10 Body Perfusion (Functional CT)

Functional CT (FCT) perfusion is a blood flow imaging application that analyzes the uptake of injected contrast bolus, in order to determine functional blood flow information about a region of interest (ROI). The region of interest is scanned in the same position and at the same time intervals, as per the expected rate of change.

NOTICE

Before continuing, refer to the “Instructions for Use” that came with your scanner.

Intravenous contrast bolus is injected into the patient, and a region of interest is scanned repeatedly for a period of time. The Hounsfield unit enhancement is tracked for each voxel over time to produce tissue specific time-density curves. Measurements made from these time-density curves and user-selected regions of interest (ROIs) are used to create various parametric functional images.

In addition to displaying color-mapped parametric functional images, statistical measurements (such as mean, and standard deviation) can be recorded for any user-selected region.

The CT perfusion application consists of the following steps:

- Load the image set;
- Select Input ROI(s);
- Calculate Perfusion; and
- Create quantitative report.

This application is intended for Oncology, for the detection and follow-up of tumor growth by examining the relationship between arterial tissue and venous enhancement after the contrast bolus injection.

Perfusion series must include at least one non-contrasted image to be used as baseline. The baseline image is subtracted from the enhanced images set to obtain time enhanced data. An ROI on this data allows the generation of the Time Enhancement Curve (TEC).

NOTICE

Depending on your Portal configuration, this application may not be available.

Indications for Use

The Functional CT application is intended for visualization, assessment and quantification of blood flow (perfusion), blood volume, time to peak and peak enhancement using dynamic CT data. The application provides whole-organ or single-location liver, lung and kidney perfusion calculations.

Open Study in Functional CT

1. Click **Directory**.
2. Select the series to open. In order to run the applications properly you must load original images. Loading derived images may cause the system to close the application and return you to the Directory, where you must select original images and launch the application again.
3. Select **Functional CT** from the Directory Applications drop-down.

Functional CT opens in the Vessel Definition stage with a tMIP image in the main viewport.

WARNING

When loading images into Functional CT, all images which contain 16 bit data are converted into 12 bit images. This means that for rescale intercept equal to -1000, HU values above 3095 are displayed as 3095. For rescale intercept equal to -1024, HU values above 3071 are displayed as 3071.

Vessel Definition Stage

Functional CT opens in the Vessel Definition stage. In this stage you select a perfusion type and define vessels for analysis.

NOTICE

The active table may be added to the clipboard using **Ctrl + C** or by right-clicking on the table and selecting copy. The measurements may then be pasted into common document types, including plain text, Microsoft Word, and Microsoft Excel documents.

Function Tabs

To access additional application functions, click the down arrow in the tab window, or hover the mouse over the tab window. The list of available functions displays.

Key Images

Save groups of images that can be reviewed in any system supporting the defined standard. See **Instructions for Use** > **Directory** > **Key Image Notes** for more information.

See **Report**, **Film**, **CT Common Processes** and **CT Common Tools** for information on using common options, tools, functions, and processes.

Batch Function

The Batch function in Vessel Definition has a Time function. It is active only when the axial image is in “average” mode - it should be grayed out in tMIP. It locks the scroll in position so that batch includes images in the same position at different times.

Mark Perfusion ROIs

The Functional CT application opens with the ROIs tab displayed. The ROIs tab contains the drawing tools for placing regions of interest on images.

Perfusion types --You must select the type of perfusion study you are working with: Liver, General, or TimeLapse.

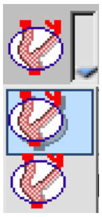
Liver Study ROIs

Liver perfusion maps include the following items:

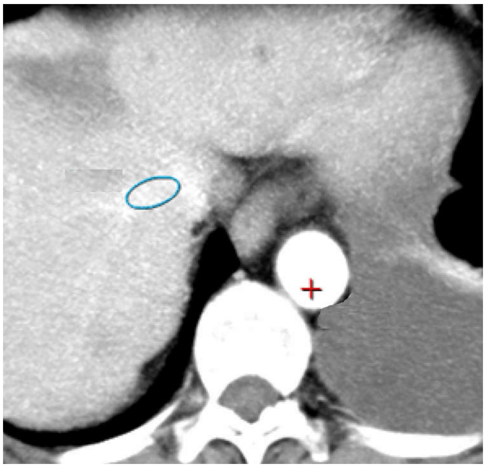
- Arterial perfusion;
- Portal venous perfusion;
- Total perfusion;
- Hepatic perfusion index; and
- All - scroll between all four of them (above).

Liver perfusion allows you to draw ROIs for the artery (Aorta), vein (Portal Vein), and spleen (draw on the spleen, ROI should be large).

Draw Artery



Use arterial ROI to set the reference ROI on the artery (Aorta), on the original (Reference) or tMIP image. Additional arterial ROIs may be drawn for viewing and comparing the contrast curves; only the ROI with the highest contrast enhancement (highest contrast peak relative to its background level before contrast enhancement) is used as reference in the functional calculations.



Select the cursor or ellipse ROI drawing tool, and drag the pencil shaped pointer across the artery (Aorta).

Draw Vein

Use venous ROI to set the reference venous ROIs on the portal vein, on the original (Reference) or tMIP image. Additional venous ROIs may be drawn for viewing and comparing the contrast curves; only the ROI with the highest contrast enhancement (highest contrast peak relative to its background level before contrast enhancement) is used as reference in the functional calculations.

Select the cursor or ellipse drawing tool, and drag the pencil shaped pointer across the vein (Portal Vein).

Draw Spleen

Use splenic ROI to set the reference ROI on the spleen, on the original (Reference) or tMIP image. Additional splenic ROIs may be drawn for viewing and comparing the contrast curves; only the ROI with the highest contrast enhancement (highest contrast peak relative to its background level before contrast enhancement) is used as reference in the functional calculations.

Mark the spleen. Draw on the spleen; the ROI should be large.

When an ROI is placed, the TLCT Graph plots the HU values over time. The TLCT Results table identifies the ROIs by vessel name and color, displaying the results for Vessel, Slice#, Enhancement, and TIP.

⚠ **WARNING**

Verify the correctness of the segmentation and labels, (manual visualization) and correct it manually if required.

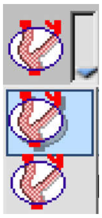
General Perfusion

General perfusion maps include the following items:

- Perfusion;
- Peak Enhanced - the highest value at each point, minus the baseline;
- TTP;
- Blood volume; and
- All - scroll between all five of them (above).

This perfusion type allows you to draw only one artery. No other vessels are used in the General perfusion type.

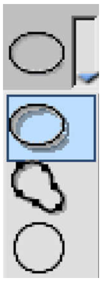
Draw Artery



Select the cursor or ellipse drawing tool, and drag the pencil shaped pointer across the artery. When an ROI is placed, the TLCT Graph plots the HU values over time, and the TLCT Results table identifies the ROIs by vessel name and color, displaying the respective results for Vessel, Slice#, Enhancement, and TIP.

When an ROI is placed, the TLCT Graph plots the HU values over time, and the TLCT Results table identifies the ROIs by vessel name and color, displaying the respective results for Vessel, Slice#, Enhancement, and TIP.

Time-lapse Perfusion



All non-relevant buttons are grayed out. Drawing tissue ROIs activates the Time Lapse CT (TLCT) graph. You can draw multiple ROIs. Select the ellipse, spline, or circle drawing tool, and drag the pencil shaped pointer across the region of interest: Ellipse; Spline; or Circle.

General Perfusion Calculation

The IntelliSpace Portal mathematical modeling technique is based on a single compartment model.

This compartmental model is used to estimate the tissue perfusion, and as the name suggests, it considers the intravascular and extra-vascular spaces as a single compartment.

This model is based on the application of the Fick’s principle of conservation of mass to a given region of interest within the target organ. The accumulated mass of contrast, Q(T), in a voxel of tissue during a time period corresponding to the complete wash in and wash out of contrast during a bolus injection is equal to the product of the volume of blood moving through a given volume of interest per unit time, (with units of milliliters of blood per 100 g of tissue per minute) and the time integral of the arteriovenous difference in contrast concentration.

The implemented calculation is also known as the Mullani-Gould formulation or single-compartment formulation.

Additional information can be obtained from http://www.ajnr.org/content/30/4/662[1].

$$(t) = a(t) \otimes \frac{F}{V} \cdot R(t)$$

[1] Konstas AA, Goldmakher GV, Lee TY, Lev MH. Theoretic Basis and Technical implementations of CT Perfusion in Acute Ischemic Stroke, Part 1: Theoretic Basis. AJNR Am J Neuroradiol. 2009 Apr;30(4):662-8. DOI: https://doi.org/10.3174/ajnr.A148.

Perfusion Maps Stage

After you have finished defining ROIs in the Vessel Definition stage, access the Perfusion Maps stage. (Once you move to the Perfusion Maps stage, you cannot change the Perfusion type.) See section “Vessel Definition Stage” on page 288.

Perfusion Map Color Schemes

Various color schemes for the Perfusion Maps are available for use as needed. The choice of color map is a user preference that affects only the types and ranges of colors used to display the perfusion parameters. The values of the perfusion parameters are not changed when selecting different color maps.

- Right mouse click on a Perfusion Map image to activate a drop-down menu.
- Select **Color Schemes**. The list of available color schemes appears.

Rainbow

In this (the default) color scheme, perfusion data is represented as a range of colors having the same sequence as a rainbow spectrum.

Black and White

Perfusion data is represented as a range of grayscale intensities. These maps are suitable for storage and display systems (e.g., PACS) that are incompatible with color maps.

Thallium

Perfusion data is represented by a range of colors similar to those used in conjunction with nuclear medicine perfusion scans (e.g., Thallium-201 SPECT).

a-LUT

Perfusion parameter color maps that use the Acute Stroke Imaging Standardization Group (Japan) recommended lookup table (a-LUT).

Perfusion Maps Stage Functions

Click the down arrow in the tab window, or hover the mouse over the tab window. The list of available functions displays. There are two additional application functions available only in stage 2, Perfusion Maps; they are Perfusion Options and Perfusion Mask.

Also, Batch is different in the Map stage than the Vessel Definition stage.

Key Images

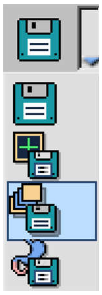
Save groups of images that can be reviewed in any system supporting the defined standard. See **Instructions for Use** > **Directory** > **Key Image Notes** for more information.

See **Report**, **Film**, **CT Common Processes** and **CT Common Tools** for information on using common options, tools, functions, and processes.

Create Batch in Functional CT

To create a batch in Functional CT:

1. Choose batch content. You can select any combination (or all) of the following content types:
   - Summary maps (Arterial, Portal, Total, HPI).
   - Original image (tMIP only).
   - Graph (TLCT).
   - Liver Perfusion Results table.
2. Sort batch content.
   - **By z-position (sort by slice).** When the batch is created, all the content you selected is grouped together: for the first slice, then for the next slice, etc.)
   - **By type.** When the batch is created, all the content you selected is grouped together by type. (The “Split batch” option is active in this mode.)
   - **Current.** The batch will only contain the selected content for the currently active slice.
3. Split batch to series. Choose **Yes** if you want each content type to be grouped together and saved as separate series.



4. When done with your selections, click **Save batch as...** in the Common tools. A dialog window opens, where you can type in the batch name, the desired format (Secondary Capture, TIFF, etc.) and the destination device.
5. Click **OK** when done. The batch is saved to the destination device. As the batch is saved, a message displays the number of images and the device.

Perfusion Options

The perfusion options include:

Portal Perfusion Type (Only for Liver)

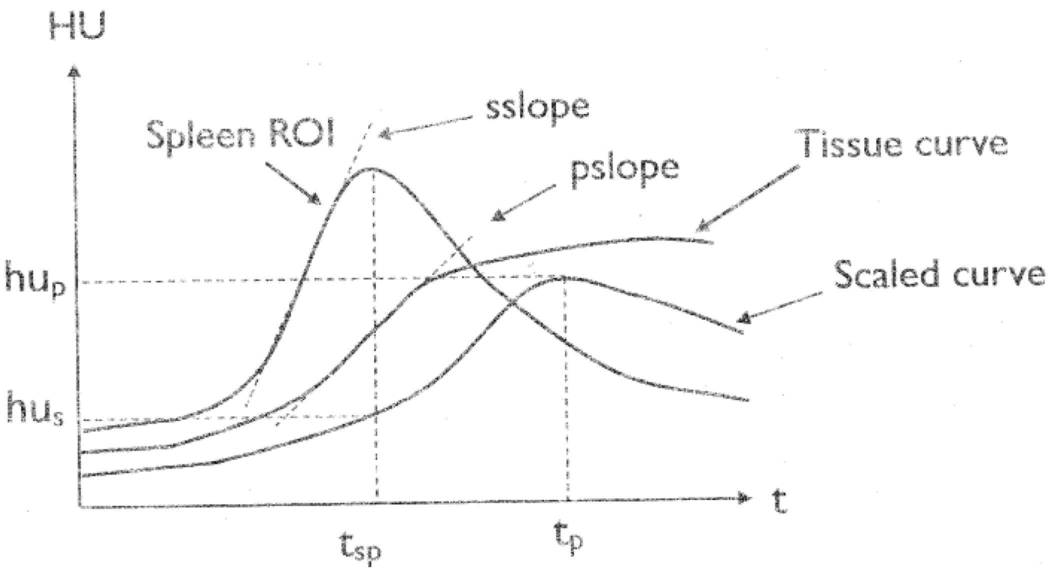
There are two perfusion methods, based on different research: the selected method affects the perfusion map. Your choices are:

- **Blomley Method (Method 1)**

  t_p–scaled tissue enhancement peak time

  hu_p–scaled tissue enhancement peak

  Scaled curve = Tissue curve pslope / sslope * Spleen curve



Portal Perfusion = $(hu_p – hu_s) * 6000 / ((t_p - t_{sp}) * \text{veneous enhancement})$

- **Mile's Method (Method 2 - default)**

  t_s–bolus start time

  t_{ap}–arterial enhancement peak time

  t_{vp}–venous enhancement peak time

  t_{sp}–spleen enhancement peak time

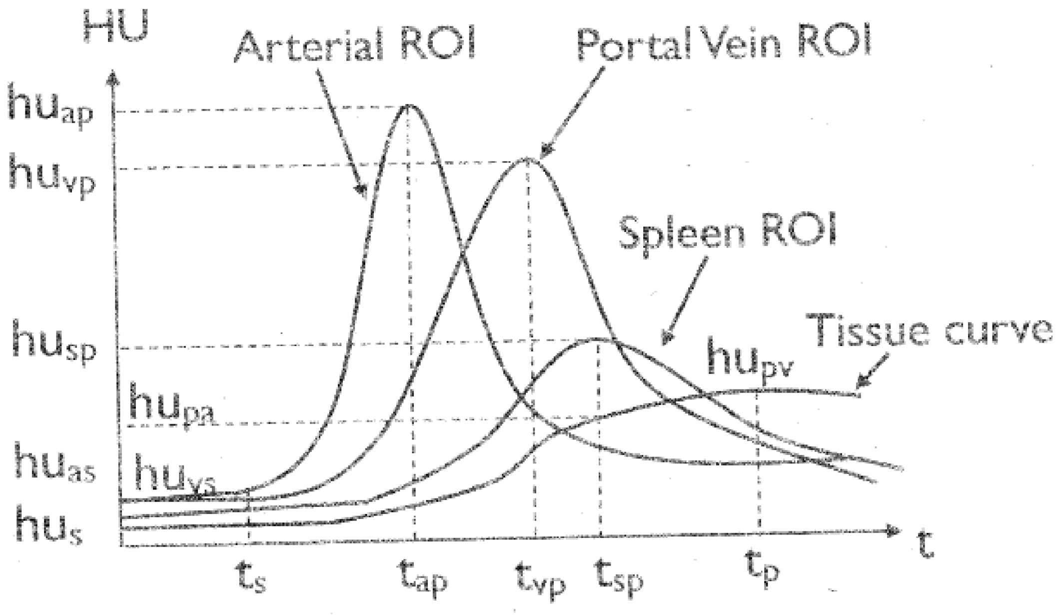
  t_p–tissue enhancement peak time

  hu_{ap}–hu_{as}- arterial enhancement

  hu_{vp}–hu_{vs}- veneous enhancement

  hu_{pa} - tissue enhancement peak on arterial stage

  hu_{pv} - tissue enhancement peak on portal stage



  Arterial Perfusion = (hu_{pa}–hu_s) * 6000 / ((t_{sp} - t_s) * arterial enhancement)

  Portal Perfusion (by Miles method) = (hu_{pv}–hu_{pa}) * 6000 / ((t_p - t_{sp}) * veneous enhancement)

  Total Perfusion = Arterial Perfusion + Portal Perfusion

  HPI (hepatic perfusion index) = Arterial Perfusion / Total Perfusion * 100%

Set as Default

Brings back the factory defaults settings.

Smooth Maps

Smoothing size: x4 = 256 x 256.

Thresholds to Exclude

Checkbox to turn on/off.

- Bone - above the HU threshold, area is in white in the perfusion maps
- Air - below the HU threshold, area is in black in the perfusion maps
- Vessels - to remove vessels from the maps. If Y=20% and the maximum of the artery enhancement is 100 HU, it colors in black all the areas that are above 20% out of 100 (meaning above 20 HU). In 100%, you see perfusion on all vessels. If Y is reduced, you see more black holes.

  Values are saved on exit and reload.

Perfusion Mask

This tab is grayed out by default when a new perfusion study is opened. To Draw a New Mask: Click the Show Perfusion Mask checkbox. Then select one of the mask drawing tools from the drop-down arrow: FreeHand or Spline.

Liver Perfusion Maps

You can display Liver Perfusion Maps viewport in 5 forms. Click on a tab at the top of the viewport to select:

- ALL - (default) click to display all 4 perfusion maps in the viewport.
- TOTAL PERFUSION - display the Arterial + Venous Perfusion map.
- ARTERIAL PERFUSION - display the Arterial Perfusion map.
- PORTAL VENOUS PERFUSION - display the Portal Venous Perfusion map.
- HEPATIC PERFUSION INDEX - display the Hepatic Perfusion Index map.

General Perfusion Maps

You can display General Perfusion Maps viewport in 4 forms. Click on a tab at the top of the viewport to select:

- ALL - (default) display all 4 perfusion maps.
- PEAK ENHANCED - display the Peak Enhanced perfusion map, which shows peak enhancement from injected contrast.
- TTP (time-to-peak) - display the TTP perfusion map, which shows the time it takes for peak enhancement to be reached at each x, y location. The color bar is scaled in seconds.
- BLOOD VOLUME - display the Blood Volume perfusion map, which shows the total volume of blood.

Perfusion Results Table

The following information is included in the table:

- ROI name;
- Slice number; and
- All measurements of the selected type (General and Liver), as shown in the maps in the upper right viewport.

NOTICE

The active table may be added to the clipboard using **Ctrl + C** or by right-clicking on the table and selecting copy. The measurements may then be pasted into common document types, including plain text, Microsoft Word, and Microsoft Excel documents.

Recommended Scan Protocol

Before continuing, see the "Instructions for Use" that came with your scanner.

1. Position the slice location to include the liver, spleen, portal vein, and aorta.
2. Inject Contrast. (Recommended injection parameters: 40-50 ml total, >300 mgl/ml, 5-7 ml/second.)
3. Obtain axial, contrast-enhanced scans at the same location during patient's breath-hold for the duration, from the injection to the end of the portal phase. (Recommended scan parameters: 5 mm slice thickness, 1 second scan duration, 3 second cycle time, 360 degree rotation, 120kpV, 150-200 mAs, breath hold.)
4. For a Liver study the Scan Range should include: Liver, Spleen, Portal vein, Aorta.

WARNING

A proper scanning procedure is essential for obtaining meaningful perfusion images. Special care must be taken to ensure that:

- **The scan duration is sufficient to cover a pre-contrast period as well as the entire first pass of the injected contrast bolus. (Recommended: minimum 60 second scan duration.)**
- **The scans are spaced no more than 5 seconds apart. (Recommended: 3.0 second temporal spacing.)**
- **The contrast injection is sufficiently rapid to preserve a narrow bolus. (Recommended: injection of 5-6 cc per second contrast for 8-10 seconds.)**
- **The Patient is able to breath-hold for the duration of the scanning. (Recommended: breath-hold test and patient hyperventilation preceding scanning.)**

Failure to meet these requirements will result in the creation of unreliable functional images.