# TRISTAN Rat Assay v3.1
# *Standard Operating Procedures for image post-processing in PMI*

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## Contents

# PMI installation

## System requirements

PMI is only available for windows, and requires a free IDL virtual machine to run, which can be obtained here:

https://docs.google.com/file/d/0B3--rFa0c7TQSzRNOW1uN1Z1bzg/edit

A compiled version of PMI for analysis of TRISTAN rat data is available on sharepoint (WP2>Software):

https://eortchq.sharepoint.com/:u:/r/Tristan/Shared%20Documents/WP2/Software/PMI-TRISTAN-RATS%20v2.0.zip?csf=1&e=yHC2wq

Some general background on PMI can be found here:

https://sites.google.com/site/plaresmedima/home

## Install and run PMI

- Download and extract the full folder /PMI-TRISTAN-rats
- Double-click on PMI.sav to run PMI (For ease of use, place a shortcut to PMI.sav on your desktop and double-click that instead)
- The interface will look like this:


## Updating PMI

- When an update of PMI is introduced you will be provided with a new PMI.sav file
- To install: close PMI and replace the previous file PMI.sav by the new one.

# Log of changes

## New features in version 3.1 (introduced 06 aug 2020)

- **Baseline liver R10:**
  - Replaced with literature values:
    - 4.7T liver: changed from 1.285 to **1.281**
    - 7T liver: changed from 0.8350 to **1.109**

## New features in version 3.0 (introduced 28 july 2020)

- **Flip angle:**
  - The flip angle of the DCE sequence was hard-wired to FA=20 after it was discovered that some scanners exported an inaccurate FA value in the DICOM header.
- **Baseline:**
  - Default value for the number of baseline scans changed from 4 to 5
- **Field strength:**
  - If the field strength is not saved in the DICOM header, the user is asked to confirm the value (previous versions assumed a value of 7.0T in that case, which affected only the Antaros data)
- **Baseline R10:**
  - Replaced with final TRISTAN measured values:
    - 4.7T liver: changed from 1.3203 to **1.285**
    - 4.7T spleen: changed from 0.7458 to **0.631**
    - 7T liver: changed from 0.8346 to **0.8350**
    - 7T spleen: changed from 0.6313 to **0.611**
- **SOPs:**
  - Instructions added to update PMI
  - Reformatted including Table of Contents

## New features in version 2.0

- **Upgrade of the kinetic model:**
  - Now allows for different relaxivities in extracellular and intracellular space, using the relaxivity values measured by Bayer & MSD (Zieman et al).
  - Correction of fixed volume fractions based on data provided by Dan Scotcher:
    - extracellular_volume_fraction in the liver: 0.230 (unchanged)
    - hepatocyte_volume_fraction: 0.722
    - spleen_extracellular_volume_fraction: 0.314
- **Optimisation:**
  - Uptake rates constrained to be positive
  - Can now handle data where ROIs in liver or spleen are deleted on one or more time points
- **DICOM import:**
  - Fixed issue with import of MSD data after scanner upgrade
- **Display Model Fit:**

    - Spleen curve displayed on same plot as liver curve
    - Outputs also fit error (Root-mean-square of difference between best fit and data as a percentage of root-mean-square of data)
- **Added feature:**
    - VFA T1mapping button (optional)
- **Update of these SOPs:**
    - Final section added showing how to edit ROIs at individual time points

# Image processing pipeline

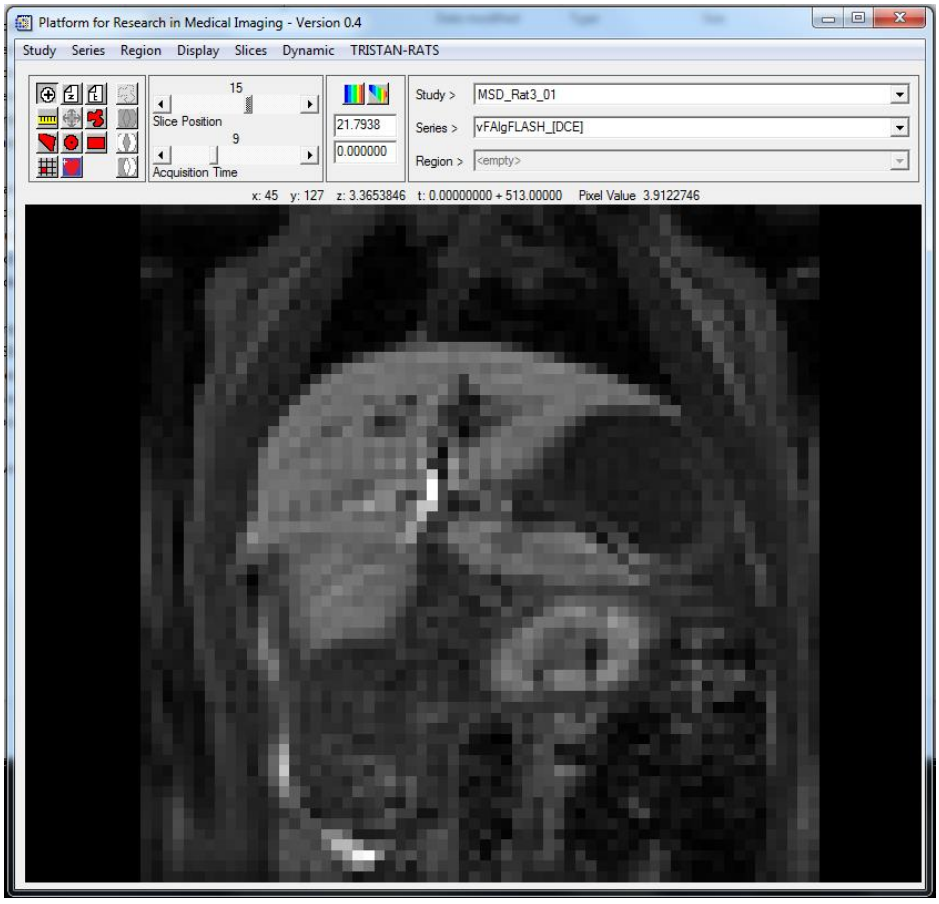
Perform steps 1-7 in order. Steps 8 is an optional procedure to correct ROIs manually at different time points.

## 1. Create a new study

a. Click on the button - **Study > New**.
b. In the open dialog box, navigate to the folder where you want to save the results.
c. Give a name to the PMI file to be created and click 'Open'.
d. You can close the study and exit PMI at any point during the following process, and continue at a later stage, but please remember to save the study first to avoid losing any work.

## 2. Import images

a. Click on the button – **TRISTAN-Rat Assay > Import DICOM v 2.0.**
b. In the open dialog box, select the folder containing the rat DICOM data
c. Click OK. After the import is finished you should see the latest series on display (see below)



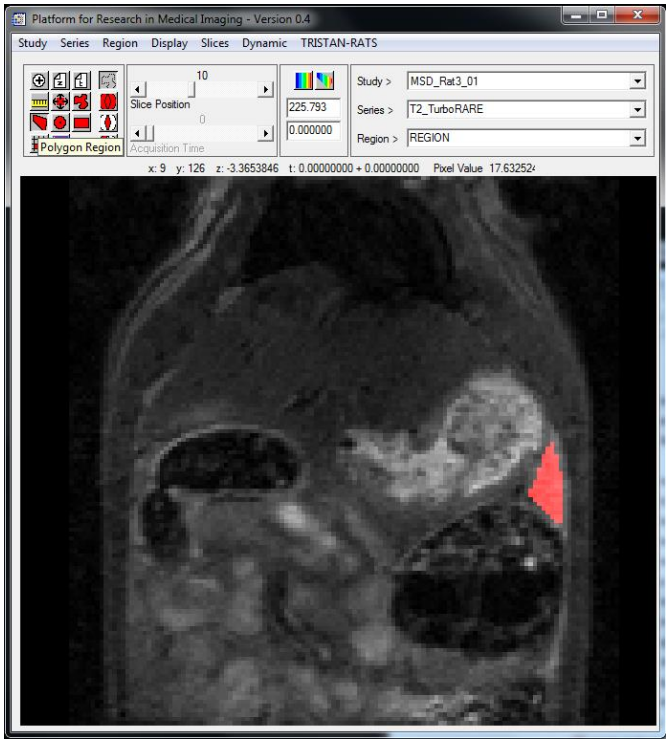
## 3. Verify imported images

a. Browse through the imported series using the **Series** dropdown list.
b. DCE images end with ‘ _[DCE]’.
c. Area under the curve and Time-MIPs are automatically created and should be shown in the list.
d. Use the **Slice Position** and **Acquisition Time** sliders to browse images in each series. (Alternatively, click on the image and use the up/down and left/right arrows of your keyboard)

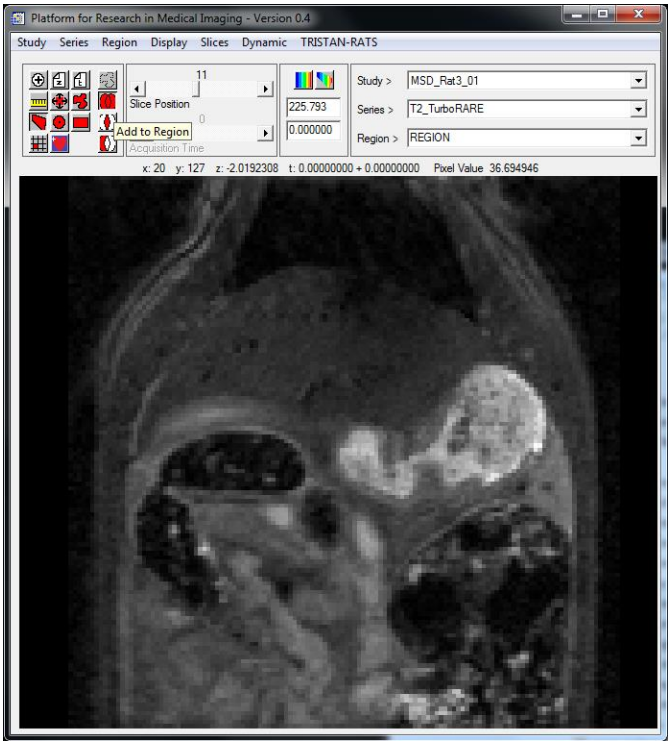
## 4. Define spleen ROI

### Draw the ROI on the T2-RARE series:

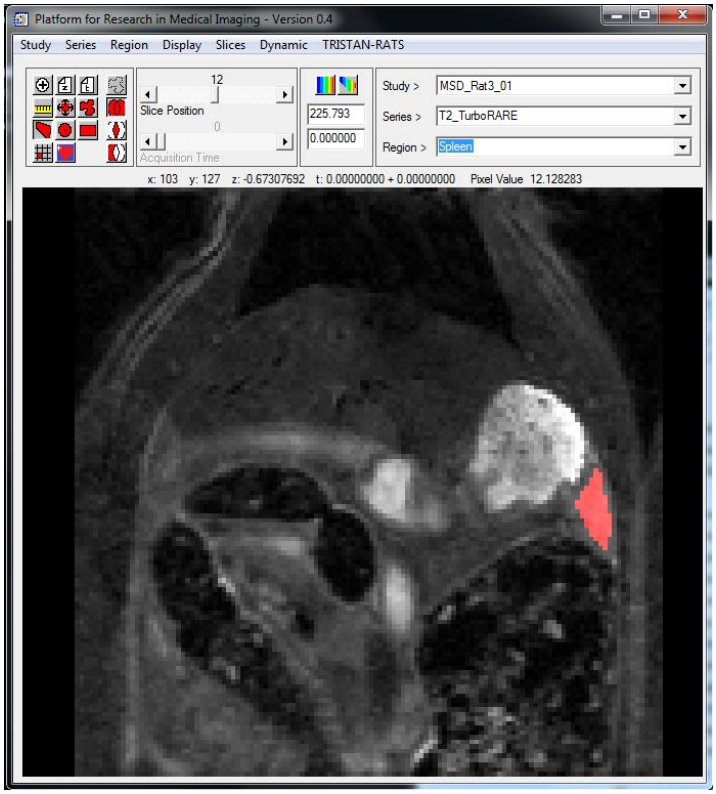
- Select the T2-RARE series in the **Series** dropdown list.
- Identify slices where the spleen is clearly visible. Use the **Slice Position** slider to browse through the slices.
- Click on the **Polygon Region** tool 
- Draw a polygon ROI outlining the spleen on one slice.




- Click on the **Add to Region** tool 
- On the next slice, draw another polygon ROI outlining the spleen.

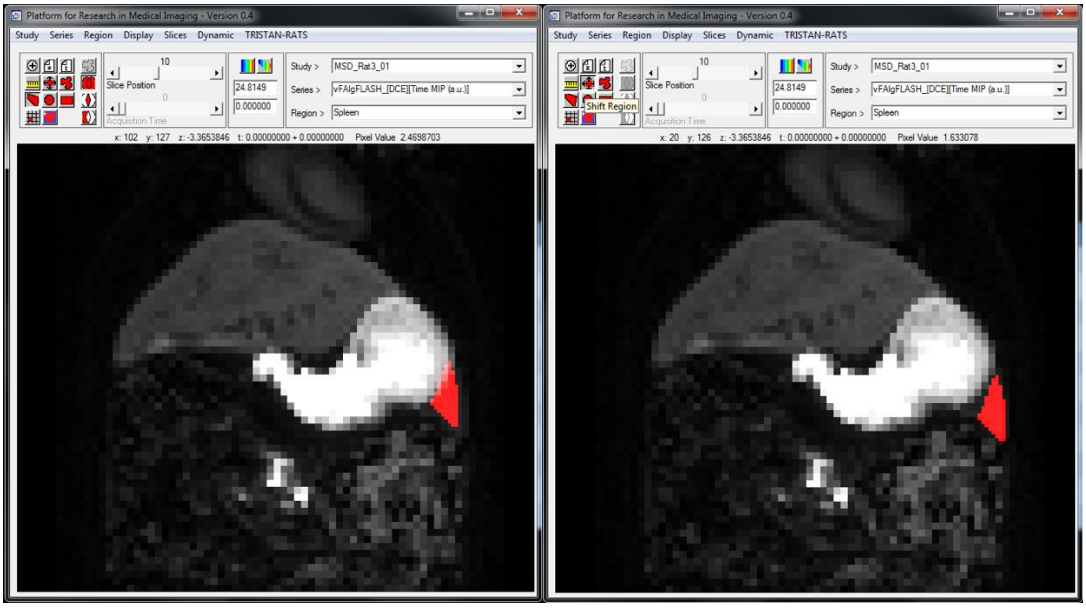



- Continue to draw ROIs around the spleen on all slices where the spleen is clearly visible, while ensuring that the **Add to Region** tool is selected.
- When finished, change the name of the ROI to 'Spleen' in the **Region** drop-down list and press ENTER.



Verify ROI positioning on the DCE time-MIP series and correct if needed:

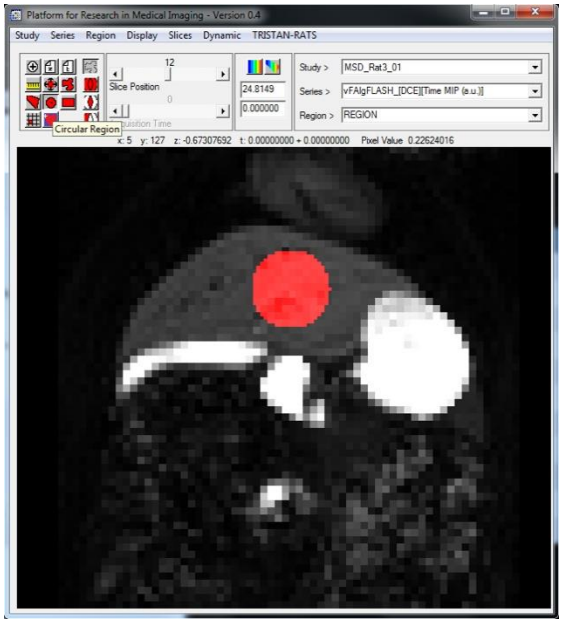
- Select the DCE Time-MIP series in the **Series** dropdown list.
- Visually verify that the Spleen ROI in each slice does not include voxels from kidney or stomach.
- If needed, correct ROI position using the **Shift Region** tool. 
- In some cases it may help to check the ROI on the original DCE series as well especially of the model fit is poor. There are various tools available in PMI under the Region menu to manually edit and combine ROIs (see point 7 and 8 below).



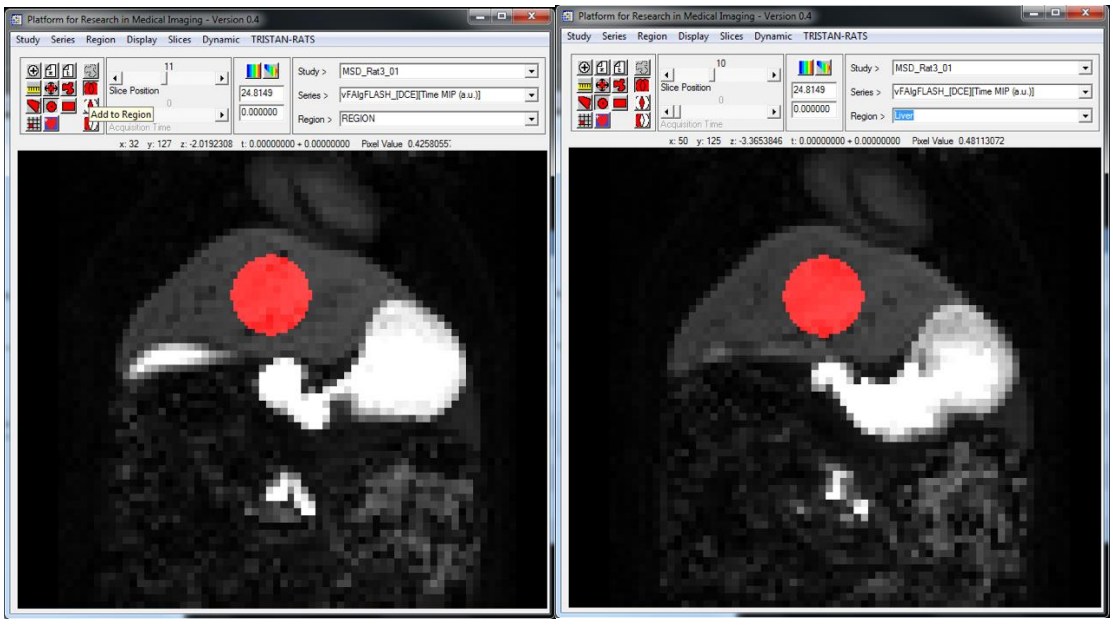

## 5. Define Liver ROI

Draw the ROI on the DCE Time-MIP series:

- Select the DCE Time-MIP series in the **Series** dropdown list.
- Using the **Slice Position** slider, navigate to the slice that is ventrally closest to the caudate processes. The liver should not contain large blood vessels in this slice.
- Click on the **Circular Region** tool  and select the **New Region** mode
- Draw a circular ROI of approximate diameter 10 voxels.



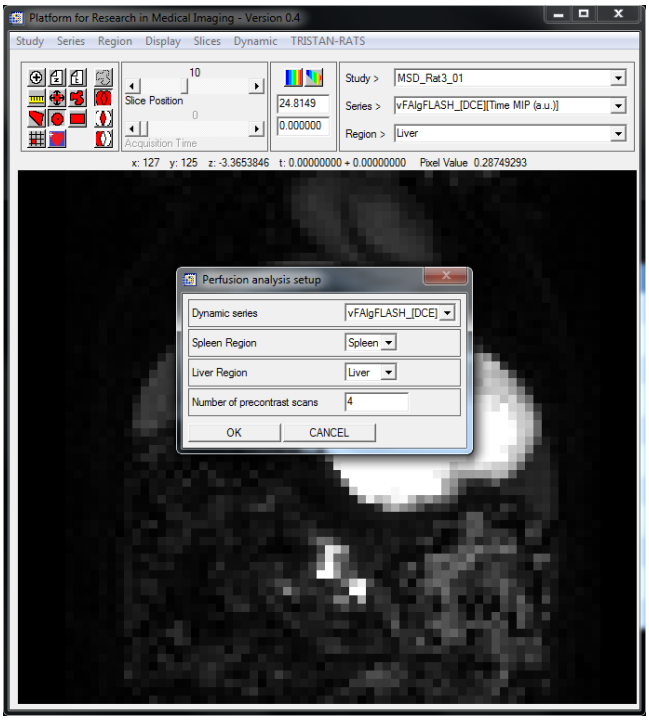

- Click on the **Add to Region** mode
- Go to the previous slice and select another circular ROI of the same diameter; repeat with one more slice (total of 3 slices for the liver ROI).
- When finished, change the name of the ROI to 'Liver' in the **Region** drop-down list and press ENTER.




## 6. Fit to gadoxetate model

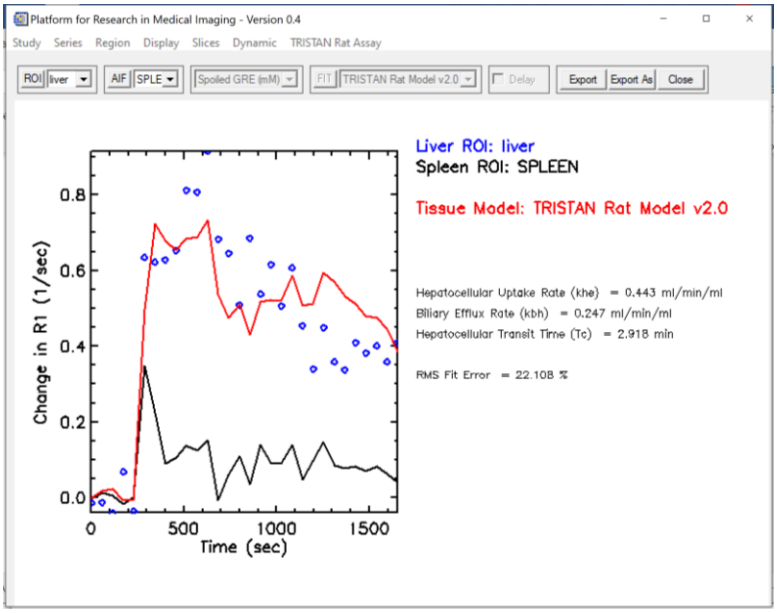
a. Click on the button – **TRISTAN Rat Assay > Fit Rat Gadoxetate model v2.0.**
b. In the open dialog box, select the DCE series from the dropdown list.
c. Select the Spleen Region and Liver Region from the dropdown lists.
d. The number of precontrast scans is by default set to 4. Don't change this unless the MRI protocol changes.

e. Click OK.




## 7. Export results

a. Click on the button – **Export**. A new folder named '[Study name]_TRISTAN Rat Model v2.0 (ROI)'will be created in the same location as the dataset. This folder will contain a plot of the fit, the fitted parameters, the concentration-time data and the signal-time data.
b. Note: if you have created multiple ROIs for liver and spleen then you can toggle between them using the droplists on the top left. The display shows the liver curve (blue), the spleen curve (black) and the model fit (red).
c. Click **Close** to return to PMI interface.
d. If you exit PMI at this point (via the **Study** menu) please remember to save the study or you will lose any ROIs defined




## 8. Optional: manual editing of ROIs at individual time points.

- It is possible to edit ROIs for liver or spleen at individual time points (eg. Those corrected by motion) or remove them on individual time points alltogether (eg. Those corrupted by artefacts).
- In order to do this, select the DCE series on the display (Series droplist) and the ROI you want to edit (Region droplist).
- Then in the menu "**Region**" click "**Extrude..**" and apply default settings. This produces a new Region in the list which is now visible on all time points.
- Scroll to the time point you want to edit and either edit the ROI (e.g. shift, remove pixels, etc) or delete it. Here is a youtube clip showing how to use the ROI editing tools in the display:
    - https://www.youtube.com/watch?v=0aQ-WV_SkdU&t=34s
- Now go back to **TRISTAN Rat Assay > Fit Rat Gadoxetate model v2.0.** and use this new ROI.