# Standard operating procedure for cardiac DCE-MRI (at rest) analysis using PMI

1. Save new study file in the folder of a participant study > new. Name the file "studyID.pmi"

2. Import DICOM files from same study participant data folder: Series > Import > DICOM. After import is finished a window appears which says 'Please select which series to load'. Select motion corrected images of mid-short axis slices at rest and click OK. Loading will begin.
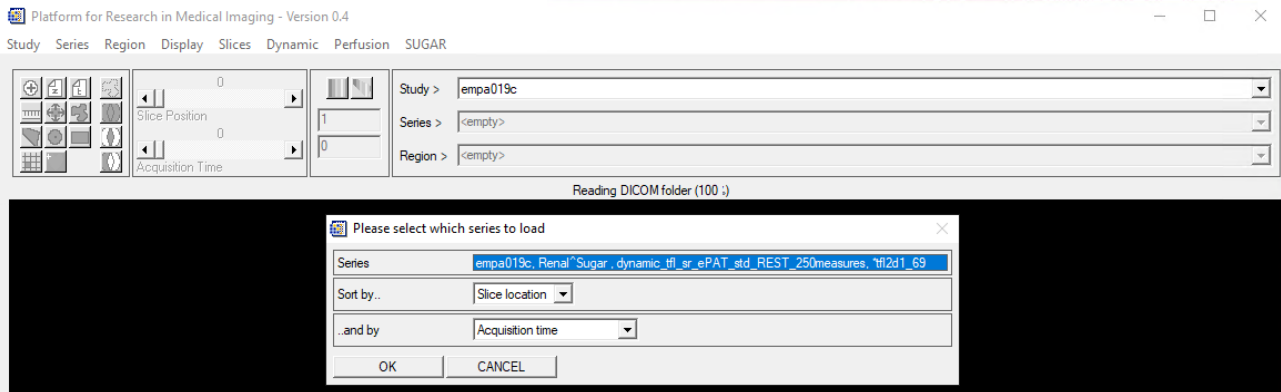


3. Find the Acquisition Time (# of dynamics) to contrast arrival:
   a. Alter # until contrast first arrives in left ventricle (LV) blood pool, then make a note of corresponding Acquisition Time (e.g. # 32 = 45 seconds in example)
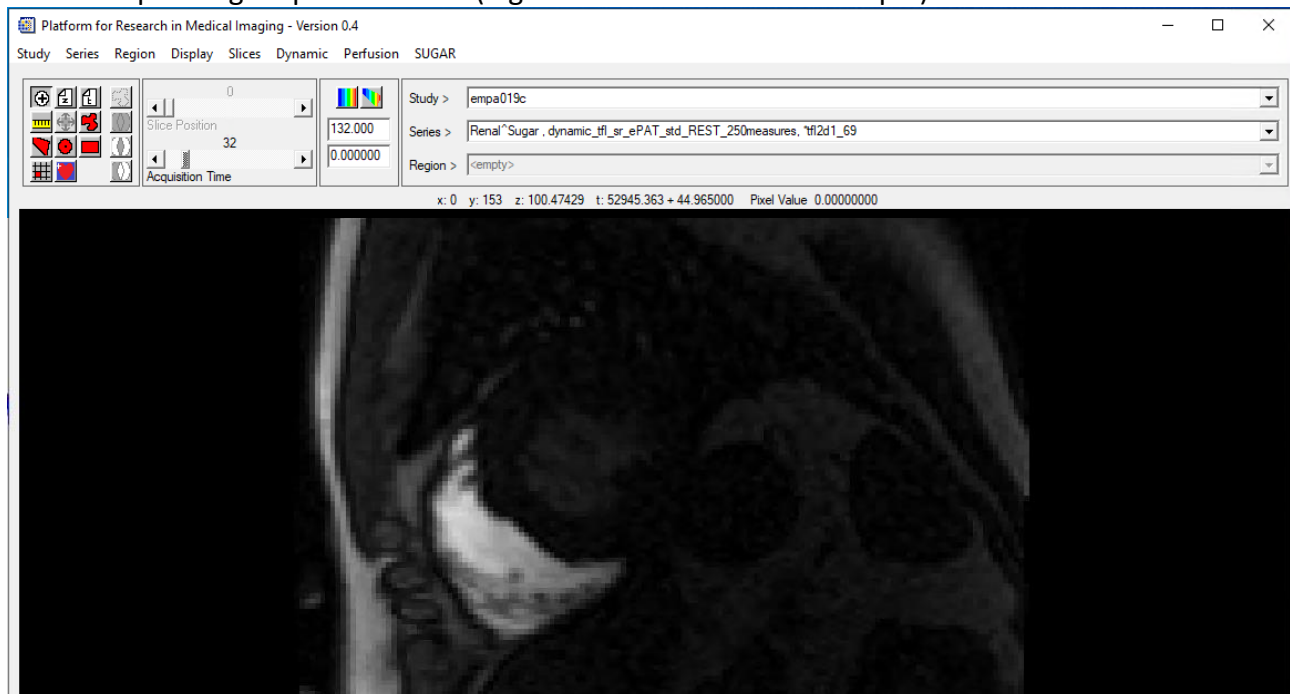


   b. Reduce # until LV blood pool turns black just prior to contrast arrival
   c. Go to # 20 to double check absence of contrast in LV blood pool
   d. If above check is satisfactory, we will fix baseline at # 20

4. **Crop # of dynamics (minimizes poor motion correction):** Select Series > Extract:
   a. Take t from index: # 2 (fixed value – avoids any problematic values at # 0 / # 1)
   b. Take t until index: # corresponding with time of contrast first arriving in LV blood pool + 60 secs (e.g. # 78 = 105 seconds in example)
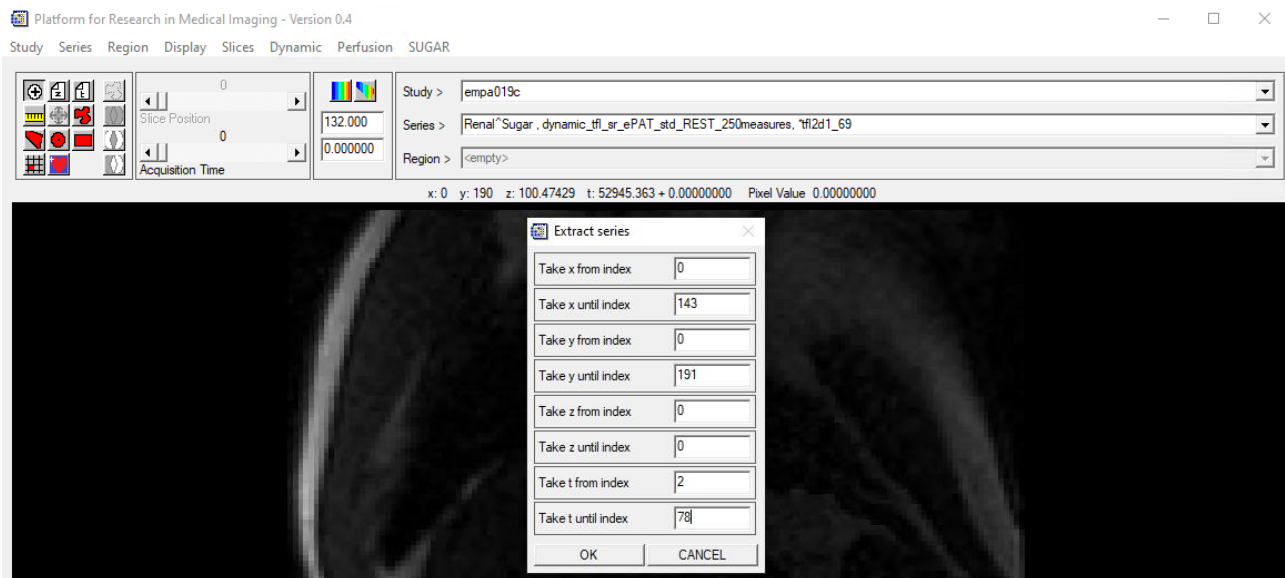
c. Rename Series (e.g. 'DCE_t78=105s' in example)

5. **Calculation of descriptive parameter maps**: Select SUGAR > Cardiac: Descriptive parameter maps > a window appears (shown below). The length of baseline will be fixed at # 20. Click OK, a calculation occurs and three parameter maps [Area under the Curve (a.u. *sec), Area:Maximum (sec), Maximum (a.u.)] appear in the Series dropdown menu.
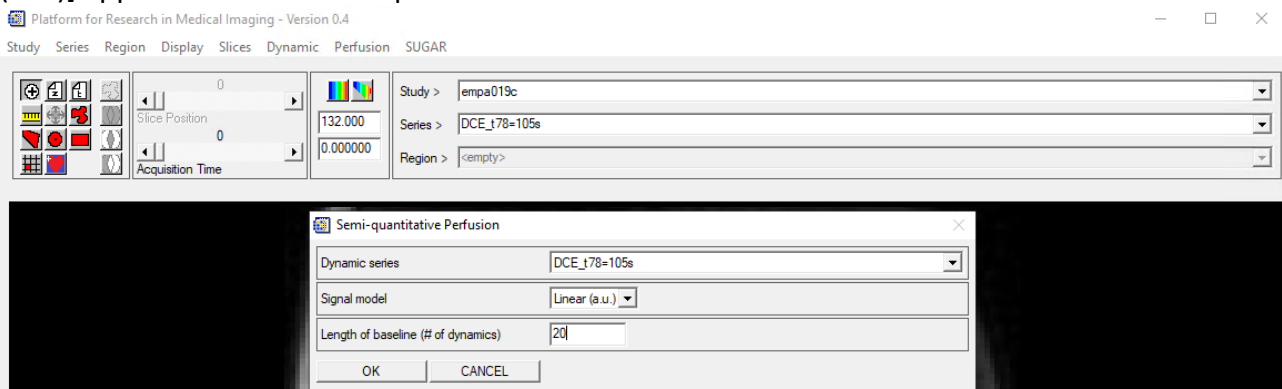


6. **Determination of ROI for arterial input function (AIF)**: Select cropped dynamic series 'DCE_t#=***s[Area under the Curve (a.u.*sec)]' from Series dropdown menu. Select Region > Threshold. A window appears as shown below.
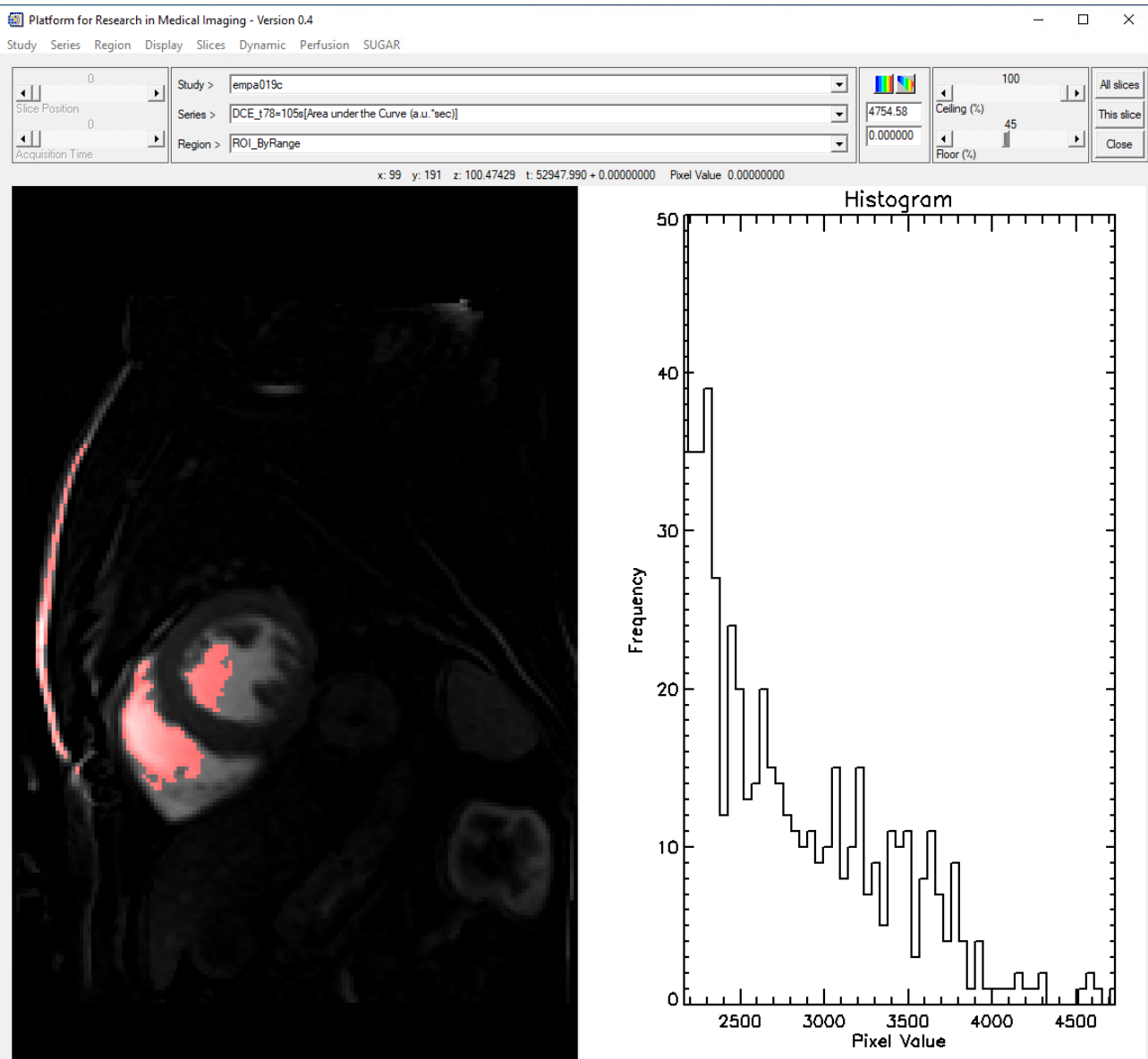
Adjust Ceiling to 100. Adjust Floor so that red region fills LV blood pool (but not LV myocardium) > click 'This slice' > click 'Close'. A new region appears in the Region dropdown menu, rename it as AIF. Click 'Polygon Region' ▼ then click 'select from region' ◐ and outline LV blood pool as shown.
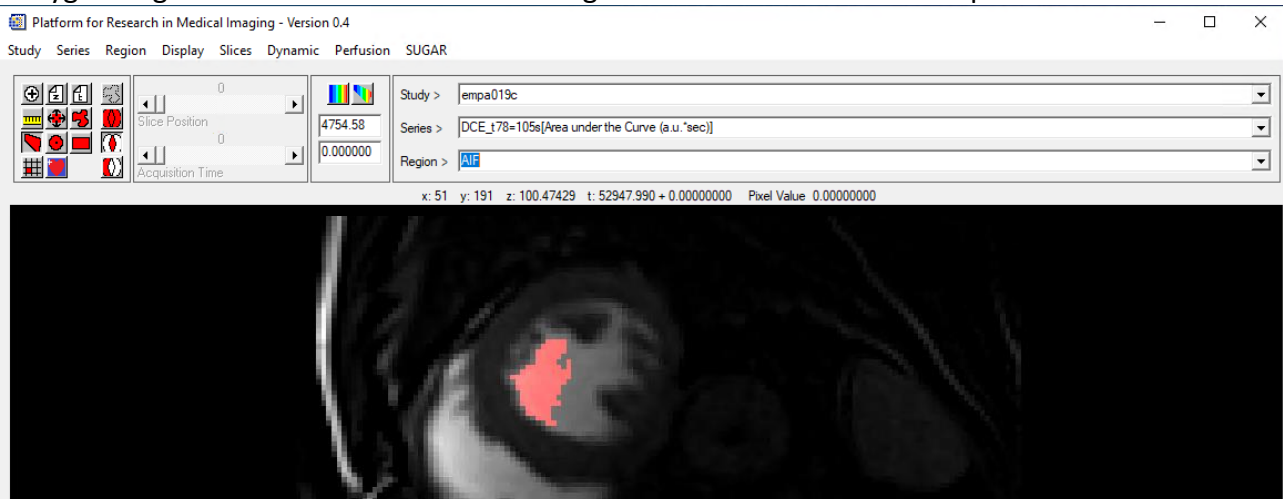


7. **Calculation of perfusion parameter maps**: Select SUGAR > Cardiac: Perfusion parameters maps > a window appears. Choose parameters as shown below. A calculation occurs and three new series for perfusion parameters [Extracellular Volume (ml/100ml), Mean Transit Time (sec), Blood Flow (ml/min/g)] appear in the Series dropdown menu.
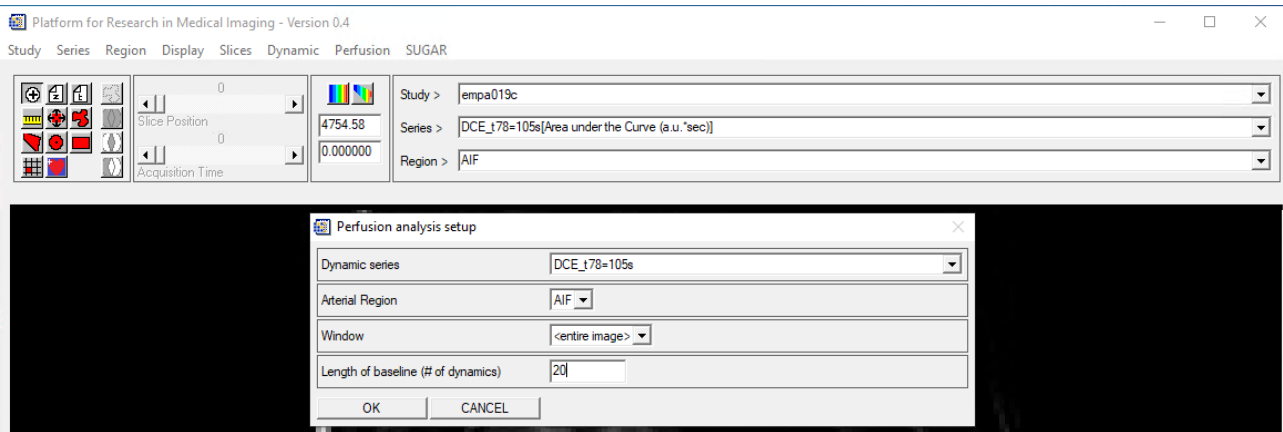
8. **Determination of myocardial ROI:** Select '1C: Blood Flow (ml/min/g)' from Series dropdown menu. Click 'Zoom (Rectangle)' ⊕ then draw rectangle around LV myocardium to zoom. Click 'Polygon Region' ◤ and outline outer ring as shown below. Rename new red region as 'MYO'in Region dropdown menu.
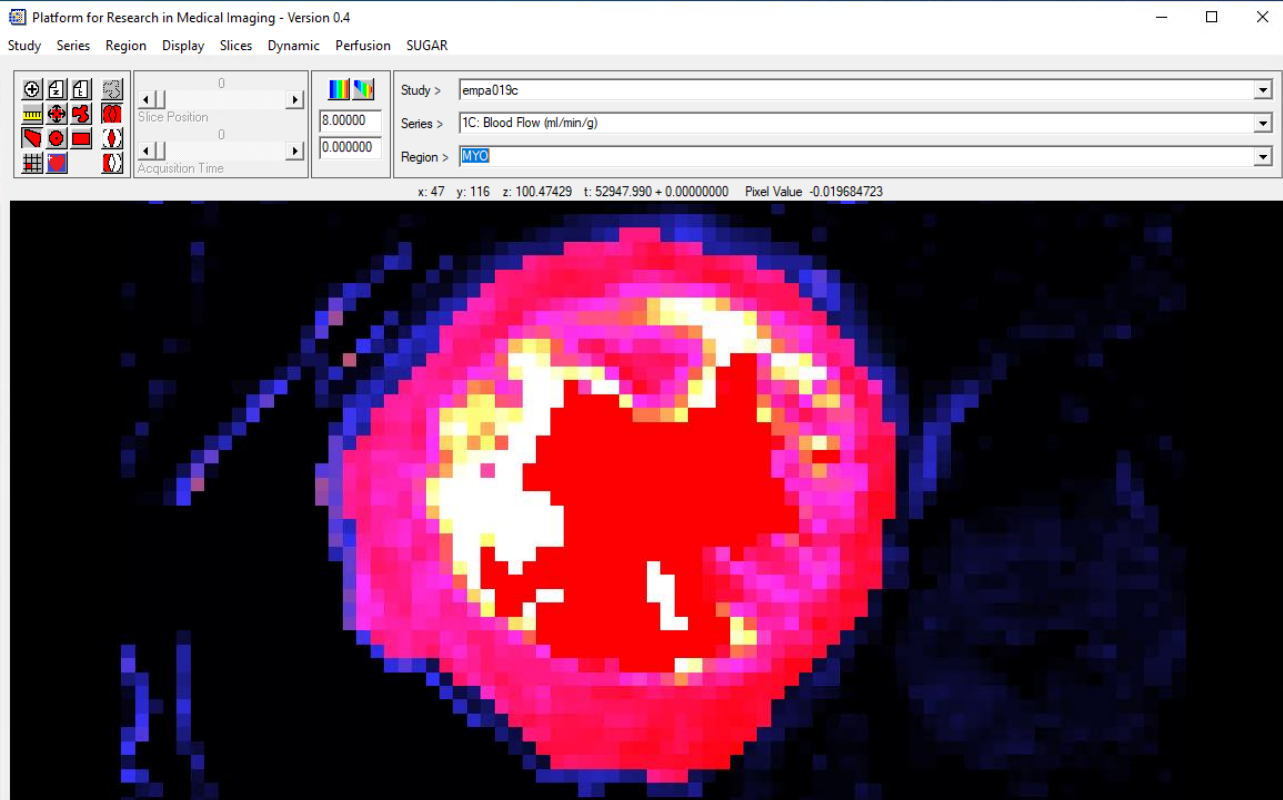


Click on 'Remove from Region' ◑ and outline LV blood pool to remove it:
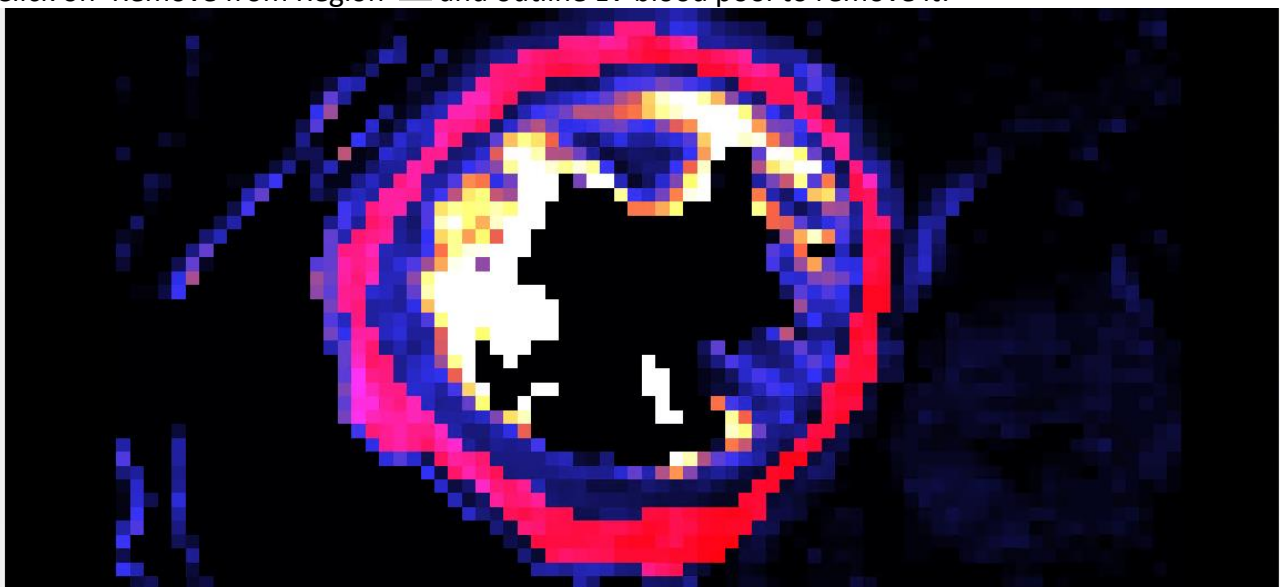
Optional steps to assess quality of motion correction: Select 'DCE_t#=***s' from Series dropdown menu. Adjust windowing. Region > Extrude > a window appears (keep default settings as shown).
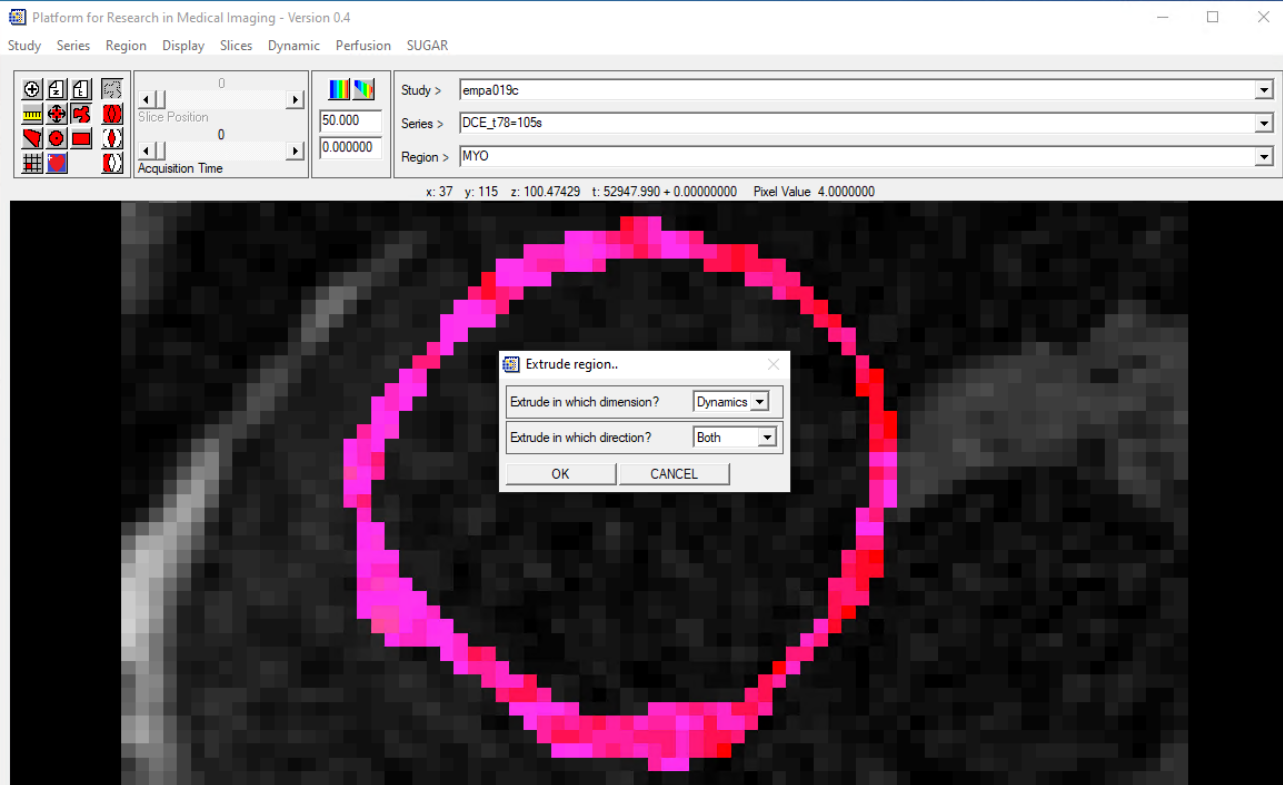


New region 'MYO[Extrude]' is created across all acquisition times. Alter 'Acquisition Time' # to review 'MYO[Extrude]' fit and if required, adjust with 'Shift Region' ✛.

9. **Determine AHA segmentation and calculate segmental mean & median of parameters**: Select '1C: Blood Flow (ml/min/g') from Series dropdown menu > click 'AHA segmentation' ❤ > click on image at LV-RV insertion point. ROI divides into 6 segments; mean & median of blood flow calculated over these segments are written in a folder within parent folder. Repeat for other parameters.
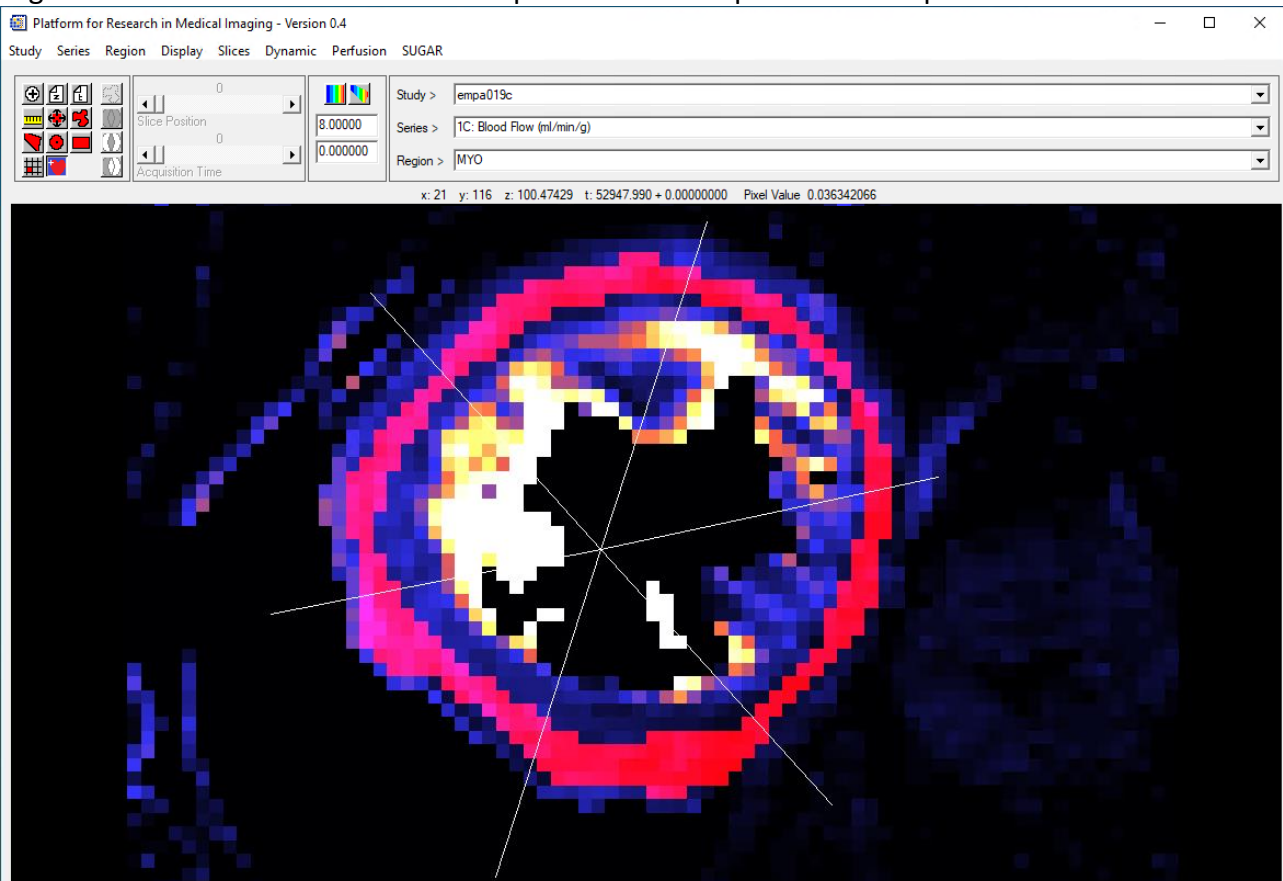
10. **Permeability calculations**: Select SUGAR > Cardiac: Perfusion ROI compartment models > a window appears. Select series, regions and other parameters as shown below. If extruded myocardium was adjusted, select 'MYO[Extrude]' instead of 'MYO' in Tissue Region. The default hematocrit of '0.45' can be used at this stage - a correction formula can be applied later to adjust to actual hematocrit.
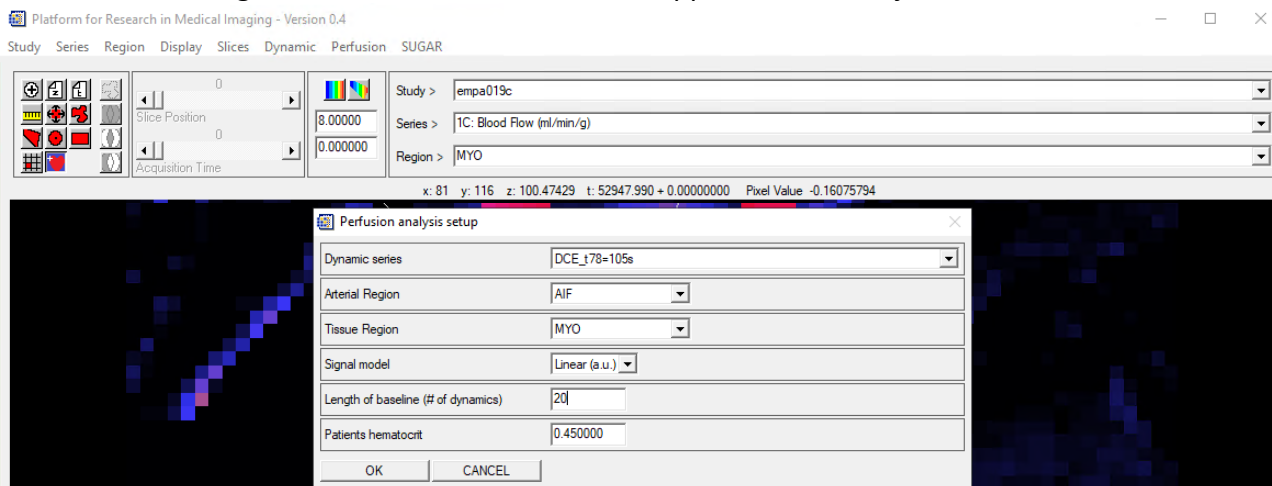


Click OK, output will appear on screen. Change model to 'Compartment' in 'FIT' window (NB: '2C Uptake' model can be used for <u>stress</u> perfusion). Click checkbox 'Delay' (incorporates time it takes for contrast to travel from LV blood pool to LV myocardium) which might improve model fit.
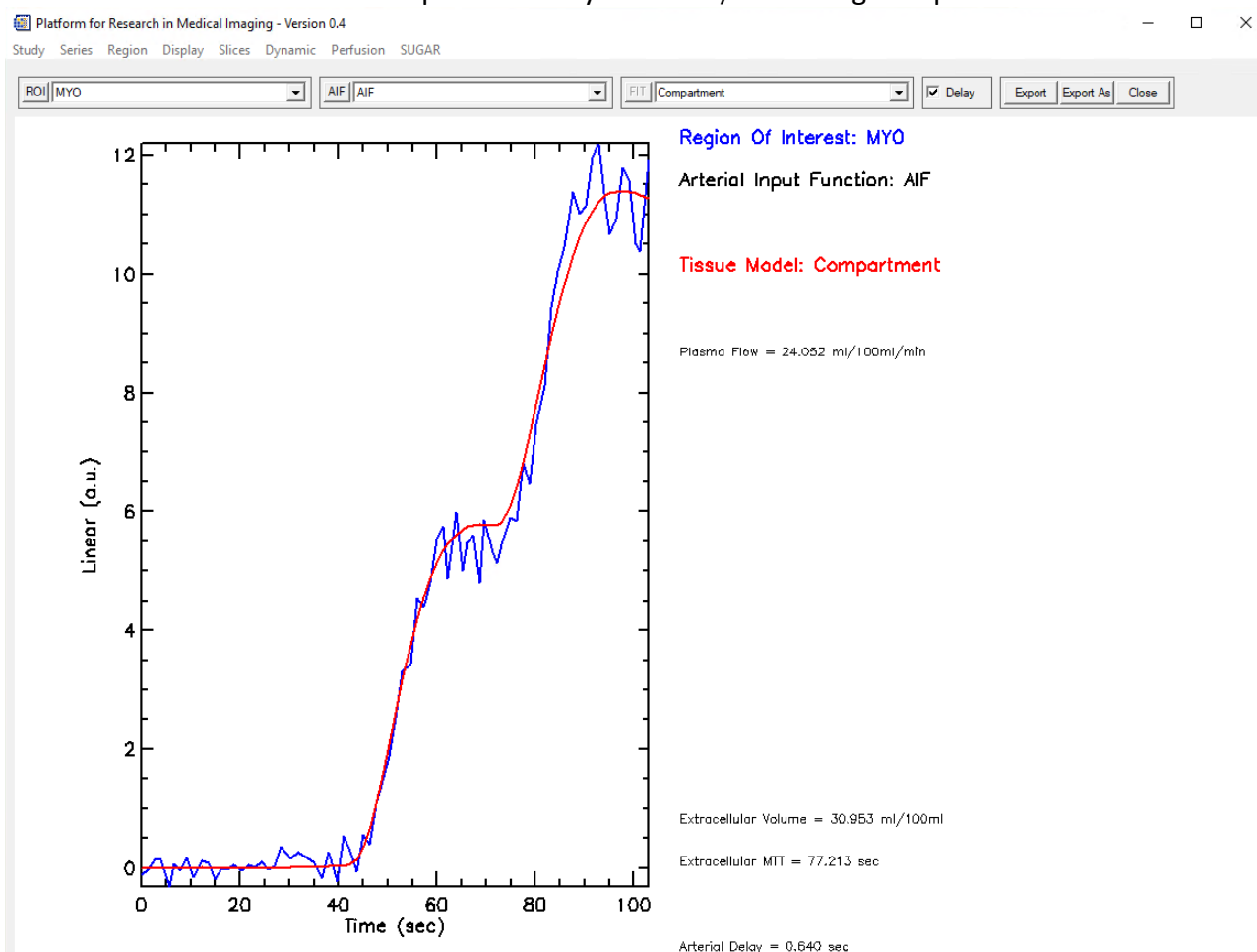


**Assess for quality of fitted red line:** If 'contamination' is present (e.g. from right ventricle or LV blood pool), scroll between different AHA segments to localize – assess if red line ignores or includes this contamination – then readjust contours if required.

**Choose ROI to fit:** Move between ROIs 'MYO', 'MYO_[slice_0_seg_1]', 'MYO_[slice_0_seg_2]', etc. clicking 'FIT' each time to generate a new fitted line.

**Exporting:** The plot and the fitting parameters displayed on screen can be saved using 'Export/Export As'. When finished, click 'Close'.

11. **Saving images with overlay**: Select blood flow map from series dropdown menu > click on 'Change series colormap' button ▮▮▮ > choose STD GAMMA-II. Select Display > Color Image > a window appears. Choose parameters as shown below. Click OK, the images will be saved in the parent folder.
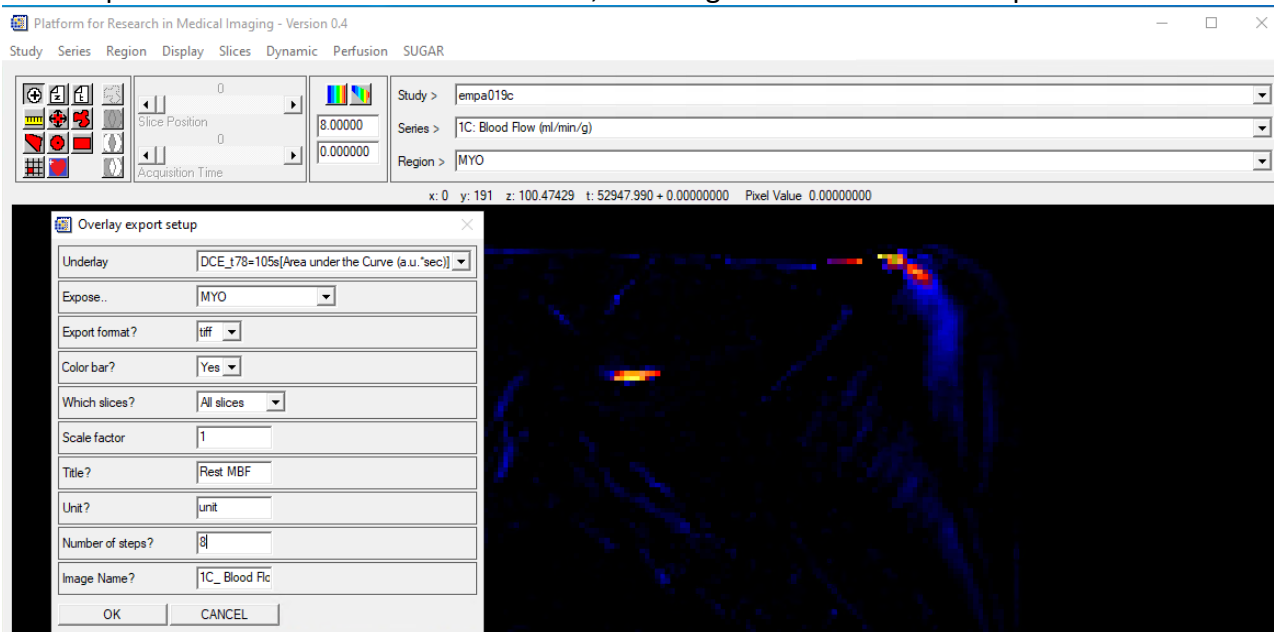


12. **Save study:** Study > Save.

13. **Close study:** Study > Close.