5 AutoSPECT Pro

AutoSPECT Pro is a fast and accurate application that allows you to automatically or manually reconstruct one or more SPECT, gated SPECT, Total Body SPECT, Vantage SPECT, or SPECT-CT projection datasets. SPECT datasets that you can manually reconstruct include cardiac, bone, brain, liver, and other SPECT datasets.

When reconstructing data, you can view three instances of the data and change filter settings on each one for comparison.

NOTICE

Multiple patient launch is not supported by the AutoSPECT Pro application.

NOTICE

Vantage is the trade name for the Philips nonuniform attenuation correction option using a gadolinium transmission line source.

NOTICE

In this manual, “CT-AC” indicates that CT is used for attenuation correction. “AC” indicates generic attenuation correction.

For Brightview XCT data, CT images are paired with projection data. The result is that when SPECT data is loaded, the CT data is automatically placed in the AC map bucket. If you have edited the DICOM information for the CT images (for example, the Series Description), the pairing is broken. When the data is no longer paired, it is handled the same way as data from machines that do not support pairing, which is often the case: automatching is attempted. If automatching fails, you can bucket data manually.

The AutoSPECT Pro workflow differs from that of the other applications. It has the standard Setup workstep to start the process, and the Review workstep at the end. However, instead of the Define Regions and Results worksteps, AutoSPECT Pro has the following:

- AC Map Generation: This workstep is available when you load the appropriate data. It allows you to create or inspect an AC map for processing.
- Reconstruction: This allows you to reconstruct unprocessed datasets, including SPECT, gated SPECT, and Total Body SPECT datasets.
- Reorientation: This allows you to reorient transverse datasets. For cardiac studies, short axis, horizontal long axis, and vertical long axis datasets are automatically generated from the reoriented transverse datasets, and displayed. For all studies, you can use this workstep to manually reorient the reconstructed dataset.

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When a dataset loads in the Setup workstep, its energy window is checked against a default for the radioisotope used. If the window is absent or differs from the default, a dialog appears allowing you to select an isotope, use the default, or use the settings from the source image.

NOTICE

All worksteps appear in the workstep list, but whether you can use one may depend on the data and preference selected.

NOTICE

Images that are 256x256 pose special issues. First, this size is not supported for gated datasets. For other datasets, processing can take a long time due to memory demands. Additionally, for 256x256 Total Body SPECT data, you should process segments separately and knit them afterward, rather than using the AutoSPECT Pro AutoKnitting feature.

One possible SPECT/CT workflow might include processing in AutoSPECT Pro, viewing fusion displays, and loading the results to AutoQuant. To ensure that this sort of workflow is possible, always start with the original CT data and not a preexisting ACMap.

If the CT data is not available, the workflow may not complete correctly. However, you could still use a preexisting ACMap to perform attenuation correction of the SPECT data.

NOTICE

AutoSPECT Pro only supports images with a scan arc of 90,180 and 360. If the application is launched with any data with a scan arc other than 90, 180 or 360, a message appears and the application closes once the message is confirmed.

Scan arc is a DICOM attribute which represents the rotation of the detector. For example, Relative 90/ Relative 180 degree SPECT acquisition in a Dual Head Gamma camera will generate a scan arc of 180/360. Some camera models (Marconi’s AXIS/IRIX, Siemens Ecam, Symbia, GE Millenium MG etc.) can acquire SPECT with Relative 102 or Relative 76 degrees in cardiac mode which generates scan arc of 102/204. These type of scan arc acquisitions are not supported by the application.

NOTICE

AutoSPECT Pro does not support other vendors' dual head detector SPECT/SPECT-CT datasets.

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The AC Map Workstep

This workstep is available for some Preferences if the right data is loaded. It has four layouts, determined by the input data and Preference selected:

- A QC layout for reviewing an existing AC map using a CT-AC or Vantage preference.
- CT-AC layout: This is available if you have loaded a CT image using one of the CT-AC preferences.
- Vantage AC layout: This is available for Vantage data if you have also loaded transmission projection data using one of the Vantage preferences.
- Chang's AC layout: This is available for any SPECT image using a Chang's AC preference.

For SPECT cardiac studies acquired from BrightView XCT systems using a 1-segment protocol, the CT FOV is 14.4 cm in the axial direction. For patients with large hearts, to ensure the robustness of attenuation correction, 3D scatter correction, and Astonish resolution recovery, the attenuation maps are automatically extended by ~20 mm at both ends in the axial direction by duplicating the original end slices of the attenuation map. Hence, the effective axial map FOV is ~18.4 cm.

Some layouts allow you to adjust crosshairs to specify the slice displayed in another viewer. To use the crosshairs, click and drag near the center to move the crosshair vertically or horizontally. Click and drag near the end to rotate the crosshair.

Reviewing an AC Map

If you provide an AC map as input to AutoSPECT Pro, the AC Map workstep displays the map in a splash format so you can review it.

Using CT-AC Data

If you are processing a CT-AC dataset, a new data manager for performing registration tasks becomes available. Use the controls below in the Registration data manager to register the SPECT image relative to the CT image.

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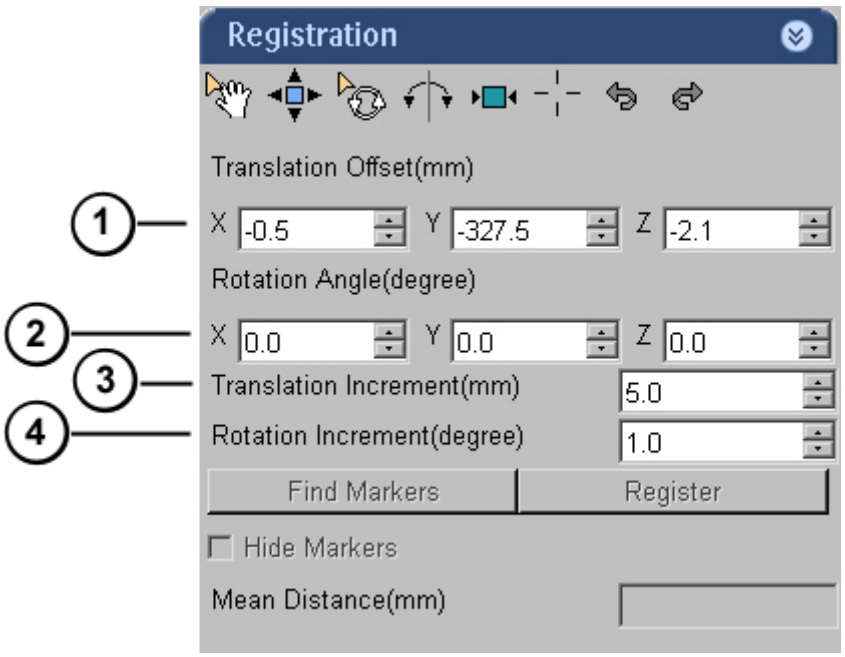

Fig. 33: CT-AC layout controls

1. Translation Offset
2. Rotation Angle
3. Translation Increment
4. Rotation Increment

When the workstep begins, the initial values of X, Y, and Z are set to zero for Philips data. For other vendor's data, the SPECT image is centered on the CT Image.

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Tool	Description
	Registration Pan: This allows you to manually translate the SPECT image in any of the three orthogonal views by dragging the image. You can also use the Translation Offset parameters to specify offset values in X, Y, and Z.
	Registration Pan (Incremental): This allows you to translate the SPECT image in increments specified by the Translation Increment control (and set as defaults: see section “Preferences for the ACMap Workstep” on page 219). To translate, click on the image. The image is divided into triangular quadrants defined by an imaginary X drawn from corner to corner (see "Triangular quadrants used in incremental translation" figure). Clicking in a quadrant moves the image in the direction of that quadrant (for example, clicking in the left quadrant moves the image left). You can also use the Translation Offset parameters to specify offset values in X, Y, and Z.
	Registration Rotate: This allows you to manually rotate the SPECT image by dragging it in any of the three orthogonal views. You can also use the Rotation Angle parameters to specify rotation values in X, Y, and Z.
	Registration Incremental: This allows you to rotate the SPECT image in increments specified by the Rotation Increment control (and set as defaults: see section “Preferences for the ACMap Workstep” on page 219). To rotate, click on the image. The image is divided in half by an imaginary vertical line. Clicking on the right half rotates the image clockwise; clicking on the left half rotates it counterclockwise. You can also use the Rotation Angle parameters to specify rotation values in X, Y, and Z.
	Reset to Zero: This sets the SPECT image translate and rotate (X,Y and Z) positions to zero for all data, Philips and other vendors.
	Center the registration: This centers the SPECT image on the CT image. If you have made any manual adjustments to the translation or rotation of the SPECT image, they are overridden. Clicking this icon returns other vendor’s data to the initial registration positions when the data is loaded.

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Tool	Description
	Undo: This undoes the previous operation. Successive clicks undo each operation you performed, in order.
	Redo: If you have used Undo, this redoes the previous operation. Successive clicks redo each operation you performed, in order.

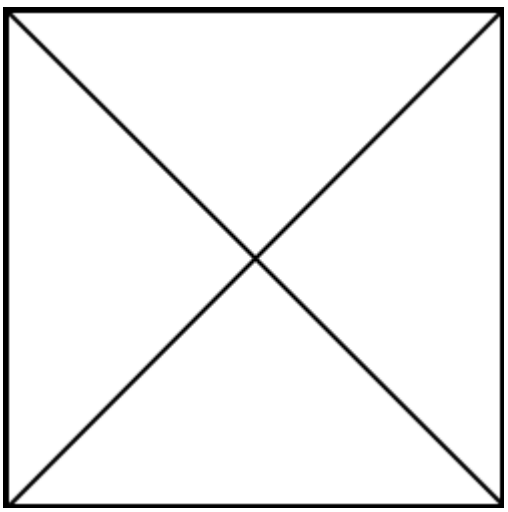

Fig. 34: Triangular quadrants used in incremental translation

If you have a dataset acquired with the Philips fiducial markers (used as a QC tool for Precedence and BrightView XCT, for example), more controls become available:

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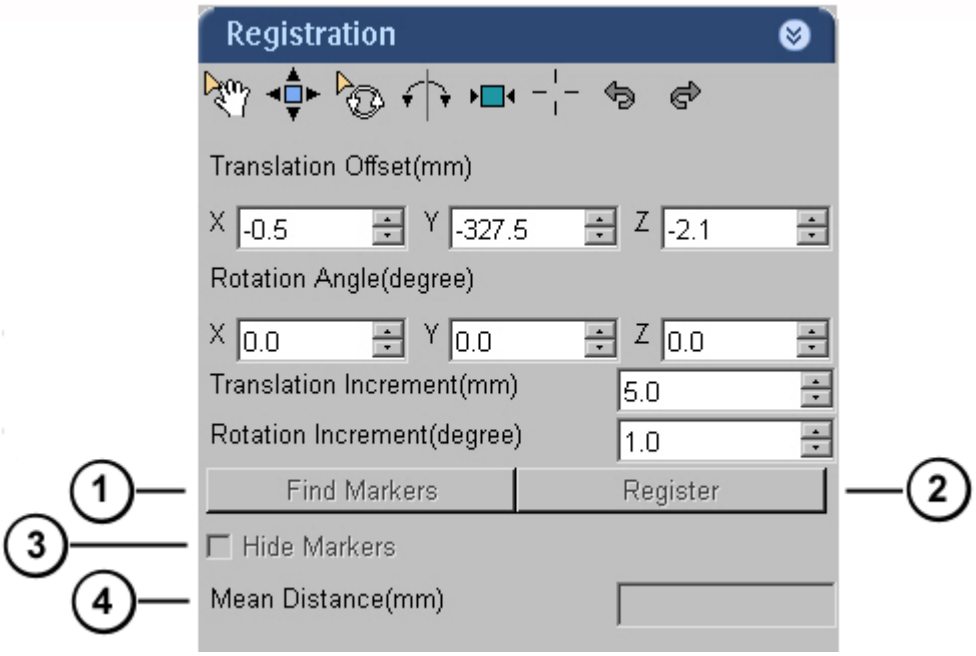

Fig. 35: ACMap workstep controls with fiducial marker functions

1. Find Markers
2. Register
3. Hide Markers
4. Mean Distance

- **Find Markers**: This searches for markers and indicates their positions with a cross.
- **Register**: This registers the images based on markers that were found.
- **Hide Markers**: This toggles the display of the crosses.
- **Mean Distance**: This is the average of the distance between all the fiducial markers in the SPECT image and the corresponding markers in the CT image for all markers that were found.

Using Vantage AC Data

If you are using Vantage AC data, you can perform transmission reconstruction using some of the same controls available in the Reconstruction workstep, but with different options.

Method (FBP)

This is a standard filtered back project reconstruction. When this is selected, you must also set the following controls:

Control	Values
Filters	Butterworth (Off, Smoothing, Analytic)
Cutoff	0.1 - 2.0

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Control	Values
Order	0.0 - 10.0
Bound	On or Off

Filter

Filter defaults to Butterworth. This is a low pass filter that smooths an image. You can control the smoothness by modifying the cutoff and order. It also has properties to ensure that the filter is applied consistently to files acquired with 64 x 64, 128 x 128, and 256 x 256 matrices.

Additionally, you can determine the smoothing applied to the reconstructed transverse dataset:

Off

No smoothing is applied to the reconstructed or projection dataset.

Smoothing

A 3 x 3 spatial filter is applied to each slice of the reconstructed dataset.

Analytic

A filter based on the settings in the Filter, Cutoff, and Order fields is applied to the reconstructed dataset. The Analytic filter is a three-dimensional filter that smooths the reconstructed dataset in the x-, y-, and z-axis. Filtering along the x-axis and y-axis smooths the counts within each slice. Filtering along the z-axis smooths the counts from slice to slice.

Cutoff

This reduces or eliminates the effects of high frequency information by applying a frequency cutoff value.

When using filters to enhance nuclear medicine images, organs or areas of uniform counts are converted to low frequency signals, and lesions with sharp edges or background noise are converted to high frequency signals. Reducing the cutoff value smooths the image by eliminating the high frequency signals. Increasing the cutoff value sharpens the image by retaining the high frequency signals. However, both the lower and higher frequencies are attenuated.

Drag the slider or type a value to set the cutoff value (the range is 0.1 to 2.00).

Important

The Cutoff and Order fields can be modified when a filter uses these fields, but they are grayed out when they are not in use by the filter.

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Order

This modifies the exponent that determines the rate that a filter attenuates a signal. The filter order modifies the region where a filter goes from passing information to attenuating information. Decreasing the order widens the transition band, that decreases the attenuation rate of high frequency signals. Increasing the order narrows the transition band, that increases the attenuation rate of high frequency signals.

The range is 0.0 to 10.0. To increase or decrease the Order value, enter a value in the field or drag the slider.

Bound

Check this to determine the body contour and reconstruct the data within that contour. Uncheck it to reconstruct all of the data within the field-of-view.

Method (Bayesian)

The **Bayesian** method uses a gradient iterative reconstruction method that assumes that the values within soft tissue will have a uniform attenuation coefficient. The output of this algorithm is significantly smoother and more accurate than the **FBP** result. This is the recommended method for performing transmission reconstruction.

When **Bayesian** is selected, you must also set the following controls:

Control	Values
Iterations	12
Start	Uniform
Truncation Correction	On or Off

Iterations

This control is only enabled if the selected method is **Bayesian Iterative**. The number of iterations depends on your data and preferences. Philips recommends 12 iterations.

Start

The initial estimate used by the iterative algorithm can be either a FBP image or an image with a uniform pixel value.

- FBP requires fewer iterations, and is recommended.
- Uniform starts with equalized pixel values and requires approximately five additional iterations to converge.

Truncation Correction

This is only available when the Bayesian **Iterative** method is selected. Enabling this applies a symmetry prior to correcting for truncation present when the patient is larger than the camera field of view. This method is identical to the regular BITGA method when no truncation is present. (BITGA, or Bayesian Iterative Transmission Gradient Algorithm, uses a prior function

that preferentially weights the current attenuation coefficient estimate at each pixel toward the value for soft-tissue region.) The only reason not to use truncation correction is if there are artifacts present in the reconstructed transmission image.

Using Chang's AC

If you are using Chang's AC, you can draw an ROI and then use these controls:

- **Identically in all Frames**: This uses the ROI in the same size and position in all frames.
- **Individually Frame by Frame**: This adjusts the ROI to the frame contents on every frame.
- **Isotope**: This dropdown menu allows you to select the isotope used in the study.
- **Coefficient**: This allows you to type in an attenuation coefficient value.
- **Reset**: This resets the ROIs to their state when the workstep began.

The Reconstruction Workstep

The Reconstruction workstep (see "A Reconstruction layout" figure) contains one or two sets (depending on the data loaded) of the following:

- Viewports that display projection data with or without motion correction, filtered projection data, and a reconstructed slice.
- Zoom controls that allow you to specify the zoom factor applied.
- Method controls that determine the reconstruction method used and any corrections to apply.
- Correction controls to apply to the data.
- Filter controls that determine the filter settings used to reconstruct the selected datasets.
- Limit parameters to specify the reconstruction range.

The reconstruction methods, controls, and suggested parameters depend on the dataset type selected for processing. However, some of the controls and recommended settings are the same for all datasets.

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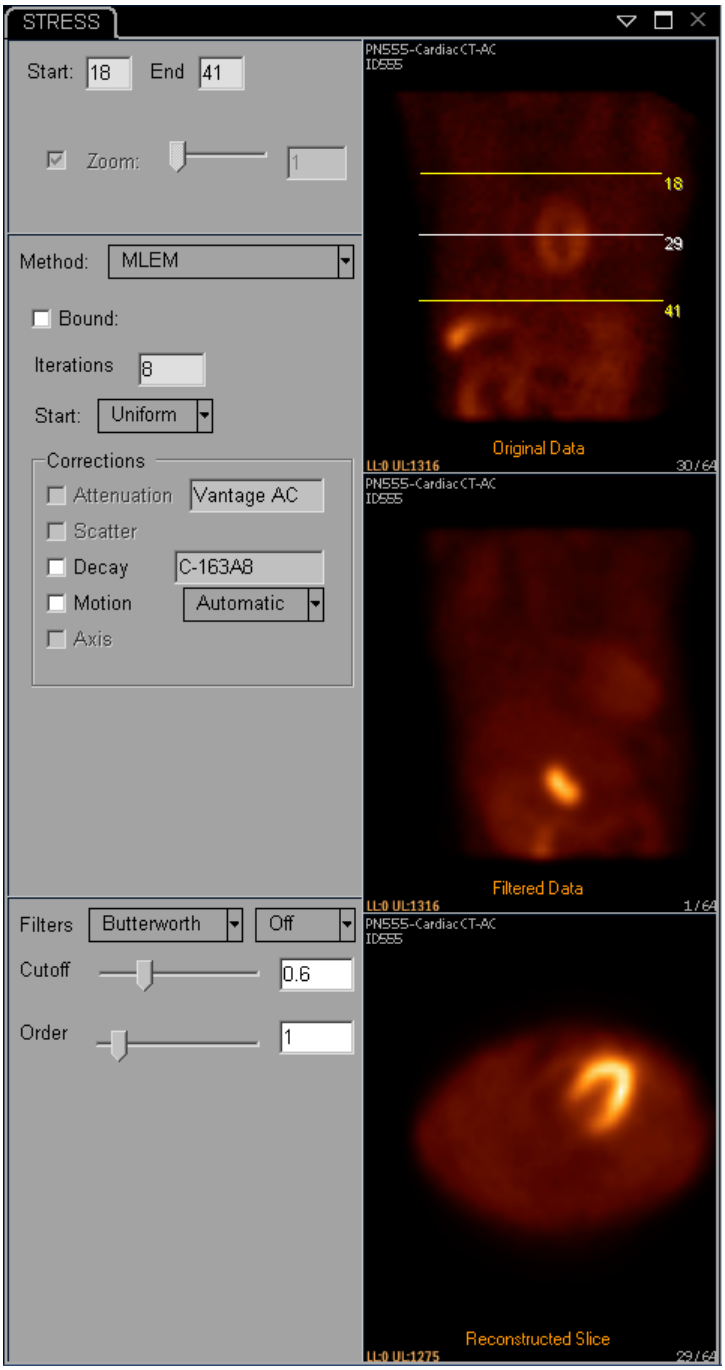

Fig. 36: A Reconstruction layout

To use the Reconstruction page, first adjust the start and end slice of the dataset. For cardiac datasets, these are set by the software, but you can adjust them to improve the results. You can either drag the reconstruction limit lines with the mouse or type values into the Start and End fields.

After adjusting the slices, use the controls described in the following sections.

CAUTION

Visually verify the reconstruction results before saving to ensure images are reconstructed properly.

Improperly reconstructed images may result in misdiagnosis.

Important

Reconstructed transverse images are not created until the Reorientation workstep is available without any error. Reconstructed transverse images are only available to save at the Reorientation workstep and the Review workstep.

Start/End

Start and **End** display the start slice and end slice of the reconstructed transverse dataset. You can change the values by dragging the reconstruction limit lines or by typing values into the fields.

NOTICE

If you have multiple reconstructions of the same data, adjusting the slice limits for one reconstruction setting automatically adjusts them for all other settings. Similarly, if you have concurrent data (for example, gated and summed, dual isotope, etc.), adjusting the slice limits for one automatically adjusts them for the other.

NOTICE

If a CT dataset is loaded for AC correction, the start and end are limited by the range of the CT.

Zoom

Zoom allows you to apply a zoom factor to the reconstructed datasets. AutoSPECT Pro applies the zoom factor to the reconstructed transverse dataset. Short axis, horizontal long axis, and vertical long axis datasets created from this transverse dataset are reconstructed using the same zoom factor.

NOTICE

Zoom is disabled for all methods except FBP.

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Philips

Checking **Zoom** displays a box on the reconstructed slice. The box shows the image area corresponding to the zoom value. You can drag the box to reposition it on the image. Drag the zoom slider or type a value to set the zoom factor (the range is 1.0 to 3.0).

Method

AutoSPECT Pro provides four methods for reconstructing the transverse data.

- Standard FBP - Filtered Backprojection: Reconstruction is performed by backprojecting with a ramp filter.
- Iterative MLEM - Maximum Likelihood Expectation Maximization: Reconstruction is performed in an iterative fashion, with updates based upon a comparison of the estimation to the measured projection data. This method reduces streak artifacts found in FBP reconstructions.

NOTICE

MLEM only supports attenuation correction for Tc-99m and Tl-201. To use AC for other data, use OSEM or Astonish instead.

- 3D OSEM - Ordered Subsets Expectation Maximization: Reconstruction is similar to MLEM method, but only a subset of the projections are used in each update. This method offers faster reconstruction than MLEM with similar accuracy.
- Astonish - If you have the Astonish option enabled, you can select this method. Astonish uses Ordered Subsets Expectation Maximization with resolution recovery to reconstruct the dataset. Resolution recovery compensates for detector and collimator performance as a function of radius from the detector to the center of the image. It uses a deconvolution method based on measured collimator parameters that are stored in a configuration file. It also includes noise control that is independent of the number of iterations and subsets used. For more information on Astonish, see section “Astonish Reconstruction” on page 349.

NOTICE

Vantage data that is labeled “_EMSCR” has already had resolution recovery applied. It is inappropriate to apply Astonish to this data, so it is not available for “_EMSCR” data.

After changing the method, review the available controls to be sure they are set as you intended. Refer to the table below for specific information about the controls.

The controls available for each method are listed in the table below.

Control	FBP	MLEM	OSEM	Astonish
Start		FBP or Uniform	Uniform	Uniform
Iterations		12 is recommended - then evaluate the image (range is 1- 60)	2 is recommended - then evaluate the image (range is 1- 60)	4 is recommended - then evaluate the image (range is 1- 60)
Subsets			16	16
Filter	None, Butterworth, Gaussian, Hamming, Hanning, Parzen	Butterworth	Butterworth	Hanning, None
Y-Axis	Off, Smoothing, Analytic, Prefilter	Off, Smoothing, Analytic	Analytic	
Cutoff	0.1 - 2.0	0.1 - 2.0	0.1 - 2.0	0.1 - 2.0
Order	0.0 - 10.0	0.0 - 10.0	0.0 - 10.0	
Start and End	First and Last Slice Numbers	First and Last Slice Numbers	First and Last Slice Numbers	First and Last Slice Numbers
Matrix	Same as input matrix, 64, 128, 256			
Zoom	1.0 - 3.0			
Attenuation Correction		On or Off	On or Off	On or Off
Scatter Correction			On or Off	On or Off
Decay Correction	On or Off	On or Off	On or Off	On or Off
Number of Detectors	Single, Dual, Triple (auto-selected based on image header)	Single, Dual, Triple (auto-selected based on image header)	Single, Dual, Triple (auto-selected based on image header)	Single, Dual, Triple (auto-selected based on image header)
Axis Correction	-5.0 - +5.0			
Motion Correction	On or Off	On or Off	On or Off	On or Off
Motion Correction method	Auto, Manual	Auto, Manual	Auto, Manual	Auto, Manual
Changs AC	On or Off			

Iterations

This control is only enabled if the selected method is **Iterative MLEM**, **3D OSEM**, or **Astonish**. The number of iterations depends on your data and preferences. The number of iterations is also affected by the initial estimation used. If FBP is used, 10 to 15 iterations are usually adequate. The effect of this control on an image involves a tradeoff. Generally, higher values yield a sharper image, but at the expense of increased noise. The range is 1-60.

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Matrix Size

The **Matrix Size** menu is only available when the method is **FBP**. **Matrix** allows you to specify the matrix size of the saved reconstructed datasets. The X1 option creates a reconstructed dataset that contains the same matrix size as the input dataset. Selecting 64, 128, or 256 creates a saved reconstructed dataset that contains the specified matrix size.

NOTICE

Reconstructed datasets using a 256 matrix sizes can become very large, and may be incompatible with some software (AutoQuant, for example).

Subsets

This control is only enabled if the selected method is 3D OSEM or Astonish. The number of subsets depends on your preferences, and the number of projections in the loaded dataset. The number of projections divided by the number of subsets should be a whole number. For instance, if there are 64 projections, there could be 64, 32, 16, 8, 4 or 2 subsets. For 120 projections, there could be 120, 60, 40, 30, 15, 10, 5, 3, or 2 subsets. Requesting more subsets does not extend the reconstruction time, but requesting more iterations does. If you enter an invalid number of subsets, your value is replaced by the nearest valid value. Using the full number of projections as the number of subsets is not recommended. Philips recommends using a subsets value that is close to the number of projections divided by 4. Using 1 subset is valid, but this is essentially the same as using Iterative MLEM reconstruction, and does not take advantage of the ordered subsets algorithm.

Start

This control is only enabled if the selected method is Iterative **MLEM** (it is set to **Uniform** for **OSEM** and **Astonish**). The initial estimate used by the iterative algorithm can be either a FBP image or an image with a uniform pixel value.

- FBP requires fewer iterations, and is recommended.
- Uniform starts with equalized pixel values and requires approximately five additional iterations to converge.

Attenuation Correction

If you are processing a Vantage or CT-AC dataset or using a Changs AC preference, check this to apply attenuation correction to the reconstructed dataset.

NOTICE

Do not neglect to check this option for Vantage datasets, or attenuation correction will not be applied.

Scatter Correction

If you are processing a CT-AC or Vantage dataset, or using a saved attenuation map with **OSEM** or **Astonish** as the reconstruction method, you can check this to apply scatter correction during reconstruction. Scatter correction is based upon an estimated slab model. See References 7 and 9 in the *NM Application Suite Reference Manual* for a full description and validation of the method. Scatter correction can reduce the impact of detecting scattered photons from hot organs near the organ of interest. Scatter correction is only available when **OSEM** or **Astonish** is the reconstruction method, and when **Attenuation Correction** is **ON**. In general, Philips recommends using scatter correction whenever you perform **OSEM** or **Astonish** with Attenuation Correction.

NOTICE

Vantage data that is labeled “-EMSCR” has already had scatter correction performed. It is inappropriate to apply AutoSPECT scatter correction to this data, so the scatter control is disabled if “-EMSCR” data is loaded.

Scatter Correction uses a pre-calculated estimation (a kernel) of the scatter expected from a point source in water, which is stored on your hard drive. These kernels are specific to the isotope used, the energy window, and the pixel size. You can only perform scatter correction for combinations of parameters for which a kernel exists. The current release of AutoSPECT Pro supports scatter correction for seven isotopes; the following combinations of parameters are supported:

Isotope	Window 1 settings	Window 2 settings	Window 3 settings	Supported Zoom Factors
Tc-99m	15 or 20% @ 140 keV	NONE	NONE	All zooms
Tl-201	15 or 20% @ 72 keV	15 or 20% @ 167 keV (or NONE)	NONE	All zooms
In-111	15 or 20% @ 173 keV	15 or 20% @ 245 keV	NONE	All zooms
Ga-67	15 or 20% @ 92 keV	15 or 20% @ 185 keV	15 or 20% @ 300 keV (or NONE)	All zooms
I-123	15 or 20% @ 159 keV	NONE	NONE	All zooms
I-131	15 or 20% @ 364 keV	NONE	NONE	All zooms
Lu-177	15 or 20% @ 113 keV	15 or 20% @ 208 keV (or NONE)	NONE	All zooms

NOTICE

Additionally, scatter correction for SPECT images with a 256x256 matrix size is only supported for Tc-99m.

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NOTICE

Using scatter correction in AutoSPECT may add several minutes to your reconstruction times, especially for isotopes with multiple scatter windows (e.g., Ga-67).

Decay Correction

Check this to apply decay correction to the projection dataset prior to reconstruction. This automatically pulls isotope information from the projection dataset.

The **Detector** is automatically determined based on the dataset's header information. However, if you need to change it, select **Single**, **Dual**, or **Triple**, depending on how the dataset was acquired.

NOTICE

Because of DICOM issues on some systems, the number of detectors may be misidentified. Be sure to always check this field and change it if necessary.

Motion Correction

If Motion is checked in a Preference and it is set to **Automatic**, motion correction will happen with no intervention. However, if **AutoProceed** is off for Reconstruction, automatic motion correction happens when you enter the Reconstruction workstep, so you see the corrected images when the application pauses at the Reconstruction workstep. Also, if Motion is set to Manual but AutoProceed is on, Manual will override the autoproceed and the study will pause at the Reconstruction workstep in the motion correction layout.

If you are in the Reconstruction workstep you can still perform automatic motion correction. To do this, **Motion** must be checked and set to **Automatic**. As soon as both of these conditions are met, motion correction is performed.

There are two ways to perform and review motion correction:

- Automatic Motion Correction: Use this for Cardiac datasets to have the AutoSPECT Pro algorithm automatically locate the heart, evaluate it for motion artifacts, and make the appropriate adjustments. Selecting this automatically selects Auto as the mode, and performs the automatic corrections. The motion corrected projection image will cine in the upper viewport. Review the images in cine mode to determine if motion correction has been successfully applied. The heart should remain at the same level for all projections—no sudden jumps should occur.
- Manual Motion Correction: Use this for non-cardiac datasets, and for cardiac datasets where the automatic motion correction induces artifacts. To perform manual motion correction, see section “Using Manual Motion Correction” on page 201.

If a Gated dataset is selected, any correction made to a Summed file is automatically made to the corresponding Unsummed file.

NOTICE

If you check Motion after making manual corrections, AutoSPECT Pro replaces the manual corrections with automatic corrections. To use automatic motion correction, the Motion box must be checked in addition to Automatic being selected.

Axis Correction

Axis applies an axis of rotation correction or center of rotation (COR) to the reconstructed datasets. Check **Axis** to enable the option. Then enter the amount of correction. This correction is only necessary for older Philips/ADAC cameras. It is not necessary if the camera includes this information in the acquired data as the newer Philips cameras do: Skylight, Forte, BrightView, and Precedence, for example.

NOTICE

This is only available when the selected Method is Standard FBP.

Filter

Filter allows you to select the filter applied to the data during reconstruction.

When the reconstruction method is **FBP**, each filter modifies a ramp filter to smooth or enhance image details.

When the reconstruction method is **MLEM** or **OSEM**, the filter is applied after reconstruction. When the reconstruction method is **Astonish**, the filter is applied to the projections before and during reconstruction.

Depending on the reconstruction method, the **Filter** menu contains combinations of the following options:

None

No filter modifies the ramp filter applied to the data during reconstruction. This may produce sharp but noisy images.

Butterworth

This filter is available only with the FBP, MLEM, and OSEM methods, not Astonish. The Butterworth filter is a low pass filter that smooths an image. You can control the smoothness by modifying the cutoff and order. It also has properties to ensure that the filter is applied consistently to files acquired with 64 x 64, 128 x 128, and 256 x 256 matrices.

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Gaussian

This filter is available only with the FBP method. The Gaussian filter is a frequency filter based on an exponential function that takes the form: F(x) = a*exp(-b), where a and b are based on the mean and standard deviation. This equation is referred to in statistics as “normal” or “bell” curve. Because of its exponential drop-off, it also behaves well in filtering.

An advantage of the Gaussian filter is that it can become almost any kind of filter (low pass, high pass, or band pass) and it can have a gradual or sharp cutoff. The shape of the filter is controlled by the cutoff frequency and the filter order. It also has properties to ensure that the filter is applied consistently to files acquired with 64 x 64, 128 x 128, and 256 x 256 matrices.

The cutoff frequency is entered as a percentage of the Nyquist frequency. The Nyquist frequency is the highest possible frequency in the image. The resolution limit is set by the linear sampling distance. Therefore, the cutoff frequency can range from 0.0 to 1.0. A cutoff frequency of 0.5 represents 50% or 1/2 of the Nyquist frequency.

The filter order specifies the steepness of the cutoff. In general, the higher the filter order, the steeper the cutoff. A steep cutoff is necessary to eliminate structures that may overlap in frequency. For example, if you have high frequency data and high frequency noise, a sharp cutoff helps isolate the data. Otherwise, a gradual cutoff is more desirable.

Choice of filter parameters is dependent on the nature of the data, personal preference of the user, counting statistics and camera performance.

Hamming

This filter is available only with the FBP method. It is a modified Hanning window with a more abrupt cutoff at the high frequency limit.

Hanning

This filter is available only with the FBP and Astonish methods. It is a low pass filter that smooths an image. Its falloff, which controls the attenuation of the high frequencies, is determined by the $\cos^2$.

Parzen

This filter is available only with the FBP method. It is a low-pass filter that smoothes an image using a linear falloff.

Y Axis

This menu is unlabeled, but is next to the **Filters** menu.

Off

No smoothing is applied to the reconstructed or projection dataset.

Smoothing

This filter is available only with the FBP, MLEM methods. A 3 x 3 spatial filter is applied to each slice of the reconstructed dataset.

Analytic

This filter is available only with the FBP, MLEM, and OSEM methods. A filter based on the settings in the **Filter**, **Cutoff**, and **Order** fields is applied to the reconstructed dataset. The **Analytic** filter is a three-dimensional filter that smooths the reconstructed dataset in the x-, y-, and z-axis. Filtering along the x-axis and y-axis smooths the counts within each slice. Filtering along the z-axis smooths the counts from slice to slice.

Prefilter

This is a smoothing filter used before reconstruction. This filter is used only with the Standard FBP method.

Cutoff

This reduces or eliminates the effects of high frequency information by applying a frequency cutoff value.

When using filters to enhance nuclear medicine images, organs or areas of uniform counts are converted to low frequency signals, and lesions with sharp edges or background noise are converted to high frequency signals. Reducing the cutoff value smooths the image by eliminating the high frequency signals. Increasing the cutoff value sharpens the image by retaining the high frequency signals. However, both the lower and higher frequencies are attenuated.

Generally, too low a cutoff value produces over-smoothed data, possibly disguising a lesion. Too high a cutoff value produces noisy images which appear patchy. The filter choice must reflect both the frequency context of the noise and the frequency context of the organ in the image.

Drag the slider or type a value to set the cutoff value (the range is 0.1 to 2.00).

NOTICE

The Cutoff and Order fields can be modified when a filter uses these fields, but they are grayed out when they are not in use by the filter.

Order

The Order value, used in the **Butterworth** and **Gaussian** filter functions, modifies the exponent that determines the rate that a filter attenuates a signal. The filter order modifies the transitional band (the region where a filter goes from passing information to attenuating information). Decreasing the order widens the transition band, which decreases the attenuation rate of high frequency signals, and can decrease the smoothing. Increasing the order narrows the transition band, which increases the attenuation rate of high frequency signals, and can increase the smoothing. So the higher the filter order, the narrower the transition band and the steeper the drop-off.

The value ranges from 0.0 to 10.0. To increase or decrease the **Order** value, enter a value in the field or drag the slider.

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Comparing Parameters

You can compare parameter settings using the **Compare** page. This displays three copies of a slice, and all the controls available for the data. The parameter values on the Reconstruction page are used for the middle slice; for comparison, the top slice has slightly lower values, and the bottom slice has slightly higher values. You can adjust any of the values to create a more meaningful comparison. When you are done adjusting the copies, click **Apply** for the one that you want to save. For studies with multiple datasets, click **Apply** once for each dataset. Click the **Reconstruction** button to go back to the Reconstruction page. The reconstructed slice will reflect the changes you made, and the controls will retain the settings you made.

Using Manual Motion Correction

Use the **Motion Correction** feature to analyze and correct for patient motion that may have occurred during an acquisition or to verify that motion artifacts have been corrected when automated motion correction is applied.

Perform motion correction on summed emission data only. This feature is not available for transmission data, and should be used for review purposes only for unsummed (gated) data. Unsummed data is automatically summed when loaded, and you can motion correct that. The motion corrected values are automatically applied to the unsummed data as well, and view it using a layout for the gated data.

The **Motion Correction** panel displays the original and corrected projection dataset with sliders and horizontal reference bars, a sinogram or cyclogram of the original projection and corrected dataset, a motion graph, and the current slice:

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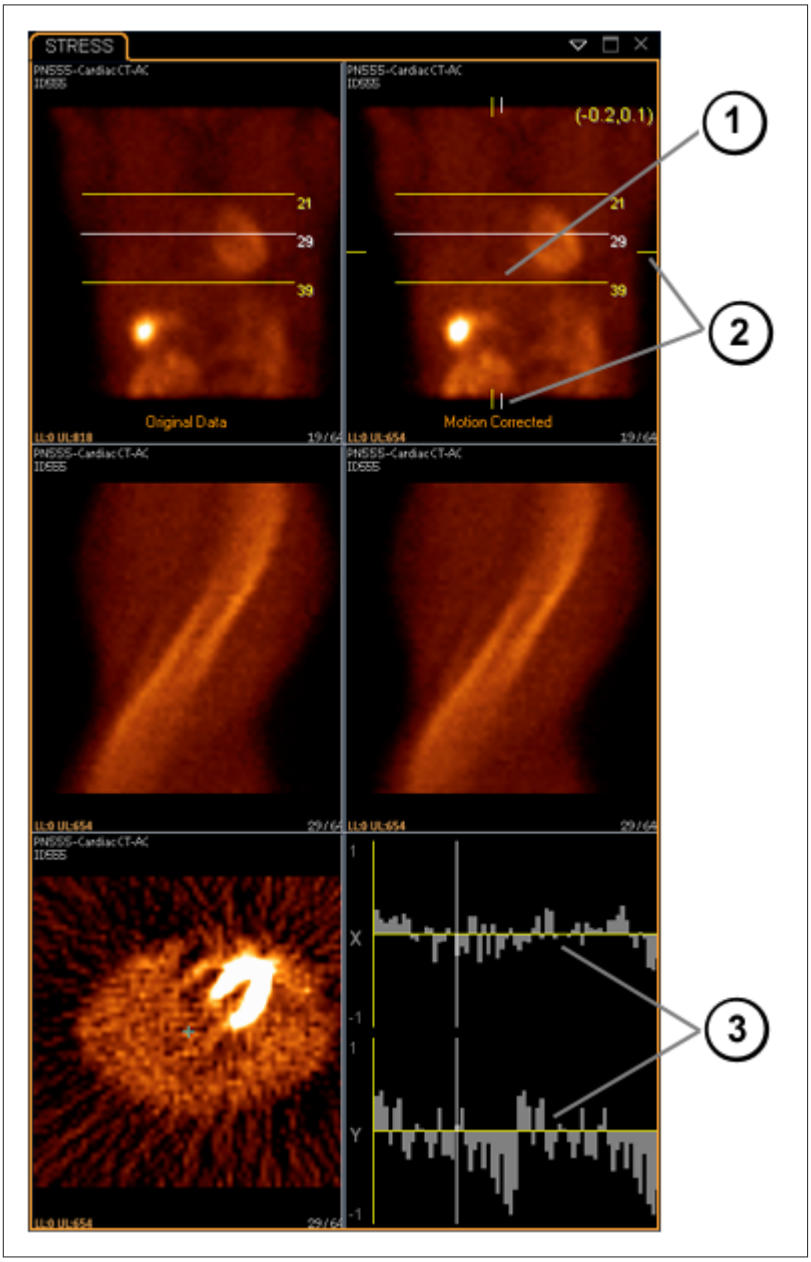

Fig. 37: Motion correction page

1. Horizontal reference bars
2. Motion correction sliders
3. Motion graph of slices

Here are the controls for Motion Correction:

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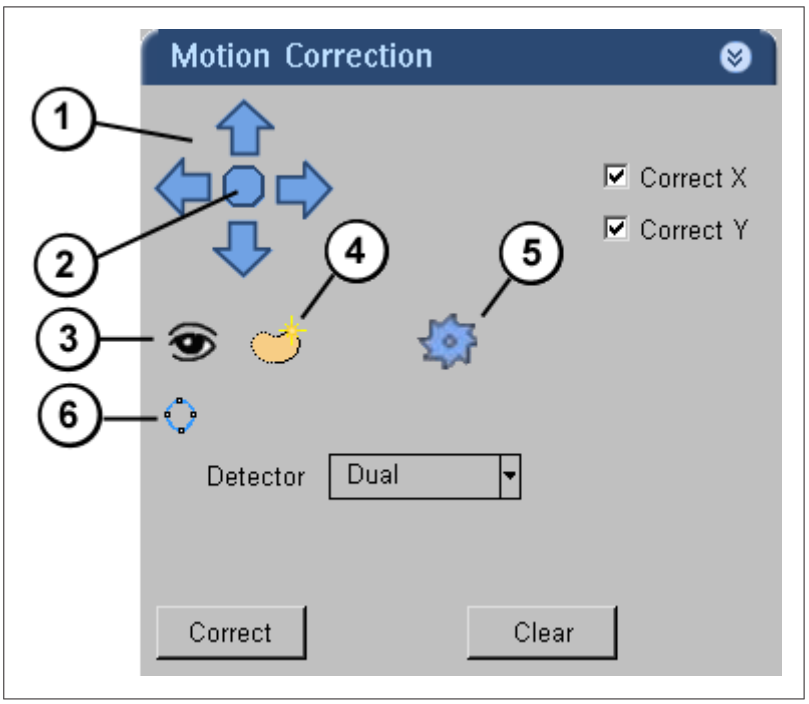

Fig. 38: Motion correction controls

1. Motion correction arrows
2. Reset
3. Show/Hide Markers
4. Enhance
5. Sinogram/Cyclogram
6. Mask

See the next section for information on sinograms and cyclograms. Use the controls below to perform motion correction.

CAUTION

Review the motion corrected projection datasets in cine mode to ensure that motion has been corrected for accuracy. Improperly applied motion correction may create artifacts resulting in misdiagnosis.

Correct X, Y

This allows you to apply automatic motion correction changes to the X and Y axes individually. By default, only **Correct Y** is checked.

Show/Hide Markers

This toggles the display of the hash marks and coordinates in the Corrected viewport.

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Enhance

Use this to display the pixel count differences between frames. Image brightness is proportional to the amount of inter-projection movement present. When displayed with cine on, the areas of motion artifacts are accentuated.

Sinogram/Cyclogram

By default, a sinogram is displayed when the Motion Correction page appears. A sinogram assists in identifying vertical motion, whereas a cyclogram assists in identifying horizontal motion. You can toggle between a sinogram and a cyclogram using this button (this control is also available when you right-click on a sinogram image). They both update as you make adjustments to an image. For more on sinograms and cyclograms, see section “Analyzing Sinograms and Cyclograms” on page 207.

Mask

This allows you to specify the region of interest that should be the focus when the motion correction is performed. Drag the crosshairs in the center to move the mask; drag the small circles to resize the mask.

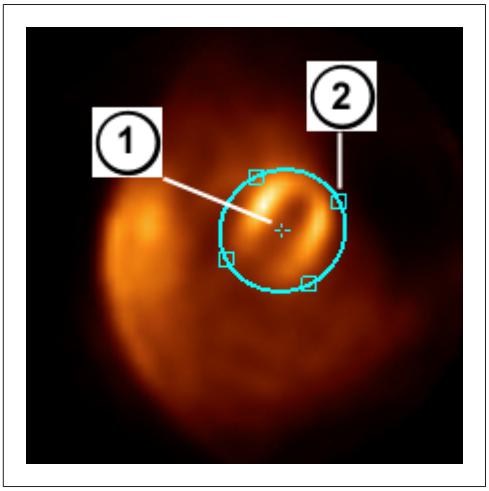

Fig. 39: Mask controls

1. Move
2. Resize

Detector

Select the detector type (**Single**, **Dual**, **Triple**) used during acquisition from the **Detector** pulldown menu. See the note in the next section for information about applying manual motion correction to Dual-Head data.

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NOTICE

This is automatically detected when the information is available in the patient header. However, be sure to review this setting to verify that it matches the acquisition, and change it if necessary.

In all cases, you can use **Single** to correct any data, even if it was acquired with two or three heads. The program can use the information about the correct number of heads to speed up and simplify motion correction, but it can successfully motion correct each frame individually if **Single** is selected.

Manually Correcting for Motion

To manually correct for motion, you need to step through each slice in the reference viewport, move the image up or down or side to side as needed to align the images, and reconstruct the image for motion correction.

Important

To minimize the number of slices you need to correct, examine the entire dataset for motion and note the slices where correction is needed. Determine the minimum number of slices you can correct to align the entire study. For example, if slices one and two are offset from all other slices, correct the first two slices relative to the last.

NOTICE

When applying manual motion correction to dual-head data, the software enforces the following rules:

- For Dual- and Triple-Head datasets, corrections in the Y direction that are applied to the Nth projection image of one detector head are also applied to the Nth projection image of the other detector head. For example, if you correct frame 6 of a 64 frame dual head study by an amount 0.5 pixels, NM Application Suite will also correct frame 38 (6 + 32) by an amount 0.5 pixels.
- For Dual-Head datasets that are acquired in the relative 180 degree configuration, an additional rule is enforced (but not for the 90 degree configuration). Corrections in the X direction that are applied to the Nth projection image of one detector are applied in the opposite direction to the Nth projection of the other detector. For example, if you correct frame 6 of a 64 frame dual head study by an amount 0.5, Autospect will also correct frame 38 (6 + 32) by an amount -0.5 pixels.
- For Triple-Head data, corrections in the X direction on one head must take into account the angles of the other heads when calculating corrections for them. This means that, for example, correcting by 0.5 pixels on one head may mean correcting by 0.25 on another, and by -0.25 on the other.

For the following procedure, refer to the "Motion correction controls" figure. To manually correct a dataset for motion:

1. Analyze the sinogram, cyclogram, or the cine display of the projection dataset to determine if the study contains a motion artifact.

   To accentuate motion artifacts, click on Enhance and analyze the cine display of the projection dataset. With Enhance enabled, the pixel count difference between frames is displayed. Therefore, regions of increased motion are displayed as brighter regions.

2. In the Original Data viewport (labelled at the bottom of the viewport), align the three horizontal reference bars with a constant point of reference. This automatically adjusts the reference bars in the Motion Corrected Data viewport. For example, in a cardiac study, align the top reference bar with the superior ventricular surface, the bottom reference bar with the inferior ventricular surface and the middle reference bar with the mid-ventricular cavity.

   You can use the reference lines as a visual cue when determining whether the patient has moved. It may help to Ctrl-click the viewport and use the cine controls in the Viewer Tools manager.

3. Step through the projections using the arrow keys on the keyboard. You can also use the mouse wheel to step through the projections.

   Analyze the image as you step through the projections until you reach the image needing correction.

4. Align the image in the Corrected viewport with the reference bars, as necessary. To do this, do one of the following:

   - Click on the motion correction arrows (see the " Motion correction controls" figure) to move the image vertically or horizontally 0.1 pixel per click.

     Click the RESET button (see the figure above) to return to the original settings of the currently active frame.

   - Drag the motion correction sliders (the yellow hash marks) in the Corrected viewport to move the image vertically or horizontally.

     The pixel values appear in the upper right corner of the Corrected viewport.

     As you move the images a bar appears in the Graph viewport (see the " Motion correction page" figure). These bars give a visual representation of where the slices are motion-corrected, how far they have been corrected, and in what direction.

Important

Do not press Correct when manually correcting for motion. If you press Correct after manually moving the data, your entries will be overwritten by the automatic motion control.

When the image is reconstructed the motion correction changes are applied.

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Analyzing Sinograms and Cyclograms

AutoSPECT Pro allows you to create sinograms and cyclograms to analyze motion artifacts in SPECT studies.

Understanding Sinograms

To create a sinogram, a single row of pixel values in each projection image forms a row of pixel values in the sinogram (see "Sinogram generation" figure). For example, to create a sinogram displaying the data used to create the Nth slice in a reconstructed dataset, the count values contained in the Nth row of each projection image would be assigned to the corresponding row in the sinogram. The count values contained in the Nth row of Image 1 form the first row of the sinogram. The count values contained in the Nth row of Image 2 form the second row of the sinogram. The number of rows in the sinogram equals the number of projections in the SPECT dataset. The number of images in the sinogram dataset equals the number of slices in the reconstructed dataset.

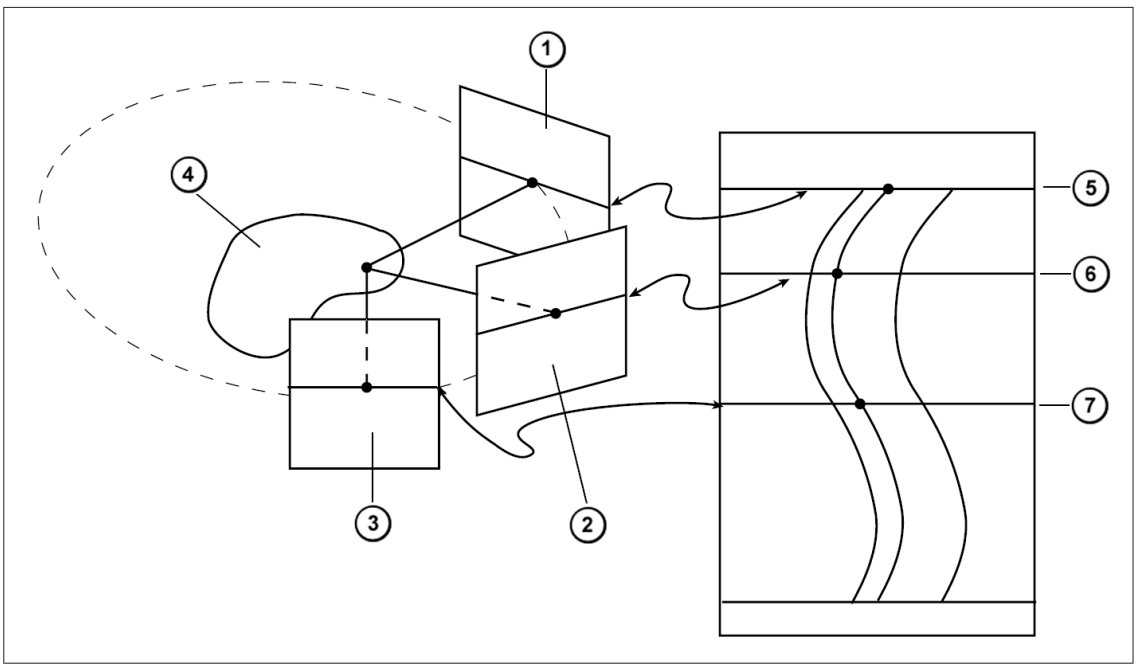

Fig. 40: Sinogram generation

1. Image 1
2. Image 2
3. Image 3
4. Nth slice
5. Row N from Image 1
6. Row N from Image 2
7. Row N from Image 3

Analyzing Sinograms

1. If the cyclogram is displayed, click on **Toggle Cyclogram** in the **Motion Correction** window to switch from the cyclogram display to the sinogram display.
2. Display the sinogram from the desired slice.
3. Drag the reference line in the Reference viewport. The sinogram display is updated to the current slice.

   The viewport for the original SPECT dataset displays the dataset as a series of individual projection images. Each projection image contains the counts acquired by a detector at a specific azimuth. Displaying other projection images in the SPECT dataset allows you to view the counts acquired at different azimuths.

   However, an image in a sinogram displays the counts from the same row in all of the projection images that are used to create a single tomographic slice. Moving the reference line up or down displays sinograms at different slice levels.

Analyze the sinogram for evidence of motion.

Viewing a dataset as a sinogram allows you to easily detect motion artifacts. A sinogram created from a dataset without motion artifacts appears as a smooth spiral, but a sinogram created from a dataset containing motion artifacts contains horizontal breaks or discontinuities in the spiral (Figure 44).

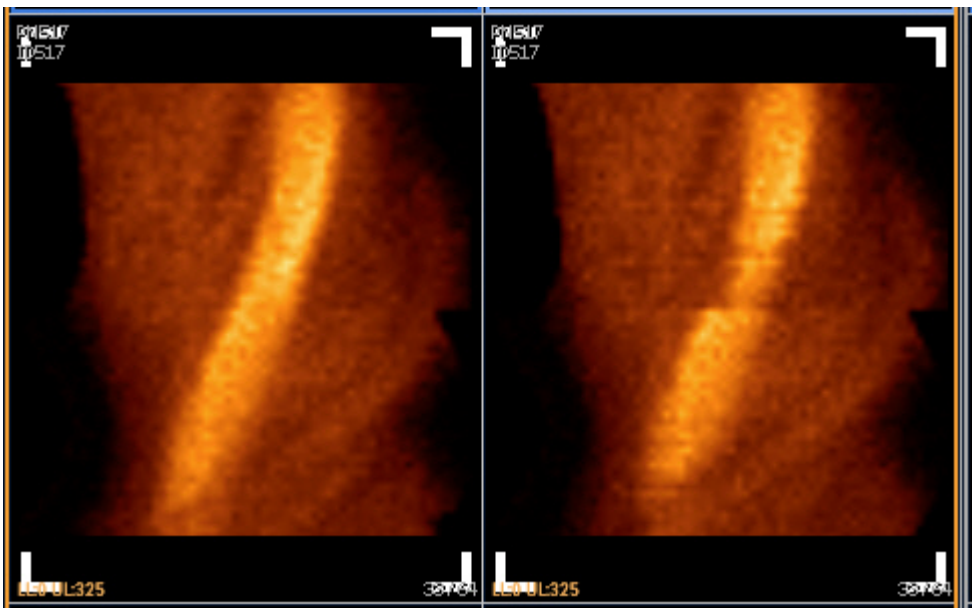

Fig. 41: Sinogram without (left) and with (right) motion artifacts

Understanding Cyclograms

Understanding Cyclograms Cyclograms are similar to sinograms but are generated by selecting a point in a transverse slice and then concatenating from each projection image the vertical strip that passes through that point (see "Sinogram without (left) and with (right) motion artifacts" figure).

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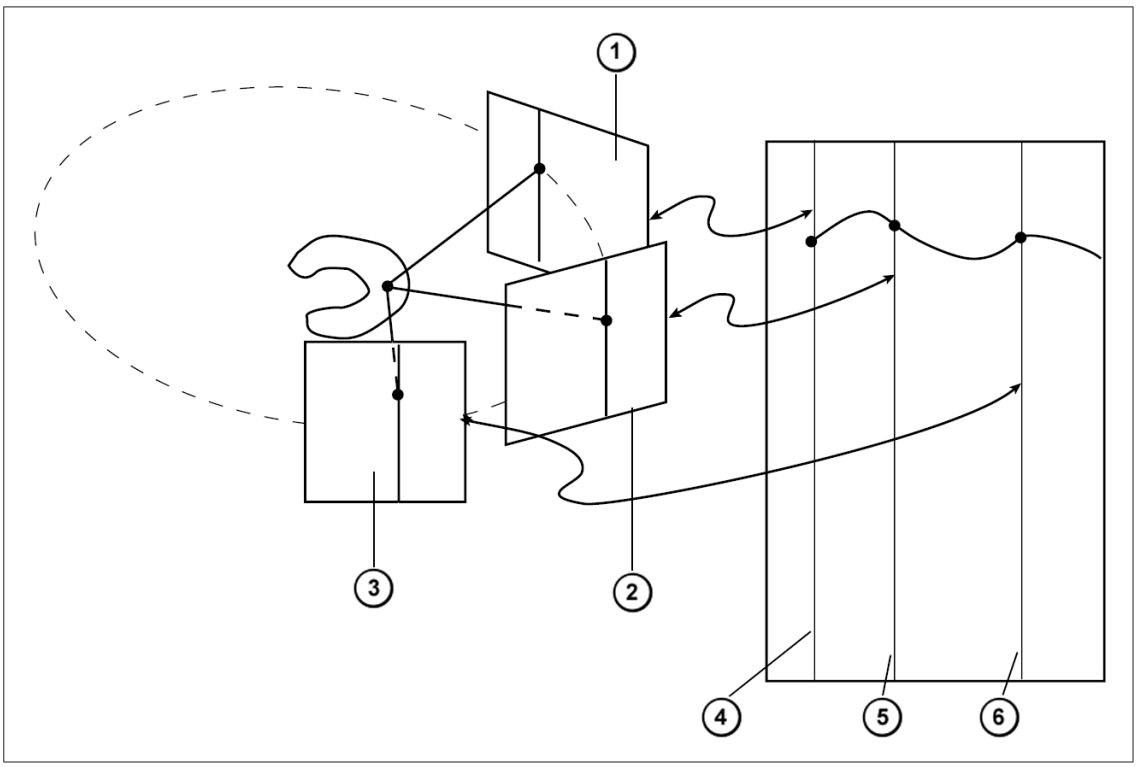

Fig. 42: Cyclogram generation

1. Image 1
2. Image 2
3. Image 3
4. Column N from Image 1
5. Column N from Image 2
6. Column N from Image 3

Analyzing Cyclograms

1. In the Motion Correction window, click on Cyclogram to enable the cyclogram display.

   A transverse sample slice will appear based on the reference line in the original projection image.

2. Drag the reference line in the original viewport.

   The sample transverse slice is updated to the current slice corresponding to the position of the reference line.

3. Use the crosshair in the sample transverse slice to determine the transverse column to be used to generate the cyclogram. Ensure that the crosshair is within the correct ROI.

   If the crosshair is not within the ROI, right-click and drag the crosshair within the ROI.

4. Analyze the cyclogram for evidence of motion.

Cyclograms display evidence of motion similar to sinograms except in the vertical plane. A cyclogram created from a dataset without motion artifacts appears as a smooth wavy image, but cyclograms created from datasets containing motion artifacts contain vertical breaks or discontinuities in the image (see "Cyclogram without (left) and with (right) motion artifacts" figure).

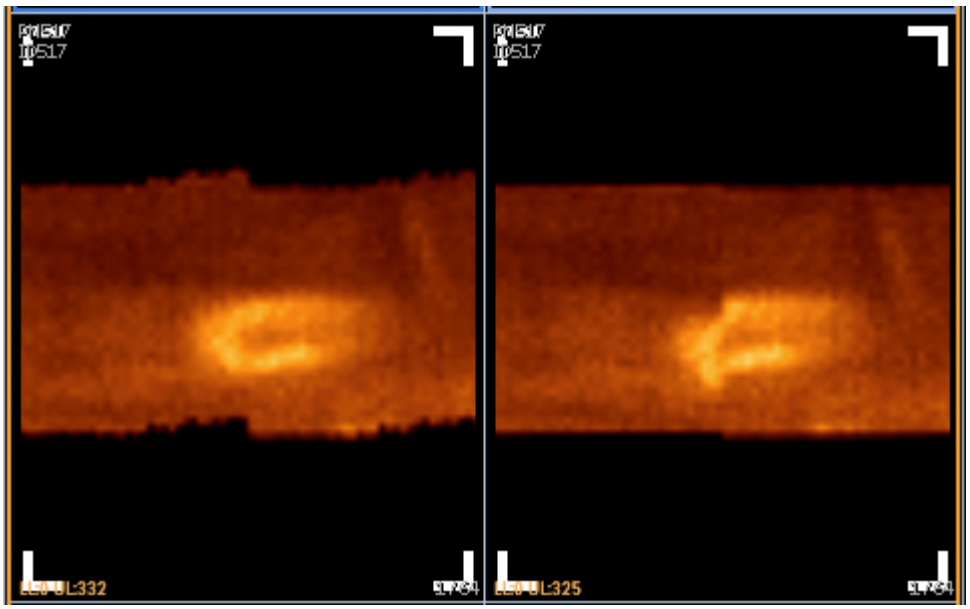

Fig. 43: Cyclogram without (left) and with (right) motion artifacts

The Reorientation Workstep

The **Reorientation** workstep (see "Reorientation page" figure) allows you to automatically or manually reorient SPECT or gated SPECT datasets. When you select the Reorient workstep, cardiac datasets are automatically processed and reoriented. If you are not satisfied with the automatically identified reorientation, or if the dataset is non-cardiac, you must adjust the limits manually.

NOTICE

Reoriented cardiac data is saved in the ACC format: the apex points to the right in the vertical long axis, and upward in the horizontal long axis (see the figure below). Additionally:

- Short Axis images in the dataset are sliced from apex to base.
- Vertical Long Axis images in the dataset are displayed from septum to lateral wall.
- Horizontal Long Axis images in the dataset are displayed from inferior to anterior.

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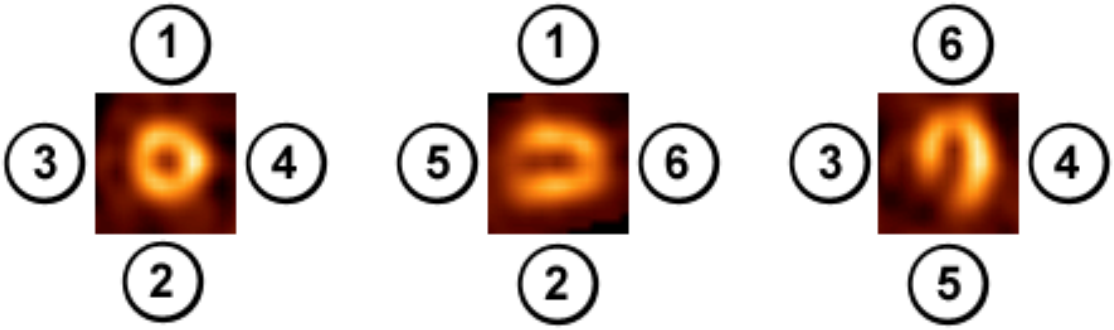

Fig. 44: Cardiac ACC orientation (SAX at left, VLA in middle, HLA at right):

1. Anterior
2. Inferior
3. Septal
4. Lateral
5. Base
6. Apex

Philips recommends making changes to the reorientation only on the Summed Emission data page. Changes made to the reorientation on the summed emission data are applied to the unsummed data, and vice versa.

For multiple reconstructions of the same dataset in the same processing session (for example, with and without attenuation correction), changes made to the reorientation of one reconstruction are automatically made to any other reconstruction in the session.

NOTICE

If you have used scatter correction or Astonish for reconstruction, the transverse slice in the Reorientation page may look different from the sample Reconstructed Slice image on the Reconstruction page. This is because calculations for the sample slice do not use the full 2D or 3D information used for the final reconstruction displayed in the Reorientation page.

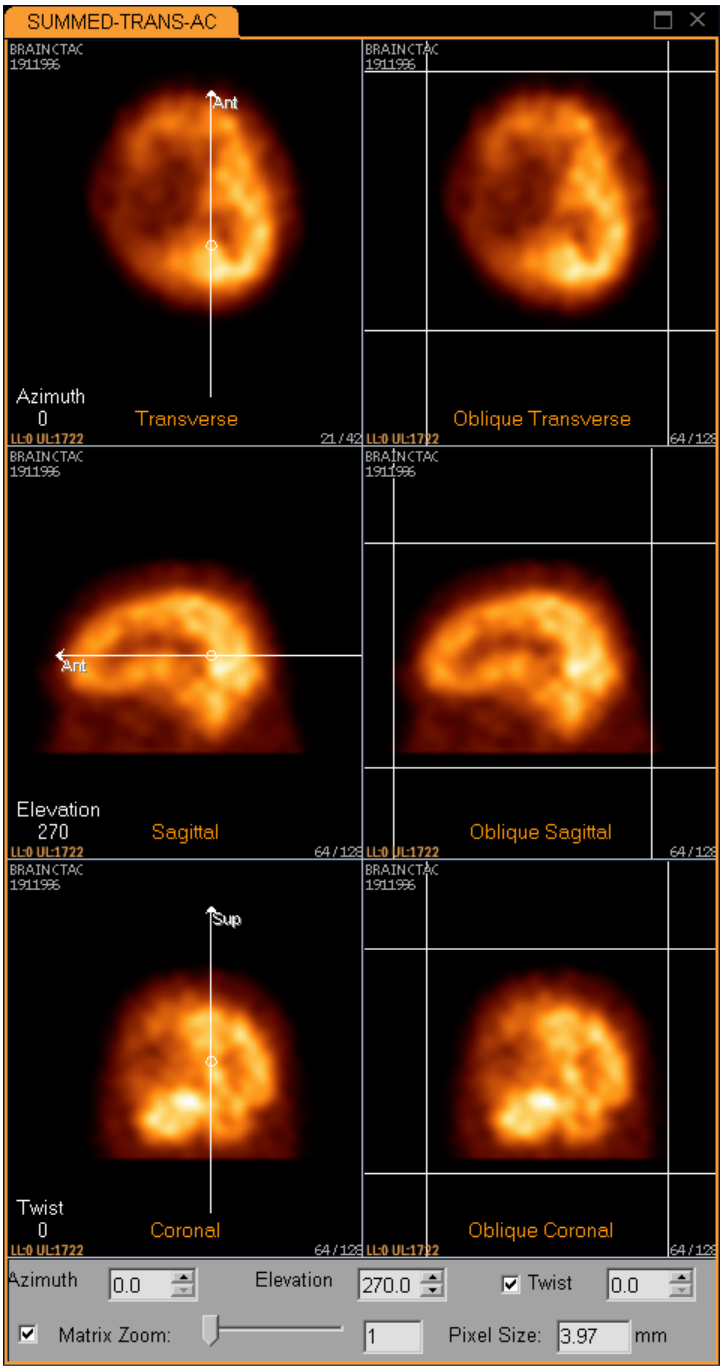

Fig. 45: Reorientation page

CAUTION

Visually verify the reorientation results before saving to ensure images are reconstructed properly.

Improperly reoriented images may result in misdiagnosis.

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Reorienting Datasets

The **Reorient** workstep (see "Reorientation page" figure) contains Azimuth and Elevation reference lines that you can drag and rotate. If the **Twist** option is enabled, an axial tilt reference line is displayed in the bottom viewport. The orientation of the reference lines determines the orientation of the reconstructed datasets.

To manually reorient the organ of interest:

1. Position each reference arrow in the organ of interest: for each viewport, drag the circle in the middle of the reference arrow to the center of the organ of interest.
2. Drag an end of a reference arrow to rotate it to align the organ of interest. Alternatively, type a value in the **Azimuth** and **Elevation** boxes at the bottom.
3. If necessary, check the **Twist** box at the bottom to display the Twist reference arrow and adjust that as well.
4. If necessary, check the **Mask** box at the bottom to enable masking the organ:
   - Edit the shape of the mask by dragging the top, bottom, left, or right of the line.
   - Change the location of the mask by dragging the ‘x’ in the center.
   - Use the button next to **Mask** to toggle whether to drag the limit lines or the mask (in case they are very close to each other).
   - The mask line is propagated to all slices. Scroll through the slices to confirm the mask shape and position.

NOTICE

Mask is only available in cardiac preferences.

5. Specify the slices to save by dragging the reference lines on the right side of each viewport to enclose the organ of interest. Use the **Matrix Zoom** control at the bottom to control the apparent size of the image: either drag the slider or type in a zoom value (the range is 1-3). If you need a specific pixel size, use the Pixel Size box to type in a value.

NOTICE

You cannot adjust the viewports individually with Zoom.

NOTICE

When positioning the reference lines, allow sufficient space between the lines and the organ so that you do not clip it.

You can save the following data and image types:

Data Type	Image Type
Tomo/Emission	Motion Corrected Tomo
Gated Tomo	Gated Motion Corrected Tomo
Gated ReconTomo (Emission)	Summed Tomo, Motion Corrected summed Tomo, Motion Corrected gated Tomo, Gated Transverse, Gated Short Axis, Gated Horizontal Long Axis, and Gated Vertical Long Axis
Recon Tomo (Emission)	Non cardiac: Oblique/Reoriented Transverse, Sagittal, and Coronal Cardiac: Transverse, Short Axis, Horizontal Long Axis and Vertical Long Axis
Recon Tomo (Transmission)	AC Map

AutoSPECT Tutorial for 1-Day Data

This protocol reconstructs gated and summed STRESS and REST cardiac studies without attenuation correction. This default uses FBP with parameters previously established in AutoSPECT Plus for a 1 day protocol.

NOTICE

This tutorial is designed to use a particular sample patient that works well to illustrate certain features of the software. Nothing prevents you from substituting your own patient, but be aware that it may not load the same way or produce similar results. If you try to load your own data and it fails because of automatching, see section “Preferences for the Setup Workstep” on page 218.

If you would like to start this tutorial over at any time, just click Restart in the application. This reloads the data as it does in the first workstep, as long as the default Preference has not been changed.

Setup

1. In the IntelliSpace Portal Patient Directory’s Local Devices list, select the NM Demo Data studies.
2. From the list of patients, select the Patient Name **AutoSPECT Pro/ 3rd Party Cardiac** with Patient ID **Cardiac Astonish**.
3. Click on the arrow in the Analysis menu and select the AutoSPECT Pro application.
4. If the “1 DAY” Preference is not selected, double-click it to set it as the current Preference.
5. Notice that the Gated Rest bucket has a red exclamation point.

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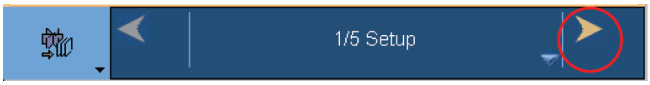
Philips

Ordinarily, this indicates that it requires data. But in the case of cardiac studies, there may be cases where you cannot gate the study, yet you still need to process using the standard Preference. When this is the case, in AutoSPECT Pro you can proceed to the next workstep and the study can be processed.

6. Click the Next Workstep button to proceed to the Reconstruction workstep:



Reconstruction

1. The top and bottom limit lines in the top viewer may enclose the heart well enough for your purposes. If not, adjust them accordingly. Use the middle line to set the position of a sample slice, visible at the bottom of the viewer.

NOTICE

Adjusting the non-gated data performs the same operation on the gated data simultaneously, so you do not need to make adjustments twice.

2. Select a Method that works best for the data by checking the sample slice at the bottom.

   Since the heart jumps around a little, apply motion correction to improve the results:

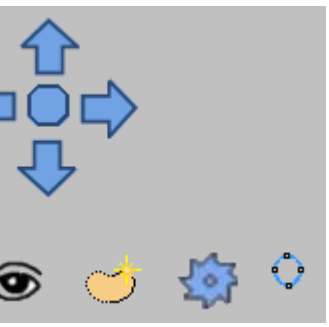
3. Click the **Motion Correction** button in the Control Panel. This opens the Motion Correction Data Manager.

   By default, **Correct Y** is checked, since this is the most common case.

4. Click **Correct**.
5. Notice that the heart has stabilized.

   You can improve the motion correction reults by masking the area to be corrected:

6. Click **Clear** to refresh the page.
7. Click Toggle Mask in the Motion Correction panel:



   Notice the elliptical ROI in the sample slice at the bottom of the viewer.

8. Drag and edit the ROI so it encloses the heart.
9. Click **Correct.**

   Verify that the heart motion has been corrected.

   The Stress and Rest data are corrected separately. If you want to correct the Rest data, you can do that using the same process.

10. Click **Reconstruction** to go back to the Reconstruction page.
11. Click **Next Workstep** to proceed to the Reorientation workstep.

Reorientation

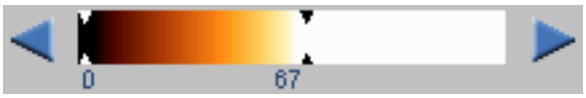
This page allows you to adjust the orientation of the images so they display correctly.

1. If you would like to adjust any of the orientations, drag one end of an arrow to rotate it.
2. Click Next Workstep to proceed to the Review workstep.

Review Images

This workstep provides multiple layouts to view the images. Click on each layout to view its contents.

1. Use the Image Colorbar to adjust the background (white bar) and brightness (black bar).
2. Right-click on the Image Colorbar to open a menu that lets you select Colormap, Intensity, and Pixel Values:



When you save images, the summed motion corrected images are available to save as well:

1. In the Image Tools manager, click **Save all images**.

   The **Save Image(s)** dialog appears.
2. Check **Summed Moco** to include the motion corrected images.
3. Click **Save** to save the images.
4. When you are done, click **Exit** to exit to the Patient Directory.

If you are prompted to save images, click **No** unless you want to save any new images.

Setting Preferences for AutoSPECT Pro

AutoSPECT Pro handles preferences differently from the other applications in the NM Application Suite. This section describes how to set preferences in AutoSPECT Pro only, not in any other application.

There are 22 factory preferences for AutoSPECT Pro:

- 1 Day
- 2 Day
- Astonish Cardiac CTAC
- Astonish Cardiac
- Astonish Vantage Pro
- Astonish Bone SPECT
- Bone SPECT
- Astonish Brain SPECT
- Brain Chang AC
- Brain CTAC
- Brain SPECT
- Cardiac CTAC

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- Cardiac Vantage Pro
- Cardiac Reorientation
- Cardiac Dual Isotope
- Gated BloodPool SPECT
- General Chang AC
- General CTAC
- General Reorientation
- General Dual Isotope CTAC
- TB SPECT
- Thallium

To use Preferences, select the **Preferences** Data Manager. This manager contains a list of all the AutoSPECT Pro preferences, and some controls at the bottom:

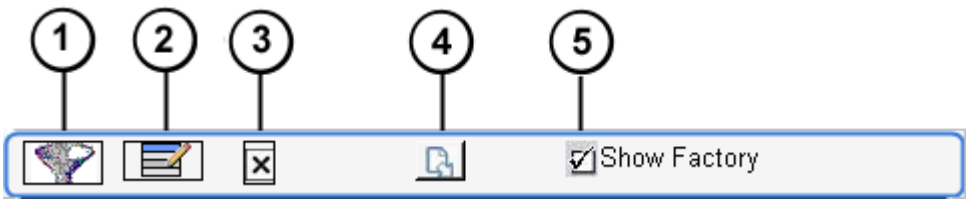

Fig. 46: Preferences controls

1. Spect Global DataFilter
2. Edit Preference
3. Delete Preference
4. Apply Preference
5. Show Factory

- To specify image types to exclude from the gated and tomo buckets, click **Spect Global DataFilter** and use the dialog. Type a value in the text box and use the '+' and '-' buttons to add and delete image types. These are the types that will be excluded when autobucketing.
- To edit a preference, select the preference from the list and click **Edit Preferences**. See the sections below for details on editing preferences.
- To apply a preference, double-click it, or select it and click **Apply Preference**.
- To delete a preference, select the preference from the list and click **Delete Preference**.
- To toggle the display of the factory-installed preferences, check the **Show Factory** checkbox.

General Preferences

In an AutoSPECT Pro preference, each workstep has its own preference settings. In addition, you can set some parameters for the preference as a whole (ones that apply to all worksteps):

- **AutoProceed**: This determines whether the workflow automatically continues through the workstep if all the required input is present. If this is unchecked, the workflow will always stop at the workstep. If it is checked, it will stop only if the required input is not present.

NOTICE

AutoProceed is available for all worksteps except the first one, Setup. You must manually proceed from the Setup step even if AutoProceed is checked for it in the Preference.

- **Acquisition Matching String**: This allows you to set strings for exam matching based on the DICOM attributes Study Description, Protocol Name, or Body Part Examined. Separate strings with a comma. Matching succeeds if any of the DICOM attributes contains one of the matching strings.
- **CT Window Preset**: These translate the values of an image into a range of gray levels suitable for optimal viewing of the specified organ or area.
- **SPECT ColorMap**: These convert gray levels to colors using different schemes.

NOTICE

CT images loaded into the AC Map workstep are always displayed in grayscale.

All other parameters are specific to the worksteps and are described below.

Preferences for the Setup Workstep

The following controls appear in the Setup workstep.

- **Matching String**: Strings you type in here are used to match datasets and exams that will use the preference. Separate strings with a comma. Matching succeeds if the value of any of these DICOM attributes contains one of the matching strings:
  - For exams: Study Description, Protocol Name, and Body Part Examined (organ)
  - For datasets, the matching proceeds in this order: Acquisition Context, Image ID, Series Description and Image Comment
- **Active**: Check this to set whether the bucket appears in the Setup step.
- **Alternate Name**: This is an additional string to use with the default bucket name.

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Preferences for the ACMap Workstep

The controls available in this workstep depend on the preference you are editing. For a Changs AC preference, there are no relevant controls. For a Vantage preference, the controls are a subset of the Reconstruction workstep controls (Method, Corrections, Filters, etc.); see the descriptions in section “The Reconstruction Workstep” on page 190 for details. For most other preferences, the following controls are present:

- Rotation: This sets the increment by which the SPECT image rotates when you click on it using the **Incremental Rotate** tool.
- Translation: This sets the increment by which the SPECT image moves when you click on it using the **Incremental Translate** tool.

Preferences for the Reconstruction Workstep

The following controls appear in the Reconstruction workstep.

- You can have up to three reconstructions configured within a preference. You can set the preferences for each one using the buttons on the left. Click a button to select it, and set the preferences described below. Use the checkboxes to specify whether the reconstruction is available.
- **Link concurrent data**: If concurrent data is loaded, this links some controls for the two datasets:
  - Limit lines (and **Start** and **End**) in Reconstruction and Motion Correction
  - **Correct X** and **Correct Y**, and the Correct button in Motion Correction
  - All controls in the Reorientation workstep
- **Auto Knitting**: Checking this automatically knits loaded segments during reconstruction. However, for this to work, adjacent segments must be contiguous, and they must all use the same reconstruction settings (Method, Iterations, Filter, etc.).
- **Mode**: This determines whether there is a single set of reconstruction and reorientation controls or a dual set.
- Reconstruction controls: The Reconstruction controls allow you to set the default settings seen in the workstep: the default Method, Iterations, Filter, whether the Corrections are on or off, etc. For explanations of these, see the sections that describe them.

NOTICE

If Motion is checked and set to Manual, this will override the AutoProceed setting, and the process will stop at the Reconstruction workstep to allow manual motion correction.

- **Saving Options**: These are the datasets to save. Check a dataset to have it saved; type a string in the text box to save the dataset with that name instead of the one displayed.
- **Buckets**: This specifies the bucket that is to be a required dataset in the Setup workstep.

Preferences for the Reorientation Workstep

The following controls appear in the Reconstruction workstep.

- Oblique Twist: This determines whether **Twist** is on or off.
- Matrix Zoom: This specifies a default zoom factor.
- Mask: This allows you to mask an organ.

Preferences for the Review Workstep

This is a list of all the viewing protocols. Select a **Default** protocol by clicking on its radio button. Select the protocols to make available by using the **Active** checkboxes. For protocols you have created on previous workstation versions (listed under **User Viewing Protocols**), you can check **Delete Protocol**, which deletes the protocol on saving the Preference.

Saving and Applying Preferences

When you are done making changes to a preference, you have the following options:

NOTICE

Before saving, be sure to verify that you have configured the options in all the appropriate worksteps.

- **Save As**: This displays a dialog that allows you to save the changes you have made as a new Preference.
- **Save**: This saves the changes you have made to the preference. To save it as a new preference, type a name in the Preference Name field before clicking Save.

NOTICE

When you save a new preference, that preference can only be accessed by the login you used when you created the preference. If you want the newly saved preference to be accessible by all user logins for the system, include ".shared" at the end of the name. For example, a preference named "CTAC 3 Segment.shared" will be accessible by all users of the system.

The shared preference can only be seen after users log off and then log back into the IntelliSpace Portal client application.

NOTICE

If you make changes to a factory default Preference and Save it, a new user Preference is saved with the same name; the factory Preference remains unchanged. You can also use Save As and save it as a new Preference.

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NOTICE

Save does not apply the changes to the current dataset; for that, use Save Apply (below).

- **Apply**: This applies the current settings to the workstep, but does not save them to the preference.
- **Save Apply**: This saves the changes you have made to the preference, and also applies it to the current dataset.
- **Close**: This closes the Preferences Editor without saving changes.

AutoSPECT Pro Factory Preferences

Here are descriptions of all the factory preferences used in AutoSPECT Pro.

1 Day

This protocol reconstructs gated and summed STRESS and REST cardiac studies without attenuation correction. This default uses FBP with parameters previously established in AutoSPECT Plus for a 1 day protocol.

2 Day

This protocol reconstructs gated and summed STRESS and REST cardiac studies without attenuation correction. This default uses FBP with parameters previously established in AutoSPECT Plus for a 2 day Cardiolite protocol.

Astonish Cardiac CTAC

This protocol reconstructs gated and summed STRESS and REST cardiac studies with and without CT-based attenuation correction. This default uses Astonish for emission data with parameters suitable for cardiac studies.

Astonish Cardiac

This protocol reconstructs gated and summed STRESS and REST cardiac studies without attenuation correction. This default uses Astonish with parameters determined from clinical studies. See the for references.

Astonish Vantage Pro

This protocol reconstructs gated and summed STRESS and REST cardiac Vantage studies with and without attenuation correction. This default uses Bayesian reconstruction for transmission data and Astonish for emission data with parameters determined from clinical studies. See the for references.

Astonish Bone SPECT

This protocol reconstructs bone scans, or general SPECT studies, without attenuation correction. This default uses Astonish with parameters determined by clinical users.

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Bone SPECT

This protocol reconstructs bone scans, or general SPECT studies, without attenuation correction. This default uses FBP with parameters previously established in AutoSPECT Plus.

Astonish Brain SPECT

This protocol reconstructs brain studies without attenuation correction. This default uses Astonish with parameters previously established in AutoSPECT Plus.

Brain Chang AC

This protocol reconstructs brain studies with and without Chang's attenuation correction. This default uses FBP with brain parameters previously established in AutoSPECT Plus.

Brain CTAC

This protocol reconstructs brain studies with and without CT-based attenuation correction. This default uses OSEM with generic parameters.

Brain SPECT

This protocol reconstructs brain studies without attenuation correction. This default uses FBP with parameters previously established in AutoSPECT Plus.

Cardiac CTAC

This protocol reconstructs gated and summed STRESS and REST cardiac studies with and without CT-based attenuation correction. This default uses OSEM for emission data with parameters previously established in AutoSPECT Plus.

Cardiac Vantage Pro

This protocol reconstructs gated and summed STRESS and REST cardiac Vantage studies with and without attenuation correction. This default uses Bayesian reconstruction for transmission data and MLEM for emission data with parameters previously established in AutoSPECT Plus.

Cardiac Reorientation

This protocol reorients previously reconstructed gated and/or ungated cardiac SPECT volumes.

Cardiac Dual Isotope

This protocol reconstructs gated and summed STRESS and REST cardiac studies without attenuation correction. This default uses FBP with parameters previously established in AutoSPECT Plus for a thallium REST, technetium STRESS protocol.

Gated BloodPool SPECT

This protocol reconstructs gated blood pool SPECT images without attenuation correction. This default uses FBP with parameters suitable for gated blood pool SPECT images.

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General Chang AC

This protocol reconstructs general SPECT studies, both with and without Chang's attenuation correction. This default uses FBP with generic parameters.

General CTAC

This protocol reconstructs up to 3 TB SPECT segments concurrently both with and without CT attenuation correction. This default uses OSEM with generic parameters.

General Reorientation

This protocol reorients previously reconstructed non-cardiac SPECT volumes.

General Dual Isotope CTAC

You can use this for concurrently reconstructing two SPECT data sets (e.g., ventilation and perfusion studies, dual isotope studies, etc.) both with and without CT-based attenuation correction. This default uses OSEM with generic parameters.

TB SPECT

This protocol reconstructs up to 6 TB SPECT segments concurrently. This default uses MLEM with no axial filter to minimize knitting artifacts, and no attenuation correction.

Thallium

This protocol reconstructs gated and summed STRESS and REST cardiac studies without attenuation correction. This default uses FBP with parameters previously established in AutoSPECT Plus for a thallium protocol.

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Supplemental Information

- In AutoSPECT Pro, the reorientation positions do not match for the concurrent non-gated and gated SPECT images.

  During the concurrent acquisition setup, it is possible to adjust the roving mask independently between the parent and child acquisitions. Ensure you check all reconstruction and reorientation settings prior to proceeding to the review workstep and confirm the appropriate positioning of the limits, azimuth and elevation.

- There is a difference seen in the Chang’s AC images generated from ICMT versus AutoSPECT Pro. These differences are caused by the following factors:
  - The reconstruction parameters that are used to generate the transverse data are different between the ‘rough’ transverse data created for the AC Map workstep in AutoSPECT Pro and the final transverse images that are generated with the desired parameters that are applied in the reconstruction workstep.
  - The edge-detected ROIs can vary slightly depending on the initial input transverse data.

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- AC Map workstep is unavailable when you are unable to apply Astonish while using the Astonish Vantage Pro preference. The Astonish Vantage Pro preference was specifically generated to perform Astonish on Vantage data. So when you are unable to perform Astonish (when no radial information exists, for example), you should not use the Astonish preference. To perform Vantage reconstruction without Astonish, use the Cardiac Vantage Pro preference instead.
- If legacy data (for example, Vantage) is loaded into the AutoSPECT Pro application on IntelliSpace Portal, the header of the loaded files is updated and these newly updated files are automatically saved to the database. These files are available to another application launched from within AutoSPECT Pro.

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