Lung SPECT

PulmoGam-Clinical Background and Rationale

Ventilation-perfusion tomography

Pulmonary scintigraphy is used to display regional ventilation (V) and perfusion (P). In the healthy persons there is a balance between regional ventilation and perfusion to get optimal gas exchange. The most important application of lung scintigraphy is the diagnosis of pulmonary embolism (PE). Pulmonary embolism causes areas with perfusion defects. Because other cardiopulmonary diseases, including lung inflammation, obstructive lung disease, tumor, asthma and left heart failure may cause deficient perfusion, imaging is combined with ventilation imaging to improve the specificity for PE diagnosis. In pulmonary embolism a perfusion defect is due to an embolus blocking blood flow. Ventilation remains normal, as tissue viability is maintained by the bronchial circulation. Hence, diagnosis of PE is based on absent perfusion with preserved ventilation, a so-called mismatch. When interpreting combined ventilation and perfusion images, it is possible to identify characteristic patterns of other diseases than pulmonary embolism [1-4].

Studies of ventilation and perfusion scintigraphy are still generally based on planar imaging although single photon emission tomography (SPECT) signifies a new era in nuclear medicine making planar imaging obsolete in several fields. For lung function studies ventilation/perfusion tomography (V/P SPECT) has undeniable advantage over planar technique such as very low non-diagnostic findings and high sensitivity and specificity [2-8]. Unfortunately, obsolete planar scintigraphy caused by non-

standardized method and probabilistic interpretation[9] is still used for comparison with up to date contrast enhanced computed tomography (CTPA).

The crucial problem in studying diagnostics of PE is that an accepted gold standard is missing. Angiography is no longer in common use due to limitations [10]. The results of clinical strategies in terms of clinical outcome have been used to illustrate the power and limitations for diagnosis of PE [11].

Radiopharmaceuticals

Ventilation Scintigraphy - Gases

Ventilation can be performed with radioactive gases or labelled aerosols. A particular aerosol is Technegas, regarded as a pseudo-gas because of its very small particle size yielding aerodynamic properties simulating a gas.

^{99m}Tc Technegas has hydrophobic particles with size 0.005-0.2 microns. These particles penetrate to alveolar level similar to a gas which makes them preferable for studying ventilation.

Perfusion Scintigraphy

Perfusion scintigraphy is based on microembolization with radio-labelled particles injected in peripheral vein. The commercially used particles are labelled macro-aggregate of human albumin (MAA). They are sized 15-100 microns and will lodge in the pulmonary capillaries and pre-capillary arterioles. The particle distribution accurately illustrates regional perfusion. The number of injected particles is essential. Minimum of 60,000 is required to obtain an even distribution of activity reflecting regional perfusion. Normally the range should be 200,000 - 700,000. The routinely administered particles will result in obstruction of only small fraction of pulmonary vessels. However, a special preparation of 100,000 - 200,000 particles is usually given to patients with known pulmonary hypertension, right to left shunt or after single lung transplantation.

V/P SPECT Method

Acquisition

The lung scintigraphy should always include V and P in order to increase the specificity, lung delineation and the pattern recognition typical for other lung diseases than PE.

A large field of view dual head gamma camera and low-energy, all-purpose collimator; a 64 x 64 matrix zoomed to a pixel size of 6.8 mm, are used with 128 projections over 360°. In supine position the patient inhales the aerosolized Technegas until 30 MBq are deposited in the lungs. Each projection takes 10 s. Immediately thereafter and without patient movement, 100 - 120 MBq of ^{99m}Tc-MAA is given i.v. for the perfusion study. Perfusion tomography follows in which each projection takes 5s.

Data Processing

Iterative reconstruction is performed using OSEM with 8 subsets and 2 iterations. The ventilation background is subtracted from the perfusion tomograms, and a normalized V/P image set calculated. In clinical routine the procedure is made fully automatic. In short, the main consideration in the creation of quotient images is to define a suitable scaling factor between the reconstructed and appropriately smoothed ventilation and perfusion data sets. The scaling was designed with the aim of producing quotient images that would be displayed in a fixed grey-scale value in lung regions deemed to be normal based on a simple automatic criterion. In the original work [2] the normal region was selected by threshholding from the maximum count after automatic hot-spot removal in the reconstructed volumes. In the last version a more robust normalization threshholding was applied. Thus, the reconstructed volume was first truncated at a lower threshold of 10% of its maximum value. An upper threshold was then obtained by iteration to the count level at which 90% of the lung volume was included. The voxels within the count range 50 - 100% of the upper threshold were used to define a preliminary 'normal' sub-volume. This process was applied to ventilation and perfusion independently. The volume in which both ventilation and perfusion were 'normal' comprised the final normalization volume. When, in exceptional cases, no such common volume was recognized, each region was used separately. The average voxel count in the normalization volume was scaled to be equal for ventilation and perfusion. The final display was set to always span a quotient range of 0 to 4000, with equality being represented by 1000 [12].

Ventilation, perfusion and V/P quotient tomograms are simultaneously presented in 13.6 mm thick coronal, sagittal and transverse slices, and as rotating volume rendered "Maximum Intensity Projection" images. The computer display allows adjustment of thresholds and colours.

The time needed for V/P examination is about 30 minutes including acquisition time of 16 minutes. Reconstruction, automatic processing including all slices and 3D rendered cine images takes approximately 9 minutes. Interpretation and reporting takes 5-10 minutes.

Validation Results of V/P SPECT

The sensitivity for V/P SPECT was tested in a porcine model using latex emboli labeled with ^{201}Tl to enable precise localization of the emboli, sized 2.2 - 3.7 mm in diameter. With the planar modality, sensitivity among the 3 readers was on average 64% and specificity was 79%. On tomographic images, sensitivity was on average 91% and specificity was 87% [14].

In clinical study, 53% more mismatch points were identified with V/P SPECT as compared to planar technique [15]. Similar results have been found by Reinertz [16].

The number of non diagnostic findings are 1-3% [3-5, 7] compared to 65% in the PIOPED study [9]. In clinical data Leblanc et al [7] showed high negative predictive value and Bajc et al showed high negative and positive predictive value in 1785 patients followed up clinically for 6 months [17].

References:

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Data Types

The following table describes the data types used in this application.

Table 1.1

Data Type	Description
Volume data	One perfusion volume and one ventilation volume. The earliest study reflects the ventilation scan.
Tomographic Projection data	One set of raw tomographic projections for ventilation, and one set of raw tomographic projections for perfusion.

WARNING — *This application is designed to interpret ventilation data acquired through the use of Tc99m-Technegas, an ultrafine aerosol of technetium-radiolabeled carbon particles. Use of ventilation data acquired with Tc99m-DTPA (diethylenetriaminepentaacetic acid) is not supported by this application, and may adversely affect the interpretative results. For more information, contact your customer service representative at Support@segamicorp.com.*

Registering Images

The V/P*q* application automatically sizes, orients, and registers the ventilation and perfusion data when the application is executed. No intervention is required.

Starting the Application

The application can be run by choosing “Segami LungSPECT” from the Start Menu.

Figure 1.1 Starting the Lung SPECT application.

The application will appear both on the display and on the Windows Task bar.

Figure 1.2 The Segami LungSPECT task bar item.

After installation, a End-user license agreement appears. Read and accept the terms of the agreement by pressing the **[I Agree]** button.

You may check the box beside the button “Do not show again” to prevent the reappearance of the EULA. The EULA can be viewed at any time by clicking on the [About] button inside the application.

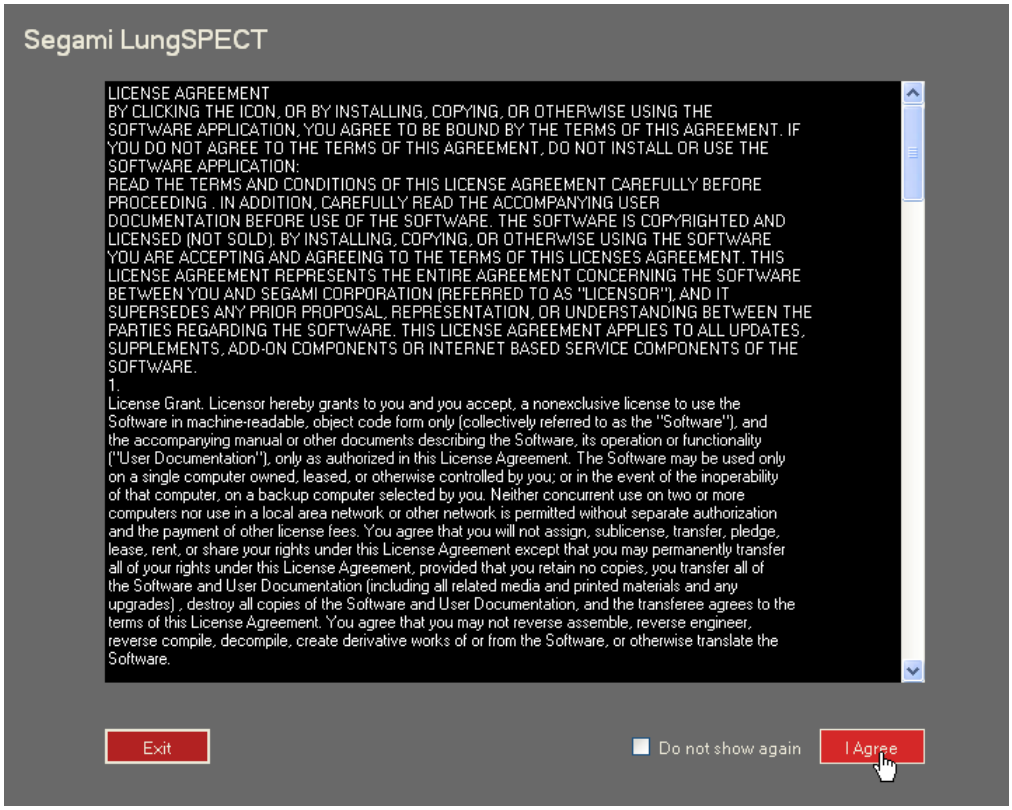

Figure 1.3 The Segami LungSPECT license agreement dialog.

Upon startup, the LungSPECT Series Chooser Dialog appears, from which ventilation and perfusion datasets can be browsed, verified and loaded.

Note — By default, datasets are stored in the C:\LungData subdirectory.

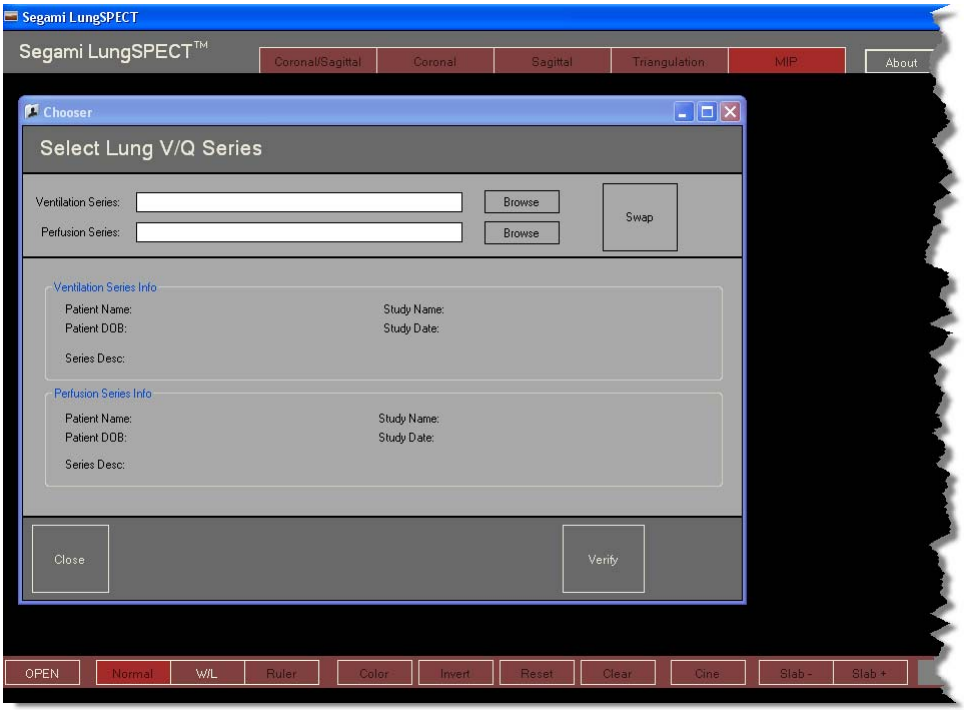

Figure 1.4 The LungSPECT Series Chooser dialog. Press the [Browse] button.

Loading the Data

Click the [**Browse**] buttons in the Series Chooser Dialog to pick the ventilation and perfusion data files. The “Select Ventilation Series” dialog opens.

If patient data is exists inside the default directory called C:\LungData, it will be shown as records at the top of the dialog.

If the series data is located in a different directory, the upper portion of the “Select Ventilation Series” dialog remains blank. Press the **[Browse]** button at the bottom of the dialog to choose a subdirectory.

Figure 1.5 The LungSPECT Series Chooser: Click the [**Browse**] button.

A “Browse for Folder” dialog appears, showing a tree of the directories available on the file system. Choose the folder where the patient series data is stored, and press the **[OK]** button.

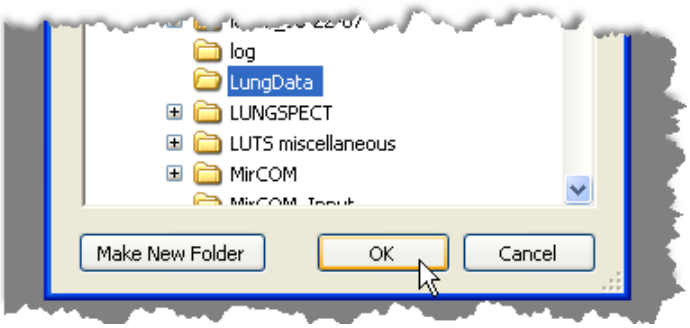

Figure 1.6 Navigate the file system and select the directory where the patient series data are found.

The directory you select will become the default directory for future.

Select Ventilation

Press the **[Refresh]** button at the bottom of the "Select Ventilation Series" dialog, and the data files will be displayed.

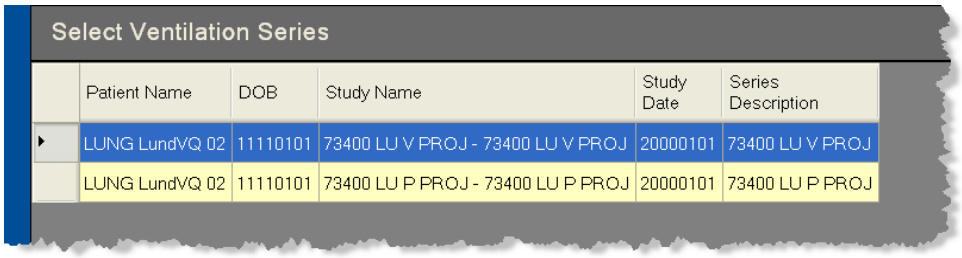

Figure 1.7 Left-click the record. Check the "Study Name" field to be sure to select a ventilation dataset.

To choose the series, right-click the record and press the [**Select**] button. The Series data file name and path will appear in the Chooser, with the ***.dat** file extension.

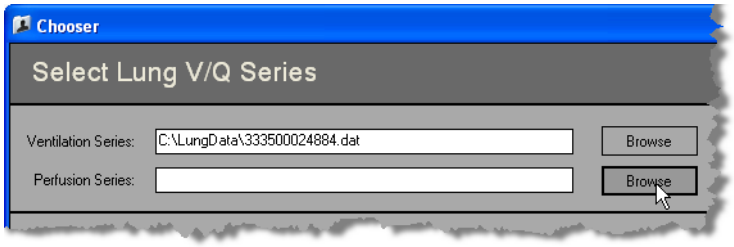

Figure 1.8 Browse the default directory for the Perfusion series. Check the "Study Name" field to be sure you select a "Perfusion" dataset.

The dialog will close, and you will be returned to the Chooser.

Select Perfusion

Repeat the process by left-clicking the **[Browse]** button in the Chooser, beside the "Perfusion Series" field.

A "Select Perfusion Series" dialog appears.

Right-click the perfusion record, and press the **[Select]** button.

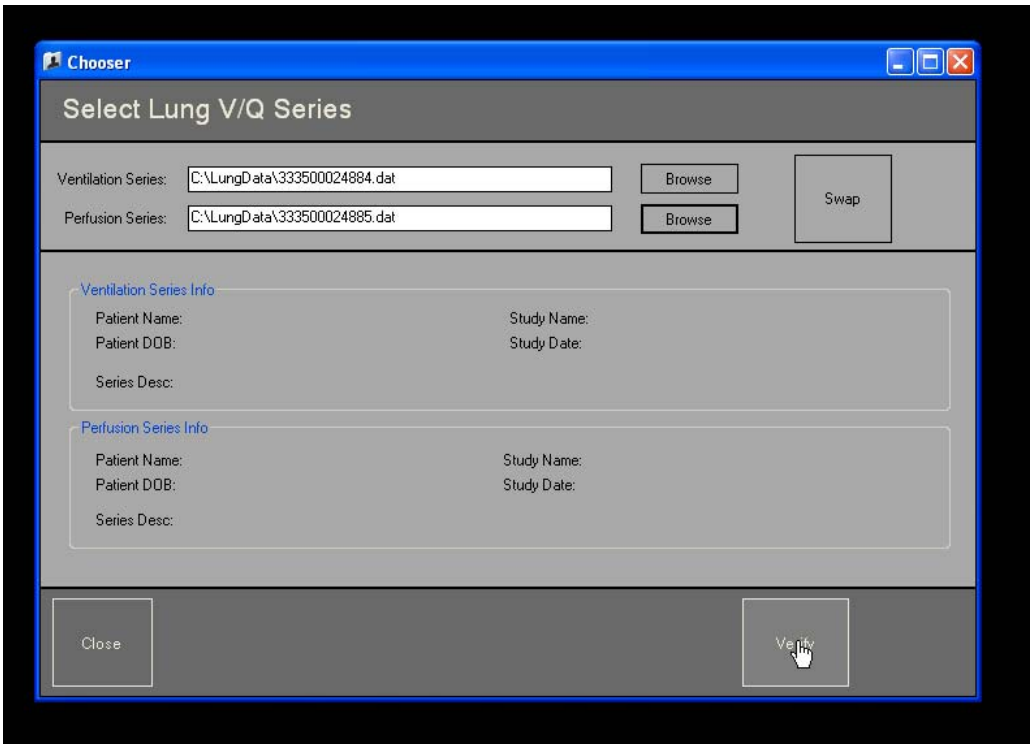

Figure 1.9 After both files have been chosen, press the second [**Verify**] button.

When complete, two series data files will be visible in the Series Chooser Dialog.

Verify the Files

Verify the nature of the data files by pressing the [**Verify**] button.

When the **[Verify]** button is pressed, the DICOM header data is read and the relevant patient, series, and study information will be displayed as details.

Figure 1.10 Press the [**Verify**] button to examine the makeup of the series, and to ensure the ventilation and perfusion data sets are in the proper sequence on the form.

The series description will identify whether the data acquisition is a ventilation scan or a perfusion scan (e.g. “V” or “P” will appear in the series information). Similarly, the study name will also distinguish ventilation from perfusion studies.

Figure 1.11 Check the Study Name or Series Description to distinguish ventilation data from perfusion data.

Swapping

If you discover that you have inadvertently placed a Perfusion dataset in the ventilation field, you can use the **[Swap]** button to correct the mistake. by reordering the form fields.

Press [**Verify**] again and examine the information that is displayed for each data file.

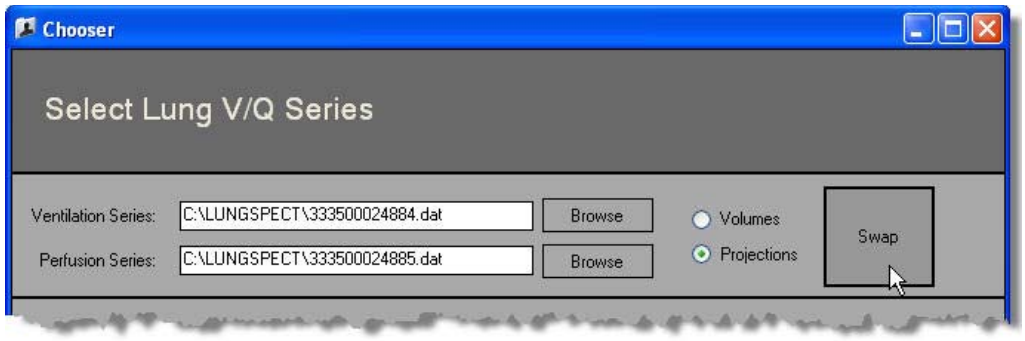

Figure 1.12 If necessary, you can swap the files between the form fields if accidentally reversed. Press [**Verify**] again, to parse the header data to double-check.

Verify that the swapped “Ventilation Series Info” is correct.

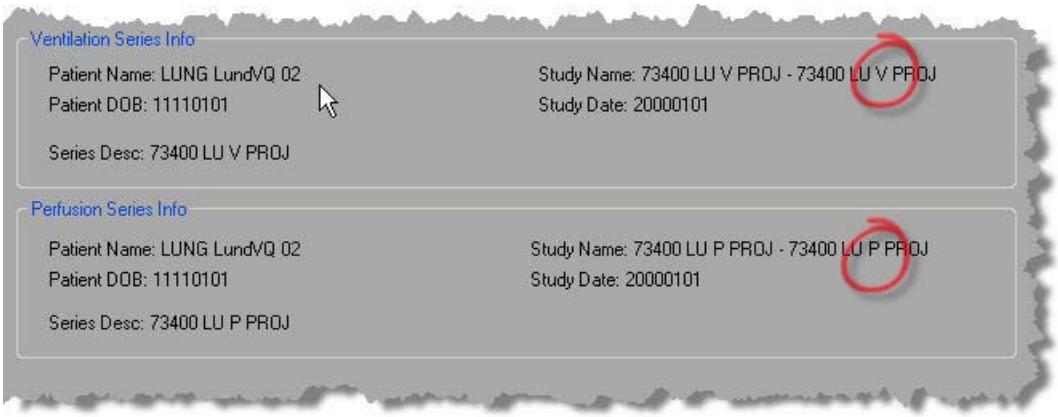

Figure 1.13 Ventilation and perfusion series information in their proper order.

Note — The [**Load Projections**] button is not available until the header data has been parsed.

Load the Files

When the data files are in the correct order, press the [**Load Projections**] button to transmit those data files to the application.

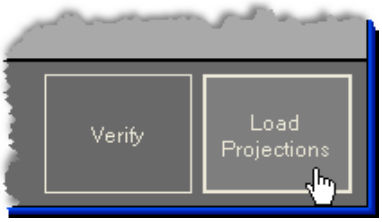

Figure 1.14 LungSPECT Chooser Dialog: Press the [**Load Projections**] button.

LungSPECT will require a few moments to process the datasets; as the data is loaded into the application, the Series Chooser Dialog will close and the M.I.P. page will be displayed.

You can load another set of data at any time, by clicking the [**Open**] button in the application. Whenever pressed, the [**Open**] button displays the Series Chooser Dialog.

The Application Interface

LungSPECT consists of a large display with navigation tabs positioned at the top, and a toolbar arranged beneath. The toolbar contains a series of buttons and a slider control to adjust “Window width and Leveling” settings.

Whenever the Series Chooser Dialog exits, the rotating Maximum Intensity Projection (M.I.P.) is displayed by default.

Use the navigation tabs found at the top of the display to switch to the following pages:

- Coronal/Sagittal Page
- Coronal Page
- Sagittal Page
- Triangulation Page
- MIP

Note — The **[About]** button opens a dismissible dialog which describes the version and build number of the application, and offers access to the End-User License Agreement.

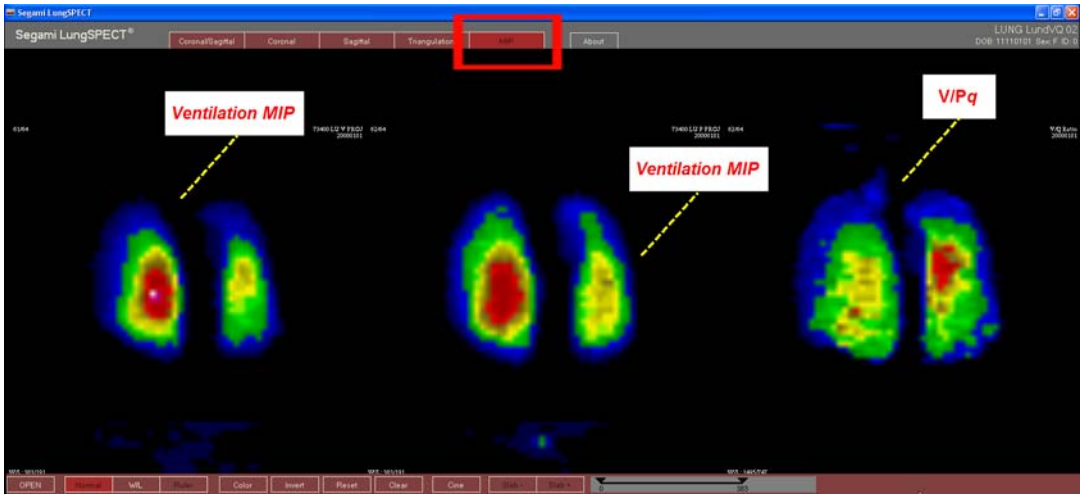

Figure 1.15 The initial screen displayed is the M.I.P Page (Tab identified by the red box). The page displays a Ventilation M.I.P., a Perfusion M.I.P., and a rotating cine of the Ventilation Perfusion Ratio image (V/P*q*).

Elements of the Display

The various display pages share a common set of screen objects. This section describes the standard elements of the display.

Viewports

Viewports display the data on the screen, in 64X64 voxel images. The mouse pointer manipulates a cursor over these viewports, and can be used to interact with the data.

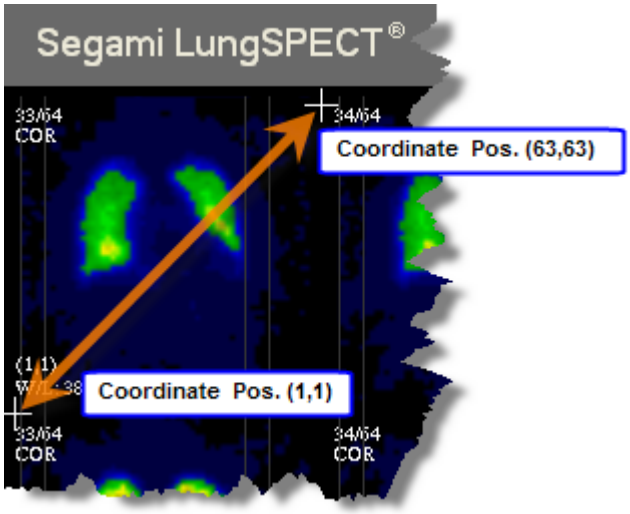

Figure 1.16 Cursor coordinates are displayed in parentheses at the lower left of the viewport. As the cursor is moved across the screen (yellow arrow) its coordinate position is constantly updated.

The position of the cursor is tracked; its (x,y) coordinate position is displayed at the lower left of the viewport as long as the cursor is present.

Counts

While the cursor is inside a viewport (on all pages except for the M.I.P.), the intensity count is displayed just below and to the right of the cursor itself. The intensity is measured at the central focus of the cursor.

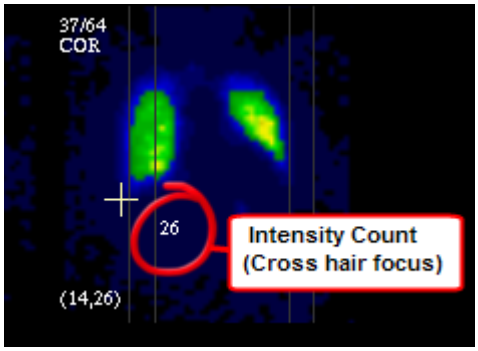

Figure 1.17 Cross hair intensity is displayed.

Note — To visualize the absolute maximum intensity in the data, use the rainbow [**Color**] scale and adjust the Window Width and Leveling [**W/L**] so the maximum pixel in the scan is displayed as white. Position the focus of the cursor over the white area for a reading.

Image Layout

By default, LungSPECT displays slices in multiple rows of eleven (except in the Triangulation and M.I.P. pages).

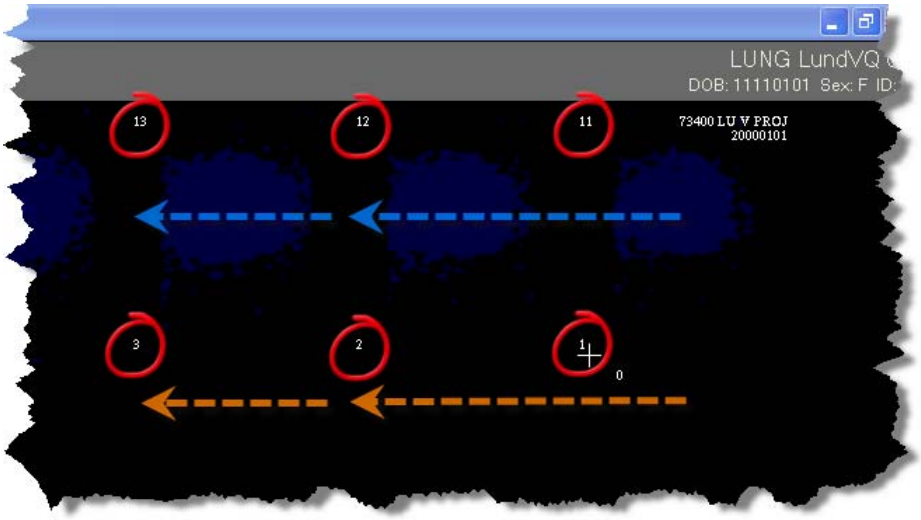

Figure 1.18 Image Slice IDs in sequence, from bottom right to upper left, ascending.

Each individual slice is shown in a viewport, and each viewport displays textual information pertaining to the image displayed in it.

The Slice ID appears at the upper left quadrant of the viewport. Immediately below it, the orientation (orthogonal projection) of the image is shown (e.g.Transverse, Coronal, and Sagittal).

Each set of acquired images from a dataset is also overlaid with the series information, and Study Date. This text appears only once for each dataset, appearing in the viewport of the lowest numbered Slice ID at the right side.

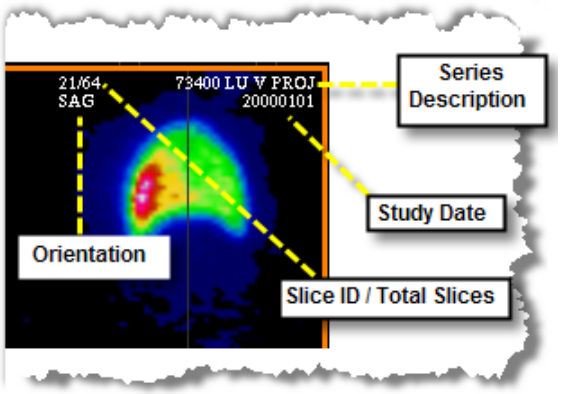

Figure 1.19 Example of the orientation guides and series information displayed on the right-most image of a set. The slice ID is shown beside the total number of slices in the dataset.

Similarly, the Patient Information (Study, Date of Birth, Sex, and ID) is displayed in the application window frame, at the upper right.

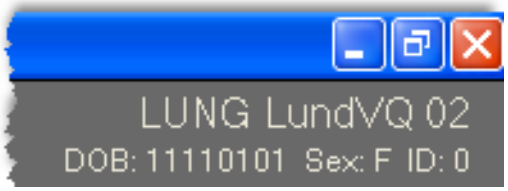

Figure 1.20 Patient Data displayed at the upper right of the Application window frame.

Study Name and Date are also shown at the upper right of each M.I.P. display.

Note — The rotating cine associated with the V/P*q* is calculated data, and no Study Name is shown, only the Study Date.

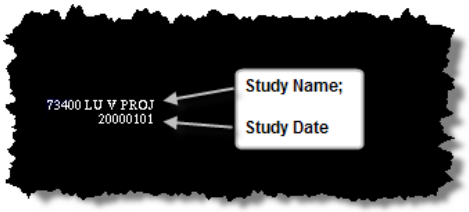

Figure 1.21 MIP Study Name and Date shown inside the viewport of a ventilation data set.

Toolbar Buttons

At the bottom of the display is a set of toolbar buttons which can be used to interact with the image data on the screen. The following table summarizes the buttons, their context, and their functions.

Table 1.1 Toolbar Buttons

Button	Context	Description
OPEN	All	Opens the Series Chooser Dialog to load new data.
Normal	All	Toggles any other button.
W/L	All	Adjusts image contrast to emphasize data values displayed in the viewport though movements of the mouse. Vertical mouse movement controls Window Width (the range of data values relative to the center value). Horizontal mouse movement controls the Window Level (the center of the window). The default Window Width is the entire dataset; the default Window Level is the center value. On the lower end of the window, all voxels are black, and upper end all voxels are shaded white. Within the window the voxels vary from black to white based upon a shading curve. When at default settings (as viewed on the slider) all values are visible in the viewport.

Button	Context	Description
Ruler	Triangulation	A left-click and drag with the mouse inscribes a straight line in any direction from the original point. A release of the button sets the line. The distance from the origin to the end-point is shown alongside in millimeters (in the patient space).
Color	All	Opens a menu bar with color scales (LUTs) which can be applied to the display. Selectable LUTs include: HSV (Hue, Saturation, Value), Geographic, Hot Iron, Rainbow, Gray Scale, and None.
Invert	All	Inverts the color scale in use into its opposite; the color values of the data and background are reversed.
Reset	All	Sets the Window Width to the default settings. The default Window Width is the entire dataset; the default Window Level is the center value.
Clear	Triangulation	When in the Triangulation tab, [Clear] dismisses all rulers that have been created.
Slab +	Coronal, Sagittal	Increases slice thickness by joining each slice with the next in the sequence. The aggregated slice is described as a range of slice ID's out of the total (e.g. 1-2/64) Pressing the button again combines another slice into the aggregate (e.g. 1-3/64).
Slab -	Coronal, Sagittal	Decreases the slice thickness of aggregated slices. Each button-press removes a slice from the joined set. Pressing [Slab -] repeatedly will restore the slices to their original state.

[Open] Button

The [**Open**] button invokes the Series Chooser Dialog, and resets the page to the default M.I.P. page. If no series are chosen, and the [**Close**] button is pressed in the Series Chooser Dialog, you are returned to the M.I.P. page.

[Normal] Button

The [**Normal**] button "Escapes" from the W/L or Ruler modes.

[W/L] Button - Window Width and Leveling

Window width and level controls are used to adjust the visualization of data values displayed in the Viewport. Certain features of the dataset may be emphasized by changing Window Width and Level values, which alter the image contrast.

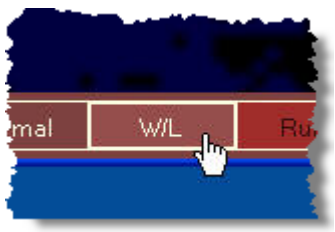

Figure 1.22 Press the [**W/L**] Button to change the shading using the mouse.

Once selected, position the mouse cursor inside the viewport, then click and hold the left mouse button.

- Drag the mouse up and down to change the width of the displayed range (the “Window Width”).
- Drag the mouse left and right to change the midpoint of the displayed range (the “Level”).

Figure 1.23 Use the W/L Slider to adjust the Window Width (left slider) and the Window Level (right slider).

Alternatively, you may use the W/L slider, at the right of the toolbar, to directly change the Width and Leveling settings. The left slider arrow controls the Window Width.

If the current Window Width and Level is undesirable, click the [**Reset**] button to set W/L back to its original default settings (i.e. Window Width is set to include the entire dataset and Window Level is set to the midpoint).

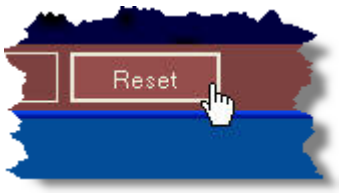

Figure 1.24 Press the [**Reset**] button to return to the default W/L settings.

Color [Button]

The [**Color**] button opens a menu list of Look Up Tables (LUTs) that can be applied to the data. Look Up Tables are used to enhance the display of one region and suppress another by altering how voxel values are represented in color.

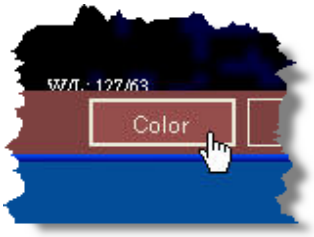

Figure 1.25 Press the [**Color**] button to choose among a set of LUTs.

The following color palettes can be chosen from the [**Color**] menu:

- HSV (Hue, Saturation, Value)
- Geographic
- Hot Iron
- Lund Color
- Rainbow
- Gray Scale
- None (Acquired values)

When one of the options are clicked, the Look Up Table (LUT) is applied to the intensity values in the image.

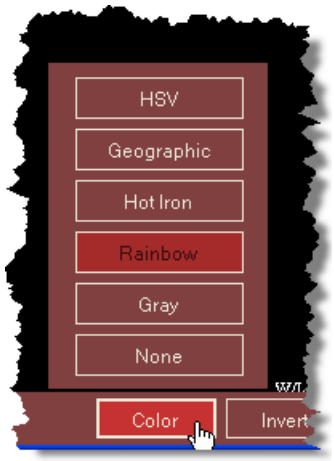

Figure 1.26 The menu which appears when the [**Color**] button is pressed.

Note — Altering the color of different pixel levels can emphasize information under study: Shifting colors assigned to pixel intensity to higher or lower ranges (or increasing or decreasing the distances between those shifts) can help bring out information not normally visible. The shifts from one color to another can be set to occur more closely together or farther apart, making the changes in color that identify different tissues more sharply defined.

Table 1.2 Look-Up Table (LUT) templates and their titles.

LUT	Title
	HSV
	Geographic
	Hot Iron
	Lund Color
	Rainbow
	Gray Scale

In addition to applying LUTs to the images, the [**Invert**] button will reverse the values and their color scheme on the display (changing a black background to white, for example).

Note — When the [**Invert**] button is pressed, the orientation guides and informational text colors are reversed to ensure that they remain visible against the altered background.

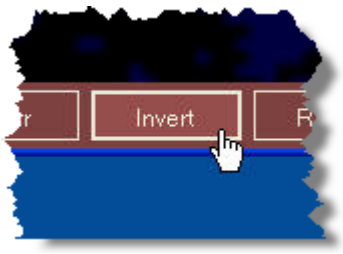

Figure 1.27 Press [**Invert**] to reverse the applied color palettes, and invert the background color.

The [**Invert**] works in all pages, including the M.I.P.

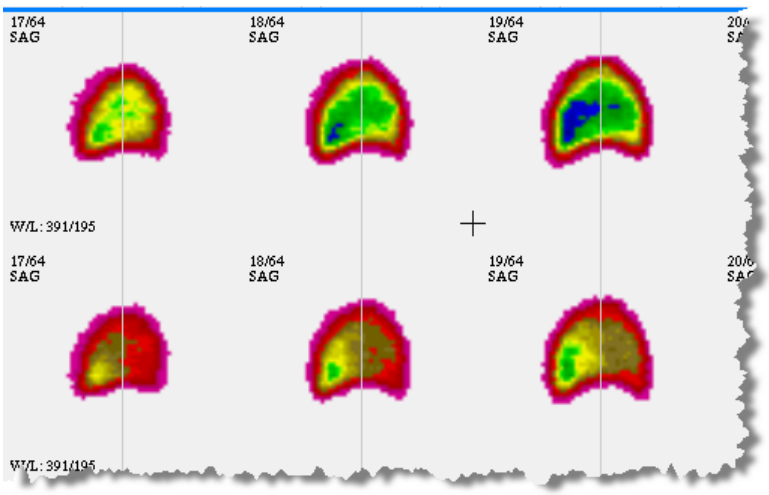

Figure 1.28 Inverted Sagittal screen.

The M.I.P. Screen

The Maximum Intensity Projection (M.I.P.) renders a series of maximum voxel values into an animated sequence of images which are shown in a repeating rotation.

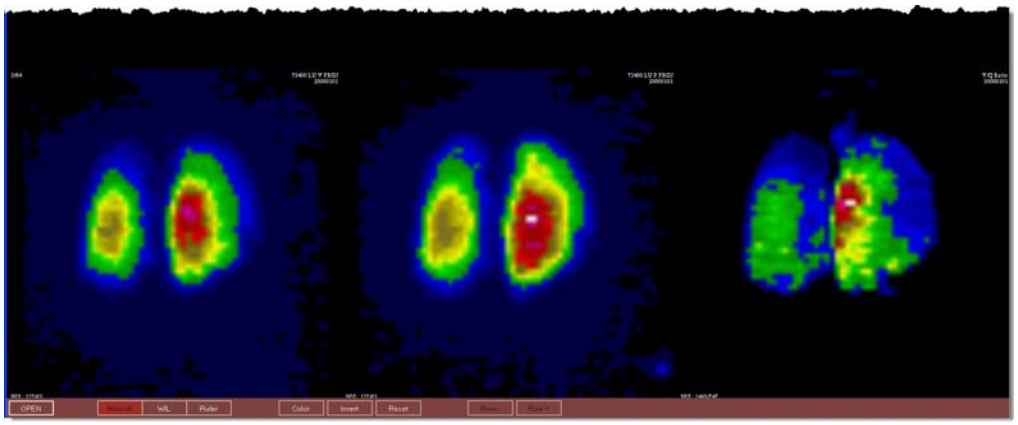

Figure 1.29 LungSPECT: M.I.P.s of ventilation and perfusion, and a V/P*q* rotating cine.

The M.I.P. Page displays a rotating cine of the ventilation, perfusion, and V/P*q* images. The rotation is synchronized.

By pressing the [**Cine**] button, the rotation is stopped and the mouse is enabled.

Figure 1.30 The [**Cine**] button halts rotation and enables manual swiveling with the mouse.

Left-click and hold, and drag to manually swivel the M.I.P. and V/P*q* cine images to the left or right. The images are synchronized and move together.

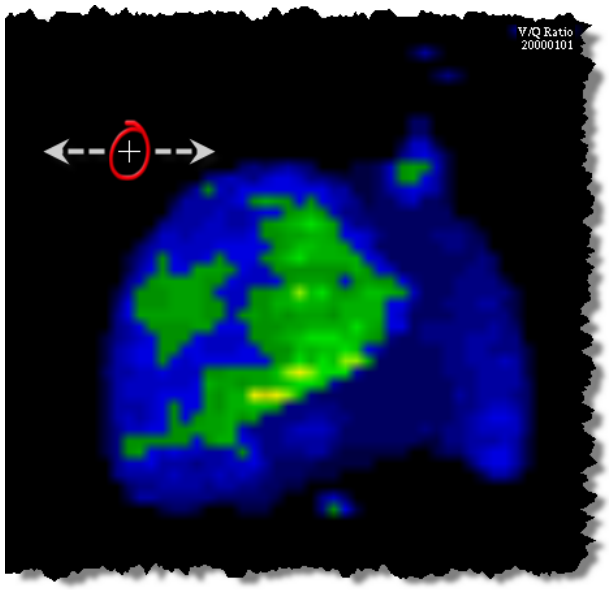

Figure 1.31 Press the [**Cine**] button to switch to manual rotation; left-click and drag the cursor (circled) left or right in the (arrows).

Coronal/Sagittal Screen

To navigate away from the default M.I.P. page, and to the dual Coronal/Sagittal projections page, click the navigation button at the top of the display.

Figure 1.32 The Coronal-Sagittal Tab.

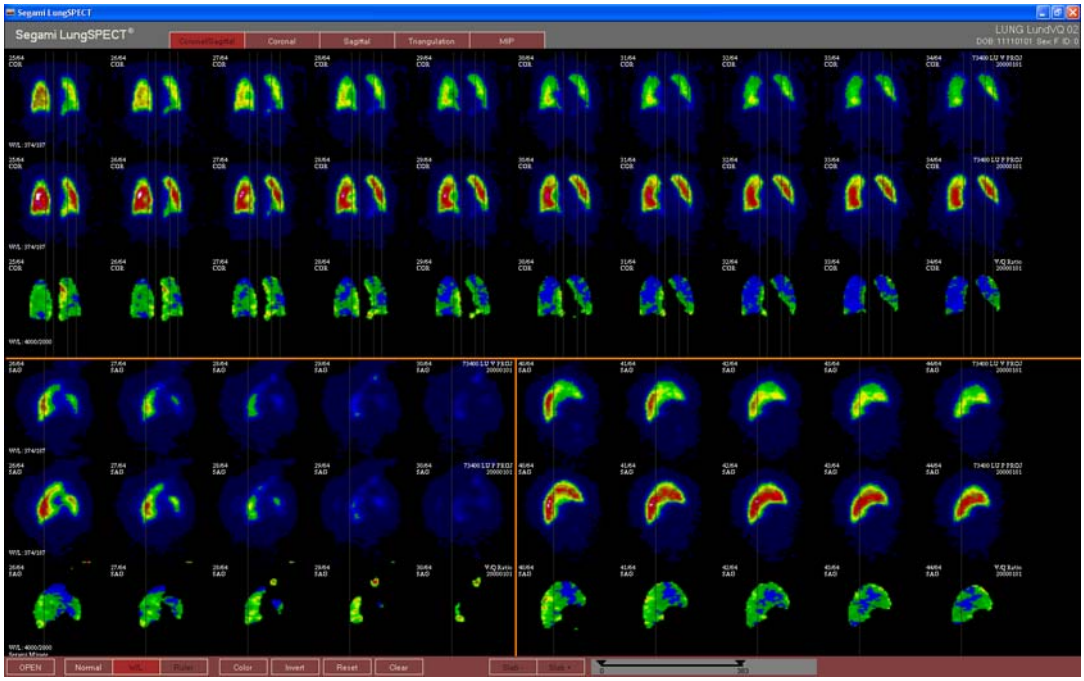

Figure 1.33 The Coronal/Sagittal Screen.

The Coronal/Sagittal Page consists of a number of viewports organized into two projections: coronal (frontal), and sagittal. The sagittal projection is divided into two sections, one for the Right Lung, and one for the Left Lung.

Stadia Cursors

Both the coronal and sagittal projections display stadia lines as triangulation cursors. The stadia lines are synchronized: changes to the left and right position of the pair of stadia lines on the coronal plane will scroll through slices in the sagittal plane.

The coronal (frontal) plane uses dual sets of twin stadia, one for the Right Lung, and another for the Left Lung. The Sagittal view contains only a single stadia line, which corresponds to the coronal plane.

Layout of the Coronal/Sagittal Page

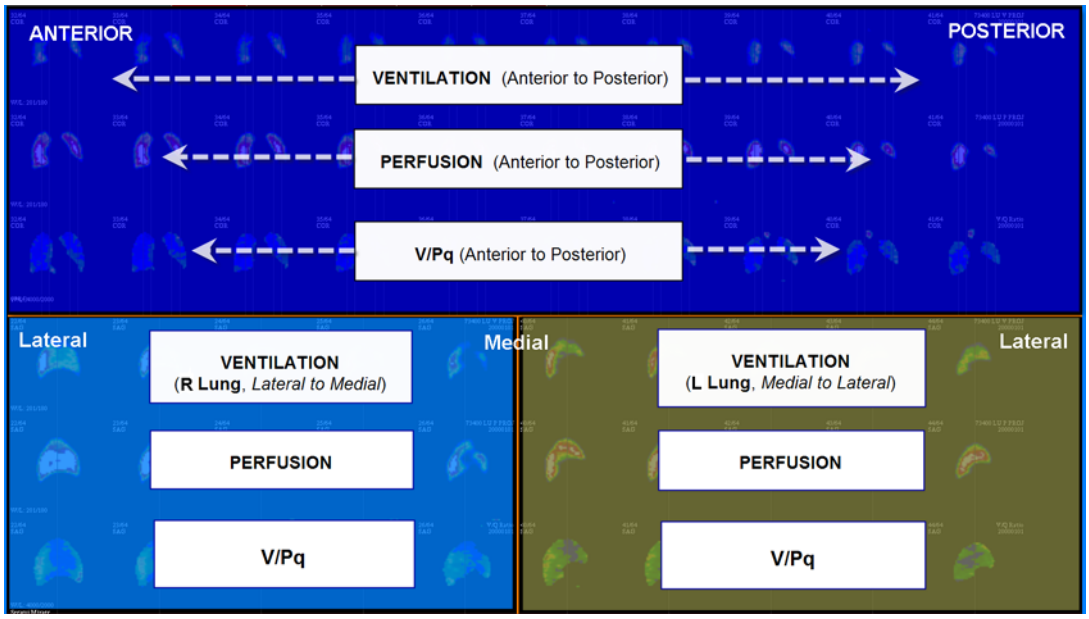

Figure 1.34 Layout of the Coronal-Sagittal Page.

The Coronal/Sagittal page is divided into three sections: A coronal section, at the top, and two sagittal sections, each corresponding to the Right and Left Lungs, respectively. Each individual section displays ventilation, perfusion, and the V/P*q* on separate rows.

The Coronal Section

This upper section displays images of the lungs from the coronal (frontal) projection, starting at the anterior and progressing down through the body to the posterior.

It consists of three horizontal rows of images: ventilation, perfusion, and the V/P*q*. The ventilation and perfusion images are acquired; the V/P*q* images are calculated.

Note — To produce the V/P*q* images, the ventilation and perfusion datasets are registered and the hot spots subtracted from the original ventilation data. The lung borders are statistically delineated and the pixel intensity values are automatically renormalized between **0** and **4000** to arrive at the V/P Quotient image set.

Dual Stadia Lines

The Left and Right Lungs in the Coronal Section are each overlaid with dual stadia cursors, which triangulate their positions with the sagittal plane, shown in the Sagittal Section below it.

The Right Lung and Left Lung each have their own independent set of dual stadia markers, triangulated to the appropriate sagittal sections (RL, LL).

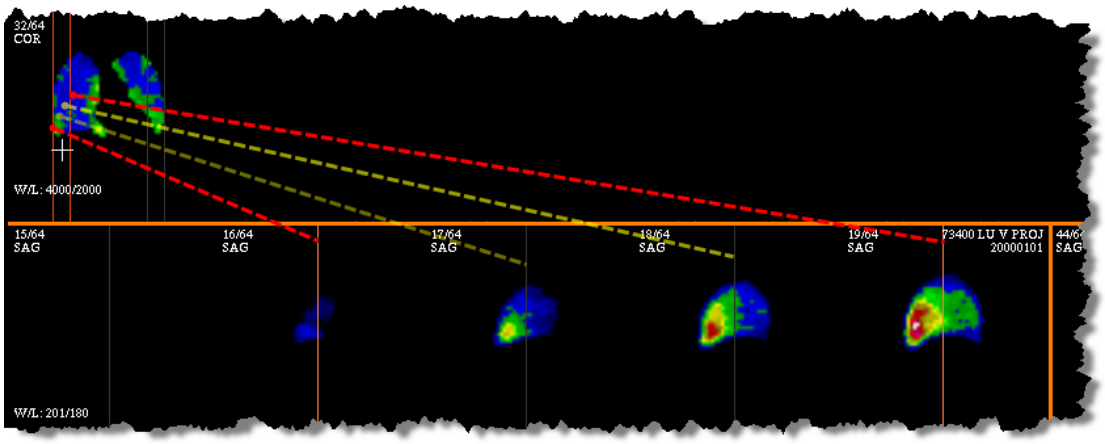

Figure 1.35 Example of how stadia lines from the Coronal Section (RL) map to sagittal images.

The distance separating the dual stadia markers corresponds to the uniform set of slices displayed on the sagittal section (four slices, by default). The first stadia line indicates the position of the first slice of four, the second stadia line indicates the last slice of the set, as shown in the sagittal view. This provides a simple way to control the examination sagittal slices while using the coronal projection for orientation.

Counts

Pixel intensity at the focus of the cursor is displayed adjacent to it. Counts appear as whole numbers in both ventilation and perfusion images.

When the cursor is moved into the V/P*q* Image, the ratio of ventilation counts to perfusion counts is shown instead. This calculated ratio is shown with four decimal places. The V/P*q* counts are used to estimate the degree of mismatch between ventilation and perfusion.

The Sagittal Sections

Below the coronal section, are two separate sections depicting a sagittal projection of the Right and Left Lungs (progressing from lateral to medial, and then medial to lateral).

Both sagittal sections consists of three rows of images:

- ventilation,
- perfusion,
- V/P*q*.

The stadia lines in the sagittal sections can be adjusted to traverse slices in the coronal section.

Coronal Screen

To navigate to the coronal projection, click the navigation button at the top of the display.

Figure 1.36 Click Coronal Tab

The Coronal Page displays the ventilation images in the top row, the perfusion images in the middle row, and the V/P*q* images below.

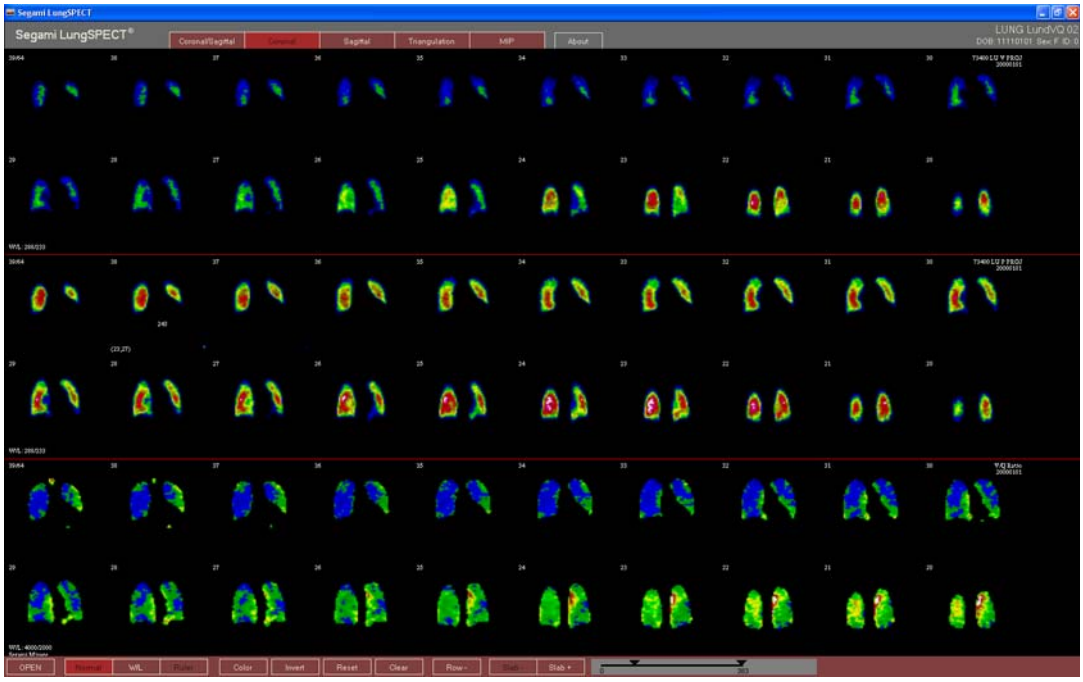

Figure 1.37 The Coronal Page showing two rows each for ventilation, perfusion, and V/P*q*).

The images in each column are synchronized; the slice IDs correspond with one another across ventilation, perfusion, and V/P*q*.

Roll the mouse wheel forward or backward to scroll through the slices in all three datasets or alternatively, left-click and drag the mouse vertically to advance or retreat through the slices.

Intensity counts are displayed adjacent to the cursor.

Layout of the Coronal Page

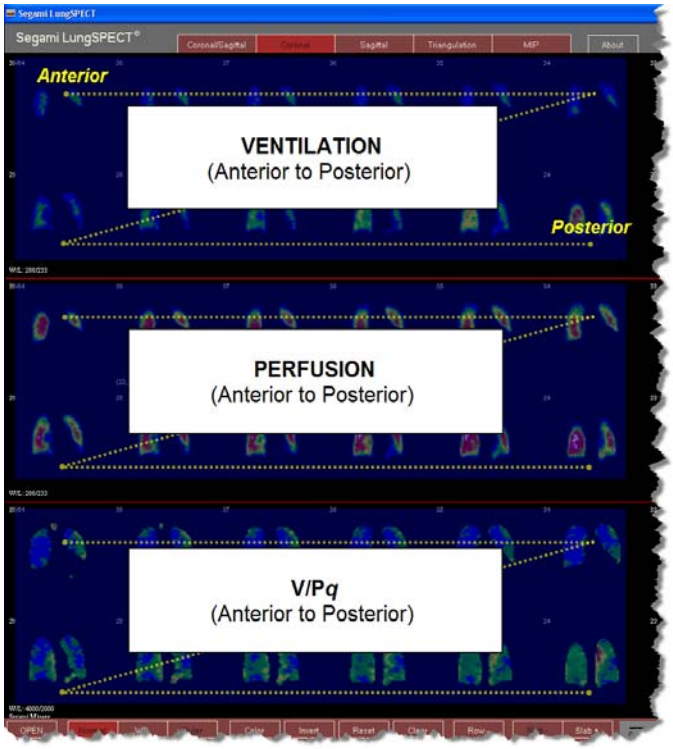

Figure 1.38 Layout of the Coronal Page

The three sections of the Coronal Page all show three rows of synchronized images: ventilation, perfusion, and the V/P*q*.

By default, the images of each dataset are shown in two columns. Press the [**Row**] button to display only a single row of images for each dataset.

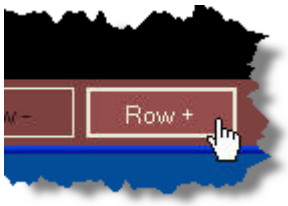

Figure 1.39 Press [**Row]** button to toggle between single and double rows of data.

In this configuration, images in each column correspond with one another. The [**Row**] button toggles the display between showing one or two rows for each data set.

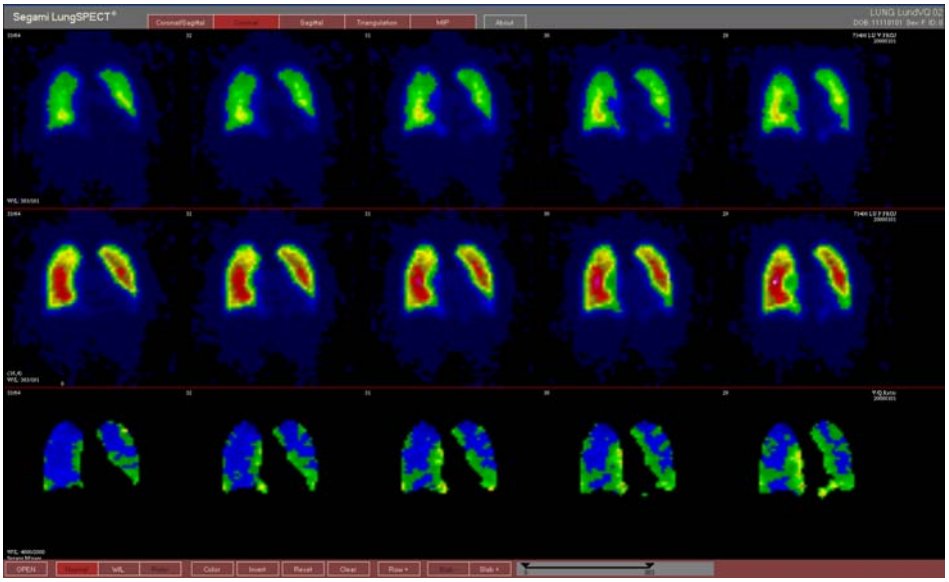

Figure 1.40 The Coronal Page after being set to display single rows.

Slabbing

The slice thickness of the displayed images can be increased and decreased by pressing the [**Slab +**] or [**Slab −**] buttons.

Figure 1.41 The [**Slab +**] button aggregates slices.

When the [**Slab +**] button is pressed, each slice in the dataset is merged with the slice that follows it, creating a thicker slice. The Slice ID which is displayed is changed into a range, reflecting the composite nature of the slices. Pressing the [**Slab +**] button repeatedly joins new slices to the existing range.

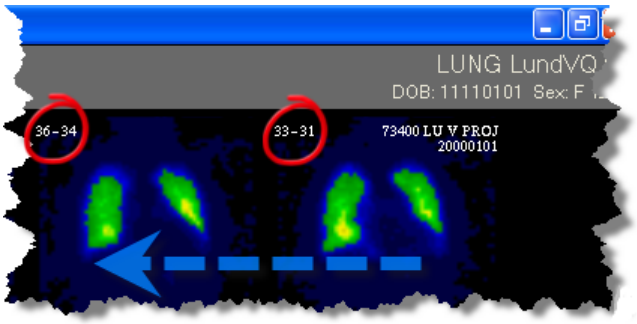

Figure 1.42 The Slice ID of each composite slab reflects the members of the set.

As slabs are extended, the datasets remain synchronized with one another, ensuring that each ventilation slab directly corresponds to both the perfusion and V/P*q* slabs that are simultaneously created.

The [**Slab −**] removes the last slice that had been added to the composite. When pressed repeatedly, [**Slab −**]will return to slices to their individual configuration.

Sagittal Screen

To navigate to the Sagittal Page, click the navigation button at the top of the display.

Figure 1.43 Click the [**Sagittal**] Tab.

The Sagittal Page displays the images from the sagittal projection only. It partially spans both lungs from lateral to medial/medial to lateral, and can be scrolled in either direction.

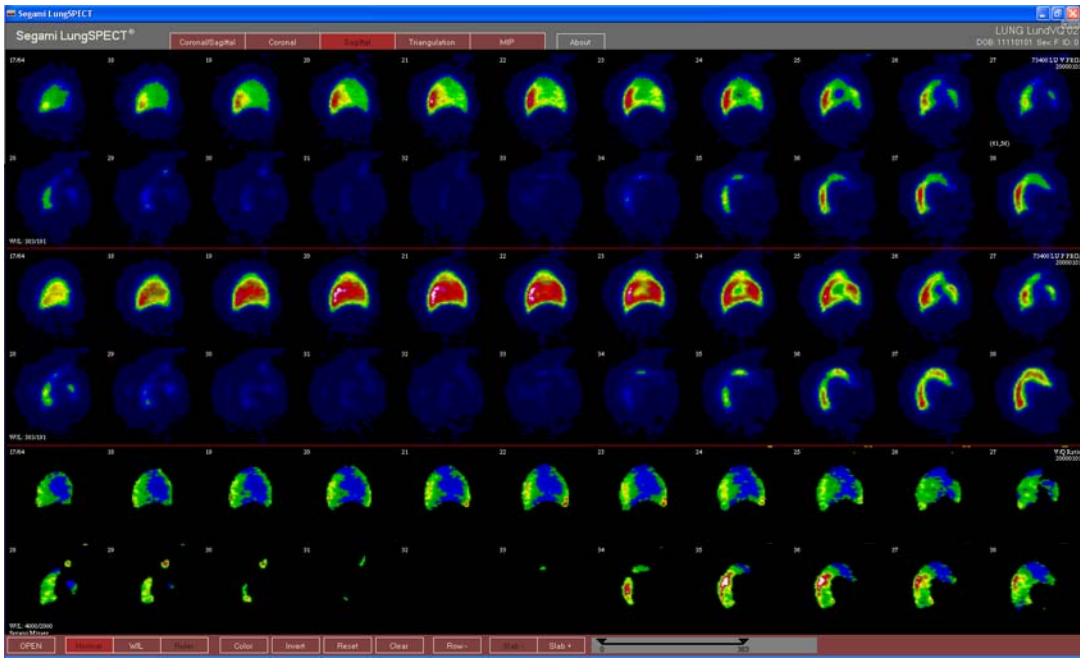

Figure 1.44 The Sagittal Page, presenting perfusion, ventilation, and V/P*q* for both lungs (shown: lateral RL to medial LL).

Layout of the Sagittal Page

Images on the Sagittal Page are displayed in three horizontal rows:

• Ventilation (lateral to medial/medial to lateral),

• Perfusion,

• V/P*q*

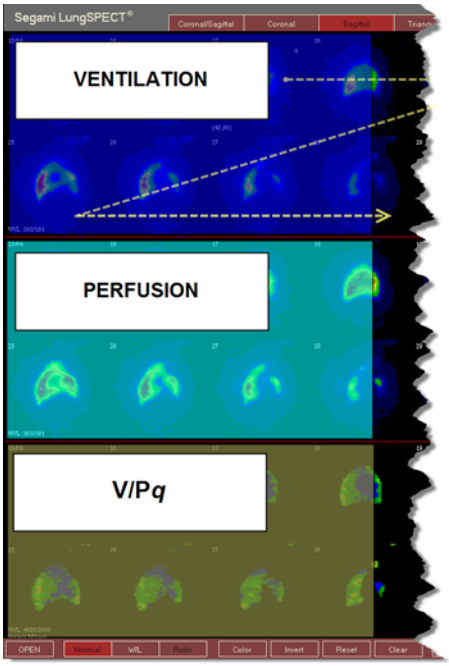

Figure 1.45 The Sagittal Page displays the acquired ventilation and perfusion in rows, and calculates the V/P*q* images and displays them at the bottom.

The images in each column are also synchronized; the slice IDs correspond between ventilation, perfusion, and V/P*q* images.

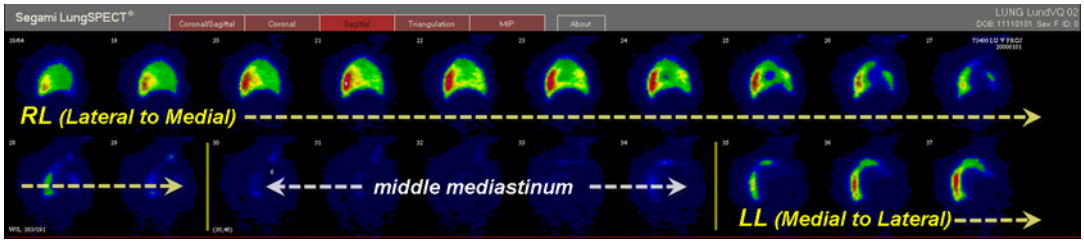

Figure 1.46 The Sagittal Page partially traverses both lungs (RL to the medial LL). Use the mouse wheel to scroll through the images.

In the Sagittal page, you can scroll the slices with the mouse in two ways:

Roll the mouse wheel forward or backward to scroll through the images in all three datasets, or alternatively, left-click and drag the mouse vertically to advance or retreat through the datasets.

As in the Coronal Page, by default the images of each dataset are shown in a two rows.

Press the [**Row +−**] button to display only a single row of images for each dataset. In this configuration, images in each column correspond with one another and their Slice IDs match.

Figure 1.47 Press the [**Row +−**] button to toggle between single and double rows of data.

The [**Row +−**] button toggles between presenting each data set in one or two rows. .

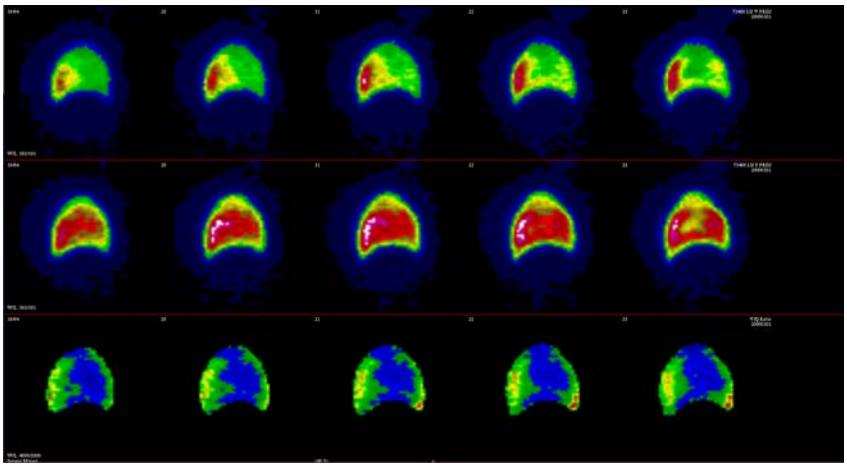

Figure 1.48 The Sagittal Screen showing a single row for each dataset after the [**Row +**] button has been pressed.

Slabbing

The slice thickness of the displayed images can be increased or decreased by pressing the [**Slab +**] or [**Slab −**] buttons.

Figure 1.49 The [**Slab +**] button aggregates slices.

When the [**Slab +**] button is pressed, each slice in the dataset is merged with the slice that follows it, creating a thicker slice. The Slice ID is changed into a range, reflecting the composite nature of the slices.

Pressing the [**Slab +**] button repeatedly joins new slices to the existing range.

Note — Slices cannot be thinned to less than the width of a single slice; they return to their initial acquired state.

Triangulation Screen

To navigate to the Triangulation Page, click on the navigation button at the top of the display.

Figure 1.50 Click the [**Triangulation**] Tab.

The Triangulation Page displays the ventilation, perfusion, and V/P*q* images in transverse, sagittal, and coronal projections.

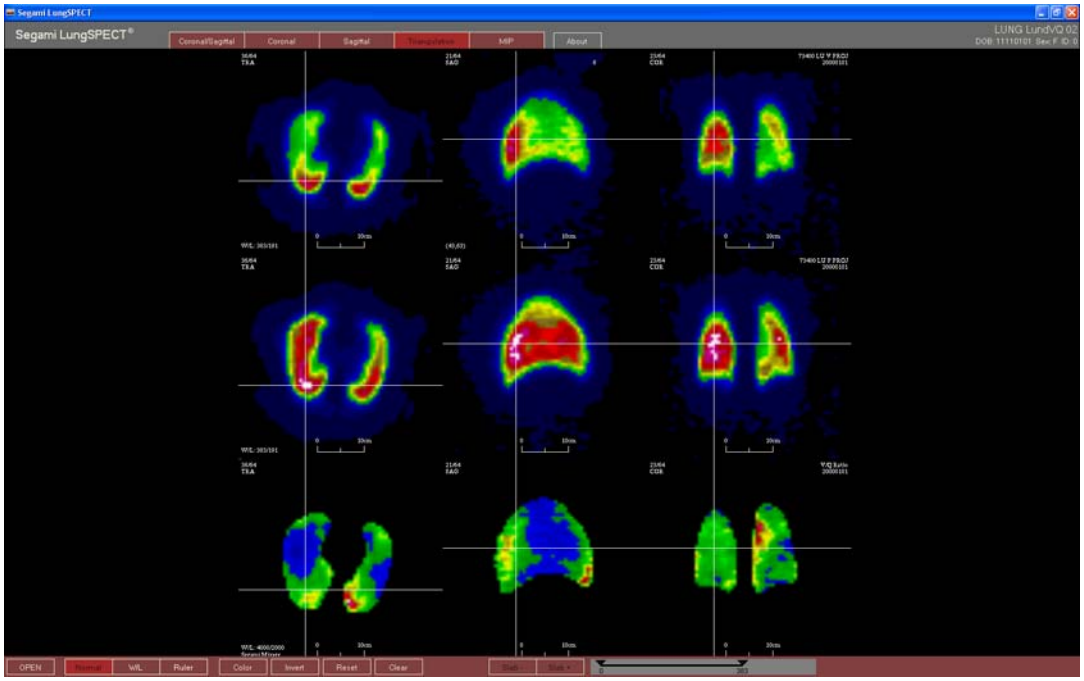

Figure 1.51 The Triangulation Page shows transverse, sagittal, and coronal projections for the ventilation, perfusion, and V/P*q* datasets.

Layout of the Triangulation Page

For each row, a single image is shown in three orthogonal projections, with cross hairs for triangulation. The triangulation images are organized into three horizontal rows:

- Ventilation,
- Perfusion,

• V/P*q*

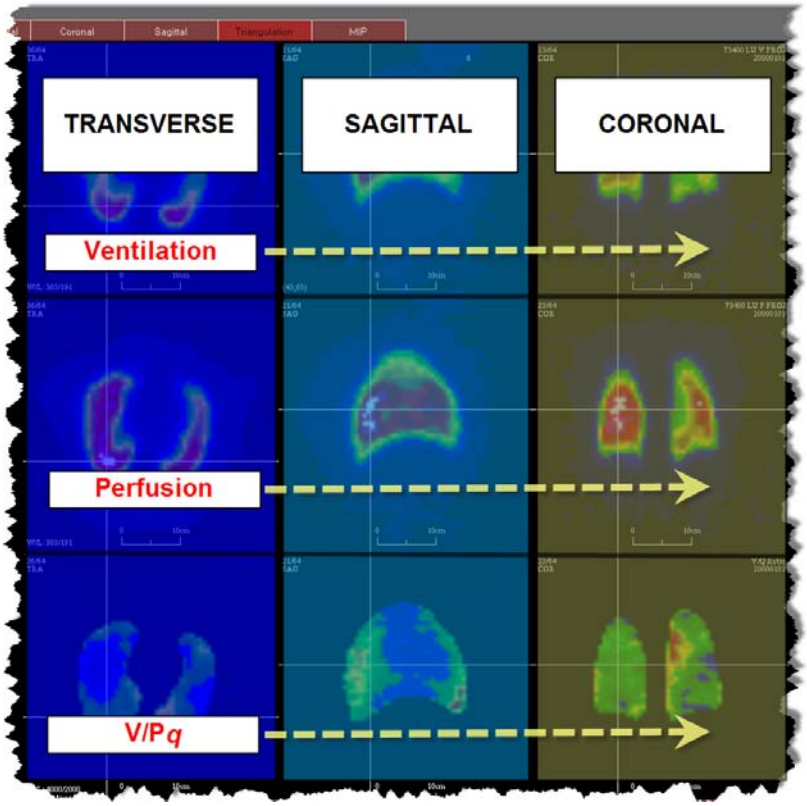

Figure 1.52 The layout of the Triangulation Page.

The Triangulation Page organizes the datasets horizontally in rows. Each dataset contains three projections. Cross hairs are triangulated between the projections, and the datasets are linked so their Slice IDs are correlated.

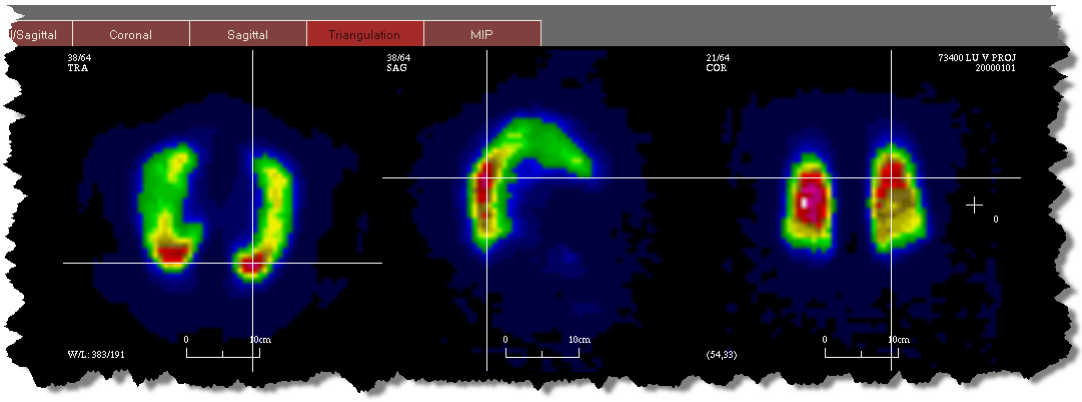

Figure 1.53 The ventilation row in the Triangulation Page, showing the transverse, sagittal, and coronal projections and their synchronized cross hairs.

The images in each column are synchronized; each slice ID corresponds between ventilation, perfusion, and V/P*q* images.

Note — When inside the Triangulation Page, adjustments to the left and right position of a cross hair on the coronal plane will scroll through slices in the sagittal plane. Vertical motions in the coronal plane translate to scrolling in the transverse plane.

Measurements

In the Triangulation Page, pressing the [**Ruler**] button draws line segments to measure areas of interest. The ruler exists as an overlay in one orthogonal projection, but is reproduced inside the viewport of each dataset. The [**Ruler**] button works only when in the Triangulation Page.

Figure 1.54 Click the [**Ruler**] button to inscribe a measured line segment in the Triangulation Page.

To draw one or more measurement lines, click the [**Ruler**] button and position the cross hair at the point in the image where you wish the line to begin (the origin).

Left-click and hold, then drag the cross hair in any direction, while holding the left mouse button down. The measurement ruler will unspool as you drag, with a distance reading appearing alongside the cross hair, showing the ruler length in millimeters from the origin.

At the terminal point, release the mouse button and the ruler is set in place.

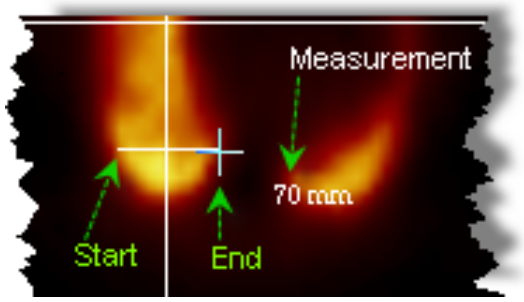

Figure 1.55 The ruler is drawn with the cross hair in any direction, and displays its length in millimeters.

The ruler you create is generated in all three rows; it appears in the ventilation, perfusion, and V/P*q* images in the same orthogonal projection that it was inscribed in originally. You may create any number of rulers in any projection.

To remove all rulers from the Triangulation Page, press the [**Clear**] button.

Figure 1.56 The [**Clear**] button removes all rulers from the Triangulation Screen.

Note — You cannot delete individual rulers; the [**Clear**] button removes ***all*** rulers on the Triangulation Page.