

## Finding the Center of the Left Ventricle

Prior to finding the endocardial and epicardial surfaces of the left ventricle (LV), the center ( $x_c, y_c, z_c$ ) and axial limits ( $z_{\text{apical}}, z_{\text{basal}}$ ) of the LV need to be determined. To find  $x_c$  and  $y_c$ , a summed image from the axial mid third of the short axis (SA) image volume is made. The initial estimate for  $x_c$  is the first moment of a linegram constructed from the upper half of this summed image. The initial estimate for  $y_c$  is the first moment of a linegram constructed from the right 5/8 of this summed image (columns 24-64 for a 64x64 image matrix). Using these seeds as the center of an 8x8 neighborhood, the final estimates for  $x_c$  and  $y_c$  are assigned by fitting an ellipse to the radial information from the circumferential profile analysis. For the axial estimates ( $z_c, z_{\text{apical}}, z_{\text{basal}}$ ), a linegram involving only the anterior portion of the mid axial slice down to the  $y_c$  estimate is used. A threshold of 55% of max activity is applied to the linegram, from which the  $z_{\text{apical}}$  and  $z_{\text{basal}}$  are determined. The value for  $z_c$  is the integral midpoint between  $z_{\text{apical}}$  and  $z_{\text{basal}}$ .

In Corridor4DM, an intuitively easy interface is provided so that the user can adjust the center and axial limits, if they are considered to be in error.

## Left Ventricular Surface Detector

Knowing the center and axial limits for the left ventricle, long axis (LA) images are created using bilinear interpolation from the SA volume. These images are created every  $5^\circ$  from 3:00 in clockwise direction (36 images total). The LA images are centered in-plane based on the Corridor4DM or user defined  $x_c$  and  $y_c$  values. Since the variable  $z_c$  is only permitted integer values, the LA images are not precisely centered axially and there is no interpolation in this dimension. This was done to have one-to-one correspondence between axial location in LA space and the SA slice number.

For this geometry, the program creates the sampling structure based on a cylindrical-spherical coordinate system. The cylindrical coordinate system is used to sample the LV from the basal to distal aspects, approximately 75% of the length of the LV. The spherical coordinate system is used to sample the apex. In plane angular sampling for both the cylindrical and spherical systems is done in  $5^\circ$  increments. Azimuthal sampling in the spherical system is performed in  $10^\circ$  increments.

The LV surface detector uses a 2D gradient image to determine initial estimates for the endocardial and epicardial surfaces. Weights based on activity, motion, and consistency of the endo- and epicardial surface estimates in space and time are assigned. A series of one- and two-dimensional weighted splines are used to refine the surfaces estimates. Since splines insure the continuity of the first derivative, the natural curvature of the myocardium is preserved even in the presence of large severe perfusion defects. Using the new surface estimates, threshold values as a function of position are determined and used in conjunction with a morphological operator to create a segmented image of the LV volume. The segmented image is used for contiguity information in updating the spline weights, and the spline interpolators are applied again to better refine the surface estimates utilizing the contiguity information. With the new surface estimates, the LV wall activity is fitted to a Gaussian function to estimate the mid wall position and thickness. For gated studies, the volume curve is estimated to determine the end-diastolic (ED) and end-systolic (ES) frames. The average FWHM value for ED is used to determine the physical wall dimensions and is scaled to be an average thickness of 10mm. Wall thickness estimates for the remaining frames in the R-R cycle are adjusted based on the wall thickness scale factor used at ED, and myocardial mass is conserved. For ungated studies, the average wall thickness is assigned to be 15mm. The spline interpolating functions are used a final time to provide smooth estimates for the endocardial, epicardial and wall thickness estimates.

Surface estimates vary depending on the location of the LV center and apical limit as defined on the SETUP page. To decrease this dependence and variability, Corridor4DM iteratively finds the LV surfaces and refines the position of the LV center and apical limit using the ungated frame. The steps are as follows

- Retrieve seeds for LV center and axial limits from SETUP page
- Find surfaces
- Find LV center by fitting an ellipse to the mid-ventricular surface estimated for the mid-SA slice. Find apical limit from mid-ventricular surface estimated for the mid-VLA slice.
- If LV center has changed by  $> 0.01$  and we have not exceeded the 5 iterations, go to step 2
- Surfaces estimation is complete.

The additional processing time is approximately 1-2 seconds per study.

## Functional Assessments (Volumes and Ejection Fraction)

Using the endocardial surface estimates, LV volumes are calculated for each frame or gate interval. The end-systolic (ES) frame is the frame where the LV volume is a minimum while the end-diastolic (ED) frame has the maximum LV volume. The LV ejection is computed from  $100\% * (ED \text{ vol} - ES \text{ vol}) / ED \text{ vol}$ .

## 3D Sampling Template

The 3D sampled data are (x,y,z) locations of the endocardial and epicardial surfaces for each gating interval. Sampling starts at the lateral wall (3:00) and proceeds clockwise. Axial sampling goes from apex to base. There are 12 axial samples or rings and angular sampling is in 15° increments.

## Polarmap Sampling Template

For all polarmap data (i.e. perfusion, wall thickening, wall motion), the polarmap sampling starts at the mid lateral wall (3:00) and proceeds clockwise. Axial sampling goes from base to apex and is equidistantly sampled along the length of the mid-ventricular surface from base to apex. There are 15 axial samples or rings to the polarmap. Rings 1 through 12 have angular samples at 10° increments. Rings 13,14, and 15 are sampled at 20°, 40° and 360°, respectively. There are 460 total sectors in a polarmap.

## Perfusion Polarmap Generator

Using the template defined by Polarmap Sampling Template, perfusion polarmaps are created from the heart volume by radial sampling the maximum value within the myocardium defined by the endo- and epicardial surfaces at each sector position (n=460).

## Wall Thickening Polarmap Generator

Using the template defined by Polarmap Sampling Template, wall thickening polarmaps are created from perfusion polarmaps created at each gating interval. At each sector, the wall thickening is defined as the relative difference between the polarmap values sampled at end-diastole and the max perfusion value sampled from all frames. The max perfusion values typically occur within +/- 1 frame of the end systolic (ES) frame. It is very rare that the max value occurs outside of this frame range. At each sector  $i$  in the polarmap template, wall thickening is defined as:

$$WTHK[i] = 100\% * (MAX[i] / ED[i] - 1);$$

where

MAX[i] is the max perfusion value at sector  $i$  found over all gating frames.

ED[i] is the perfusion value at sector  $i$  for the ED frame.

The following constraints are also imposed on the WTHK[i] values:

- if any sector value for ED[i] is less than 10% of the peak value found in the heart from any gated frame, WTHK[i] is set to 3%.
- if WTHK[i] as defined above is found to be negative, it is set to 0%.

The final step is a 5x5 kernel [1,1,1,1,1] smooth of the WTHK[i] data.

## Wall Motion Polarmap Generator

Using the template defined by Polarmap Sampling Template, the wall motion polarmap is estimated from the 3-D LV surfaces using a 3-D extension of the centerline method used in contrast ventriculography.

## Polarmap Normalization

Perfusion polarmaps are normalized to 100% peak activity by finding the maximum regional activity in a region consisting of 2 rings by 50° between the basal and distal rings. Rings 13,14,15 are excluded from this search. Wall thickening and wall motion polarmaps are never normalized.

For Perfusion database comparison, there are two options.

- 1) Find regional peak as defined above and normalize to 100%.
- 2) Find regional peak as defined above and normalize to the peak in the database for the same region.

Method (1) is the default. Method (2) can be used by setting PmapDefectNorm=1 in the preferences file. There currently is no GUI for setting this parameter.

For wall thickening and wall motion database comparison, there is no normalization. The comparison is made in absolute units.

## Raw Polarmap Types

The 4D-MSPECT application supports the following raw data types

- Ungated, ED and ES Perfusion
- Wall Motion
- Reversibility
- DIFF12
- Washout
- Wall Thickening
- 2-study Comparison Maps
- Viability
- DIFF21
- T ½

The raw polarmap is always displayed on the RAW panel on the Polarmaps screen and on the Imgs+Scores screen. The characteristics of the raw maps for perfusion, wall thickening and wall motion are defined in the following table.

**TABLE 1: RAW POLARMAP PROPERTIES**

Raw Data Type	Computation	Display Range
Perfusion (Ungated, ED, ES)	See Polarmap normalization	The display range is (0,max) where max is the maximum value in the polar map. The data is in units of reconstructed intensities.
Wall Thickening	See Wall Thickening Polarmap Generator	The display range is (0,100%). All display values greater 100% are set to 100%. This range limit affects only the displayed polar map, it does not affect the raw data used in subsequent calculations (i.e. database comparison).
Wall Motion	See Wall Motion Polarmap Generator	The display range is (-3mm, 9mm). All display values less than -3mm are set to -3mm, and all values greater than 9mm are set to 9mm. This range limit affects only the displayed polar map, it does not affect the raw data used in subsequent calculations (i.e. database comparison).

The raw polarmap can also be displayed on the Polarmaps screen in the DB-Comparison panel by selecting the “Raw” option from the DB-Comparison menu. The display range and units as defined above applies to this map and the generated regional statistics.

**TABLE 2: DB-COMPARISON MAP PROPERTIES**

Type	Perfusion	Wall Thickening	Wall Motion
Norm	Computation: See Polarmap Normalization Display Range: (0,100%)	Computation: Map is not normalized. Display Range: (0,100%)	Computation: Map is not normalized. Display Range: (-3mm,9mm)
Severity	Computation: See Polarmap Severity Maps Display Range: (-10σ,10σ)		
Blackout	Computation: See Polarmap Blackout Maps		
	Display Range: (0,100%)	Display Range: (0,100%)	Display Range: (-3mm,9mm)  NOTE: Any wall motion ≤ 0mm is considered abnormal regardless of the defect threshold.
Defect Severity	Computation: See Polarmap Defect Severity Maps Display Range: (0,10σ)		
DB Mean	Computation: This is independent of the raw data type. The values represent a measurement of the mean for the database population at each sampled sector position.		
	Display Range: (0,100%)	Display Range: (0,100%)	Display Range: (-3mm,9mm)
DB StDev	Computation: This is independent of the raw data type. These values represent a measurement of the square root of the variance for the database population at each sampled sector position. Display Range: (0,10σ)		

## DB-Comparison Maps

### POLARMAP SEVERITY MAPS

Using a normal database providing mean (mean) and standard deviation (stdev) data, severity values are computed for each polarmap sector,  $i$ , from

$$\text{severity}[i] = (\text{mean}[i] - \text{pmap}[i]) / \text{stdev}[i];$$

The intensity of the severity values are in units of standard deviations. Positive severity values represent areas that are less than the mean (i.e. increasingly abnormal), while negative values represent areas that are greater than the mean (i.e. normal).

### POLARMAP DEFECT SEVERITY MAPS

Using the Polarmap Defect Thresholds page in the Preferences Dialog, the user defines regional defect thresholds,  $D[j]$ , in units of standard deviations below the normal database mean. The user defined regional defect thresholds are then interpolated to  $DT[i]$  to match the polarmap sampling template, where  $i$  is the sector in the polarmap template. Using a normal database providing mean (mean) and standard deviation (stdev) data, defect limits are computed for each polarmap sector,  $i$ , from

$$\text{defect\_limit}[i] = \text{mean}[i] - DT[i] * \text{stdev}[i];$$

Given polarmap data for each sector  $\text{pmap}[i]$ , a defect severity map is computed using the following

$$\begin{array}{ll} \text{severity}[i] & = 0 & \text{for } \text{pmap}[i] > \text{defect\_limit}[i] \\ & = (\text{mean}[i] - \text{pmap}[i]) / \text{stdev}[i]; & \text{for } \text{pmap}[i] \leq \text{defect\_limit}[i] \end{array}$$

So a defect severity will display normal sectors as black and the intensity of the defect sectors will be proportional to its severity in units of standard deviations.

### POLARMAP BLACKOUT MAPS

Using the Polarmap Defect Thresholds page in the Preferences Dialog, the user defines regional defect thresholds,  $D[j]$ , in units of standard deviations below the normal database mean. The user defined regional defect thresholds are then interpolated to  $DT[i]$  to match the polarmap sampling template, where  $i$  is the sector in the polarmap template. Using a normal database providing mean (mean) and standard deviation (stdev) data, defect limits are computed for each polarmap sector,  $i$ , from

$$\text{defect\_limit}[i] = \text{mean}[i] - DT[i] * \text{stdev}[i];$$

Given polarmap data for each sector  $\text{pmap}[i]$ , a blackout map is computed using the following

$$\begin{array}{ll} \text{blackout}[i] & = \text{pmap}[i] & \text{for } \text{pmap}[i] > \text{defect\_limit}[i] \\ & = 0; & \text{for } \text{pmap}[i] \leq \text{defect\_limit}[i] \end{array}$$

So a blackout map will preserve normal sectors and display defect sectors as black.

## 2-Study Comparison Maps

The following 2-study comparison maps are supported

- Reversibility
- Viability
- DIFF12
- DIFF21
- Washout
- T  $\frac{1}{2}$

Two-study comparison maps are computed for all raw data types, perfusion (ungated, ED and ES), wall thickening and wall motion. By definition, reversibility is specific to perfusion data; thus, reversibility maps do not apply to the wall thickening and wall motion. To handle this, 4D-MSPECT will compute the absolute difference maps DIFF21 for reversibility.

### REVERSIBILITY

**Raw Map:** In computing raw perfusion reversibility, the stress and rest perfusion polarmaps are normalized and the normalized stress map is subtracted from the rest map. In the normalization process, the regional maximum is found in the stress map and the central sector for that region is noted. The regional max in the rest map is determined at the central sector from the stress map. The rest map is then normalized to the regional maximum of the stress map, and the raw reversibility map is the difference of the rest - stress map.

NOTE: For wall motion and wall thickening, raw reversibility is the absolute difference between the rest and stress maps.

**Norm Map:** Reversibility maps are not normalized. The normalized reversibility map is equal to the raw reversibility map.

**Blackout:** For the blackout reversibility map where reversible regions are displayed in a white cross-hatched pattern, only defect sectors in the stress map are checked. If the raw reversibility value in a stress defect sector is  $>$  the reversibility threshold, then the sector is considered reversible and is displayed in a white cross-hatch pattern. If it is  $\leq$  the reversibility threshold, the defect is considered fixed and is assigned a value of 0 (black).

**Defect Severity:** For the severity reversibility map, the algorithm for determining reversible regions applies. In the display of a severity reversibility map, reversible regions are also displayed as white cross-hatched regions, but fixed defect sectors are displayed in units of severity, the number of standard deviations the sector is below the normal mean.

### VIABILITY

An FDG image set is assumed to be input for the viability study.

**Raw Map:** The FDG polar map distribution is normalized to 100% in the location where the stress study's intensity is a maximum.

**Norm Map:** Same as raw map.

**Blackout:** For the blackout viability map where viability regions are displayed in a white cross-hatched pattern, only defect sectors in the stress map are checked. If the raw viability value in a stress defect sector is  $>$  the viability threshold, then the sector is considered viable and is displayed in a white cross-hatch pattern. If it is  $\leq$  the viability threshold, the defect is considered fixed and is assigned a value of 0 (black).

**Defect Severity:** For the defect severity viability map, the algorithm for determining viable regions applies. In the display of a defect severity viability map, viable regions are also displayed as white cross-hatched regions, but fixed defect sectors are displayed in units of severity, the number of standard deviations the sector is below the normal mean.

### DIFF12

**Raw Map:** In computing raw DIFF12, Study\_1 and Study\_2 perfusion polarmaps are normalized independently and the normalized Study\_2 is subtracted from normalized Study\_1 map. Unlike the reversibility calculation, the two maps are not normalized to the same spatial sector.

NOTE: For wall motion and wall thickening, raw DIFF12 is the absolute difference between the Study\_1 and Study\_2 maps.

**Norm Map:** DIFF12 maps are not normalized. The normalized DIFF12 map is equal to the raw DIFF12 map.

**Blackout:** Since a value of 0 is normal for a DIFF12 map and defect sectors are sectors whose value is GREATER than the defect threshold, a modification was made for the DIFF12 blackout maps compared to the procedure described in Polarmap Blackout Maps. For sectors that are  $\leq$  defect thresholds, the sector is set to the defect threshold to signify normal. Sectors  $>$  than the defect threshold are set to 0 (black). Thus, with the displayed data does not preserve any of the normal values from the raw DIFF12 map.

**Defect Severity:** For the severity DIFF12 map, sectors that are  $>$  the defect threshold are set the number of standard deviations the sector value is above the database mean. For sectors that are  $\leq$  the defect threshold, the sector is set to 0 to signify normal.

### DIFF21

This difference map is identical to the DIFF12 map with the exception that  $\text{DIFF21} = \text{Study}_2 - \text{Study}_1$  while  $\text{DIFF12} = \text{Study}_1 - \text{Study}_2$ .

### WASHOUT

**Raw Map:** In computing raw washout, Study\_1 and Study\_2 perfusion polarmaps are normalized independently based on acquisition duration time and Study\_1 is scaled for decay to time of Study\_2. After time and decay normalization, a washout value for each polar map sector  $i$  is calculated as follows

$$\text{washout}[i] = 100\% * (\text{Study}_1[i] - \text{Study}_2[i]) / \text{Study}_1[i]$$

NOTE: If the acquisition duration time for either study is not known, a washout map will not be estimated.

**Norm Map:** Normalization for the washout map is identical to the normalization for perfusion maps. See Polarmap normalization

**Blackout:** Blackout maps are calculated in the same manner used for perfusion maps.

**Defect Severity:** Blackout maps are calculated in the same manner used for perfusion maps.

**T  $\frac{1}{2}$** 

**Raw Map:** In computing a T  $\frac{1}{2}$  map, Study\_1 and Study\_2 perfusion polarmaps are normalized independently based on acquisition time. After time normalization, a T  $\frac{1}{2}$  value for each polar map sector i is calculated as follows

$$T_{1/2}[i] = \ln(2.0) * \text{deltaT} / \ln(\text{Study\_1}[i] / \text{Study\_2}[i]) \text{ (for Study\_1}[i] > 0 \text{ and Study\_2}[i] > 0)}$$
$$= 0 \text{ (for Study\_1}[i] \leq 0 \text{ or Study\_2}[i] \leq 0)}$$

where

**deltaT** is the time in minutes between acquisition start times for Study\_1 to Study\_2.

T  $\frac{1}{2}$  maps are not computed if any of the following are true

1. deltaT < 0
2. Acquisition start times are not known for either study
3. Acquisition duration times are not known for either study.

**Norm Map:** T  $\frac{1}{2}$  maps are not normalized. The normalized T  $\frac{1}{2}$  map is equal to the raw T  $\frac{1}{2}$  map.

**Blackout:** Blackout maps are calculated in the same manner used for perfusion maps Polarmap Blackout Maps.

**Defect Severity:** Blackout maps are calculated in the same manner used for perfusion maps Polarmap Defect Severity Maps.