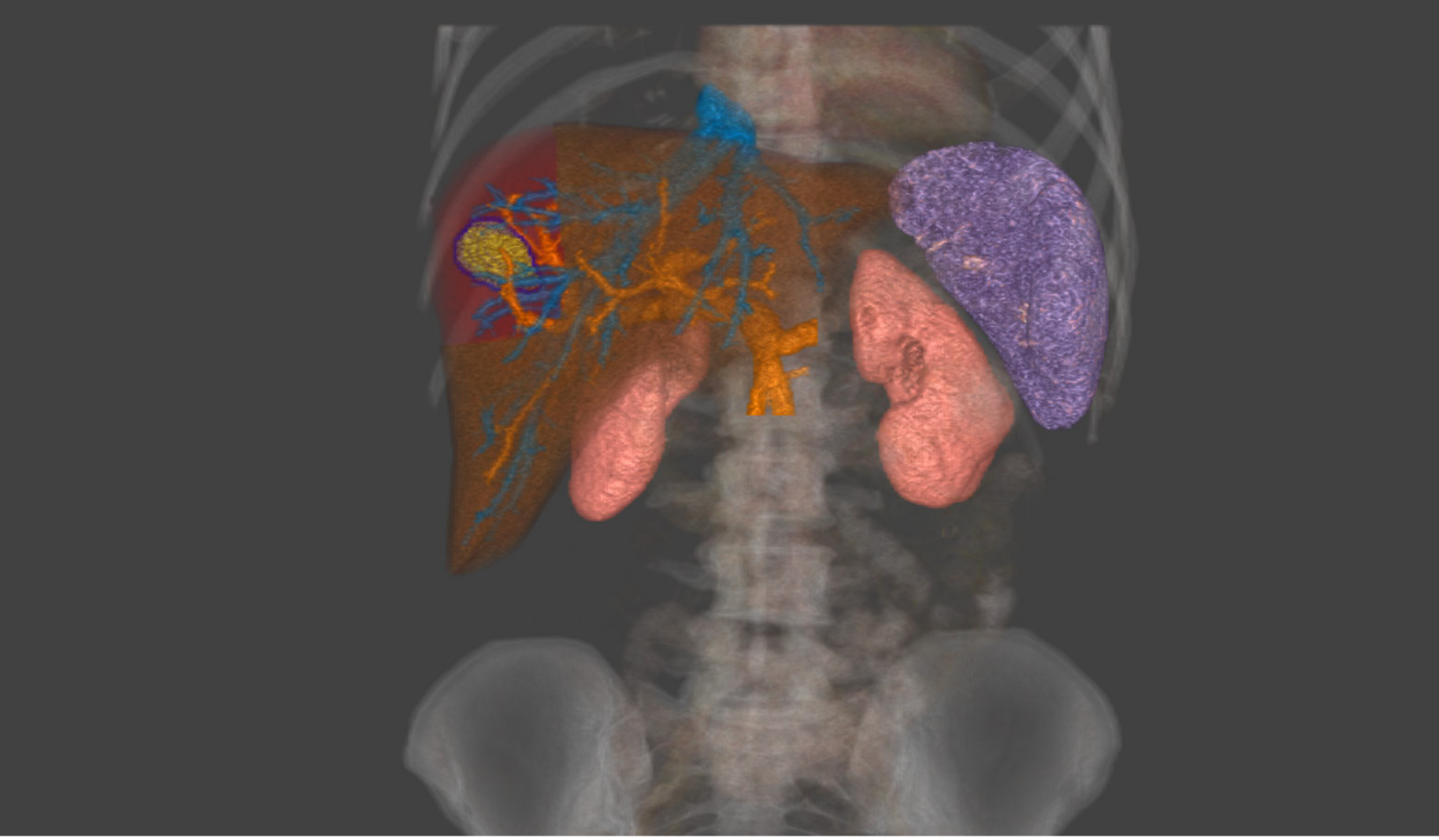

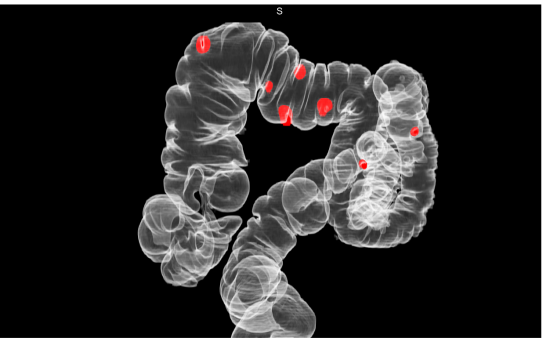

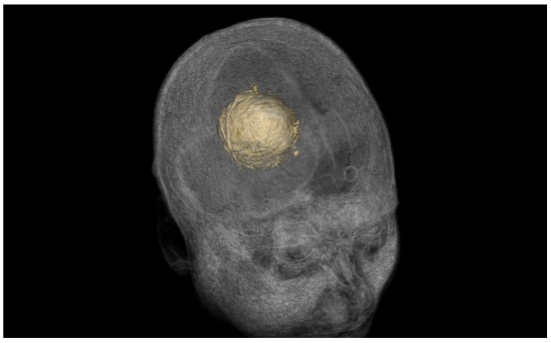

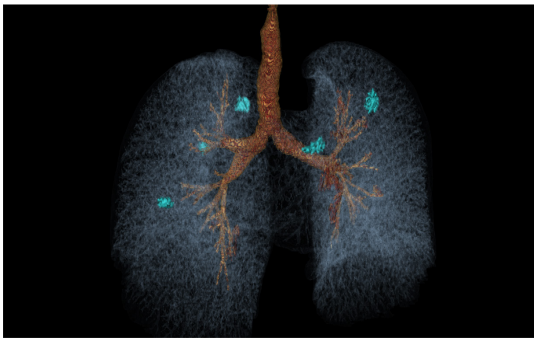

Vitrea Advanced®
Vitrea Workstation™

Education and Reference Guide
Oncology

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Safety and Regulatory Considerations

PLEASE REFER TO THE **ABOUT VITAL IMAGES MEDICAL IMAGING SOFTWARE** DOCUMENT BEFORE USING THIS PRODUCT. This document includes important information regarding general Vitrea Safety and Regulatory considerations.

CAUTION: Federal law restricts this device to sale by or on the order of a physician, as directed by 21 CFR 801.109(b)(1).

Contact Us

- For general, non-technical support questions, contact us through our Web site: www.vitalimages.com.
- For customer technical support, contact us:
  - In the U.S., call the Customer Support line at 1.800.208.3005.
  - Outside the U.S., contact your Vital distributor.
  - Send an email to support@vitalimages.com.
- For a printed version of the Release Notes, Education and Reference Guide, or Installation Guides, contact Customer Support at 1.800.208.3005.

Release Notes

Vitrea® Release Notes contain late-breaking information not available at the time the Education and Reference Guide was released. This document is available from your System Administrator or from Vital Images.

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CT Colon Analysis

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CT Colon Analysis Overview

CT Colon Analysis generates 2D and 3D images of the colon to allow close examination of the lumen of the colon, thereby increasing the speed and ease of locating and analyzing suspected polyps. CT Colon has the following features:

- Auto-segmentation of the colon
- Segmentation editing
- Axial imaging, multi-planar reformatting and 3D views
- Manual and automatic endoluminal fly-through of the colon
- Eye-based navigation for performing fly-through and target-based navigation for examining POI and Reverse View mode
- MPR eye placement to adjust view direction down lumen
- Transparent wall view of the colon with a field-of-view cone to act as a reference during fly-through
- Dual Volume Viewer window format for side-by-side comparison of prone and supine studies
- Ability to mark points in the colon with arrows; arrow are hidden from view when you fly too close
- SPACE BAR to step through images containing arrows
- Prone/supine registration
- Polyp Probe tool to select and characterize polyps
- Polyp assessment using the C-RADS guidelines
- Fly-through image batches and digital movies
- Special report template that contains an anatomically-labeled diagram of the colon for easier documentation of findings, as well as a C-RADS report template
- Fly-through keyboard shortcuts

CT Colon Analysis Tools

Tool	Description
Viewer Window Layouts	
Dual Vol Dual Volume	Display Axial view and POI view (2D-directed) or Flythrough view (3D-directed) for both volumes side-by-side.
Four-up 3D	Display POI view (2D-directed) or Flythrough view (3D-directed) and three MPR views.
Five-up 3D	Display Transparent Wall view, POI view (2D-directed) or Flythrough view (3D-directed), and three MPR views.
Five-up Axial	Display large Axial view, POI view (2D-directed) or Flythrough view (3D-directed), the other two MPR views, and Transparent Wall view.
Runoff	Display large POI view (2D-directed) or Flythrough view (3D-directed), and three MPR views.
Filet View (Comparative)	Display Axial view, POI view (2D-directed) or Flythrough view (3D-directed), and Filet view for both volumes.
3D Filet View (Comparative 3D)	Display Transparent Wall view, POI view (2D-directed) or Flythrough view (3D-directed), and Filet view for both volumes.
Filet View (Single)	Display POI view (2D-directed) or Flythrough view (3D-directed), three MPR views, and Filet view.
Colon Refinement Tools	
Show Colon Line Show Colon Line	Display the colon centerline in the Transparent Wall and MPR views
Edit Edit colon	Display a blue tint in the Transparent Wall view on colon areas that are not included in the Colon region and display a red tint in the MPRs on the Colon region areas.
Sculpt Sculpt colon	Draw a contour to remove unwanted areas from the Colon region.

Tool	Description
Compute	Recreate colon segmentation after all edits are complete.
Rectum Cecum Set Rectum or Cecum	Override the software-generated rectum or cecum location
Swap	Swap the rectum and cecum locations.
Anal Verge Set Anal Verge	Identify the anal verge.
Colon Tools	
Fly Through controls	Fly backward, pause, and fly forward.
180°	Reverse flight direction 180°.
Slower Faster Speed control	Adjust the flight speed.
Update All Views Update All Views	Update related views in real time.
Flythrough/MPR Flythrough/MPR	Display an MPR cross-section overlaid on the Flythrough view.
Register To supine - 01 Jan 2002 Register to	Select the volume to primarily investigate so the other volume registers to the primary volume and navigates to the general vicinity in the lumen.
Polyp Analysis Tools	
Select Select	Probe a suspected polyp.
Edit Edit polyp	Edit polyp boundaries.
Clear Clear	Clear all polyps listed in the Polyp Management area.
Polyp Overlay Polyp Overlay	Show or hide polyp measurements and bounding boxes.

Tool	Description
Rename Rename	Rename a probed polyp in the Polyp Management area.
Delete Delete	Delete a probed polyp in the Polyp Management area.
Match UnMatch Match or UnMatch	Match or unmatch polyps from both studies in the Polyp Management area.
Polyp Assessment area	Assign Size, Location, Morphology, and Attenuation values to probed polyps for the C-RADS report.
Comments... Comments	Add comments and impressions for probed polyps for the C-RADS report.

CT Colon Analysis Lesson

I. Select Study

Load both prone and supine colon studies.

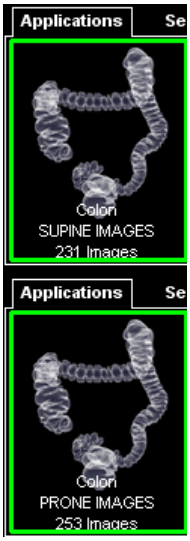
See the instructions for your Vitrea type (VitreaAdvanced Through the Data Manager or VitreaWorkstation) in the **Select Study** chapter of the **VitreaAdvanced-VitreaWorkstation General Education and Reference Guide**.

II. Choose Protocol and Preset

Use one of these procedures:

Data Manager

Press CTRL and select both the prone and supine colon application and double-click one of the application thumbnails:



NOTE: This application opens to the 3D Directed (Prone & Supine) preset. To use the 2D Directed (Prone & Supine) preset, click the 3D mode buttons in the 3D views of the Viewer window to display the POI mode.

Gallery Window

There are four Gallery choices:

- **2D Directed** – viewing a single volume at a time
- **2D Directed (Prone & Supine)** – viewing two volumes at once
- **3D Directed** – viewing a single volume at a time
- **3D Directed (Prone & Supine)**– viewing two volumes at once

This lesson covers the **2D Directed (Prone & Supine)** and **3D Directed (Prone & Supine)** workflows.

1. Select **Colon CT** protocol.

2. Click Pick next to the **2D Directed (Prone & Supine)** preset to start the 2D Directed workflow.

   OR

   Click Pick next to the **3D Directed (Prone & Supine)** preset to start the 3D Directed workflow.

3. Continue with the appropriate Perform Analysis section.

III. Perform Analysis – 2D Directed (Prone & Supine) Workflow

Review Segmentation

Review the study to verify the semi-automatic segmentation is accurate.

1. Click **Five-up 3D** to display the Transparent Wall view.

2. Select **Show Colon Line** to display the colon centerline in the Transparent Wall and MPR views.

   NOTE: Distance measurements are based on the colon centerline. Verify the colon line is appropriate before relying on distance measurements. For optimal distance measurements, be sure the placement of the rectum point, cecum point, and anal verge (if set) is accurate.

   See the Edit Rectum or Cecum Location section of Additional Procedures to reset the rectum or cecum placement.

3. Rotate the Transparent Wall view to verify the colon is accurately segmented.

   See the Edit Colon Region Segmentation section of Additional Procedures if the Colon region is not accurately segmented (portions of the colon are not included in the segmentation, or the segmentation includes unwanted areas, such as the small bowel).

4. Press F10 to display the other volume.

5. Repeat step 3.

6. Click **Dual Volume** to return to the dual volume layout.

Register to a Primary Viewing Volume

Select the volume to primarily investigate, and the other volume “registers to” the primary volume and navigates to the general vicinity in the lumen.

1. Decide which volume, prone or supine, to investigate.

2. Verify the check box in the **Registered To** area is selected.

3. Click the dropdown menu and select the volume to investigate.

Scroll through the MPR Views

Scroll through the MPR views to track the colon cross-sectionally.

4. In the primary MPR view, right-click and drag up and down.

   TIP: To use a larger MPR view, click in the lower-left corner of the view.

   TIP: To use the coronal or sagittal view, click in lower-left corner of the view.

5. Verify is active.

   TIP: The cursor indicates that the volumes are registered.

6. When you find a suspected polyp, click it, or in the surrounding lumen, in the primary view to place the crosshairs on it.

   TIP: The other view “jumps” to the same approximate area of the lumen and the primary 3D POI (point of interest) View displays the crosshair area.

7. Scroll a small amount in the secondary view until you see the same suspected polyp and click it.

Inspect a Suspected Polyp

When you find a suspected polyp, examine it to characterize what it may be.

8. In either 3D POI View, click and drag to rotate the view.

   TIP: To add or remove surrounding tissue around the crosshairs, right-click and drag.

9. Press INSERT (W/L blue key) to toggle between three window/level presets and determine whether air is inside the suspected polyp.

   TIP: Looking for air may help you determine whether the structure is a polyp or stool.

10. Verify

is active.

11. Click and drag over the suspected polyp in the MPR image.

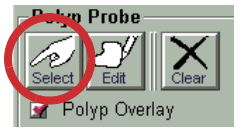
    TIP: The HU value displays for the crosshair location.

Probe the Polyp

Probe polyps for easy identification and navigation.

12. Click

.



13. Click the polyp in the primary view (either the MPR view or the 3D POI view).

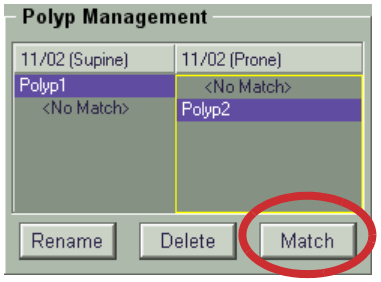
    TIP: In the 3D POI view, Vitrea shades the polyp red and displays its measurements. In the MPR view, Vitrea displays a yellow bounding box around the polyp and gives it a unique label. Vitrea adds a listing of the probed polyp in the Polyp Management area.

NOTE: Distance measurements are measured from the rectum unless you set the anal verge point.

See Identify Anal Verge section of Additional Procedures for information on setting the anal verge point.

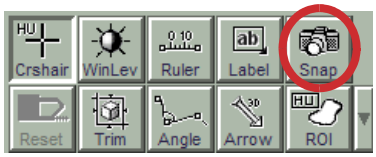
14. Repeat steps 12 and 13 for the same polyp in the secondary view.

15. Click Match in the Polyp Management area.



See the Additional Procedures section of this module for information on editing polyp boundaries and managing polyp listings.

16. Click Snap and click in a view to save a snapshot.



TIP: To take several snapshots, click Snap, hold ALT, and click in each view.

OR

To take one snapshot that includes all views, click Snap, hold CTRL, and click in any view.

NOTE: If the resulting image is viewed on a PACS, the measurements on the image may be difficult to read.

TIP: Move the measurements box if it blocks the view.

Mark Areas of Interest

Use arrows to identify other areas of interest.

17. Right-click in the MPR view and click .

18. Click and drag in the MPR view to draw the arrow.

TIP: Be sure to keep the arrow within the lumen.

TIP: Arrows are listed as “Xtra” in the Polyp Management list.

19. Press SPACEBAR to scroll through marked areas.

Take Snapshots

20. Click

and click in a view to save a snapshot.

Continue Scrolling Through the MPR Views

21. Continue from step 4 until you review the entire colon, and you mark all the suspected polyps and other features.

III. Perform Analysis – 3D Directed (Prone & Supine) Workflow

Review Segmentation

Review the study to verify the semi-automatic segmentation is accurate.

1. Click **Five-up 3D** to display the Transparent Wall view.

2. Select **Show Colon Line** to display the colon centerline in the Transparent Wall and MPR views.

   NOTE: Distance measurements are based on the colon centerline. Verify the colon line is appropriate before relying on distance measurements. For optimal distance measurements, be sure the placement of the rectum point, cecum point, and anal verge (if set) is accurate.

   See the Edit Rectum or Cecum Location section of Additional Procedures to reset the rectum or cecum placement.

3. Rotate the Transparent Wall view to verify the colon is accurately segmented.

   See the Edit Colon Region Segmentation section of Additional Procedures if the Colon region is not accurately segmented (portions of the colon are not included in the segmentation, or the segmentation includes unwanted areas, such as the small bowel).

4. Press F10 to display the other volume.

5. Repeat step 3.

6. Click **Dual Volume** to return to the dual volume layout.

Register to a Primary Viewing Volume

Select the volume to primarily investigate, and the other volume "registers to" the primary volume and navigates to the general vicinity in the lumen.

1. Decide which volume, prone or supine, to investigate.

2. Verify the check box in the **Registered To** area is selected.

3. Click the dropdown menu and select the volume to investigate.

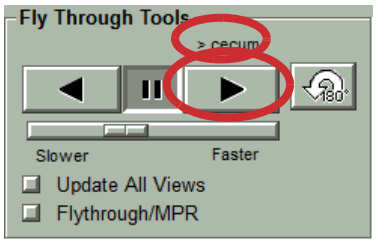
Fly Through the 3D Views

Navigate the passageway by flying through the lumen to search for suspected polyps. The direction of the flight path is indicated in the Fly Through Tools area.

4. Click to begin flying.

   TIP: Click and drag

   to adjust autofly speed.



   TIP: Roll the mouse wheel or right-click and drag towards you in the 3D view to manually fly.

TIP: If you come to blocked portion of the colon,

click ▶ again to continue at the next inflated portion.

TIP: As you fly through the 3D view, review the MPR view to assist with navigation.

5. To update the related views in real time, select **Update All Views**.

6. When you see a suspected polyp, click ❚❚ to stop flying then click the polyp in the primary view to place the crosshairs on it.

   TIP: The other view "navigates" to the same approximate area of the lumen.

7. Fly a small amount in the secondary view until you see the same suspected polyp and click it.

8. To change flight direction 180°, Click

9. Select **Flythrough/MPR** to display an MPR cross-section, external to the lumen, overlaid on the Flythrough view so you can view anatomy outside the colon lumen.

Inspect a Suspected Polyp

When you find a suspected polyp, examine it to characterize what it may be.

10. Click in the lower-right corner of the 3D Fly-Through View to switch to the 3D POI View.

11. In the 3D POI View, click and drag to rotate the view.

    TIP: To add or remove surrounding tissue around the crosshairs, right-click and drag.

12. Press INSERT (W/L blue key) to toggle between three default window/level presets to determine the presence of air inside the suspected polyp.

13. Click .

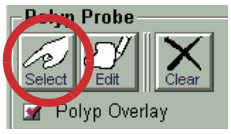
14. Click and drag over any part of the MPR image.

The HU value displays and changes as you move the mouse.

Probe the Polyp

Probe polyps for easy identification and navigation.

15. Click .



16. Click the polyp in the primary view (either the MPR view or the 3D Fly-Through View).

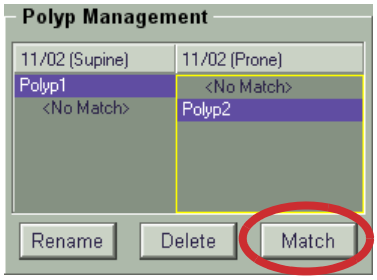
TIP: In the 3D Fly-Through View, Vitrea shades the polyp red and displays its measurements. In the MPR view, Vitrea displays a yellow bounding box around the polyp and gives it a unique label. Vitrea adds a listing of the probed polyp in the Polyp Management area.

NOTE: Distance measurements are measured from the rectum unless you set the anal verge point.

See Identify Anal Verge section of Additional Procedures for information on setting the anal verge point.

17. Repeat steps 15 and 16 for the same polyp in the secondary view.

18. Click Match in the Polyp Management area.

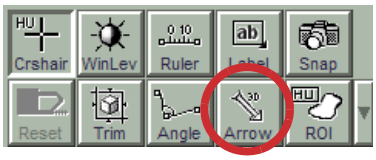


See the Additional Procedures section of this module for information on editing polyp boundaries and managing polyp listings.

Mark Areas of Interest

Use arrows to identify other areas of interest.

19. Right-click in the MPR view and click .



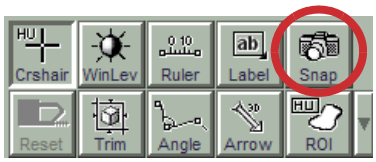
20. Click and drag in the MPR view to draw the arrow.

TIP: Keep the arrow within the lumen.

TIP: Arrows are listed in the Polyp Management area with “Xtra” as the label.

Take Snapshots

21. Click Snap and click in a view to save a snapshot.



TIP: To take several snapshots, click Snap, hold ALT, and click in each view.

OR

To take one snapshot that includes all views, click Snap, hold CTRL, and click in any view.

TIP: Move the measurements box if it blocks the view.

Continue Flying Through the 3D Fly-Through Views

22. Click in the lower-right corner of the 3D view to return to fly-through mode.

23. Continue from step 4 until you review the entire colon in both directions and mark all suspected polyps and other features.

IV. Distribute Findings

The snapshots, batches, and movies you save in the Viewer window are saved to the Report window.

CAUTION: Verify the accuracy of all contours and confirm all measurements when restoring snapshots from previous software versions created through the use of region editing.

1. Select Report at the bottom of the window.

2. Export your findings

OR

Create a report.

The Colon report displays by default. Select the C-RADS (CT Colon Reporting and Data System) report for the Polyp findings table.

NOTE: The distances listed on the C-RADS report are to the rectum unless the anal verge location has been set.

See the **Distribute Findings** chapter of the **VitreaAdvanced-VitreaWorkstation General Education and Reference Guide** for instructions on exporting findings, restoring workflow, and creating reports.

Additional Procedures

This section addresses some less common procedures you may need to complete your workflow.

Edit Colon Region Segmentation

When you load a colon study, Vitrea segments the colon and adds it to a Colon region. If necessary, edit the Colon region by adding inflated areas that were missed on initial segmentation or by removing unwanted areas that were included on initial segmentation, such as the small bowel.

TIP: Select a Viewer Window layout that includes the Transparent Wall view.

1. Click

.

   In the Transparent Wall view, a blue tint displays on colon areas that are not included in the Colon region.

2. Edit in the Transparent Wall view:

   a. To add to the Colon region, hover on a blue area so that it turns green and click.

   b. To remove unwanted areas from the Colon region, hover on a white area so that it turns magenta and click.

   OR

   Edit in the MPR views:

   a. To add to the Colon region, hover on an insufflated area that is not tinted in the MPR so that it turns green and click.

   NOTE: Areas that Vitrea deems as too small or not within a certain HU range can also be added.

   - Hover on an insufflated area that is not tinted in the MPR so that it turns yellow and click.

     NOTE: It is possible that Vitrea will tint a large region yellow (especially if the area to be added is attached to the large

region). In this case, Vitrea will only segment the small portion to be added regardless of how much of the colon is tinted yellow.

b. To remove unwanted areas from the Colon region, hover on a tinted area so that it turns solid magenta (filled in) and click.

3. Sculpt unwanted areas from the Colon region:

a. Click

.

b. Draw a contour around the unwanted area.

c. Click **Remove from Colon**.

TIP: If there are many areas that need to be removed, use **Sculpt** to remove all visible areas from the Transparent Wall view, then use **Edit** to add the colon back into the Colon region.

TIP: If you want to remove a portion of the Colon region, but **Edit** tints too large a region, divide it by using **Sculpt** to remove a small portion in the middle, then use **Edit** to remove one of the remaining areas.

4. Click

after all edits are complete to recreate the Colon region.

5. Review the colon to ensure edits are applied correctly.

NOTE: If the message “More edits are required...” displays after you click **Compute**, you may need to add or remove more areas or edit the rectum or cecum points.

6. If you have the Filet view displayed, click **Regenerate Filet Views** to recompute the Filet views after all edits to the colon segmentation are complete.

Edit Rectum or Cecum Location

NOTE: Use the MPR views to edit the rectum or cecum location for optimal placement. If you use the Transparent Wall view to edit, be sure to rotate the view fully to verify the location point.

1. Scroll the MPR views to display the correct rectum or cecum location.

2. Click

or

.

3. Click in an MPR view to set the point.

TIP: If Vitrea initially reversed the rectum and cecum points upon segmentation, click

.

Identify Anal Verge

NOTE: Use the MPR views to set the anal verge location for optimal placement. If you use the Transparent Wall view, be sure to rotate the view fully to verify the location.

1. Scroll the MPR views to display the anal verge location.

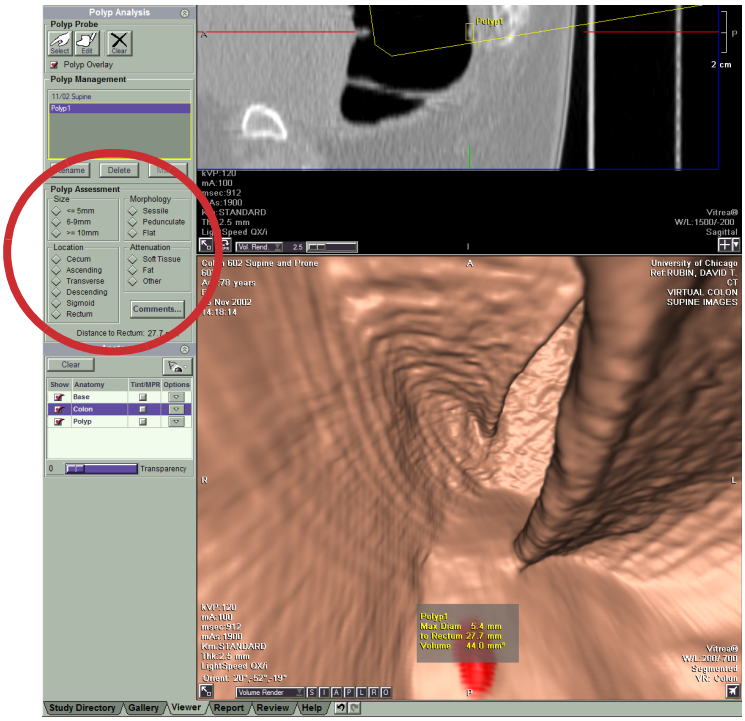
2. Click

.

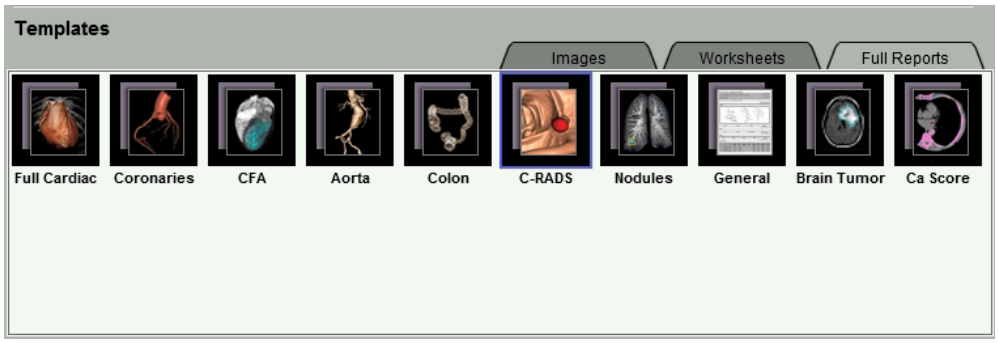
3. Click in the MPR view to set the point.

Polyp Assessment

1. To assess the polyps, make your selections (size, morphology, location, and attenuation) in the Polyp Assessment area of the Viewer tab.



2. From the Report tab, select the C-RADS report template and click New Report.



Your selections in the Polyp Assessment area Auto-populate in the C-RADS report.

Findings

Polyp	Scan	Vol. (mm³)	Max Diam (mm)	Distance To Rectum/Anal Verge (cm)	Morphology	Location	Attenuation	Size (mm)	Comments
Polyp1	05 Nov 2002 14:18:14	219.0	8.3	75/--	Pedunc.	Descending	Soft Tissue	6-9mm	---
Polyp3	05 Nov 2002 14:18:14	161.1	8.9	94/--	Flat	Transverse	Soft Tissue	6-9mm	---
Polyp5	05 Nov 2002 14:18:14	712.2	14.0	102/--	Pedunc.	Transverse	Soft Tissue	>= 10mm	---
Polyp7	05 Nov 2002 14:18:14	970.9	15.5	105/--	Sessile	Transverse	Soft Tissue	>= 10mm	---
Polyp9	05 Nov 2002 14:18:14	352.0	11.4	106/--	Flat	Transverse	Soft Tissue	>= 10mm	---

NOTE: The distances listed on the C-RADS report are to the rectum unless the anal verge location has been set.

Work With Single Volume Presets

If you prefer to work with one volume at a time rather than both volumes side-by-side, select the 2D Directed or 3D Directed preset.

- Press F9 (PREVIOUS on blue keys) or F10 (NEXT on blue keys) to toggle between volumes.

Edit Polyp Boundaries

If Vitrea did not shade an entire polyp, edit the polyp boundary.

NOTE: Vitrea does not allow using the Sculpt tool for editing an existing polyp. Use the Edit tool to edit existing polyps.

1. Select the polyp in the Polyp Management area,
2. Click

.

3. In the axial view, drag the contour to the desired shape and size.

Navigate to Polyp Findings

Use the Polyp Management list to navigate to the findings in the volumes.

To	Do This
Navigate to a finding in a volume	Click the finding name in the Polyp Management list.
Navigate forward through images containing findings	Press SPACEBAR.
Navigate backward through images containing findings	Press SHIFT + SPACEBAR.

Manage Polyp Findings

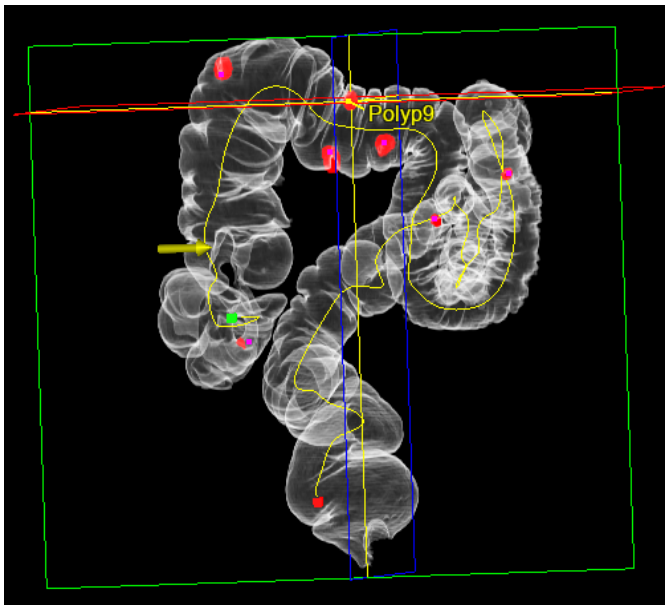
Vitrea adds listings of probed polyps and arrows to the Polyp Management area. Use this list to manage the findings.

- Select the finding in the Polyp Management list, then:

Click	To
Rename	Rename the finding.
Delete	Delete the finding.
UnMatch	Unmatch matched findings.

Review the Colon Centerline

Show the colon centerline in Transparent Wall view and MPR views.



1. Click .

2. Select **Show Colon Line** in the Colon Edit Tools area.

   OR

   Right-click and select **Show Colon Line**.

3. Click

to return to the dual volume view.

Use the Reverse View while Flying

Use the Reverse View mode to see behind your viewpoint while flying.

1. Click .

2. In the upper 3D view, click to switch to Reverse View mode.

Create Fly-Through Image Batches and Movies

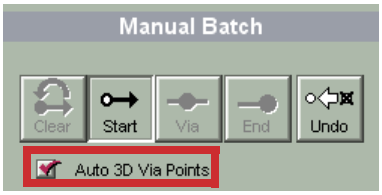
Create Fly-Through image batches or movies to burn to a CD or post to the intranet.

1. Fly to the starting position in the 3D View.

2. Select

.

3. Verify **Auto 3D Via Points** is selected.



4. Click in the 3D view.

5. Press SHIFT + > to autofly.

   TIP: To navigate past a collapse, press SHIFT + > again.

6. To end flying:

   Click

   OR

   Click in the image.

7. Click

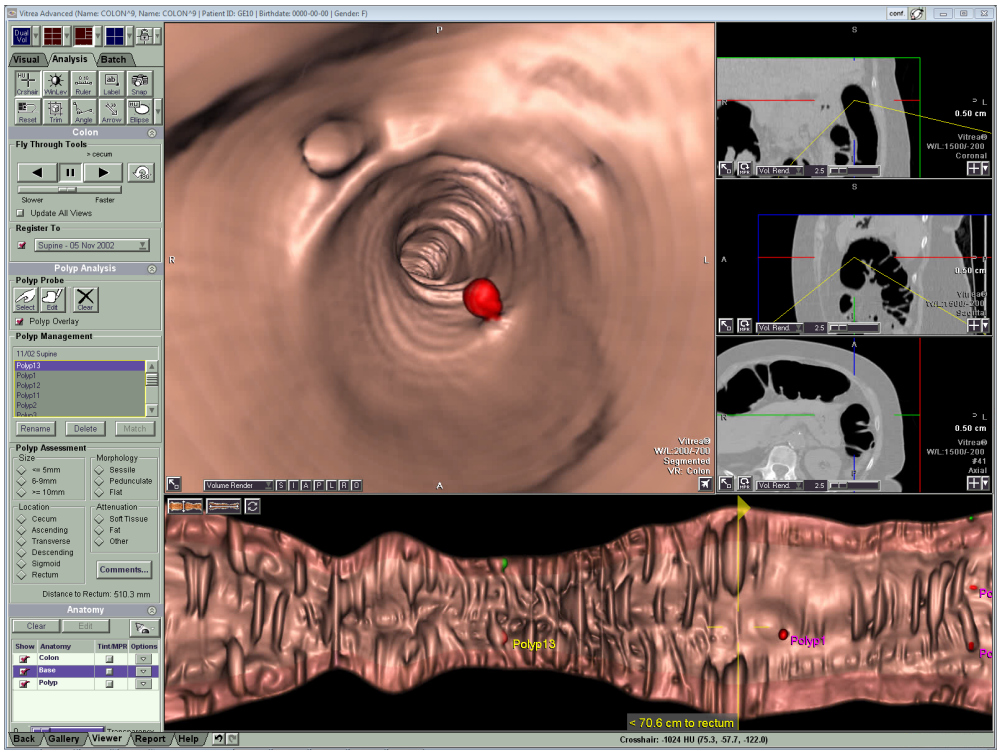
or

.

   TIP: A preview of the batch or movie plays in a separate window and then it is saved to the Report window.

Display the Colon Filet View

Display the colon as an unfolded tube along the centerline axis by switching to the Filet view. Vitrea uses the colon centerline to generate the filet view. Review the Transparent Wall view to verify the centerline.



1. Click to display the single-volume filet view.

   OR

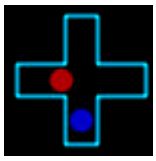
   Click to display the dual-volume filet view.

   The Filet view displays with a vertical line that indicates the crosshair location of the other views. The flag on the vertical line indicates the direction of the Fly-Through view. The approximate distance from the crosshair to the rectum is indicated at the bottom of the view.

   NOTE: The shaded area on the edges of the Filet view indicates the overlap band. This is repeated data to provide context to features on the edges.

2. To fit the image width in the Filet view window, click . To fit the image length in the Filet view window, click .

3. Press the ARROW keys to rotate the filet view. Click to reset the rotation. The dots within the cross icon in the upper-right corner of the filet view indicate the direction and amount of rotation.



TIP: The Filet view behaves like any other 3D view in regard to pan, zoom, crosshair placement, and window/level.

4. Fly through the 3D view.

NOTE: It is recommended that you use the 3D or MPR views as the primary views for finding and investigating polyps. Use the Filet view for secondary viewing.

As you move along the colon in the Fly-Through view, the vertical line in the Filet view moves along the flattened image.

TIP: Select the **Update All Views** check box to enable this behavior.

5. Probe polyps in the MPR, 3D, or Filet view.

VitreaAdvanced annotates polyps in the Filet view.

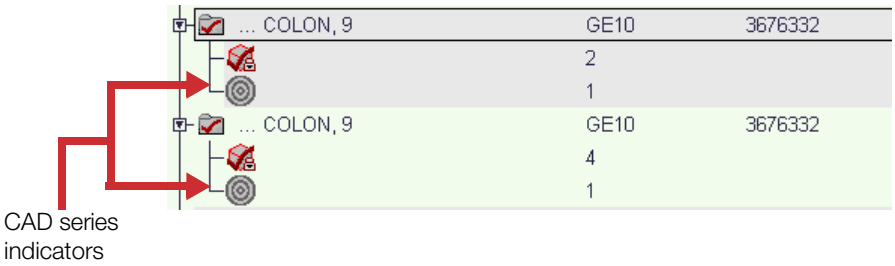
NOTE: Polyps within the overlap band are shaded green. A polyp in the overlap band may display twice, but is annotated once.

VeraLook Workflow

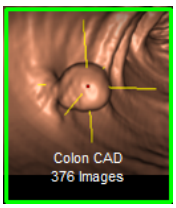
Processing the CAD Results

The CAD series process automatically if the study description matches the protocol selector for CT Colon. Vitrea builds the CAD series and links it to the corresponding volume. A special icon identifies the CAD series on the Study Directory.

CAD Series (Vitrea Standalone):



CAD Studies (VES and PACS-integrated Data Manager):



Processing the CAD results manually (VitreaWorkstation only)

If Vitrea did not process the CAD results automatically, you can generate CAD results manually.

1. Right-click the study.
2. From the menu, select **Process Colon CAD**.

   Vitrea will build the CAD results. A progress bar will display across the CAD icon.

   NOTE: If Vitrea did not process the CAD results automatically for a VES system, please contact your System Administrator regarding re-pushing the data.

Loading a CAD Series

You load a CAD series just like any other Vitrea study. The CAD series is linked to the volume and will load with the rest of the study.

Vitrea will load the series associated with the CAD results generated. If there is more than one series with corresponding CAD results, use the Data Selection screen to select specific series to load.

Any CT Colon preset can be used with VeraLook.

Displaying CAD Candidates

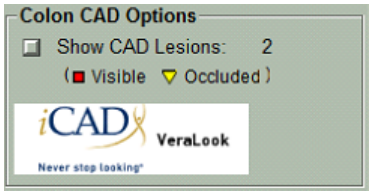
CAUTION: Examine the colon in its entirety, either all slices of the MPRs or both directions of fly-through, prior to displaying the CAD results.

When you display the CAD candidates in the Viewer window, the software displays marks on the Fly Through and MPR views

- Select the **Show CAD Lesions** check box.

  OR

  Press D.

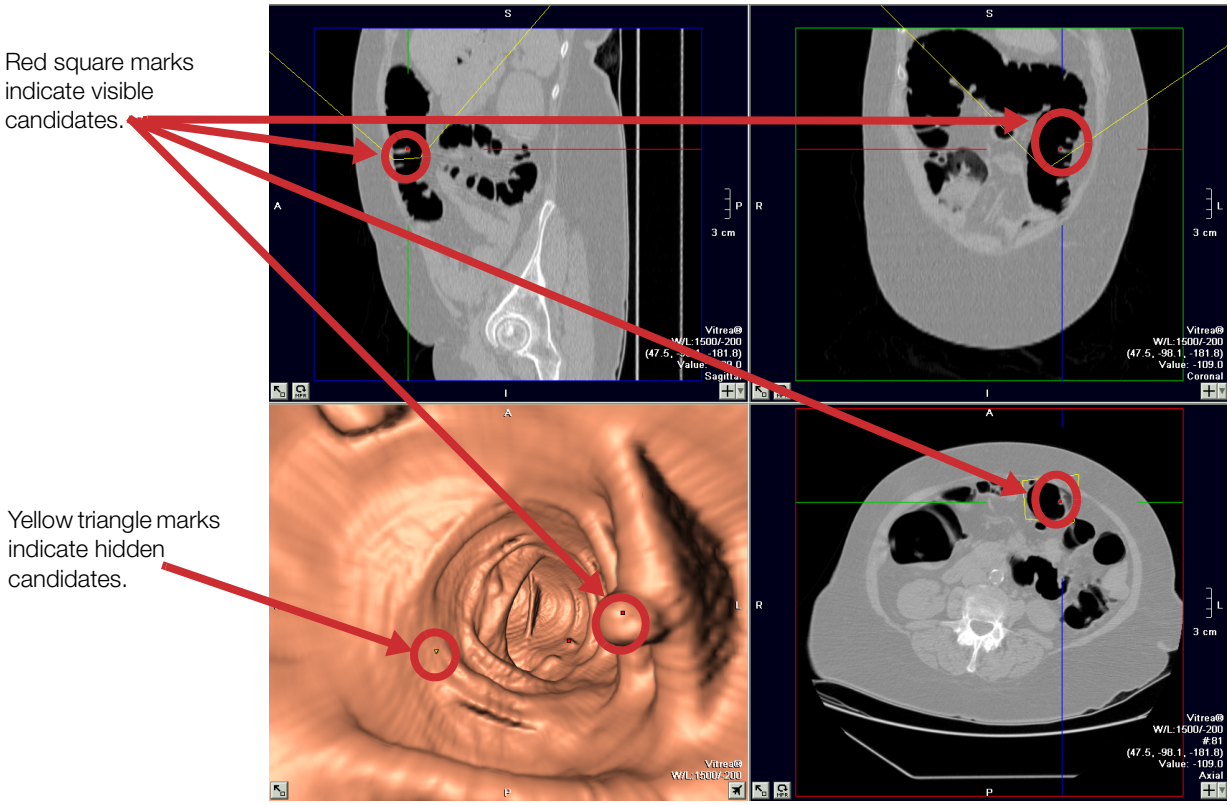


  Red square marks, indicating visible candidates, display in the Fly Through and MPR views.

  Yellow triangle marks, indicating occluded (hidden behind a fold) candidates, display in the Fly Through view.

  Vitrea adds a listing to the Polyp Management area for each candidate.

  NOTE: The accuracy of the number of candidates found and placement of CAD marks depends on a number of factors, many of which are beyond the control of the software. It is important that you do not base a treatment or diagnostic decision solely on the results of the CAD analysis.



To hide CAD marks:

- Clear the **Show CAD Lesions** check box.

  OR

  Press D.

CT Lung Analysis

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Additional Procedures

- Select Viewer Window Layout
- Edit Nodule Boundaries
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- Manage Nodule Findings
- Characterize Nodules
- Nodule CAD Analysis
- Pulmonary Artery Analysis
- Filling Defects CAD Analysis

Appendix

- Fleischner Criteria

CT Lung Analysis Overview

CT Lung Analysis is intended for the review and analysis of thoracic CT images for the purposes of semi-automatic segmentation and quantification/characterization of nodules in the lung. Lung Analysis has the following features:

- User selection of single study or multiple studies
- Nodule Analysis preset that automatically displays the lung airways
- Segmentation of solitary pulmonary nodules (SPNs), nodules fed by vessels, and nodules attached to the chest wall; limited to segmenting nodules less than 30mm in diameter and unable to segment ground glass opacifications (GGOs)
- Automatic software calculation of the following measurements for each segmented nodule:
  - Volume (mm^3)
  - Effective diameter (mm): Diameter of a sphere with the same volume
  - Maximum Diameter (mm) (RECIST)
  - Short Axis Diameter (mm) (WHO)
  - Average/Minimum/Maximum densities (HU)
- Manual edit of the nodule segmentation contour lines with automatic recalculation of all measurements post-editing
- Manual specification of the following characteristics for each nodule:
  - Lobe Location
  - Shape
  - Border

- Ability to enter and edit observations on each nodule
- Comparison feature that allows establishing correspondence between nodules in two or three studies, and automatic calculation of the following temporal measurements between each follow-up scan and the previous scan:
  - Elapsed time in days
  - Doubling time in days
  - Percent (%) growth in nodule volume
- Automated tracking for lung nodules in longitudinal exams
- Report generation summarizing nodule finding and measurements with comparison formats and temporal measurements to evaluate changes in nodule characteristics over time

CAUTION: You are responsible for reviewing the placement and accuracy of all system-generated nodule boundary contour lines and editing them, deleting them, and drawing new boundary lines wherever necessary.

CAUTION: Review all automatically-probed nodules to verify they are correctly identified and matched.

CT Lung Analysis Lesson

I. Select Study

Load a lung series, or load one series from two or three studies for the same patient from different study dates.

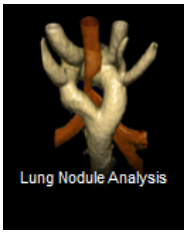
See the instructions for your Vitrea type (VitreaAdvanced Through the Data Manager or VitreaWorkstation) in the **Select Study** chapter of the **VitreaAdvanced-VitreaWorkstation General Education and Reference Guide**.

II. Choose Protocol and Preset

Use one of these procedures:

Data Manager

- Double-click the **Lung** application thumbnail.



Gallery Window

1. On the Gallery window, select the Lung CT protocol.

   The Gallery choices update automatically.

2. Double-click in the Nodule Analysis preset.

III. Perform Analysis

Restore Nodules

If you load a scan that has been previously worked up in Vitrea, Vitrea detects the results and allows you to restore the previously probed nodules.

- Click

in the Nodule Management area.

NOTE: Vitrea looks for restorable nodules of the second-most recent study first. If nodules are not found on that study, Vitrea looks for restorable nodules of the earliest study. If no prior studies have nodules, Vitrea looks for restorable nodules of the most recent study.

NOTE: When you restore nodules from previous studies, be sure to verify against previous reports or snapshots that Vitrea restored all nodules appropriately.

Viewer Synchronization

Viewer synchronization lets you lock views so visualization and spatial operations are replicated across views in a locked set. When views are synchronized any manipulations made in one view are immediately reflected in the other synchronized view(s).

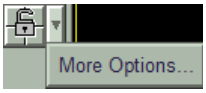
NOTE: The viewer synchronization feature only applies to MPR views and 3D views.

- Lock cine, window/level, pan, zoom, and crosshair for MPR viewers.
- Lock window/level, pan, zoom, crosshair, and rotate for 3D views.

Specific presets may have additional link choices. The preset file determines how VitreaAdvanced links a particular manipulation. The two choices are:

- Manual lock — you must manually align viewers across datasets to the desired starting points.
- Auto lock — start manipulating in one dataset and the other dataset either takes the same value of the first dataset or creates a corresponding value based on an algorithm.

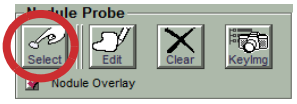
NOTE: When Vitrea is installed, synchronization options in each available preset (with multi-volume view format) in Vitrea are configured based on an estimate of your specific clinical requirements. To change this configuration, contact your System Administrator or Technical Support.

Button	Description
	Global Link Click to set all available views **Linked** or **Unlinked**. Global Link Button **NOTE:** When set, and every view is linked, manipulations performed with Auto Link have the active dataset as the reference value, and the other datasets take the active dataset's value. The More Options dialog includes settings found in the loaded preset. Use this dialog to change defaults set in the preset by checking or clearing options shown.  **NOTE:** Zoom and Pan are set to be linked in the preset and cannot be changed using the Configuration dialog.
	Each view has a Link/Unlink button in the lower left corner. This button controls the view the button belongs to, adding it or removing it from a link set. Manipulations performed with the Auto Link feature have the active dataset as the reference value, and other datasets take on the active dataset's value.

Probe Nodules

Use Nodule Probe to detect and measure nodules. Match nodules to display comparison measurements.

3. In the Nodule Probe area, click .



4. Right-click and drag in one of the views and look for suspected nodules.

TIP: Nodules may be easier to see if the rendering is set to MIP, and you increase the MPR thickness to about 10. Slide the thickness bar at the bottom of the axial view to adjust.

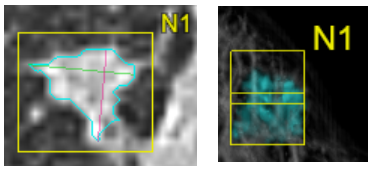
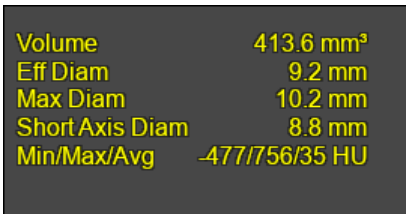
5. When you find a nodule, click it in the left view.

TIP: If Vitrea is unable to probe the nodule, it will sound a tone. Decrease the thickness if this happens.

TIP: If Vitrea is unable to probe the nodule with minimum thickness applied, press CTRL and click. An elliptical contour displays that you can then edit.

See the Additional Procedures section for information regarding editing nodule contours.

Vitrea gives the nodule a unique label, adds a listing to the Nodule Management area, and displays:

Feature	Description
Nodule contour and axes	• The cyan contour indicates the nodule boundary. Hover on the nodule contour line and drag to edit it. **NOTE:** The thickness must be set to the minimum to edit nodule contours. • The green line indicates the Max Diam (RECIST) measurement. A RECIST measurement is the measurement of the maximum diameter on the axial plane of a nodule. • The pink line indicates the perpendicular Short Axis to the Max Diam line (WHO).
Yellow bounding box	Displays around currently selected nodule in the axial and 3D Transparent Map views. 
Green bounding box	Displays around non-selected nodule in the axial and 3D Transparent Map views.
Measurements	Display in the axial view.  **TIP:** To move the measurements box, hover over the box and click and drag to move the box to a location where it will not block the view.

TIP: To examine the 3D image of the nodule more closely:

a. Click in the lower-right corner of the 3D view.

b. Click and drag in the view to rotate.

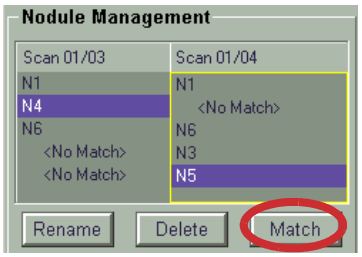
c. Click in the lower-right corner of the view to return to the 3D Transparent Map view.

6. If the same nodule is evident in the a follow-up study view, Vitrea probes it. Verify that the nodule(s) Vitrea probed is correct.

CAUTION: Review all automatically-probed nodules to verify they are correctly identified and matched.

See the Additional Procedures section of this module for information regarding editing nodule boundaries and managing nodule listings.

7. Click Match in the Nodule Management area.



NOTE: In the axial view for the follow-up scan, Vitrea displays comparative measurements.

Take Snapshots

8. Right-click in the view and click .

TIP: For important (key) images, click KeyImg then click in the image.

These snapshots are listed separately in the Image Findings list on the Report window.

See the Distribute Findings section of this module for information on sorting and reporting images.

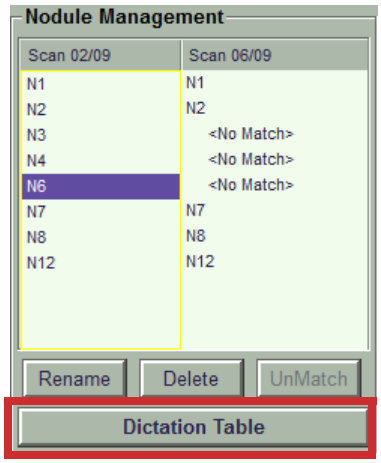
9. Repeat from step 4 for all nodules in the study.

TIP: Select new nodules in follow-up exams that do not have a match in the baseline exam.

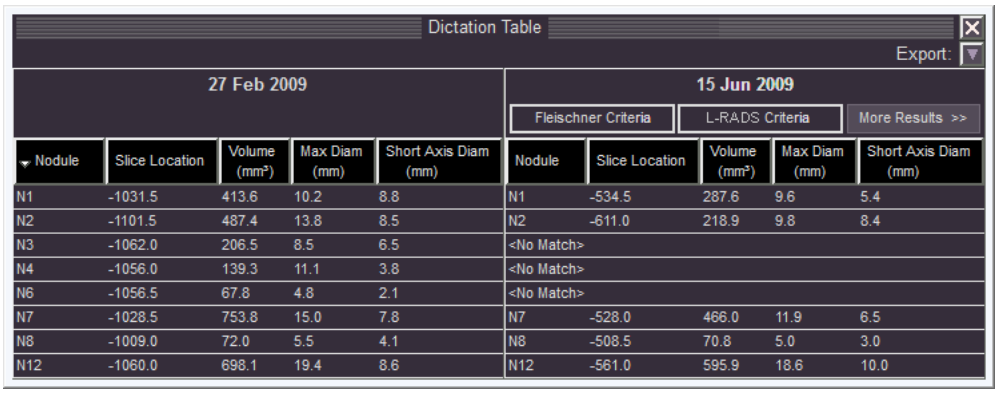
Display the Dictation Table

Display a dictation table that lists the nodule name, slice location, and measurements for each nodule, grouped by exam date.

10. In the Nodule Management area, click **Dictation Table**.



Vitrea displays the Dictation Table.



Dictation Table

Export:

27 Feb 2009					15 Jun 2009				
					Fleischner Criteria	L-RADS Criteria		More Results >>	
Nodule	Slice Location	Volume (mm³)	Max Diam (mm)	Short Axis Diam (mm)	Nodule	Slice Location	Volume (mm³)	Max Diam (mm)	Short Axis Diam (mm)
N1	-1031.5	413.6	10.2	8.8	N1	-534.5	287.6	9.6	5.4
N2	-1101.5	487.4	13.8	8.5	N2	-611.0	218.9	9.8	8.4
N3	-1062.0	206.5	8.5	6.5	<No Match>				
N4	-1056.0	139.3	11.1	3.8	<No Match>				
N6	-1056.5	67.8	4.8	2.1	<No Match>				
N7	-1028.5	753.8	15.0	7.8	N7	-528.0	466.0	11.9	6.5
N8	-1009.0	72.0	5.5	4.1	N8	-508.5	70.8	5.0	3.0
N12	-1060.0	698.1	19.4	8.6	N12	-561.0	595.9	18.6	10.0

11. To sort on the nodule name column, click the **Nodule** column header.

12. To sort by slice location (z-position of the centroid in the patient coordinate space) of the nodules, click the **Slice Location** column header.

13. To display the comparative measurements for matched nodules (multiple studies loaded), click More Results >> .

Elapsed Time (days)	Percent Growth	Doubling Time (days)
108	-30.5	
108	-55.1	
108	-46.7	
108	-31.4	
108	-40.3	
108	80.5	127

14. To display the Fleischner Criteria, click Fleischner Criteria .

The following charts display:

- Recommendations for Follow Up and Management of Nodules Smaller than 8 mm Detected Incidentally at Nonscreening CT[1]
- Recommendation for the Management of Subsolid Pulmonary Nodules Detected at CT: A Statement from the Fleischner Society[2]

See the Appendix for the Fleischner Criteria charts.

OR

To display the L-RADS Criteria, click L-RADS Criteria .

The Lung-RADS™ Assessment Categories[3] chart displays.

See the Appendix for the L-RADS Criteria chart.

15. Click the Export dropdown Export: and select:

- **Take Snapshot**, to capture an image of the dictation table to include in a report
- **Export to CSV**, to create a CSV file that can be viewed in a spreadsheet
- **Copy to Clipboard**, to copy to the Windows clipboard so you can paste in another application

1. Ways to improve radiologists' adherence to Fleischner Society guidelines for management of pulmonary nodules. Eisenberg RL.J Am Coll Radiol. 2013 Jun;10(6):439-41. doi:10.1016/j.jacr.2012.10.001. Epub 2013 Mar 29.
2. Recommendations for the management of subsolid pulmonary nodules detected at CT: a statement from the Fleischner Society. Naidich DP. et al. Radiology. 2013 Jan;266(1):304-17. doi: 10.1148/radiol.12120628. Epub 2012 Oct 15.
3. Lung Imaging Reporting and Data System (Lung-RADS™) by American College of Radiology; http://www.acr.org/Quality-Safety/Resources/LungRADS

IV. Distribute Findings

The snapshots, batches, and movies you save in the Viewer window are saved to the Report window.

CAUTION: Verify the accuracy of all contours and confirm all measurements when restoring snapshots from previous software versions created through the use of region editing.

1. Select Report at the bottom of the window.

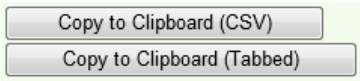
2. Export your findings or create a report.

   See the **Distribute Findings** chapter of the **VitreaAdvanced-VitreaWorkstation General Education and Reference Guide** for instructions on exporting findings, restoring workflow, and creating reports.

   TIP: Lung Analysis has a specific Nodules Worksheet and Nodules Full Report template.

To copy the Nodules Worksheet to the clipboard:

1. From the Nodules Worksheet (page 2 of the Nodules Full Report), click either **Copy to Clipboard** button.

2. Paste into any application compatible with .csv or tabbed lists.

Additional Procedures

This section addresses some less common procedures you may need to do to complete your workflow.

Select Viewer Window Layout

Vitrea provides these Viewer window formats for lung nodule detection:

Button	Description
	Single Lung Format for slice-by-slice or volume-by-volume review and analysis. This format contains the following views for a single loaded study: • MPR views (axial, coronal, and sagittal) • 3D POI (point-of-interest) volume • Semi-transparent 3D lung • Nodule characteristics
	Basic Comparative Lung Format for side-by-side comparison. This format contains the following views for a maximum of three loaded studies or volumes: • Axial MPR view • Semi-transparent 3D lung **NOTE:** In comparative lung format, all the views corresponding to the active volume are enclosed by a yellow rectangle.
	Advanced Comparative Lung Format for side-by-side comparison and analysis. This format contains the following views for a maximum of three loaded studies or volumes: • Axial MPR view • 3D POI volume • Nodule characteristics **NOTE:** In comparative lung format, all the views corresponding to the current volume are enclosed by a yellow rectangle.

NOTE: The basic and advanced comparative lung format buttons display only if you load more than one volume.

Edit Nodule Boundaries

If necessary, edit the nodule boundaries.

NOTE: Vitrea does not allow using the Sculpt tool for editing an existing nodule. Use the Edit tool to edit existing nodules.

3. Adjust the Thickness Slider to minimum slice thickness available.

4. Verify the Nodule Overlay check box is selected.

5. Select the nodule in the Nodule Management area.

6. Click

.

7. In the axial view, drag the contour to the desired shape and size.

8. Roll the mouse wheel to scroll through the axial image, then repeat step 7 as necessary.

9. To remove a contour at the top or bottom margin of a nodule, scroll to that contour, then press DELETE or BACKSPACE.

Navigate to Nodule Findings

Use the Nodule Management list to navigate to the findings in the volumes.

To	Do This
Navigate to a finding in a volume	Click the finding name in the Nodule Management list or Dictation Table.
Navigate forward through images containing findings	Press SPACEBAR.
Navigate backward through images containing findings	Press SHIFT + SPACEBAR.

Manage Nodule Findings

Vitrea adds listings of probed nodules in the Nodules Management area. Use this list to manage the findings. Findings changed in the Nodules

Management area will also be changed in the dictation table and report table.

- Select the nodule in the Nodule Management list, then:

Click	To
Rename	Rename the nodule.
Delete	Delete the nodule.
UnMatch	Unmatch matched nodules.

Characterize Nodules

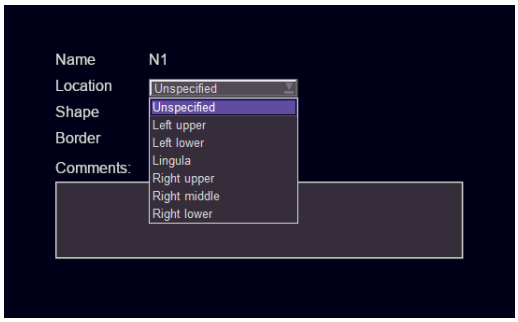
Specify characteristics for each nodule:

- Lobe Location
- Shape
- Border

1. Click or .

2. Select the nodule in the Nodules Management area.

3. In the Nodule Characteristics view, click any of the dropdown arrows, then select a value.



4. Click in the comments box, then type observations or other information about the nodule.

TIP: Vitrea imports the values and comments you specify for each nodule on the second page of the Nodules report template.

5. Repeat from step 2 for other nodules.

Nodule CAD Analysis

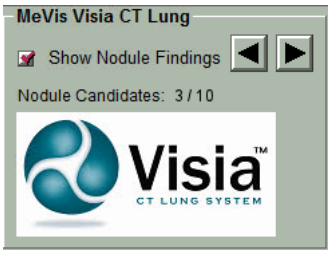
NOTE: CAD Analysis is available for use with the separately-licensed Visia CT Lung system

Use the Visia CT Lung option to automatically display nodule findings.

CAUTION: The CAD software is a detection aid, not an interpretive aid. It should only be used after the first reading of the images. You should always read first before turning on CAD, and then never change your mind about a potential finding if CAD does not mark it.

1. Follow the steps in the **Perform Analysis** section of this module to complete the first reading.

2. Check the **Show Nodule Findings** check box Show Nodule Findings.



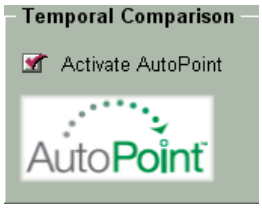
3. Click ◀ or ▶ to step through the potential findings within the currently selected scan.

   OR

   Press PAGE UP or PAGE DOWN to step through potential findings within the currently selected scan.

   TIP: The currently selected scan has a yellow border.

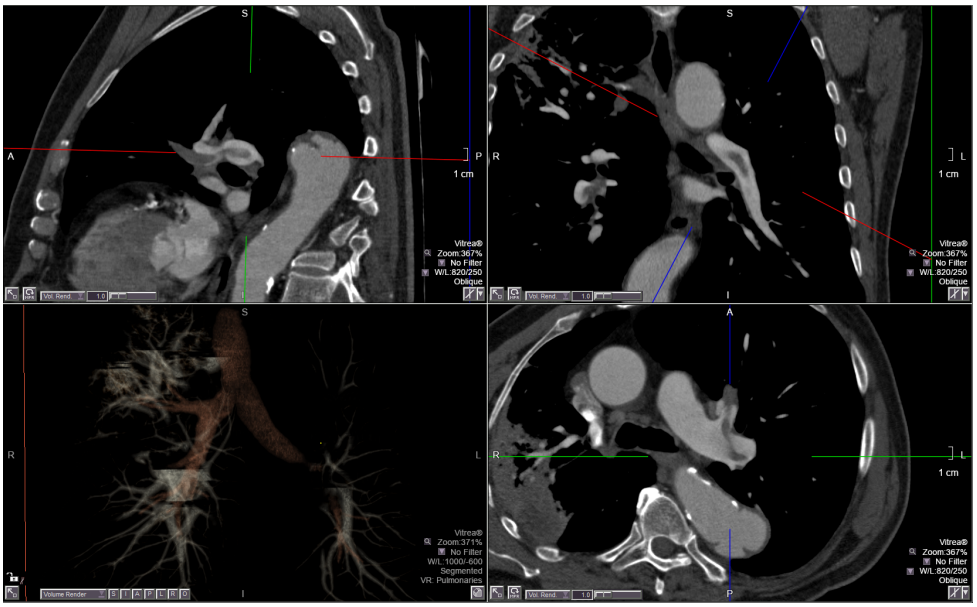
4. If the CAD software has found potential findings that match in multiple studies, select the **Activate AutoPoint** check box to cause Vitrea to indicate matching nodules when you probe a potential nodule.



5. If you decide a CAD finding is a nodule, probe it using the Nodule Probe tools.

Pulmonary Artery Analysis

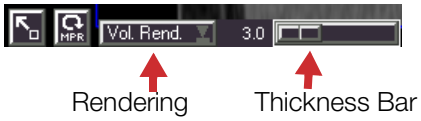
Perform pulmonary artery examinations in MPR and 3D views to evaluate the presence of suspected filling defects or other pathology in the pulmonary arteries.



Examine the MPR Views

1. Select a Pulmonary Artery study.
2. Choose the **Lung CT** protocol and the **Pulmonary Analysis** preset.
3. Roll the mouse wheel in the MPR views and look for suspected filling defects or other pathology.

   TIP: Filling defects may be easier to see if the rendering is set to MIP, and you increase the MPR thickness to about 10. Slide the thickness bar at the bottom of the MPR view to adjust.



4. Apply the Oblique MPR mode and “walk” the vessels.
5. Take snapshots.

6. Repeat from step 3 for the other MPR views.

Examine the 3D View

7. Click in the lower-left corner of the 3D view.

8. On the Visual tab, select the Oblique Trim check box. Oblique Trim

9. Right-click and drag up and down to scroll through the image.

10. Middle-click and drag up and down to rotate the trim plane around a pivot point.

11. Take snapshots.

Filling Defects CAD Analysis

NOTE: CAD Analysis is available for use with the separately-licensed Visia CT Lung system

Use the Visia CT Lung option to automatically display nodule findings.

CAUTION: The CAD software is a detection aid, not an interpretive aid. It should only be used after the first reading of the images. You should alway read first before turning on CAD, and then never change your mind about a potential finding if CAD does not mark it.

1. Follow the steps in the **Pulmonary Artery Analysis** section of this module to complete the first reading.

2. Check the **Show Filling Defects** check box Show Filling Defects .

3. Click or to step through the filling defects within the currently selected scan.

OR

Press PAGE UP or PAGE DOWN to step through the filling defects within the currently selected scan.

TIP: The currently selected scan has a yellow border.

Appendix

Fleischner Criteria

Recommendations for Follow-up and Management of Nodules Smaller than 8mm Detected Incidentally at Nonscreening CT[1]

Nodule Size (mm)*	Low-Risk Patient†	High-Risk Patient‡
≤4	No follow-up needed§	Follow-up at 12 mo; if unchanged, no further follow-up‖
>4—6	Follow-up at 12 mo; if unchanged, no further follow-up‖	Initial follow-up CT at 6—12 mo the at 18-24 mo if no change‖
>6—8	Initial follow-up CT at 6—12 mo the at 18-24 mo if no change	Initial follow-up CT at 3—6 mo then at 9—12 and 24 mo if no change
>8	Follow-up CT at around 3, 9, and 24 mo, dynamic contrast-enhanced CT, PET, and/or biopsy	Same as for low-risk patient

Note.—Newly detected indeterminate nodule in persons 35 years of age or older.

* Average of length and width.

† Minimal or absent history of smoking an of other known risk factors.

‡ History of smoking or of other known risk factors.

§ The risk of malignancy in this category (<1%) is substantially less than that in a baseline CT scan of an asymptomatic smoker.

‖ Nonsolid (ground-glass) or partly solid nodules may require longer follow-up to exclude indolent adenocarcinoma.

1. Ways to improve radiologists' adherence to Fleischner Society guidelines for management of pulmonary nodules. Eisenberg RL.J Am Coll Radiol. 2013 Jun;10(6):439-41. doi:10.1016/j.jacr.2012.10.001. Epub 2013 Mar 29.

Recommendations for the Management of Subsolid Pulmonary Nodules Detected at CT: A Statement from the Fleischner Society[1]

Nodule Type	Management Recommendations	Additional Remarks
Solitary pure GGNs		
≤5 mm	No CT follow-up required	Obtain contiguous 1-mm-thick sections to confirm that nodule is truly a pure GGN
>5 mm	Initial follow-up CT at 3 months to confirm persistence then annual surveillance CT for a minimum of 3 years	FDG PET is of limited value, potentially misleading, and therefore not recommended
Solitary part-solid nodules		
	Initial follow-up CT at 3 months to confirm persistence. If persistent and solid component <5mm, then yearly surveillance CT for a minimum of 3 years. If persistent and solid component ≥5 mm, then biopsy or surgical resection	Consider PET/CT for part-solid nodules >10 mm
Multiple subsolid nodules		
Pure GGNs ≤5 mm	Obtain follow-up CT at 2 and 4 years	Consider alternate causes for multiple GGNs ≤5 mm

1. Recommendations for the management of subsolid pulmonary nodules detected at CT: a statemet from the Fleischner Society. Naidich DP.etal. Radiology. 2013 Jan;266(1):304-17. doi: 10.1148/radiol.12120628. Epub 2012 Oct 15.

Nodule Type	Management Recommendations	Additional Remarks
Pure GGNs > 5 mm without a dominant lesion(s)	Initial follow-up at 3 months to confirm persistence and then annual surveillance CT for a minimum of 3 years	FDG PET is of limited value, potentially misleading, and therefore not recommended
Dominant nodule(s) with part-solid or solid component	Initial follow-up CT at 3 months to confirm persistence. If persistent, biopsy or surgical resection is recommended, especially for lesions with >5 mm solid component	Consider lung-sparing surgery for patients with dominant lesion(s) suspicious for lung cancer

L-RADS Criteria

Lung-RADS™ Version 1.0 Assessment Categories[1]

Category Descriptor	Category Descriptor	Primary Category	Management
Incomplete	-	0	Additional lung cancer screening CT images and/or comparison to prior chest CT examinations is needed
Negative	No nodules and definitely benign nodules	1	Continue annual screening with LDCT in 12 months
Benign Appearance or Behavior	Nodules with a very low likelihood of becoming a clinically active cancer due to size or lack of growth	2	

1. Lung Imaging Reporting and Data System (Lung-RADS™) by American College or Radiology; http://www.acr.org/Quality-Safety/Resources/LungRADS

Category Descriptor	Category Descriptor	Primary Category	Management
Probably benign	Probably benign finding(s) - short term follow up suggested; includes nodules with a low likelihood of becoming a clinically active cancer	3	6 month LDCT
Suspicious	Findings for which additional diagnostic testing and/or tissue sampling is recommended	4A	3 month LDCT; PET/CT may be used when there is a greater than or equal to 8 mm solid component
		4B	Chest CT with or without contrast, PET/CT and/or tissue sampling depending on the [1]probability of malignancy and comorbidities. PET/CT may be used when there is a greater than or equal to 8 mm solid component.
Significant - other		S	
Prior Lung Cancer		C	

1 Link to McWilliams Lung Cancer Risk Calculator
Upon request from the authors at: http://www.brocku.ca/lung-cancer-risk-calculator
At UptoDate http://www.uptodate.com/contents/calculator-solitary-pulmonary-nodule-malignancy-risk-brock-university-cancer-prediction-equation

Lung Density Analysis

(Not available for sale in the United States)

Contents

Lung Density Analysis Lesson

- **I** Select Study
- **II** Choose Protocol and Preset
  - Data Manager
  - Gallery Window
- **III** Perform Analysis
  - Evaluate Segmentation Results
  - Edit Segmented Regions
  - Set the Lung Density Settings
  - View Table Results
  - Take Snapshots
- **IV** Distribute Findings

Additional Procedures

- Create a Batch
- Dual Volume Comparison
- Denoising

Lung Density Analysis Lesson

I. Select Study

Load Lung Density Analysis studies.

See the instructions for your Vitrea type (VitreaAdvanced Through the Data Manager or VitreaWorkstation) in the **Select Study** chapter of the **VitreaAdvanced-VitreaWorkstation General Education and Reference Guide**.

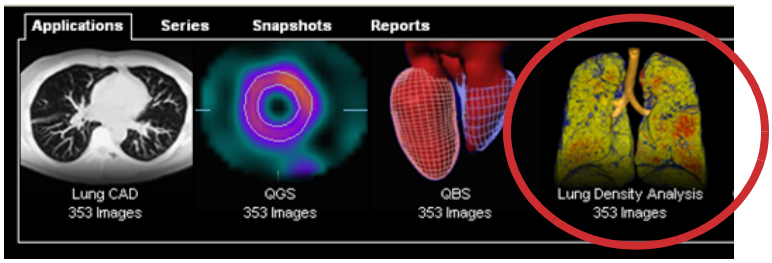
Lung Density Analysis loads one or two series of a chest CT exam.

II. Choose Protocol and Preset

Choose a visualization protocol and preset using either the Data Manager or the Gallery:

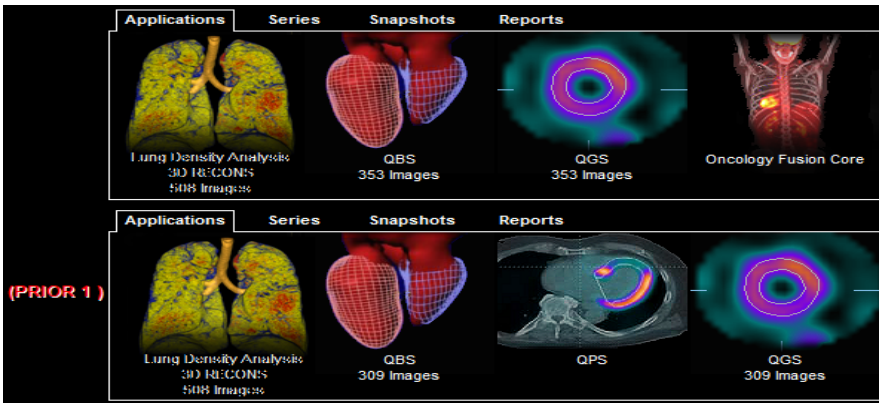
Data Manager

1. From the Applications tab, double-click the **Lung Density Analysis** thumbnail.



NOTE: To compare two studies, press CTRL and select both Lung Density Analysis studies and double-click. The Dual Vol icon

displays when two volumes are selected.



Gallery Window

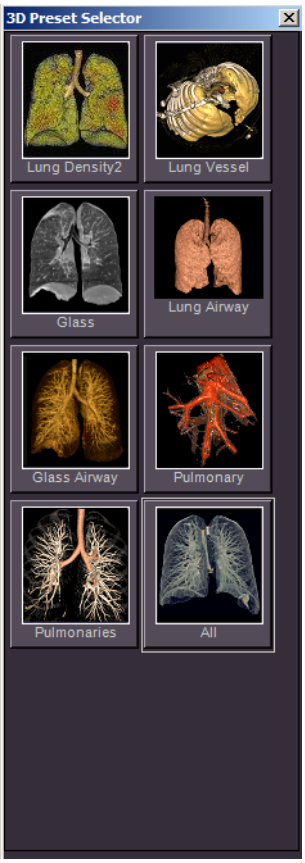
1. Select the **Lung CT** protocol.
2. Click Pick next to the **Lung Density Analysis** preset to start the workflow.
3. Continue with the appropriate Perform Analysis section.

III. Perform Analysis

Evaluate Segmentation Results

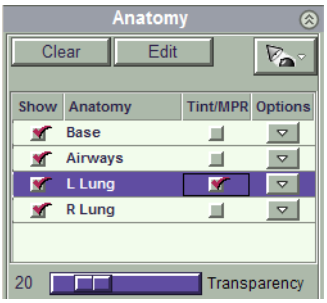
Lung Density Analysis segments the airways (including the trachea, main bronchi, and some larger bronchioles), left lung, and right lung.

You must review and verify the automatic segmentation results.



1. Scroll through the MPRs.

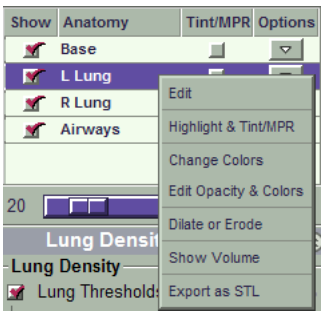
2. Select the appropriate Tint/MPR box to review the tinting for each region.



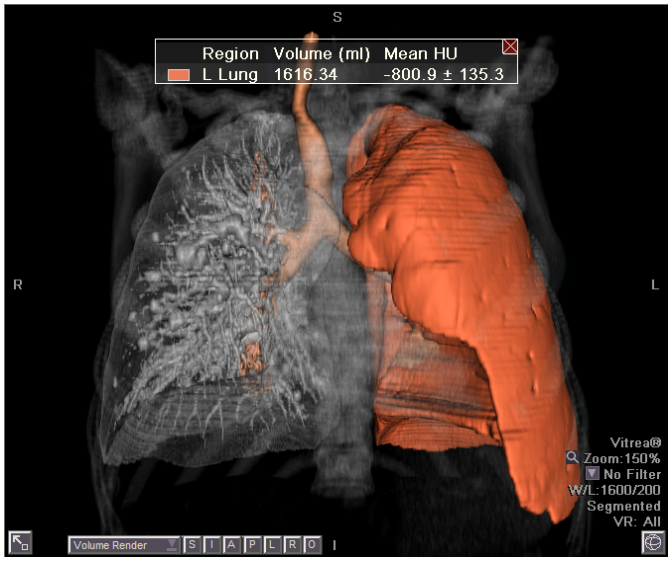
NOTE: Be sure to clear the **Lung Thresholds** check box to tint the MPR.

3. From the 3D Preset Selector, select additional 3D presets to better visualize lung segmentation and regions.

4. From the Anatomy area, select the appropriate anatomy selection and select the Options dropdown.



5. Select **Show Volume** to better visualize the corresponding region between MPR and 3D.



Edit Segmented Regions

If necessary, manually edit each segmented region except the Base.

1. Select a region.

2. Click Edit .

   Contours defining the region display in the MPR views.

3. Choose which MPR view to work in.

4. To maximize the MPR view, click .

5. Click and drag the edge of the contour.

6. Scroll, and continue editing.

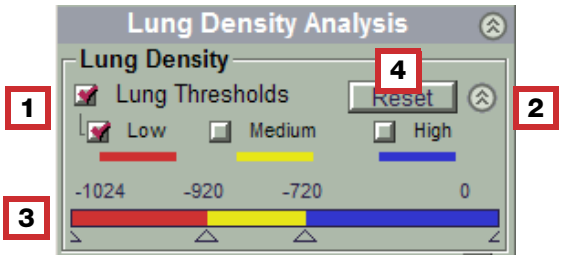
7. Click **Apply**.

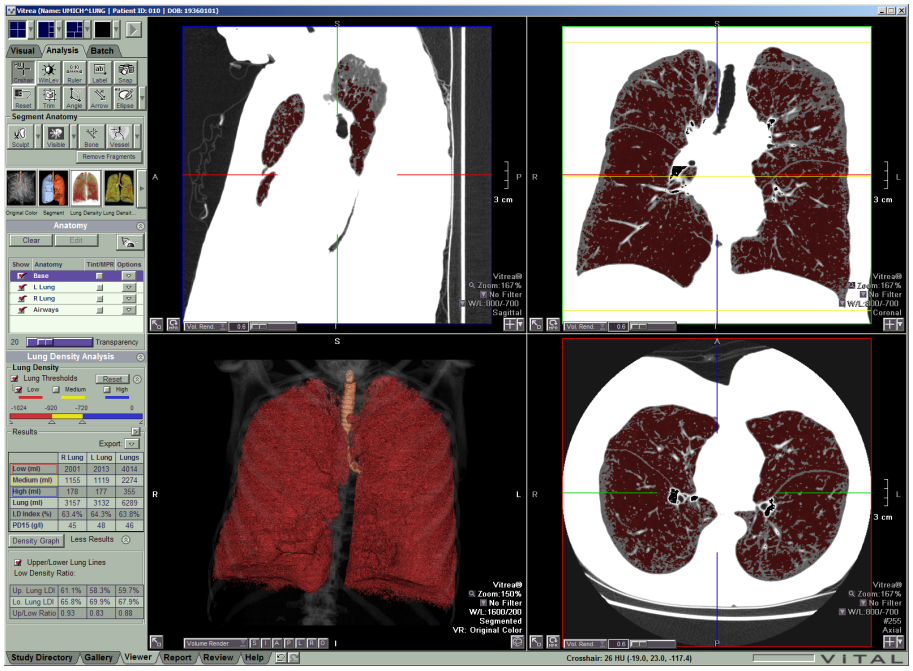
Set the Lung Density Settings

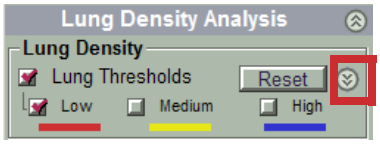
8. Select the Lung Thresholds check box to enable density visualization.

   Lung Density displays:

   - a 3-color overlay in the MPR viewer.
   - a 3-color, 3D, volume rendered lung region (for each lung).

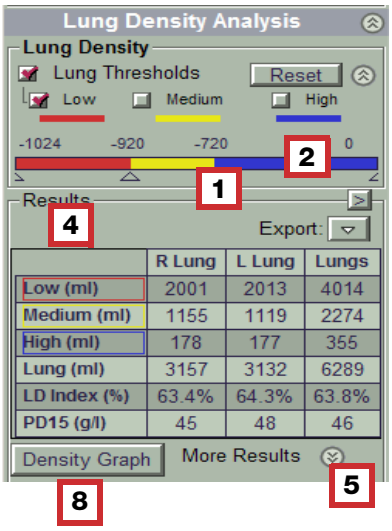


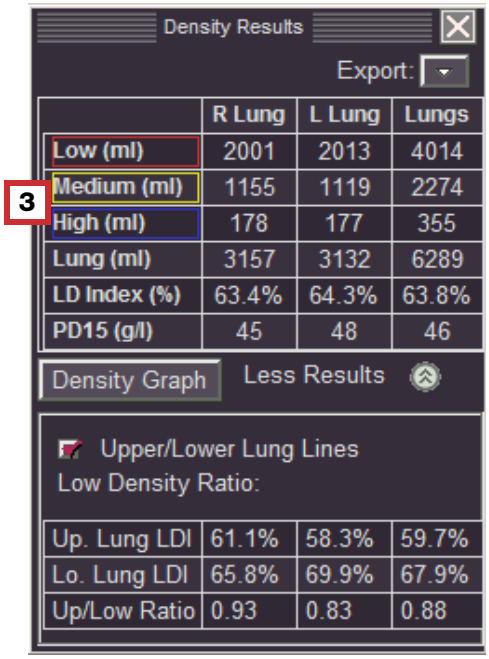
Callout	Description
1	**Lung Thresholds** check box — Select to display the color overlay for all lung density components and measurements. Clear to hide. You can select one, two, or all colors by selecting and clearing the appropriate check boxes. By default, the **Low** check box is selected and the **Medium** and **High** check boxes are cleared. The HU value settings for each lung density component is initialized from the preset. When you clear the Lung check box, the color overlay disappears. When the values are not specified in the preset, the following settings are used: • **Low** Check box: -1024 to -920 is the default HU range. Select to display red for areas of low density. • **Medium** Check box: -920 to -720 is the default HU range. Select to display yellow for areas of medium density. • **High** check box: -720 to 0 is the default HU range. Select to display blue for areas of high density (such as vessels). If you make changes to the settings, press CTRL-P (modified preset) to save the new settings for future sessions. 

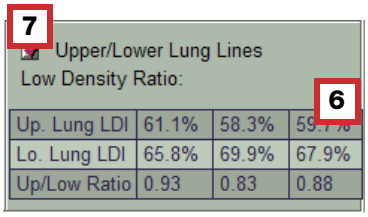
Callout	Description
2	**Expand/Collapse** button — Click to show or hide the Lung Density Settings bar. 
3	**Lung Density Settings** bar — Adjust the HU value settings defining lung density components. Click the HU value text to activate a text box. The box turns white. Type a new value in the box to adjust the HU value. The following HU settings are updated: • quantification of the associated lung regions. • visualization of the associated lung regions. Click and drag a triangle or separation bar to increase or decrease the HU value range. **TIP:** Settings in a dual volume are linked. When you change the settings in one volume of a dual display, the settings in the second volume also change.
4	**Reset** button — Click Reset to change the lung density settings bar to default HU values.

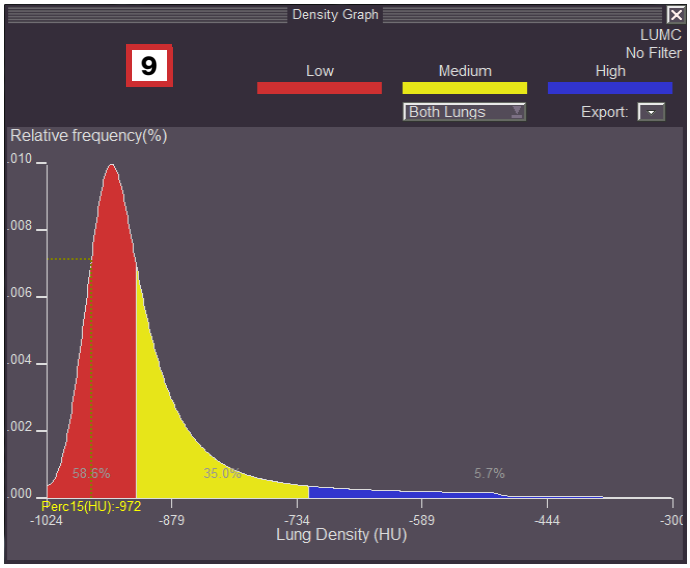
View Table Results

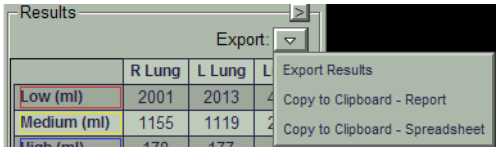
9. View the Lung Density Analysis results.



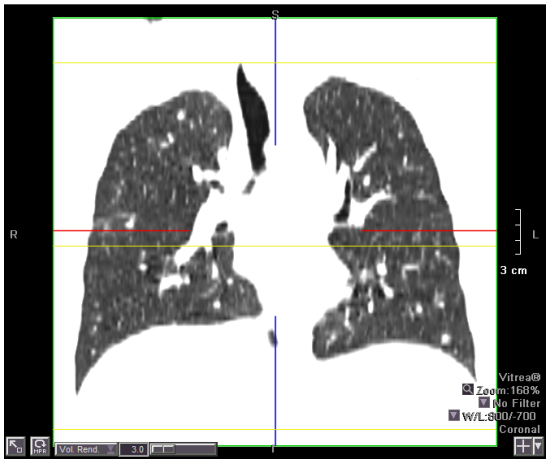






Callout	Description
1	**Export** button — Click to display the Export Results.  • **Export Results** — Select this option to export the results as a .csv file. • **Copy to Clipboard - Report** — Select this option to copy the report to the clipboard, then paste into other, compatible applications (e.g. Microsoft Word). • **Copy to Clipboard - Spreadsheet** — Select this option to copy the spreadsheet to the clipboard, then paste into other, compatible applications (e.g. Microsoft Word).
2	**Expand Results** button — Click to show the in-viewer Density Results.
3	**In-viewer Density Results** — The in-viewer Density Results display on top of the 3D view or MPR view, which is convenient for taking snapshots because the results are overlaid on the viewer image. They are the same results that display on the Analysis tab.

Callout	Description
4	**Lung Density Results** — The results automatically display for right, left, and both lungs. • **Low (ml)** —The volume of lung voxels in the lowest HU density range as defined by the density thresholds. • **Medium (ml)** — The volume of lung voxels in the middle HU density range as defined by the density thresholds. • **High (ml)** — The volume of lung voxels in the highest HU density range (such as vessels) as defined by the density thresholds. • **Lung (ml)** — The functional lung volume including only the voxels designated as Low and Medium lung tissue. • **LD (Low Density) Index (%)** — Low volume / (Low volume + Medium volume). • **PD15 (g/l)** — The HU value which a certain percentage (15%) of the voxels in the frequency distribution histogram have a lower density. Expressed as g/l by the addition of 1000(HU). See the Appendix for more information on Lung Density Results.
5	**More/Less Results** button — Click or to display more or less results for the lung density quantification results.
6	**Ratio** table — Displays results for the right lung, left lung, and both lungs. • Up. Lung LDI (upper lung index) — Displays the Low Density Index for the upper lung(s) only. • Lo. Lung LDI (lower lung index) — Displays the Low Density Index for the lower lung(s) only. • Up/low ratio — Displays the Upper lung ratio/Lower lung ratio.

Callout	Description
7	**Upper/Lower Lung Lines** check box — Click to display the lung lines. **TIP:** Crosshair must be selected for the upper and lower lung lines to display. The lung lines display in the coronal MPR viewer. The lung lines are automatically placed using automatic lung segmentation:  • The upper line is the most superior point of the lungs. • The lower line is the most inferior point of the lungs. • The middle line is equidistant between the upper and lower lines. To modify lung line positions: • Click and drag the upper, middle, and lower lung (yellow) line in the MPR coronal view.

Callout	Description
8	**Density Graph** button — Click Density Graph to display the Density Graph Results on top of the 3D view. • contains data to identify the patient, exam settings, and date/time. • displays on top of the 3D viewer. Click and drag to move it to a different location. • The Density Graph dropdown provides options to display the density graph of both lungs, right lung, or left lung.
9	**In-viewer Density Graph** — Represents the smooth histogram of the relative frequencies of the lung voxels following the thresholds defined for the different lung densities and an indicator for the 15th percentile point. See the Appendix for information regarding the 15th percentile point. • **Export Curves** — Select this option to export the values of the density curves as a .csv file. • **Copy Curves to Clipboard** — Select this option to copy the values of the density curves to the clipboard, then paste into other, compatible applications (e.g. Microsoft Word). • **Copy Graph to Clipboard** — Select this option to copy the graph of the visible curve. Then paste into any graphic application, and save it as a .png or any other graphic format.

Take Snapshots

10. Click Snap and click in a view to save a snapshot.

TIP: To take several snapshots, click Snap, hold left-ALT, and click in each view.

OR

To take one snapshot that includes all views, click Snap, hold CTRL, and click in any view.

11. Click

and click on the Density Results, either in the left panel or expanded in the view, to save a snapshot of the results.

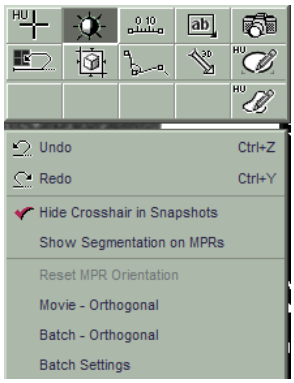
12. Click

and click on the Density Graph to save a snapshot of the graph.

Create a Batch

13. From the Axial view, right-click and select **Batch - Orthogonal** or **Movie - Orthogonal**.

14. A batch preview window opens for you to review the batch or movie.



IV. Distribute Findings

The snapshots, batches, and movies you save in the Viewer window are saved to the Report window.

1. Select

at the bottom of the window.

2. Export your findings or create a report.

See the **Distribute Findings** chapter of the **VitreaAdvanced-VitreaWorkstation General Education and Reference Guide** for instructions on exporting findings, restoring workflow, and creating reports.

CAUTION: Restoring snapshots from previous versions of software may result in slightly different calculations than in the original snapshot, as the formula for calculating PD15 has changed. The snapshots usually only store the inputs to complex calculations, and those calculations are re-run during snapshot restore.

Additional Procedures

This section addresses some less common procedures you may need to do to complete your workflow.

Dual Volume Comparison

The Dual Volume Comparison displays side-by-side axial images on top and 3D images on the bottom (shown in the “All” combo preset display).

See the Choose Protocol and Preset section for information on how to load dual volumes.

- Displays the results of the selected series. When changing between volumes, the results are updated accordingly.
- Allows threshold modification with automatic updates to the quantification and visualization of the associated lung regions.
  - The settings are linked so when there are changes to settings in one volume, the settings in the second volume are also changed.
- The Density Graph displays in the 3D view. The Density Graph displays as the currently selected volume.

Denoising

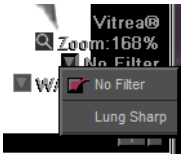
Use Denoising to filter images with regard to noise reduction.

NOTE: Be sure to view images with Denoising applied in conjunction with the original images by switching between the primary image and the denoised image.

- After you have applied a Denoising filter, press D to switch between an image with Denoising applied and the image with no filter.

1. Click the Denoising dropdown arrow to display the menu.

2. Select **Filter: Lung Sharp**.



NOTE: This process may take some time to complete.

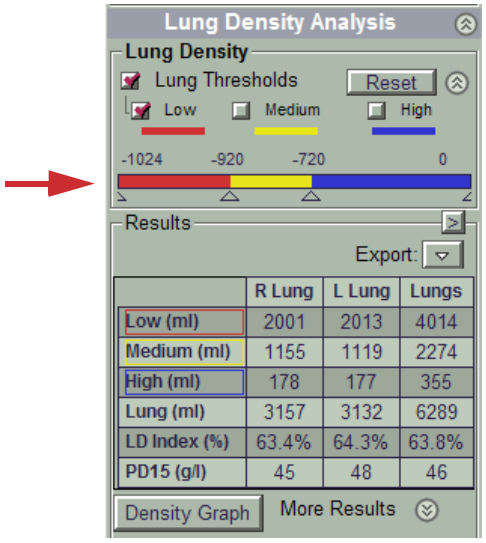
Appendix

Notes on the Lung Density Results: Low Density Index%, Lung Tissue Volume, Upper/Lower Ratio, 15th Percentile Point (HU), and PD15% (g/l).

NOTE: These notes provide more detailed information regarding the main lung quantitative imaging biomarkers (QIBs) available in the Lung Density Analysis application.

LD Index (%)

The Low Density Index (LDI%) is defined as the ratio between the lung volume under a low density threshold for lung density (red area in slider bar) and the volume of the lung parenchyma including the lung voxels under the upper density threshold (red and yellow areas in the slider bar). The LDI% is the 3D counterpart of the 2D relative area index (RA%) used in early lung density studies[1].



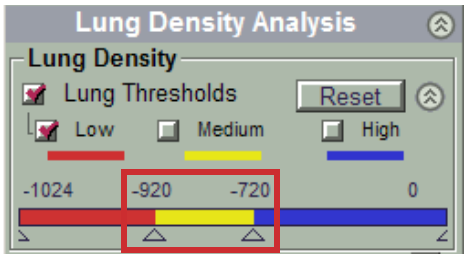
LDI%=Lung volume below threshold/total lung parenchyma volume, expressed in percentage.

1. Stoel BC, Stolk J. Optimization and standardization of lung densitometry in the assessment of pulmonary emphysema. Invest. Radiol. 2004 Nov;39(11):681-8.

Lung Tissue Volume (ml)

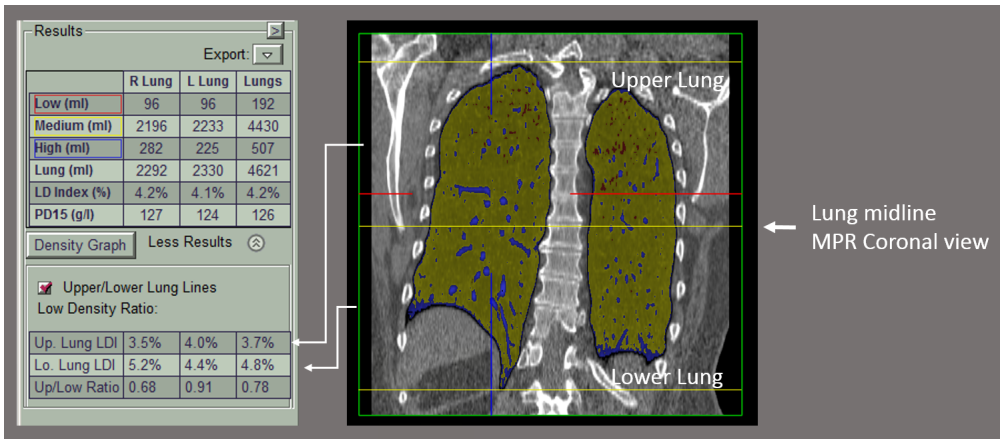
The lung tissue volume is computed from the automated lung segmentation and includes all the lung voxels under an upper threshold.

Both low density threshold (default value: -920HU) and upper threshold (default value: -720HU) vary in the chest radiology community and in the radiologic literature. They are user-adjustable in the Vitrea Lung Density Analysis application.



The Upper/Lower Lung Ratio

The percentage of the low lung density is calculated for the upper and lower halves of the lungs, divided midpoint between lung apices and the diaphragm. The default midpoint appears as a horizontal yellow midline in the coronal MPR view. Upper/lower density ration grater than 1 indicates a relative lower density in the upper lung region compared to the lower lung[2]. If needed, the user can modify the vertical position of the midline. The default semi-automatic midline uses the lowest and highest points of the lungs in the coronal plane.



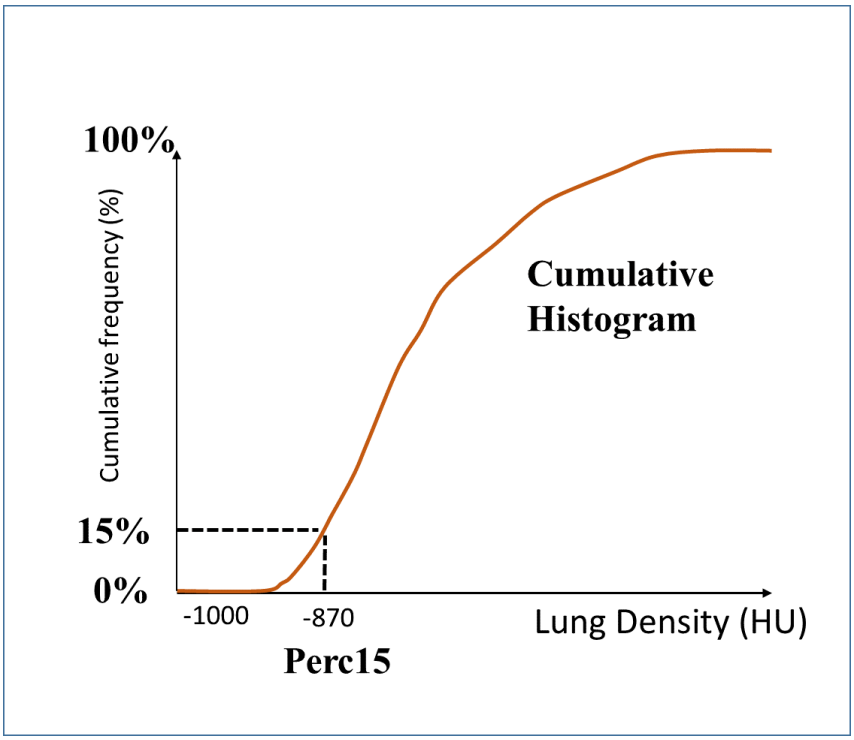
	R Lung	L Lung	Lungs
Low (ml)	96	96	192
Medium (ml)	2196	2233	4430
High (ml)	282	225	507
Lung (ml)	2292	2330	4621
LD Index (%)	4.2%	4.1%	4.2%
PD15 (g/l)	127	124	126

Up. Lung LDI	3.5%	4.0%	3.7%
Lo. Lung LDI	5.2%	4.4%	4.8%
Up/Low Ratio	0.68	0.91	0.78

2. Flaherty KR, Kazerooni EA, Curtis JL, Iannettoni M, et al.: Short-term and long-term outcomes after bilateral lung volume reduction surgery: prediction by quantitative CT. Chest. 2001 May; 119(5):1337-46.

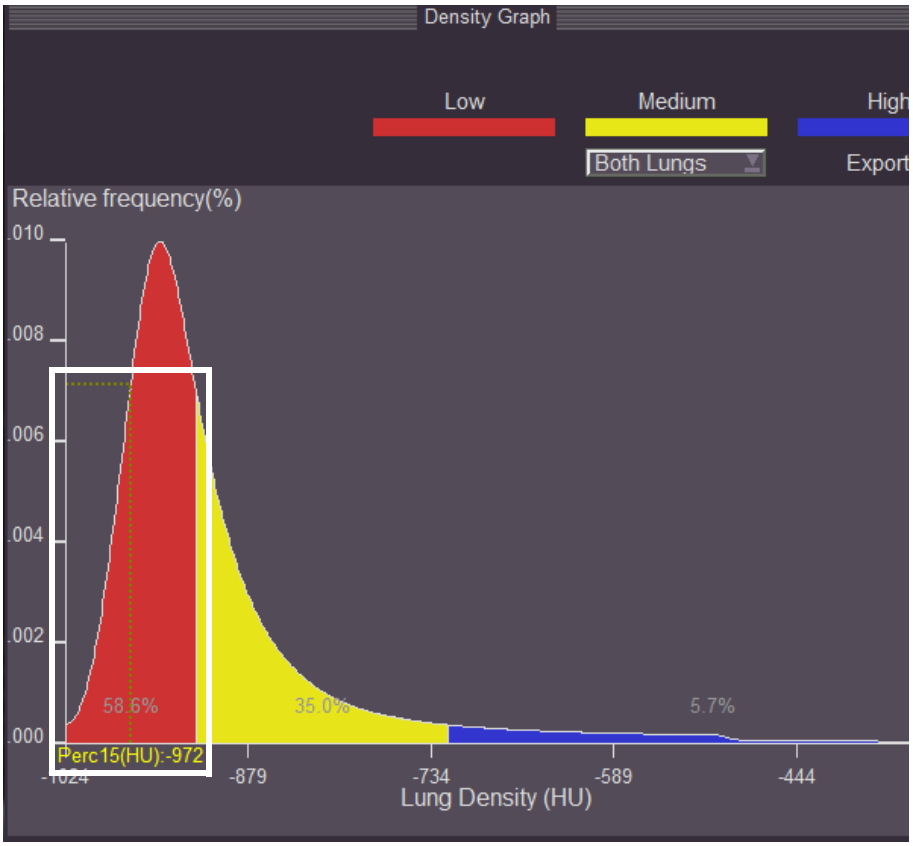
15th Percentile Point (Perc15)

Following [Parr2009][3] and [Stoel2004][4], the 15th percentile point (Perc15) is defined as the cut-off value, in Hounsfield Units (HU), below which are distributed the 15% of lung voxels with the lowest density.



3. Parr DG1, Dirksen A, Piitulainen E, Deng C, Wencker M, Stockley RA. Exploring the optimum approach to the use of CT densitometry in a randomised placebo-controlled study of augmentation therapy in alpha 1-antitrypsin deficiency. Respir. Res. 2009 Aug 13;10:75.
4. Stoel op. cit., 681-8.

The 15th percentile point is shown in the lung density graph.



Percentile Density PD15%(g/l)

The 15th percentile point (HU) index is converted to the Percentile Density PD15% by the addition of 1000 (HU), assuming the air density of 0g/l and -1000HU for air CT attenuation.

For example, a 15th percentile point index of -883HU corresponds to a percentile density of PD15% of (-883 + 1000) = 117 g/l.

CT Liver Analysis

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  - Segment Hepatic Artery Using Vessel Grow
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  - Probe Tumors
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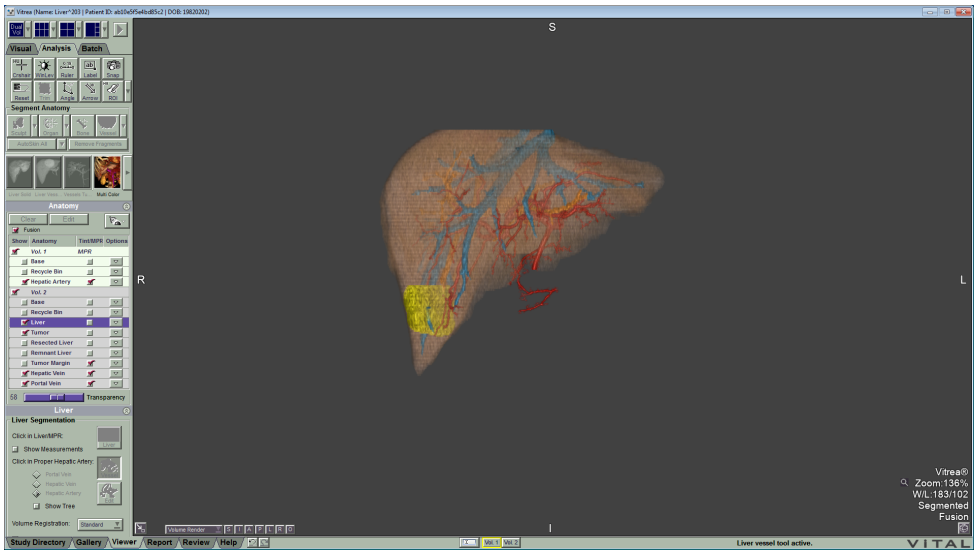
CT Liver Analysis Overview

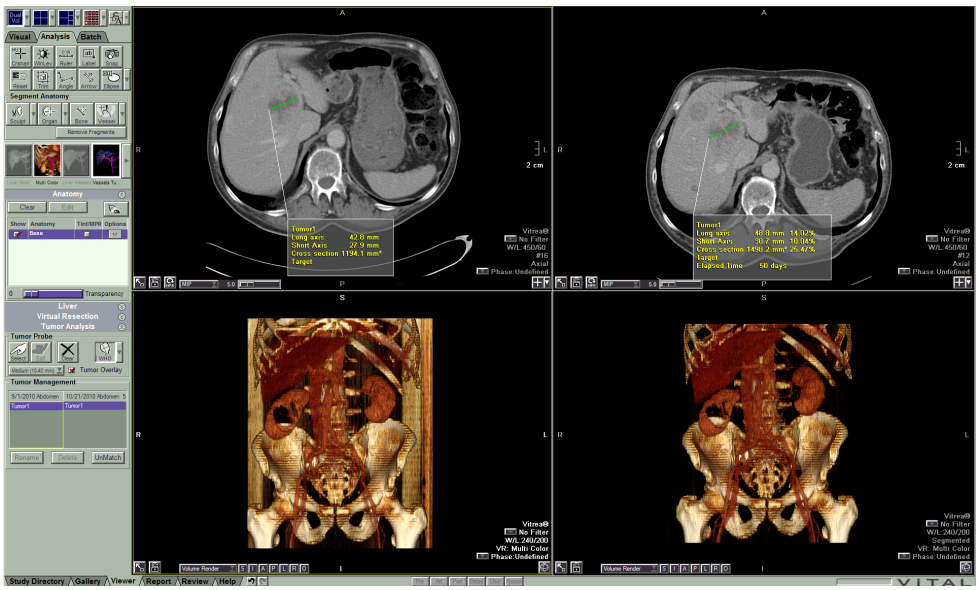
The CT Liver Analysis Education and Reference Guide includes the **Resection Planning** and **Tumor Response** workflows.

The software supports Liver CT studies. The software does not support MR studies.

Use the **Resection Planning** workflow for surgical planning.



Use the **Tumor Response** workflow for tumor tracking.



CT Liver Analysis Lesson

I. Select Study

Load CT Liver studies.

See the instructions for your Vitrea type (VitreaAdvanced Through the Data Manager or VitreaWorkstation) in the **Select Study** chapter of the **VitreaAdvanced-VitreaWorkstation General Education and Reference Guide**.

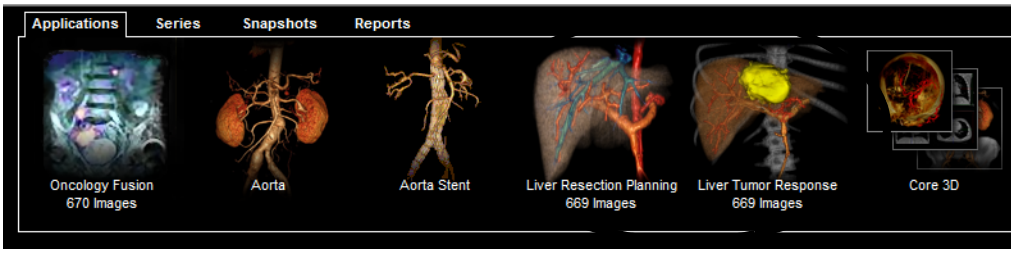
NOTE: You have the option to select single/multiple series. Load any series to define the liver anatomy. During the workflow, you do not have the option to return and add additional series.

II. Choose Protocol and Preset

Choose a visualization protocol and preset using either the Data Manager or the Gallery:

Data Manager

1. From the Applications tab, double-click the **Liver Resection Planning** or the **Liver Tumor Response** thumbnail.



2. Continue with the appropriate Perform Analysis section.

Gallery Window

1. Select the **Liver CT** protocol.

2. Click Pick next to the **Resection Planning** preset to start the workflow.

   OR

   Click Pick next to the **Tumor Response** preset to start the workflow.

3. Continue with the appropriate Perform Analysis section.

III. Perform Analysis – Resection Planning Workflow

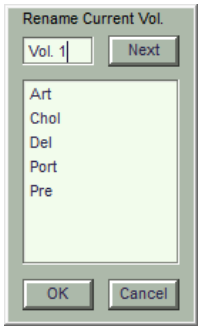
Use the Resection Planning workflow to create liver and vessel regions. For best results, load the arterial and portal phases. You may also load the pre-contrast, delay, or cholangiogram phases.

Select and Relabel the Phases

1. Use the Volume Navigation buttons to select the phases.

   The yellow highlight around the MPR and 3D views indicates the active phase.

2. To change the labels on the Volume Navigation buttons, click and select a label from the list: pre-contrast, arterial, portal, delay, or cholangiogram, or type a new name in the entry field.



Choose a Layout

Choose a layout scheme depending on the number of volumes loaded:

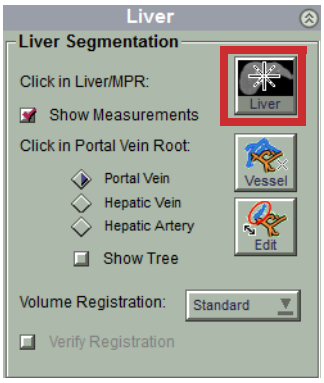
- **Dual Vol** layout for two volumes, or
- **Triple Volume** layout for three or more volumes.

NOTE: Either viewer layout is available with two or more volumes loaded.

Segment the Liver

Use the Liver tool to segment the liver. You can also use a combination of segmentation tools to create a liver region.

See the Additional Procedures section for information on how to manually sculpt the liver.



3. From the Liver section on the Analysis tab, click **Liver** to segment the liver.

   NOTE: The portal phase is recommended to segment the liver due to the increased contrast in the liver.

4. In the MPR view, hover on the liver.

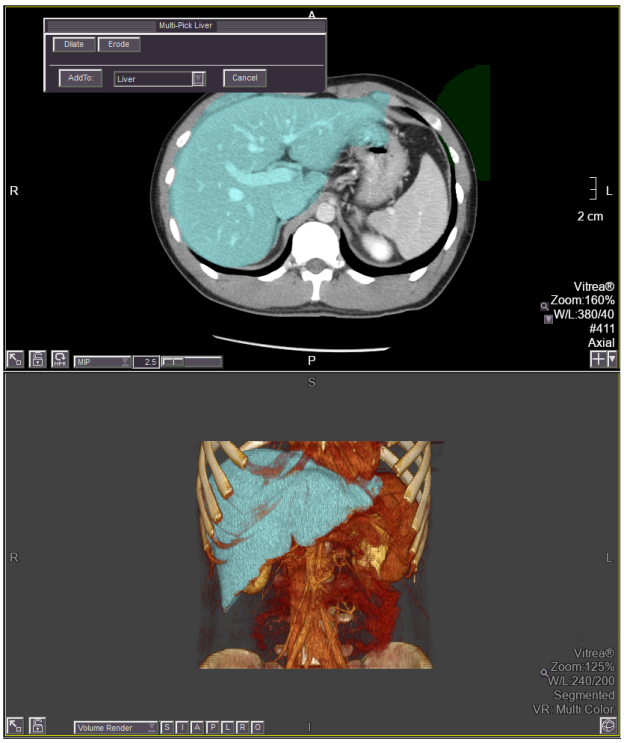
   TIP: An overlay displays on areas that will be segmented. Use this as a guide to determine if you need to hover in another location.

5. Click the liver to segment.

   The preview indicates what will be selected or de-selected.

   - Click the green overlay to add sections.
   - Click the purple overlay to remove sections.

- Press the + or - keys to include more or less in the preview.

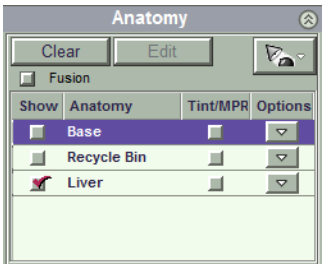


6. From the Multi-Pick Liver dialog box, click Dilate or Erode as needed.

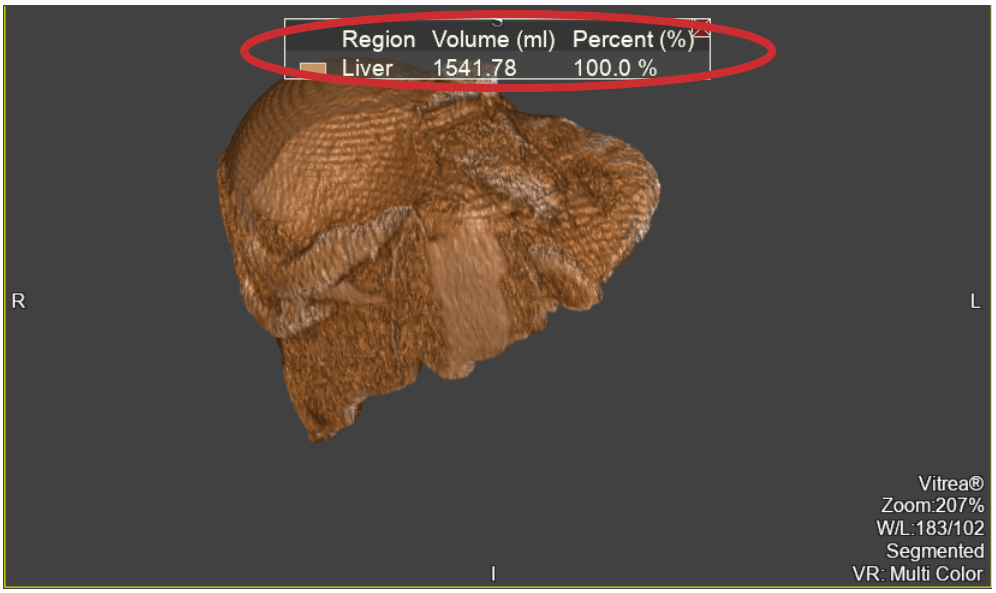
   TIP: The **Dilate** and **Erode** buttons decrease or increase the selected area by 1 voxel per click.

7. Click **AddTo:** from the Multi-Pick Liver dialog box.

A listing is added to the Anatomy Management area.

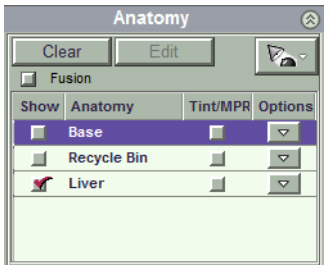


The Liver region Volume displays and the Base region is hidden.



Edit the Liver Segmentation

If necessary, edit the liver segmentation.

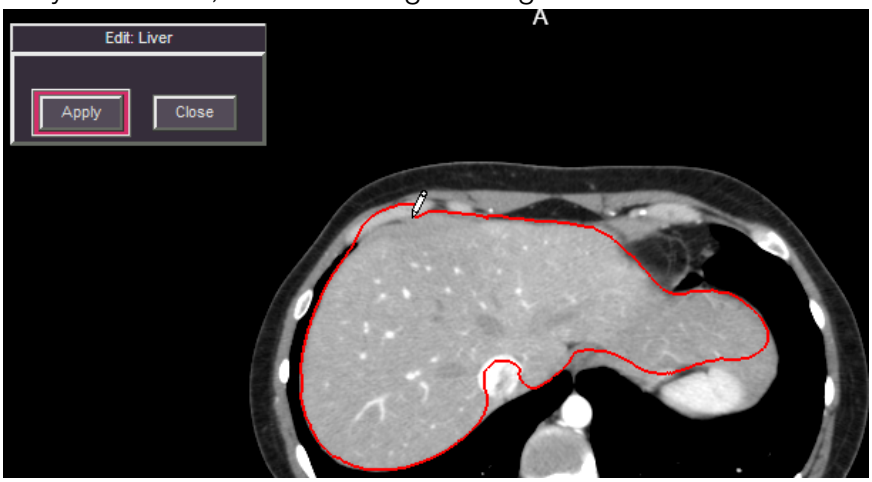


See the Additional Procedures section for information on how to manually sculpt the liver.

8. Select and highlight **Liver** in the Anatomy area.

9. Click Edit to edit the liver.

10. In any MPR view, click and drag the edge of the contour.

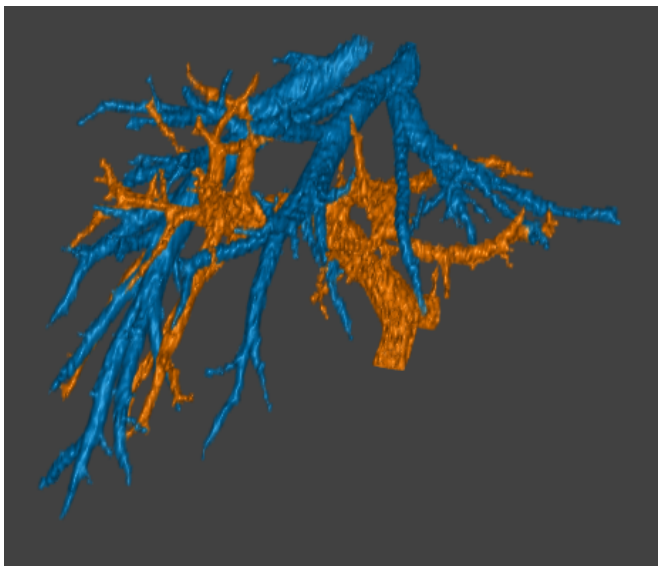


11. Scroll a few slices and continue editing.

NOTE: Vitrea performs interpolation between edited contours when you click Apply.

12. When you finish editing, click **Apply**.

Segment Portal Vein and Hepatic Vein Using One-Click Segmentation



Use this workflow to segment the portal vein and hepatic vein with a single click. This procedure may also be used to segment the hepatic artery in the arterial phase.

13. Select the portal phase using the Volume Navigation button.

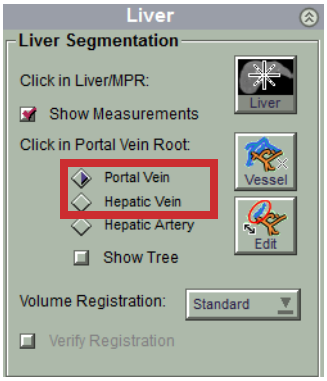
14. In the Liver area, click

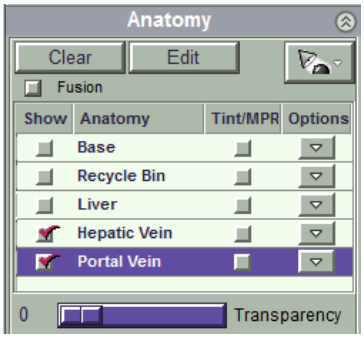
.

15. Select the target vessel type.

16. In an MPR view, click in the portal vein root outside the liver.

Portal Vein and Hepatic Vein regions are created in the Anatomy area.

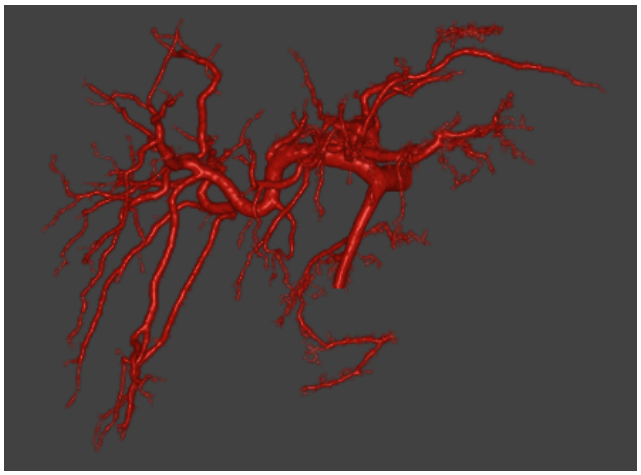




TIP: Press ESC to cancel the segmentation while it is running.

NOTE: In order to retain the ability to edit the Portal Vein and Hepatic Vein regions, do not rename them.

Segment Hepatic Artery Using Vessel Grow



Use this workflow to segment the hepatic artery. This procedure may also be used to segment the hepatic and portal veins in the portal phase.

17. Select the arterial phase using the Volume Navigation button.

18. Select **Hepatic Artery** in the Liver Segmentation area.

19. In the Segment Anatomy area, click

.

20. Hover over a point in the mid to distal part of the artery.

21. Click and hold on the vessel to grow the vessel branches.

22. Adjust the selection area with the Vessel Grow slider. Use the cyan area in the image as a guide.

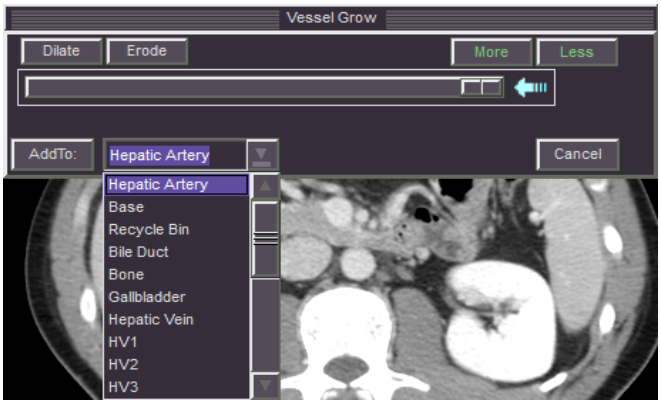
TIP: Apply MIP rendering and some thickness to the MPR views to better visualize the selected area.

23. From the Vessel Grow dialog box, click Dilate / Erode or More / Less.

TIP: The **Dilate** and **Erode** buttons decrease or increase the selected area by 1 voxel per click. The **More** and **Less** buttons increase or decrease the selected area by HU threshold.

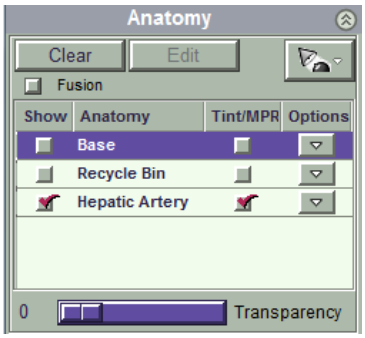
24. Verify the Hepatic Artery region is listed in the text field.

TIP: To change the region listed, click the dropdown and select a region.



25. Click AddTo:.

A Hepatic Artery region is created in the Anatomy area.



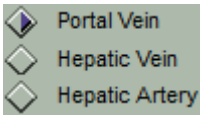
See the Common Tasks chapter of the VitreaAdvanced Education and Reference Guide for detailed information on changing the appearance of a region and creating a custom color scheme.

NOTE: In order to retain the ability to edit the Hepatic Artery region, do not rename it.

Edit the Vessels

NOTE: It is important that you verify the vessel segmentation and edit if necessary.

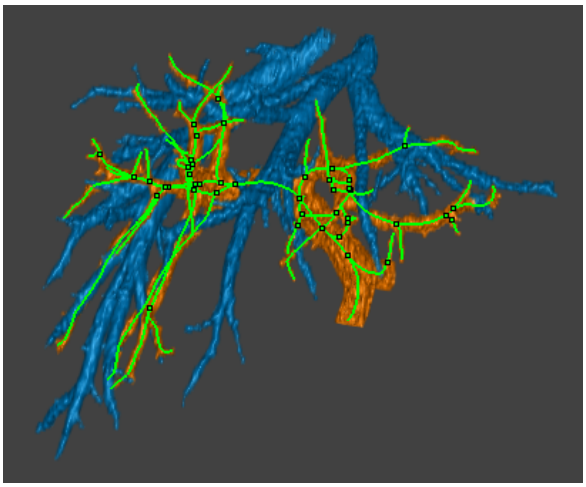
26. Select the radio button for the vessel you want to edit.



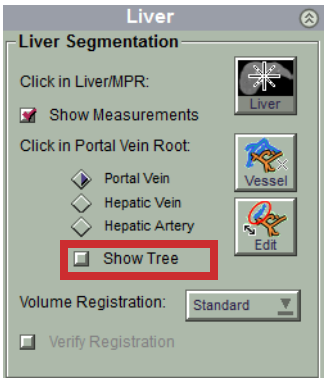
27. Click

.

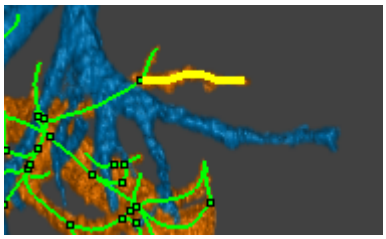
The vessel tree displays in the 3D view.



TIP: To display the vessel tree without editing the vessel centerlines, select the **Show Tree** check box.

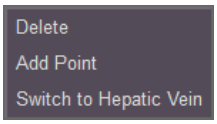


28. Hover over a branch to highlight it.



TIP: To expand the highlighted portion to more of the connected branch, scroll the mouse wheel.

29. Right-click the highlighted branch, then select:



- **Delete**
- **Add Point,** to split a branch by adding a new control point
- **Switch to,** to move this branch to another vessel (for example: Portal Vein to Hepatic Vein, Hepatic Vein to Portal Vein, or Hepatic Artery to Portal Vein)

TIP: Click the highlighted branch to switch the branch to another vessel. Press DELETE or BACKSPACE to delete the highlighted branch.

30. To lengthen a segmented vessel:

a. Select the vessel radio button.

b. Click

.

c. Click and hold in an MPR or 3D view distally.

d. Add to the correct region.

Probe Tumors

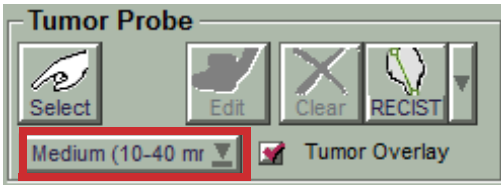
Use Tumor Probe to isolate and probe tumors.

31. In the Tumor Probe area, click

32. Right-click and drag in one of the views and look for suspected tumors.

33. When you find a tumor, review it to determine the approximate size.

34. From the Tumor Probe dropdown, select the appropriate size of the tumor (small, medium, or large).



35. Click in the tumor.

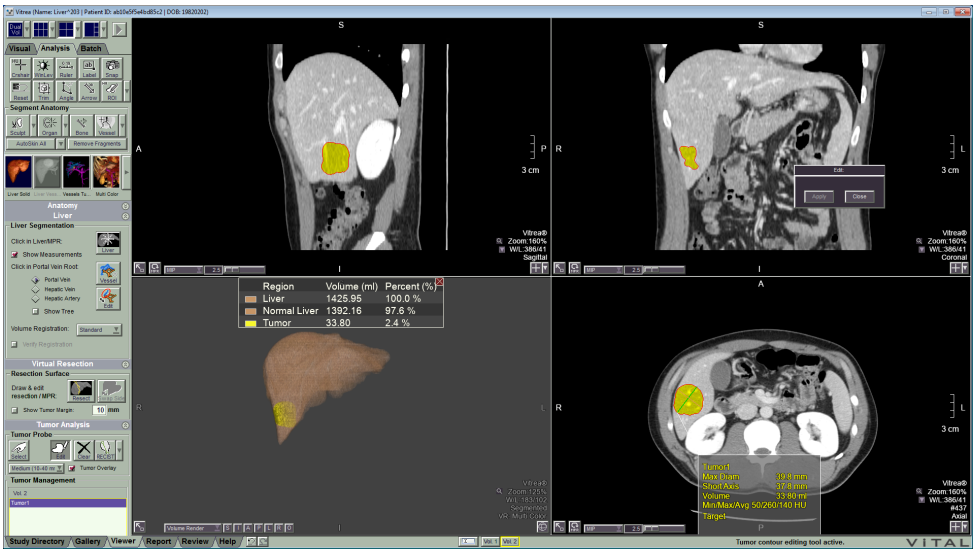
36. To modify the tumor segmentation, click **+** or **-**.

37. To examine the 3D image of the tumor more closely:

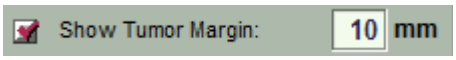
- **a.** Click in the lower-right corner of the view to switch to the point-of-interest view.
- **b.** Click and drag in the view to rotate.
- **c.** Click in the lower-right corner of the view to return to the full 3D view.

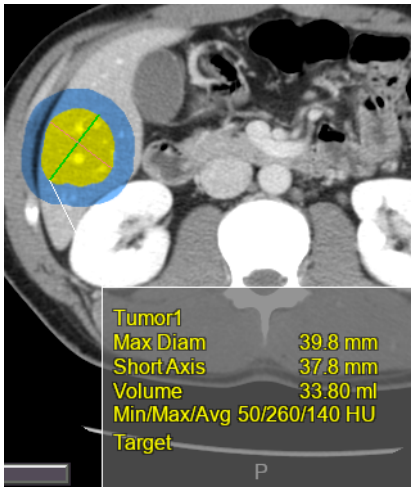
38. From the Tumor Probe dropdown, select the appropriate size of the tumor (small, medium, or large).

39. If necessary, edit the probed tumor.



40. From the Virtual Resection section, select **Show Tumor Margin** and enter the distance.





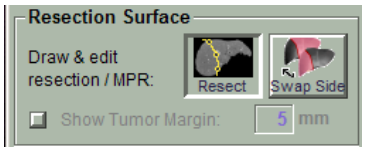
Perform Resection Planning

Use this tool to divide the liver into Remnant and Resected Liver to get two liver volumes.

NOTE: The system automatically determines which part is resected and remnant for liver segmentation. The table showing the volumes in the application will be color coded to match the region colors.

41. Select

.



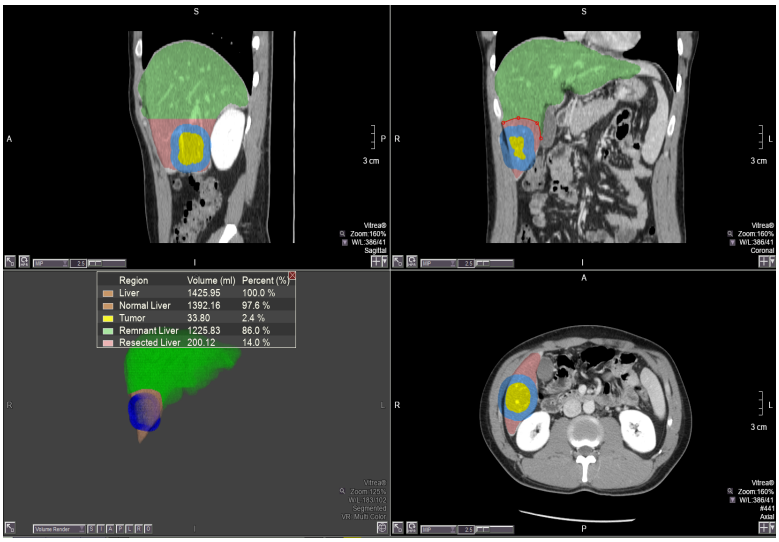
TIP: If a surface is already created, the 3D surface is visible when you select Resect. If you select Resect for the first time, there is not a surface.

42. In the 2D view, move the cursor along the plane and click to plot a point.

43. Continue to plot all additional points.

44. Double-click to end.

As you plot points, a new red line displays. The Remnant Liver displays in green and the Resected Liver displays in pink.



CAUTION: Verify that the system-generated assignments for remnant liver and resected liver are correct.

TIP: To switch the automatic selection for remnant liver and resected liver, click

to swap sides.

45. To edit, hover over a plotted point to change the cursor to a hand. Click to move the plotted point.

NOTE: Vitrea does not allow using the Sculpt tool to edit the Resected Liver and Remnant Liver regions. Use the procedure above to edit the regions.

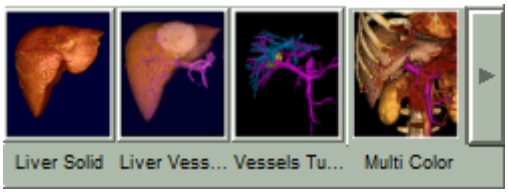
46. Click and drag the line and it dynamically shows the resulting line as you drag. The point displays after you release the mouse.

47. Right-click and select **Delete Curve** or **Delete All Curves** to delete.

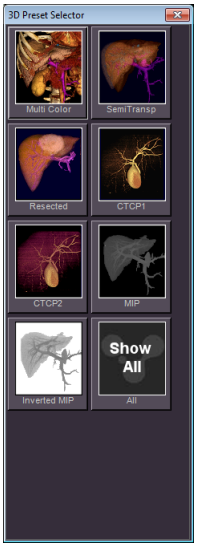
48. Hover over the line to highlight it and press **Delete** to delete a line.

Apply Visualization Presets to the 3D View

49. Select a visualization preset button to change the look of the 3D view.

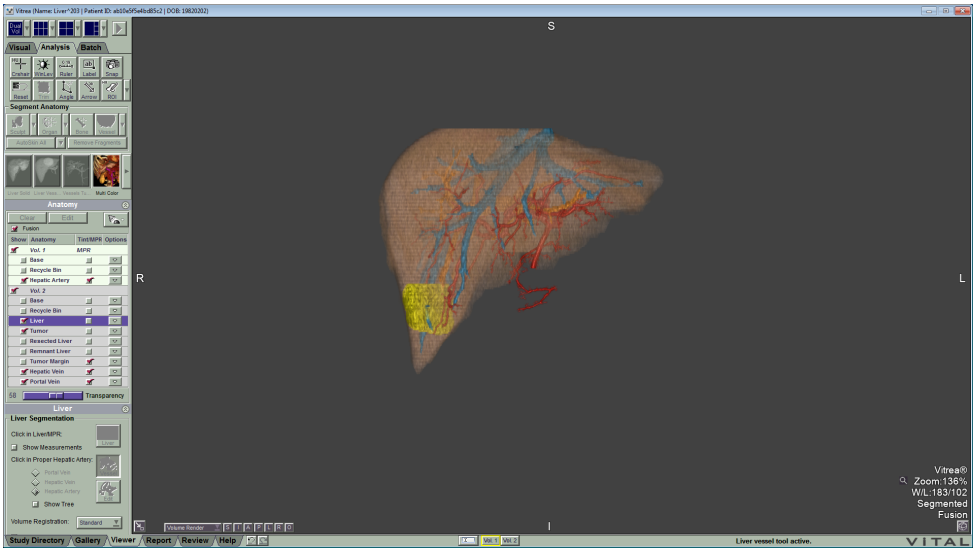


TIP: Click the arrow to the right of the preset buttons to display a panel of additional presets.



Create Multi-phase Volume Fusion

Use this option to visualize the liver, vessels, and tumor(s) in a single fused view.



NOTE: Before creating a multi-phase volume fusion, you must create all regions. Use of the resection tool should be performed before fusion.

CAUTION: Check your registration before using a fused volume.

50. Click the Volume Navigation button for the portal phase to make it the current volume.

51. From the Volume Registration dropdown, select one of the following options:

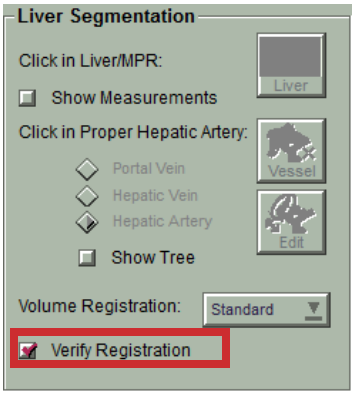
- **Standard** (a general rigid registration),
- **Rigid** (a liver-centric rigid registration), or
- **Deformable** (a deformable registration that takes breathing into account).

The fusion volume displays.

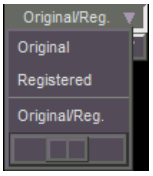
NOTE: If there is too much motion in the liver region, try another type of registration. If there is still too much motion, do not use the fused volume.

52. In the Liver Segmentation area, select the **Verify Registration** check box.

The MPRs display showing the Original volume in the default gray coloring and the Registered volume in pink coloring.



53. Select the Original/Registered drop down to view:



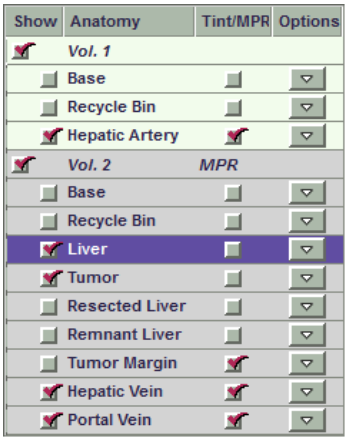
- just the Original volume,
- just the Registered volume, or
- a combination of the Original and Registered volumes.

TIP: To adjust the percentage of Original and Registered volumes displayed in the combination volume, adjust the slider.

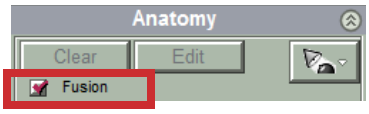
NOTE: There should be little movement in the liver area.

54. Continue to select from the lower dropdown list to verify each volume.

55. Select or clear the Show check boxes for each region you want to show or hide.

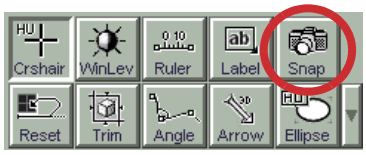


56. In the Anatomy area, clear or select the **Fusion** check box to toggle the fusion off or on.



Take Snapshots

57. Click and click in a view to save a snapshot.



OR

To take several snapshots, click , hold ALT, and click in each view.

OR

To take one snapshot that includes all views, click , hold CTRL, and click in any view.

III. Perform Analysis – Tumor Response Workflow

Use the Tumor Response workflow to compare studies over time.

NOTE: This version does not support restoring previously segmented tumors.

Auto-Lock Exams Together

Synchronize the views and link them so visualization and spatial operations can be replicated across views in a locked set. When you lock views, manipulations made in one view are reflected in synchronized views.

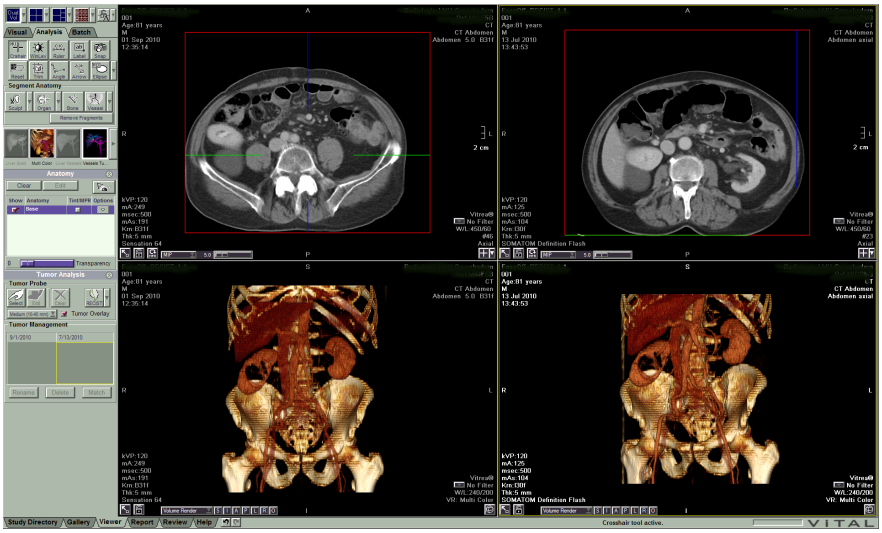
- Select

.

See the Additional Procedures section for information on how to lock exams together using manual lock.

Assess the Comparative Exams

- Compare the two images to view the exams.

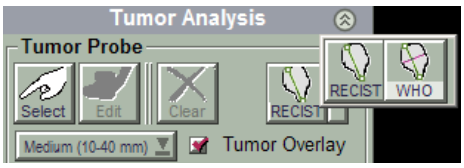


Locate Lesions in Datasets

Perform one of the procedures below to locate lesions, detect, and measure tumors. Match the tumors to display comparison measurements.

- Simple Rulers (RECIST 1.1 or WHO)
- Tumor Probe
- Manual Sculpt or Organ Pick

Simple Rulers (RECIST or WHO)



1. From the Tumor Analysis section on the Analysis tab, select **RECIST** (1.1) (measures the longest diameter) or **WHO** (measures the longest diameter, short diameter, and cross-sectional information).
2. Draw the diameter.

CAUTION: Place ruler endpoints as precisely as possible, exactly where you want them to display on the image.

3 If necessary, edit the short diameter (WHO measurements only).

4 Draw the diameter for the same tumor in the other volume.

CAUTION: Verify the lesions you are matching are correct.

5 Click Match in the Tumor Management area to calculate the difference.

See the Additional Procedures - Manage Tumors section for more information on how to manage tumors.

6 Continue with the Tumor Findings Results section.

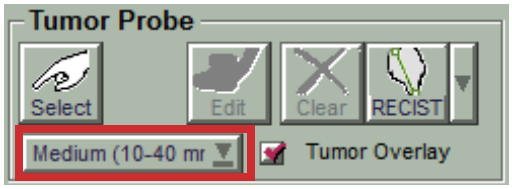
Probe Tumors

1. In the Tumor Probe area, click Select

2 Right-click and drag in one of the views and look for suspected tumors.

3 When you find a tumor, review it to determine the approximate size.

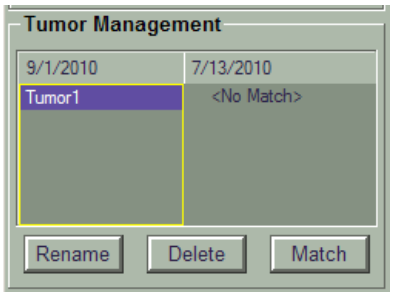
4 From the Tumor Probe dropdown, select the appropriate size of the tumor (small, medium, or large).



5 Click in the tumor.

6 To modify the tumor segmentation, click **+** or **-**.

Vitrea gives the tumor a unique label and adds a listing to the Tumor Management area.



7 To examine the 3D image of the tumor more closely:

a. Click in the lower-right corner of the view.

b. Click and drag in the view to rotate.

c. Click in the lower-right corner of the view to return to the full 3D view.

8 Probe the same tumor in the other volume.

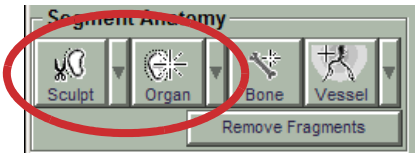
9 Click Match in the Tumor Management area to calculate the difference.

See the Additional Procedures - Manage Tumors section for more information on how to manage tumors.

10 Continue with the Tumor Findings Results section.

Use Manual Sculpt or Organ Pick to Define a Tumor

1. In the Segment Anatomy area, click **Sculpt** or **Organ**.



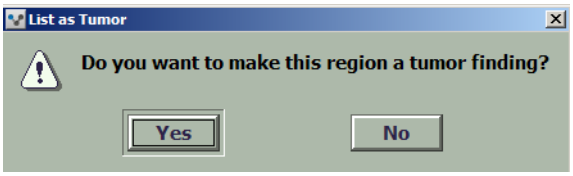
2 Sculpt or click the tumor.

3 From the dialog box, select the Liver Tumor from the dropdown.

4 Click AddTo: .

Vitrea adds a listing to the Anatomy Management area.

5 When the following dialog box displays, click **Yes**.



See the Additional Procedures - Manage Tumors section for more information on how to manage tumors.

6 Sculpt or pick the same tumor in the other volume.

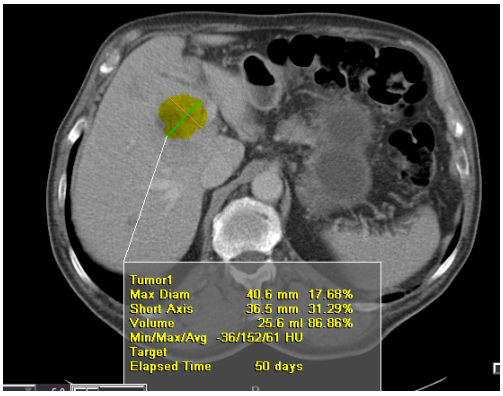
7 Click Match in the Tumor Management area to calculate the difference.

See the Additional Procedures - Manage Tumors section for more information on how to manage tumors.

8 Continue with the Tumor Findings Results section.

Tumor Findings Results

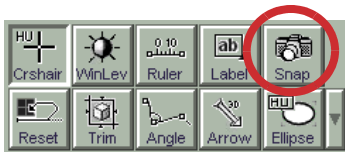
The results display in a yellow box.



Type	Results
RECIST (1.1)	Long axis
WHO	Long axis Short axis Cross-sectional (long axis x short axis)
Tumor Probe	Maximum Diameter Short Axis Volume

Take Snapshots

9. Click Snap and click in a view to save a snapshot.



TIP: To take several snapshots, click Snap, hold ALT, and click in each view.

OR

To take one snapshot that includes all views, click

, hold CTRL, and click in any view.

IV. Distribute Findings

The snapshots, batches, and movies you save in the Viewer window are saved to the Report window.

CAUTION: Verify the accuracy of all contours and confirm all measurements when restoring snapshots from previous software versions created through the use of region editing.

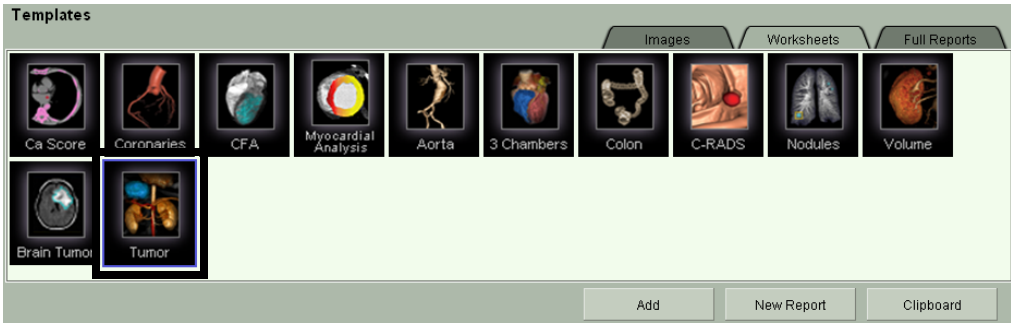
1. Select Report at the bottom of the window.

2. Export your findings or create a report.

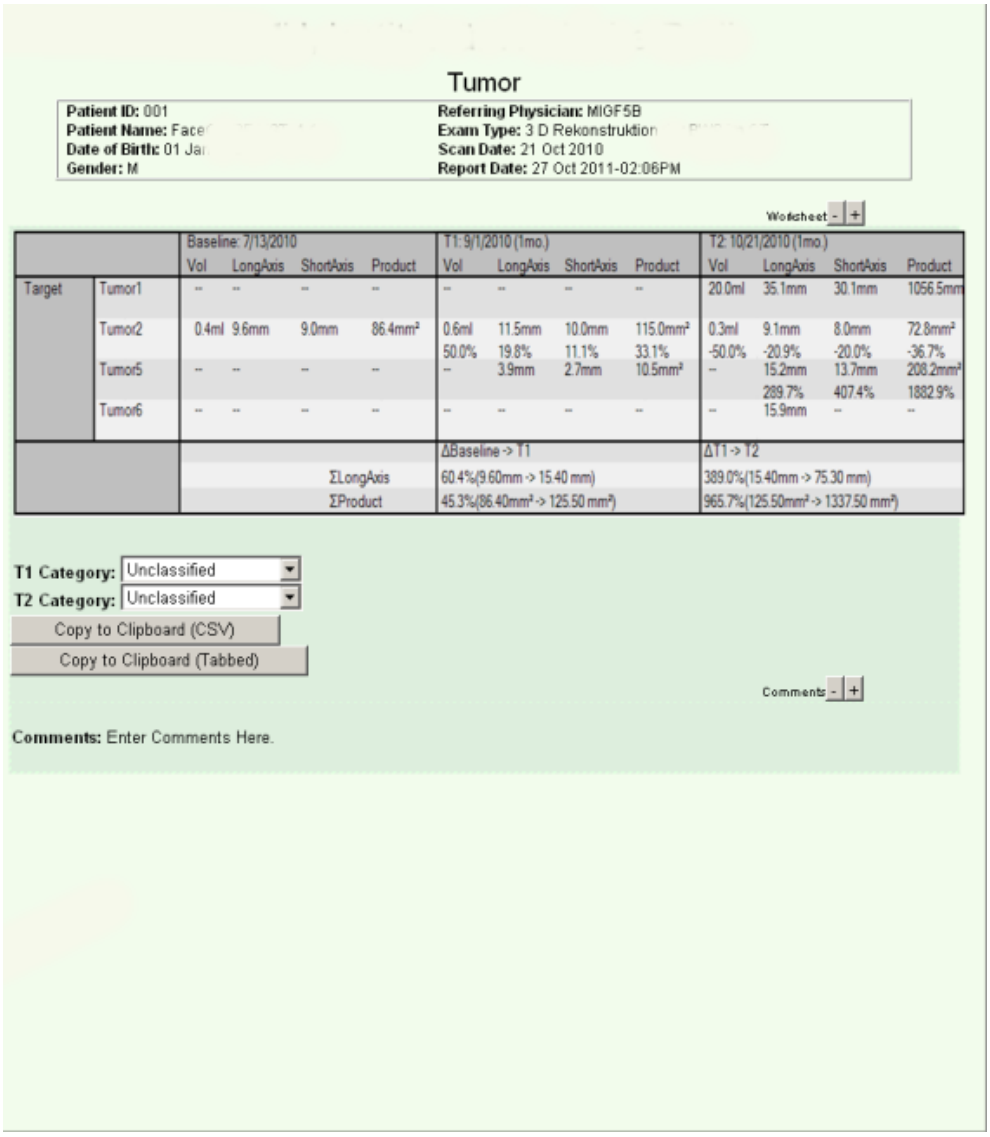
   See the **Distribute Findings** chapter of the **VitreaAdvanced-VitreaWorkstation General Education and Reference Guide** for instructions on exporting findings, restoring workflow, and creating reports.

3. The Tumor template contains a report specific to CT Liver Analysis.

   NOTE: Use the Tumor template for Tumor Response workflow.



The report displays a table with the results.



Tumor

Patient ID: 001
Patient Name: Face
Date of Birth: 01 Ja
Gender: M

Referring Physician: MIGF5B
Exam Type: 3 D Rekonstruktion
Scan Date: 21 Oct 2010
Report Date: 27 Oct 2011-02:06PM

Worksheet - +

		Baseline: 7/13/2010				T1: 9/1/2010 (1mo.)				T2: 10/21/2010 (1mo.)			
		Vol	LongAxis	ShortAxis	Product	Vol	LongAxis	ShortAxis	Product	Vol	LongAxis	ShortAxis	Product
Target	Tumor1	--	--	--	--	--	--	--	--	20.0ml	35.1mm	30.1mm	1056.5mm
	Tumor2	0.4ml	9.6mm	9.0mm	86.4mm²	0.6ml	11.5mm	10.0mm	115.0mm²	0.3ml	9.1mm	8.0mm	72.8mm²
						50.0%	19.8%	11.1%	33.1%	-50.0%	-20.9%	-20.0%	-36.7%
	Tumor5	--	--	--	--	--	3.9mm	2.7mm	10.5mm²	--	15.2mm	13.7mm	208.2mm²
											289.7%	407.4%	1882.9%
	Tumor6	--	--	--	--	--	--	--	--	--	15.9mm	--	--
						ΔBaseline -> T1				ΔT1 -> T2			
					ΣLongAxis	60.4%(9.60mm -> 15.40 mm)				389.0%(15.40mm -> 75.30 mm)			
					ΣProduct	45.3%(86.40mm² -> 125.50 mm²)				965.7%(125.50mm² -> 1337.50 mm²)			

T1 Category: Unclassified
T2 Category: Unclassified
Copy to Clipboard (CSV)
Copy to Clipboard (Tabbed)

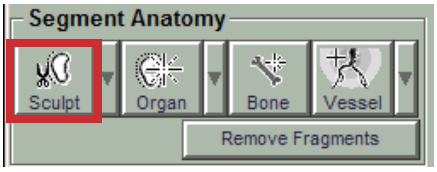
Comments - +

Comments: Enter Comments Here.

Additional Procedures

This section addresses some less common procedures you may need to do to complete your workflow.

Manually Sculpt the Liver



1. In the Segment Anatomy area, click **Sculpt**.

2. Draw contours around the region to sculpt.

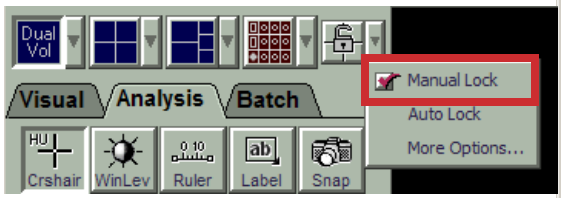
3. In the Sculpt dialog, verify Liver is selected in the dropdown and select **Add To**.

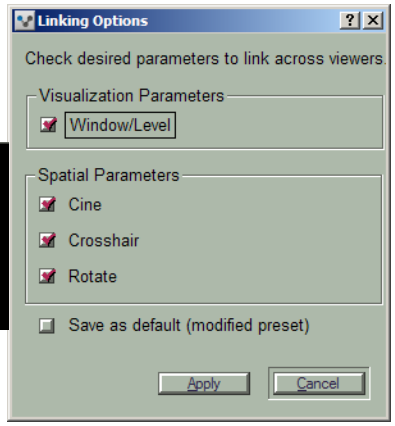
   NOTE: Vitrea does not allow using the Sculpt tool for editing an existing tumor region or resected liver/remnant liver regions. Use the Edit tool to edit existing tumor region and the steps in the Resection Planning section on page 93 to edit the resected/remnant liver.

Manual-lock

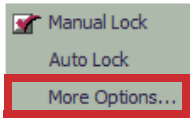
1. Right-click and adjust the axial views until they show the corresponding anatomy in both views.

2. Select the dropdown arrow next to the Lock button and select **Manual Lock,** then click the **Lock** button.



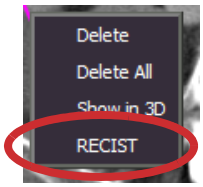


To change the lock settings, select the dropdown arrow next to the Lock button and click **More Options...** The Linking Options dialog box displays.



TIP: The views can be “locked” with respect to window/level, scroll/cine, zoom and pan, crosshair location, and rotating. If you manipulate one view, the other view(s) update automatically.

Manual RECIST



If you draw a regular ruler in an axial MPR, you can convert it to a tumor finding.

- Right-click on the ruler and select **RECIST**.

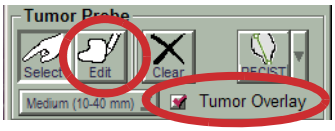
Edit Tumor Boundaries

If necessary, edit the tumor boundaries.

NOTE: This procedure applies if you created a tumor region with Tumor Probe, Organ segmentation, or manual Sculpt. It does not apply if you used WHO or RECIST.

1. Adjust the Thickness Slider to 1 (or minimum slice thickness available).

2. Verify the Tumor Overlay check box is selected.



3. Select the tumor in the Tumor Management area.

4. Click

.

5. In an mpr view, drag the contour to the desired shape and size.

6. Roll the mouse wheel to scroll through the axial image, then repeat step 5 as necessary.

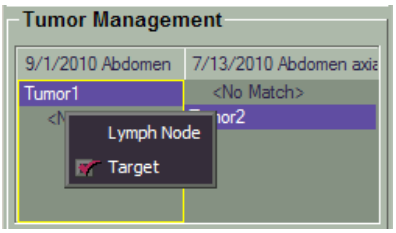
7. Click **Apply**.

8. Click **Close**.

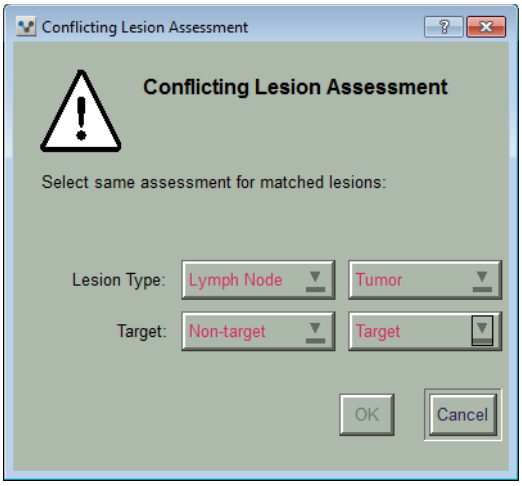
Manage Tumors

Vitrea adds listings of probed tumors in the Tumor Management area. Use this list to manage the findings.

Optional From the Tumor Management area, right-click and select **Lymph Node** and/or **Target**.



NOTE: If the same assessment is not selected for matched lesions, you will receive the following message. Make the appropriate selections and click **OK**.



Navigate to Tumor Findings

Use the Tumor Management list to navigate to the findings in the volumes.

To	Do This
Navigate to a finding in a volume	Click the finding name in the Nodule Management list.
Navigate forward through images containing findings	Press SPACEBAR.
Navigate backward through images containing findings	Press SHIFT + SPACEBAR.

Manage Tumor Management Findings

Select the finding in the Tumor Management list, then:

Click	To
Rename	Rename the finding. **TIP:** Only findings that are not matched can be renamed.
Delete	Delete the finding.
UnMatch	Unmatch matched findings.

CT Body Perfusion 4D for fX

Contents

CT Body Perfusion 4D for fX Overview

- Perfusion Study
- Perfusion Maps
- DICOM Export Limits
- Bolus Injection
- Body Perfusion Presets

CT Body Perfusion 4D Tools

CT Body Perfusion 4D for fX Lesson

I Select Study

- Loading a Pre-registered Study
- Loading a Non-registered Study

II Choose Protocol and Preset

- Data Manager
- Gallery Window

III Perform Analysis

- Examine the View
- Identify the Input Selections
- Compute Results
- Inspect the Perfusion Map(s)
- Review the Time-Density Graph
- Take Snapshots
- Create a Time-Series Batch or Movie

- Create an Orthogonal Batch or Movie
- Create a Collage Batch

IV Distribute Findings

Additional Procedures

- Undo Motion Correction
- Apply a Preset Window/Level Setting to the MPR
- Set the Window/Level Setting for the Perfusion Maps
- Adjust Measurement Colors
- Rescale the Curves in the Time-Density Graph
- Perform Patlak Plot Analysis (Single-input only)

Appendix

- Single-input Perfusion
- Dual-input Perfusion
- Region of Interest (ROI) Inputs
- Time-Density Graph
- Perfusion Image Map Calculations
- Patlak Plot Algorithm (Single-input Perfusion)
- Patlak Flow Line

CT Body Perfusion 4D for fX Overview

Vitrea® CT Body Perfusion 4D is a noninvasive post-processing software that calculates perfusion characteristics from dynamic CT image data. It displays blood flow parametric maps for single-input and dual-input workflows.

This application is available only on VitreaAdvanced fX and VitreaWorkstation fX systems and requires workstations with a minimum

of 16 GB of RAM. This is necessary to allow support for the datasets requirements and enough overhead for processing.

Perfusion Study

CAUTION: Vitrea CT Body Perfusion 4D does not support shuttle acquisition studies. Any shuttle acquisition studies loaded into CT Body Perfusion 4D will have inaccurate results.

CT Body Perfusion 4D requires certain data characteristics. If these conditions are not met, the Body Perfusion protocol will not be available.

- At least 5 volumes must be loaded, although 10 or more is recommended.

  NOTE: A blue informational icon will display in the Time-Density graph if 5 - 9 volumes are loaded.
- The maximum total slice count for all volumes is 10,000 slices.
- The loaded volumes must be coincident.

CAUTION: Verify the quality of motion correction by using the playback feature and ensuring that anatomical structures remain stationary across phases. Automatic deformable registration attempts to correct for motion due to breathing and other factors. In some cases, motion correction may not be able to correct for all possible motions. Regions where motion is still present will not contain correct perfusion results because the time curves at that region will not represent the same anatomical location across all phases.

A time gap of 5 seconds or less between volumes is recommended. A blue informational icon will display on the Time-Density Graph if Vitrea detects a time gap of greater than 5 seconds. In these cases, be sure to confirm that the time gaps between volume acquisitions are appropriate for perfusion analysis.

Vitrea uses the first volume from the dynamic scan prior to contrast enhancement as the baseline for the time intensity curves.

NOTE: In older versions, Vitrea used an average of the first two volumes prior to contrast enhancement as the baseline. Keep this difference in mind when restoring snapshots from previous versions of Vitrea.

Perfusion Maps

After input and reference points are identified, VitreaAdvanced calculates the following perfusion maps depending on the type of study:

Name	Abbrev.	Units	Model	Algorithm
Arterial Flow	AF	ml/min/100ml	single- and dual-input	maximum slope
Portal or Pulmonary Flow	PF	ml/min/100ml	dual-input	maximum slope
Perfusion Index	PI	%	dual-input	maximum slope
Flow Extraction Product	FE	ml/min/100ml	single-input	Patlak plot
Equivalent Blood Volume	EquivBV	ml/100ml	single-input	Patlak plot

DICOM Export Limits

You can export a CT Body Perfusion 4D report to DICOM servers or PACS devices. Keep these limitations in mind when using exported reports:

CAUTIONS:

- **You should not rely on Vitrea perfusion color maps viewed in grayscale on PACS workstations in making a diagnosis, as the conversion from color may be inaccurate.**
- **Vitrea exports each image in a report as a DICOM Secondary Capture image. Therefore, taking measurements (Hounsfield unit readings or dimensional rulers) and performing other similar operations on PACS or other devices on these Secondary Capture images will not yield accurate results.**
- **If you export images to a DICOM image server, the exported images may not have the same detail as the original scanned images.**

Bolus Injection

The operator should take care to capture the entire time of bolus transit, from just before wash-in to wash-out.

Body Perfusion Presets

Consult with your scanner manufacturer for specific scanning parameters for the Body Perfusion 4D protocol.

CT Body Perfusion 4D Tools

Tool	Description
	Viewer Window Formats
	Single-input Perfusion
	Maximum Slope Method
One-up MPR	2D axial view
Four-up 3D	AF perfusion map in three planes and CT only 3D
Two-up MPR Map	CT only and AF perfusion map in axial view
Two-up 3D Map	CT only and AF perfusion map in 3D
	Patlak Plot Method
Four-up 3D	AF perfusion map in three planes and CT only 3D **NOTE:** Click the map selector dropdown in the view to switch to the Equiv BV or FE perfusion maps.
Four-up MPR Map	CT only, Equiv BV map, AF map, and FE map in the axial view
Four-up 3D Map	CT only, Equiv BV map, AF map, and FE map in 3D
Twelve-up 3D	CT only, AF map, Equiv BV, and FE in axial, coronal, and sagittal orientations

Tool	Description
Dual-input Perfusion	
One-up MPR	2D axial view.
Four-up 3D	AF perfusion map in three planes and CT-only 3D. **NOTE:** Click the map selector dropdown AF in the view to switch to PF or PI perfusion maps.
Four-up MPR	Axial, sagittal, coronal, and 3D.
Four-up MPR Maps	AF, PF, PI perfusion maps and CT-only view in axial plane.
Four-up 3D Maps	AF, PF, PI perfusion maps and CT-only view in 3D.
Twelve-up 3D	AF, PF, PI, and CT-only view in axial, sagittal, and coronal planes.
Perfusion Analysis Tools	
Undo Motion Correction	Undo the motion correction Vitrea performed (non-registered studies)
Artery Tissue Portal Spleen PA LA Input Selection Buttons	Click a button, then draw a contour in the designated area.
Compute	Compute the maps
CT/Map Map CT/Map	Toggle between a Map only and a CT/Map fused view.

CT Body Perfusion 4D for fX Lesson

I. Select Study

Loading a Pre-registered Study

If you have used an external registration algorithm from your scanner to correct for motion during the scan, follow these steps to load a study:

VitreaAdvanced Through the Data Manager:

1. Click the patient name.
2. Select the **Series** tab.
3. Select the BODY-REG series.
4. Right-click and select **Load in VitreaAdvanced**.

OR

VitreaWorkstation:

1. Click the patient name.
2. Select the REGISTERED sub-study.
3. Click **Load in Vitrea**.

Loading a Non-registered Study

To have Vitrea perform motion correction, follow these steps to load a study:

VitreaAdvanced Through the Data Manager:

1. Click the patient name.
2. Select the **Series** tab.

3. Select the non-registered series.

4. Right-click and select **Load in VitreaAdvanced**.

OR

VitreaWorkstation:

1. Click the patient name.

2. Select the non-registered sub-study.

3. Click **Load in Vitrea**.

   NOTE: Allow Vitrea several minutes to perform the registration and motion correction.

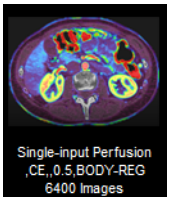
II. Choose Protocol and Preset

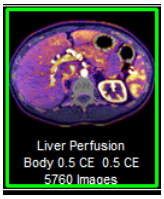
NOTE: The Single-input Body Perfusion preset is intended for organs other than the liver.

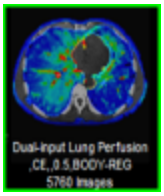
Use one of these procedures:

Data Manager

- Double-click the **Single-Input Perfusion**, **Liver Perfusion**, OR the **Dual-input Lung Perfusion** application thumbnail.







Gallery Window

1. On the Gallery window, select the **CT Body Perfusion** protocol.

2. Click Pick next to the **4D Single Input Perfusion**, **4D Liver Perfusion** OR the **4D Dual Input Lung Perfusion** preset.

III. Perform Analysis

Examine the View

1. To scroll through view, right-click and drag up or down in the view.

   OR

   Roll the mouse wheel in the view.

2. To cine through time in the view, right-click and drag left or right in the view.

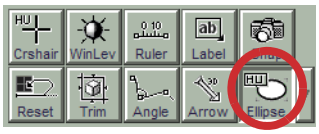
   NOTE: Cine through time in the view to be sure that motion correction registration has properly completed.

3. If the aorta does not appear to be fully enhanced, cine through time until it does.

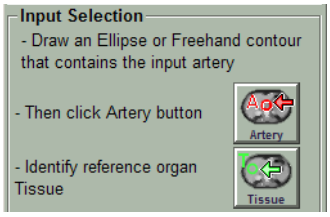
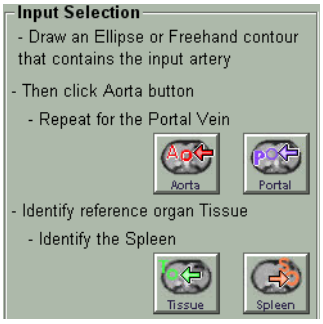
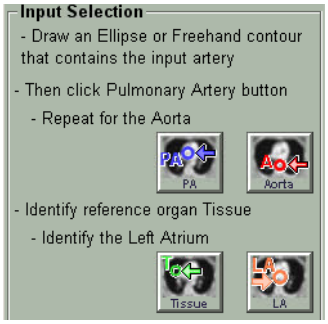
Identify the Input Selections

4. Verify

is active.



5. Complete the input selection steps:

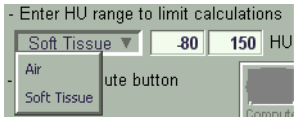
Single-input	Liver	Lung
		

Single-input	Liver	Lung
a. Draw a contour in the aorta. **TIP:** Be sure the contour is of significant size but still fully within the lumen. **b.** Click **Artery** . **c.** Press F10 to scroll through series to be sure the contour is within the lumen in all series. **TIP:** If the contour does not display on a series, press the SPACEBAR. **d.** Draw a contour within the organ. **TIP:** The representative sample should be healthy tissue with good contrast. **e.** Click **Tissue** .	**a.** To enlarge the view, click . **b.** Draw a contour in the aorta. **TIP:** Be sure the contour is of significant size but still fully within the lumen. **c.** Click **Aorta** . **d.** Press F10 to scroll through series to be sure the contour is within the lumen in all series. **TIP:** If the contour does not display on a series, press the SPACEBAR. **e.** Draw a contour within the portal vein. **TIP:** It may be easier to draw the contour in the portal vein in the coronal view. **f.** Click **Portal** . **g.** Draw a contour within the liver. **TIP:** The representative sample should be healthy tissue with good contrast. **h.** Click **Tissue** .	**a.** To enlarge the view, click . **b.** Draw a contour in the pulmonary artery. **TIP:** Be sure the contour is of significant size but still fully within the lumen. **c.** Click **PA** . **d.** Draw a contour within the aorta. **e.** Click **Aorta** . **f.** Press F10 to scroll through series to be sure the contour is within the lumen in all series. **TIP:** If the contour does not display on a series, press the SPACEBAR. **g.** Draw a contour within the lung. **TIP:** The representative sample should be healthy tissue. **h.** Click **Tissue** .

Single-input	Liver	Lung
	i. Draw a contour within the spleen. **TIP:** The representative sample should be healthy tissue with good contrast. **j.** Click **Spleen** .	**i.** Draw a contour within the left atrium. **TIP:** The representative sample should be healthy tissue with good contrast. **j.** Click **LA** .

Compute Results

6. If necessary, select a preset HU value from the dropdown or manually enter a HU range.



7. Click .

   The following display:

   - **Single-input**: An Arterial Flow (AF) perfusion map displays overlaid on a CT image.
   - **Liver**: An Arterial Flow (AF) perfusion map, a Portal Flow (PF) perfusion map, and a Hepatic Perfusion Index (PI) perfusion map display overlaid on CT images.
   - **Lung**: A Pulmonary Flow (PF) perfusion map, an Arterial Flow (AF) perfusion map, and a Pulmonary Perfusion Index (PI) perfusion map display overlaid on CT images.

8. To toggle between the CT/Map overlay view and the Map only view, click the CT/Map dropdown in the image.

9. To change the transparency of the perfusion map overlay(s), slide the Transparency slider in the CT/Map dropdown. To make this transparency setting a modified preset, press CTRL-P.

Inspect the Perfusion Map(s)

10. Verify

is active.

11. Click and drag in the CT/Map or Map view to display arterial flow values for the crosshair location.

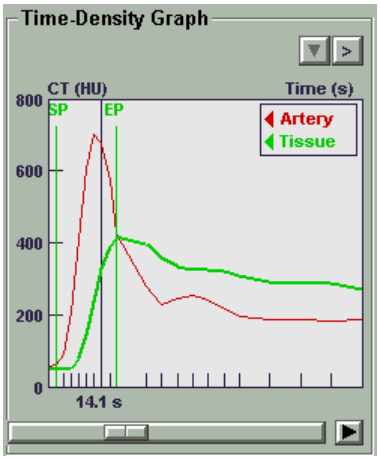
Review the Time-Density Graph

The Time-Density Graph plots the contrast density over time.

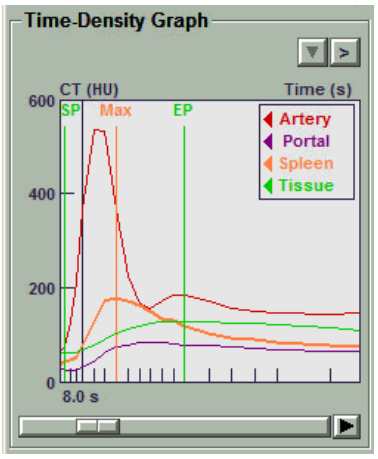
The black vertical line indicates the time of the currently displayed image. The green vertical lines indicate the start point (SP) and the end point (EP) of the range of maximum slope.

For Liver graphs, the orange vertical line indicates peak spleen enhancement.

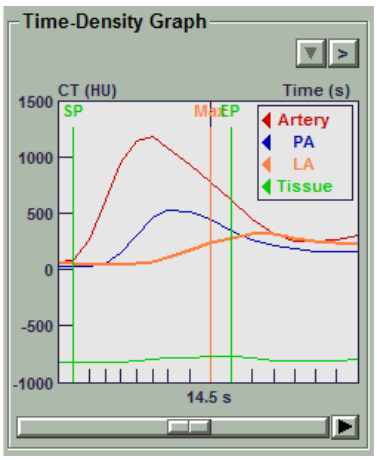
For Lung graphs, the orange vertical line indicates peak left atrium enhancement.



Single-input



Liver



Lung

For more information regarding the elements on the Time-Density graph and the methods of calculation, see the Appendix of this chapter.

The colored arrows indicate the y-axis the corresponding curve used for scaling.

See the Additional Procedures section for information on re-scaling the curves.

12. If necessary, drag the SP or EP lines in the Time-Density Graph to define the optimal slope range.

13. For Liver or Lung graphs, if necessary, drag the Max line in the Time-Density Graph to indicate peak vessel enhancement.

14. To review the contrast density over time, drag the **Time Slice** slider.

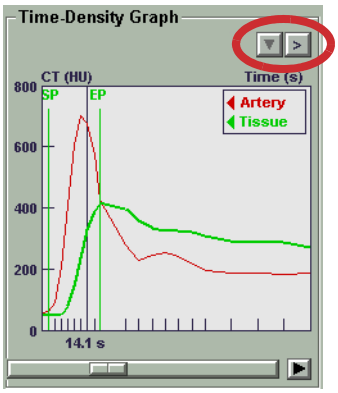
OR

Click .

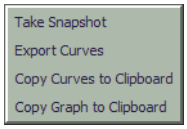
TIP: Drag the small slider to change the cine speed.

15. To view a larger version of the Time-Density graph, click .

TIP: You can take snapshots of this enlarged graph.



16. To distribute the graph, click and select an option.



NOTE: Export Curves, Copy Curves to Clipboard, and Copy Graph to Clipboard available for Standalone Workstations only.

Take Snapshots

Take snapshots to save your work and to put into a report.

17. Right-click and select , then click in each view.

TIP: Hold ALT to keep taking snapshots without having to activate the snapshot tool each time.

OR

Hold CTRL to take one snapshot that includes all views.

Create a Time-Series Batch or Movie

Create an image batch or a movie of a 3D time-series study.

18. Right-click in the 2D or perfusion map view.

19. Select **Movie -4D Cine** to save it as a movie, or select **Batch - 4D Cine** to save it as a batch.

Create an Orthogonal Batch or Movie

Make orthogonal slice batches or movies of the perfusion map.

20. Right-click in a perfusion map view and select **Movie - Orthogonal** or **Batch - Orthogonal**.

Create a Collage Batch

Create a single batch that includes the MPR and perfusion map views.

21. Right-click in a perfusion map view and select **Batch - Collage**.

IV. Distribute Findings

The snapshots you save in the Viewer window are saved to the Report window.

1. Click Report at the bottom of the window.

2. Export your findings or create a report.

See the **Distribute Findings** chapter of the **VitreaAdvanced-VitreaWorkstation General Education and Reference Guide** for instructions on exporting findings, restoring workflow, and creating reports.

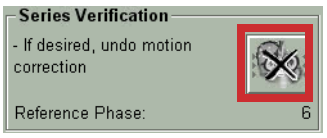
Additional Procedures

This section addresses some less common procedures to complete your workflow.

Undo Motion Correction

You can undo the motion correction Vitrea performs on non-registered studies.

1. Click .



Apply a Preset Window/Level Setting to the MPR

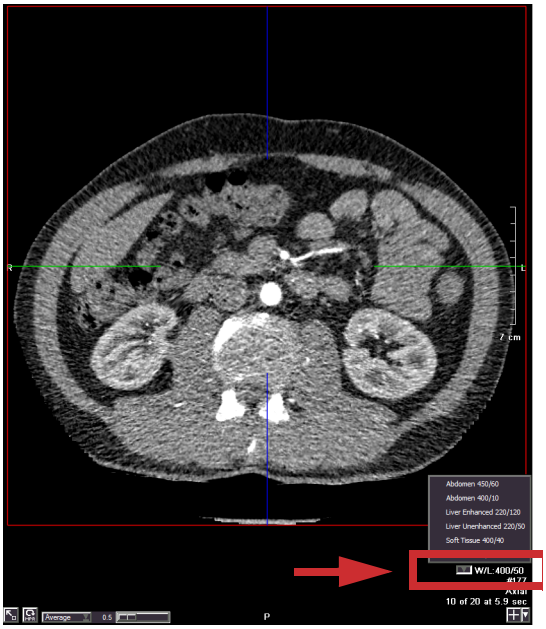
Apply window/level settings in the MPR view.

1. Click the Window/Level dropdown in the view.

   W/L:400/50

2. Select a setting.

   Abdomen 450/60
   Abdomen 400/10
   Liver Enhanced 220/120
   Liver Unenhanced 220/50
   Soft Tissue 400/40
   Vascular 600/150

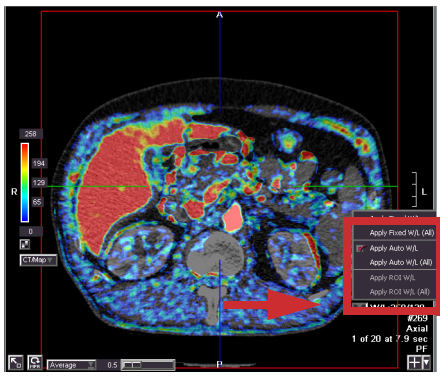


Set the Window/Level Setting for the Perfusion Maps

Set the window/level settings in the maps based on fixed, automatic, or user-defined ROI settings.

1. Click on the Window/Level dropdown in a map view. W/L:335/167

2. Select a setting:
   - **Apply Fixed W/L** - a fixed setting for the map
   - **Apply Fixed W/L (All)** - a fixed setting for all maps
   - **Apply Auto W/L** (default setting)
     - Vitrea assesses the map and computes a setting based on scan-specific factors
   - **Apply Auto W/L (All)** - Auto W/L for all maps
   - **Apply ROI W/L** - Vitrea assesses the ROI and normalizes the map to the region
   - **Apply ROI W/L (All)** - ROI W/L for all maps



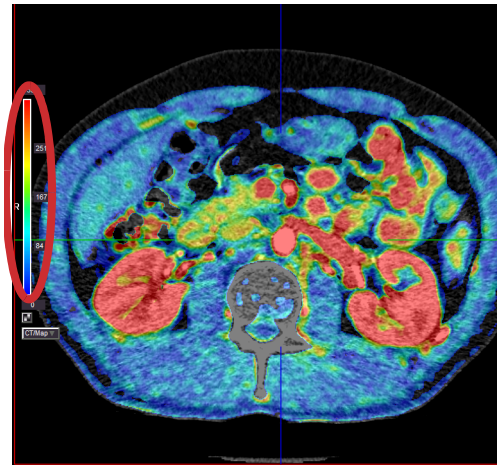
TIP: To activate the Apply ROI W/L option, draw a representative ROI in the view.

CAUTION: Manually window/level the maps if the automatic window/level does not apply or applies incorrectly.

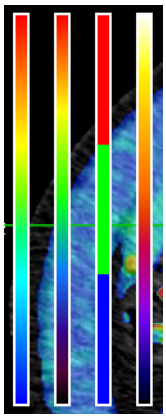
Adjust Measurement Colors

Change the color on the perfusion maps to highlight areas of tissue in different color schemes.

1. Click the color scale bar in the map view.



2. Click the desired color scheme.

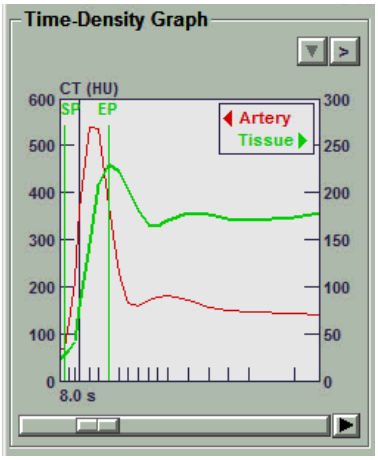


TIP: The 3-color scheme allows you to adjust the HU range for each color. Drag the dividing line between colors.

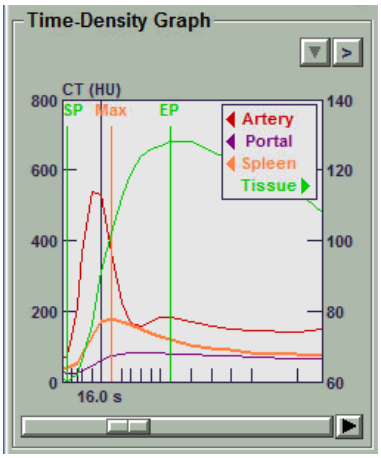
TIP: To invert the color scale, click under the color scale bar.

Rescale the Curves in the Time-Density Graph

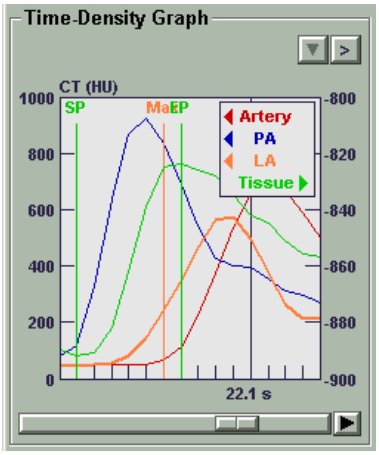
The Tissue, Spleen, and LA curves have smaller peaks than the Artery and Portal curves. You can apply separate scaling for the **Tissue** curves for single-input studies, **Spleen** and **Tissue** curves for liver studies, and the **LA** and **Tissue** curves for lung studies to better visualize the quality of the corresponding ROIs.



Single-input



Liver



Lung

NOTE: The Artery and Portal curves in single-input and liver studies and Artery and PA curves in lung studies are not re-scalable.

The colored arrows next to the curve labels indicate which y-axis the corresponding curves are scaled to.

1. Hover on the Tissue label for single-input studies, Spleen or Tissue label for liver studies, or the LA or Tissue label for lung studies.

2. Click the outline arrow to the right of the label.

A new y-axis displays to the right of the Time-Density Graph and the colored arrow switches to indicate the new y-axis.

Curve (Single-input)	Y-axis Scale
Tissue	0-300 HU

Curve (Liver)	Y-axis Scale
Spleen	50 to 100 HU
Tissue	60 to 85 HU

Curve (Lung)	Y-axis Scale
LA	0 to 500 HU
Tissue	-810 to -780 HU

3. To return to regular scaling, click the outline arrow on the left side of the label.

Perform Patlak Plot Analysis (Single-input only)

The Patlak Plot method computes **AF Max Slope** (Arterial Flow), **Equiv BV Patlak** (Equivalent Blood Volume), and **FE Patlak** (Flow Extraction product) maps.

NOTE: This analysis method requires a special scan protocol that captures not only the initial contrast bolus but also the full wash-out phase. The Patlak Plot analysis uses this extended wash-out phase where contrast enters the extravascular space.

1. Identify the Arterial Input and click .

2. Identify the Organ Tissue and click .

3. Click the dropdown arrow next to the Compute button, and select **Patlak Plot**.

4. Click .

   AF Max Slope (Arterial Flow), **Equiv BV Patlak** (Equivalent Blood Volume), and **FE Patlak** (Flow Extraction product) perfusion maps display overlaid on CT images.

5. Review the Time-Density Graph to verify that the scan captured the entire time of bolus transit, from just before wash-in to full wash-out.

6. Click to switch to the Patlak Plot Graph.

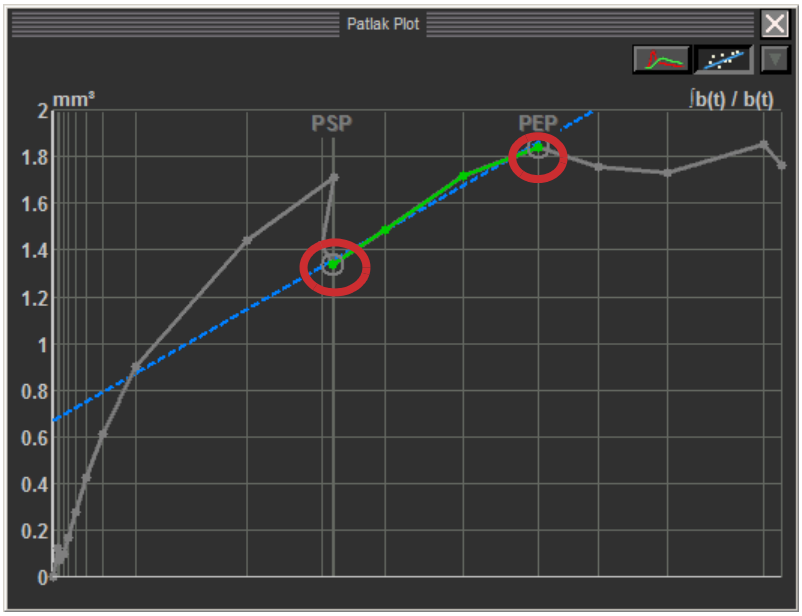
   TIP: Click to expand the Patlak Plot on to the Viewer window.

7. Verify that the Patlak Flow Line (blue line) is the best linear fit between the time when contrast enters the extravascular space (first time point - PSP) and the time when contrast reabsorbs to the intravascular space (last time point - PEP).

   See the Patlak Flow Line section of the Appendix for more information.

   TIP: To edit the Patlak Flow Line:

   a. Click an endpoint on the plot line and drag to appropriate time point.



   b. Click

.

Appendix

Single-input Perfusion

Vitrea uses a maximum slope model to calculate blood flow, which is based on the Fick principle.

For single-input organs, a maximum slope model is used to calculate blood flow. The maximum slope algorithm requires a reference arterial input (typically the abdominal aorta).

The Time-Density Graph displays the average image density over time curve for the artery in red; and the average image density over time curve in the tissue sample in green.

Dual-input Perfusion

Vitrea uses a dual-input maximum slope model to separately calculate blood flow:

- from the hepatic artery (arterial flow) and the portal vein (portal flow) for **liver** studies.
- from the pulmonary artery (pulmonary flow) and bronchial artery (arterial flow) for **lung** studies.

The Time-Density Graph for **liver** studies displays the average image density over time curves:

- for the artery in red
- for the tissue sample in green
- for the portal vein in purple
- for the spleen in orange.

The Time-Density Graph for **lung** studies displays the average image density over time curves:

- for the aorta in red
- for the tissue sample in green
- for the pulmonary artery in blue

- for the left atrium in orange.

Region of Interest (ROI) Inputs

You specify the ROI (region-of-interest) to be used for the arterial input and portal vein. ROI inputs, instead of a single-voxel location, are used to generate an average time-density curve. When you place the arterial input ROI, Vitrea performs vessel tracking across all phases in case the location of the vessel shifts.

You specify a representative sample of the target organ. This provides a reference curve for the tissue that you can use to control the range for the maximum slope calculations.

For dual-input method, you specify a representative sample of the spleen (for the liver) or the left atrium (for the lungs). This provides a reference curve you can use to identify the transition for arterial to portal flow (for the liver) or for the pulmonary to arterial flow (for the lungs). Use the curve to control the ranges for the two maximum slope calculations.

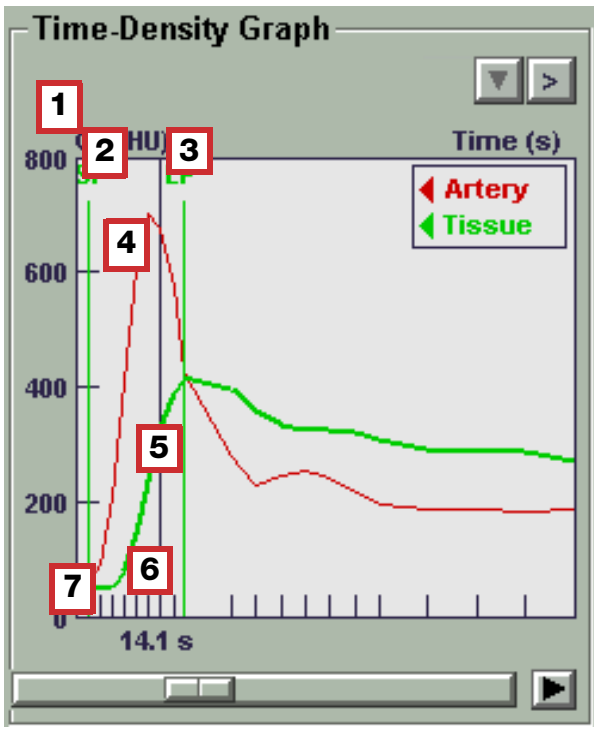
Time-Density Graph

The Time-Density Graph plots the contrast density over time.

The black vertical line indicates the time of the currently displayed image, and the corresponding time value is displayed along the horizontal axis. Drag this line to adjust the time of the currently displayed image.

The green vertical lines indicate the start point (SP) and end point (EP) of the range of maximum slope. If the tissue curve indicates “noise” at the beginning of the scan, you can adjust these lines to identify the optimal slope range.

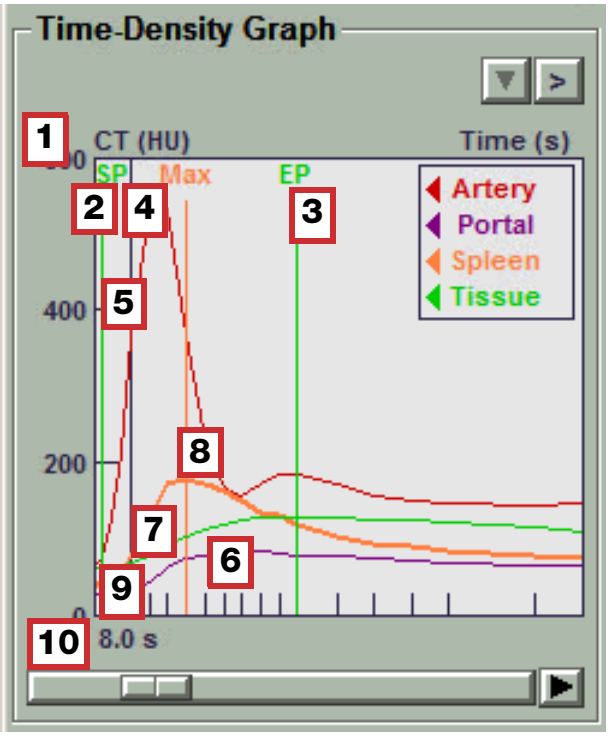
Single Input Studies



No.	Description	Details
1	HU Value Axis (y-axis)	Image density value.
2	Adjustable Start Point line	Indicates the start of the maximum slope range of tissue sample. Adjust as necessary.
3	Adjustable End Point line	Indicates the end of the maximum slope range of tissue sample. Adjust as necessary.
4	Artery (red) curve	Image density over time for the artery location.
5	Tissue (green) curve	Image density over time for the tissue sample.
6	Adjustable Cross-reference line	Indicates the time of the displayed image.
7	Time Axis (x-axis)	Time, in seconds.

Liver Studies

The orange vertical line indicates peak spleen enhancement. Use this in conjunction with the two tissue markers to identify the ranges for the artery and portal phases. The calculation for the maximum slope for the artery and portal phases are restricted to these ranges.

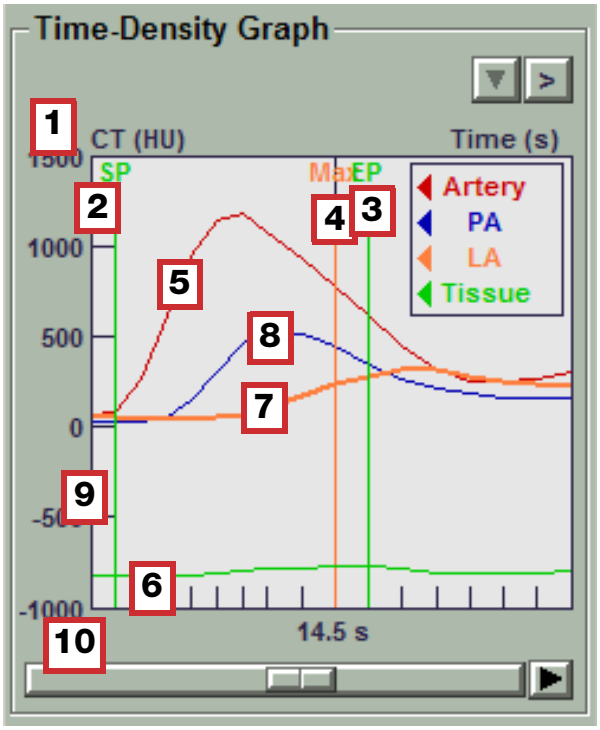


#	Description	Details
1	HU Value Axis (y-axis)	Image density value.
2	Adjustable Start Point line	Indicates the start of the maximum slope range of tissue sample. Adjust as necessary.
3	Adjustable End Point line	Indicates the end of the maximum slope range of tissue sample. Adjust as necessary.
4	Adjustable Maximum Spleen Enhancement Line	Indicates the location of peak spleen enhancement. Adjust as necessary.
5	Artery (red) curve	Image density over time for the artery location.
6	Tissue (green) curve	Image density over time for the tissue sample.
7	Spleen curve (orange)	Image density over time for the spleen sample.
8	Portal Vein curve (purple)	Images density over time for the portal vein location.

#	Description	Details
9	Adjustable Cross-reference line	Indicates the time of the displayed image.
10	Time Axis (x-axis)	Time, in seconds.

Lung Studies

The orange vertical line indicates peak left atrium enhancement. Use this in conjunction with the two tissue markers to identify the ranges for the pulmonary and arterial phases. The calculation for the maximum slope for the pulmonary and arterial phases are restricted to these ranges.



#	Description	Details
1	HU Value Axis (y-axis)	Image density value.
2	Adjustable Start Point line	Indicates the start of the maximum slope range of tissue sample. Adjust as necessary.
3	Adjustable End Point line	Indicates the end of the maximum slope range of tissue sample. Adjust as necessary.

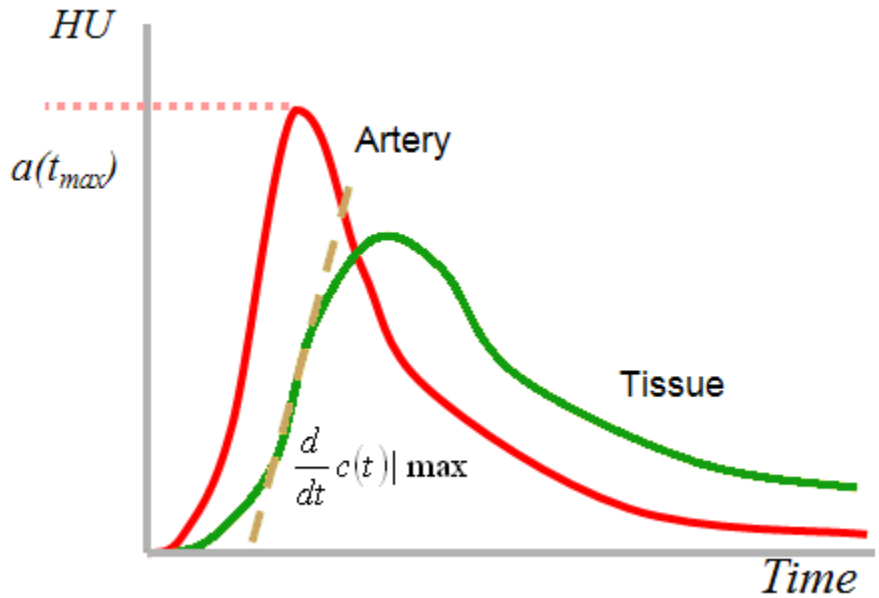
#	Description	Details
4	Adjustable Maximum Left Atrium Enhancement Line	Indicates the location of peak left atrium enhancement. Adjust as necessary.
5	Aorta (red) curve	Image density over time for the aorta location.
6	Tissue (green) curve	Image density over time for the tissue sample.
7	Left Atrium curve (orange)	Image density over time for the left atrium sample.
8	Pulmonary Artery curve (blue)	Images density over time for the pulmonary artery location.
9	Adjustable Cross-reference line	Indicates the time of the displayed image.
10	Time Axis (x-axis)	Time, in seconds.

Perfusion Image Map Calculations

Vitrea uses the maximum slope method to calculate the blood flow for each voxel then computes the perfusion map(s).

For all organs, besides the liver and the lungs, Vitrea uses a single-input maximum slope model to calculate blood flow.

Single-input Perfusion:



The blood flow for each voxel is then calculated as follows:

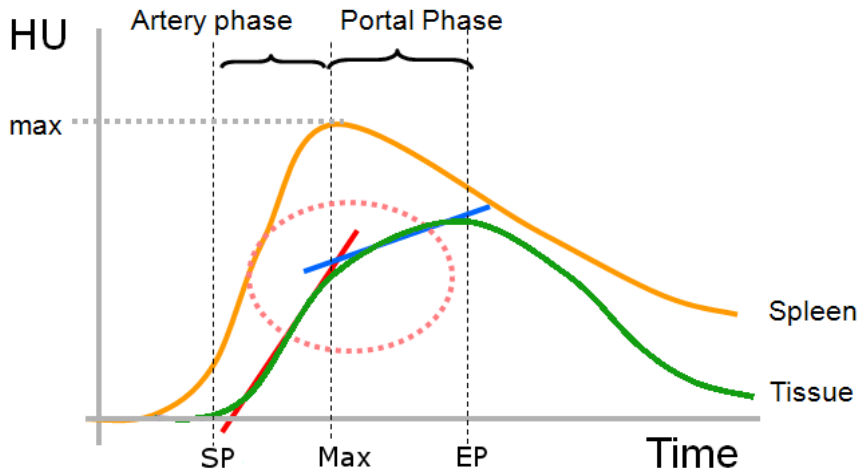
$$BloodFlow = \frac{F}{V} = \frac{\frac{d}{dt}c(t)|max}{a(t_{max})}$$

In other words, the blood flow is equal to the maximum slope of the tissue curve divided by the maximum value of the arterial input function.

For the liver and lungs, Vitrea uses a dual-input maximum slope model to separately calculate:

- blood flow from the hepatic artery (AF) and the portal vein (PF) for **liver** studies
- blood flow from the pulmonary artery (PF) and bronchial artery (AF) for **lung** studies.

Dual-input Perfusion - Liver:



The two components of blood flow are calculated independently using the following formulas:

$$ArterialFlow(AF) = \frac{F_a}{V} = \frac{\frac{d}{dt}c_l(t)|max}{c_a(t_{max})}$$

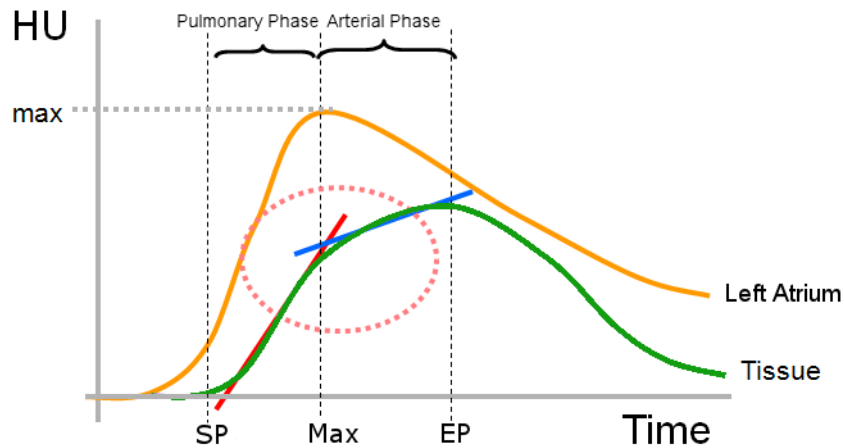
$$PortalFlow(PF) = \frac{F_p}{V} = \frac{\frac{d}{dt}c_l(t)|max}{c_p(t_{max})}$$

Where c_l is the tissue curve and $c_a(t_{max})$ is the maximum contrast enhancement of the artery curve and $c_p(t_{max})$ is the maximum enhancement of the portal curve.

In addition, Vitrea calculates the perfusion index (PI) as the following:

$$HepaticPerfusionIndex(PI) = AF/(AF + PF)$$

Dual-input Perfusion - Lung:



The two components of blood flow are calculated independently using the following formulas:

$$ArterialFlow(AF) = \frac{F_a}{V} = \frac{\frac{d}{dt}c_l(t)|max}{c_a(t_{max})}$$

$$PulmonaryFlow(PF) = \frac{F_p}{V} = \frac{\frac{d}{dt}c_l(t)|max}{c_p(t_{max})}$$

Where c_l is the tissue curve and $c_a(t_{max})$ is the maximum contrast enhancement of the artery curve and $c_p(t_{max})$ is the maximum enhancement of the portal curve.

In addition, Vitrea calculates the perfusion index (PI) as the following:

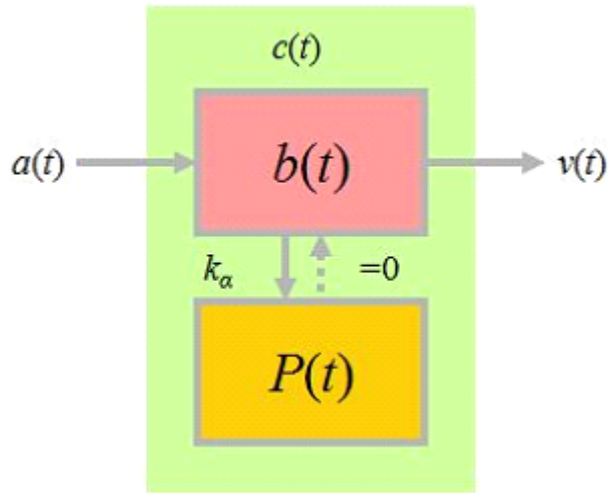
$$PulmonaryPerfusionIndex(PI) = PF/(AF + PF)$$

Once the blood flow per voxel is calculated, Vitrea displays perfusion maps as an overlay on the CT image. Use the CT/Map toggle drop down to display the Map only.

Patlak Plot Algorithm (Single-input Perfusion)

The Patlak Plot method computes **AF Max Flow** (Arterial Flow), **Equiv BV Patlak** (Equivalent Blood Volume), and **FE Patlak** (Flow Extraction product) perfusion maps.

The Patlak Plot method is a two-compartment model represented by intravascular and extracellular compartments. With injection of a contrast agent into the intravascular space, some contrast medium will pass into the extravascular space of the target tissue. This can be represented by the following illustration:



where:

- a(t) = density of contrast media in artery
- b(t) = density of contrast medium in blood
- c(t) = density of contrast medium in tissue
- v(t) = density of contrast medium in vein
- P(t) = total concentration of contrast medium outside vessel
- k_α (t) = transfer from blood to extracellular space

If we assume the transfer of contrast medium from blood to extravascular space is constant and the concentration of contrast medium in the extravascular space is sufficiently low during the scan to limit re-absorption of the contrast medium back into the blood, the system can be represented by the following:

$$C(t) = Vc(t) = B(t) + P(t)$$

where:

- C(t) = total concentration of contrast media in tissue
- B(t) = total concentration of contrast media in blood
- V = Volume of tissue

divided by the volume (V) gives:

$$c(t) = \frac{C(t)}{V} = \frac{B(t)}{V} + \frac{P(t)}{V}$$

Taking the compartment model we can write:

$$\frac{dP(t)}{dt} = k_{\alpha} b(t)$$

or:

$$P(t) = k_{\alpha} \int_0^t b(t)dt$$

Combining the above equations gives:

$$\frac{c(t)}{b(t)} = \frac{B(t)}{Vb(t)} + \frac{k_{\alpha}}{V} \cdot \frac{\int_0^t b(t)dt}{b(t)}$$

with:

$$B(t) = V_B b(t)$$

gives:

$$\frac{c(t)}{b(t)} = \frac{V_B}{V} + \frac{k_{\alpha}}{V} \cdot \frac{\int_0^t b(t)dt}{b(t)}$$

This is representative of a linear relationship after sufficient mixing has occurred (constant transfer rate) and prior to re-absorption of contrast medium (sufficient concentration of contrast in the extracellular space

reached). The slope of this line represents the clearance or flow and the y-intercept represents the equivalent blood volume.

In summary, with regard to Patlak theory, Equiv. BV is an estimate of the tissue blood volume; Patlak Flow Extraction Product is an estimate of the transfer coefficient k from IVS (intravascular space) to EVS (extravascular space); and Patlak Flow Extraction Product/unit volume = permeability.

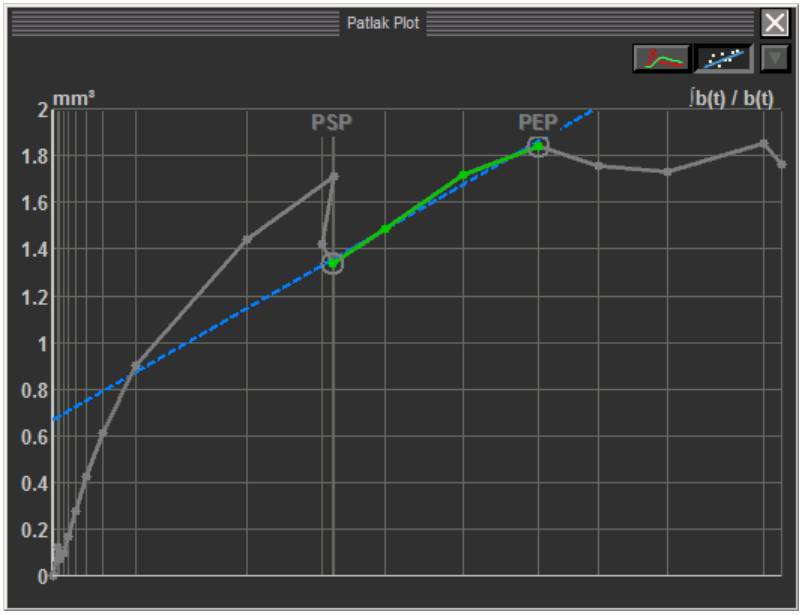
Patlak Flow Line

The Patlak Plot graph includes raw data points and the corresponding Patlak Flow Line representing the linear regression. Use the graph to check the validity of the line fit and whether the time range for the linear regression is appropriate.

The graph includes two adjustable markers, the start point (PSP) and end point (PEP), so you can modify the calculation range.

The PSP should be placed at the time point of the clearance of contrast from the intravascular space to the extravascular space. The PEP should be placed at the time point of re-absorption of contrast back to the intravascular space.

The slope of the Patlak Line represents the clearance or flow, and the y-intercept represents the Equiv. BV.



MR Tumor Volume

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MR Tumor Volume Lesson

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- **II** Choose Protocol and Preset
  - Data Manager
  - Gallery Window
- **III** Perform Analysis
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  - Display Tumor Volume Measurements
  - Edit Contour Lines Around Tumors
  - Take Snapshots
- **IV** Distribute Findings

Additional Procedures

- Examine the Tumor in 3D

MR Tumor Volume Overview

Measure the volume of single or multiple non-contiguous tumors within a region of interest using the Vitrea Tumor Volume Measurement feature. The tumor volume measurement feature is intended for the analysis/

quantification of tumor volumes obtained from MR brain series scans using a special 2D view in the **Head MR** protocol.

- Review an MR series of the brain for a patient.
- Identify regions you suspect to be brain tumors.
- The controls of Vitrea define the regions that contain the brain tumors.
- Select the tumor volume measurement feature to display highlighting of the tumors and tumor volume measurements in cubic centimeters.

NOTE: In Vitrea, the term tumor refers to any suspected or known brain lesion indicated on an MR image. The Vitrea software contains tools to help the physician measure noncontiguous tumors within a region of interest.

CAUTION: A Vitrea algorithm detects tumors based on the shape, density, and location of voxel values. Some data with values above the dynamically calculated voxel value will not indicate the presence of a tumor. You must carefully review the highlighting and tumor volume measurements to ensure accuracy. Once Vitrea has identified the tumors within the user-designated region of interest, it measures tumor volumes.

CAUTION: For best results, you must use only volumes created from MR series of the brain scanned with the manufacturer's recommended Head MR settings. This measuring tool is not intended for measuring tumors in other anatomical regions or for measuring volumes created from MR series of the brain scanned at different settings other than the manufacturer's recommended Head MR settings.

CAUTION: MR tumor volume measurements may be inaccurate when performed on studies acquired with variable slice spacing.

MR Tumor Volume Lesson

I. Select Study

Load an MR brain study.

See the instructions for your Vitrea type (VitreaAdvanced Through the Data Manager or VitreaWorkstation) in the **Select Study** chapter of the **VitreaAdvanced-VitreaWorkstation General Education and Reference Guide**.

II. Choose Protocol and Preset

Use one of these procedures:

Data Manager

- Double-click the **Brain MR** application thumbnail.

Gallery Window

5. On the Gallery window, select the **Brain MR** protocol.

   The Gallery choices update automatically.

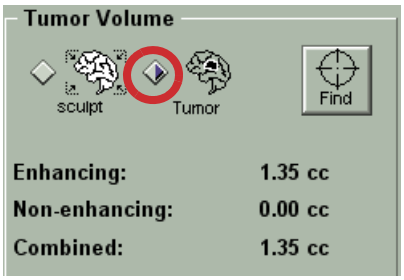
6. Click Pick next to the **2D Tumor Measurement** preset.

III. Perform Analysis

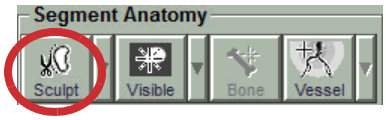
1. In the 2D Viewer window, roll the mouse wheel to view the image. The image may initially display in black.

Draw Contour Lines on Selected Slices

2. Select **Tumor**.



3. From the Segment Anatomy area, click **Sculpt**.



4. Right-click on the image and scroll to locate the tumor.

5. Move one slice beyond the margin and click and drag to create a generous contour.

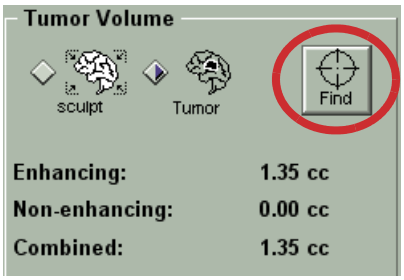
   Optional To adjust the shape of the contour line, click and drag its border. The line adjusts as you drag.

6. Move one slice beyond the margin of the end of the tumor and click and drag to create a contour.

Display Tumor Volume Measurements

7. Click

.



   Vitrea calculates the measurements.

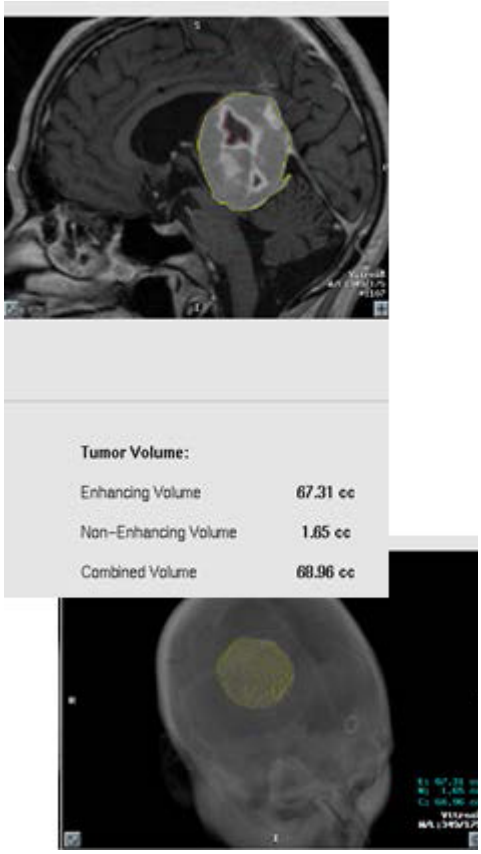
   - Enhancing tissue is circled in yellow.

     To add an enhancing (yellow) contour line, press and hold the Ctrl key.

- Non-enhancing tissue is circled in pink.

  To add an unenhanced contour (pink) line, press and hold the Shift key and trace with the mouse.

- Values for enhancing, non-enhancing, and combined are reported on the left.



CAUTION: In some cases, tumor volume measurements can represent measurements of tissue that is neither malignant nor abnormal growth. Such measurements can occur if a clinician measures a volume representing nonmalignant or normal tissue or when the effect on the data of visual settings of either Vitrea or the scanning device causes parts of the volume to be measured as a tumor.

Edit Contour Lines Around Tumors

CAUTION: The accuracy of the tumor volume measurements can be affected by the accuracy of the contour lines. It is important to review and, if needed, edit the contour lines, so the contour lines surround the region that you have determined to be tumorous or cystic. If Vitrea draws contour lines for tumors or cysts around regions for healthy or non-tumorous tissue, the measurements will include the regions for healthy or non-tumorous tissue.

8. Scroll to the slice containing the contour line you want to change.

9. Position the cursor over the contour line you want to change.

TIP: The cursor changes to look like a pencil.

10. Click and drag exactly where you want the border to display.

11. Repeat as needed to get the desired shape.

Vitrea recalculates all of the tumor volume measurements.

NOTE: Edit the contour lines in the 2D or MPR views. Vitrea does not allow editing the contour lines in the 3D views.

Take Snapshots

12. Right-click and select (or press S) to activate the camera.

13. Move the cursor to the image and click.

Snapshots, which include measurements, rulers, W/L, or segmentation option, can be restored from the Report page or the Study Directory.

IV. Distribute Findings

The snapshots you save in the Viewer window are saved to the Report window.

1. Click

at the bottom of the window.

2. Export your findings or create a report.

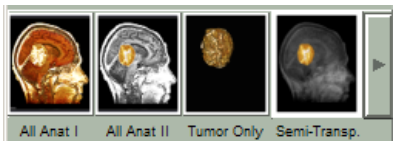
See the **Distribute Findings** chapter of the **VitreaAdvanced-VitreaWorkstation General Education and Reference Guide** for instructions on exporting findings, restoring workflow, and creating reports.

Additional Procedures

Examine the Tumor in 3D

1. Switch to a 4-up Viewer window format.

2. Click the **Tumor Only** preset button.



3. Rotate the 3D view to examine the Tumor region.

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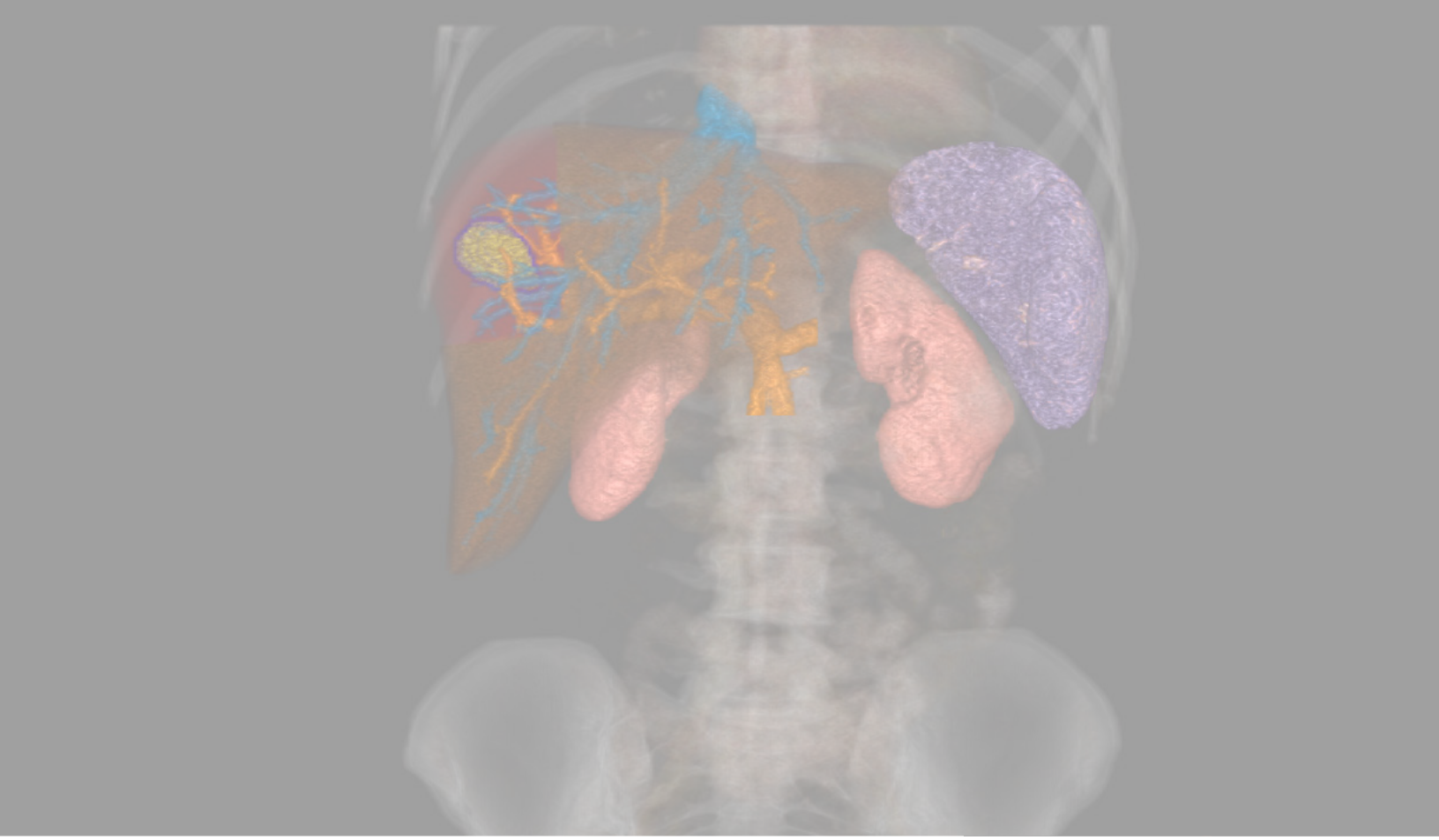

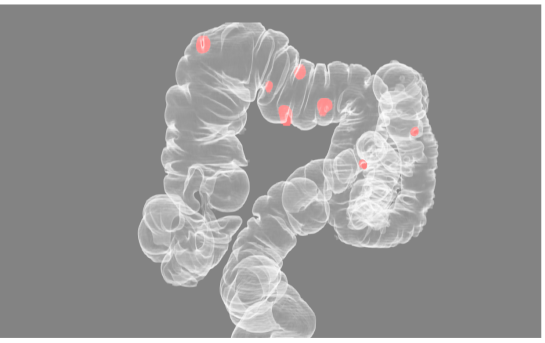

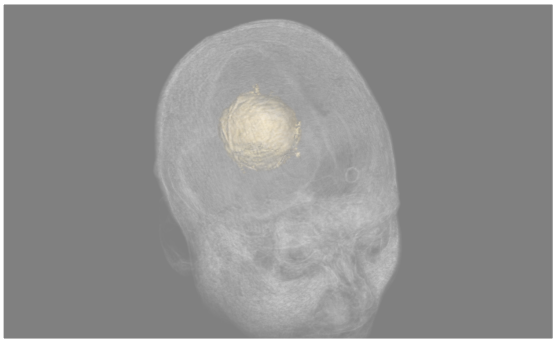

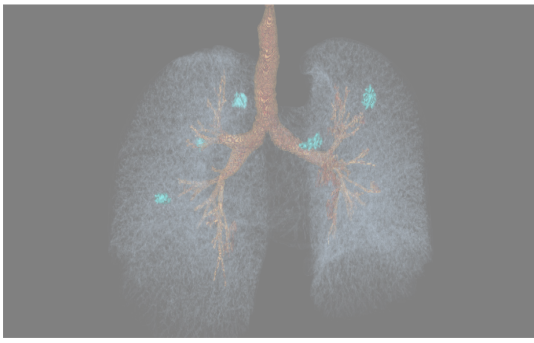

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