Clinical Guide

Philips Customer Services Clinical Education

Astonish® SPECT Reconstruction

This is an application guide for the Philips Astonish® SPECT Reconstruction Algorithm

For more detailed information, please refer to the Philips operator or user guide.

Astonish® SPECT Reconstruction:

If you have the Astonish license, Astonish appears as one of the reconstruction methods available within AutoSPECT Pro. The Astonish method consists of performing Ordered Subsets Expectation Maximization with compensation for the blurring effects of your collimator built into the reconstruction. We frequently refer to this compensation as Resolution Recovery, because it allows the recovery of some of the original resolution of the activity distribution. To model the point spread of the activity distribution at the time of acquisition, Astonish uses the distance from the detector to the object of interest recorded as a function of angle by your camera during acquisition, and the geometric properties of the specific collimator used.

When to Use Astonish®:

The accurate modeling performed by Astonish leads to excellent image quality for all images. Philips Healthcare recommends using this method for most nuclear medicine SPECT reconstructions.

Using the Astonish SPECT reconstruction method will enhance the resolution of your SPECT images, and improve the signal-to-noise ratio. The improved noise properties and appearance of the background of your images may change the appearance of the images. Your facility may need to read several Astonish images in order to become comfortable with the appearance of these reconstructed images.

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The image below shows a patient study reconstructed according to typical clinical practice (bottom), and the same study reconstructed with Astonish (top). The improved resolution of the image results in clearer separation, and detail, in the vertebrae. This is especially apparent in fine structures such as the sternum.

Figure 1

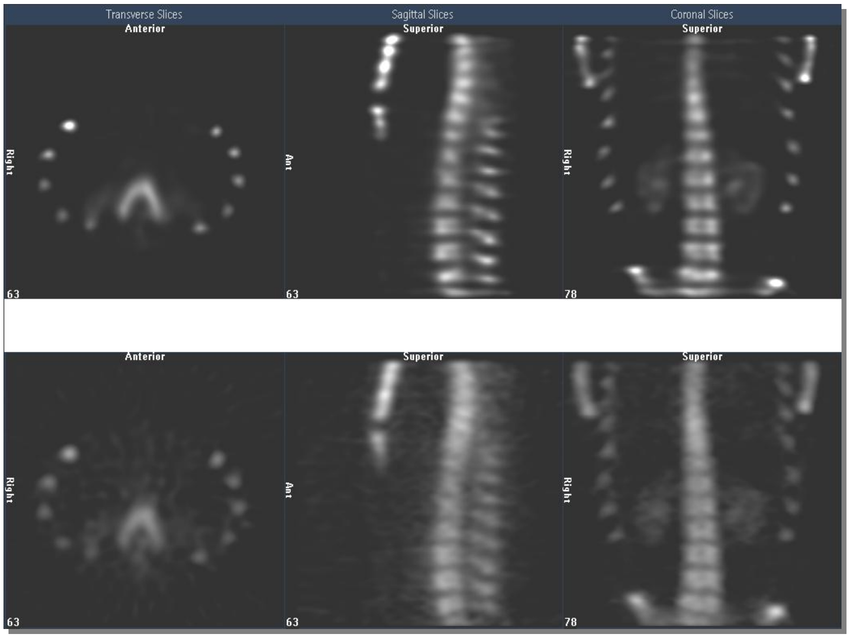

Figure 1 A comparison of Astonish reconstruction (top) with FBP reconstruction (bottom)

***Important**: When using Astonish reconstruction for Cardiac images, use appropriate cardiac normal databases for quantification. Philips Healthcare recommends that you use an Astonish Normal Database that may be supplied with your system. You may also use your cardiac review program to generate your own normal databases specific to your site, your imaging preferences, and your preferred Astonish reconstruction parameters (filtering, AC, scatter correction, etc.).*

Using Astonish® Reconstruction:

You use Astonish in the same way as the other reconstruction methods: by selecting it from the Reconstruction pull-down menu or by using factory supplied Astonish defaults. This section describes how to set reconstruction parameters such as Filtering, Iterations, and Subsets in order to optimize image quality when you use Astonish.

Astonish® Filtering and Noise:

With many iterative reconstruction methods, the noise in the reconstructed image increases with iterations. For this reason, the number of iterations is usually kept small to avoid having an overly noisy image.

Astonish incorporates a patented matched dual filter within the reconstruction to control this accumulation of noise, allowing you to use more total iterations while maintaining an acceptable image. If your images are noisy to begin with - for instance, for gated cardiac datasets, rest perfusion imaging, or for general nuclear images acquired a long time after injection - it can be helpful to use the matched dual filter during reconstruction. For this reason, Philips Healthcare provides you with a Hanning matched dual filter to use with Astonish for noisy, or count-poor, data.

The two images below show the effect of filtering on an Astonish reconstructed image. The left image shows a Maximum Intensity Projection (MIP) display of an Astonish image reconstructed with 4 iterations and 16 subsets, with no filter. The right image shows a similar display of an image reconstructed with the same parameters, but including a Hanning filter with a cutoff of 1.0. The image has become smoother without losing the fine detail available as a result of the Astonish reconstruction.

Figure 2

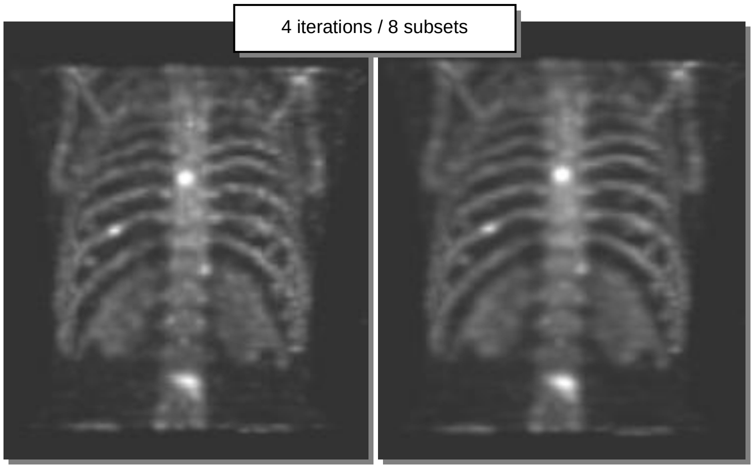

Figure 2 Astonish reconstructions without Hanning filter (left) and with Hanning filter (right)

The effect of filtering can also be seen in the cardiac images that follow. A myocardial perfusion scan was processed with 4 iterations and 8 subsets and only the Hanning filter cutoff was modified. Notice that the higher the cutoff, the sharper the image.

Figure 3

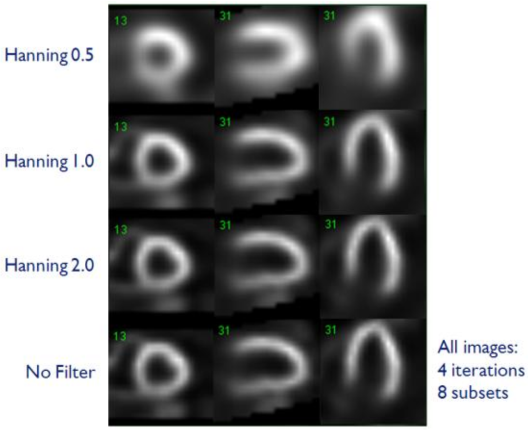

Figure 3 Astonish reconstructions (4 iterations/8 subsets) with Hanning filter cutoff of 0.5, 1.0, 2.0 and no filter.

Astonish® Iteration and Subsets:

To take full advantage of the resolution recovery provided with Astonish SPECT reconstruction, the expectation maximization algorithm must converge, which requires a large number of updates to the activity estimation.

For MLEM, the number of updates is identical to the number of iterations, for OSEM, the subsets and iterations are multiplied together to calculate the total number of updates. The higher this number of updates, the more likely the software is to have achieved convergence.

Although it is possible to achieve an acceptable nuclear medicine reconstructed image, using 2-3 iterations and 8-16 subsets, even better resolution may be achieved by iterating more. This may cause processing times to be extended, so your site must determine the acceptable number of iterations.

Philips Healthcare recommends starting from a Uniform estimate and using at least 24 updates for most nuclear medicine data, which can be achieved by performing 3 iterations with 8 subsets as a starting point.

The three images below show the effect of iteration number on an Astonish reconstructed image. The left image shows a Maximum Intensity Projection (MIP) display of an Astonish image reconstructed with 2 iterations and 16 subsets, with no filter. The center image was reconstructed with 3 iterations, and the far right image with 4 iterations. More fine detail becomes available with additional iterations, but the images also become noisier.

Figure 4

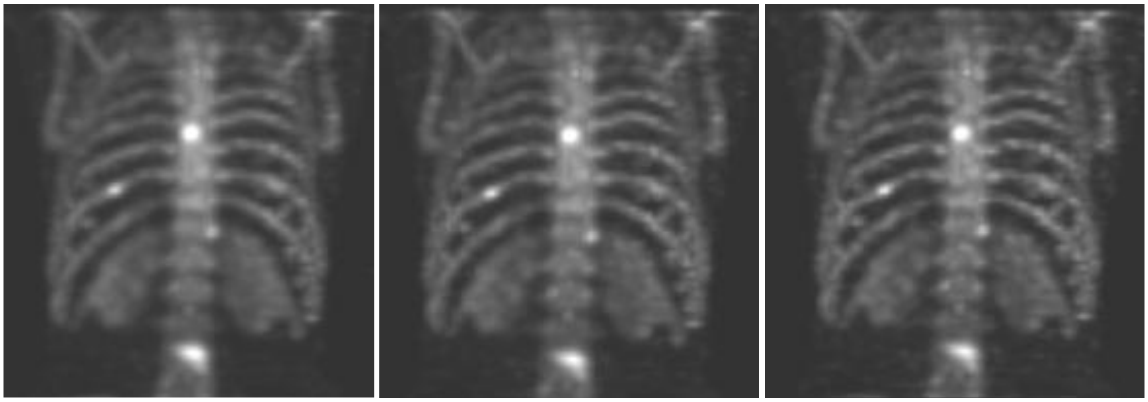

Figure 4 Astonish reconstruction with 2 iterations (left), 3 iterations (center), and 4 iterations (right). All three reconstructions used 16 subsets with no filter.

The cardiac images below also demonstrate the effect of changing iterations. The MPI scan was reconstructed with Astonish using no Hanning filter and keeping the number of subsets fixed at 8. Only the number of iterations was changed. (Remember: Iterations X Subsets = Updates)

Figure 5

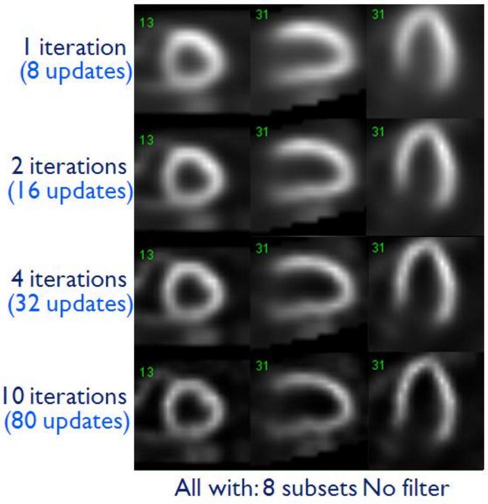

Figure 5 Astonish reconstruction with no filter and the same number of subsets (8) but with 1 iteration, 2 iterations, 4 iterations and 10 iterations.