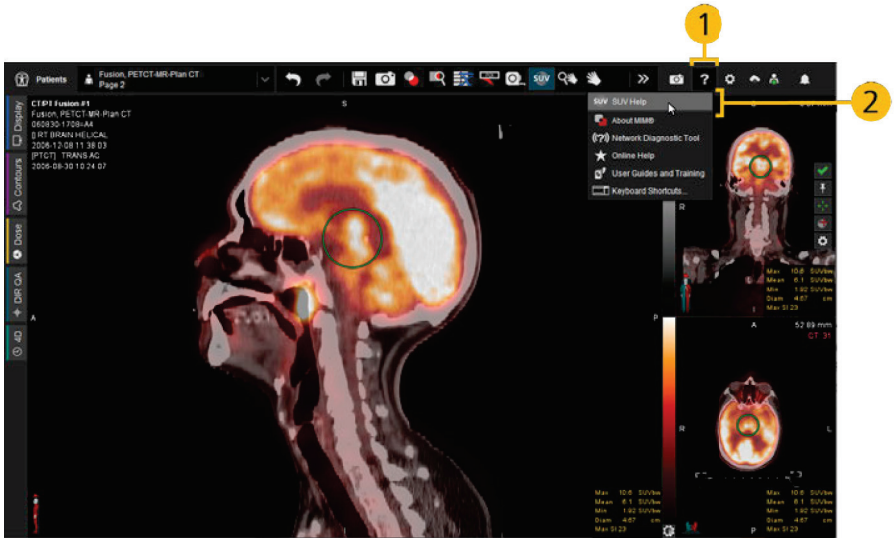
Contents

The Toolbar

The toolbar at the top of MIM contains many of the tools you use to view and process data. The toolbar begins with the Undo and Redo tools and ends with the double arrow button. Use the double arrow button to find tools that aren't currently shown in the toolbar.



- The active tool is highlighted in blue. Click the tool again to deactivate it.
- To view help information for the active tool:
    1. Click the question mark button in the upper-right corner.
    2. Select the first menu item.

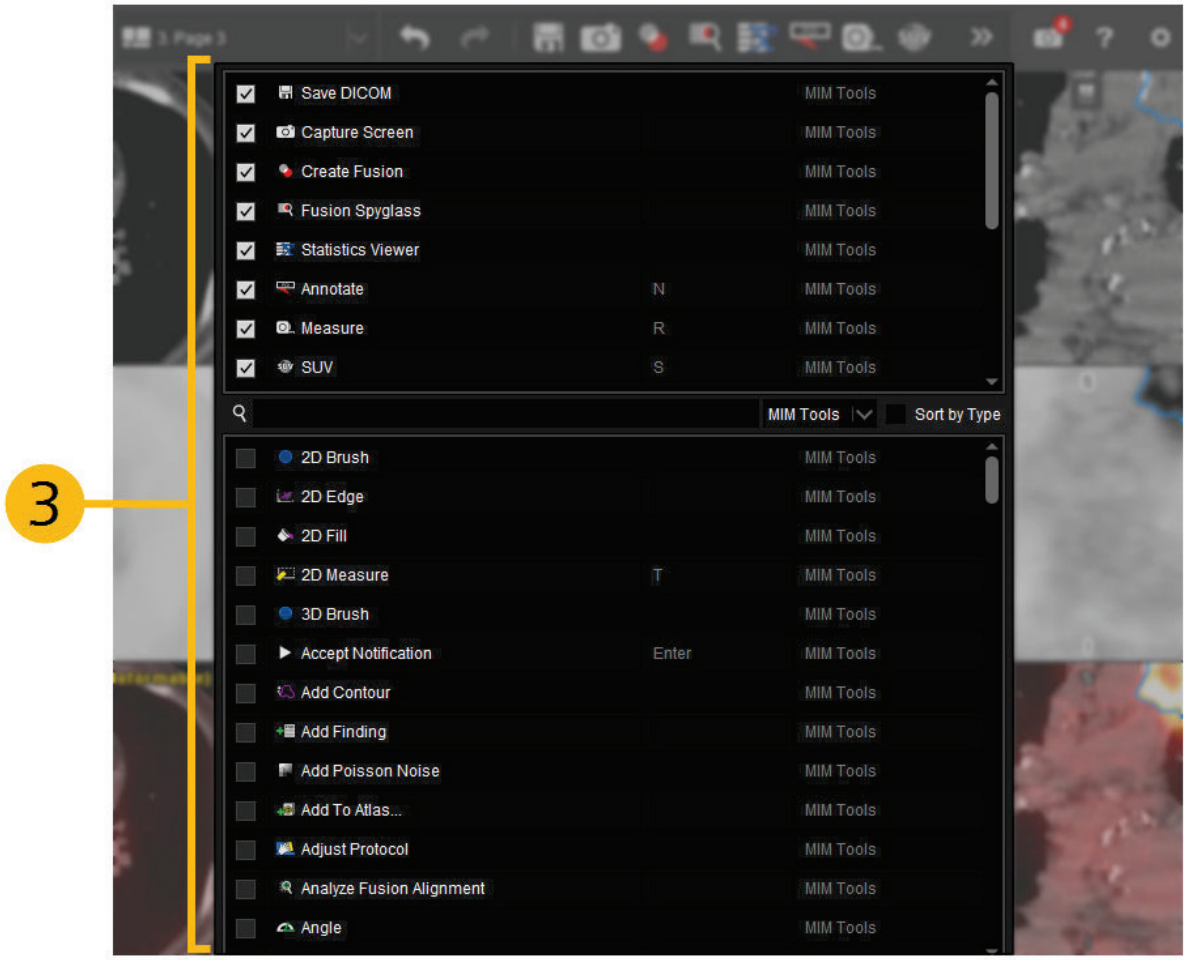


Customize the Toolbar

You can edit the toolbar to add tools you use frequently or remove tools you do not use:

1. Click the double arrow button on the far right side of the toolbar.
2. Select the **Configure Toolbar** button at the top of the menu.
3. *MIM 7.3 and later:* Select tools in the bottom half of the list to add them to your toolbar. Deselect tools in the top half of the list to remove them from your toolbar.

   MIM 7.2 and earlier: There are no checkboxes. Click tools in the bottom half of the window to add them to the toolbar. Click tools in the top half of the window to remove them from the toolbar.



4. *MIM 7.3 and later:* Click **OK** at the bottom of the menu.

   MIM 7.2 and earlier: Click the double arrow button to close the menu.

Tip: To see a list of MIM Workflows™ that can be added to your toolbar switch the dropdown menu (*MIM 7.3 and later*) or tab (*MIM 7.2 and earlier*) in the middle of the list from **MIM Tools** to **Workflow**. If you use MIM Extensions™, you can also switch the dropdown or tab to Extensions.

The Radial Menu

The radial menu lets you quickly access a set of frequently used tools with a right-click in any viewport. This reduces back-and-forth movement across your screen and lets you work more quickly.

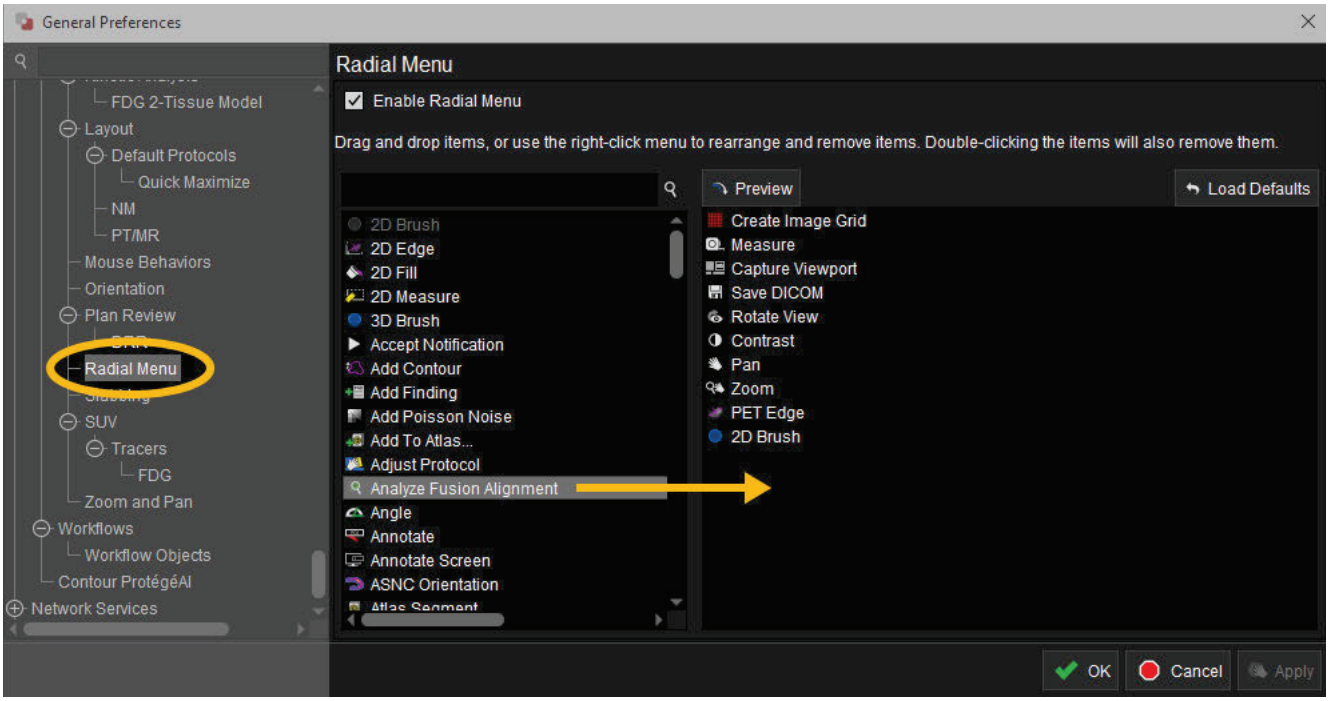
1. Access the radial menu by right-clicking on an image in an open session.
2. Click on a tool in the radial menu to activate it.
3. When you are finished using the tool, right-click again to access the radial menu. Select a new tool, or deactivate the current tool by clicking the X ⊗ button in the center.
4. Move the cursor away from the radial menu to hide it.

Customize the Radial Menu

You can edit the radial menu to add tools you use frequently or remove tools you do not use:

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**radial menu**".
3. Click **Radial Menu** on the left side.

4. Add items to your radial menu by dragging items from the left column to the right column.



5. Click **OK** to save the changes and close the window.

Create and Modify Display Layouts

MIMTD-610 • 09 Nov 2023

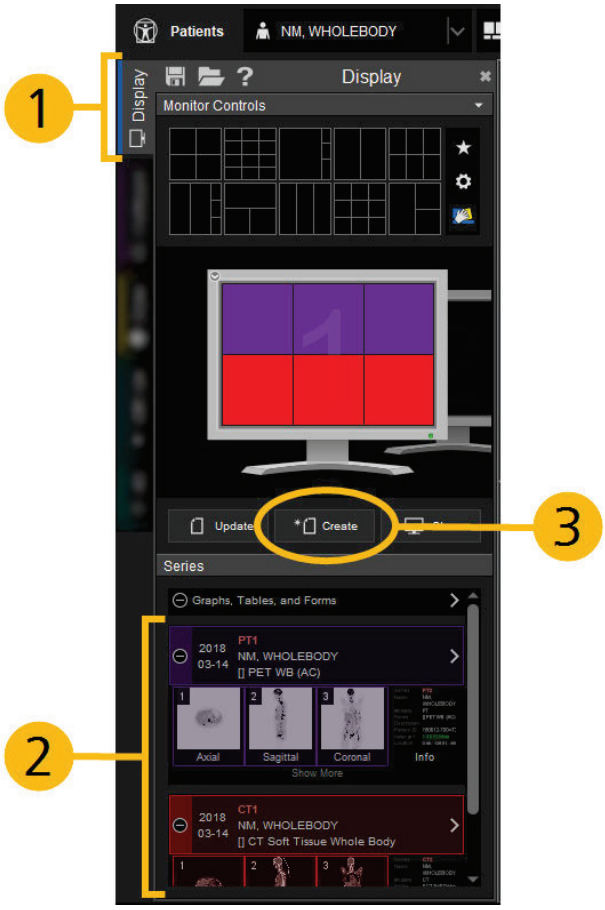
Overview

MIM® has numerous premade display layouts, also known as hanging protocols. You can also create, modify, and save your own display layouts. You can specify default display layouts to use with certain image types.

Tip: Saved display layouts can also be mapped into MIM Workflows™ so that the results are displayed exactly as you like. Please contact MIM Software Support at support.mimsoftware.com for assistance with this process.

Contents

Create a New Display Layout



Basic Steps

1. With images open in a session, click the **Display** tab to expand the Display sidebar.
2. Click the thumbnail of the series you want to add to your display, or drag and drop the thumbnail onto the preview monitor:
   - To add an entire row to the layout, click the title bar of the series.
   - To add only a single view to the layout (e.g., the axial view), click the thumbnail of that view.
   - You can add any number of series to the display layout.

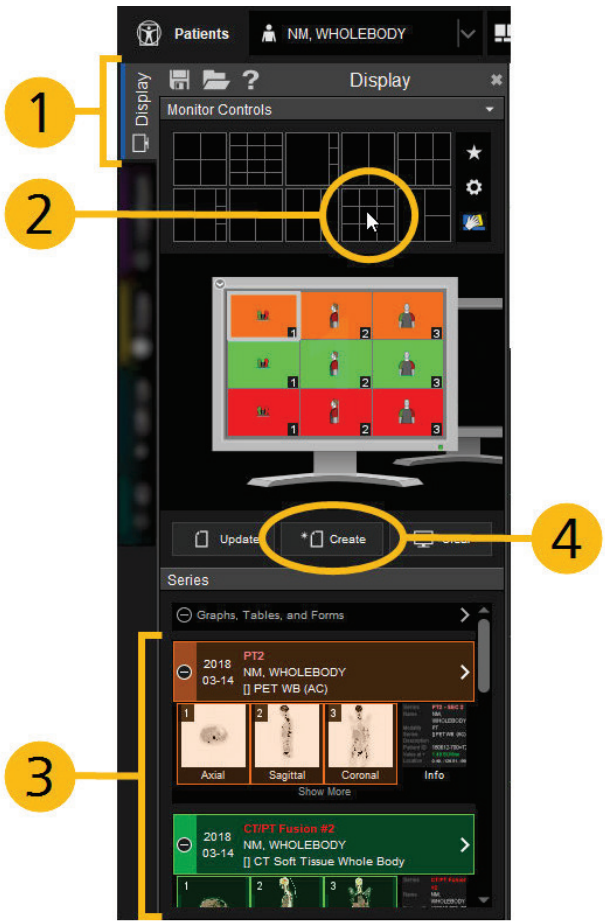
   The thumbnail is highlighted, and the corresponding color appears on the preview monitor to show where the series will be dispalyed.
3. Click the **Create** button below the preview monitor. A new page is created with the selected series.

Tip: If you don't see display layouts or the preview monitors, click **Monitor Controls** to expand the menu.

Additional Display Layout Options

- To see more data that can be added to your display, click **Show More** under the series thumbnails. Examples of available data include MIPs, DVHs, and dose constraint tables.
- If you use MIM on multiple monitors, multiple preview monitors appear in the Display sidebar. To add series to a display on a specific monitor, first click the corresponding preview monitor.
- To adjust the relative size of a particular series or view in your layout, hover over its thumbnail and use the scroll wheel of your mouse. The preview monitor updates accordingly.
- To replace your current display, rather than create a new display page, click **Update** instead of Create.

Use a Premade Display Layout



Basic Steps

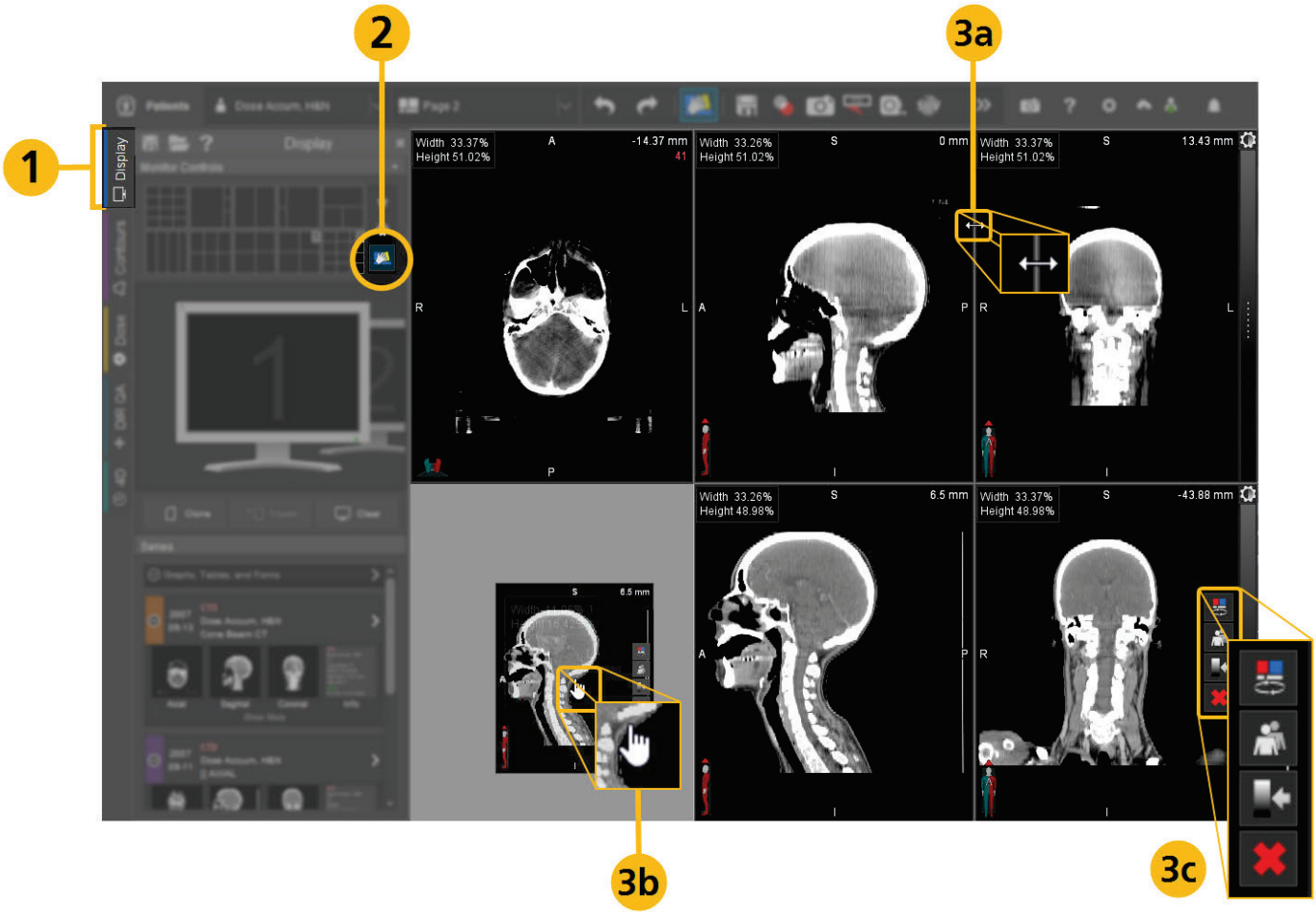
1. With images open in a session, click the **Display** tab to expand the Display sidebar.
2. Click a premade display layout at the top of the Display sidebar. The display layout appears on the preview monitor.
3. Click the thumbnail of the series you want to add to your display:
   - The display layout is filled from left to right beginning with the top row.
   - To add a series to the layout automatically, click the title bar of the series.
   - To add only a single view to the layout (e.g., the axial view), click the thumbnail of that view.

   The thumbnail is highlighted, and the corresponding color appears on the preview monitor to show where the series will be dispalyed.
4. Click the **Create** button below the preview monitor. A new page is created with the selected series and display layout.

Additional Tips for Working with Premade Display Layouts

- Multi-monitor display layouts are indicated by a small "1" in the upper-right corner. To add a multi-monitor display layout to all monitors at once, double-click the display layout.
- To view premade display layouts for a specific specialty (e.g., Radiation Oncology or Radiology), click the star ★ button near the top of the Display sidebar.
- To view all premade display layouts, click the gear icon ⚙ near the top of the Display sidebar. Use the plus ⊕ buttons and the minus ⊖ buttons to add and remove display layouts from the top of the Display sidebar.
- To replace your current display, rather than create a new display page, click **Update** instead of Create.

Adjust Your Current Display



1. With images open in a session, click the **Display** tab to expand the Display sidebar.
2. Click the **Adjust Protocol** tool near the top of the Display sidebar to activate the tool.
3. Use the following options to adjust the layout as desired:
    a. Left-click drag the borders of a viewport to resize the viewport.
    b. Left-click drag inside a viewport to rearrange or reposition the image.
    c. Hover in a viewport to see companion tools with more adjustment options. Hover over each button for more information.
4. Click the **Adjust Protocol** tool at the top of the Display sidebar to deactivate the tool.

> **Tip:** If you don't see the **Adjust Protocol** tool, click **Monitor Controls** to expand the menu.

Save a Display Layout

1. Click the save button in the upper-left corner of the Display sidebar.
2. In the **Save Hanging Protocol** window, enter a Protocol Name and click **Save**. The rest of the information in the window is filled automatically.

To find all saved display layouts, click the gear button near the upper-right corner of the Display sidebar. For more information, see Use a Premade Display Layout.

Set Default Display Layouts

1. Click the Settings button in the upper-right corner of MIM.
2. Select **General Preferences**.
3. In the General Preferences window, search for "**Default Protocols**" and select **Default Protocols** from the left-side menu.

6.1.8

4. In the Default Protocols window, select a default 2D protocol and a default 3D protocol from the available options.

Swap Series in Display Layouts

MIMTD-1756 • 06 Nov 2023

Overview

Use the following tools to replace a series in your display layout with a different series from the current session. This is useful, for example, if you want to quickly view a prior exam without changing your display layout.

PT/CT

MIM 7.3 and later: Use the **Switch PT/CT Series** tool as described below.

MIM 7.2 and earlier: Use the tools in the All Modalities section.

Switch PT/CT Series — Replace a PT/CT from one time point with a PT/CT from a different time point. This tool is also known as "PET Swapping."

Tip: This tool appears only if you are viewing a display that doesn't include all of the available PT/CT time points from your session.

Follow these steps to use the tool:

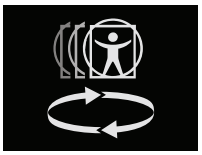
1. Hover in a viewport.
2. Click the **Switch PT/CT Series** button that appears at the top of the viewport.

3. Click the time point that you want to switch to. Your display updates to show the selected time point.

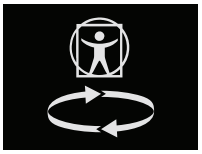
If you do not see the Switch PT/CT Series button at the top of your viewports, check the following:

- Ensure that you are viewing a display that does not include all of the available PT/CT time points from your session. If your display includes series from every time point, the Switch PT/CT Series button will not appear.
- Go to Settings >> **General Preferences** >> **Viewing** and ensure that **Show Switch PT/CT Series controls** is selected.

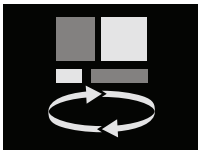
All Modalities



Swap Series — Replace a series or fusion group (i.e., the primary series of a fusion, the secondary series of a fusion, and the fusion itself) with another series or fusion group from the current session.



Swap Single Series — Replace a single series (i.e., an individual PT, CT, or fusion) with another single series from the current session.



Swap Viewports — Replace one view of one series with another view from the current session. For example, replace the axial view of one series with the axial view of another series.

Follow these steps to use **Swap Series**, **Swap Single Series**, or **Swap Viewports**:

1. Activate the desired tool from the toolbar, from the radial menu, or via keyboard shortcut:
   - To add the tools to your toolbar, click the double arrow button at the top of MIM, go to **Configure Toolbar...**, and click the checkbox next to the desired tools. For more information, see Access Tools: The Toolbar and the Radial Menu.
   - To add the tools to your radial menu, click the Settings button in the upper-right corner of MIM, go to **General Preferences** >> **Viewing** >> **Radial Menu**, and follow the instructions in the settings menu. For more information, see Access Tools: The Toolbar and the Radial Menu.
   - To add keyboard shortcuts for the tools, click the Settings button in the upper-right corner of MIM, go to **Keyboard Shortcuts**, and add a key binding next to the desired tools. For more information, see Set Keyboard Shortcuts.
2. If you activate the tool from the toolbar, follow the prompts to select the series, fusion group, or viewport that you want to replace.

   Tip: If you activate the tool from the radial menu or via keyboard shortcut, the viewport that you are hovering in determines which series, fusion group, or viewport will be replaced.

3. In the Swap Series or Swap Viewport window that appears, click the series, fusion group, or viewport that you want to replace the selected item with. Your display layout now includes the selected series.

Export Data from MIM®

MIMTD-613 • 19 Jul 2023

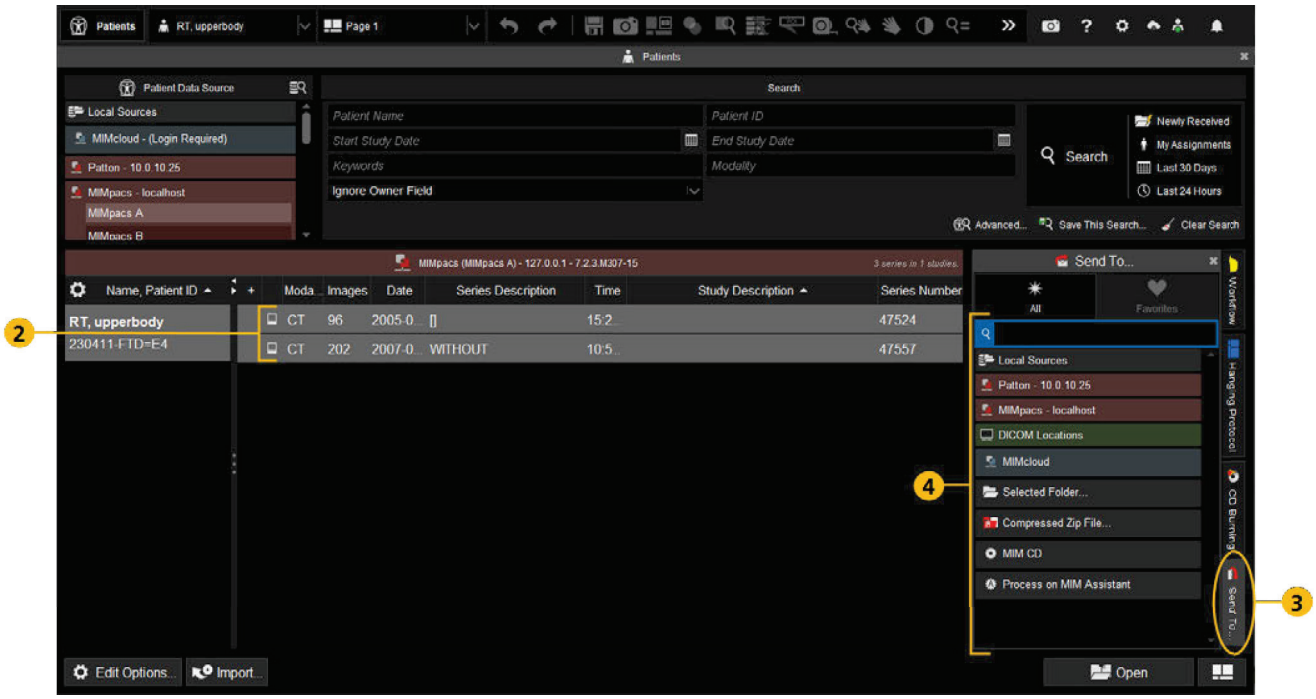
Overview

You can export data to a third-party location, burn data to a disc, send data to a folder, or create a zipped file.

Export Data

1. Search for the patient data you want to export

2. Select the patient on the left and then select individual series from the center of the screen.
3. Open the **Send To...** tab on the right side of the screen.
4. Click on the desired destination. *In MIM 7.4 and later*, you can search for a specific export destination using the search bar at the top of the Destinations section. *In MIM 7.3 and earlier*, this functionality is not available.



- If you're sending to a local patient list, MIMpacs list, or PACS, click the destination to send the data.
- If you're sending data to a **MIMcloud®** location, follow the prompts in the Notifications window.

- If you're sending data to a **MIM CD**, the **CD Burning** tab opens. Choose the desired options in the CD Burning tab and then click **Burn CD...**. Additionally, you can use the MIM CD option to send to a folder instead of a CD, similar to using the Selected Folder... option. The MIM CD option also lets you include a DICOM viewer with the exported data.

Related: See Burn Discs from MIM® for more information.

- If you're sending data to a **Selected Folder...**, browse to the desired file location.
- If you're sending data to a **Compressed Zip File...**, browse to the desired file location.

When DICOM data is exported from MIM to a folder, an initial folder is created and named with the month and year of the study (i.e., 2022-12_Studies). When the initial folder is opened, there are sub-folders with names that contain the patient name, patient ID number, modality, date of scan, time of scan, study description, series description, and number of slices in the scan. The individual DCM files are contained within these sub-folders. It is not possible to configure the file structure for DICOM exported from MIM.

Tip: You can favorite a destination so that it moves to the top of the list by clicking the ♡ next to each destination name.

Burn Discs from MIM®

MIMTD-1121 • 09 Aug 2023

Overview

You can export series from MIM to a CD/DVD, file location, or folder location. When burning to a disc, you can choose to include a copy of MIM CD along with the data. Use this option if you are giving the disc to a patient or to another party that does not have a DICOM viewer.

Related: Refer to Troubleshoot Burning Data to Discs if you encounter an error or are unable to complete the steps below to successfully burn a disc.

Prerequisites

- Data that exists on a local or MIMpacs™ patient list. If you want to burn data from MIMcloud® or a third-party PACS, first send the data to a local or MIMpacs patient list.
- A CD-R, DVD-R, or DVD+R disc. (CD-RW, DVD-RW, and DVD+RW disc types are not supported.)
- The correct drive letter entered in your MIM preferences. Go to Settings >> **General Preferences** and search for **"CD burning"**. Check the configured **Drive Letter**.

Burn a Disc from MIM

To burn a CD/DVD from MIM, follow these steps:

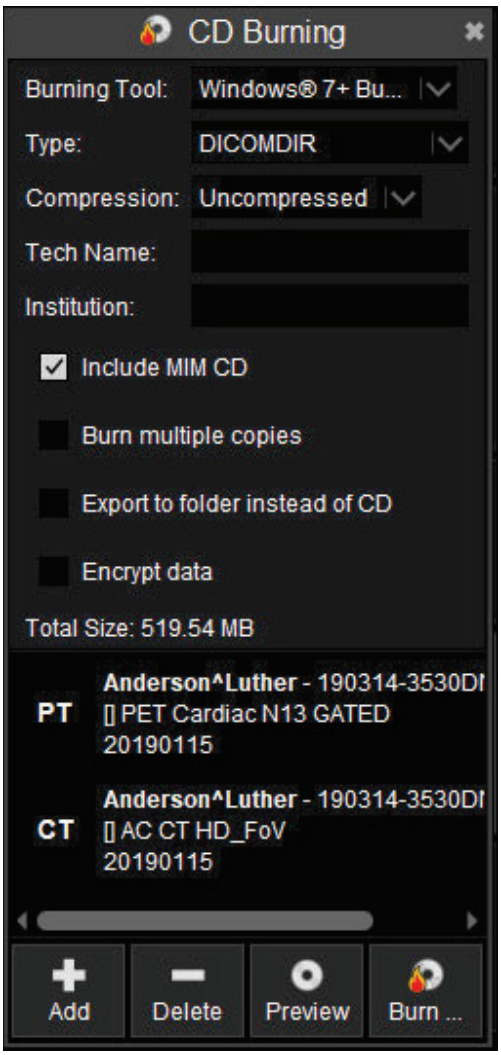
1. Search for and select the data you would like to burn from a local or MIMpacs patient list. See Find and Open Patient Data for more information.

   Tip: If you want to burn data from multiple patients or studies, or different searches, you can add data at a later step below.

2. Go to the **CD Burning** tab on the right side of the screen.

3. Click **Add** to add the data that you selected to list of data to be burned.



4. In most cases, keep the default **Burning Tool**, **Type**, and **Compression** settings. You may need to update these settings if burning initially fails or if the receiving system has specific needs. See Troubleshoot Burning Data to Discs for more information.
5. Enter a **Tech Name** and **Institution**.
6. Select **Include MIM CD** to include a DICOM viewer on the burned disc. If the receiving institution already has a way to view the DICOM, do not select **Include MIM CD**.
7. If you want to burn multiple discs that contain the same data, select **Burn multiple copies**. After the first disc is burned, MIM will prompt you to burn another copy.
8. Select **Encrypt data** if you want to encrypt the data. With this option, MIM will prompt you to configure a password when you burn the disc. You need to provide that password to the recipient so that they can access the data.

9. If there are additional series that you want to include, select them and then click the **Add** button. You can also **Delete** series from the list of series to be burned.
10. *If you want to burn a disc:*
    i. Insert a CD-R, DVD-R, or DVD+R into the disc drive.
    ii. Click **Burn...**.

    If you want to send the data to a folder or file location:
    i. Check **Export to folder instead of CD**.
    ii. Click **Export…** and browse to the desired destination.

Tip: If you frequently burn discs, you can favorite **MIM CD** as a destination by clicking the ♡ next to it. This moves it to the top of the list alongside other favorite destinations.

Import MIMneuro Normals

MIMTD-850 • 16 Aug 2023

Overview

6.1.8

MIMneuro® Normals are a collection of scans that have been reviewed by a qualified physician and found to be normal. These scans are used for comparison in MIMneuro processing. For detailed information on the acquisition parameters and the types of scans included, please see the Appendix.

Your organization has a few options for how to import the MIM normals data, as described below.

Important: Normals must be imported on every client workstation.

Important: It is strongly recommended that you validate normal images from your institution against the MIMneuro Normals before clinical use. See Validate Normals for details.

Contents

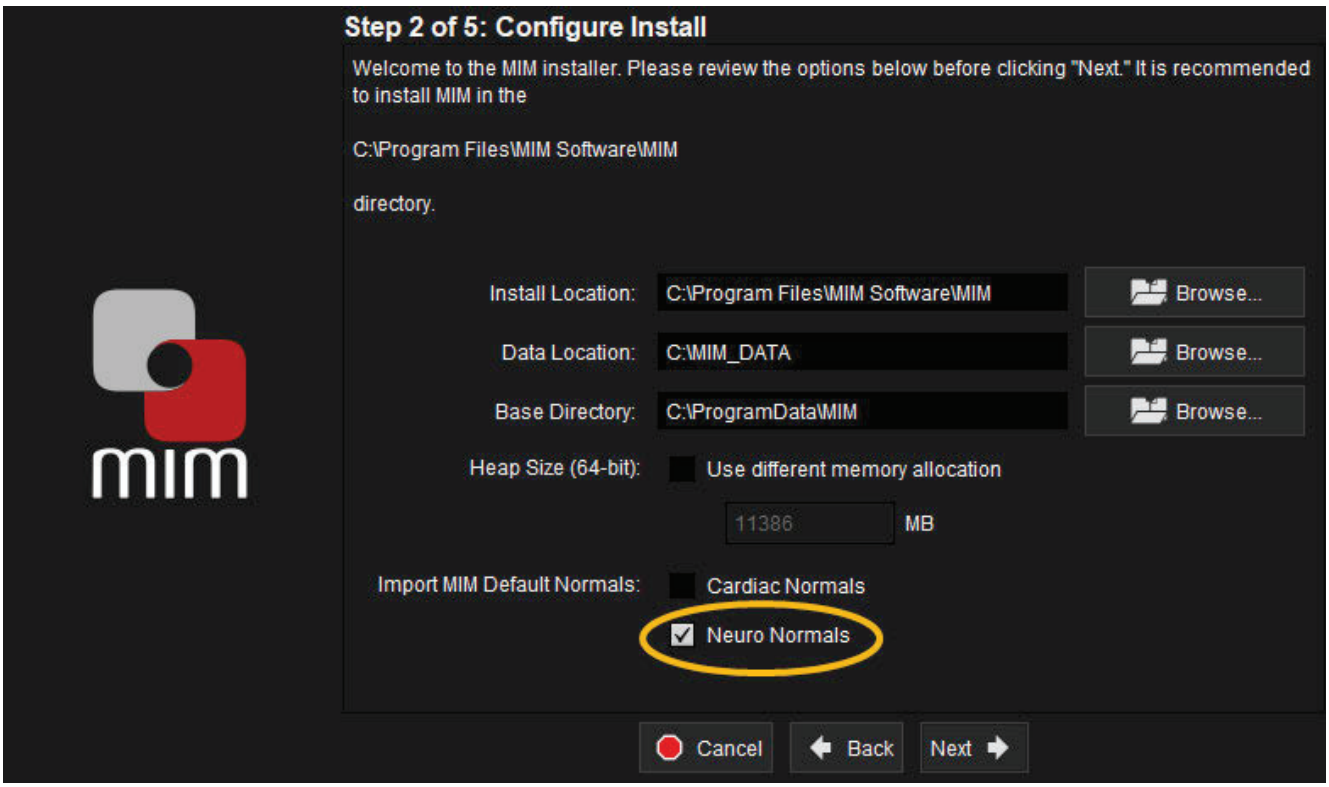
Import Normals During Install or Upgrade (MIM 7.3 and Later)

MIM 7.3 and later: You can import the normals database during install or upgrade. If you install or upgrade MIM on client workstations using MSI, you can include normals with the software install instead of manually performing these steps. *MIM 7.2 and earlier*: These steps do not apply, and you need to use a different import option.

These steps are for Windows® workstations only. If you are using a Mac®, you need to use the Import Normals from the Internet or Import Normals from a File option instead.

1. Launch the MIM installer.
2. During step 2 of the installation, select **Neuro Normals**.

3. Click **Next** to proceed with the installation.



Import Normals from the Internet

If the machine has an internet connection, import the latest normals directly from the MIM website. Complete the following steps:

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Click **Import Neuro Normals**.
3. In the Notifications window, ensure that **Import from Internet** is selected, then click **OK** to begin the import.

When you see the message *The neuro normal database has been imported successfully* in the Notifications window, the normals are ready to validate.

Import Normals from a File

If the machine does not have an internet connection or if you need to install a specific version of the MIMneuro Normals (e.g., to maintain consistency in a research study), import the normals manually from a file. Complete the following steps:

1. On an internet connected computer, go to https://www.mimsoftware.com/download/mim and find the appropriate version of the MIMneuro Normals.

2. Download the appropriate version of the MIMneuro Normals. Ensure that you save the normals to a location that can be accessed by the computer you want to import to.
3. Open MIM on the computer where you want to import the normals.
4. Click the Settings button in the upper-right corner of MIM.
5. Click **Import Neuro Normals**.
6. In the Notifications window, ensure that **Import from local file** is selected, then click **OK**.
7. In the window that opens, browse to the zipped normals file. You do not need to unzip the file. Select the file and click **Open**.

When you see the message *The neuro normal database has been imported successfully* in the Notifications window, the normals are ready to validate.

Validate Normals

To validate the MIM normals set, compare at least five normal scans acquired from each relevant camera to the MIMneuro Normals database to ensure that your images are sufficiently similar to the MIM normal data.

If you find a discrepancy, you may need to adjust reconstruction settings to appropriately match the MIMneuro normal data. Alternatively, you can create a custom normal database of images from your institution. Refer to Create a Custom Neuro Normals Database for more information.

When validation is complete, communicate to users that the normals are now ready for use. As needed, repeat the steps above to import the normals on additional workstations.

Adjust Images

Adjust Image Color Tables

MIMTD-611 • 27 Jun 2023

You can change Color Tables (Look Up Tables) in MIM® by adjusting the default settings, or make changes individually in an open session.

Set Default Color Tables

Tip: To share and standardize these settings across your organization, a MIM administrative user should make the additions or updates while logged in to the **Edit Site Defaults** login mode. See Update Default Settings for Users for prerequisites and instructions.

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**color tables**".
3. Click **Color Tables** on the left side and set color tables for various modalities. This setting applies starting with the next session.

Fusion Color Tables

By default, the secondary image in a fusion is set to the Hot Metal color table.

If desired, you can assign different default colors to different pairs of fused images:

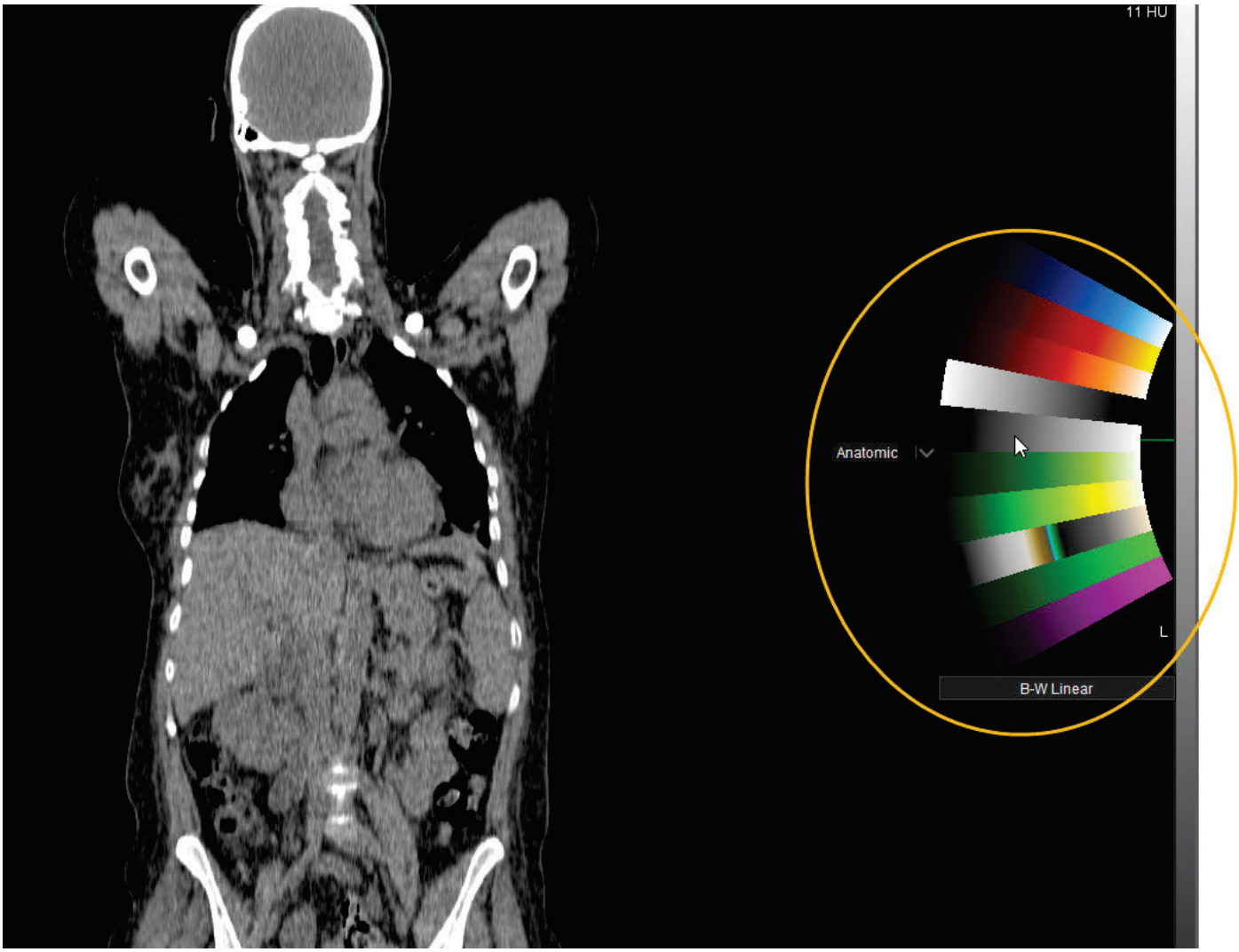
1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**color tables**".
3. Click **Fusion Color Tables** on the left side.
4. Click the **Add** button to create new pairs. This setting applies starting with the next session.

Adjust Color Tables in a Session

You can change the color table for an image in an open session:

1. Click on the contrast bar.
2. Hover over each color table to preview it on the image. Use the dropdown menu to the left of the color tables to reveal different options.
3. Click on a color table to apply it to the image.

Note: Fusion images contain two contrast bars, one that controls the primary image's color and one that controls the secondary image's color.



Adjust Image Contrast

MIMTD-612 • 24 Aug 2023

Overview

MIM® has a variety of automatic and manual contrast adjustment methods for different modalities and tissue types. You can also create your own contrast presets, which is helpful when matching contrast to other systems.

Contents

Adjust Contrast with the Mouse (MIM 7.3 and Later)

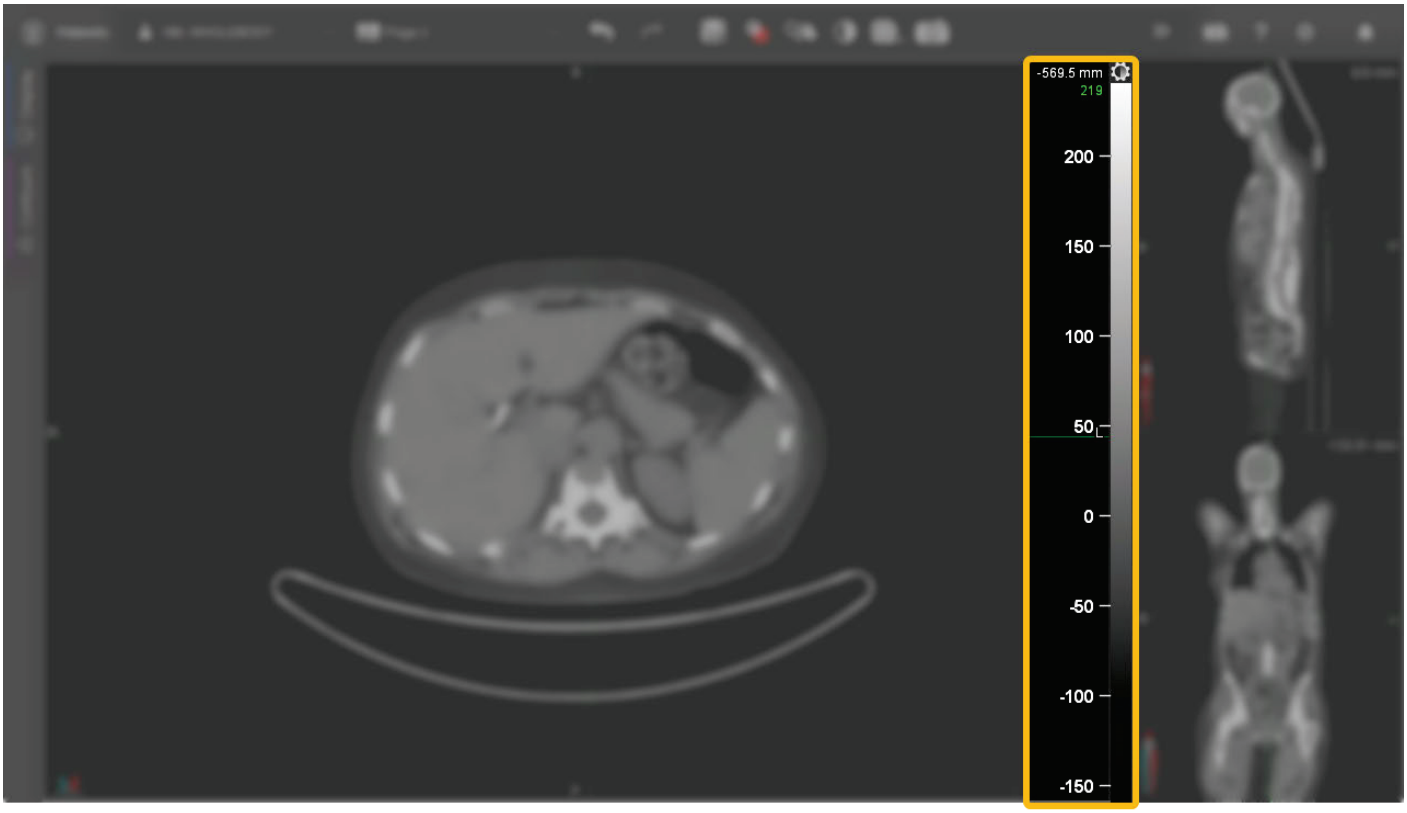
To adjust the contrast with the mouse, middle-click drag in any viewport. In MIM 7.2 and earlier, this functionality is not available.

- Drag up and down to change the window width.
- Drag left and right to change the window level.

Tip: You can configure any of your mouse buttons to adjust contrast. For more information, see Configure Mouse Behaviors.

Adjust Contrast with the Contrast Bar

The contrast bar appears on the right side of an image. Hover over the contrast bar to see the values.

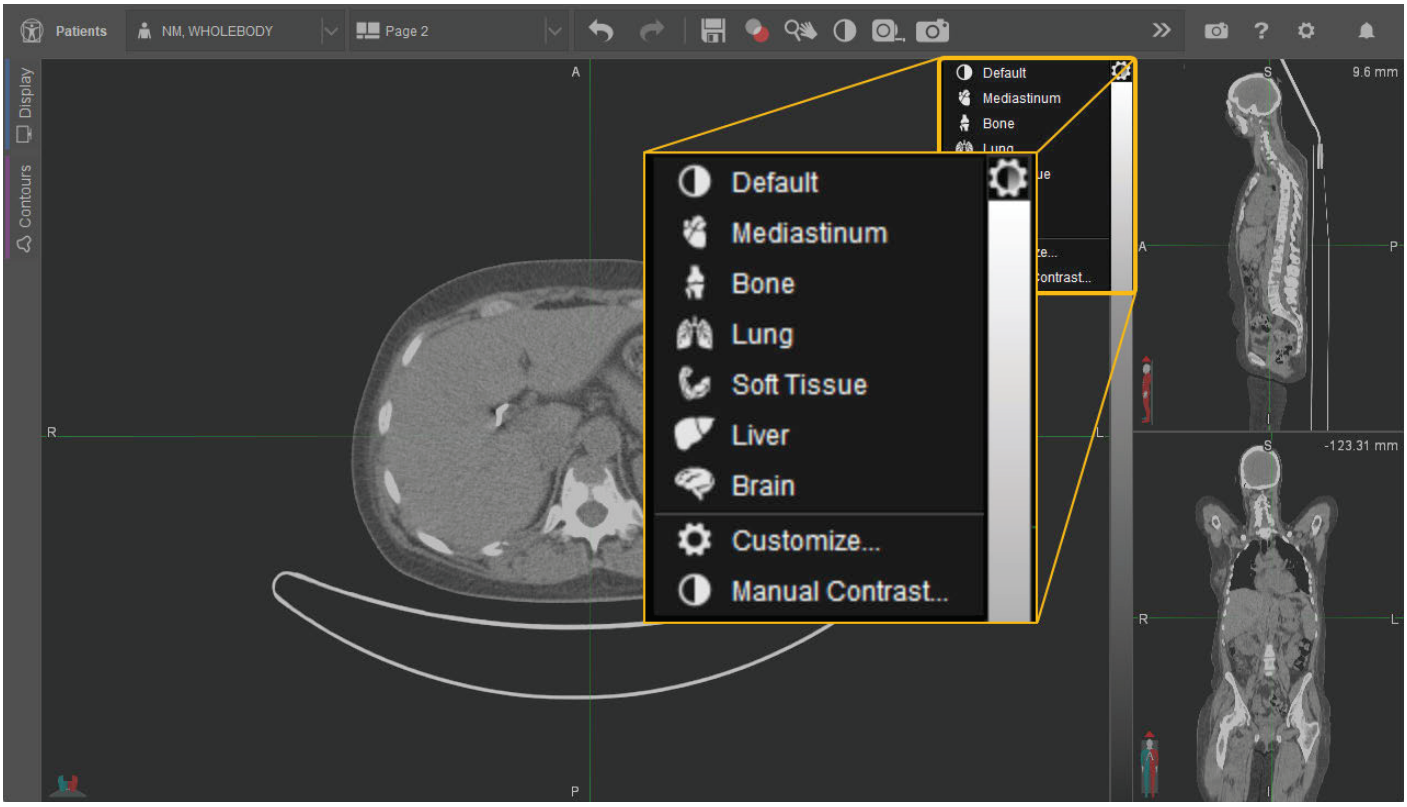


See the table below for possible contrast adjustments with the contrast bar:

Contrast Adjustment	Action
Adjust the window level	Left-click drag left/right on the contrast bar
Adjust the window width	Left-click drag up/down on the contrast bar
Reset the contrast	Right-click the contrast bar

Apply a Contrast Preset

Click the contrast preset button above the contrast bar to access the contrast preset menu.



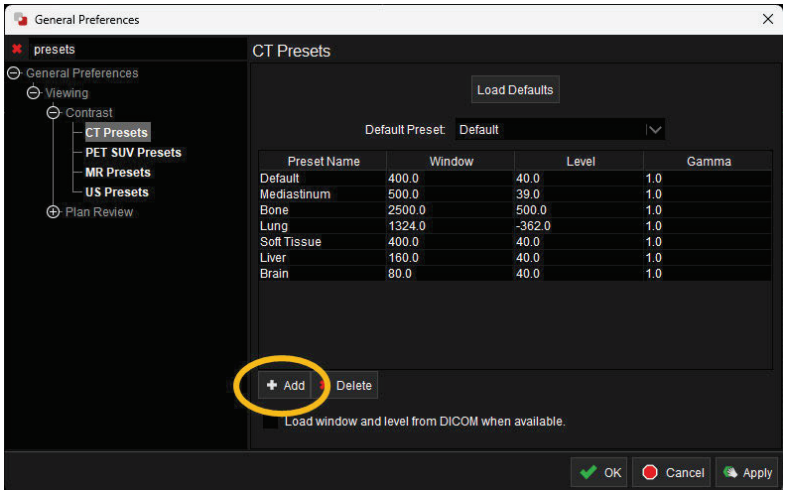
Choose a default contrast preset from the menu. The modality of the image determines which options are available.

Create Your Own Contrast Presets

Adjust MIM-provided presets or create your own presets. This is helpful when matching contrast to other systems.

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**presets**". Select the desired preset modality from the left side.

- To adjust an existing preset, double-click any value to change it.
- To create a new preset, click **Add**, then adjust the values as desired.



Tip: If you use a preset often, map it to a keyboard shortcut. For more information, see Set Keyboard Shortcuts.

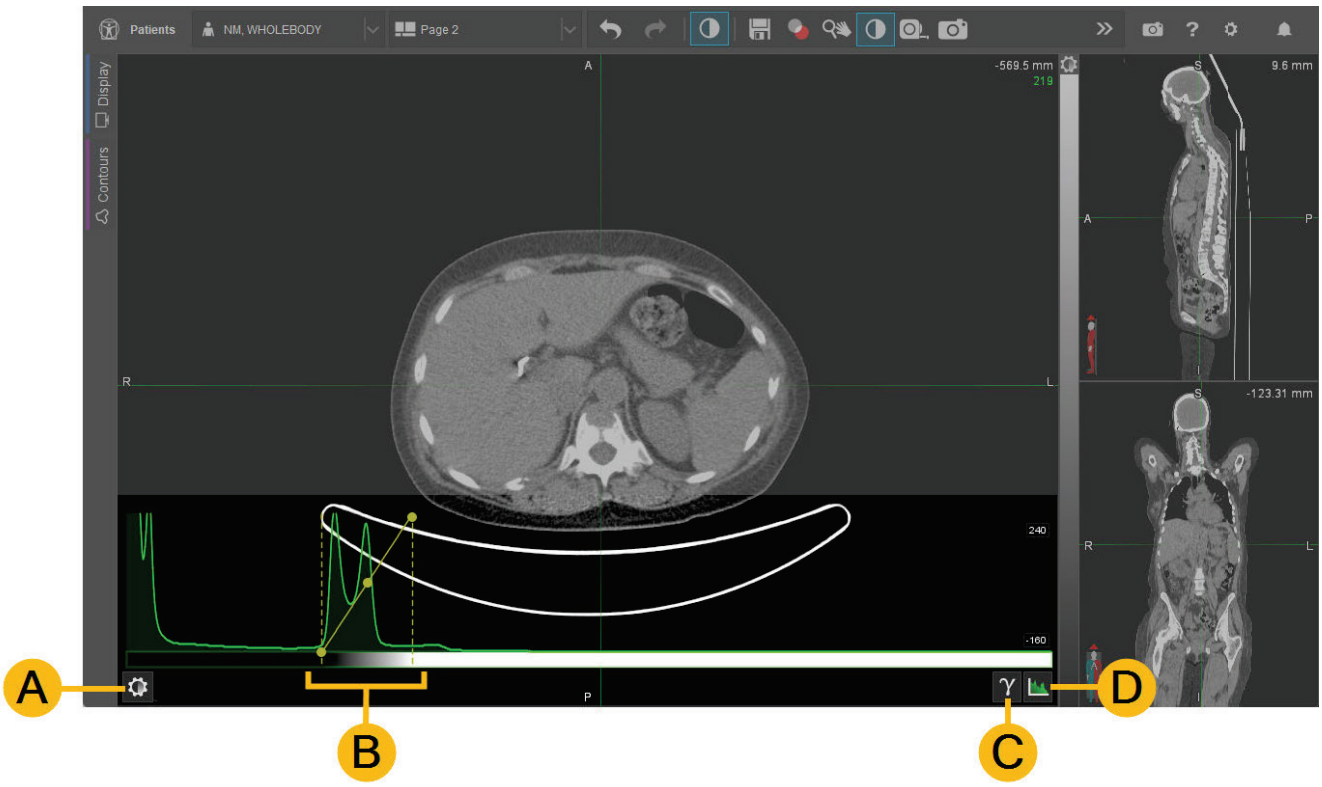
Tip: Image contrast, including presets, can also be applied in MIM Workflows™.

Adjust Contrast with the Contrast Tool

Activate the **Contrast** tool from the toolbar, radial menu, or with the W keyboard shortcut.

- To define the contrast window based on a region of interest, right-click drag on the image to define the region of interest.

- To access additional functions of the Contrast tool, hover in any viewport:



A. Contrast Preset Menu
B. Contrast Histogram
C. Gamma Correction Adjustment
D. Toggle the Contrast Histogram

Read the Contrast Histogram

The green line shows the values present in the image.

- In the screenshot above, the green line corresponds to the HU values of the CT.
- On a PT image, the green line corresponds to the SUV values of the PT.

The yellow dashed lines and dots form the contrast window. See the table below for possible contrast adjustments with the contrast histogram:

Contrast Adjustment	Action
Adjust the upper and lower contrast values	Left-click drag the yellow dots on each side

Contrast Adjustment	Action
Adjust the window center	Left-click drag left/right on the center point or anywhere inside the yellow lines
Adjust the window width	Left-click drag up/down anywhere inside the yellow lines

Adjust Contrast Bounds (MIM 7.3 and Later)

The color of the dots on the contrast histogram indicates whether the contrast bounds are locked.

Dot Color	Indication
Red	The bound is locked and cannot be adjusted
Yellow	The bound can be adjusted, but not beyond the minimum or maximum value for the series
Blue	The bound can be adjusted beyond the minimum or maximum value for the series

You can adjust the bound locks. In MIM 7.2 and earlier, this functionality is not available.

- To lock an upper or lower contrast value, click the corresponding yellow dot. It will turn red, indicating that it is locked and cannot be edited.
- To expand the upper or lower bound beyond the minimum or maximum value for the series, follow these steps:
    i. Lock the other bound, turning the dot red.
    ii. Click the dot for the bound you want to adjust. It will turn blue, indicating that it can be adjusted beyond the defined range of data.
    iii. Left-click drag to adjust the bound.

Tip: For PET images, the lower contrast bound is locked to zero by default. See the steps below to change this behavior.

Various preferences control these bounds and the lock behavior. To adjust these settings, follow the steps below:

1. Click the Settings button in the upper-right corner of MIM. .
2. Go to General Preferences and search for "**contrast**". Select **Contrast** on the left side.

3. If desired, deselect **Load PT or NM with lower contrast level locked**.
    - With this preference disabled, the lower contrast level is unlocked and can be adjusted (yellow), but not below the series minimum.
    - To adjust the lower contrast bound beyond the series minimum, either:
        - Lock the upper bound (click to make it red) and then click the lower bound (to make it blue). The lower bound can then be adjusted.
        - Deselect **For functional modalities, limit the contrast lower bound to the series minimum**. With this preference disabled, the lower bound will always be fully adjustable (a blue dot).

4. If desired, deselect one or more of the preferences that limit the contrast bound to the series maximum/minimum.

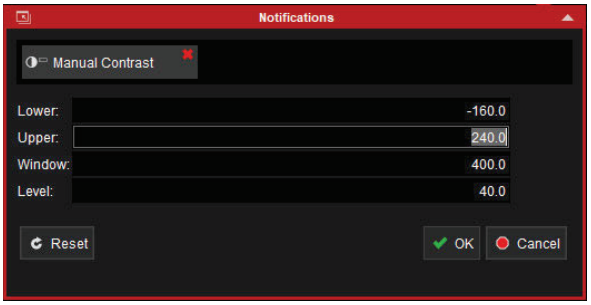
    For example, deselect **For functional modalities, limit the contrast upper bound to the series maximum**. The upper bound will be unlocked and you will be able to extend the bound above the series maximum.

Specify Manual Contrast Values

1. Activate the **Manual Contrast** tool from the toolbar or by clicking on the contrast preset menu and selecting **Manual Contrast...**.
2. *If multiple series are visible on the page,* use the **Select this series** button to choose the image you want to adjust.
3. Enter values for the **Lower**, **Upper**, **Window** (width), and **Level** (window center).

> **Tip:** The parameters automatically update as needed as you make changes (e.g., so that the window center always remains equidistant from the lower and upper values).

4. Click **OK** to save the changes and close the window.



Tip: If you regularly set the contrast manually, the Manual Contrast tool can be set to a keyboard shortcut. For more information, see Set Keyboard Shortcuts.

Create a Fusion Manually

MIMTD-620 • 21 Dec 2023

Overview

A fusion produces a link between two series that lets you localize and scroll on both series simultaneously, transfer contours, and more.

Contents

Create a Fusion

To manually create a fusion, follow these steps:

> **Tip:** When opening a series (e.g., a PET/CT series) it is possible a fusion is created automatically by MIM®.

1. Open or create a session with multiple series displayed on the same page.
2. Activate the **Create Fusion** tool from the top toolbar.

> **Related:** For more information, see Access Tools: The Toolbar and the Radial Menu.

3. Click the **Select this series** button for the series that you want to be the primary series (see Primary vs. Secondary Series for more information).
4. *If only one other series exists on the page*, MIM automatically selects it as the secondary series.

   If multiple other series exist on the page, click the **Select this series** button for the series that you want to be the secondary series (see Primary vs. Secondary Series for more information).

   A fusion is created and appears in a new row at the bottom of the current page.

5. If necessary, make adjustments to the fusion.

Related: See Adjusting Fusions for more information.

Primary vs. Secondary Series

The primary series in a fusion is the series that remains unaltered when a fusion is performed. Typically, this series is:

- The most current time point out of the two series
- The CT in a PET/CT study

The secondary series in a fusion is the series that is adjusted via rotation and translation to align with the primary series.

Break Spatial Links To Create Independent Fusions

If you have series that were acquired together (e.g., two MR sequences) and you fuse each MR to your plan CT, adjustments to one fusion (MR1/CT) affect the other fusion (MR2/CT). This is because the MR2/CT fusion preserves the pre-existing acquisition link between MR1 and MR2. You can break the pre-existing link so that adjustments to the MR1/CT fusion do not affect the MR2/CT fusion.

If you want to adjust the two fusions separately, follow these steps:

1. Break the link between the two MR series.

   Tip: Ensure you break the links between the MR series before fusing to the CT.

   i. Activate the **Link Manager** tool.

   Related: If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

   ii. Hover over any series. The Link Manager button appears in the center at the top of the viewport.

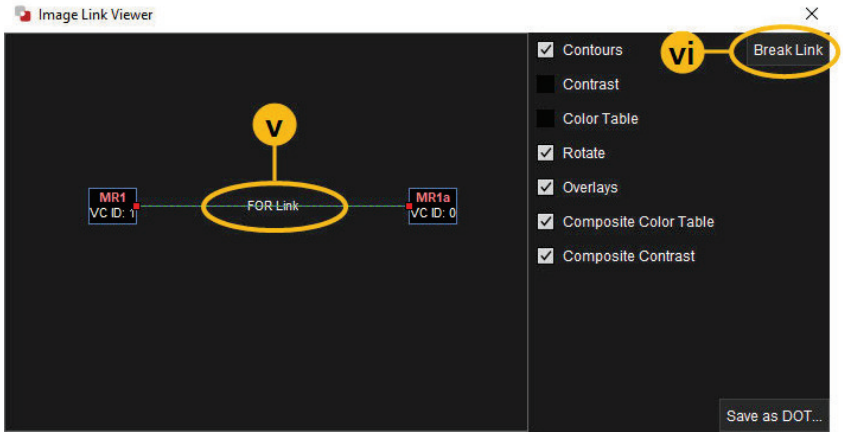
   iii. Click the **Link Manager** button in the viewport.

   iv. Select **Show Links…**. The Image Link Viewer window opens.

   Tip: You may need to reposition the series in the Image Link Viewer window to more easily visualize the links.

   v. Click the link (shown as a line) between the two MR series.

vi. Click **Break Link** in the upper-right corner of the window.



vii. When finished, click the X to close the Image Link Viewer window.

2. Fuse MR1 to the CT.
3. Fuse MR2 to the CT.

Create Multiple Fusions with the Same Series

Tip: If you would like to automate this process using a MIM Workflow™, please speak with your MIM Site Development Manager or contact MIM Software Support at support.mimsoftware.com.

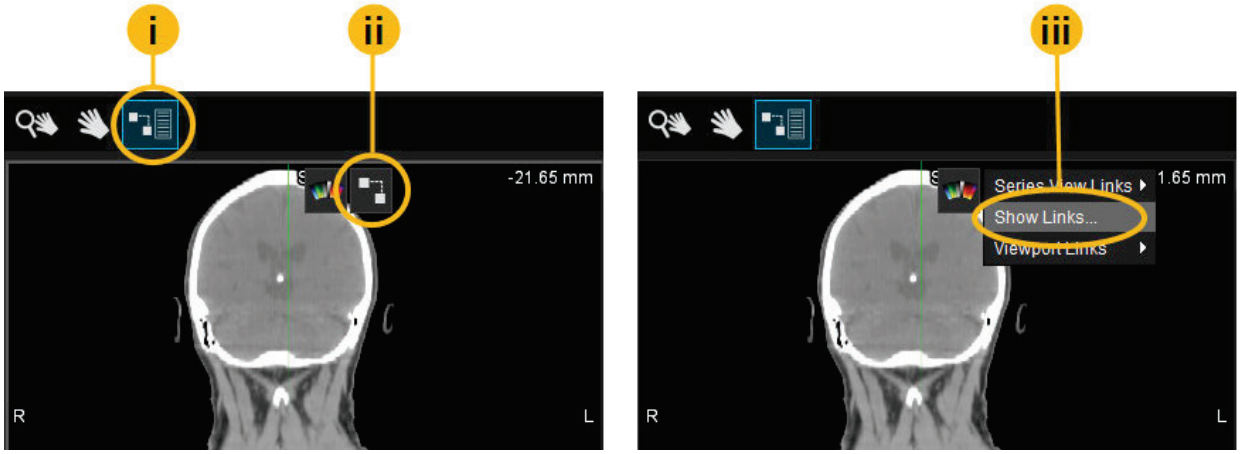
You can create multiple, but separate fusions. For example, you may want to visualize different fusions as part of the pre-planning process.

To create multiple separate fusions between the same two series, follow these steps:

1. Open the two series in a session (e.g., CT1 and CT2).
2. Return to the patient list, and double-click on the second series (the series that will be the secondary series in the fusion). A second copy of the series (CT2a) opens in the session.
   Alternatively, you can generate a second copy of the series using the Scale Image Intensity tool:
   i. Activate the **Scale Image Intensity** tool. (To find the tool, click the button at the top of MIM to search all tools.)
   ii. Select series CT2.
   iii. Enter 1 for the **Scale Factor** to create a copy of the series (CT2a).
3. Break the link between CT2 and CT2a.
   i. Activate the **Link Manager** tool.

Related: If you use this tool regularly, you can add it to your toolbar for easy access. For more information, see Access Tools: The Toolbar and the Radial Menu.

ii. Click the **Link Manager** button in the viewport.

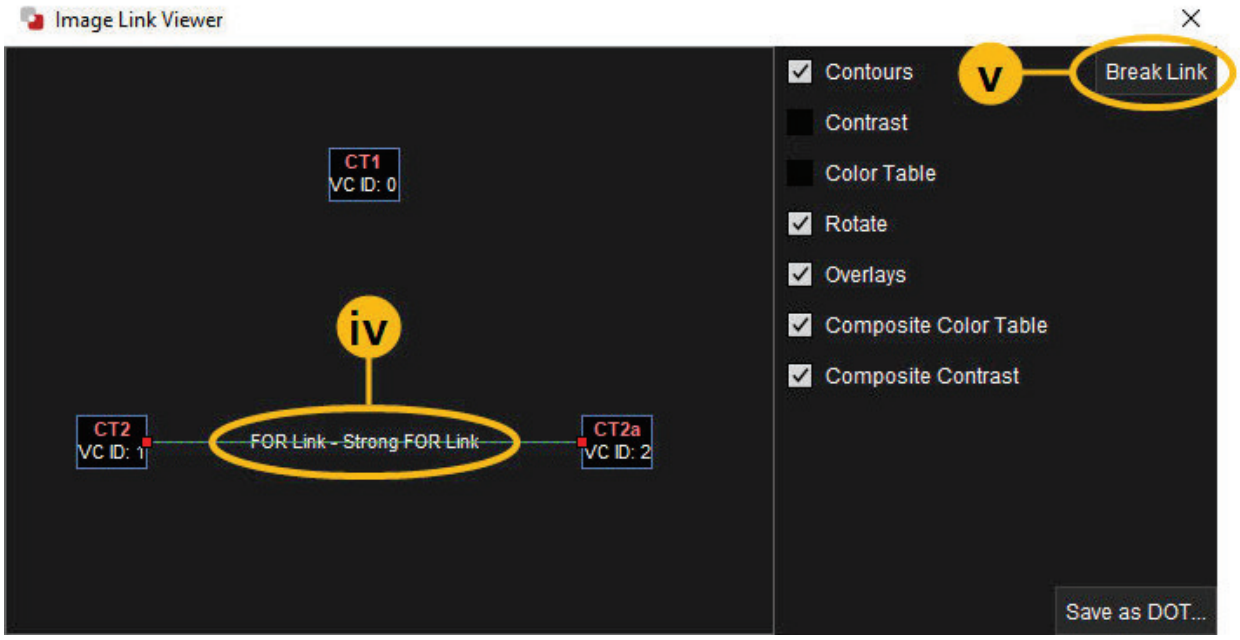


iii. Click **Show Links…**. The Image Link Viewer window opens.

Tip: You may need to reposition the series in the Image Link Viewer window to more easily visualize the links.

iv. Click the **FOR Link - Strong FOR Link** between CT2 and CT2a in the Image Link Viewer window.

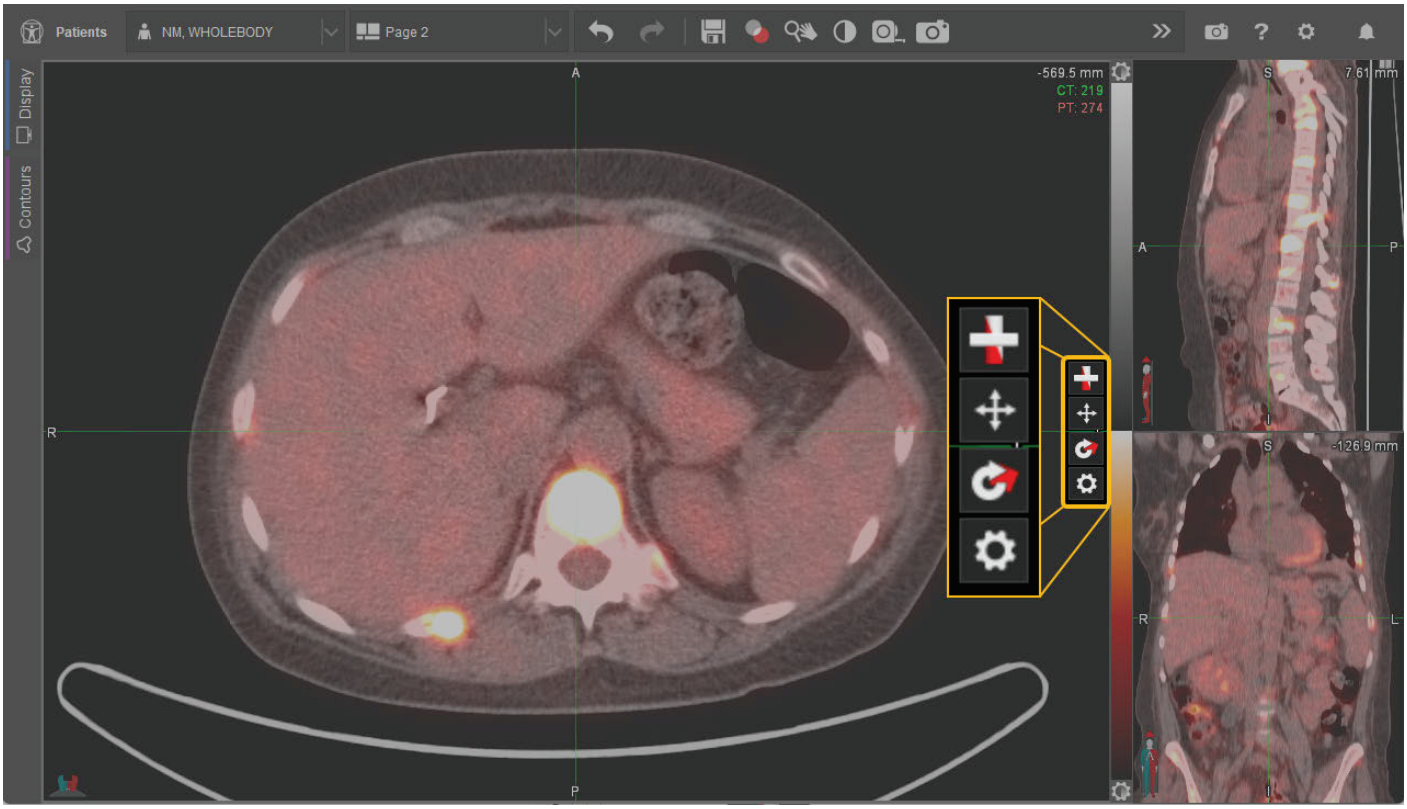
v. Click **Break Link** in the upper-right corner of the window.



vi. When finished, click the X to close the Image Link Viewer window.

4. Create and adjust the fusions.
   i. Fuse the primary and the secondary series (CT1 and CT2).
   ii. Create a second fusion between the primary and the copy of the secondary series (CT1 and CT2a).
   iii. Adjust the fusions as desired.

Show/Hide the Fusion Companion Tools



By default, the fusion companion tools always appear when hovering in a fusion viewport. To toggle the fusion companion tools on and off within a session, you can create a keyboard shortcut.

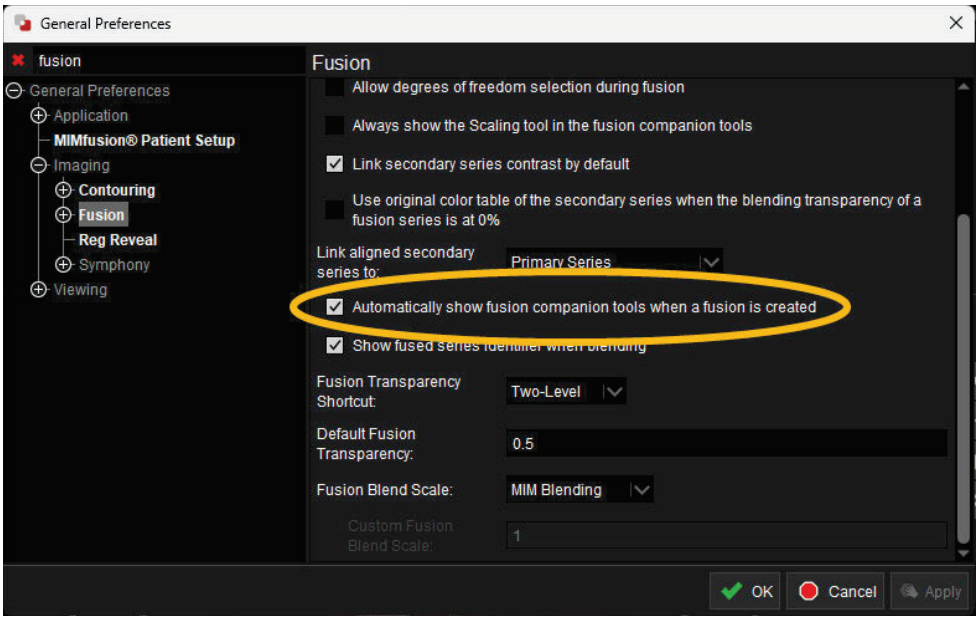
Related: For instructions on configuring keyboard shortcuts, see Set Keyboard Shortcuts.

The default behavior can also be changed. This is helpful if a viewport size is very small or zoomed in and the fusion companion tools are obstructing the image.

To hide the fusion companion tools by default, follow the steps below:

1. Click the Settings ⚙ button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion**". Select **Fusion** on the left side.

3. Deselect **Automatically show fusion companion tools when a fusion is created**.



4. Click **OK** to save the changes and close the window.

Tip: When changed, this setting takes effect in any open sessions that include a fusion.

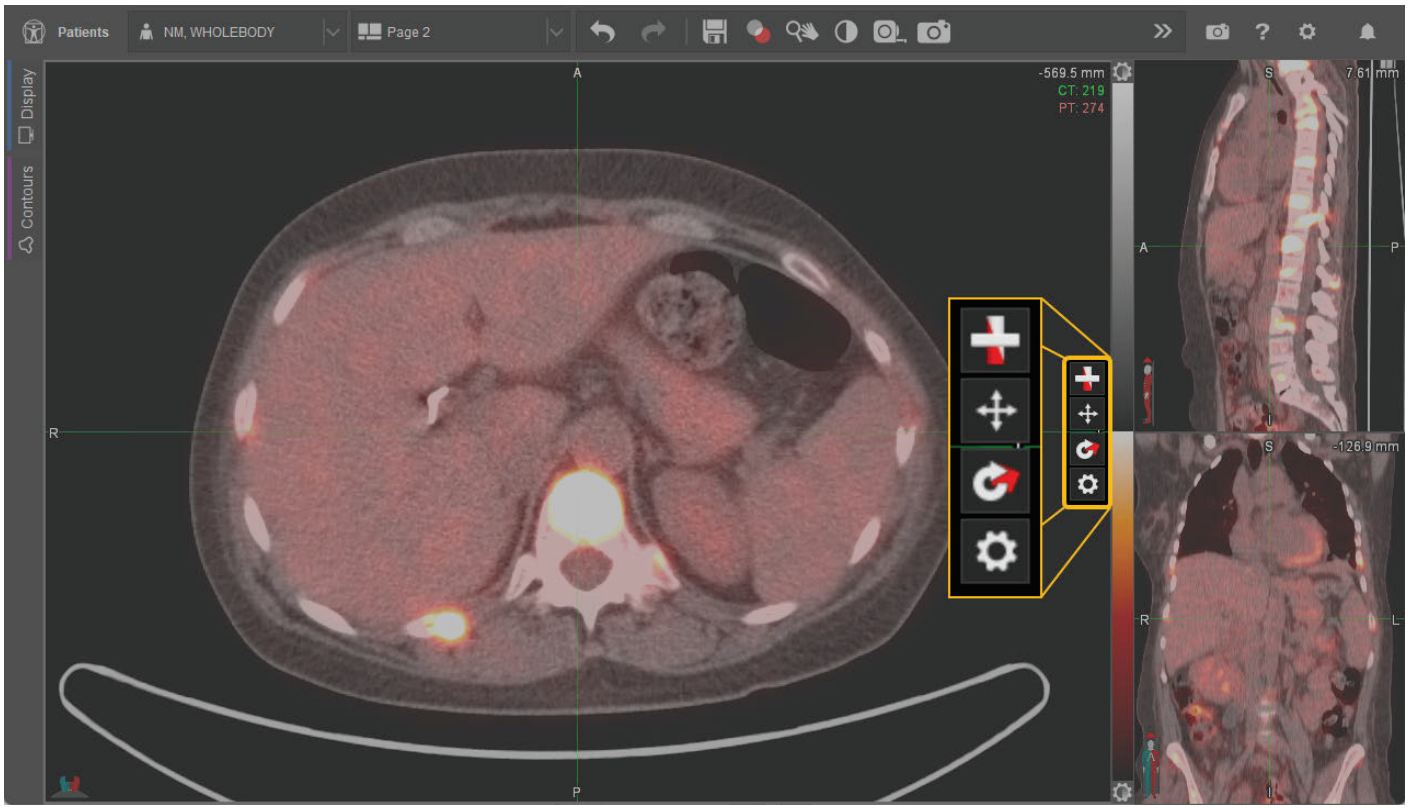
Tip: Your preference to show/hide fusion companion tools is not included when you save a session. If a saved session is opened by another user, the fusion companion tools are shown or hidden according to that user's preference.

Adjust Fusions Manually

MIMTD-621 • 02 Jan 2024

Overview

When you hover over a fusion viewport in any plane, MIM® displays companion tools on the right side. Use these tools to adjust the alignment of the two images. Fusions are typically done automatically when using a workflow, and you're prompted to review and make adjustments as desired.

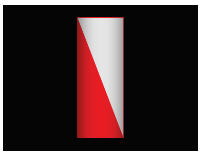


You can automatically show or hide these companion tools. For more information, see Configure Fusion Settings.

Related: For information about optimizing fusions automatically, see Optimize Fusions Automatically.

Contents

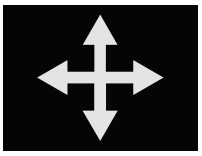
- Rotate



Blend

- Left-click drag up/down to blend between the primary series and secondary series.
- Right-click the Blend tool to reset the blend.

> **Tip:** Press the Tab key on your keyboard to toggle between the primary series and blend.



Translate

- Left-click drag to move the secondary series up/down or left/right to better align with the primary.
- Double-click on the tool to automatically rerun rigid assisted alignment.
- Right-click the Translate tool to reset the original position of the series.
- Use keyboard shortcuts to fine-tune the adjustment. Ensure the Translate tool is still activated:

	Large Adjustments	Small Adjustments	Very Small Adjustments
Windows®	Ctrl+arrow keys	Shift+arrow keys	Alt+arrow keys
macOS®	Command+arrow keys	Shift+arrow keys	Option+arrow keys

> **Tip:** To view and manually specify the exact translation in millimeters in the X, Y, and Z directions, use the **Edit Fusion Alignment Translation** tool. To access the tool, add it to your fusion settings menu. For more information, see Configure Fusion Settings.

Rotate

- Left-click drag to rotate the secondary series around the center of the primary series.

Tip: Drag straight up/down or left/right for best performance. Moving the mouse in a circular fashion results in erratic movements.

Tip: If desired, you can change the rotation center to the secondary series center, isocenter, DICOM origin, or localization point via **Settings** >> **General Preferences >> Imaging >> Fusion**.

- Right-click the Rotate tool to reset the original position of the series.

Tip: To view and manually specify the exact rotation in degrees in each plane, use the **Edit Fusion Alignment Rotation** tool. To access the tool, add it to your fusion settings menu. For more information, see Configure Fusion Settings.

Optimize Fusions Automatically

MIMTD-1724 • 17 Oct 2023

Overview

MIM® has many automatic tools and methods that let you adjust the alignment of two images. Images can be aligned by a specific region of interest, and with or without a pre-existing link.

Related: For information about adjusting fusions manually, see Adjust Fusions Manually.

Tip: Fusions are typically done automatically when using a workflow, and you're prompted to review and make adjustments as desired.

Contents

Run Rigid Assisted Alignment vs. Reset Fusion Alignment

Rigid Assisted Alignment is run when you use the **Create Fusion** tool to register two images.

If there is a pre-existing link between two series, MIM uses that link to generate a fusion. A pre-existing link results from:

- A shared Frame of Reference (FOR) between two series (e.g., when images are acquired together on the same scanner).
- A REG file that links the two images. REG files contain information that dictates how two images are aligned, and do not contain any image data.
- A link to another series. For example, if Series A and Series B share a FOR, and Series A is fused to Series C (which has a different FOR), Rigid Assisted Alignment runs. Then, if Series B is fused to Series C, the existing link between Series A and Series C is used for the new fusion.

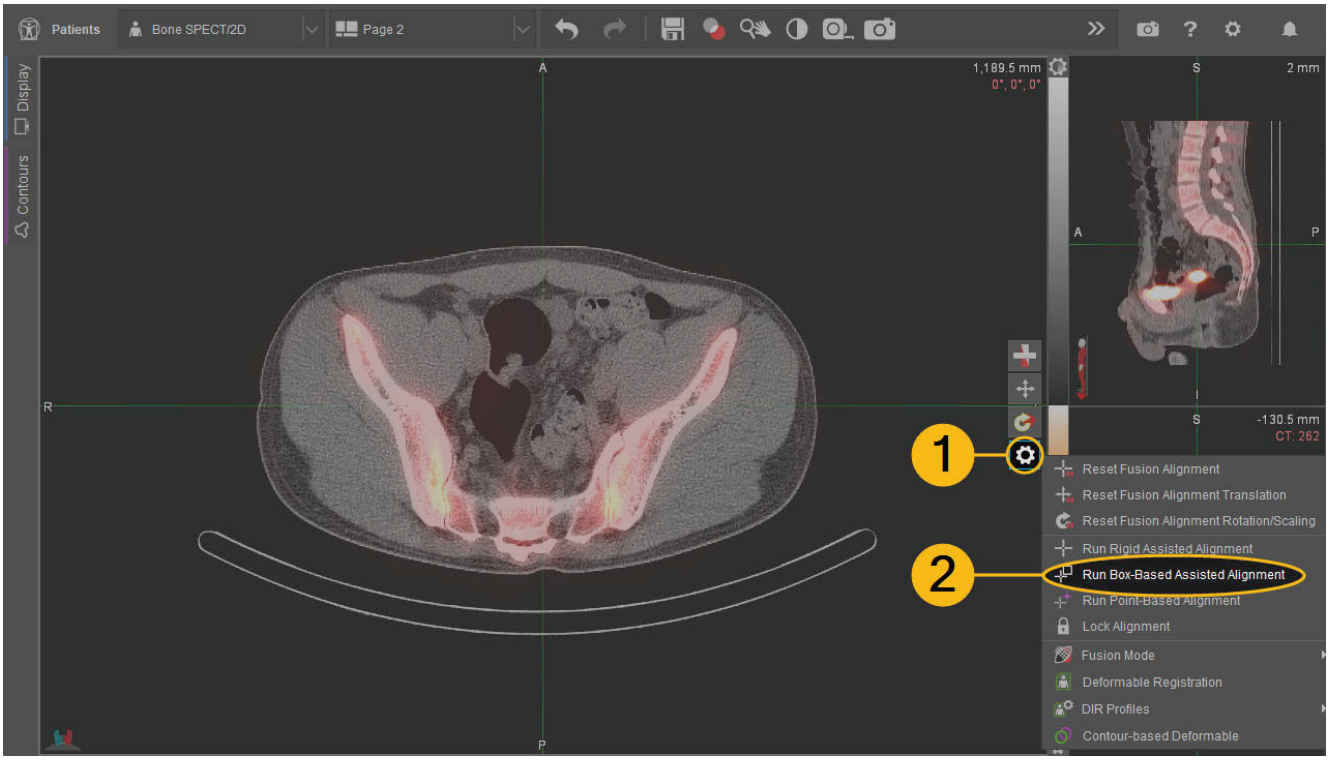
Reset Fusion Alignment resets the fusion using the DICOM orientation to attempt to orient the patient images in the same direction.

- If the scans share a Frame of Reference (FOR), the tool sets the translation based on the image's DICOM coordinates.
- If the images do not share a FOR, the tool aligns the scans center-to-center.

Box-Based Assisted Alignment

Box-Based Assisted Alignment works like Rigid Assisted Alignment by maximizing mutual information, but it restricts the data considered to what is contained within the user-specified box.

1. Click the **Fusion Settings** menu.
2. Select the **Box-Based Assisted Alignment**. A white box displays on the fusion image.



3. Adjust the size of the box to fit around the area of interest in all three planes:
   - To move the box, left-click drag with the cursor inside the box.
   - To resize the box, left-click drag any points on the box, or right-click drag up/down within the box.
4. With the box adjusted to the correct dimensions around the area of interest, click the box-based assisted alignment button located below the **Fusion Settings** menu. This reruns the Rigid Assisted Alignment algorithm with the emphasis placed on the area within the box.

Tip: You can run the Box-Based Assisted Alignment tool as many times as needed.

View Images with Various Fusion Modes

MIMTD-1298 • 09 Jan 2024

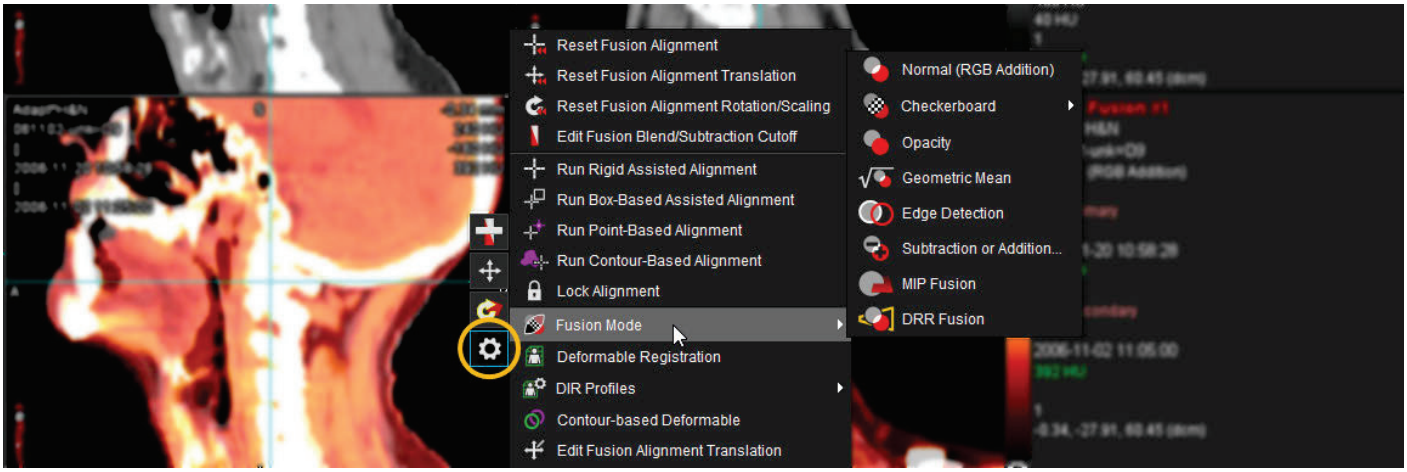
Overview

MIM® provides a number of different ways to visualize image fusions. These different fusion modes allow for the variability of personal preference and can provide specialized viewing conditions for particular types of studies.

Contents

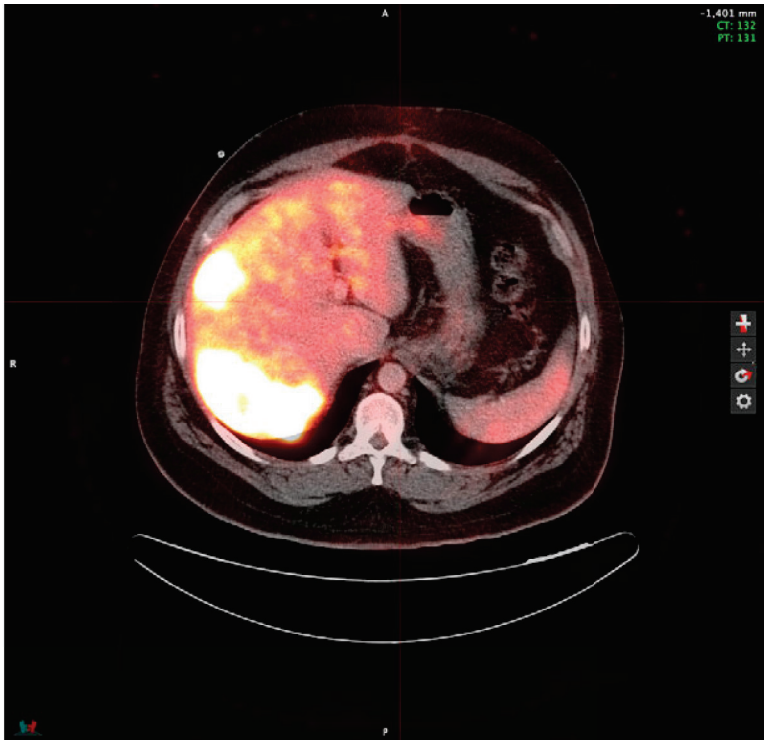
Change Fusion Modes in a Session

1. Click the gear button on the right side of any fusion viewport.
2. In the menu that opens, hover over **Fusion Mode** to see available options.



Fusion Modes

Normal (RGB Addition)



This is the default fusion mode in MIM. In this mode, MIM adds color to color (red to red, green to green, blue to blue) at each voxel location to create the fusion you see.

MIM uses a scaled blending algorithm that, at the middle point of "50%" displays 80% of the primary and 80% of the secondary. This works well in fusions where the secondary color table goes from dark to bright,

like Hot Metal (MIM's default for PT/CT fusions). However, it may not be ideal for a secondary color table, like Rainbow, that has equivalent brightness throughout. With this color table, the default blending algorithm can result in a washed-out image.

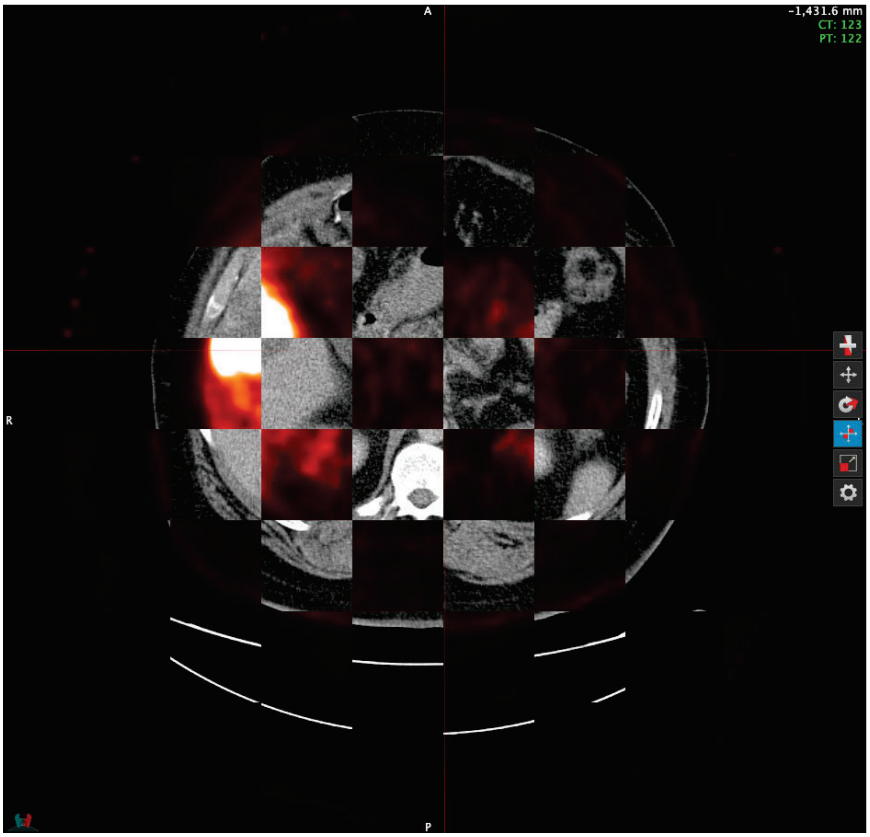
Configure Linear Fusion Blending

MIM's fusion blending algorithm is configurable. If you would like to configure MIM to use linear fusion blending, which is common in other imaging systems, follow these steps:

Tip: Linear blending matches the output produced from some other systems.

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search "**fusion**". Select **Fusion** on the left side.
3. Use the **Fusion Blend Scale** dropdown to select your preferred blending option:
    - **MIM Blending** — MIM's default blending algorithm as described above.
    - **Linear Blending** — More commonly used by other systems, such as Siemens, for fusion display.
    - **Custom** — Lets you set your own blending scale using the Custom Fusion Blend Scale field below the dropdown.

Checkerboard



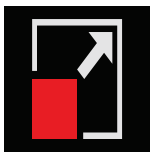
Checkerboard mode lets you see both the primary and secondary series at the same time in a checkerboard pattern. It can be useful for visualizing whether the edges of specific anatomical structures line up well between the primary and secondary images.

There are three options for viewing in Checkerboard mode:

- **Fusion Checkerboard** — A standard checkerboard display of the primary and secondary images
- **MIP Checkerboard** — Overlays the MIP of the secondary onto the primary image
- **DRR Checkerboard** — Overlays a DRR of the secondary onto the primary

When you view a fusion in Checkerboard mode, two tools are added to the Fusion Companion Tools:

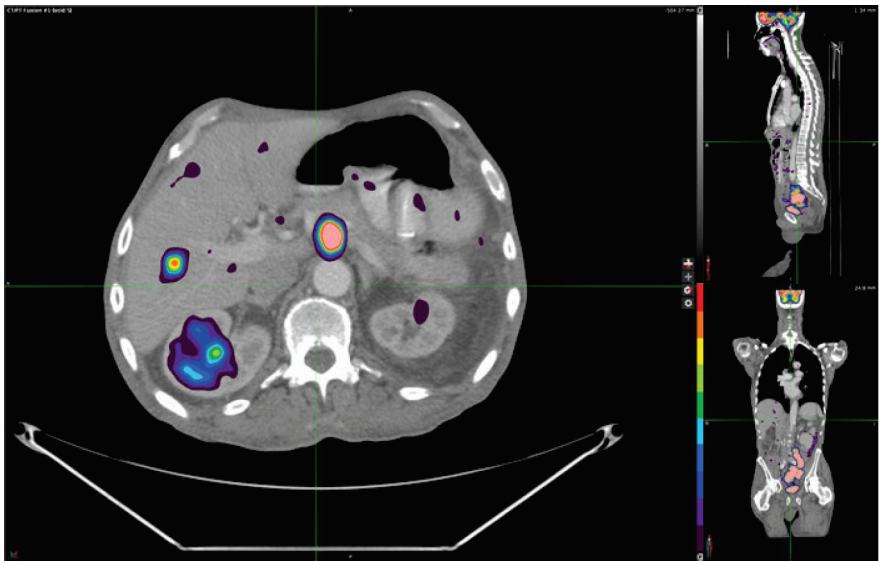
Change the position of the checkerboard grid on the images.



Change the scale of the checkerboard grid on the images.

Related: For more information on the basic Fusion Companion Tools, see Adjust Fusions Manually.

Opacity



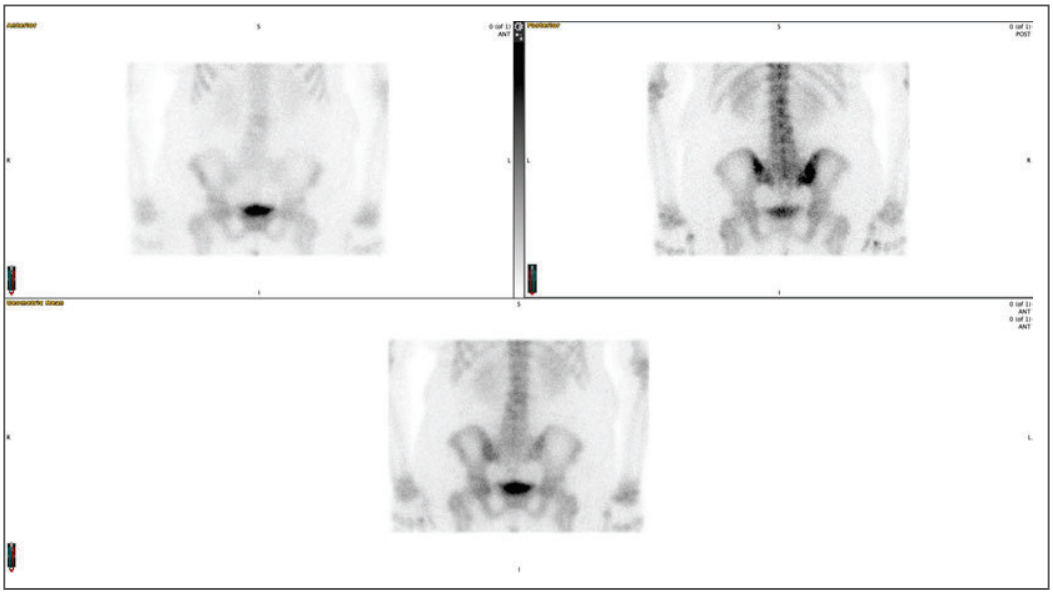
Opacity mode is similar to Normal fusion mode, except that it has special handling for low values and for blending.

In Opacity mode, the color that represents the lowest values in the image becomes transparent. Any image pixels that map to this color, including those below the contrast window, are treated as transparent.

Tip: When used with a color table like Rainbow 10, this mode lets you ignore low pixel values that are irrelevant to the analysis.

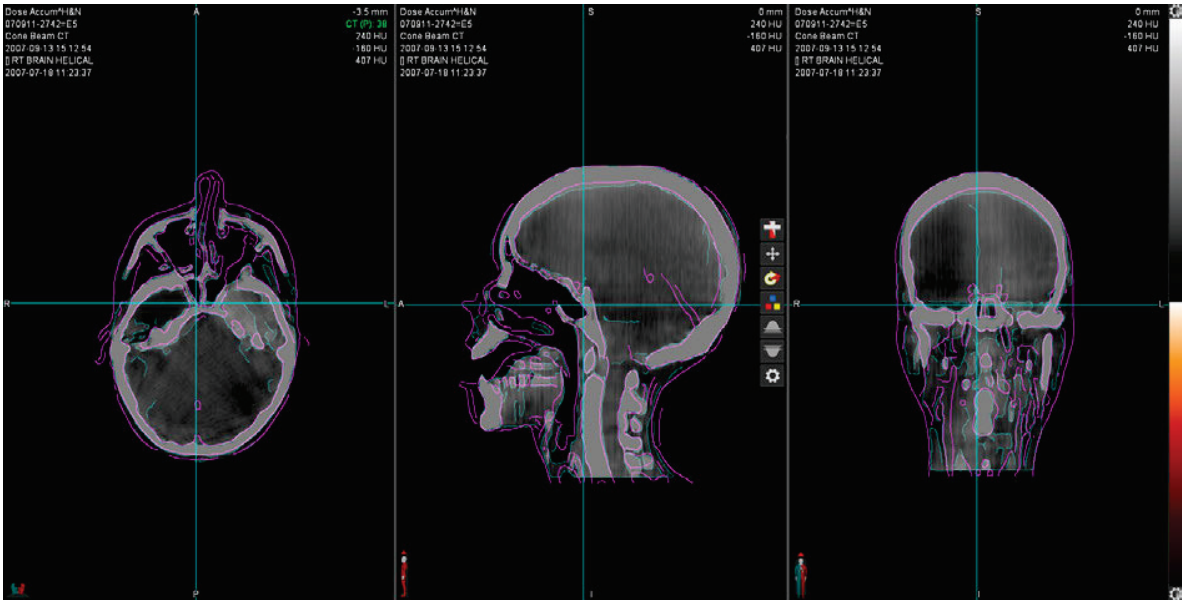
At 50/50 blend (half primary/half secondary), MIM shows the visible voxels in the secondary image according to the color table. In areas where the voxels are treated as transparent, as described above, only the primary image is shown.

Geometric Mean



This mode creates a geometric mean image comprised of the primary and secondary images. This is typically used in Nuclear Medicine when anterior and posterior images are available and a geometric mean image is needed for additional statistical calculations.

Edge Detection



This mode is typically used in MR/CT fusion cases. It shows the edges of the primary and secondary images in order to better visualize the fusion and align anatomical structures.

When you view a fusion in Edge Detection mode, three tools are added to the Fusion Companion Tools:

Choose colors for the edge indicators. Colors can be specified for both the primary and the secondary image.

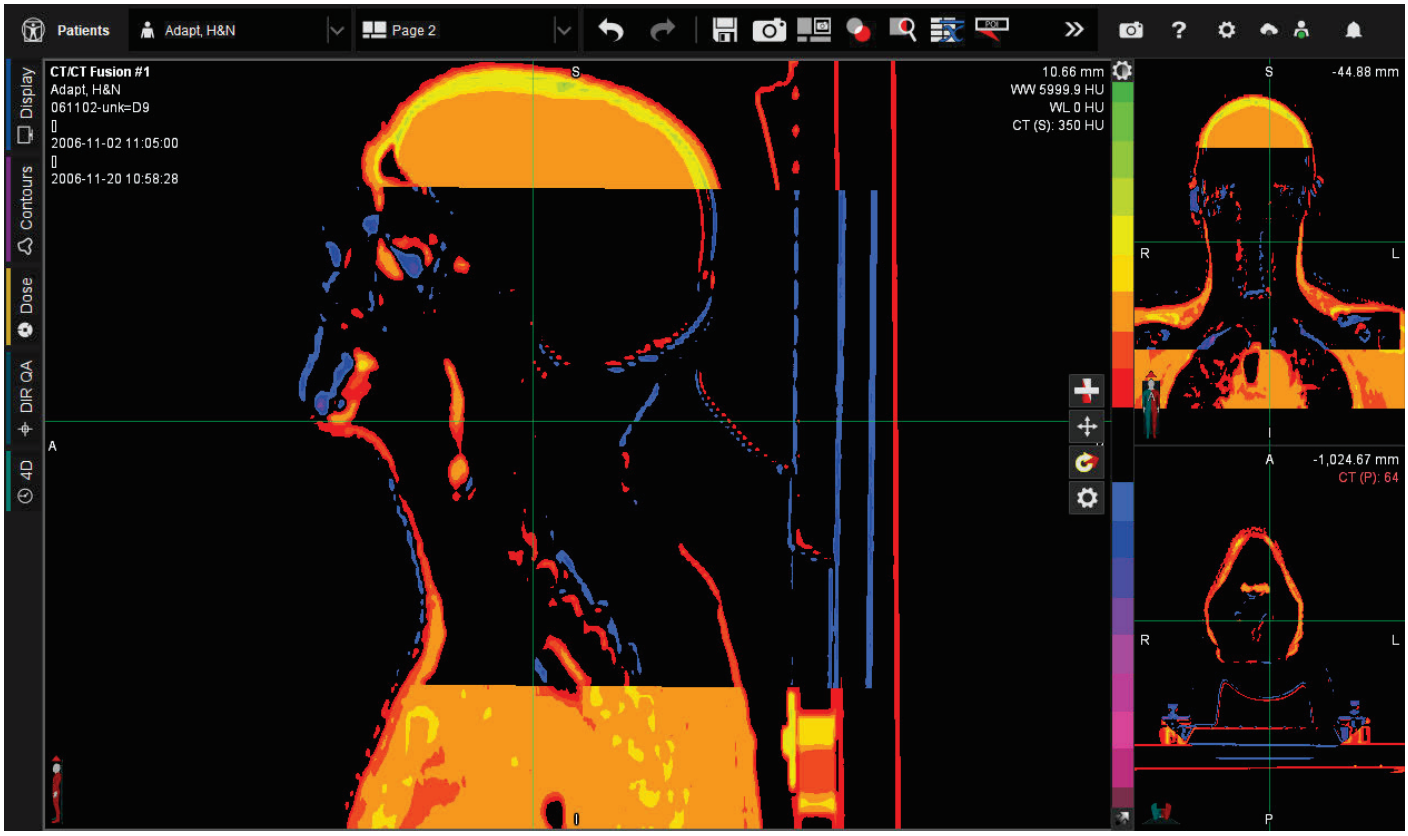
Left-click drag up or down on this button to adjust the upper threshold for detecting edges.

Left-click drag up or down on this button to adjust the lower threshold for detecting edges.

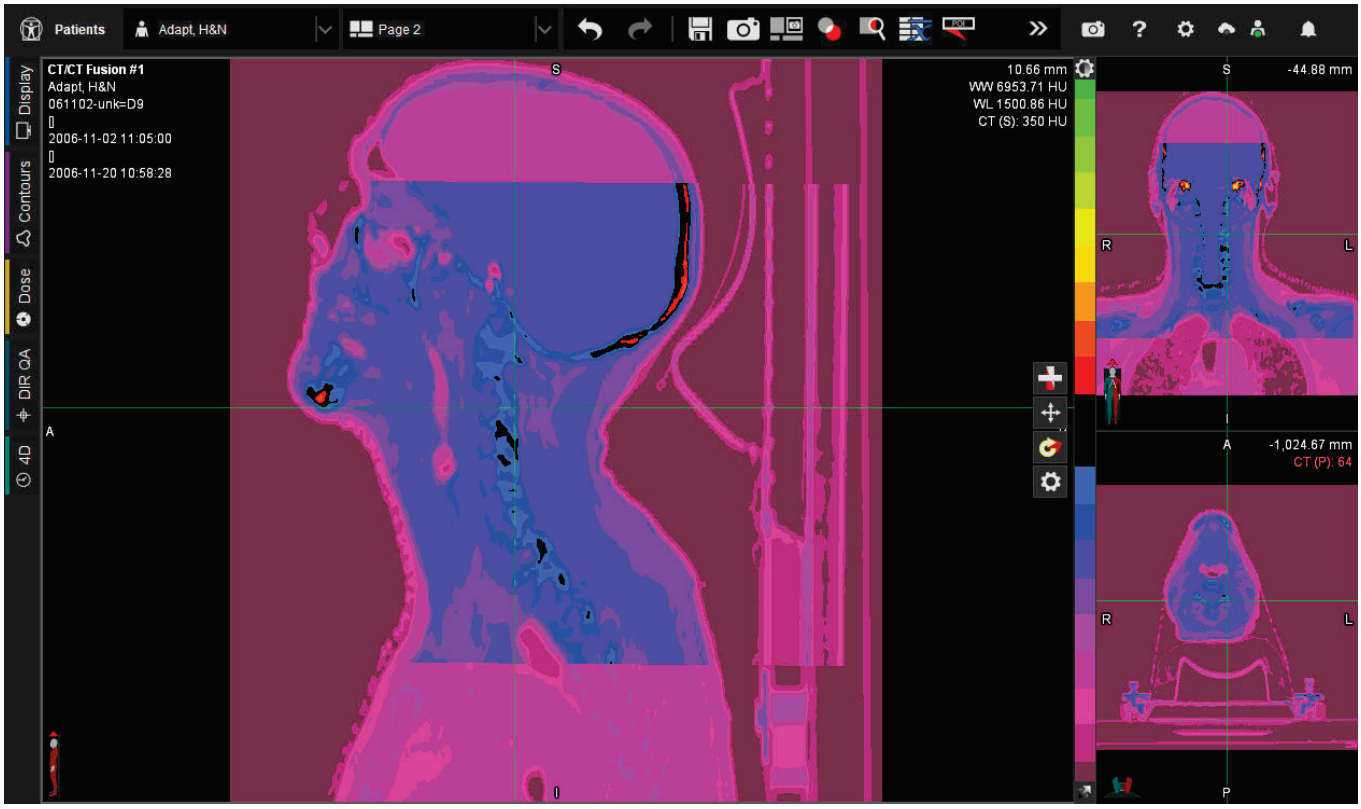
Related: For more information on the basic Fusion Companion Tools, see Adjust Fusions Manually.

Subtraction or Addition

This mode lets you create a single image by either subtracting the secondary from the primary or adding the secondary to the primary. Use subtractions when you want to see the difference between two images. Use additions to look at the summation of two images.



An example of a subtraction in MIM.



An example of an addition in MIM.

When this fusion mode is selected, the Configure Fusion Mode dialog opens. Use this dialog to define the parameters of the addition or subtraction, then click **OK** to create the new image.

MIP Fusion

This mode creates a maximum intensity projection (2D image) of the secondary to be overlaid on the primary image. This can be utilized when it is difficult to see the anatomy in the secondary due to tracer uptake.

DRR Fusion

This is designed for a special case when you have a current x-ray and want to see what an x-ray from this angle would have looked like on a different CT. This could be used to assist with patient setup for EBRT.

Create User-Defined Fusion Blending Rules (MIM 7.3 and Later)

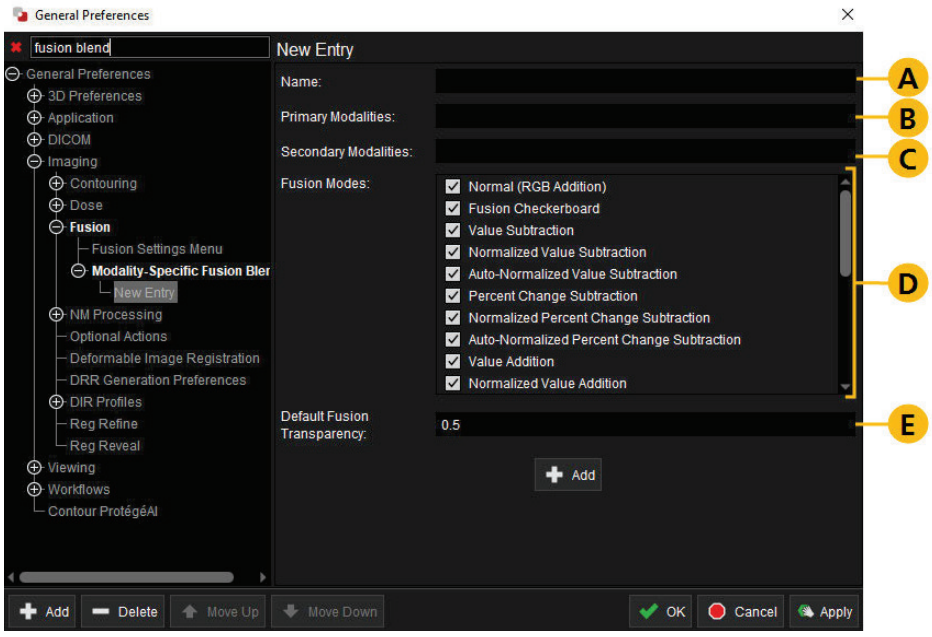
MIM 7.3 and later: It is possible to create user-defined blending rules in MIM. These rules are automatically applied to fusions based on the modalities of the images involved and the fusion mode selected. *MIM 7.2 and earlier:* This functionality is not available.

To create a Modality-Specific Fusion Blend Rule:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search "**fusion blend**". Select **Modality-Specific Fusion Blend Rules** on the left side.
3. Click **Add** to create a new entry.
4. Configure the rule by filling the fields as desired:
   A. The name of the rule.
   B. The primary image modalities that will be considered as part of the rule.
   C. The secondary image modalities that will be considered as part of the rule.

> **Important:** You are not required to define either the primary or the secondary modalities. A rule with no modalities defined will apply to all future fusions. If modalities are defined for primary modalities, secondary modalities, or both, the rule will only be applied to fusions that meet the rule criteria.

   D. The fusion modes that the rule applies to.
   E. The fusion transparency that will be automatically applied to fusions that meet the rule parameters.



5. Click **OK** to save the rule and close the window. The rule will be applied to all future fusions that meet its parameters.

Configure Fusion Settings

MIMTD-1725 • 05 Oct 2023

Overview

Adjust fusion settings to increase the usability of fusion tools, access different fusion modes, and create seamless integration between MIM® and other systems.

Related: For information about adjusting image alignment, see Adjust Fusions Manually and Optimize Fusions Automatically.

Contents

Update the Fusion Settings Menu

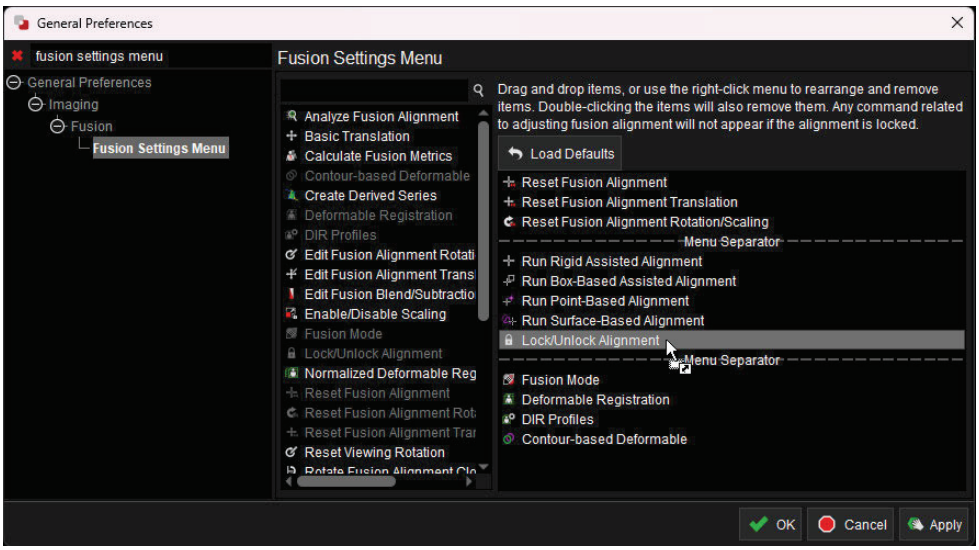
Click the gear button on the right side of a fusion viewport to open the **Fusion Settings Menu**, where you have a variety of automatic and manual alignment methods. Use an automatic method to optimize your fusion, then use the manual tools for additional refinement if desired.

Related: For more information about manual adjustment tools, see Adjust Fusions Manually.

Add to and organize the list of fusion optimization tools in the **Fusion Settings** menu:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion settings menu**". Select **Fusion Settings Menu** on the left side.

3. Drag tools from the left menu to the right menu.

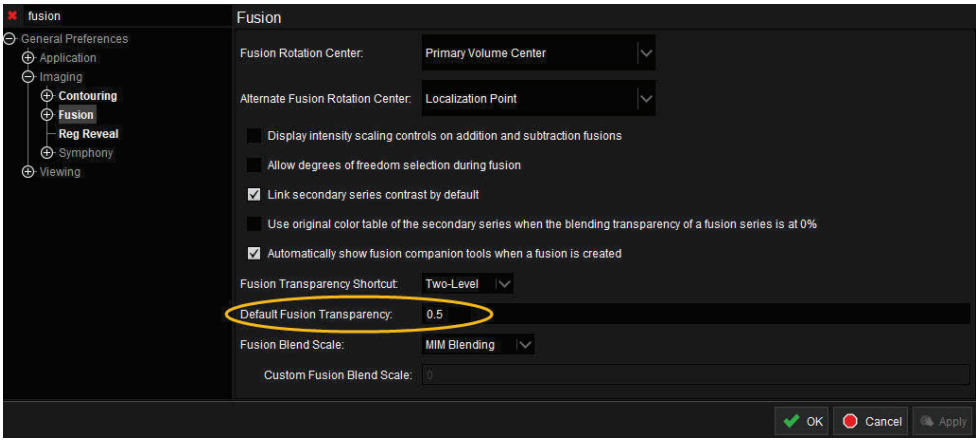


4. Click **OK** to save the changes and close the window.

Adjust the Default Fusion Transparency

When fusions are created, the default fusion transparency provides an equal display of both primary and secondary images. Make manual adjustment using the **Blend** tool (see Adjust Fusions Manually for more information). To adjust the default transparency, follow these steps:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion transparency**". Select **Fusion** on the left side.
3. Adjust the **Default Fusion Transparency** field to a value between 0 and 1.
    - 0 indicates 0% transparency, which means the secondary series is fully opaque. The primary series is not visible.
    - 1 indicates 100% transparency, which means the secondary series is fully transparent. Only the primary series is visible.



4. Click **OK**.

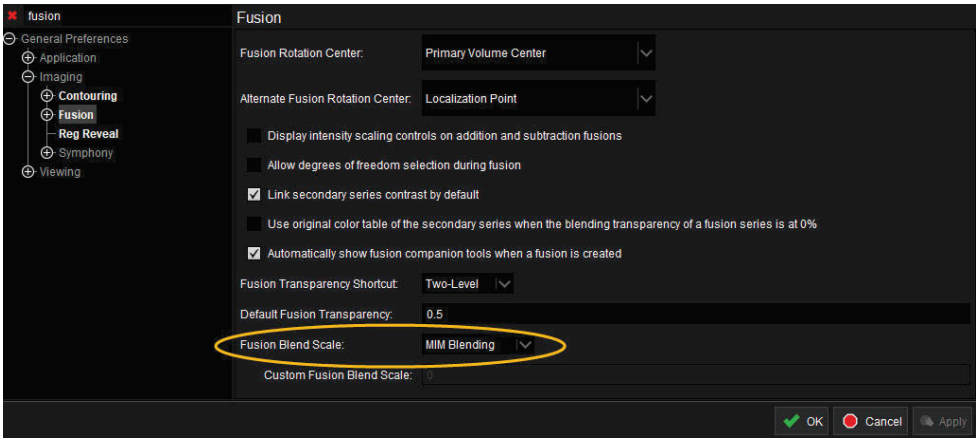
> **Tip:** When changed, this setting will take effect beginning with the next-created fusion.

Adjust the Fusion Blend Scale

MIM uses a scaled blending algorithm in its fusions that affects the brightness of the image display. The scale is determined by the **Fusion Blend Scale** preference. This preference can be adjusted to let you to see more detail in lower values on the fusion and to more closely match the output of a third-party system.

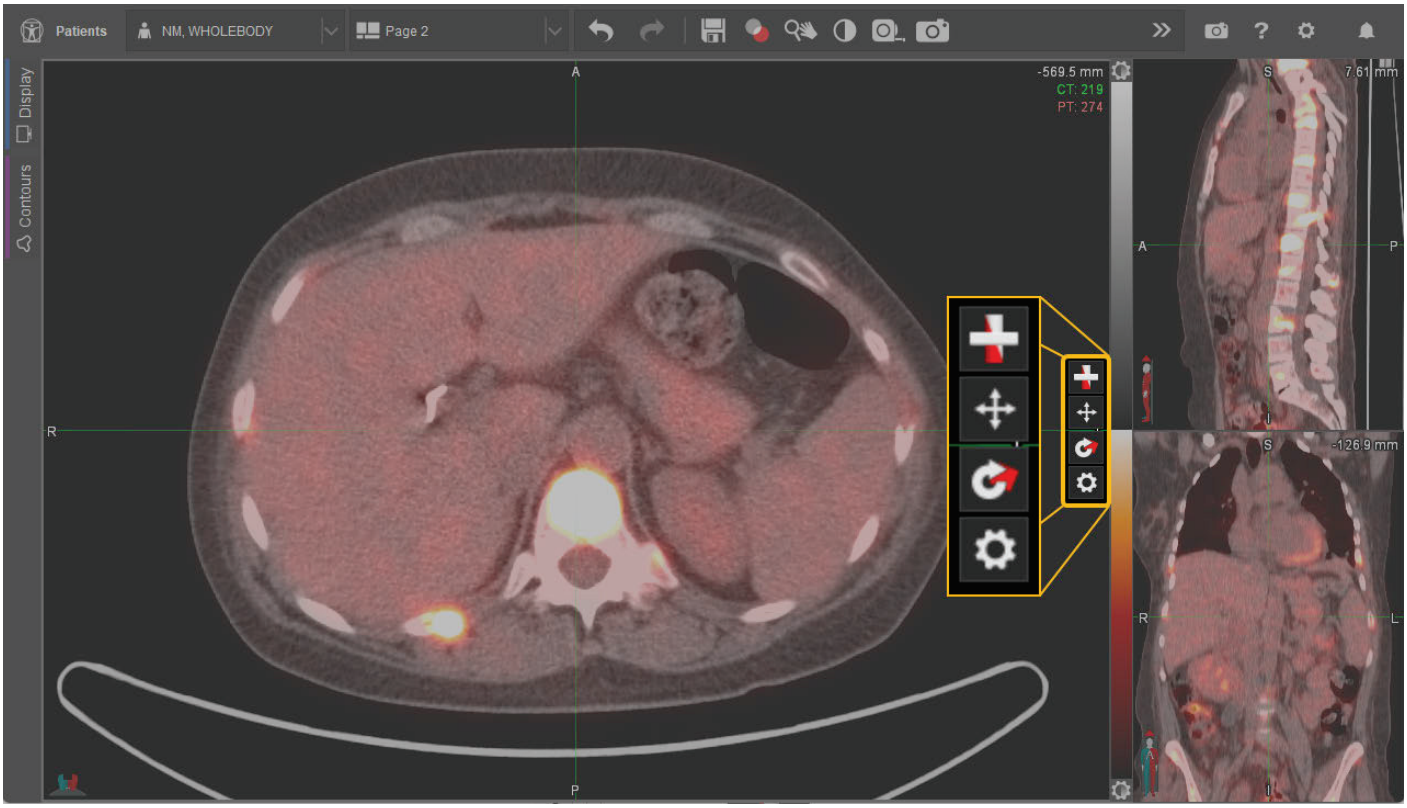
1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion blend**". Select **Fusion** on the left side.
3. Adjust the **Fusion Blend Scale** dropdown:
   - **MIM Blending** works well in fusions where the secondary color table goes from dark to bright. A good example is the Hot Metal color table option.
   - **Linear Blending** tends to more closely match the output of third-party systems.
   - **Custom** can be a value between 0 (linear blending) and 1 (MIM blending) to find a value that suits you.

> **Tip:** When changed, this setting takes effect in any open sessions that include a fusion.



4. Click **OK** to save the changes and close the window.

Show/Hide the Fusion Companion Tools



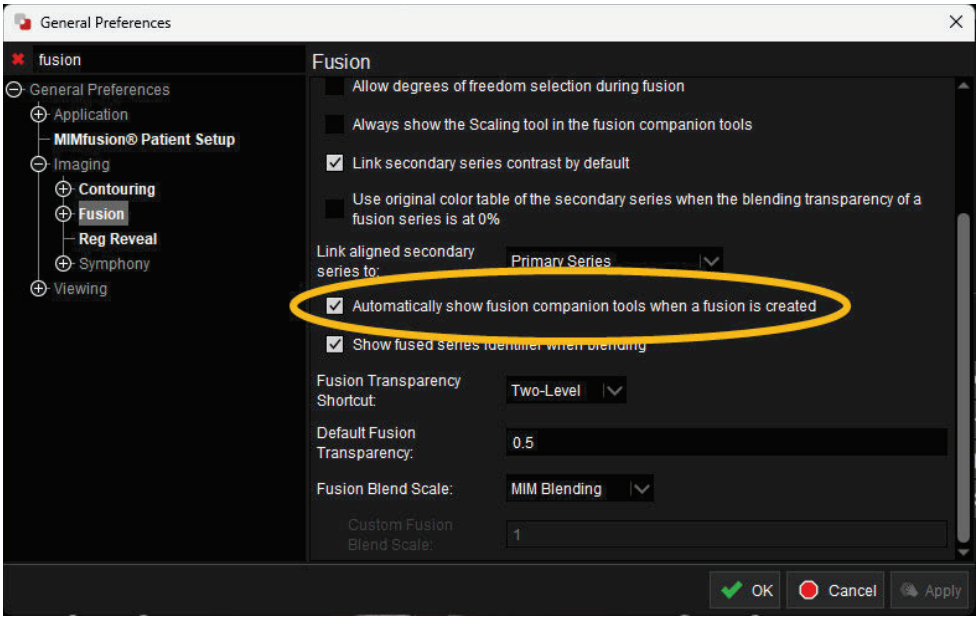
By default, the fusion companion tools always appear when hovering in a fusion viewport. To toggle the fusion companion tools on and off within a session, you can create a keyboard shortcut.

Related: For instructions on configuring keyboard shortcuts, see Set Keyboard Shortcuts.

The default behavior can also be changed. This is helpful if a viewport size is very small or zoomed in and the fusion companion tools are obstructing the image.

To hide the fusion companion tools by default, follow the steps below:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**fusion**". Select **Fusion** on the left side.
3. Deselect **Automatically show fusion companion tools when a fusion is created**.



4. Click **OK** to save the changes and close the window.

Tip: When changed, this setting takes effect in any open sessions that include a fusion.

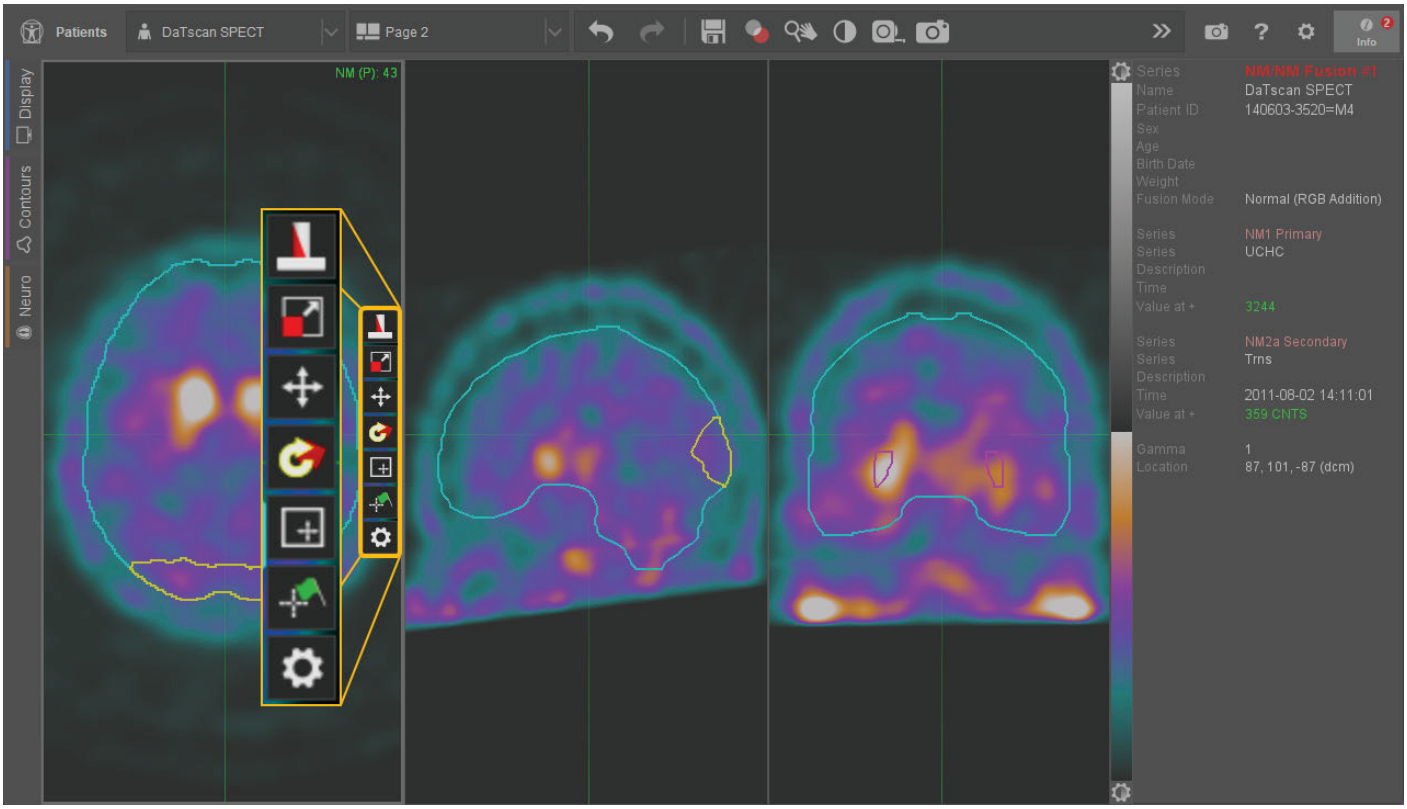
Tip: Your preference to show/hide fusion companion tools is not included when you save a session. If a saved session is opened by another user, the fusion companion tools are shown or hidden according to that user's preference.

Adjust Affine Registrations

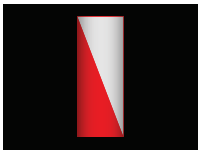
MIMTD-851 • 31 Oct 2023

Overview

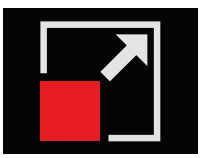
Use the affine registration tools to correct the registration if the alignment of your neuro images to the template is unsatisfactory. The tools appear when you hover over the right side of a neuro fusion window.



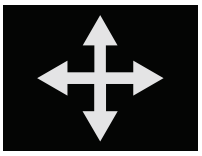
Affine Registration Tools



Use the **Blend** tool to blend between your image (slide to the bottom) and the template (slide to the top).

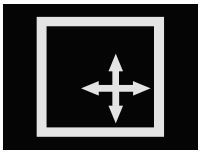


Use the **Adjust Scale** tool to scale your image to match the template.

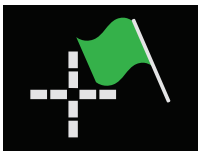


Use the **Translate** tool to move your image in any direction to match the template.

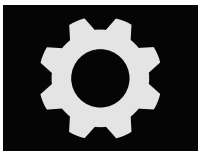
Use the **Rotate** tool to rotate your image to match the template.



Use the **Assisted Alignment** tool to rerun the registration from its current alignment.



Click the green flag button to accept the registration and proceed with processing.

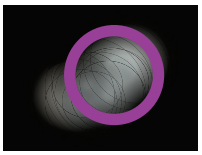


Click the **Fusion Settings...** gear to open a menu of additional fusion options.

Create Contours with the Threshold Tool

MIMTD-703 • 07 Sep 2023

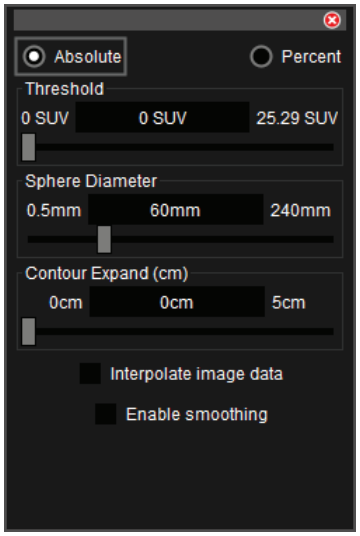
Overview



The Threshold tool contours voxels on anatomic (i.e., CT and MR) and functional (i.e., PET and NM) images above a specified threshold value within a spherical region.

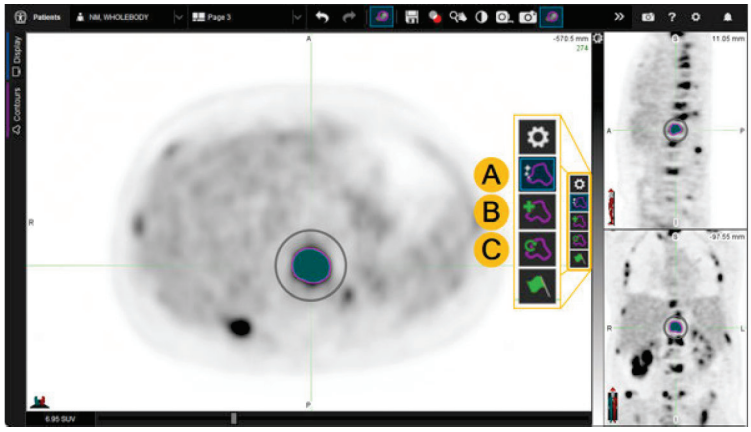
Create a Contour

1. Activate the **Threshold** tool from the top toolbar, radial menu, or Contours sidebar.
2. Position the sphere by left-clicking or left-click dragging.
3. Click the button along the right edge of any viewport to configure threshold settings.



i. Select an absolute or percent-based threshold.
ii. Adjust the threshold, sphere diameter, and contour expansion by dragging the sliders or manually specifying values.
iii. Choose whether to interpolate image data.
iv. Choose whether enable contour smoothing.

4. Click the green flag button to create the contour.
5. If you need to append to or replace the contour, click the appropriate button on the right side of the viewport, then click the green flag button again.



A. Create a new contour.

B. Append to the current contour.

C. Replace the existing contour.

Next Steps: Workflows and Customization

Import MIM Workflows™ and Other Content

MIMTD-614 • 26 Apr 2021

Overview

Use the Import Manager to import default and content from other users at your organization, including workflows, into MIM®. For information about available default workflows, see MIMneuro Workflows.

Content that you can import includes:

- Workflows
- Hanging protocols
- Structured report templates
- External report templates
- Extensions
- Custom viewport info layouts
- Findings templates
- Images
- Dose constraint sets
- Isodose settings
- ROI templates
- Contour shape templates
- BED profiles
- Color tables
- Statistics viewer layouts
- Target filters
- Sector assist segmentation models
- Anonymization templates
- Voxel S value kernels
- Public keys
- Private keys
- Structured reporting macros

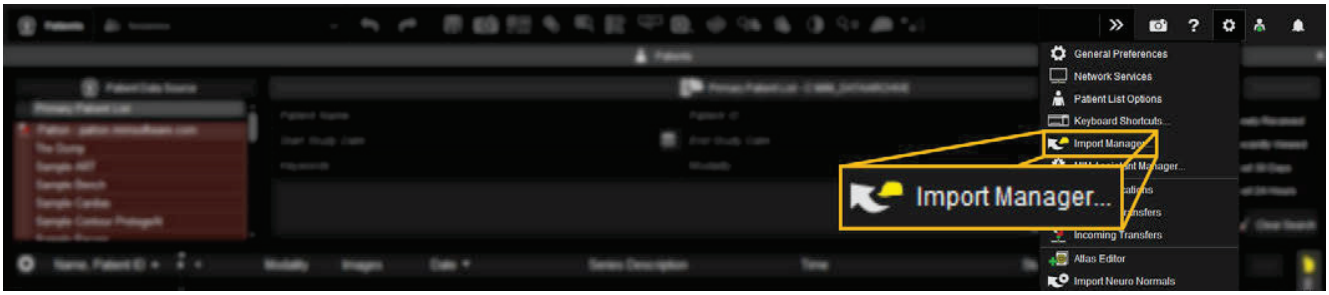
Notes:

- Some of the content types above may not apply to the MIM product or functionality that you use.
- If you are interested in developing your own site-defined content, please contact MIM Software Support at support.mimsoftware.com.

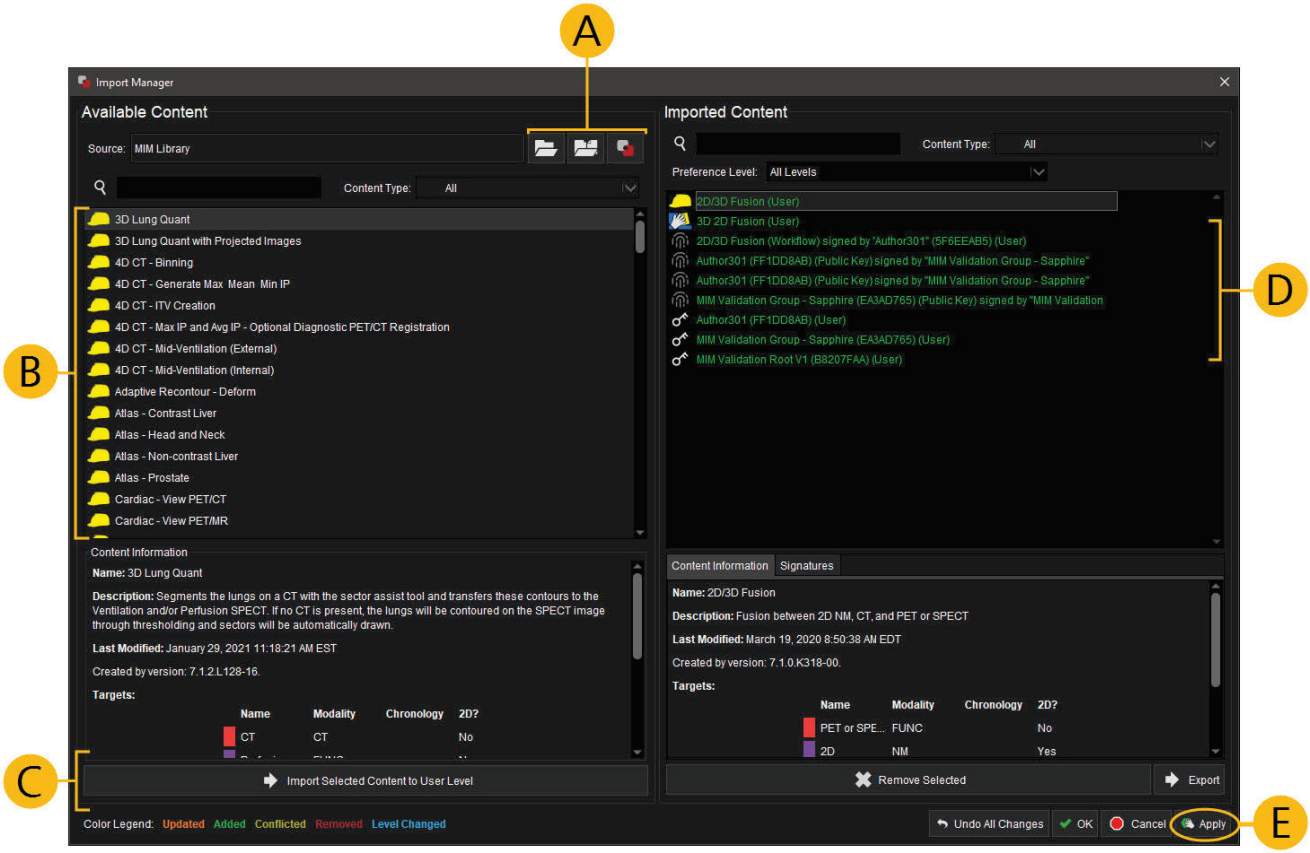
If your site has a MIMpacs™ license and MIM Network User logins are enabled, administrative users can import content for all users. For more information, see the *MIMpacs User Guide*.

To import content for one user or workstation:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **Import Manager...**.



3. View and import content:



A. Choose a content source:

- The MIM Library is automatically selected. You should keep this source selected if you want to import default workflows, for example. To change the content source back to the MIM Library anytime, click the MIM logo button.

- To import site-defined content that is stored in a local or network directory or file, click the open directory or open file buttons and go to the desired location. You should select one of these sources if you want to import a workflow that was built specifically for your site, for example.

B. Select one or more items. To select multiple items at a time, hold the Ctrl key or the Shift key while clicking.

C. Click **Import Selected Content to User Level**. After clicking the button, the selected content appears in the Imported Content column on the right side of the Import Manager.

D. Review the items in the Imported Content column.

> **Tip:** The text color of the items being imported indicates their status. Check the Color Legend in the lower-left corner of the Import Manager to see what each color means.

E. Click **Apply**. The text color of the items being imported changes to white. The imported content is now available in MIM.

Launch MIM Workflows™

MIMTD-615 • 25 Jul 2023

Overview

MIM Workflows automate tasks to increase efficiency and standardization across your organization.

Contents

Prerequisites

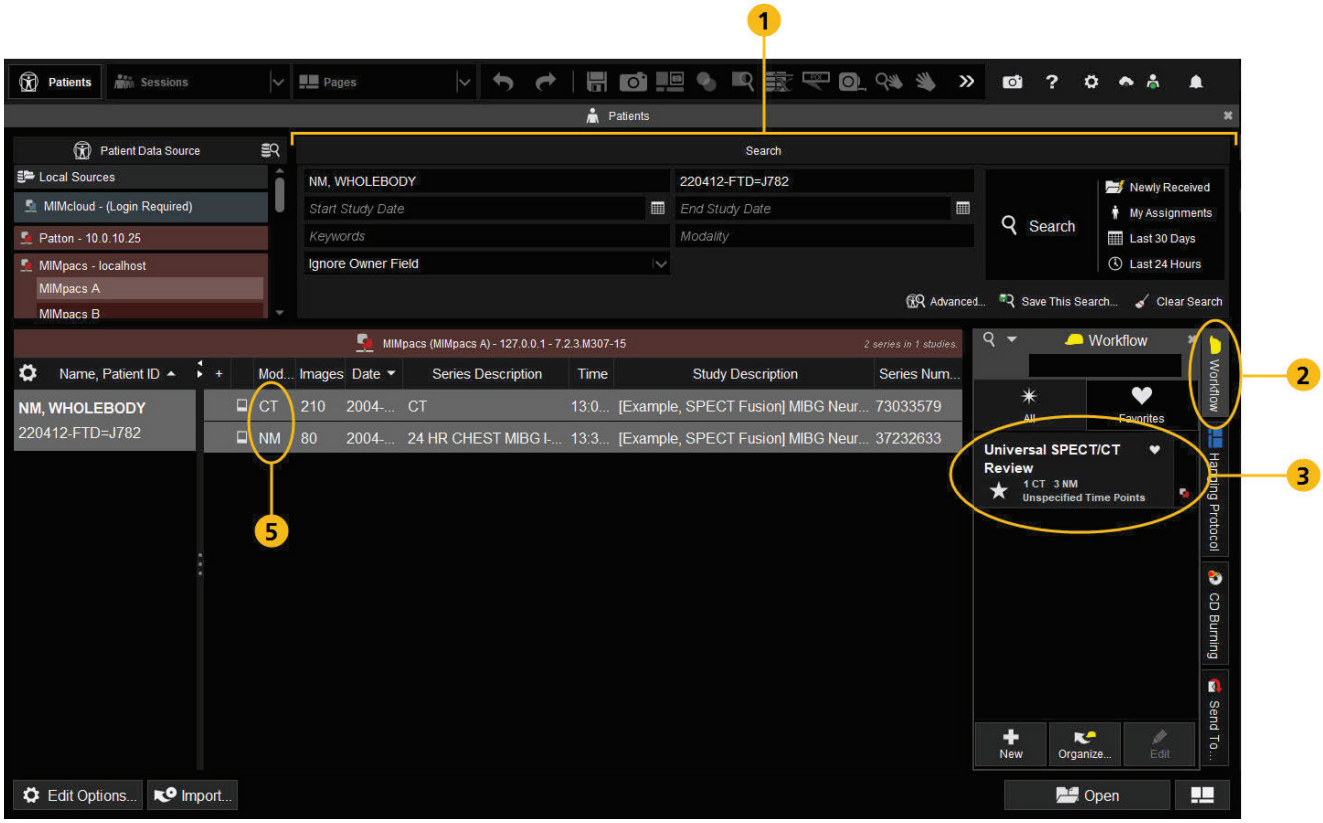
You must have workflows available to use. Available workflows can be viewed in the Workflows tab on the right side of MIM®.

Related: See Import MIM Workflows™ and Other Content to learn how to import MIM's default workflows. For assistance creating your own workflows, please contact MIM Software Support at support.mimsoftware.com.

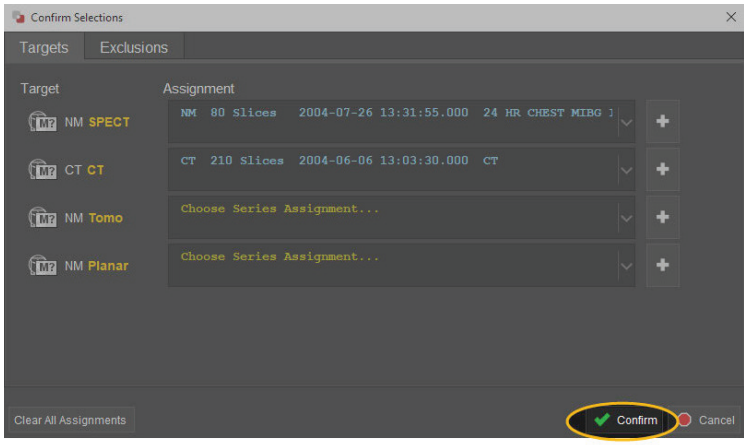
Launch MIM Workflows

1. Search for the patient whose data you want to run a workflow on.
2. Open the **Workflows** tab on the right side of MIM.
3. Find the workflow you want to launch.
4. Hover over the workflow to display the series requirements and ensure you have the correct series.
5. Select a patient or series from the patient list. The workflow lights up in white. A star indicates that MIM can use the DICOM information to map the selected series to the workflow inputs without

manual intervention.



6. Double-click the workflow name to launch it.
7. If the Confirm Selections window appears, review and confirm which series should be mapped to each workflow target. Click **Confirm** once you have confirmed the assignments for each target are correct.



8. Follow the workflow prompts in the Notifications window to complete the workflow.

You can designate a workflow as a "favorite" by clicking the ♡ next to the workflow name.

- Favorite workflows are listed first when they can be run using the selected patient data.
- If other workflows are a closer match, based on the workflow's targeting parameters, they may still be listed first.
- To only display favorite workflows, select the **Favorites** tab.

Set Keyboard Shortcuts

MIMTD-616 • 30 Aug 2023

Overview

MIM® has hundreds of commands that you can assign to keyboard shortcuts. Keyboard shortcuts give you quick access to CT contrast presets, zooming functionality, localizing functionality, and more.

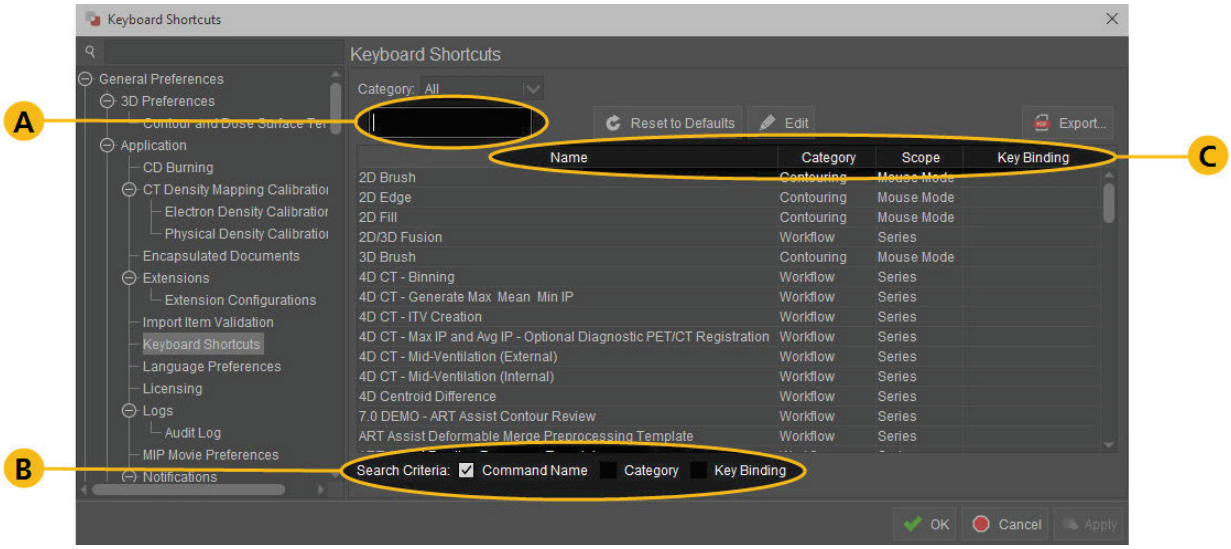
Related: By default, many commands are already assigned to keyboard shortcuts. For a list of default keyboard shortcuts, see Default Keyboard Shortcuts.

Contents

Assign or Reassign Keyboard Shortcuts

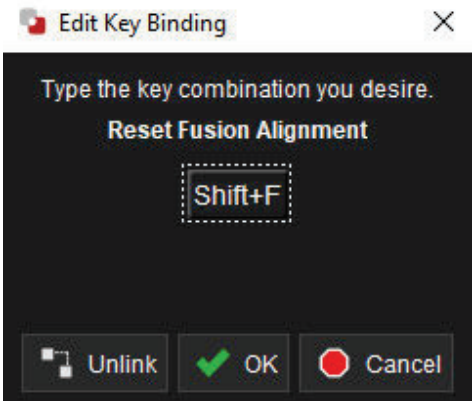
1. Click the Settings button in the upper-right corner of MIM.
2. Go to **Keyboard Shortcuts...**.
3. In the Keyboard Shortcuts window, find the command that you want to assign or reassign a keyboard shortcut to:
   A. Enter search terms in the empty field below the Category dropdown.
   B. To change the search criteria, select or deselect **Command Name**, **Category**, or **Key Binding** at the bottom of the Keyboard Shortcuts window.

C. To sort the columns, click the **Name**, **Category**, **Scope**, or **Key Binding** column headers.



Important: The **Scope** column indicates where the cursor needs to be in order for the keyboard shortcut to work. If the scope is **Series**, the cursor needs to be hovering over a specific viewport. If the scope is **Mouse Mode** or **Session**, the keyboard shortcut functions as long as the cursor is active within MIM.

4. Double-click the command that you want to change. The Edit Key Binding window opens.
5. Type the key binding that you want to assign to the command. The Edit Key Binding window updates with the key binding that you typed.



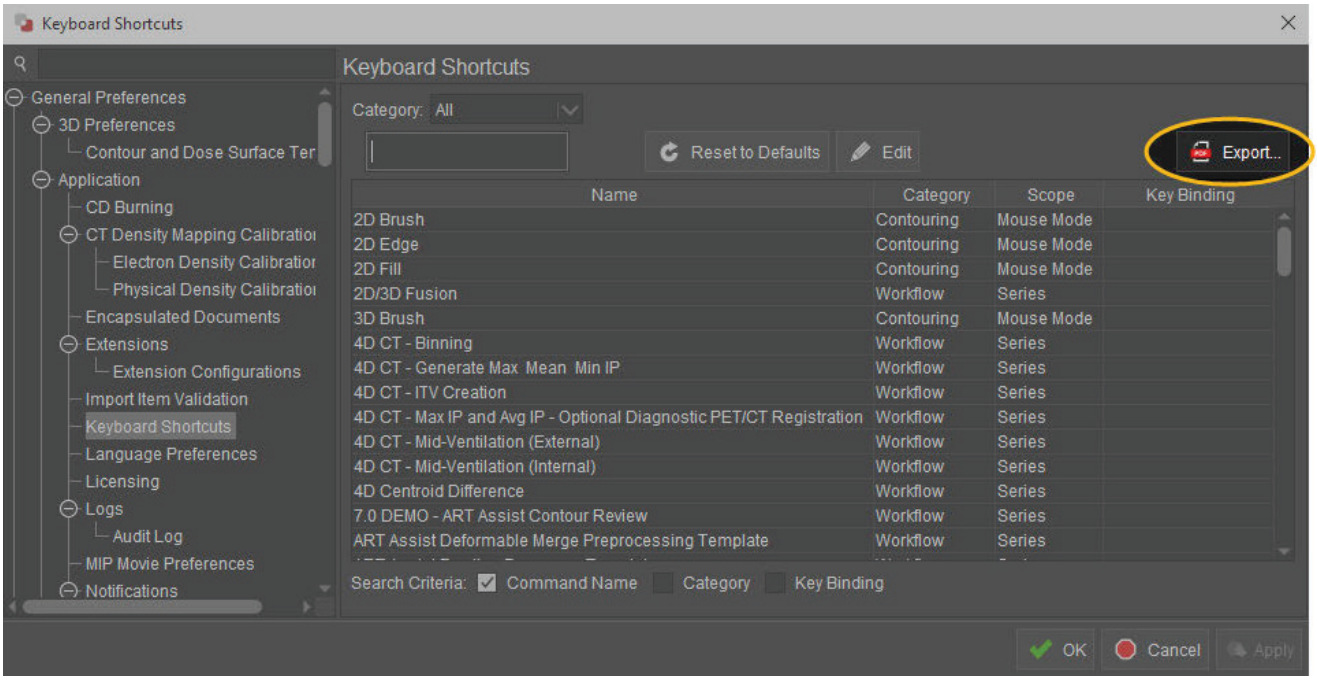
Important: If the key binding is already in use, MIM warns you and shows the command that the key binding is assigned to. Type a different key binding, or click **OK** to use the key binding that you entered and unassign the key binding from the other command.

6. Click **OK**. The Key Binding column updates to show the assigned key binding.
7. Click **OK** at the bottom of the Keyboard Shortcuts window to save your changes and close the window.

Export a PDF of Keyboard Shortcuts for Reference

To export a list of keyboard shortcuts for reference, follow these steps:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **Keyboard Shortcuts...**.
3. Click the **Export...** button in the upper-right corner of the Keyboard Shortcuts window.



4. To include or exclude keyboard shortcuts from the list, select or deselect the desired shortcuts.
5. Click **Save PDF...**.
6. Browse to the file location where you want to save the PDF.
7. Enter a filename.
8. Click **Save**. The PDF of keyboard shortcuts is now available in your save location.

Configure Mouse Behaviors

MIMTD-1282 • 07 Aug 2023

Overview

The click and drag behaviors for your mouse buttons can help you complete several actions in MIM® more quickly. *MIM 7.3 and later*: You have the ability to configure which mouse buttons control which actions based on what is most intuitive and useful for you. *MIM 7.2 and earlier*: The Default Mouse Behaviors are always used and are not configurable.

For example, you may want to scroll quickly through a series with a left-click drag instead of the default right-click drag (see Examples below for instructions).

Contents

Default Mouse Behaviors

MIM includes the following default mouse behaviors:

Action	Mouse Behavior	More Information
Localize	Left-click and left-click drag	Localize and Scroll
Adjust Contrast*	Middle-click drag	Adjust Image Contrast
Radial Menu	Right-click	Access Tools: The Toolbar and the Radial Menu
Scroll Slices	Right-click drag	Localize and Scroll

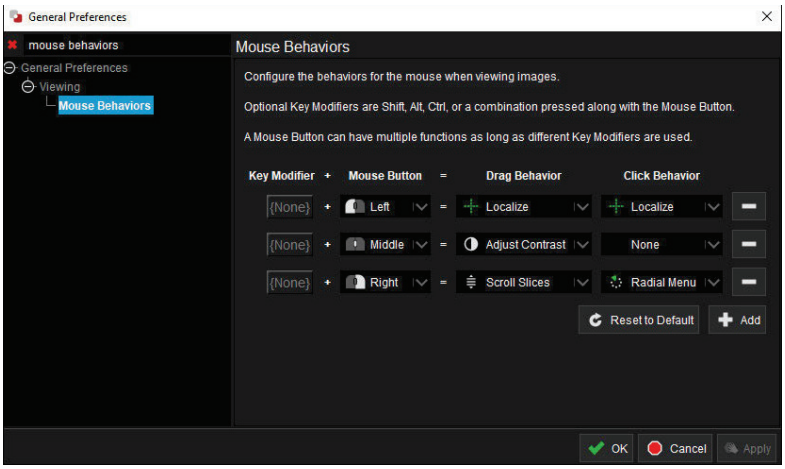
*The adjust contrast default is new in MIM 7.3 and later. In MIM 7.2 and earlier, there is no mouse behavior for this action.

Adjust Mouse Behaviors

> **Tip**: To share and standardize these settings across your organization, a MIM administrative user should make the additions or updates while logged in to the **Edit Site Defaults** login mode. See Update Default Settings for Users for prerequisites and instructions.

To adjust the mouse behaviors, follow these steps:

1. Click the Settings button in the upper-right corner of MIM.
2. Go to **General Preferences** and search for "**mouse behaviors**". Select **Mouse Behaviors** on the left side.
3. Adjust the existing behaviors or click **Add** to set a new behavior.
    - Use the dropdowns to choose the **Mouse Button**, **Drag Behavior**, and **Click Behavior**.
    - Click the **Key Modifier** field and then press a key to set the modifier.



The following options can be combined:

Key Modifiers*	Mouse Button	Behaviors

• Windows®
  • Shift
  • Alt
  • Ctrl
• Mac®
  • shift
  • option
  • control
	• Left
	• Middle**
	• Right
		• Scroll Slices
		• Adjust Contrast
		• Localize
		• Rotate View
		• Pan
		• Zoom
		• Quick MIP

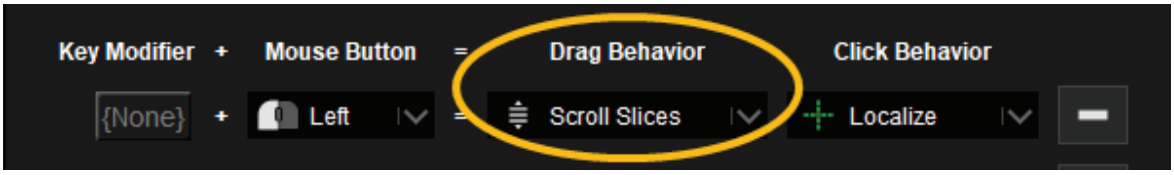
*Neither the Command key (for Macs) nor the Windows key are allowed with mouse behaviors.

**Clicking or click-dragging the middle button (usually the scroll wheel) can be configured with the behaviors listed above. Configuring the behavior for scrolling the wheel, however, is not available at this time.

Examples

If you want to scroll quickly through a series by left-click dragging:

1. Find the Left Mouse Button preference.
2. Change the Drag Behavior dropdown to **Scroll Slices**.

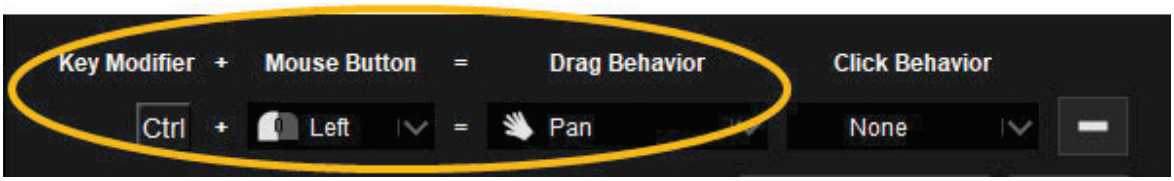


If you want to pan a series by dragging the middle button:

1. Find the Middle Mouse Button preference.
2. Change the Drag Behavior dropdown to **Pan**.

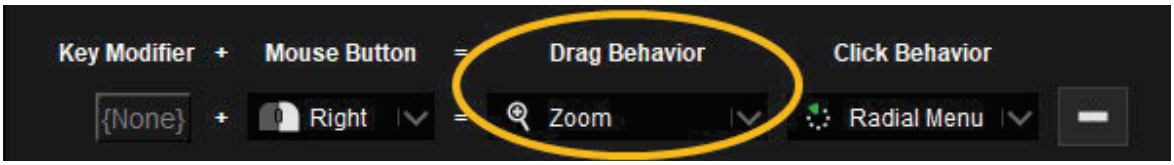
If you want to pan a series using the Ctrl key and left-click dragging:

1. Add a new behavior.
2. Set the Key Modifier to Ctrl
3. Set the Mouse Button to Left.
4. Set the Drag Behavior to Pan.



If you want to zoom a series by right-click dragging:

1. Find the Right Mouse button preference.
2. Change the Drag Behavior dropdown to Zoom.



Create and Save Secondary Captures

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Overview

You can create secondary captures, which are similar to screenshots. Consider the following examples of when to use secondary captures:

- Save data to a PACS that does not support DICOM image processing. Secondary captures are saved as OT files that can be opened by basic DICOM viewers. They do not include voxel data.
- Capture a static view. A screencapture saves exactly what you are currently looking at, which can be helpful to refer back to later.
- Send an image to another provider. Instead of sending the entire series, you can send only the screencapture of what you want them to see.
- Add the image to a structured report. See Create and Modify Structured Reports for more information about adding secondary captures to reports.

Contents

Create a Capture

You create a capture after opening a patient session and identifying what in the session that you want to capture. Then, you can use the **Capture Screen** tool on the top toolbar. Or, click the button on the right side of the toolbar to find any of the additional Capture Tools listed below.

> **Tip:** Add the capture tools that you use most to your top toolbar or radial menu for easy access. See Access Tools: The Toolbar and the Radial Menu for details.

After creating the capture, click the **Capture Gallery** button on the right side of the screen to view captures from that session.