

# Analyzing Fallypride PET data with PMOD

Chris Smith & Linh Dang

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# Initial Steps

<http://www.pmod.com/web/>

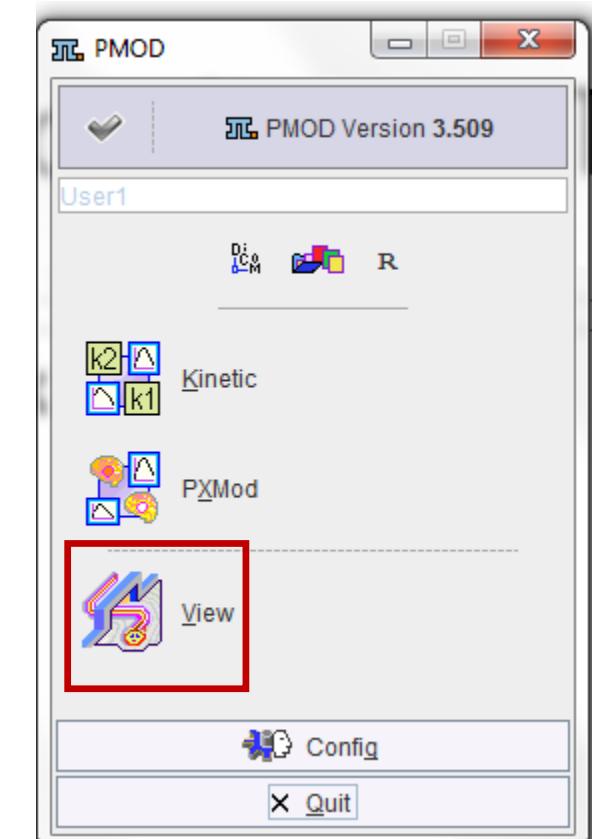
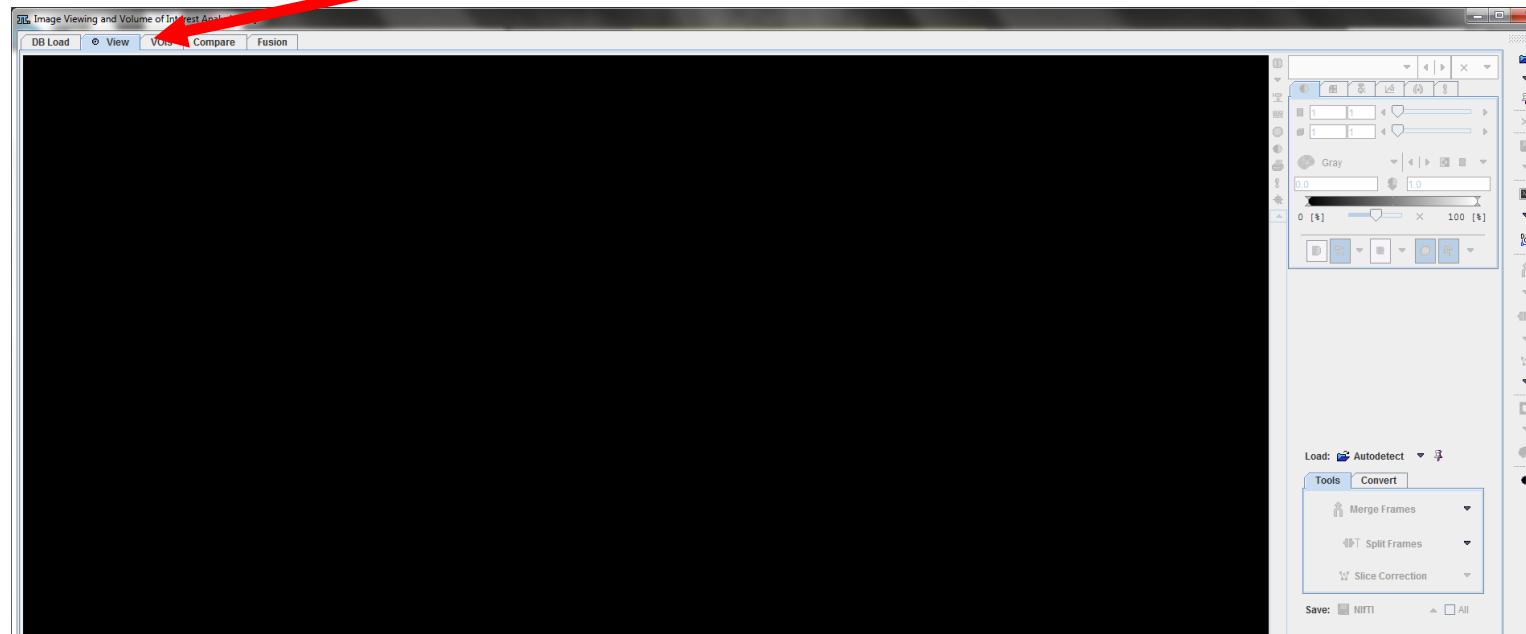
- Will have latest documents and support; you can also download a trial version @  
[http://www.pmod.com/web/?page\\_id=1051](http://www.pmod.com/web/?page_id=1051)
  - username: trial
  - Password: pmodtrial
- You will need to virtually connect to Yale to obtain the license to all the PMOD modules we need to analyze our PET data.
- You will need to be sure Cisco AnyConnect Secure Mobility Client is installed on your machine and will be asked to do so when you login at  
<https://access.yale.edu>
  - Once Cisco AnyConnect is installed and running, connect to: [access.yale.edu](https://access.yale.edu) via the client and enter:
    - Username: dhz3
    - Password: zaldlab14
    - Multifactor Identification: phone
    - ***Note, the lab phone will ring when you press OK and you will hear a recorded message telling you to press 1 if you were expecting the call, the client will then connect***

When launching PMOD for the first time, it will want to know where the license to run it is located.

- Since you are connected to access.yale.edu, you will just need to point PMOD to this IP address to obtain the license:  
**172.28.167.35 (this will be automatic after the initial setup)**
- On a PC, to launch PMOD 3.5, navigate to the location where you installed PMOD and locate the start folder: C:\Pmod3.5\Start
- Click on “RunPmod”
  - The Command Window will open and execute the commands to launch the program.

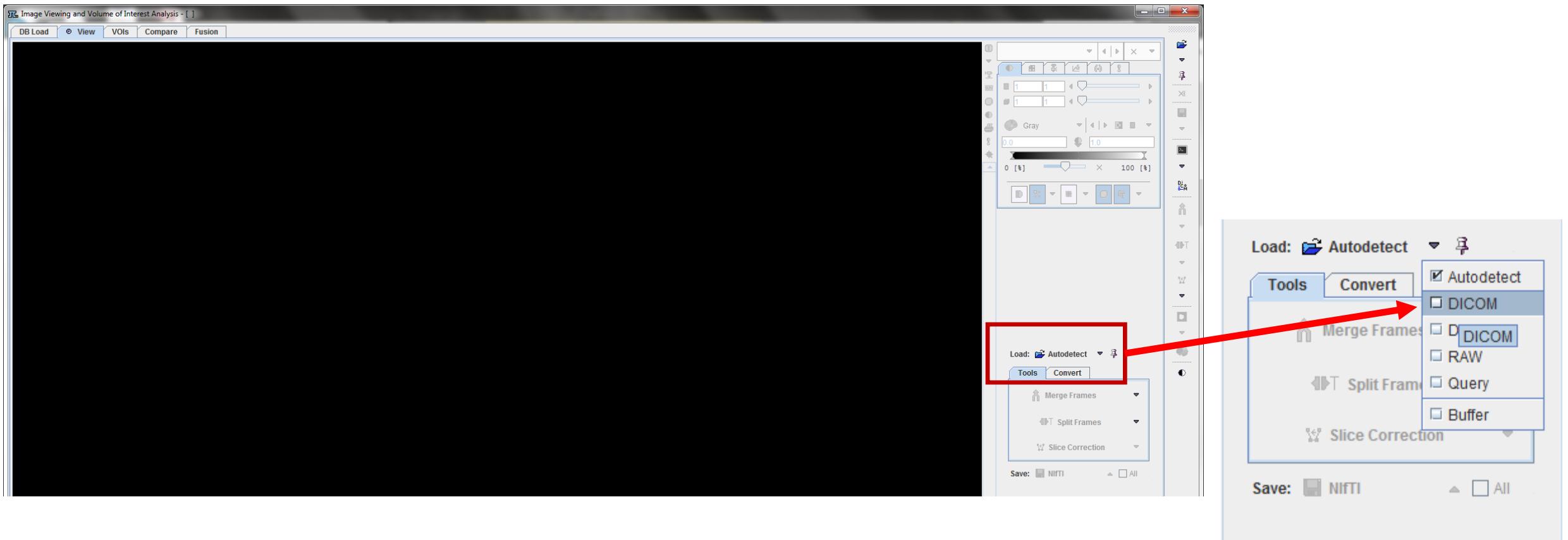
# Uploading PET data to PMOD using “VIEW”

- Once PMOD launches, select “View”
- Click on the “View” tab once PMOD View opens



# Uploading PET data to PMOD using “VIEW”

- On the right of the screen for load, select “dicom” from the drop down menu

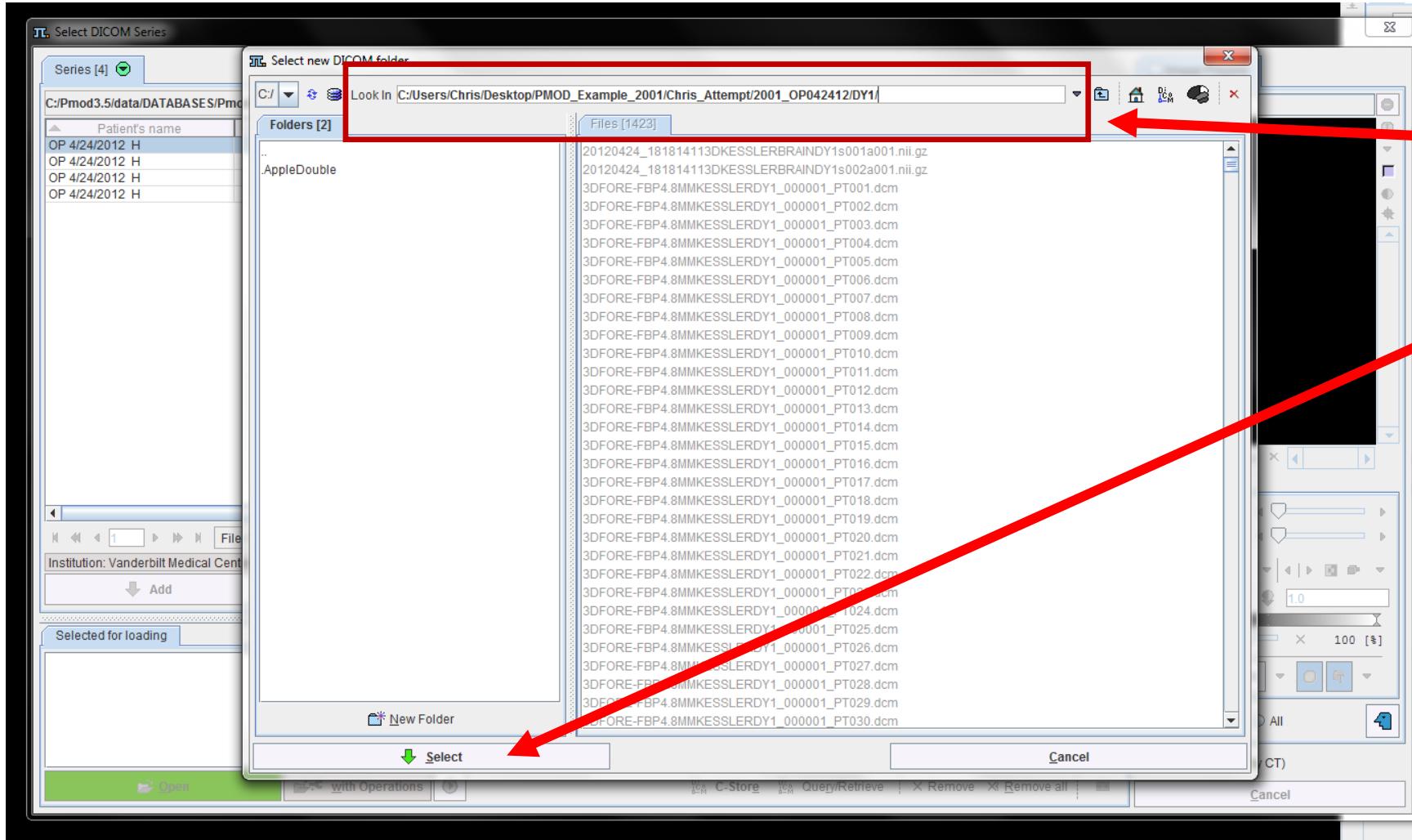


# Uploading PET data to PMOD using “VIEW”

- Use the dicom files from the “No Decay” data folder for the subject
- Each PET subject will have a raw data file containing 3 folders labeled DY1, DY2, and DY3
- These are 3 sets of dynamic PET image collections which were separated by breaks for the participant to get out of the PET scanner to stretch, use the restroom, etc...
- Note that DY1 is comprised of 28 frames (or volumes of the brain collected over time) while DY2 is 4 frames and DY3 3 frames; thus we have a total of 35 PET frames/volumes per subject

# Uploading PET data to PMOD using “VIEW”

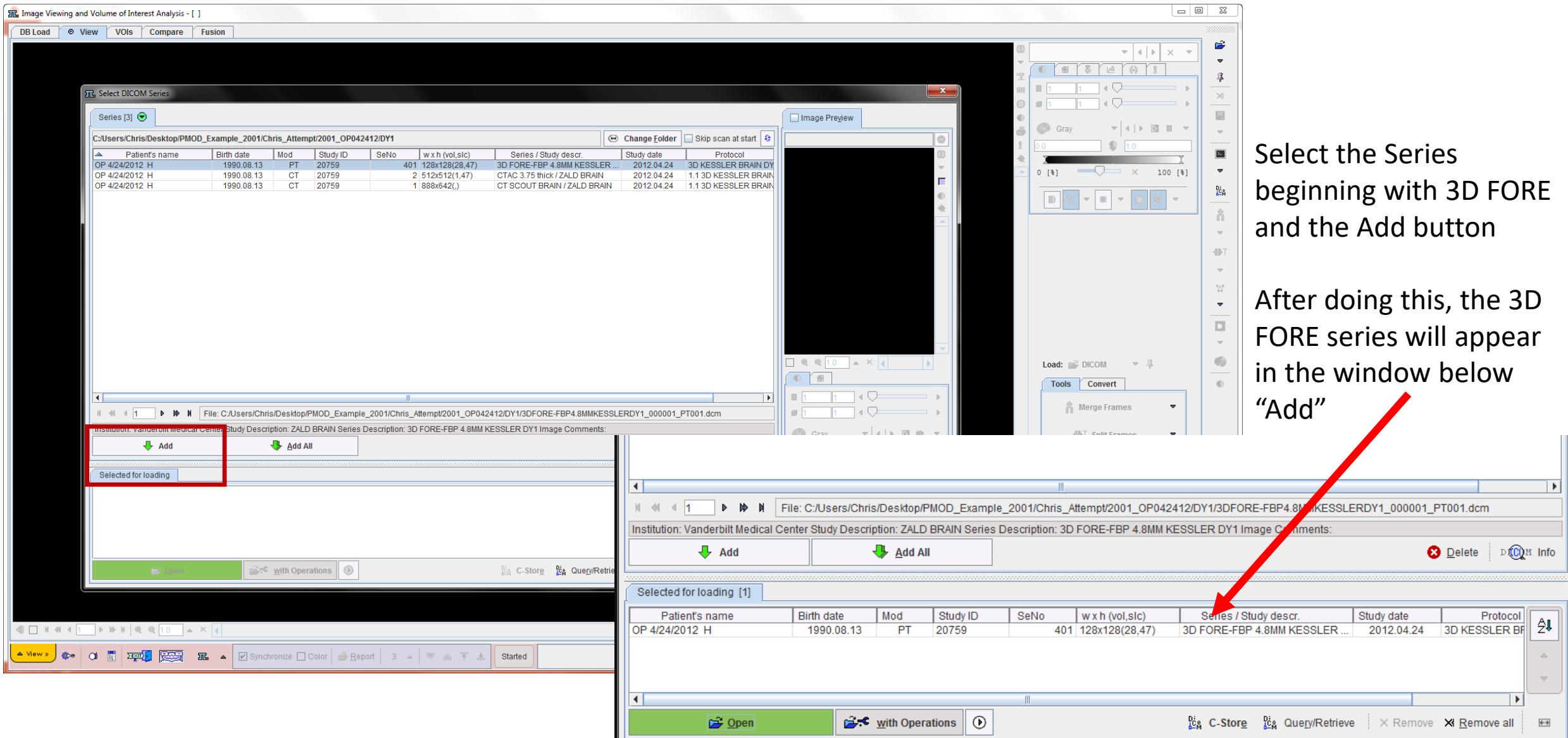
We will select each DY folder in turn to add to PMOD View;



Here we are looking in DY1 for the dicom image files of interest

Once you have the folder selected, click “**Select**” at the bottom of the loading window...that data will be loaded into PMOD View

# Uploading PET data to PMOD using “VIEW”



Select the Series beginning with 3D FORE and the Add button

After doing this, the 3D FORE series will appear in the window below "Add"

# Uploading PET data to PMOD using “VIEW”

Use “Change Folder” to navigate to the DY2 folder and add the 3D FORE series and then the DY3 folder and add the 3D FORE series

Select DICOM Series

Series [4]

C:/Users/Chris/Desktop/PMOD\_Example\_2001/Chris\_Attempt/2001\_OP042412/DY2

Patient's name	Birth date	Mod	Study ID	SeNo	w x h (vol,slc)	Series / Study descr.	Study date	Protocol
OP 4/24/2012 H	1990.08.13	PT	20760	401	128x128(2,47)	3D FORE-FBP 4.8MM KESSLER ...	2012.04.24	3D KESSLER BRAIN DY
OP 4/24/2012 H	1990.08.13	CT	20760	3	512x512(1,47)	BRAIN 30CM / ZALD BRAIN	2012.04.24	1.3 3D KESSLER BRAIN
OP 4/24/2012 H	1990.08.13	CT	20760	2	512x512(1,47)	CTAC 3.75 thick / ZALD BRAIN	2012.04.24	1.3 3D KESSLER BRAIN
OP 4/24/2012 H	1990.08.13	CT	20760	1	888x642(,)	CT SCOUT BRAIN / ZALD BRAIN	2012.04.24	1.3 3D KESSLER BRAIN

Change Folder  Skip scan at start

When you have all the 3D FORE series selected, the following series will appear in the loaded window  
Click “Open with operations”

Institution: Vanderbilt Medical Center Study Description: ZALD BRAIN Series Description: 3D FORE-FBP 4.8MM KESSLER DY3 Image Comments:

Add Add All Delete

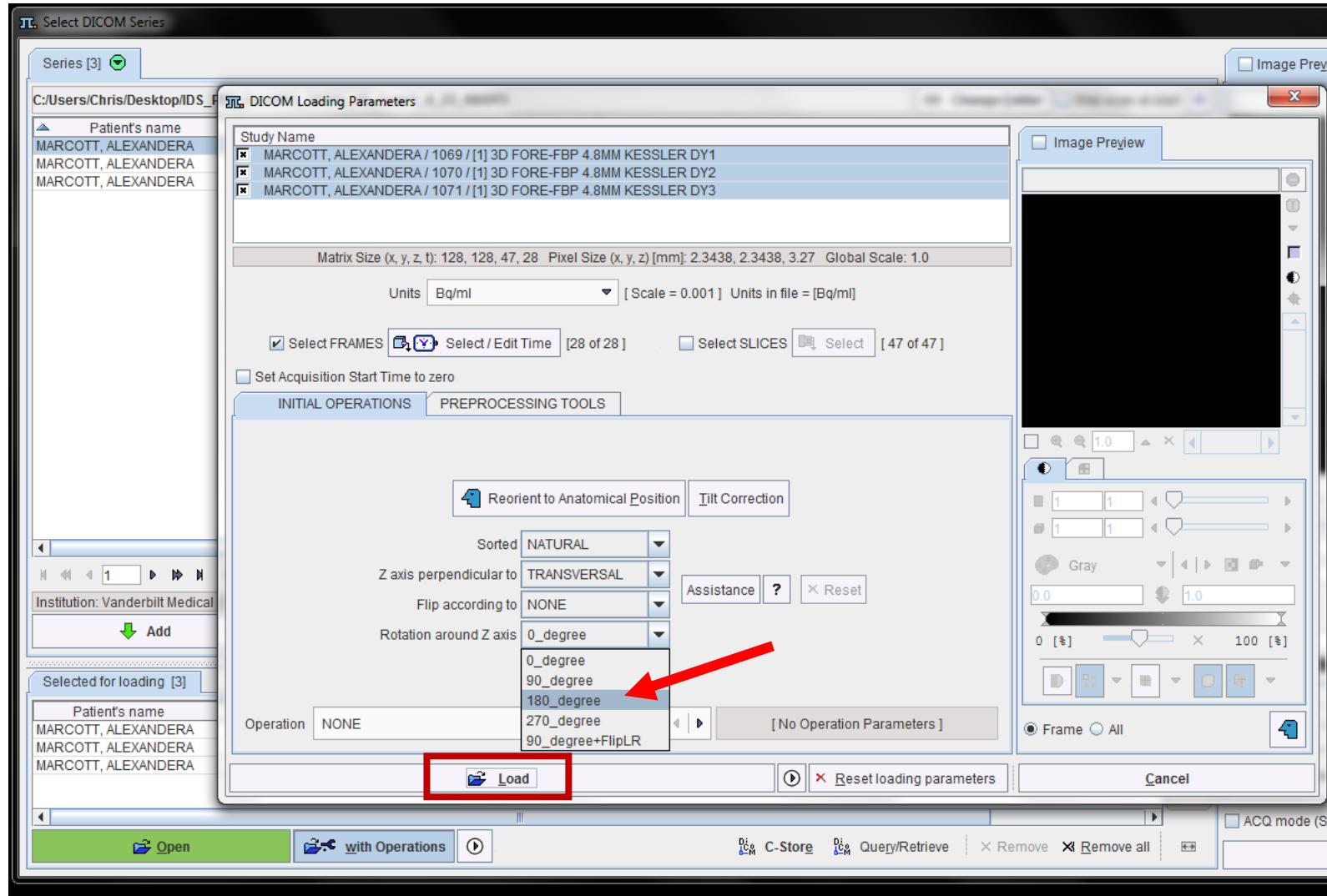
Selected for loading [3]

Patient's name	Birth date	Mod	Study ID	SeNo	w x h (vol,slc)	Series / Study descr.	Study date	Protocol	No
OP 4/24/2012 H	1990.08.13	PT	20759	401	128x128(28,47)	3D FORE-FBP 4.8MM KESSLER ...	2012.04.24	3D KESSLER BRAIN DY1	0
OP 4/24/2012 H	1990.08.13	PT	20760	401	128x128(2,47)	3D FORE-FBP 4.8MM KESSLER ...	2012.04.24	3D KESSLER BRAIN DY2	1
OP 4/24/2012 H	1990.08.13	PT	20761	401	128x128(2,47)	3D FORE-FBP 4.8MM KESSLER ...	2012.04.24	3D KESSLER BRAIN DY3	2

Open with Operations  Remove  Remove

DICM C-Store DICM Query/Retrieve X Remove X Remove

# Choose from “Rotation around Z axis”: “180\_degree”



Then, click “Load”

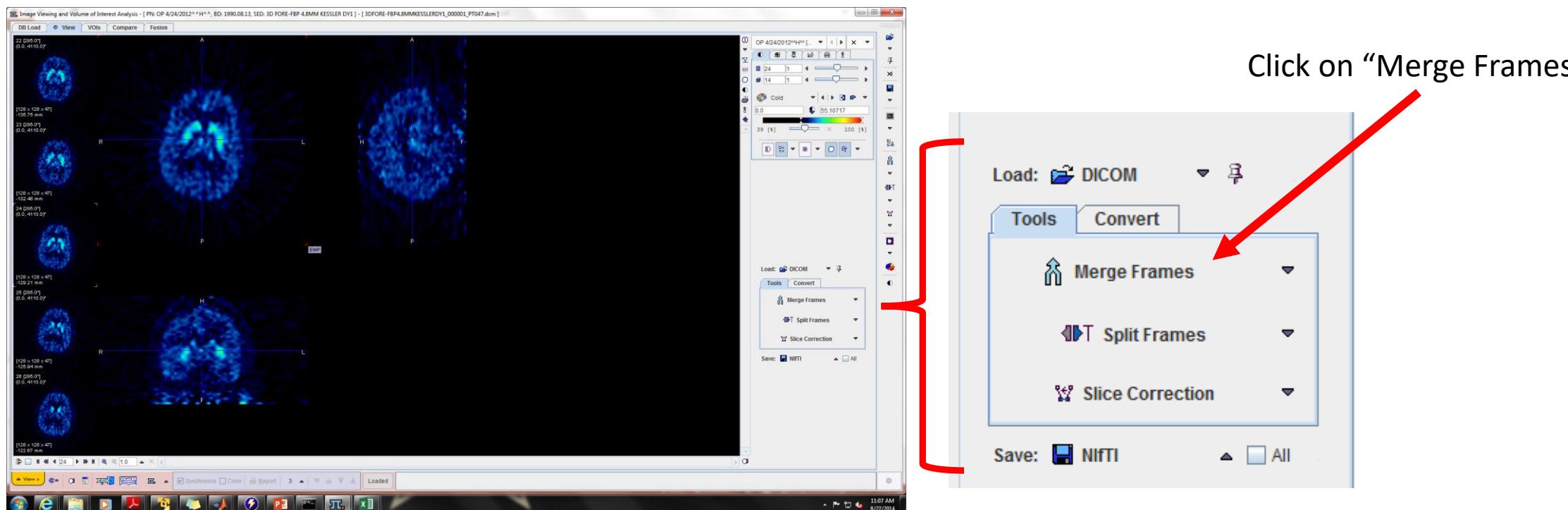
Note, this step will flip our PET image so that it is in the same orientation as the MNI template we will register this image to.

Doing this step early will have the PET data in an orientation that will allow FSL’s FLIRT operation to more easily register the subject’s brain to MNI space.

# Merging Images and Attaching timing information to the DY frames

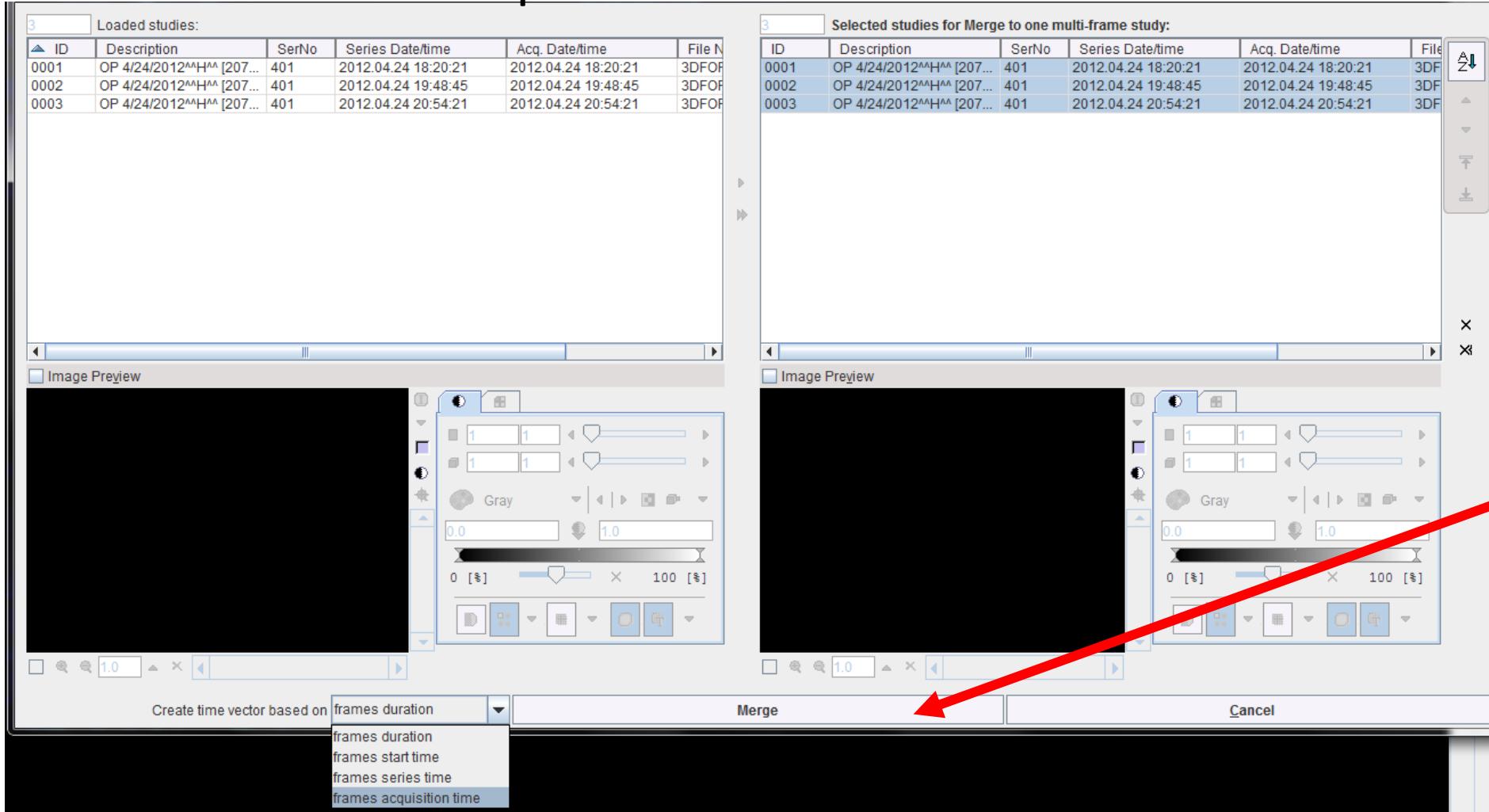
Once you have opened the DY folder dicom images together, you will get an image such as the one below.

We then need to merge the frames by acquisition time as our images were collected over time and the Fallypride PET tracer will change its distribution and signal over time.



# Merging Images and Attaching timing information to the DY frames

Select the 3 DY folders on the right and then choose create time vector based on “frames acquisition time”

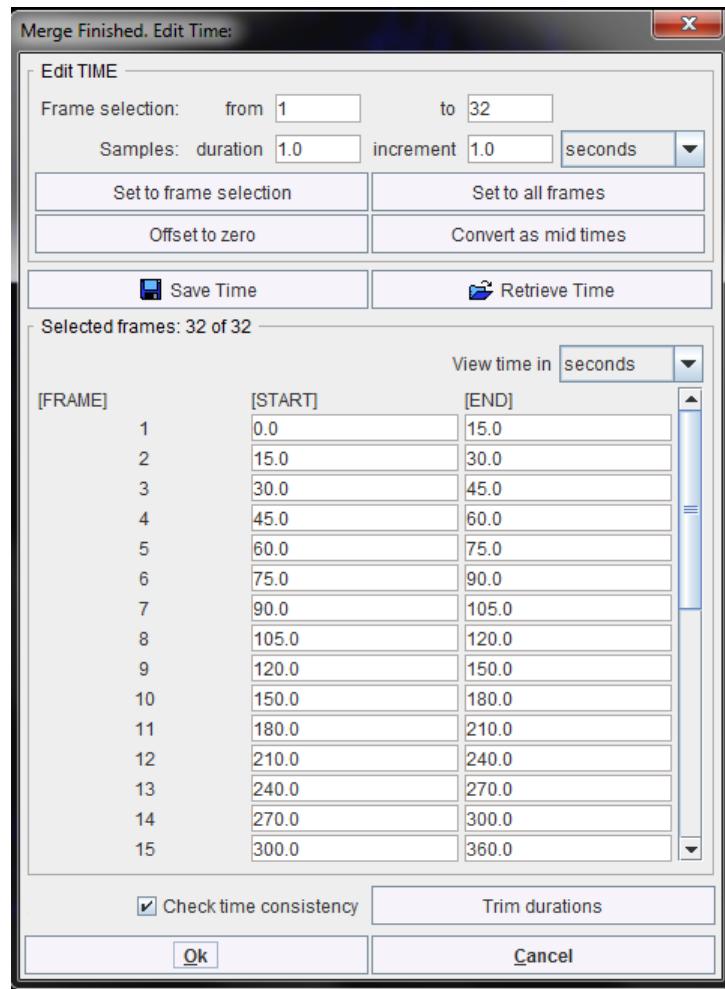


Click on “Merge”

When prompted, select  
“Add new study”

# Checking the timing file before associating it with the images

The following box will appear with the acquisition times (start and end) for each frame/volume collected.



Note that there will be 35 frames (volume images)

It is important that the end time of the preceding image matches the start time of the next for frames 1-28 (DY1).

**If you see a place where these times overlap, you need to adjust them.**

[FRAME]	[START]	[END]
1	0.0	15.0
2	15.0	30.0
3	30.0	45.0
4	45.0	60.0
5	60.0	75.0
6	75.0	90.0
7	90.0	105.0
8	105.0	120.0
9	120.0	150.0
10	150.0	180.0
11	180.0	210.0
12	210.0	240.0
13	240.0	270.0
14	270.0	300.0
15	300.0	360.0
14	270.0	300.0
15	300.0	360.0
16	360.0	420.0
17	420.0	480.0
18	480.0	540.0
19	540.0	600.0
20	599.0	659.0
21	659.0	809.0
22	810.0	1110.0
23	1110.0	1410.0
24	1410.0	1710.0
25	1709.0	2309.0
26	2309.0	2909.0
27	2910.0	3510.0
28	3510.0	4110.0

For example, here frame 19 ends at 600 sec but frame 20 is being read as starting at 599 sec. This is not possible and is a result of slight measurement/rounding issues.

So, we will adjust frame 20's start time to 600.

# Checking the timing file before associating it with the images – what proper times should look like, frames 1-28

Merge Finished. Edit Time: X

Edit TIME

Frame selection: from 1 to 32  
Samples: duration 1.0 increment 1.0 seconds

Set to frame selection Set to all frames  
Offset to zero Convert as mid times

Save Time  Retrieve Time

Selected frames: 32 of 32

View time in seconds

[FRAME]	[START]	[END]
1	0.0	15.0
2	15.0	30.0
3	30.0	45.0
4	45.0	60.0
5	60.0	75.0
6	75.0	90.0
7	90.0	105.0
8	105.0	120.0
9	120.0	150.0
10	150.0	180.0
11	180.0	210.0
12	210.0	240.0
13	240.0	270.0
14	270.0	300.0
15	300.0	360.0

Check time consistency  Trim durations

Ok  Cancel

Merge Finished. Edit Time: X

Edit TIME

Frame selection: from 1 to 32  
Samples: duration 1.0 increment 1.0 seconds

Set to frame selection Set to all frames  
Offset to zero Convert as mid times

Save Time  Retrieve Time

Selected frames: 32 of 32

View time in seconds

[FRAME]	[START]	[END]
14	270.0	300.0
15	300.0	360.0
16	360.0	420.0
17	420.0	480.0
18	480.0	540.0
19	540.0	600.0
20	600.0	660.0
21	660.0	810.0
22	810.0	1110.0
23	1110.0	1410.0
24	1410.0	1710.0
25	1710.0	2310.0
26	2310.0	2910.0
27	2910.0	3510.0
28	3510.0	4110.0

Check time consistency  Trim durations

Ok  Cancel

The timing of frames 1-28 will not deviate across subjects and should look like this example.

# Timing of frames 29-35

While frame 28 will always end at 4110 seconds, the start of frame 29 (first of 4 frames in DY2) and the start of frame 33 (first of 3 frames in DY3) will vary based on when the participant returned to the PET scanner from their break. The important things in these frame timings is that the end of frame 29 matches the start of frame 30 and the end of frame 33 matches the start of 34, etc....

28	3510.0	4110.0
29	5279.0	6029.0
30	6029.0	6779.0
31	6779.0	7529.0
32	7529.0	8279.0
33	9284.0	10484.0
34	10484.0	11684.0
35	11684.0	12884.0

Check time consistency      Trim durations

**NOTE: The start of frame 29 and start of 33 will not match the times before them (breaks for subject comfort)!!!**

Merge Finished. Edit Time:

Edit TIME  
Frame selection: from 1 to 32  
Samples: duration 1.0 increment 1.0 seconds  
Set to frame selection Set to all frames  
Offset to zero Convert as mid times  
 Save Time  Retrieve Time  
Selected frames of 32

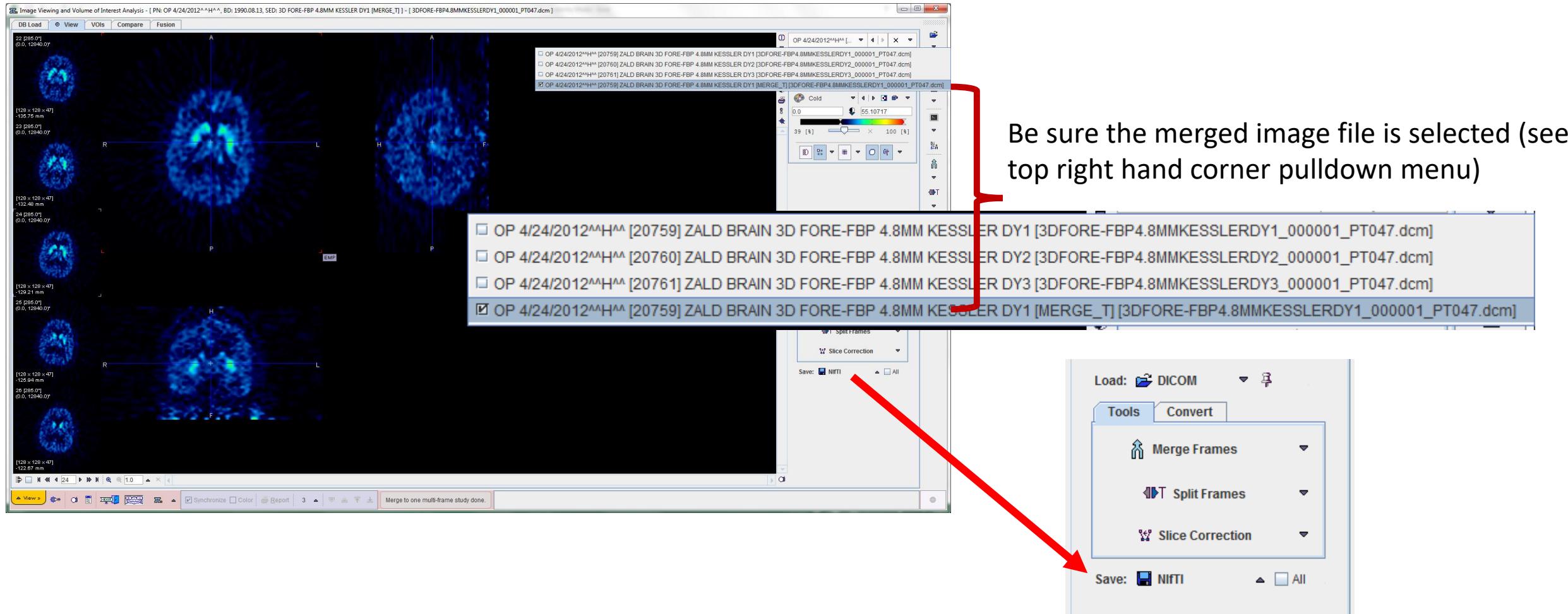
[FRAME] [START] [END]  
1 0.0 15.0  
2 15.0 30.0  
3 30.0 45.0  
4 45.0 60.0  
5 60.0 75.0  
6 75.0 90.0  
7 90.0 105.0  
8 105.0 120.0  
9 120.0 150.0  
10 150.0 180.0  
11 180.0 210.0  
12 210.0 240.0  
13 240.0 270.0  
14 270.0 300.0  
15 300.0 360.0

Check time consistency Trim durations

Once all your times look OK, select “Save Time” and save the timing file with the subject’s ID number in the subject’s PET data folder. PMOD will name the file .acqtimes (which can be read much like a text file)

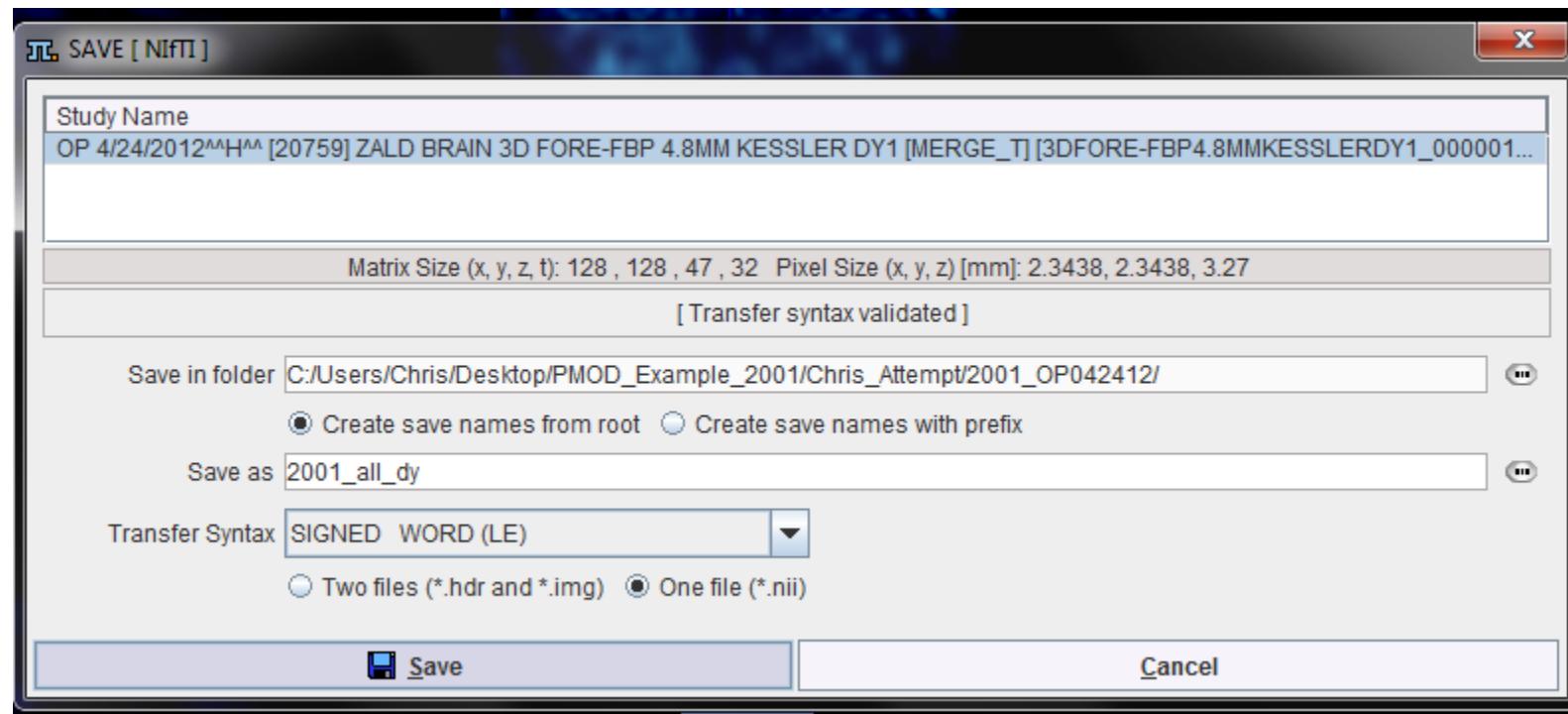
# Save the Merged image file

- Once the acqtimes file has been saved, press “Ok” to exit the timing dialogue box.



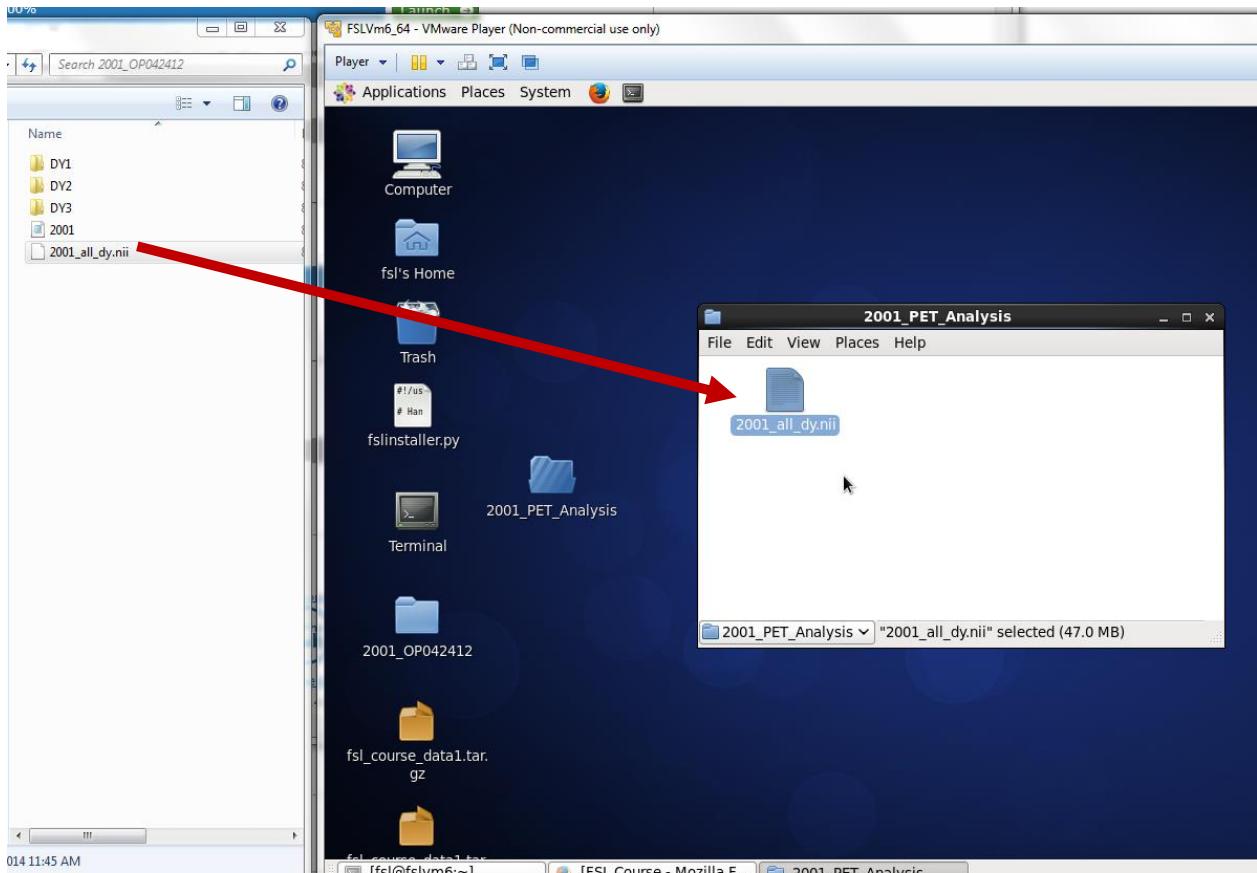
- Then, save the merged frame file as a .nii (nifti) file with the subject ID and all-dy in the file name (ex: DND001\_all-dy.nii) in the participant's PET data folder.

# Save the Merged image file

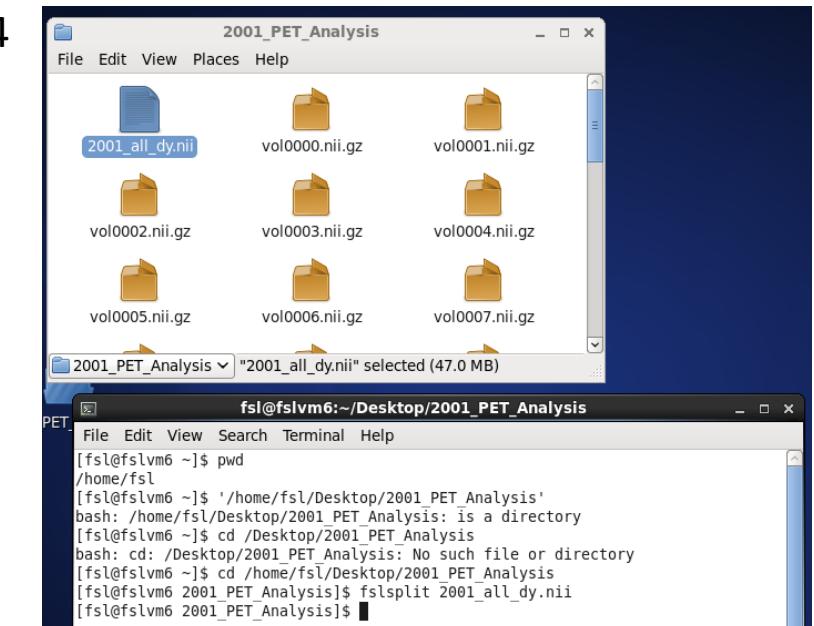


# Splitting the all\_dy.nii file into its individual components.

- Once you have created the all\_dy.nii file, we need to split it into its components using a program called FSL.
- If using Windows, you can drag the all\_dy.nii file to FSL's Vmware environment in a folder labeled with that participant's ID#.



We then use the command `fslsplit` in the terminal (type: `fslsplit 2001_all_dy.nii`) to split the all\_dy.nii file. Note that the subject's folder becomes populated with vol0000 through vol0034



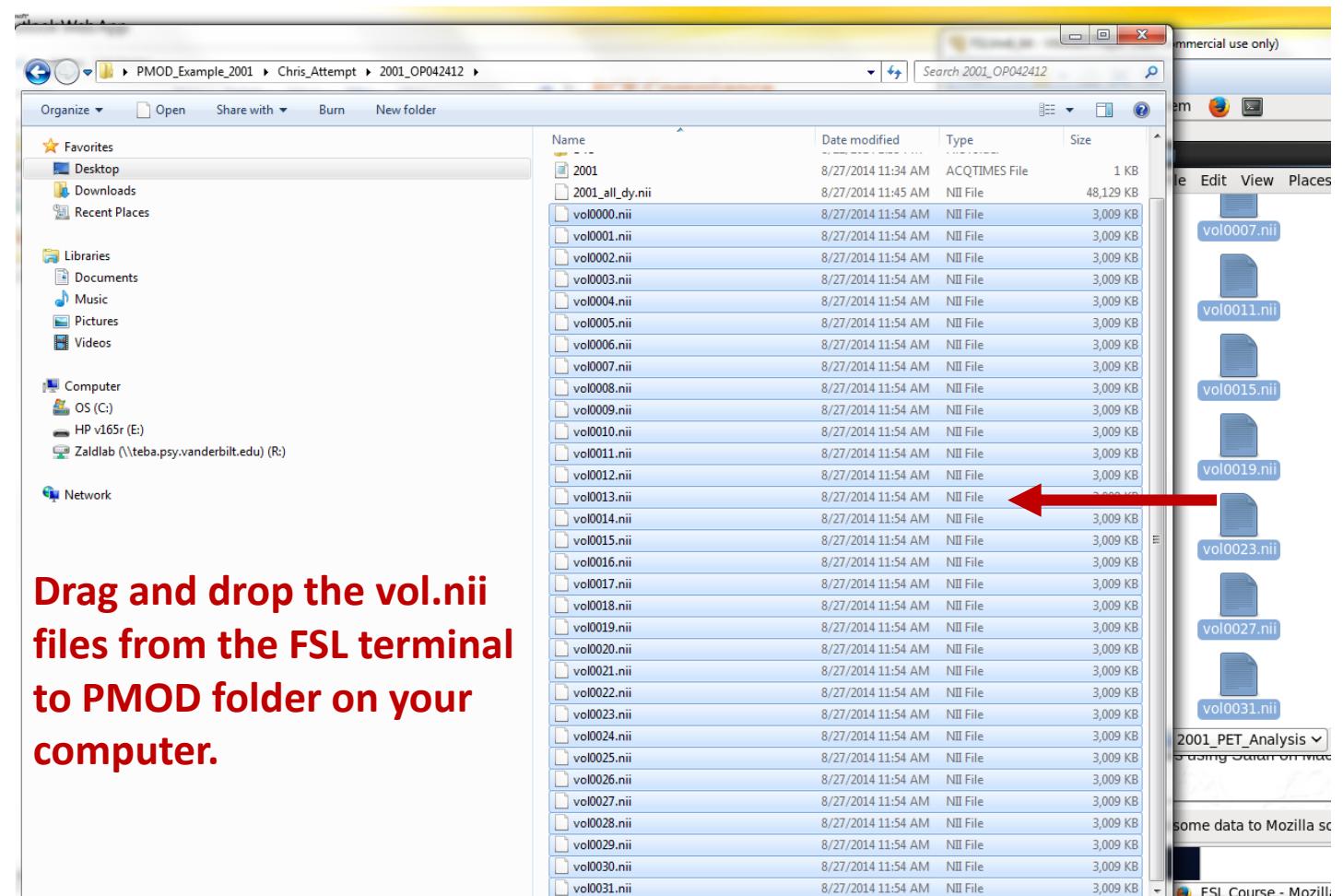
# Unzipping the unsplit volume images & Copying them into the PMOD subject analysis folder

We need to use “gunzip” to unzip all the compressed volume images so that the files can be read by PMOD.

In the terminal type: gunzip vol\*

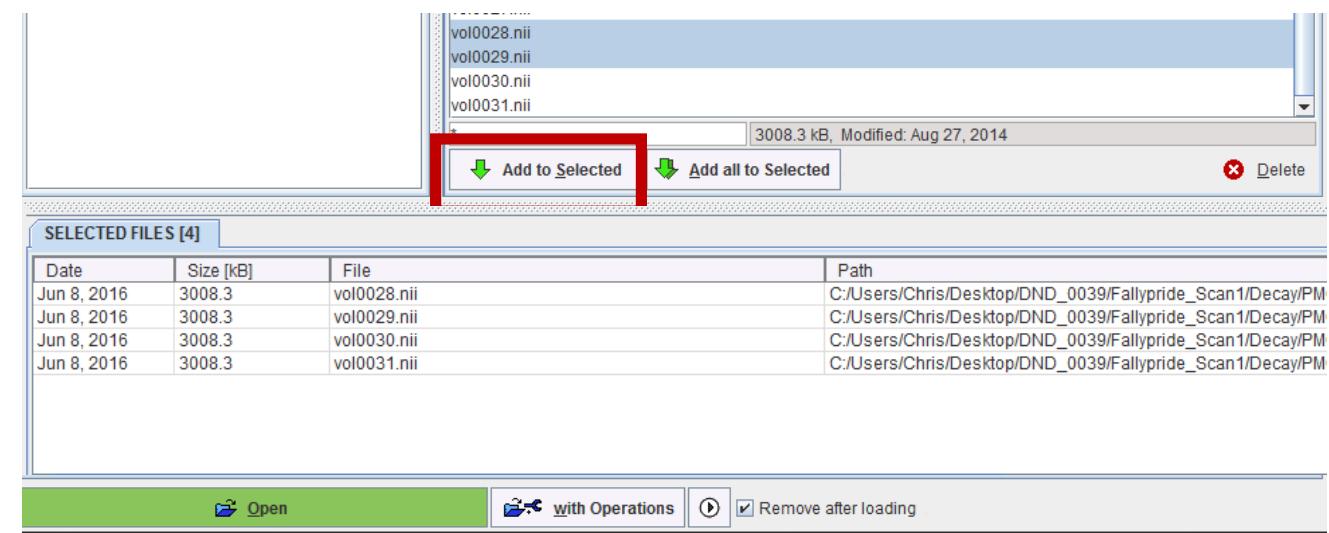
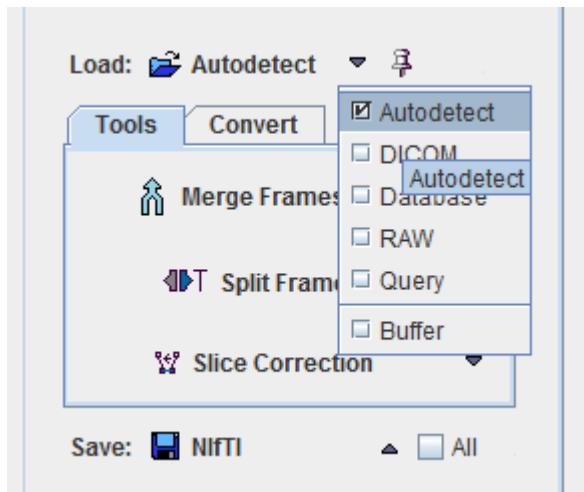
This will unzip any .gz compressed image files beginning with “vol” which are all the files we just created from our splitting of all\_dy.nii

Then, copy these vol images to the subject’s data folder being used by PMOD.



# Decay correction

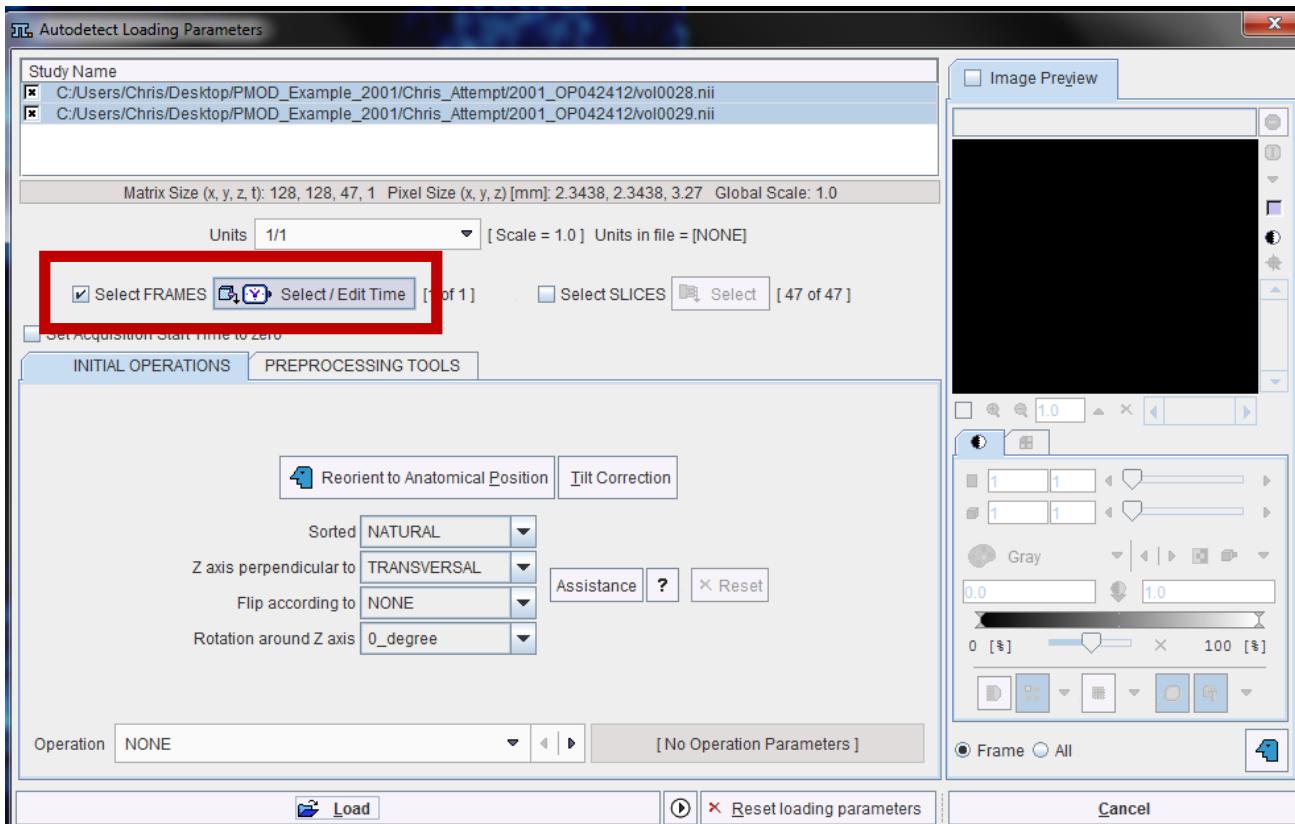
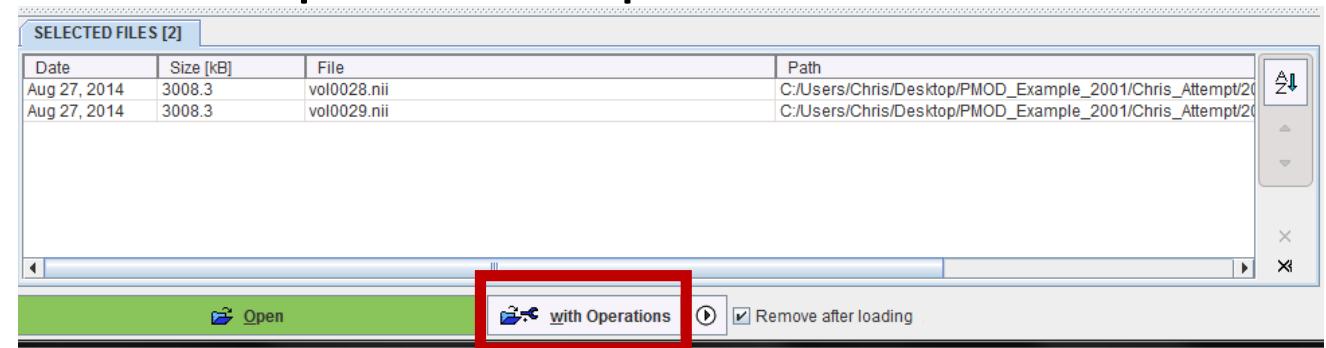
- This step is critical for proper modeling of the PET tracer timecourse. Essentially, we need to tell PMOD that the beginning of frames 29 and 33 (start of DY2 and DY3) are happening so many seconds after the initial image we got at the beginning of the PET scan.
- We must do this to allow for a correction in our Fallypride tracer signal as the tracer has a half-life of 109.77 minutes. Essentially, we are correcting for the loss in signal with time in our data.
- To start, in PMOD View, on the right of the screen, go to “Load”, choose “Autodetect” and select vol0028, vol0029, vol0030, & vol0031 (these are really frames 29-32 because the first frame is labeled vol0000).



# Decay correction

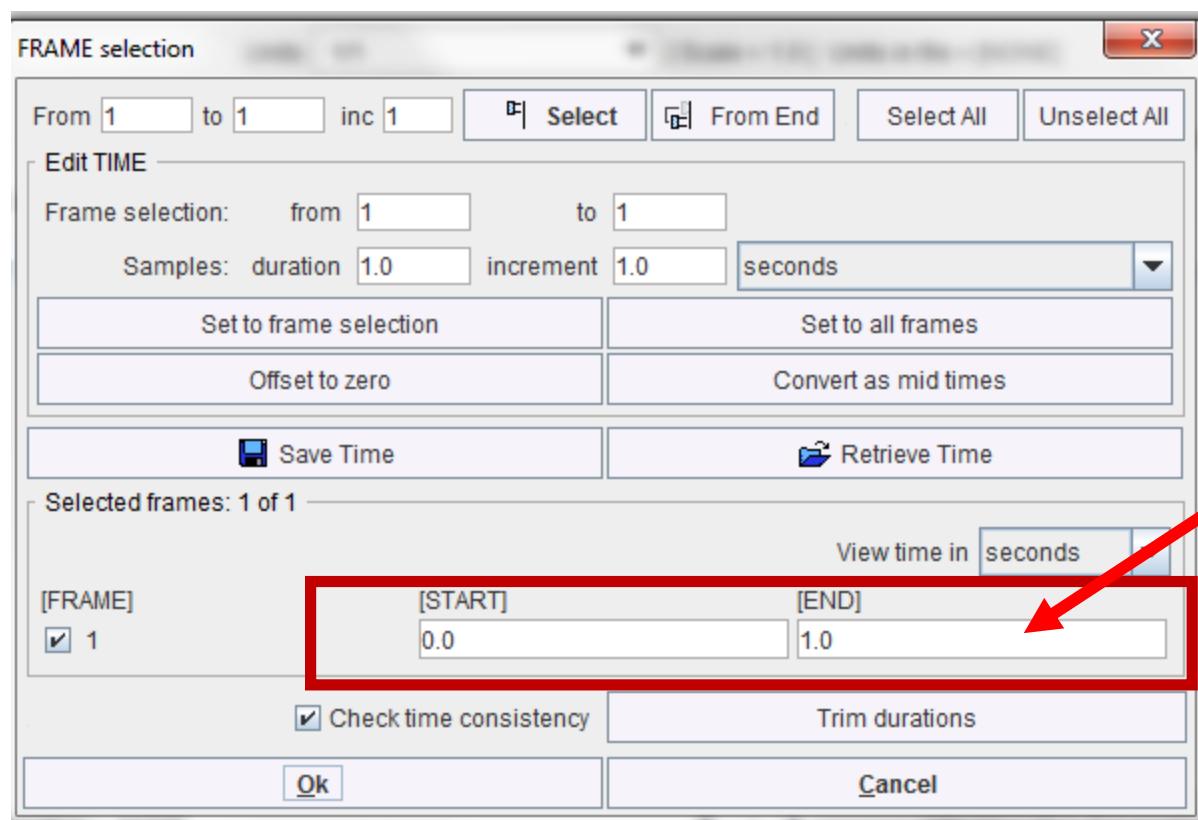
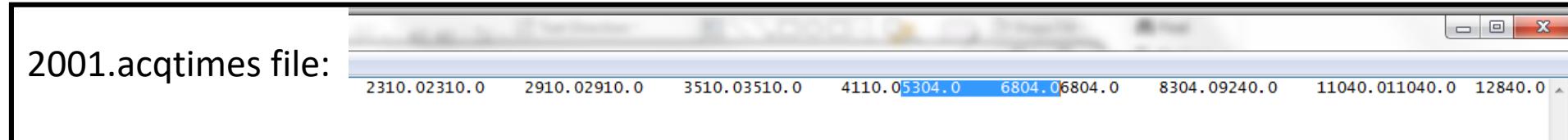
- Once these 4 volumes are added, choose “Open with operations” at the bottom of the screen

Choose, “Select FRAMES” Select/Edit Time



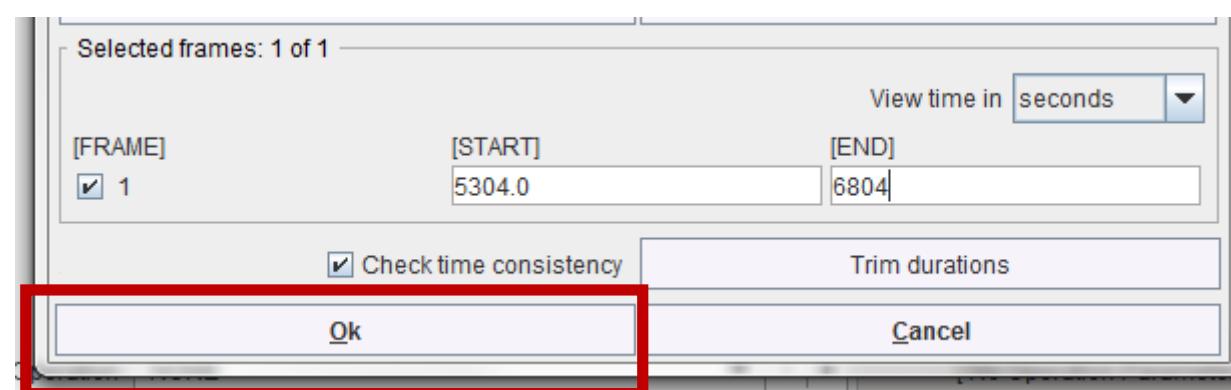
# Decay correction

Once this window appears, we are going to change the start and end times to reflect when frame 29 began and ended relative to the first frame/image. We will open our acqtimes file to get these values.



The acqtimes file opens a bit oddly in notepad. However, you know that frame 28 ends at 4110 So, that means the next pair of numbers (in this case 5304, 6804) represent the start and end of frame 29.

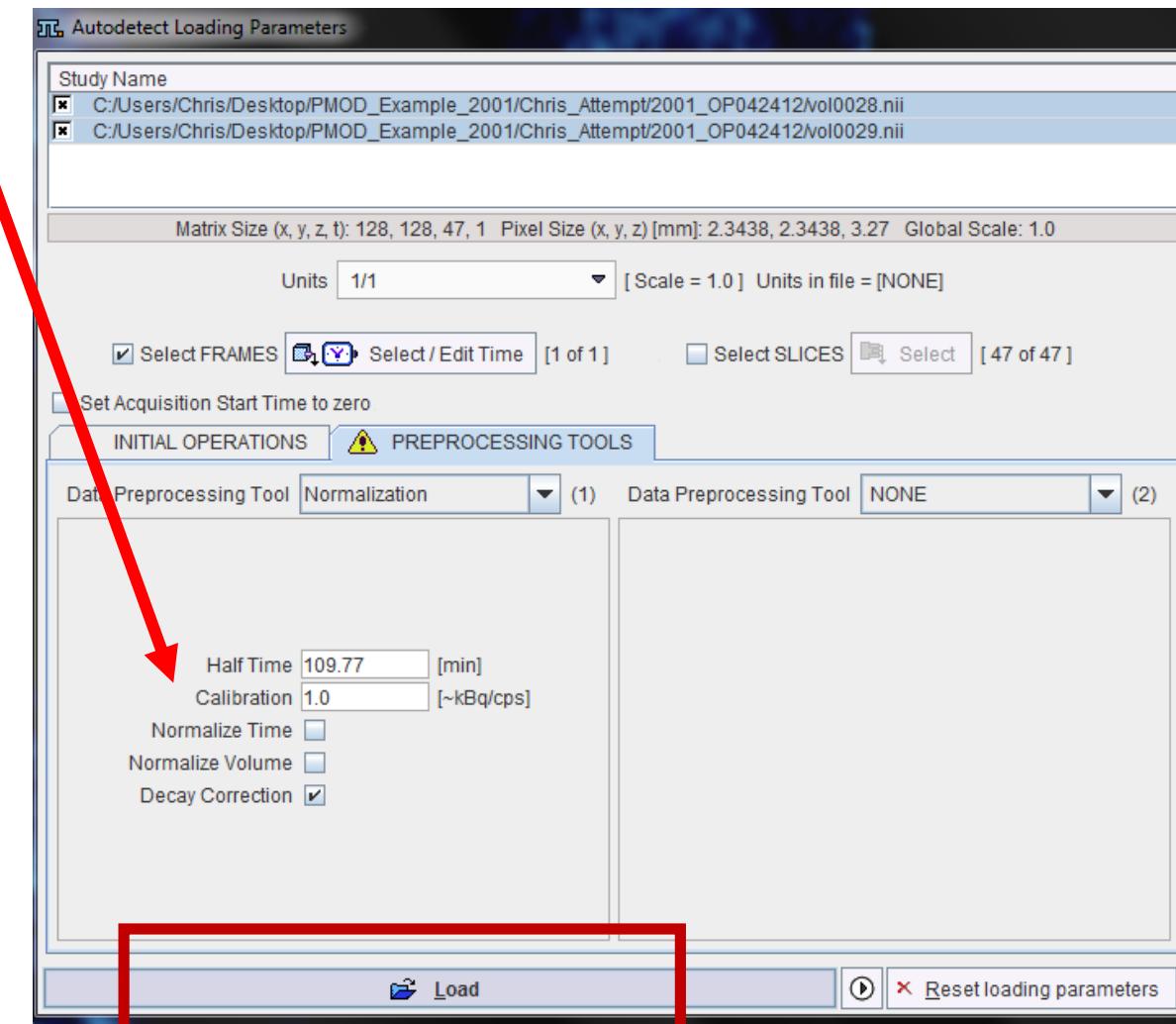
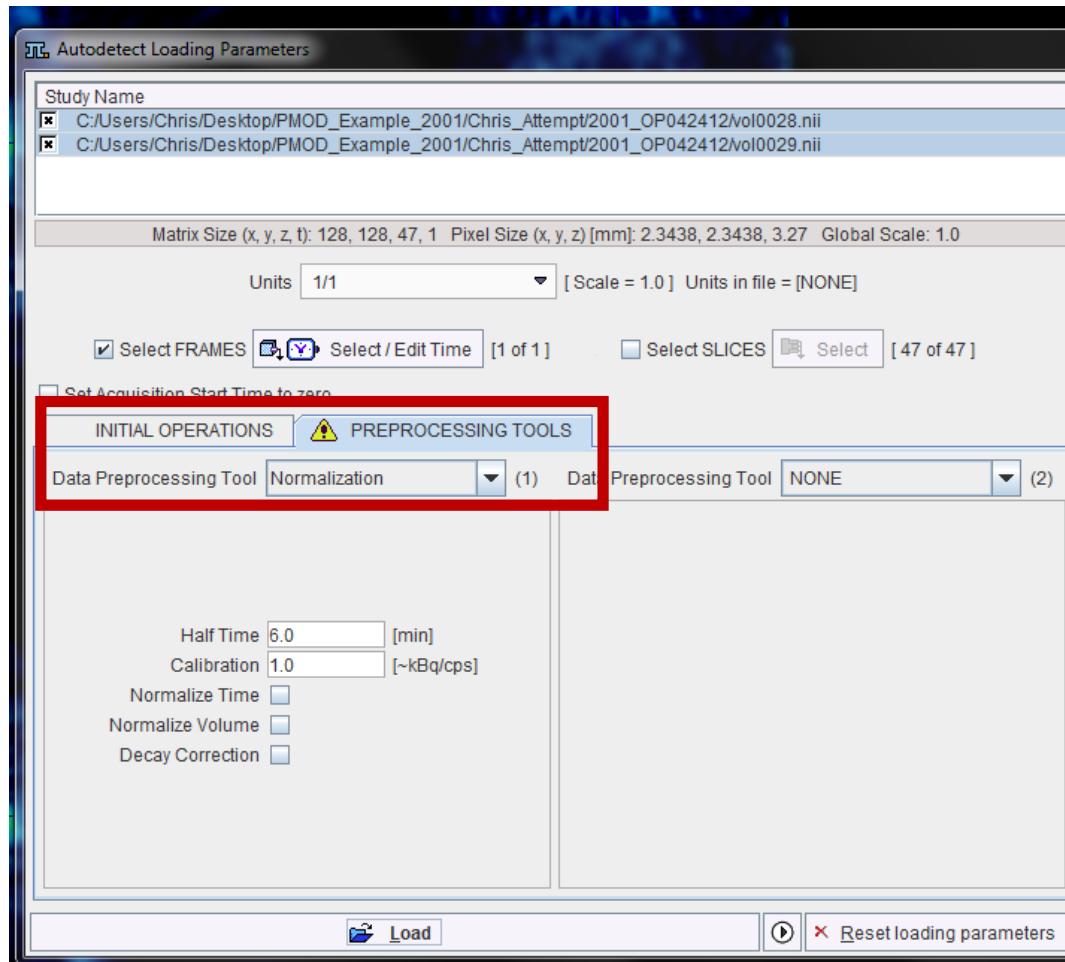
We enter those numbers into the FRAME selection box and press "Ok" when done



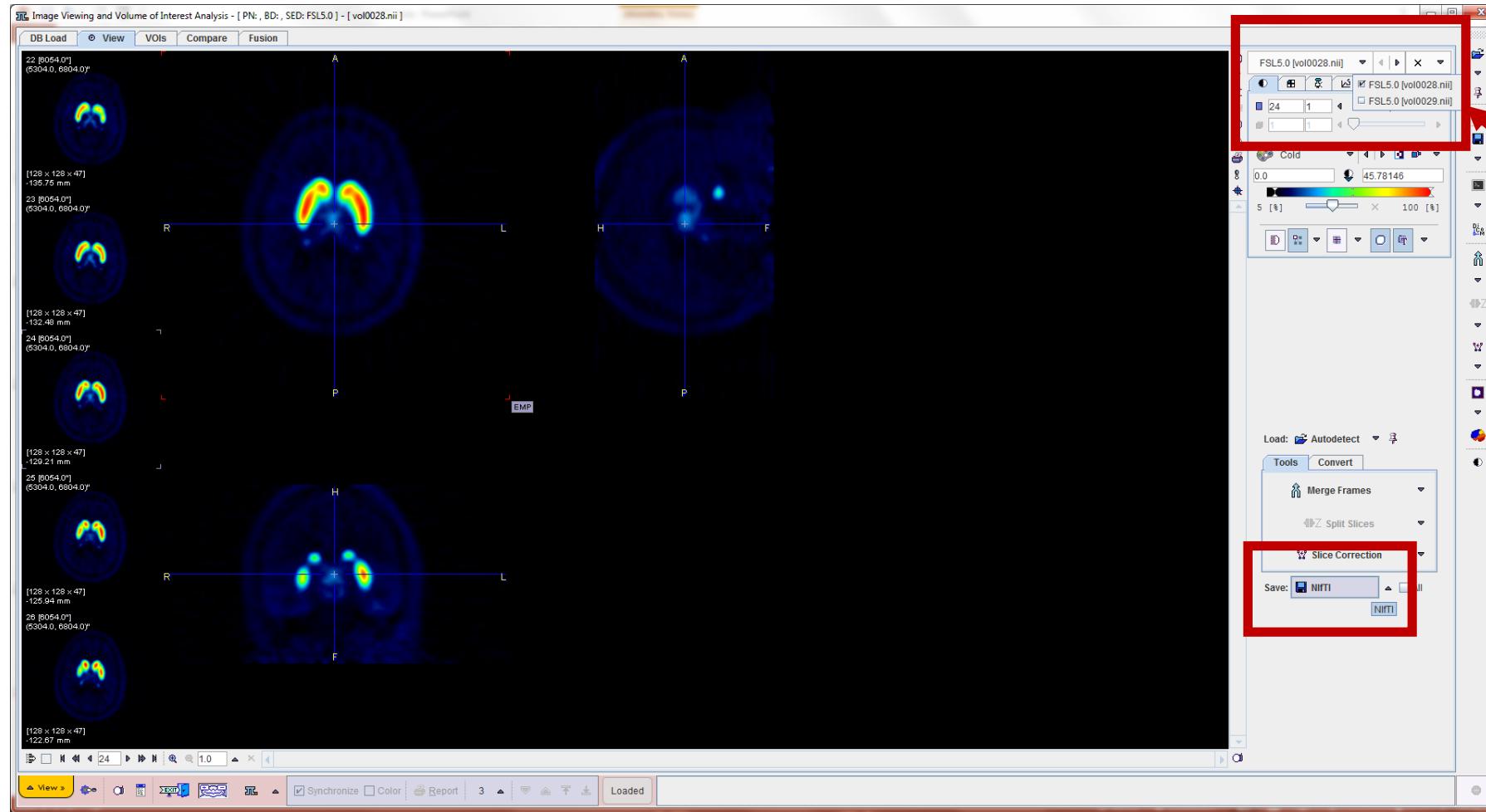
# Decay correction

Select “Preprocessing Tools” and from the drop-down menu by Data Preprocessing Tool, choose “Normalization”

Change Half Time to 109.77 & be sure Decay Correction is Checked, then click on “Load”



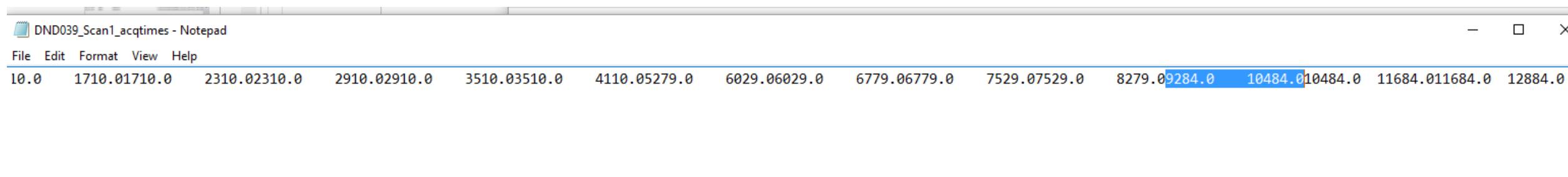
# Once the decay corrected vol0028-0031 images have been loaded, save them as vol00xx\_dc.nii files



Remember to use the pulldown menu to select each vol.nii file and save the decay\_corr version accordingly.

Repeat the Decay Correction steps for vol0032, vol0033, and vol0034

Remember to look in the acqtimes file and find the start and end time for frame 33 (vol0032), which will be the third to last pair of numbers



A screenshot of a Windows Notepad window titled "DND039\_Scan1\_acqtimes - Notepad". The window shows a single row of numerical data. The data consists of 14 columns of floating-point numbers separated by spaces. The first column is 10.0, followed by pairs of numbers such as 1710.0 1710.0, 2310.0 2310.0, etc., ending with 12884.0 12884.0. The entire row is highlighted with a blue selection bar.

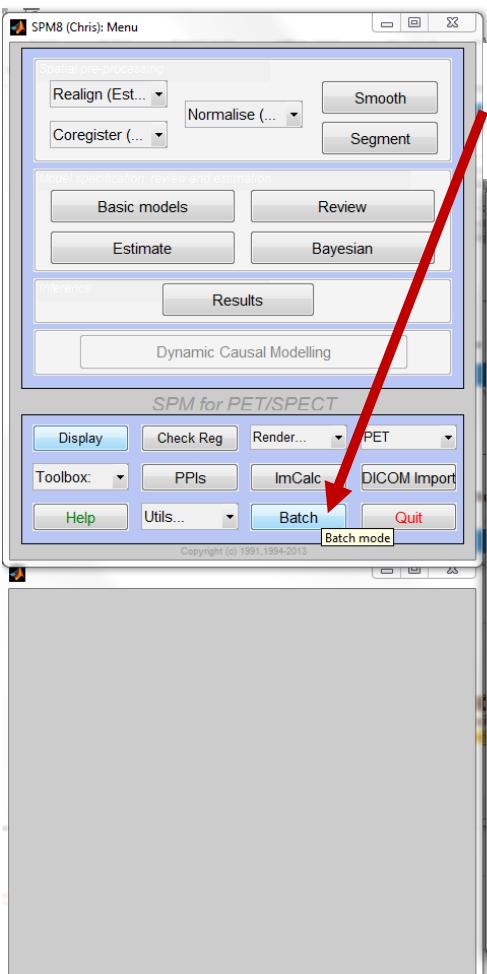
10.0	1710.0	1710.0	2310.0	2310.0	2910.0	2910.0	3510.0	3510.0	4110.0	4110.0	5279.0	6029.0	6779.0	6779.0	7529.0	7529.0	8279.0	8279.0	9284.0	9284.0	10484.0	10484.0	11684.0	11684.0	12884.0	12884.0
------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	--------	---------	---------	---------	---------	---------	---------

So, when done with these two sets of decay corrections we will have vol0028-0034.nii files in decay\_corr forms

# Realignment

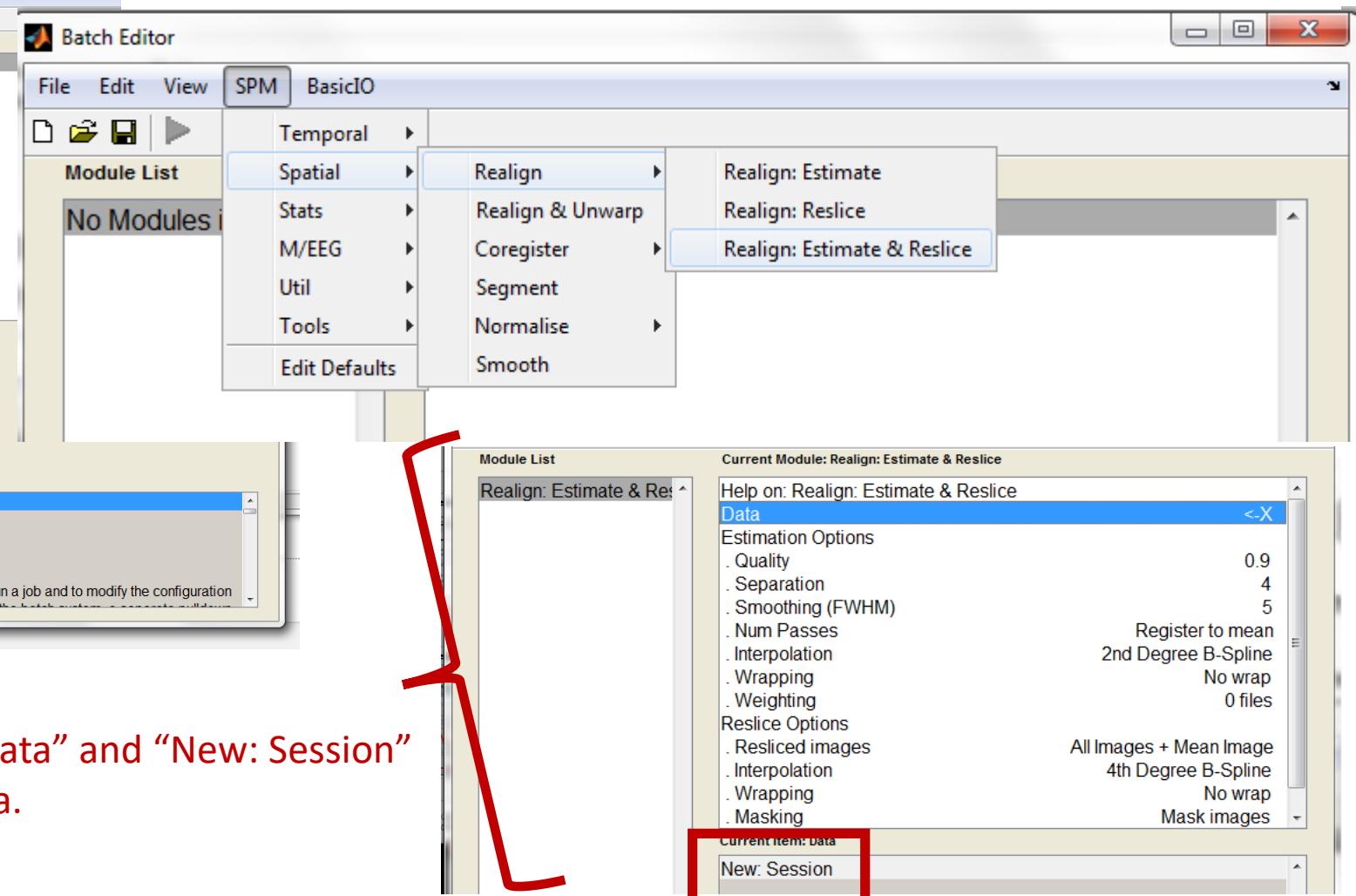
- For our next step, we will realign all of our vol images to the 20<sup>th</sup> image as it has sufficient information to serve as a reference. Essentially what we are doing here is using a software program to measure how much our images move around in time due to subject movement and then to correct them so that they are all in the same space.
- To do the realignment we will use a program called SPM (short for statistical parametric mapping) which runs in a program known as Matlab.
- So, you will need to open Matlab, navigate to the folder with the PET data you have been working on, and then type “spm pet” into the Matlab command window to launch the program.

# Realignment



From the SPM Menu, choose “Batch”  
This will open the Batch Editor.

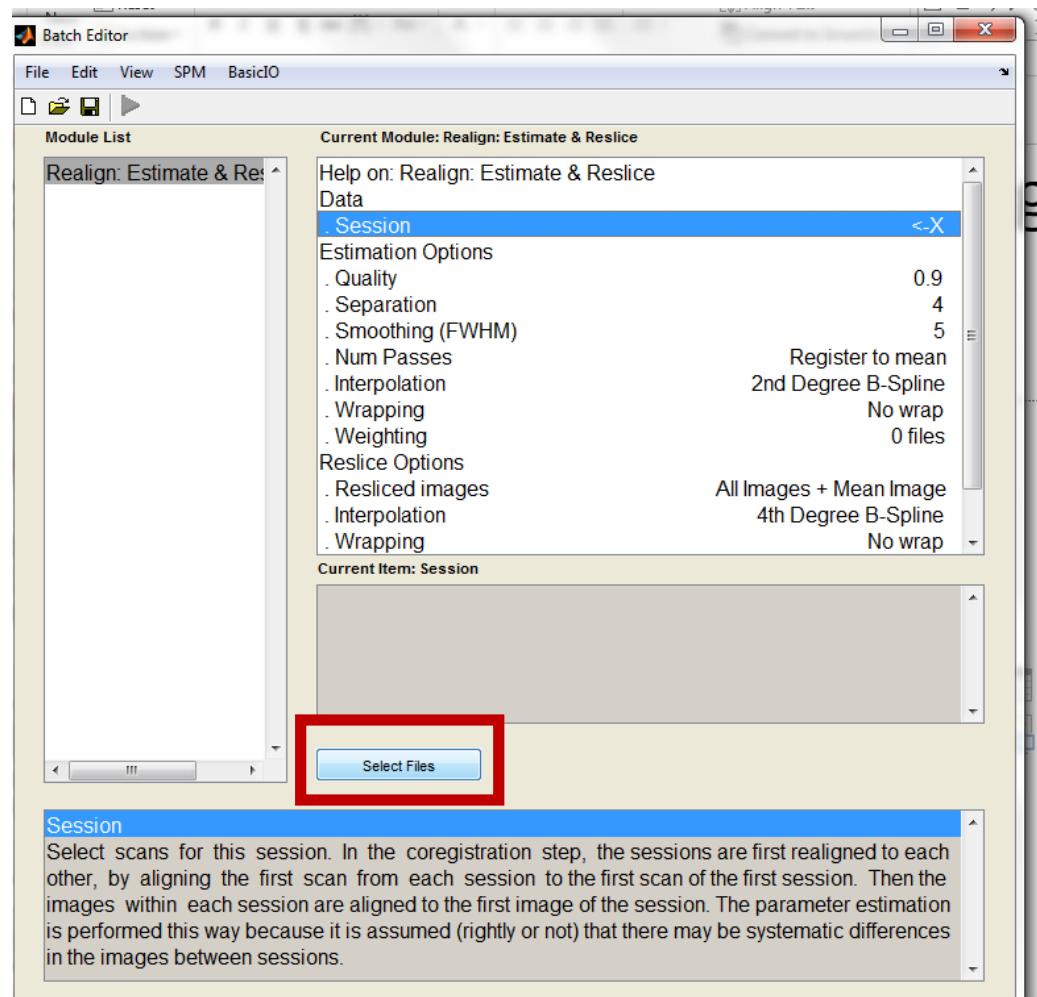
In the Batch Editor, select SPM, Spatial, Realign, Realign: Est & Reslice



When Realign: Est & Reslice opens, select “Data” and “New: Session”  
To specify we are realigning a new set of data.

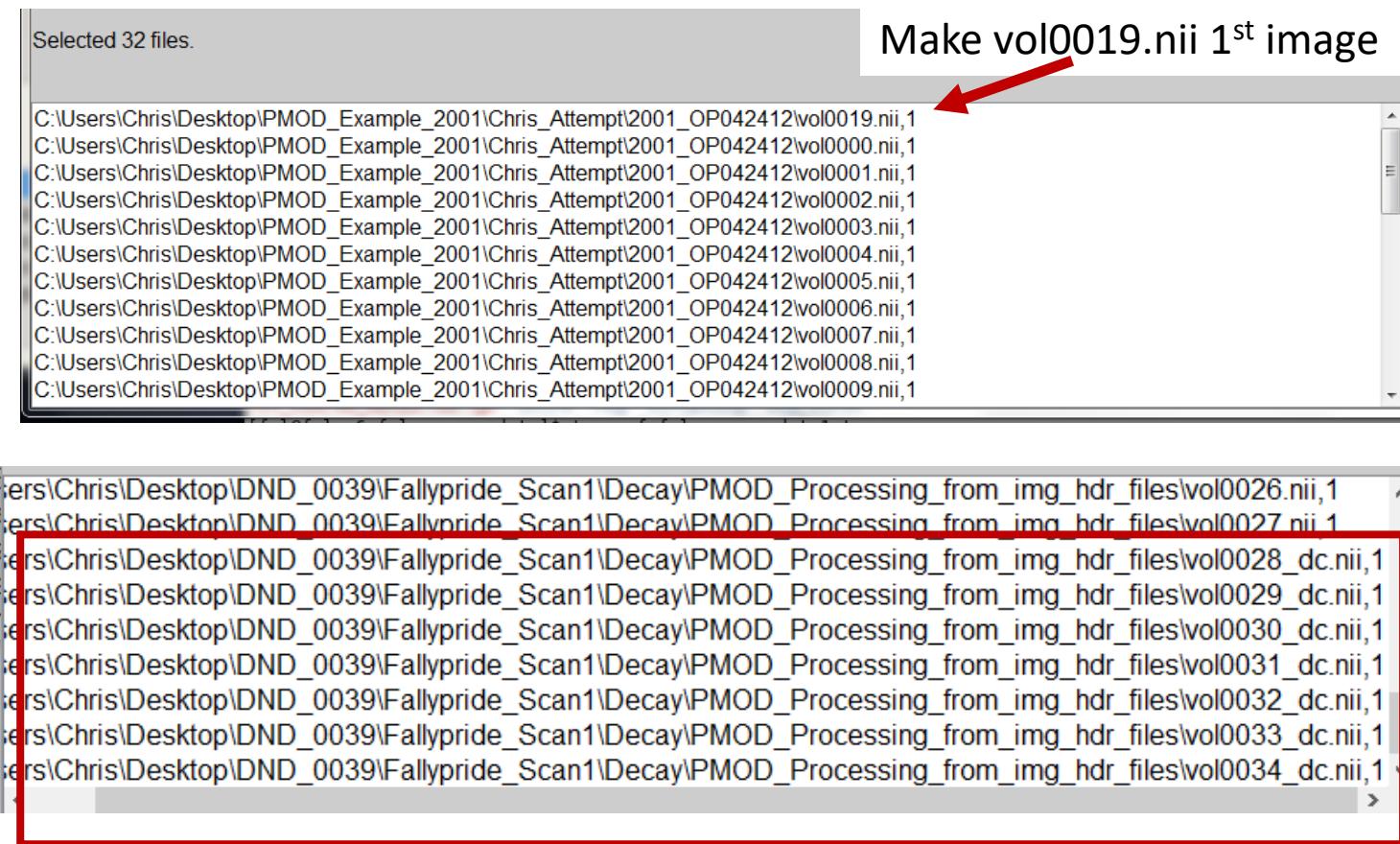
# Realignment

Click on the “X” next to Session under “Data” and then click on the Select Files button



The order in which you select the files matters. Select vol0019.nii as the first file as the realignment will be performed relative to that image. Then select vol0000 – vol0034\_dc.nii images as these are the order in which they were collected.

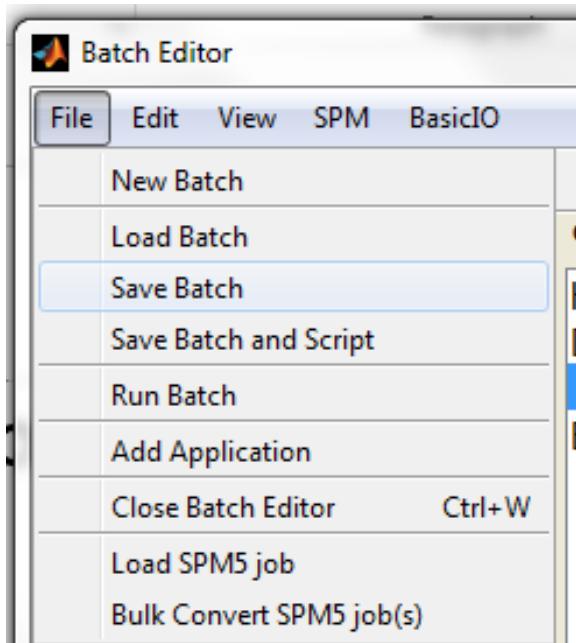
Click “Done” when all imgs selected.



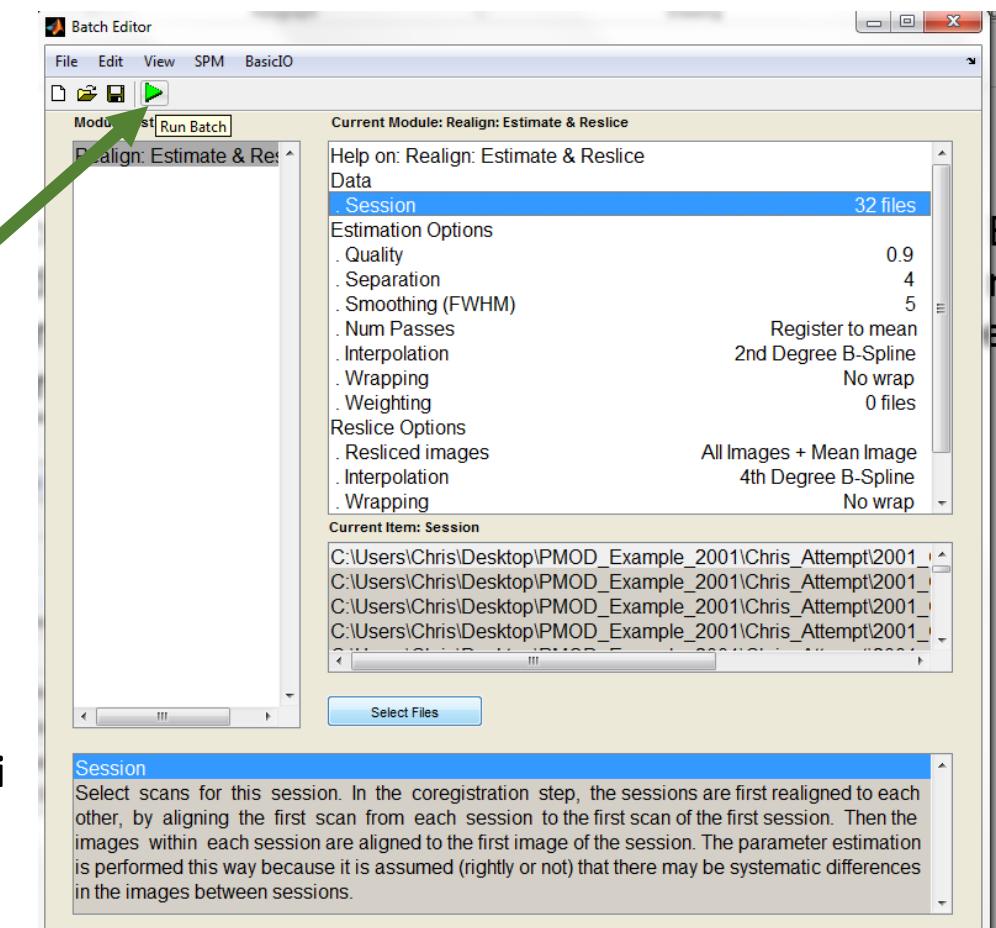
Note that we want the decay\_corr.nii files from the last 7 frames as these are the images we will be using in our subsequent analyses.

# Realignment

- I like to save my batch by going to File, Save Batch in the Batch Editor. Save this file with the subject number and PET realignment in the name and put it with the participant's PET data. This will allow us to always see what was specified in the realignment of the images.



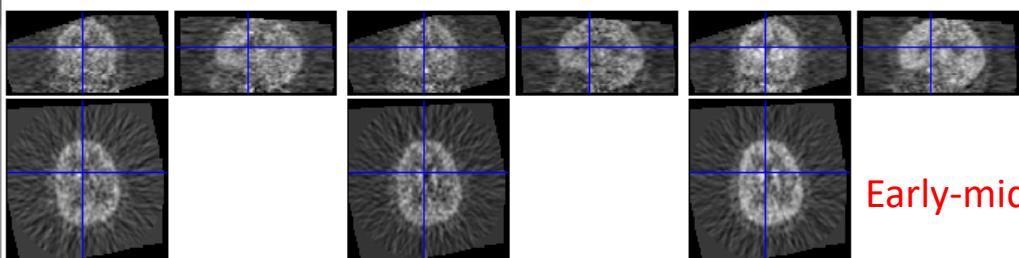
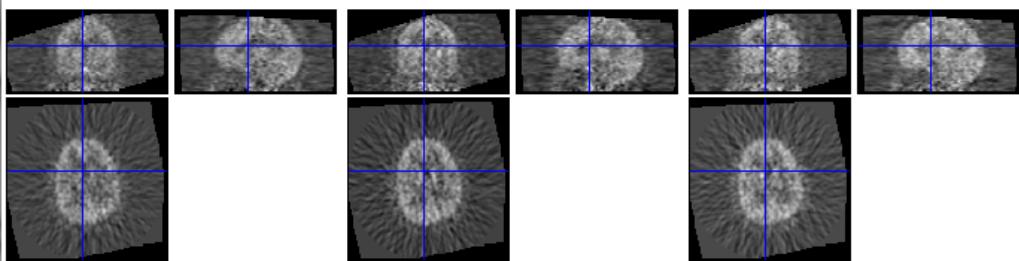
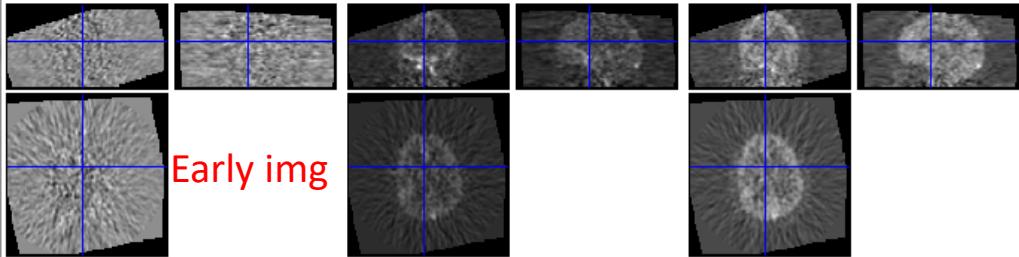
After saving the batch, click the green “play” button to run the realignment step. It will take a few minutes to complete.



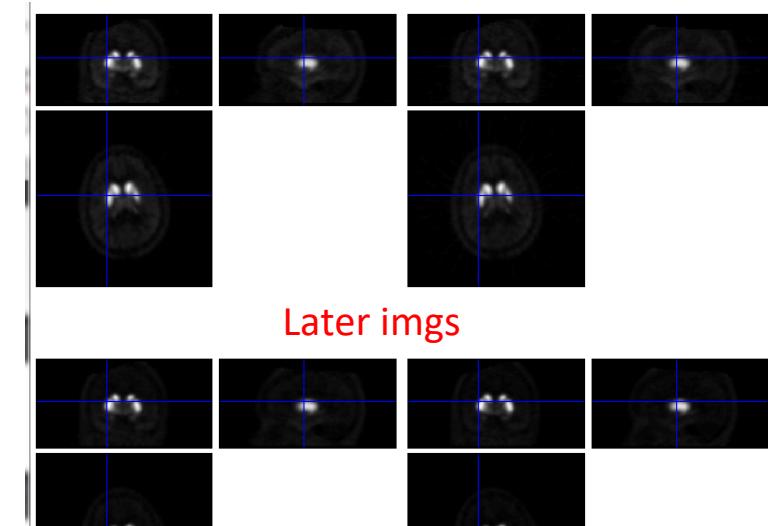
This step creates a mean PET image which will be labeled meanvol0019.nii  
As well as realigned versions of each vol.nii which will have an “r” prefix added to them.

# Checking Realignment

- It is useful to visually inspect your realigned vols to be sure the images are in the same space and that nothing weird happened during the realignment step in SPM.
- You can use the “CheckReg” button in SPM to view up to 15 images at a time. So, select some early, middle, and late img files to see how well they are aligned.



*Clicking around, you should see all images are aligned (same structures are found at the crosshairs across all images); also note that with time the images begin to look more like a brain as the Fallypride tracer is uptaken into the brain and then notice how most of the tracer is washed out by the last few images except for in areas with high levels of D2/3 dopamine receptors (the striatum).*

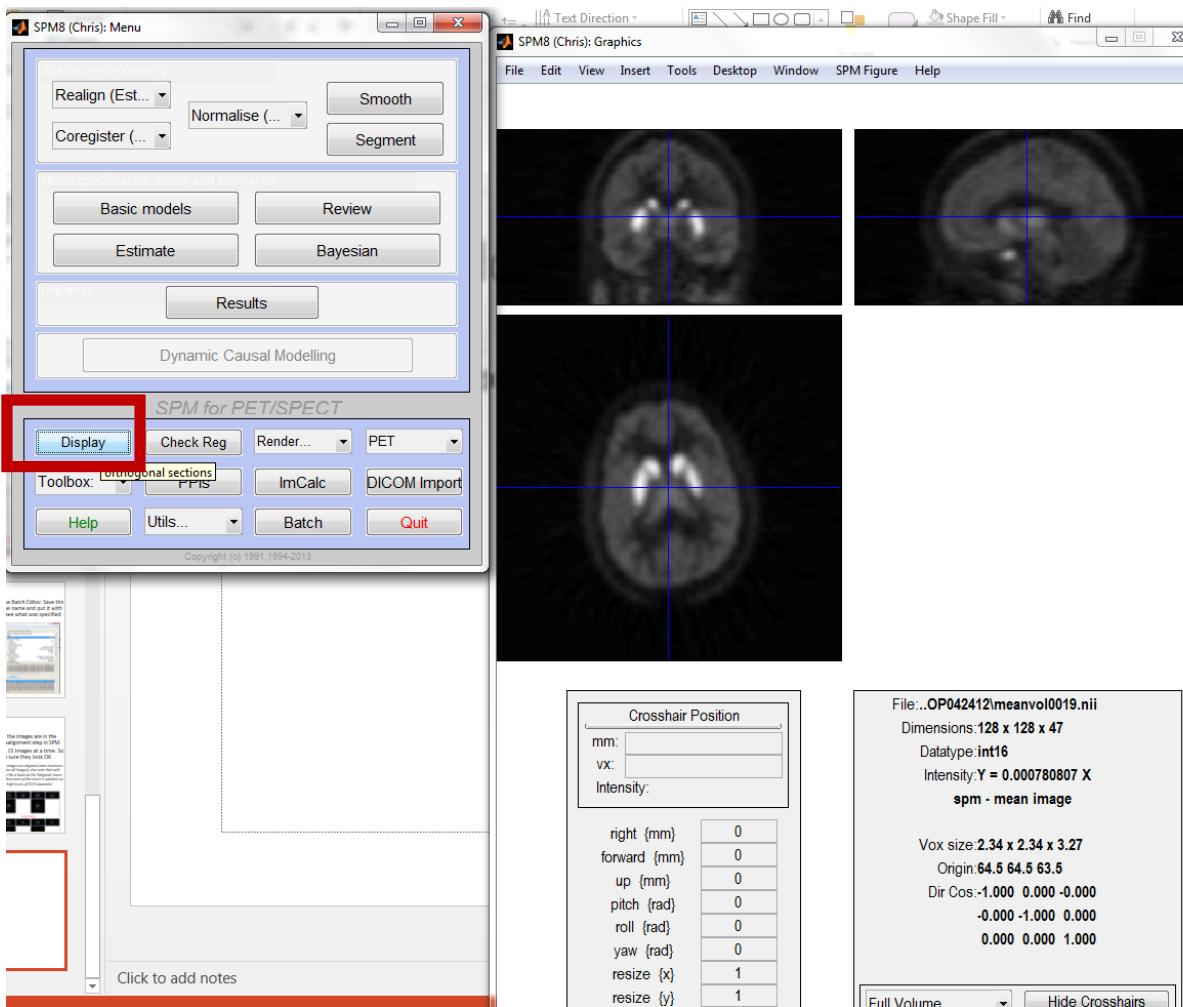


# Checking Realignment

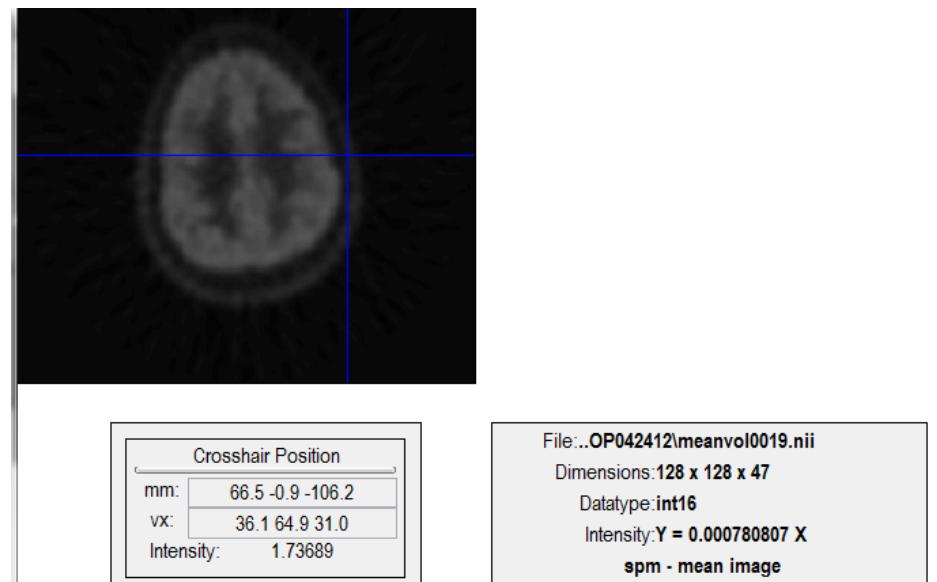
You can also click on “Display” in SPM to look at the meanvol0019.nii file

We want this image to look like a brain with no loss of signal anywhere (where the image is cutoff, etc...).

This image is important as it is the image we will use to warp standard space templates of regions of interest into the subject's PET image space.

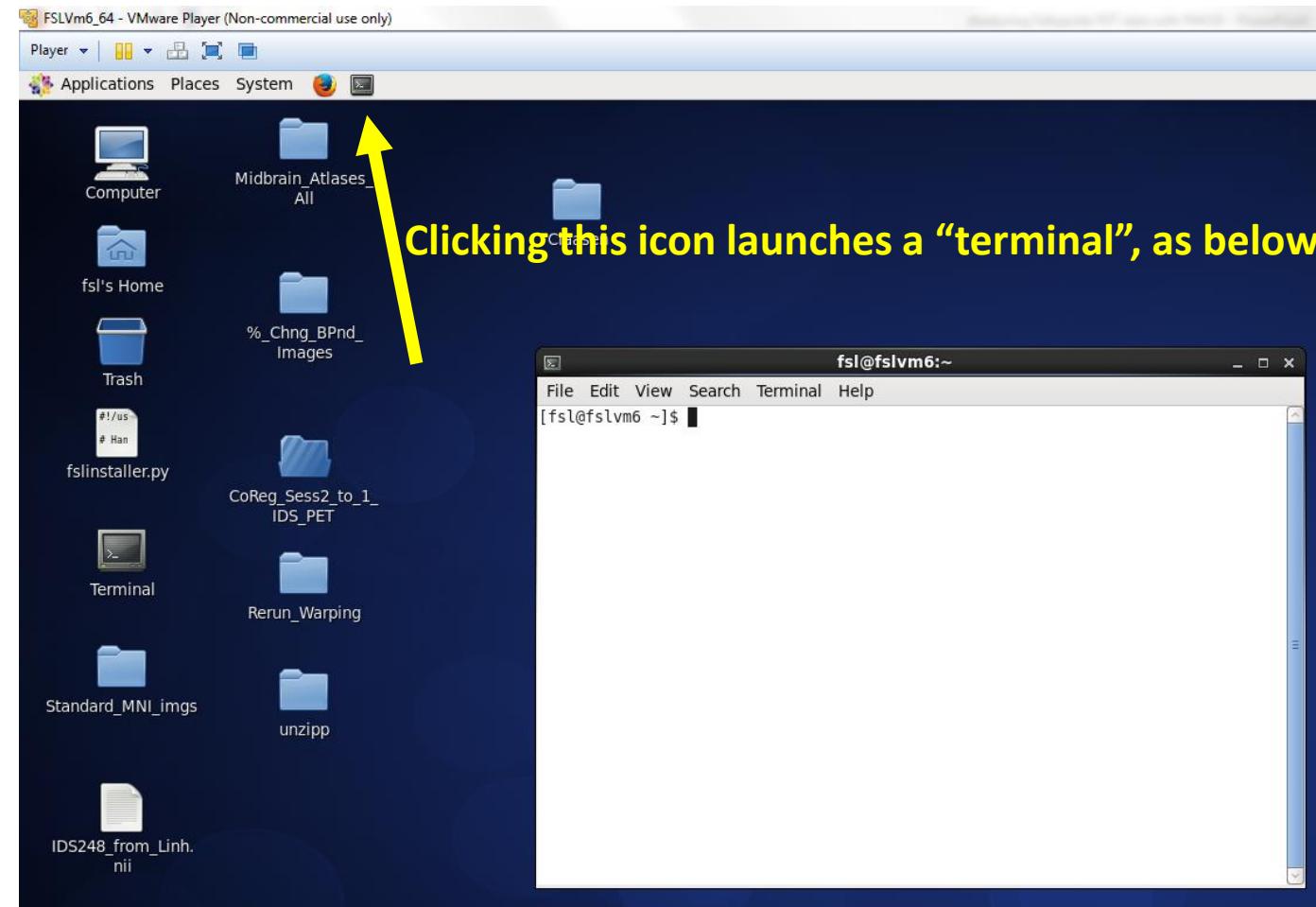


As you click around this image, note that the intensity value changes. Areas outside the brain tend to have intensities <2 in this particular subject. This will be important as we will threshold this image to only include values in the brain ( $\geq 2$ ). **Note, the intensity inside and outside the brain may vary in this image from subject to subject.**



# Using FSL commands to find transforms between PET, T1, and eventually MNI space

- In the unix terminal, type “fsl &”
- This launches the FSL gui menu from which you can view images with “fslview”, among other things
  - **Fslview will be used to verify visually that registrations are OK**
- For ease of use, it is best to use the “terminal” in the linux environment that FSL runs in and feed commands to the program



# Using FSL to find the transform for converting Standard Space Images to Subject PET Space

- We have two regions of interest (ROIs) that must be used in our kinetic modeling of the Fallypride PET data. The cerebellum serves as a reference region and the putamen serves as a D2/3 dopamine receptor-rich region.
- We have these ROIs in standard MNI (Montreal Neurological Institute) space: mni\_cerebellum\_posterior.nii, mni\_putamen.nii (These standard ROIs can be found on TEBA in (\Active\_Lab\_Projects\Chris)
- We are going to register the meanvol0019 from the PET data with the subject's structural (T1) image 1st
- To begin, threshold the mean0019vol.nii to 1 to remove signal not in the brain.
  - In the FSL terminal type: `fslmaths meanvol0019.nii -thr 1 meanvol0019_thr.nii`
  - This will create a new image with the mean volume thresholded at 1.

# Initial FSL registration Steps – PET to Subject's T1

#=info on step; 1. first command you will type in terminal; highlighted files will need to reflect name of subject and subject's data files you are using

# coreg T1 to Session\_1 PET mean vol using DOF 6

1. flirt -in T1 -ref meanvol\_thr -dof 6 -out T1\_2\_meanvol -omat T1\_2\_meanvol.mat

# invert matrix from step above

2. convert\_xfm -omat meanvol\_2\_T1.mat -inverse T1\_2\_meanvol.mat

You can open the T1\_2\_meanvol.nii.gz file and overlay it on the meanvol\_thr in **Fslview** to see how well the registration worked

# Next FSL registration Steps – Find transform between MNI (standard space) and subject's T1 space

**NOTE: These steps have been done for you in the DND data.**

All required transform files can be found on TEBA in:

Zalddlab\Active\_Lab\_Projects\DANeuromodulation\MRI\_Data\DND\_Scans\DNDXXX\T1\_2\_MNI where XXX is the subject #

# coreg linearly T1 to MNI space

3. flirt -in **T1** -ref /usr/local/fsl/data/standard/MNI152\_T1\_2mm -out T1\_2\_mni\_flirt -omat T1\_2\_mni\_flirt.mat

# coreg nonlinearly T1 to MNI space

4. fnirt --ref=/usr/local/fsl/data/standard/MNI152\_T1\_2mm --in=**T1** --aff=T1\_2\_mni\_flirt.mat --  
cout=T1\_2\_mni\_fnirt\_warpcoef --iout=T1\_2\_mni\_fnirt

# invert the nonlinear transform to move from MNI to T1 space

5. invwarp -w T1\_2\_mni\_fnirt\_warpcoef.nii.gz -o MNI\_2\_T1\_fnirt\_warpcoef.nii.gz -r **T1**

You can open the T1\_2\_mni\_fnirt.nii.gz file and overlay it on the standard MNI brain (MNI152\_T1\_2mm) in **Fslview** to see how well the registration worked

# Move MNI reference regions to T1 space and then to subject's PET space

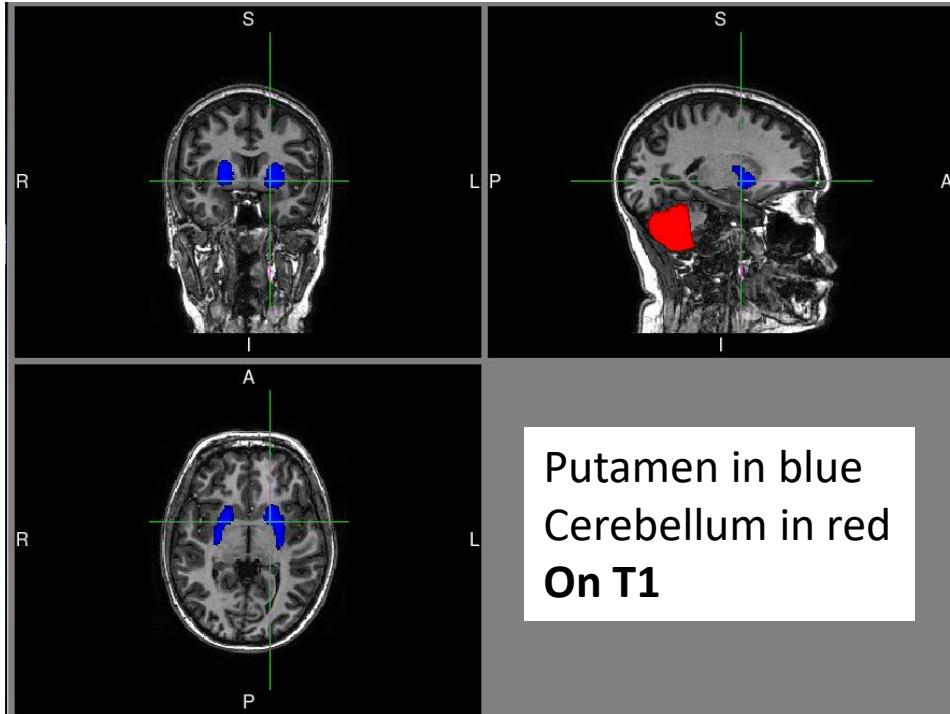
```
# apply MNI_2_T1 fnirt to bring mni_cerebellum_posterior and mni_putamen to T1 space  
6. applywarp -i mni_putamen -o putamen_T1space -r T1 -w MNI_2_T1_fnirt_warpcoef.nii.gz
```

Zaldlab\A **The putamen T1space and cerebellum T1space images can be found in:**

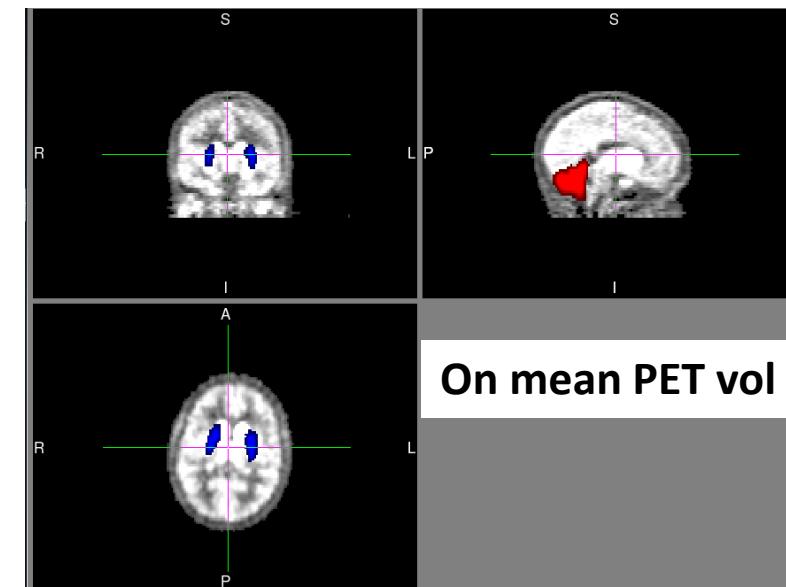
ctive\_Lab\_Projects\DANeuromodulation\MRI\_Data\DND\_Scans\DNXXXX\T1\_2\_MNI where XXX is the subject #

```
# Move cerebellum_posterior and putamen from T1 to PET space
```

```
7. flirt -in putamen_T1space -ref meanvol_thr -applyxfm -init T1_2_meanvol.mat -out putamen_PETspace
```



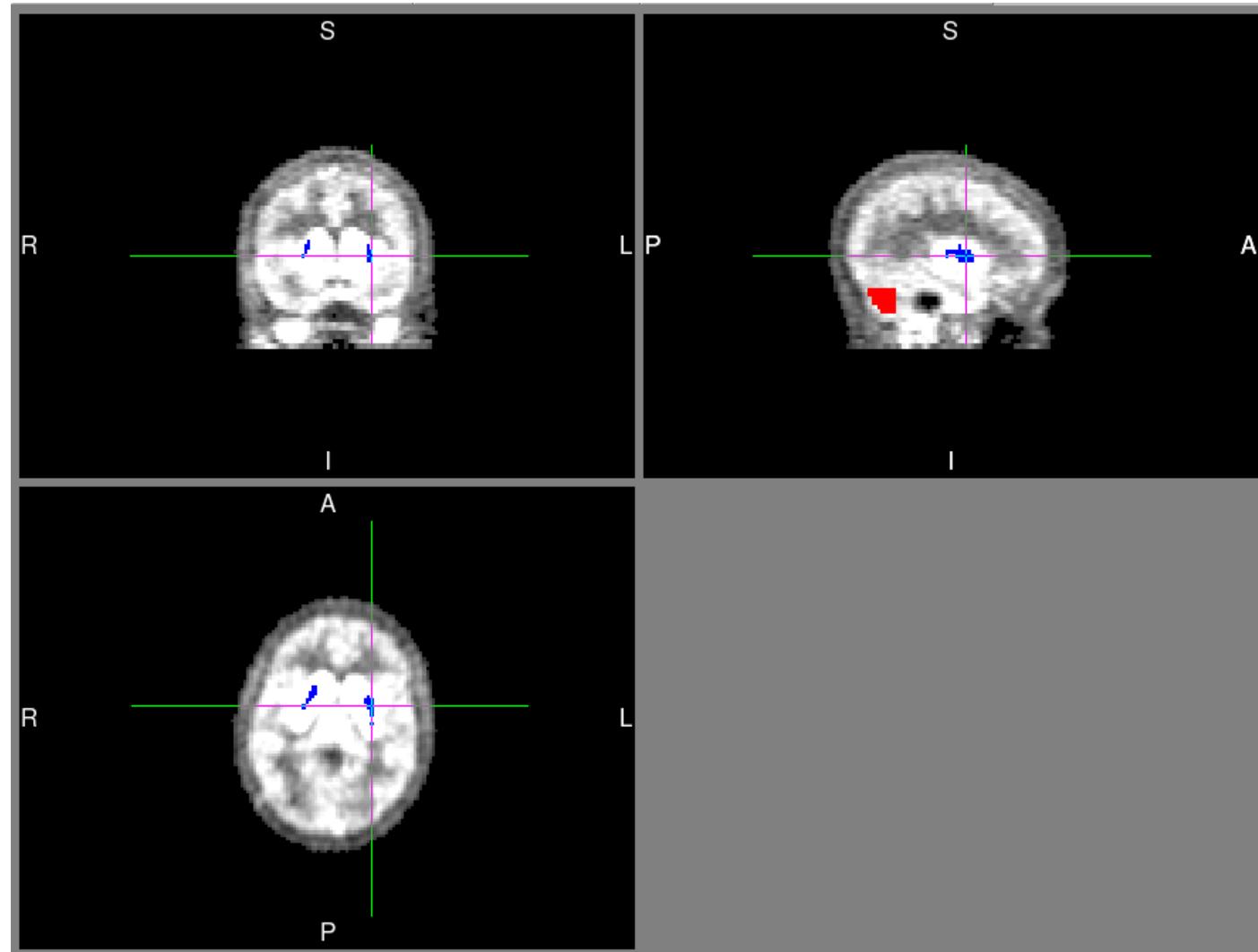
Use fslview to verify good assignment of regions in subject's T1 image and subsequent PET image (meanvol\_thr)



# Threshold the ROIs to only include areas FSL assigned to those regions with high confidence

- If you click around in FSL view enough while the ROIs are loaded, you will see while most of the ROI has an intensity value of “1” some voxels have values less than that. This means FSL was not 100% confident in assigning those voxels to the putamen or cerebellum in this particular subject.
- Thus it is good practice to threshold the ROI masks we just created to a value of **1 for cerebellum and 0.99 for putamen** to only include in each mask voxels we are confident are in each of those regions.
- To do this, in the terminal type “fslmaths putamen\_in\_PETspace –thr 0.99 putamen\_in\_PETspace\_thr” & then “fslmaths cerebellum\_in\_PETspace –thr 1 cerebellum\_in\_PETspace\_thr”
- Then unzip these files for PMOD to be able to read them;  
“gunzip \*PETspace\_thr.nii.gz”

# FSL view of thresholded ROIs

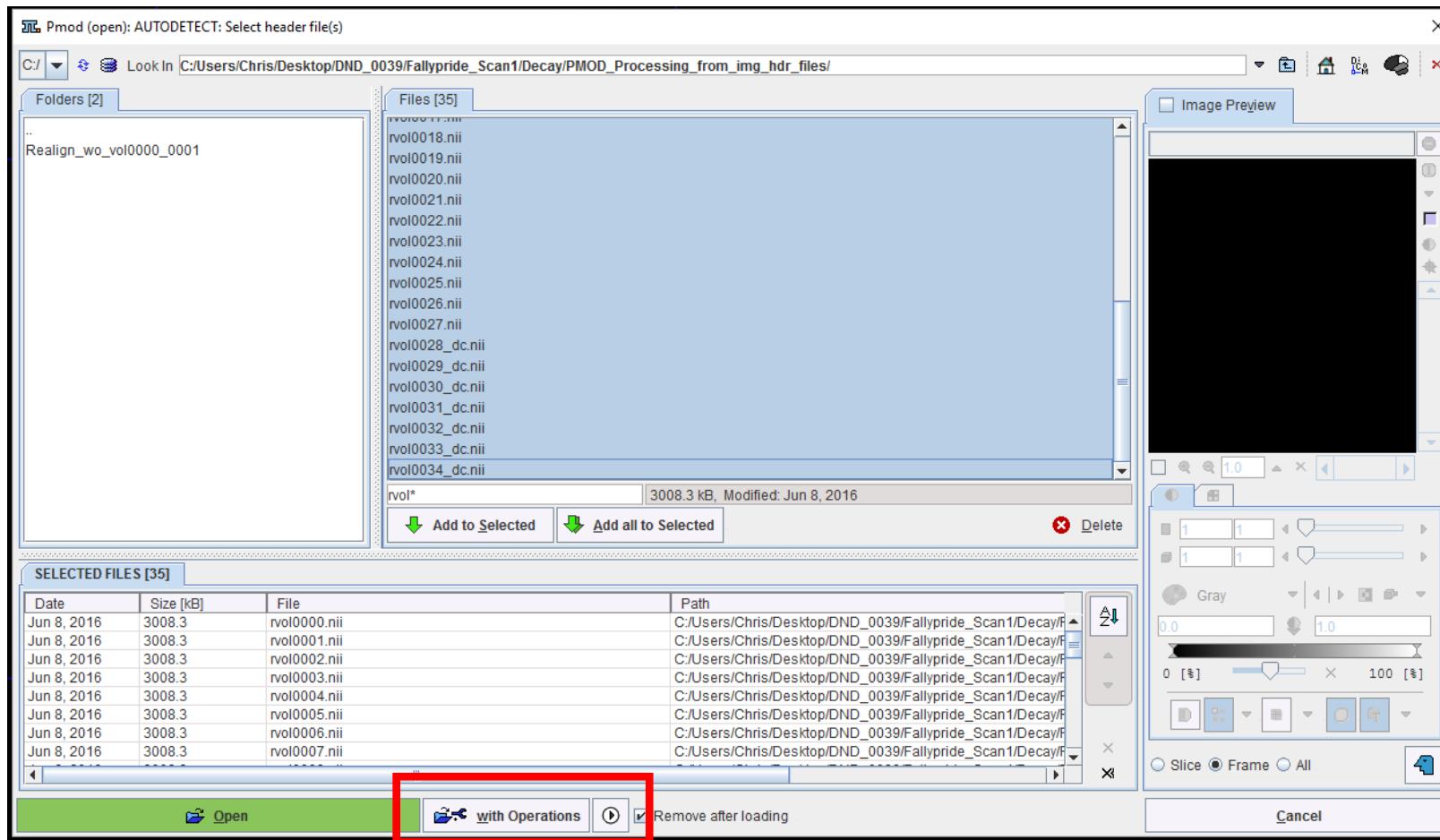
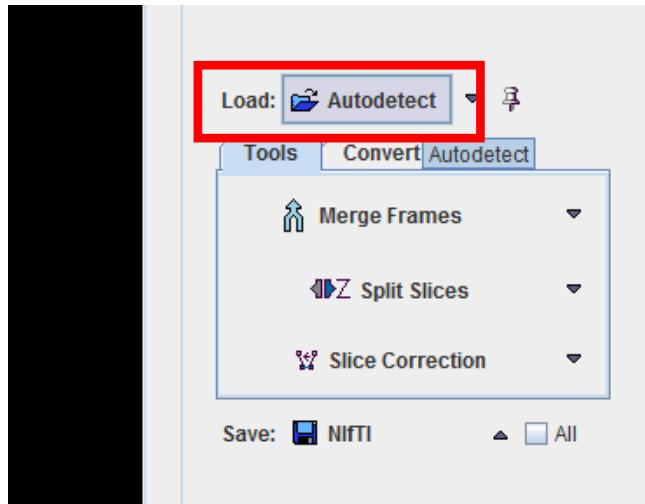


Putamen in blue  
Cerebellum in red

If ROIs look OK, copy them to the desktop space you will need them in to use them in PMOD.

# Merge realigned volumes and be sure timing file is attached

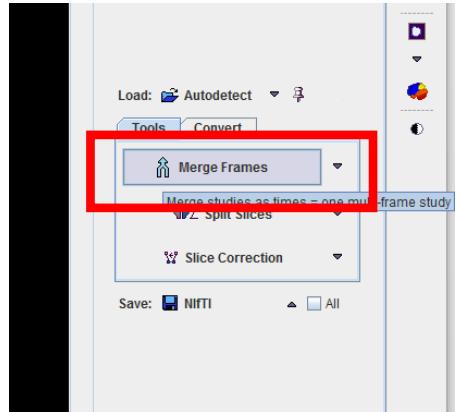
Back in PMOD View, choose LOAD “Autodetect”



Select all the rvol.nii files, in numerical (time) order, click on “Open with Operations”

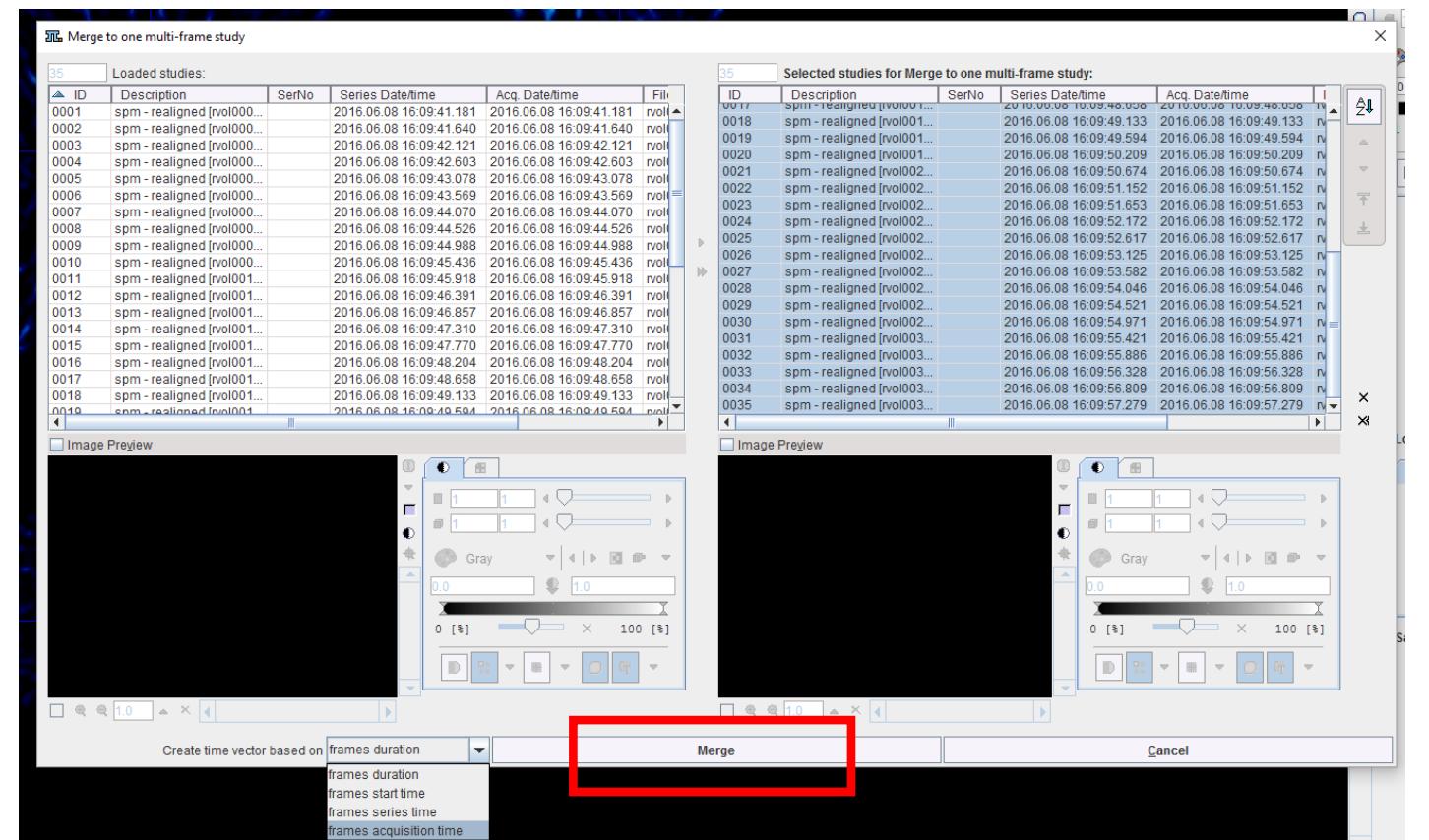
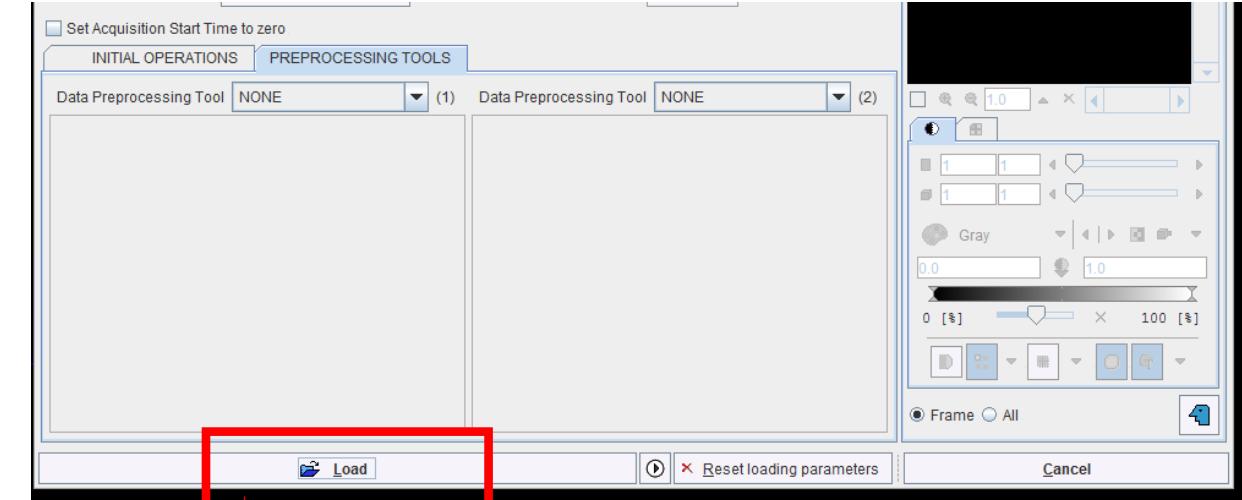
Be sure all decay correction or rotation options are turned off, then click “Load”

Once imgs load, Choose “Merge Frames”, at right

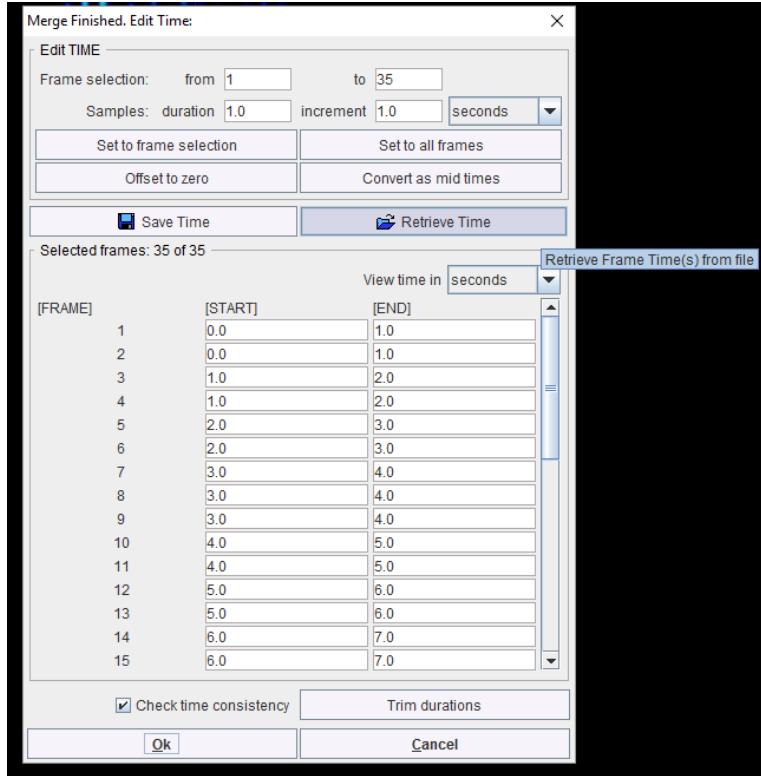


Select all 35 vol files on the right and choose Create time vector based on “frames acquisition time” from drop-down menu at bottom left, then click “Merge”

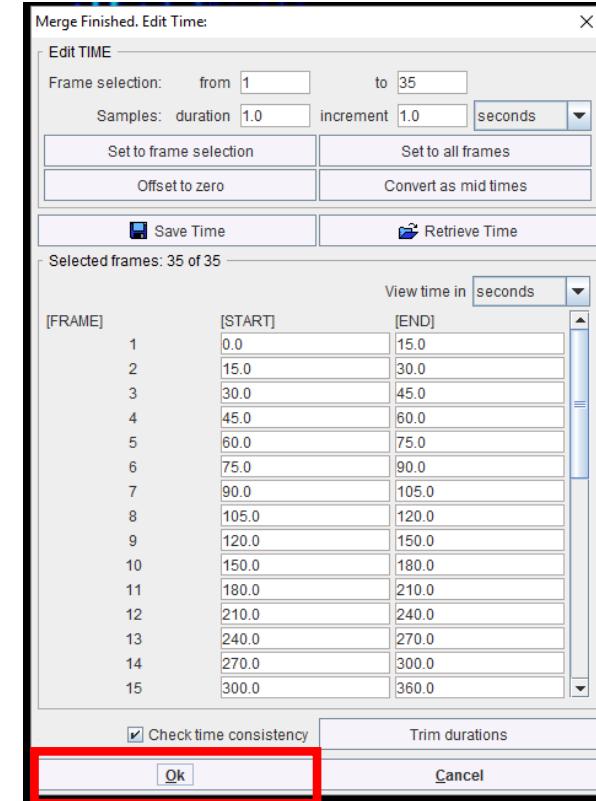
When get a pop box about creating a new study just leave the default selected and click “OK”



- When the timing window appears, select retrieve time
- Then load the .acqtimes file you created earlier and click OK



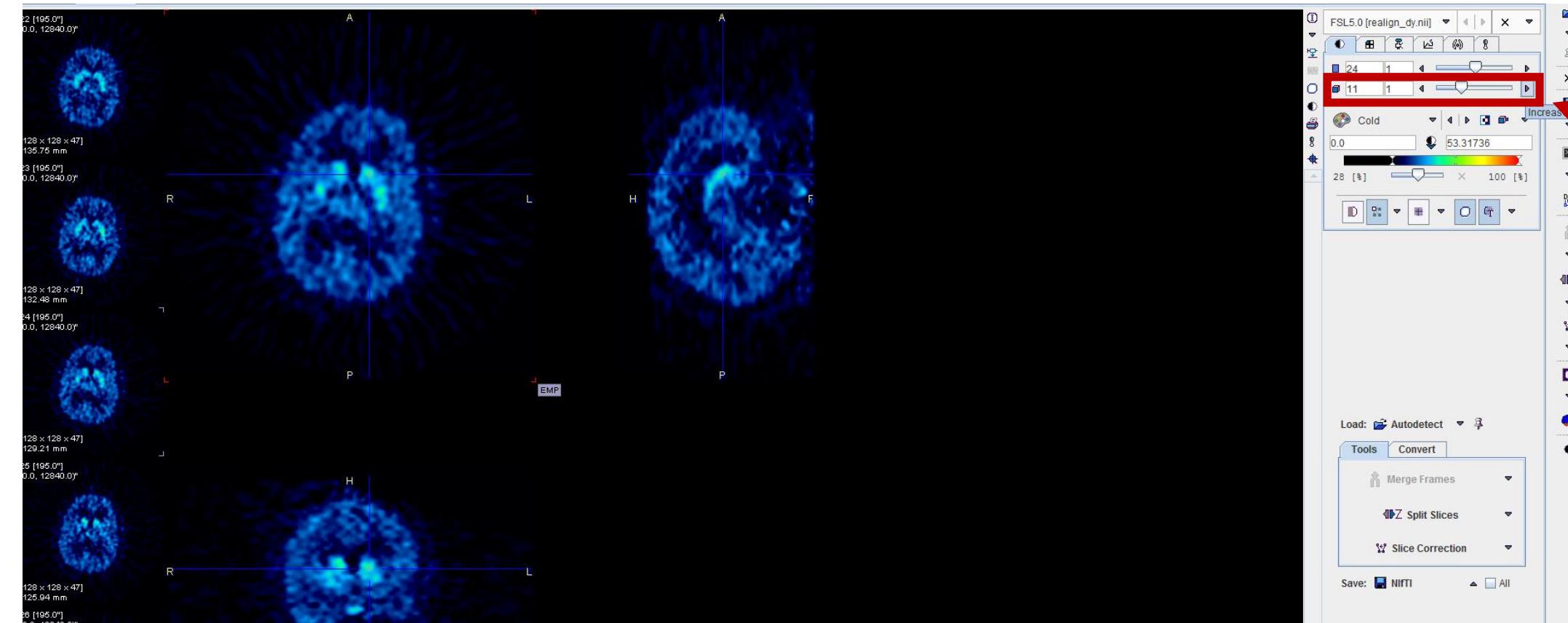
After adding .acqtimes file



This will produce a merged .nii file that contains all the realigned vols as well as the timing information you will need to do the kinetic modeling and estimate BPnd

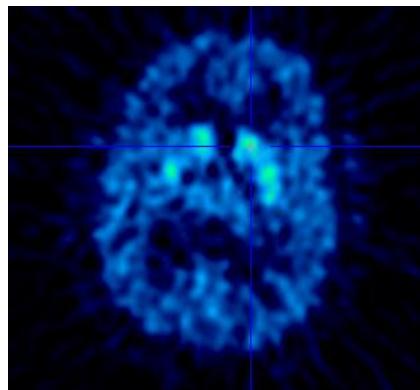
Be sure the merged img file looks OK, then save the new image as realign\_all\_dy\_with\_time.nii

- As you scroll through time, you should see the signal in the striatum continue to increase across all frames. If the intensity seems to drop off between one frame and another, especially towards frames 28-35, this could be because the decay correction was not applied correctly.

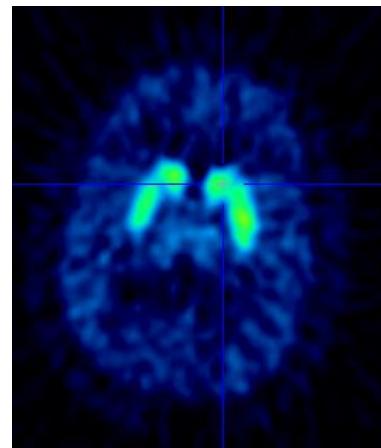


Be sure the merged img file looks OK, then save the new image as realign\_all\_dy\_with\_time.nii

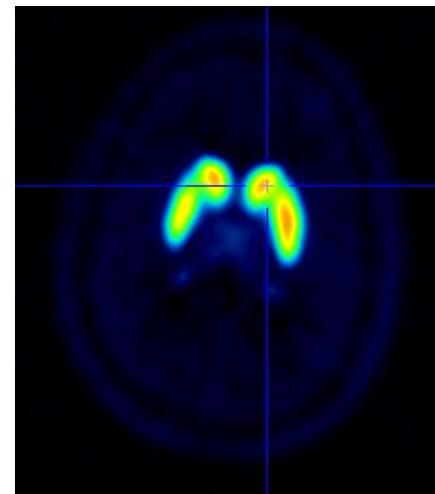
Early PET frame



Mid PET frame



Late PET frame

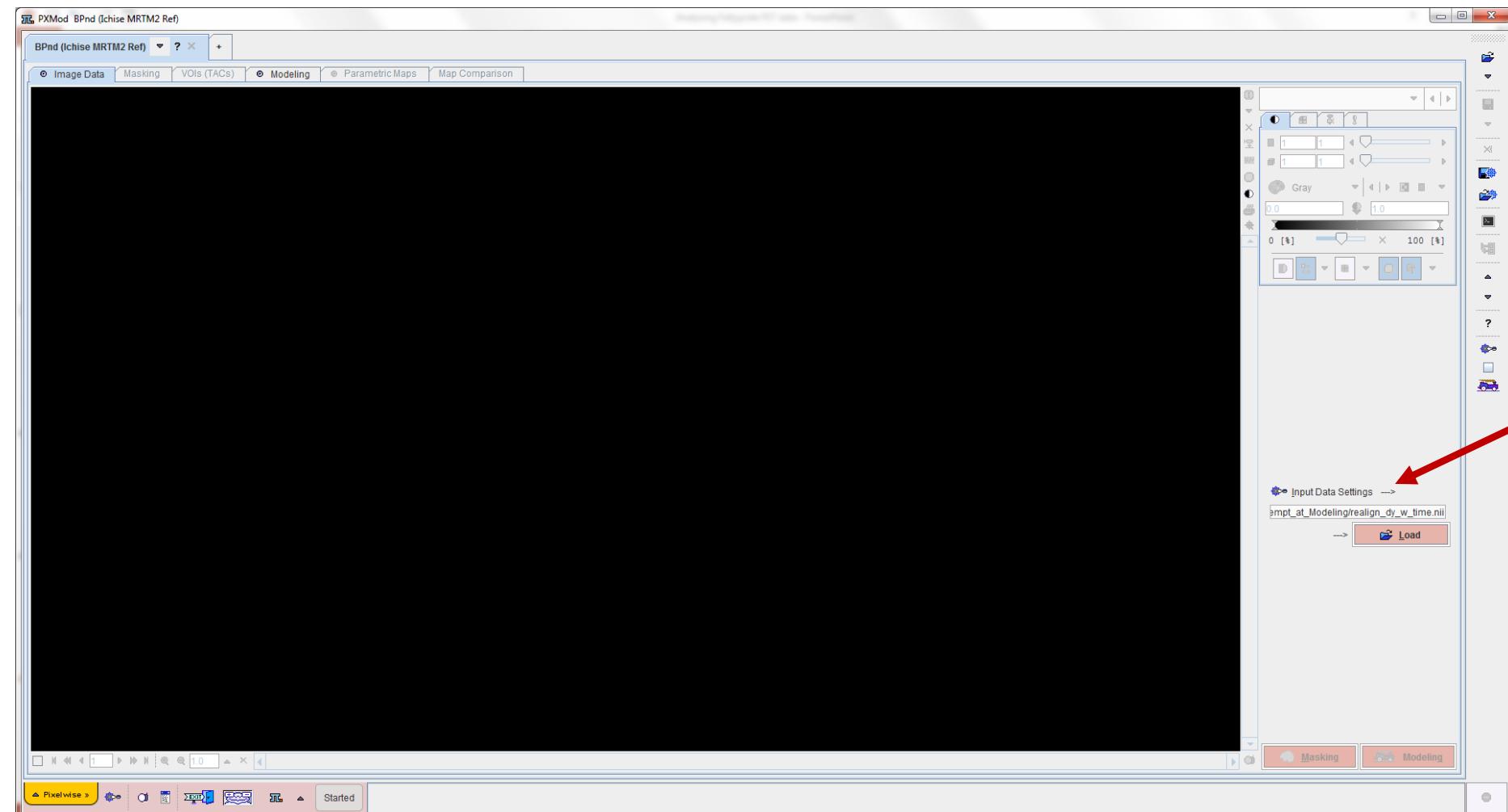


Note, there should be little to no movement in the image as you scroll through time. If you see excessive movement, try:

- 1) Running realignment on the rvol files (select rvol0019 as the reference image)
- 2) If problems persist you can delete the first vol (vol0000) or first and 2<sup>nd</sup> (vol0000 and vol0001) but only do this as a last resort as this modification will mean modifying the timing files as well; see Chris for more info if you have to do this

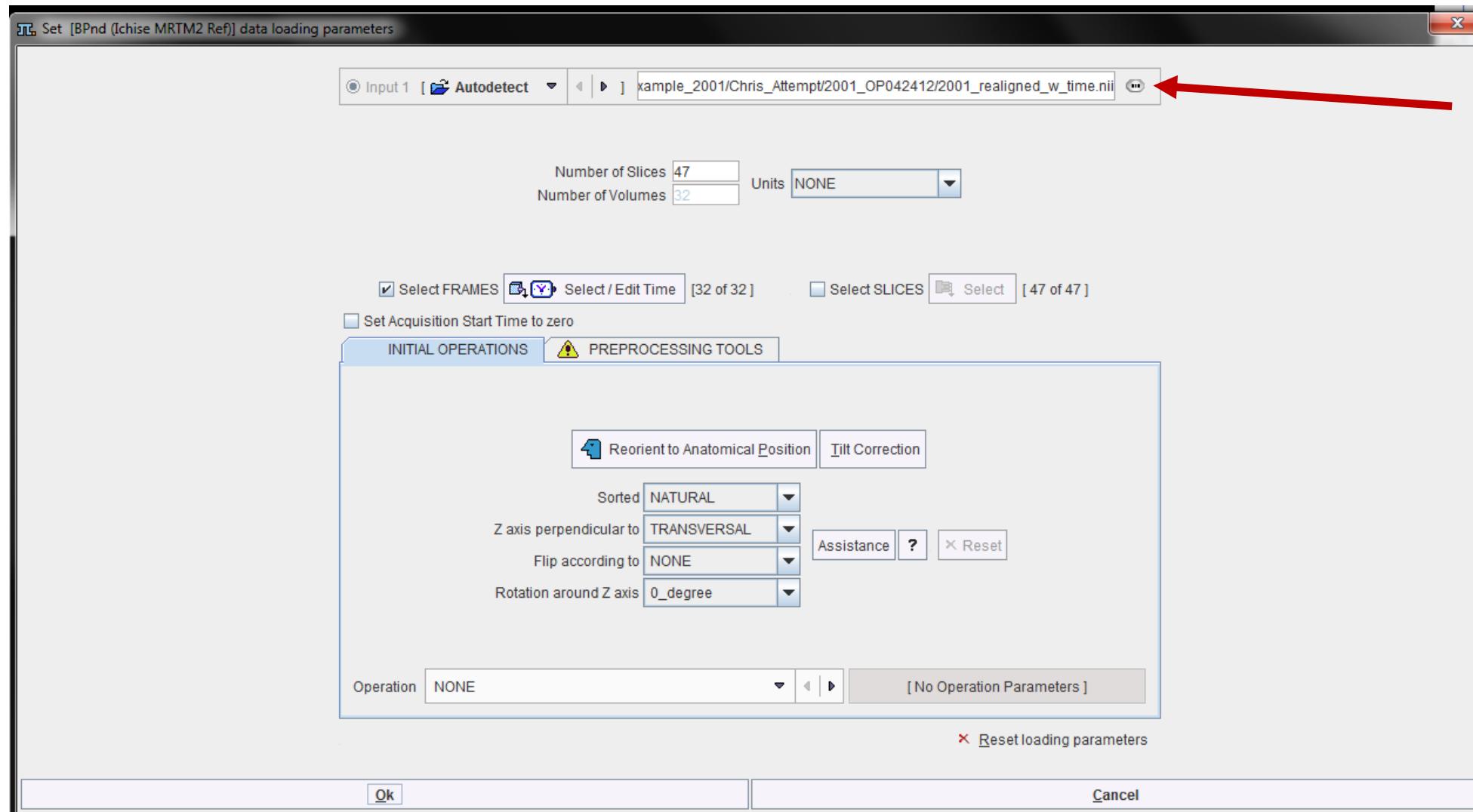
If all looks OK, save image as nifti as Subject\_realign\_dy\_with\_time.nii

# Using PXMOD to Model the Kinetics of Fallypride

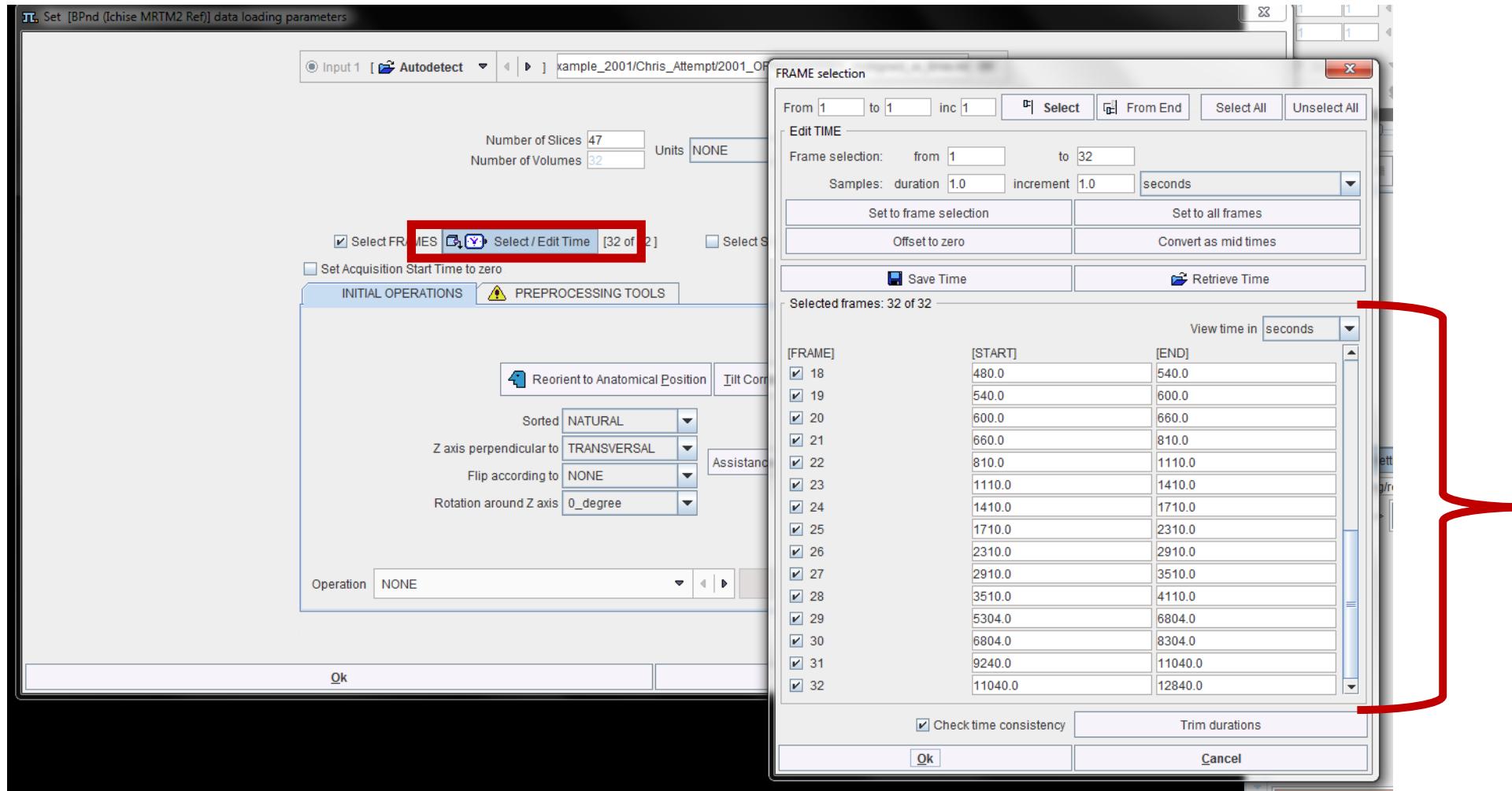


Click on  
“Input Data Settings”

# Load the realigned\_w\_time.nii file

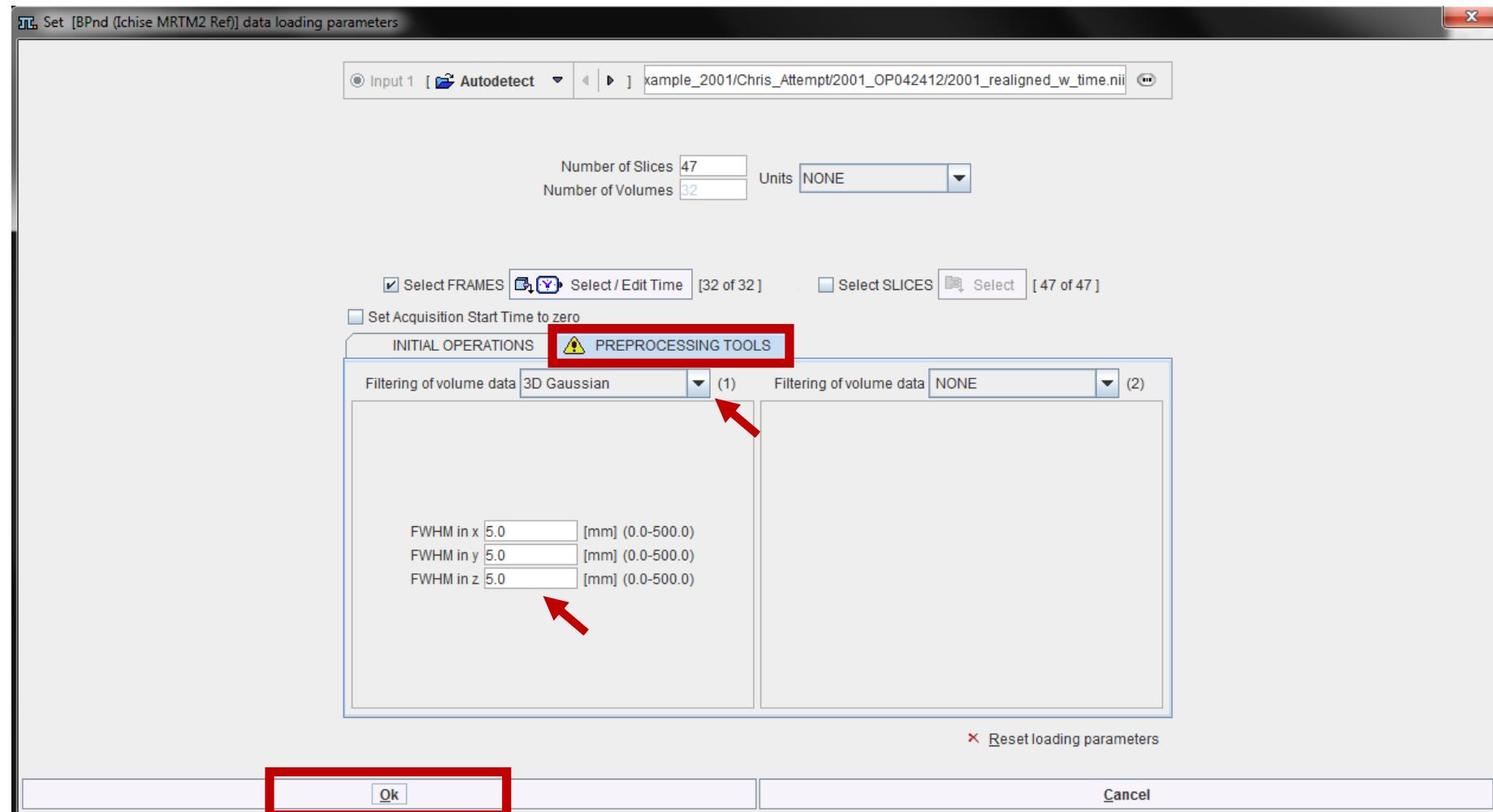


# Click on “Select/Edit Time” to be sure timing of frames is associated with the nii file

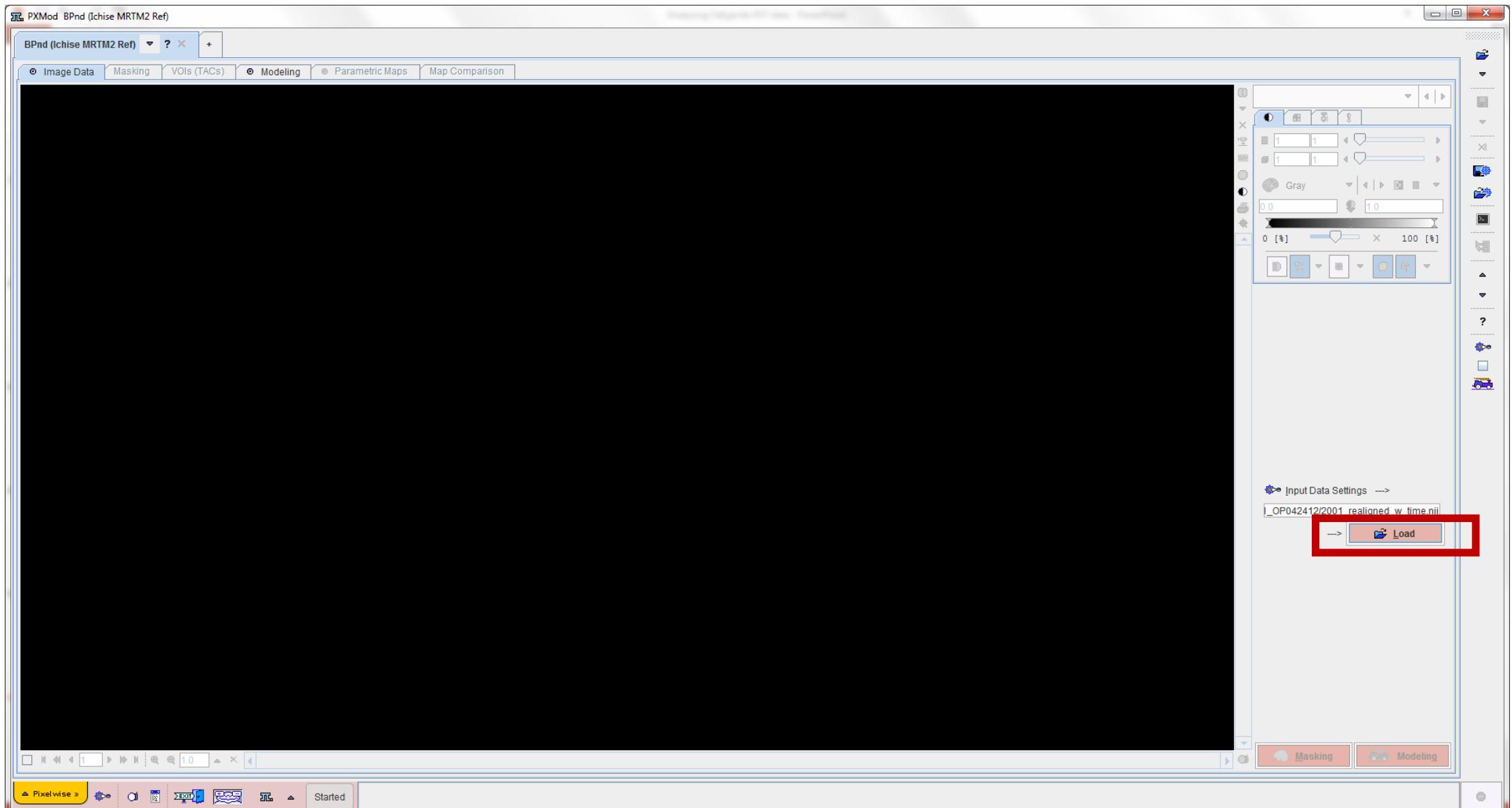


Be sure START and END times look good

Check that in “Preprocessing Tools” the 3D Gaussian is set at 5x5x5, then press “Ok”  
(this will smooth our images to increase signal to noise in the data)

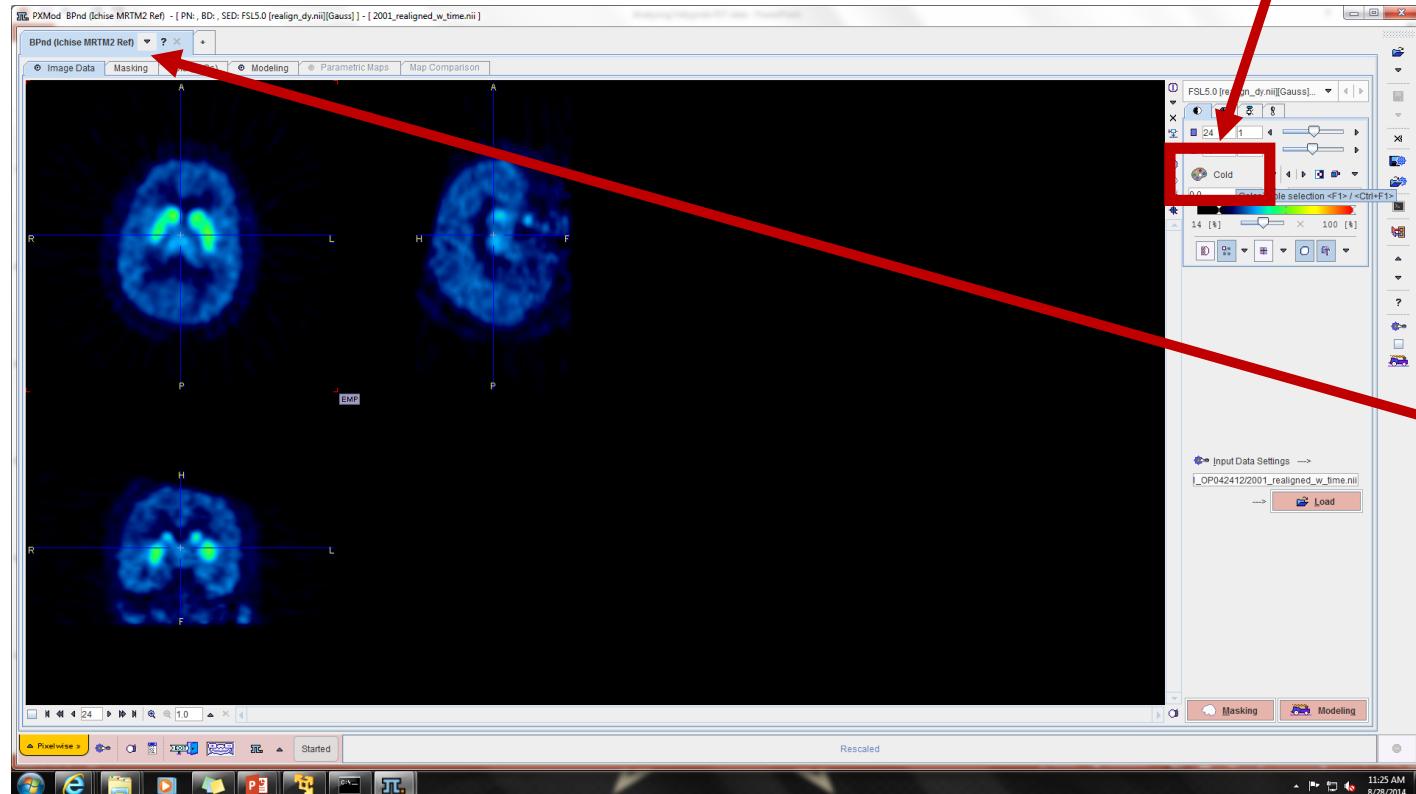


Once you return to the PXMOD main screen, press “Load”

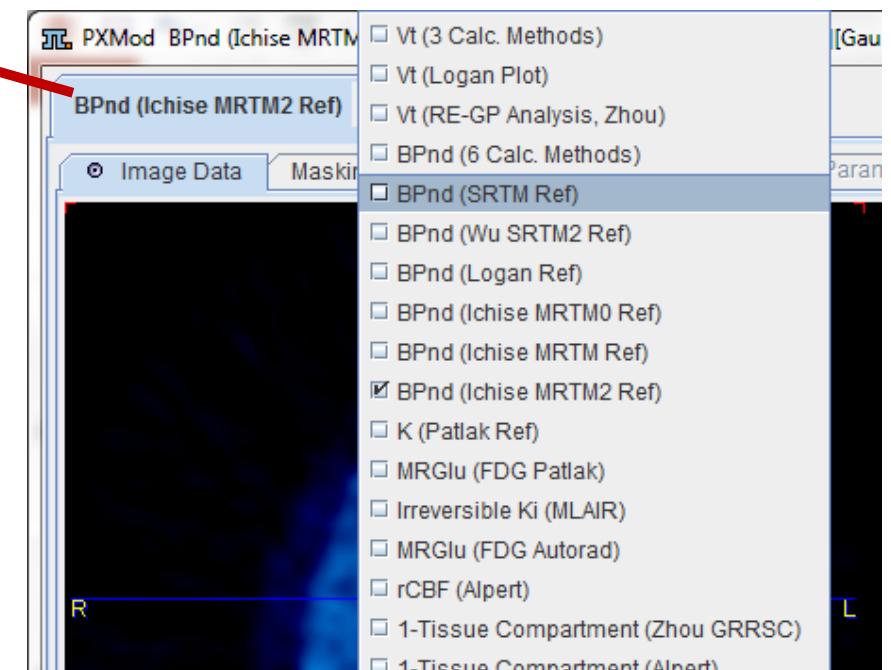


# Setting up the BPnd SRTM Model

Note: Once the realigned\_with\_time-dy.nii file has been loaded, you can change the display from “gray” to “cold” by clicking the paint palette icon to the right of the image



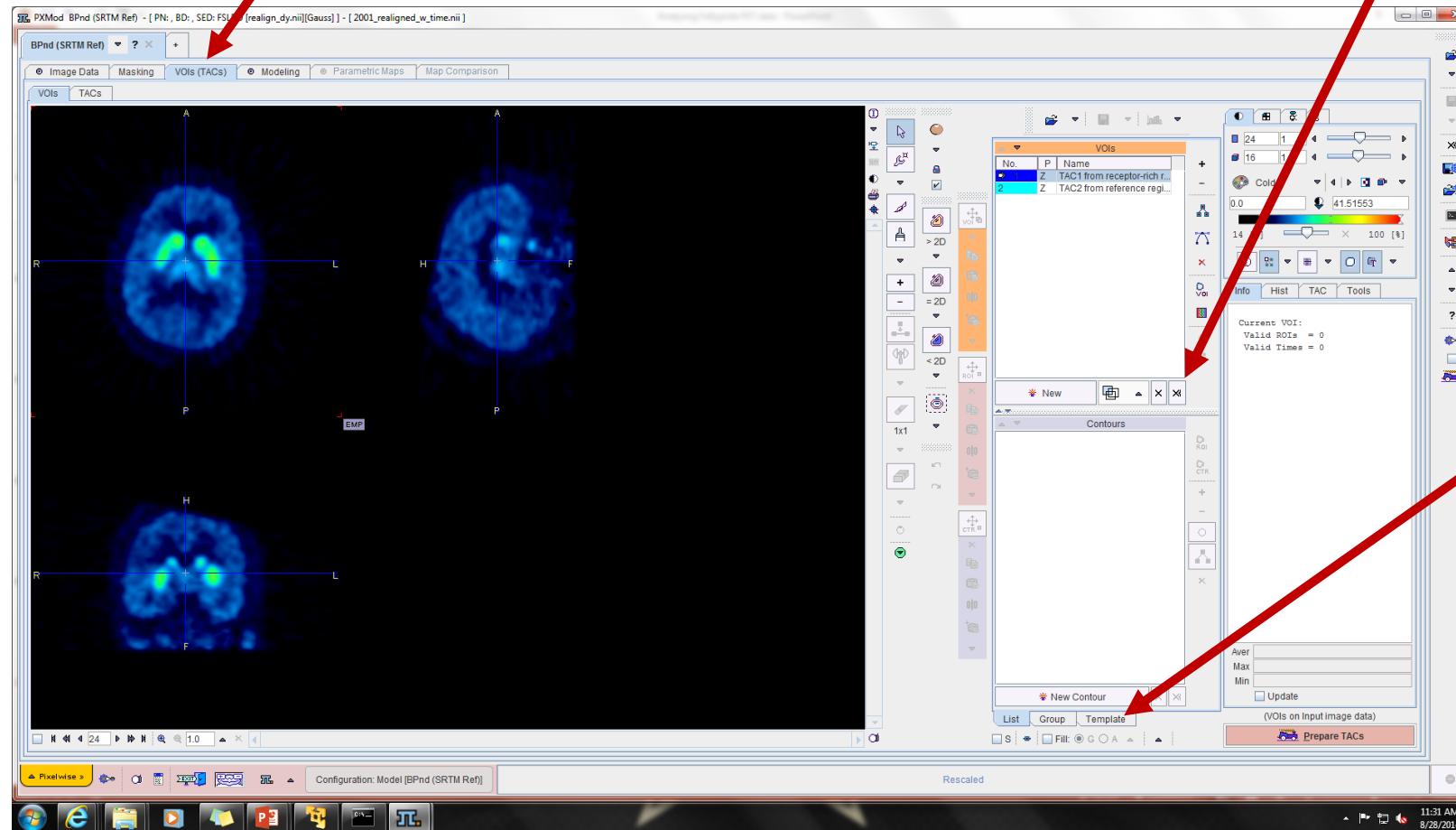
The first kinetic model we will use to get BPnd (non-displaceable binding potential) will be the SRTM Ref (simple reference tissue model), select this from the drop down menu at the top left of the PXMOD application



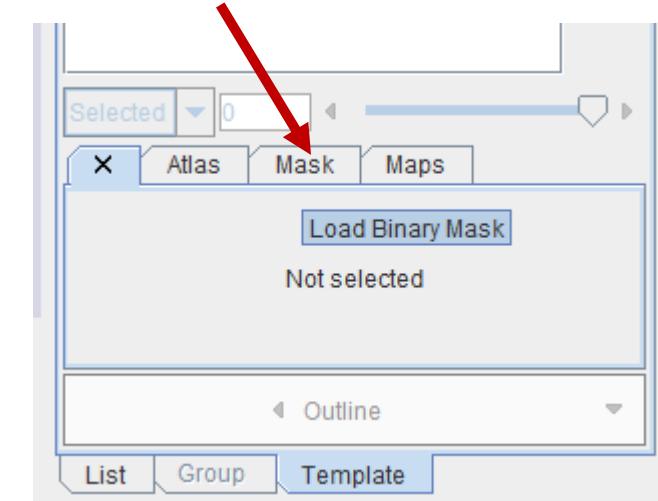
# Importing Cerebellum and Putamen ROIs

Click on the VOIs (TACs) tab

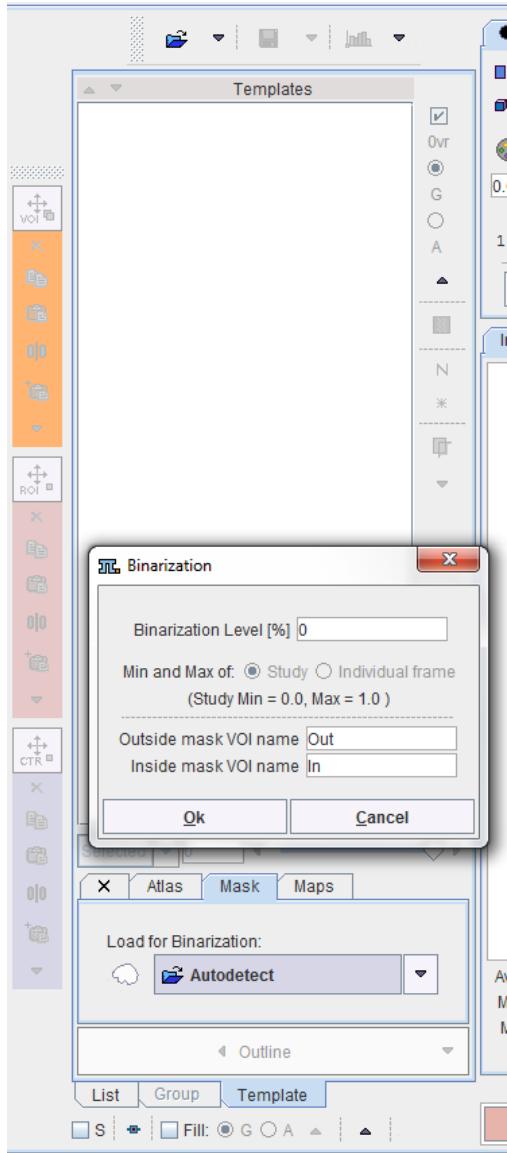
Remove preloaded TAC1 and TAC2 by clicking on the “X{“



1. Click on the “Template” tab
2. Click on the “Mask” tab



# Importing Cerebellum and Putamen ROIs

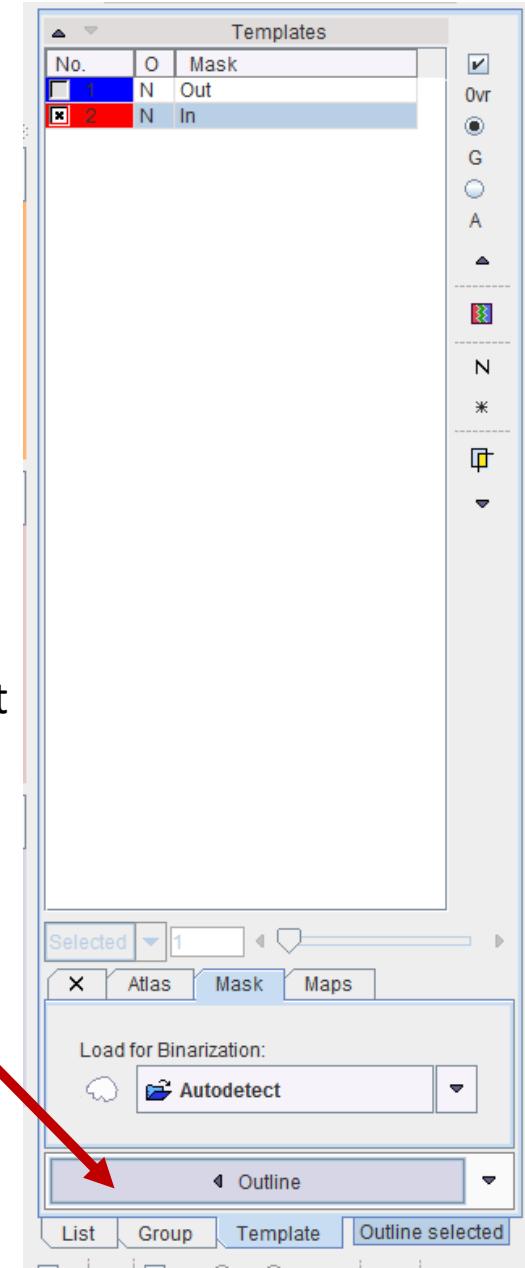


Choose to load a binary mask  
Click “Autodetect”, be sure to load the thresholded putamen.nii file that is in subject space (**always load putamen first as it is the receptor rich region!!**)  
Also be sure the binarization level is set to 0 (we already thresholded our ROI to include only voxels FSL was 100% confident were in the putamen)

Once the ROI image is loaded, click on “Outline” to move it into the main VOI list

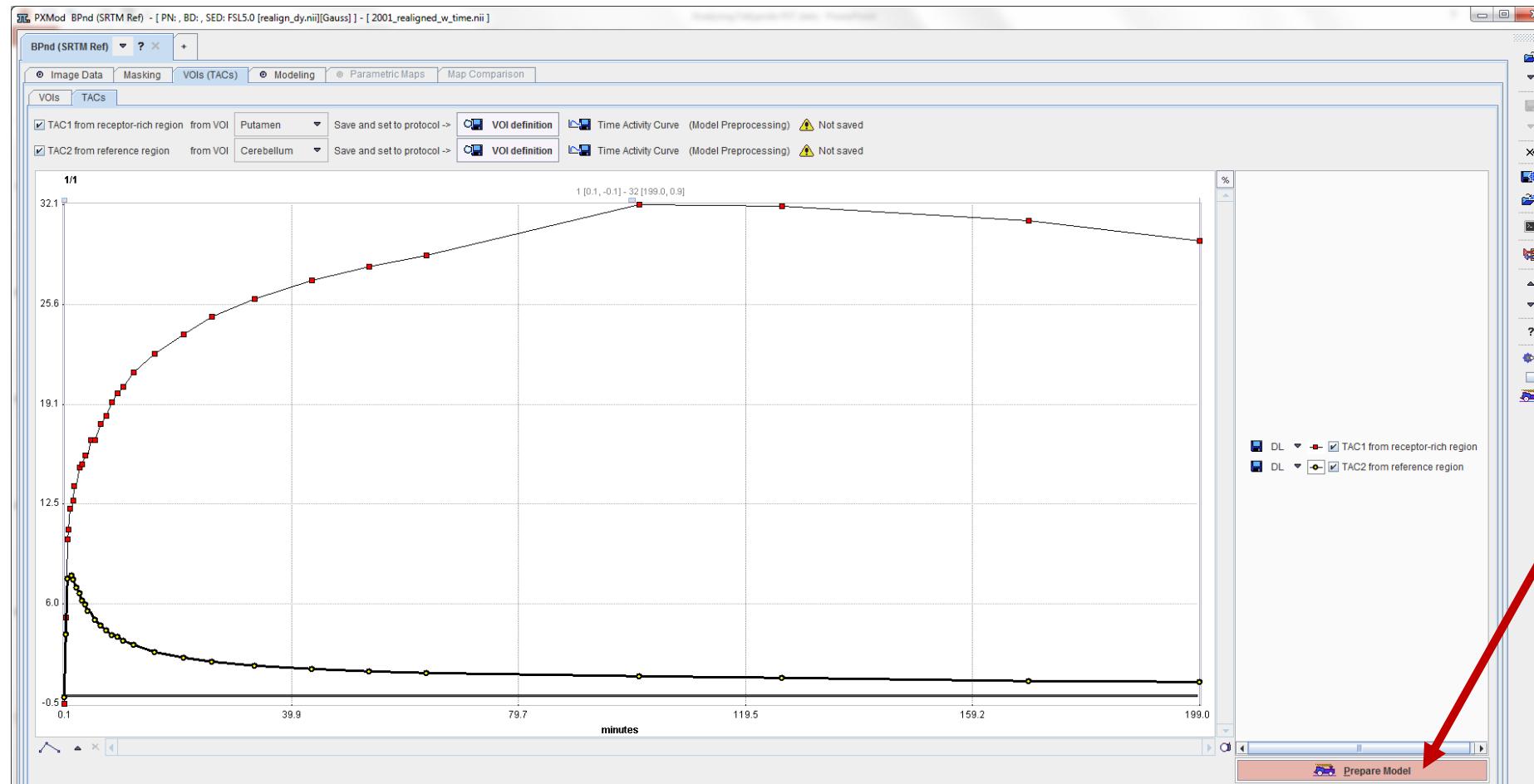
No.	P	Name
1	Z	Putamen
2	Z	Cerebellum

Be sure to name each VOI; add the cerebellum after you finish with the Putamen



# Running the kinetic model

- Once the VOIs are loaded, click “Prepare TACs” at the bottom right corner of the PXMOD application; you will be presented with the time activity curves (TACs) plotting the amount of fallypride tracer uptaken by the putamen (red dots) and cerebellum (yellow dots)

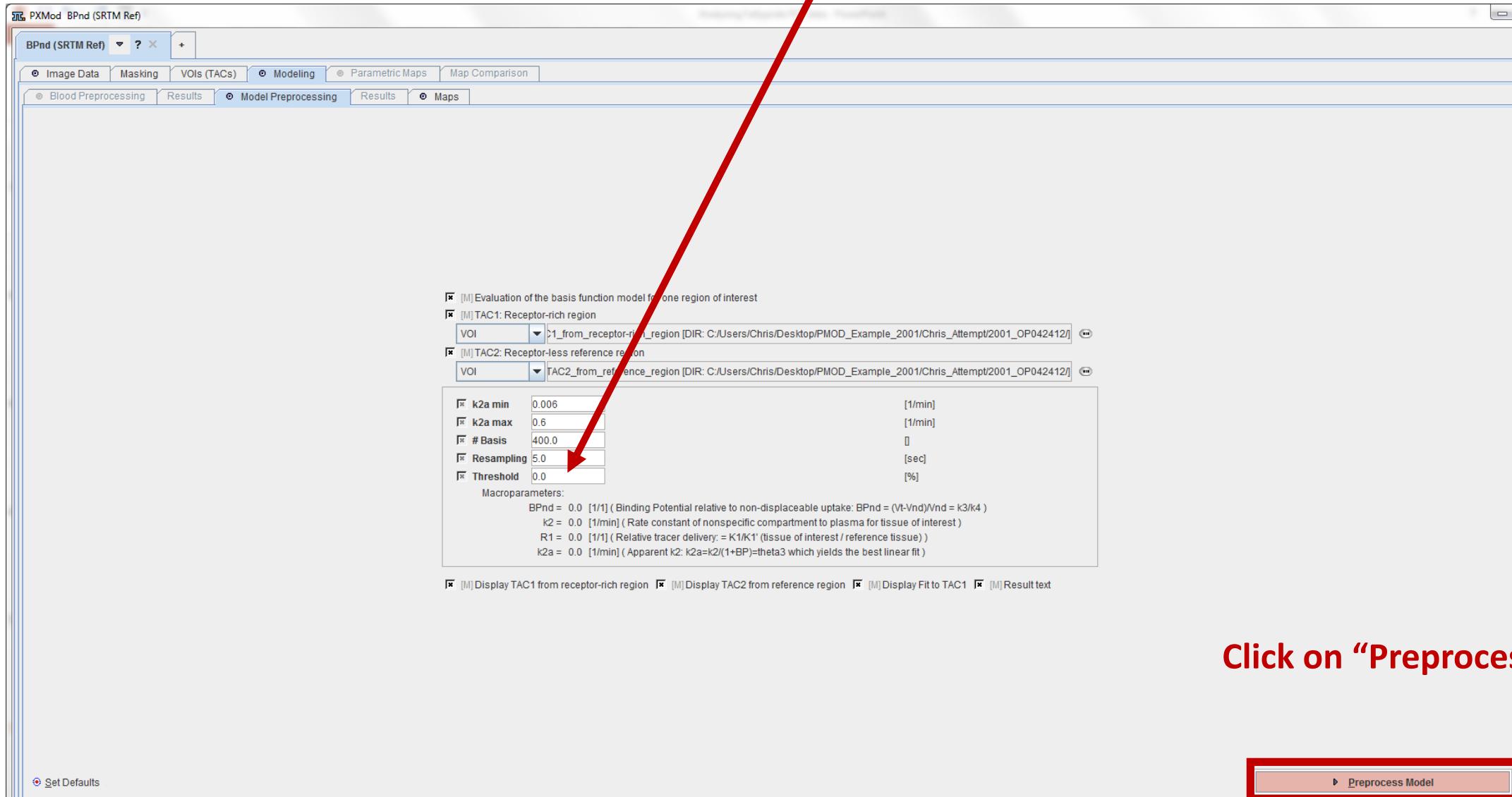


Click on “Prepare Model”

You will be prompted  
whether you want to save the  
VOIs, which you should do  
with that subject’s PET data

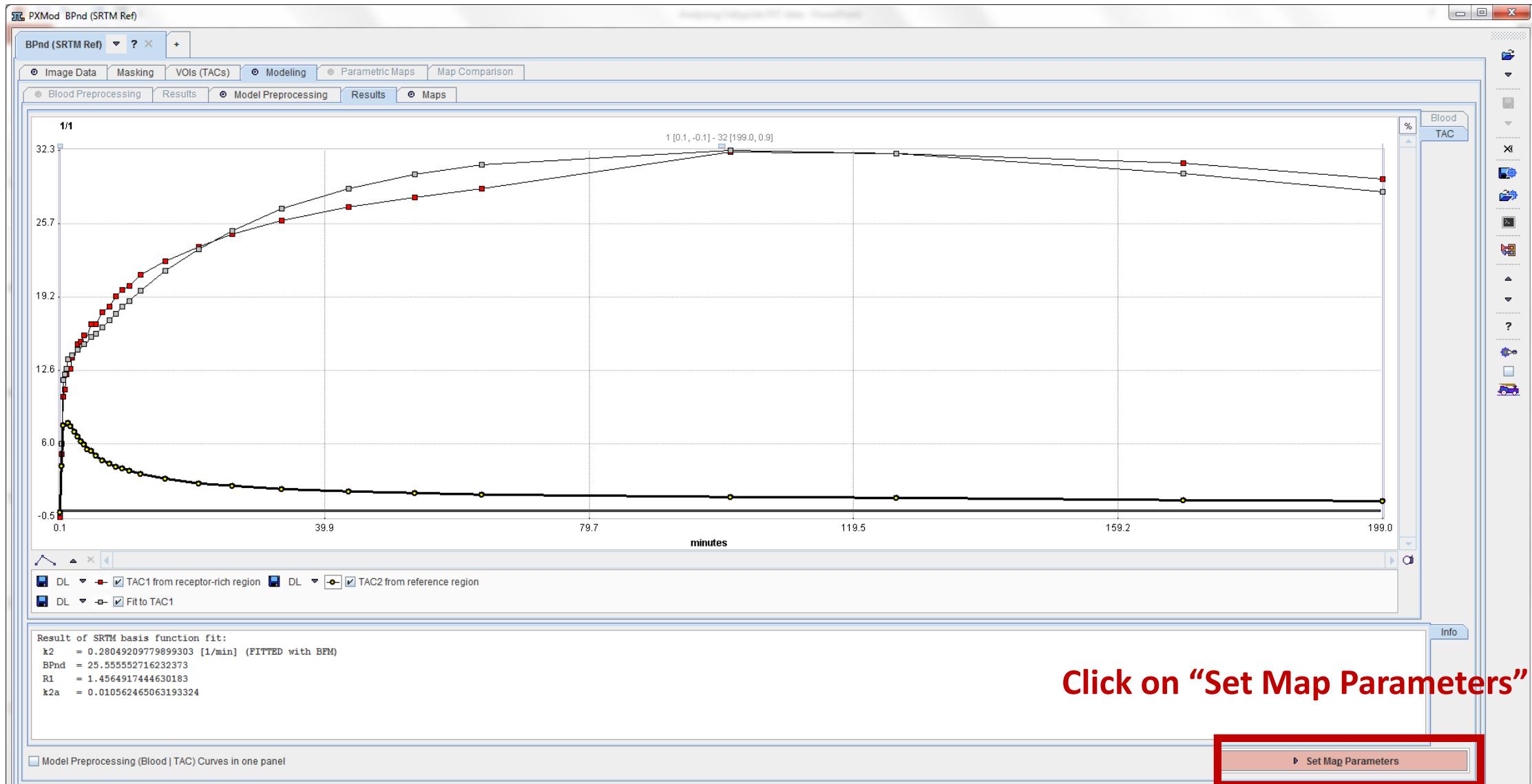
# Running the kinetic model

Be sure that in the model parameters, you set the “Threshold” to 0 (the default is 3)



Click on “Preprocess Model”

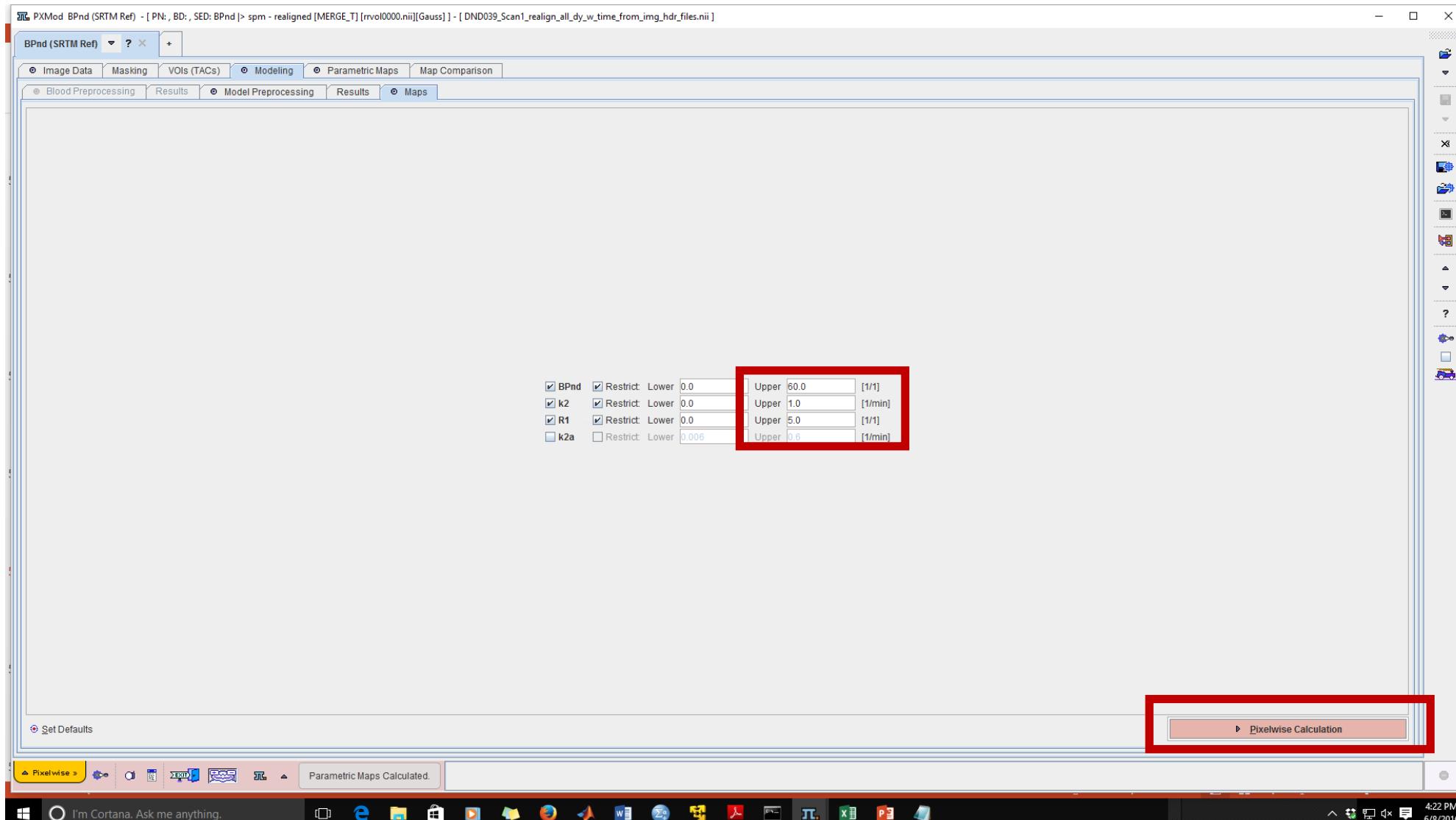
# Modeled fit (gray) vs Actual data (red)



# Set Map Parameters – getting BPnd Image

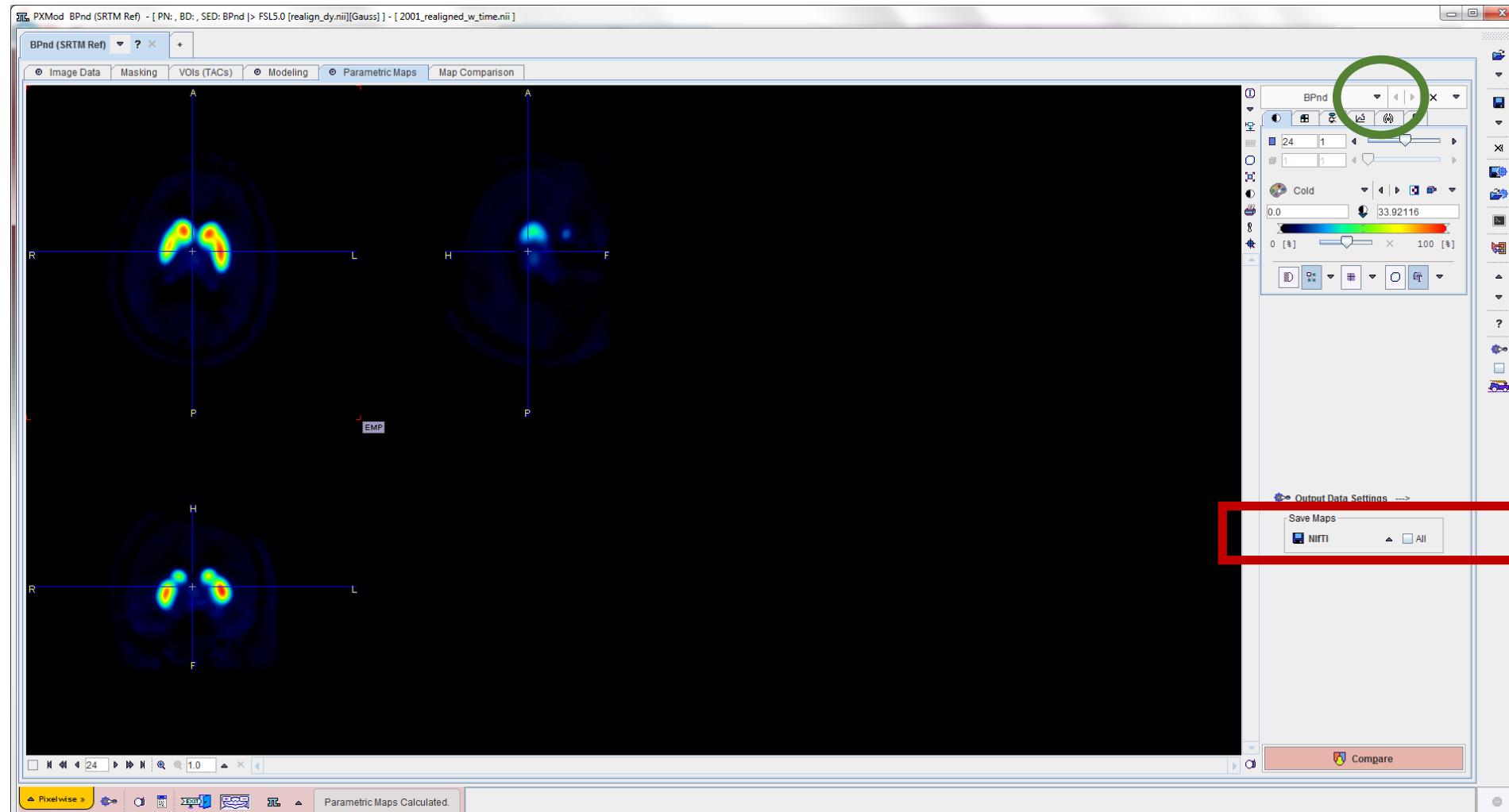
After clicking “Set Map Parameters”, select BPnd and be sure the upper limit is set at 60; then click on “Pixelwise Calculation”

**ALSO, select k2 and R1**

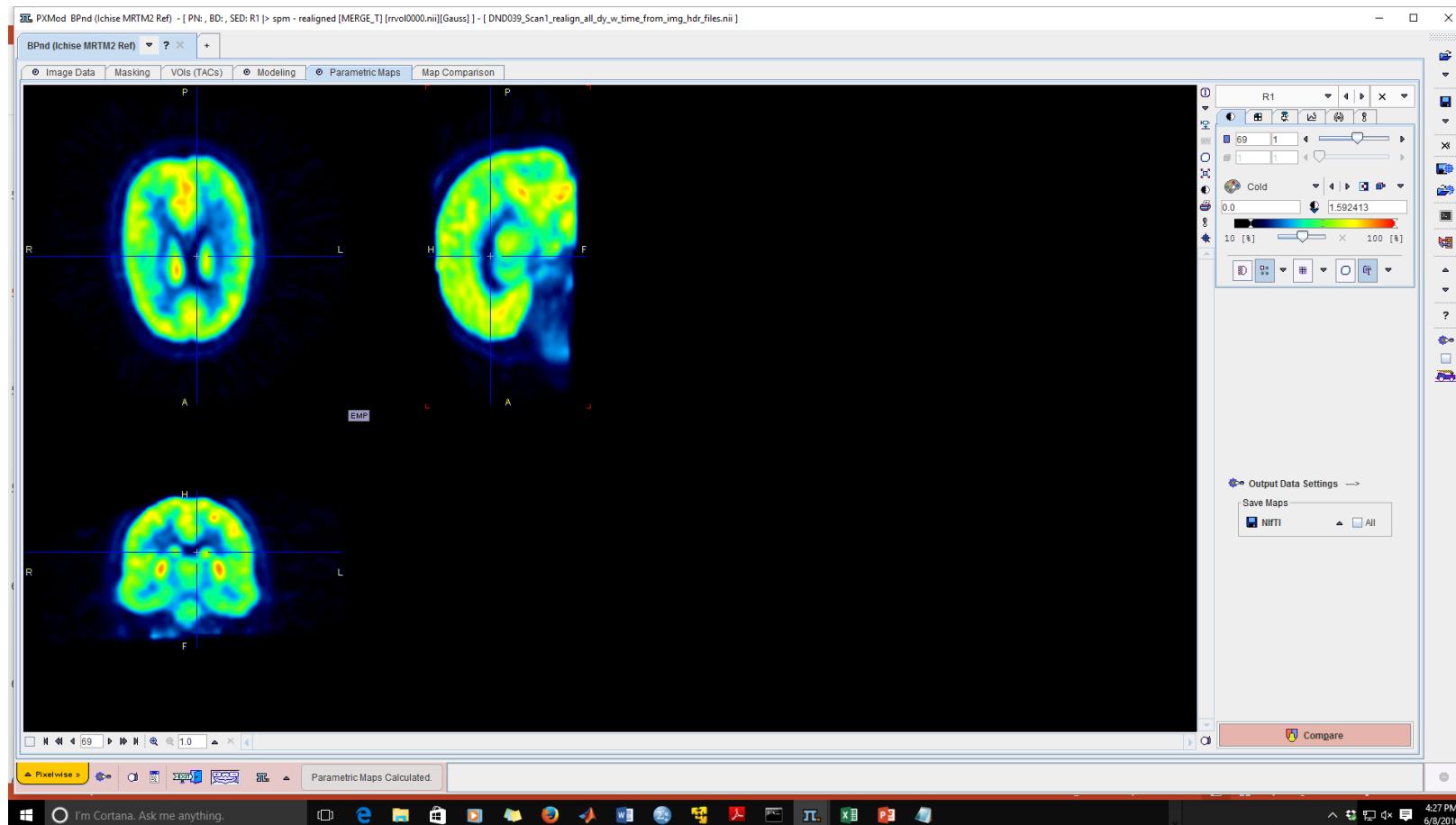


# BPnd Image Generated from SRTM

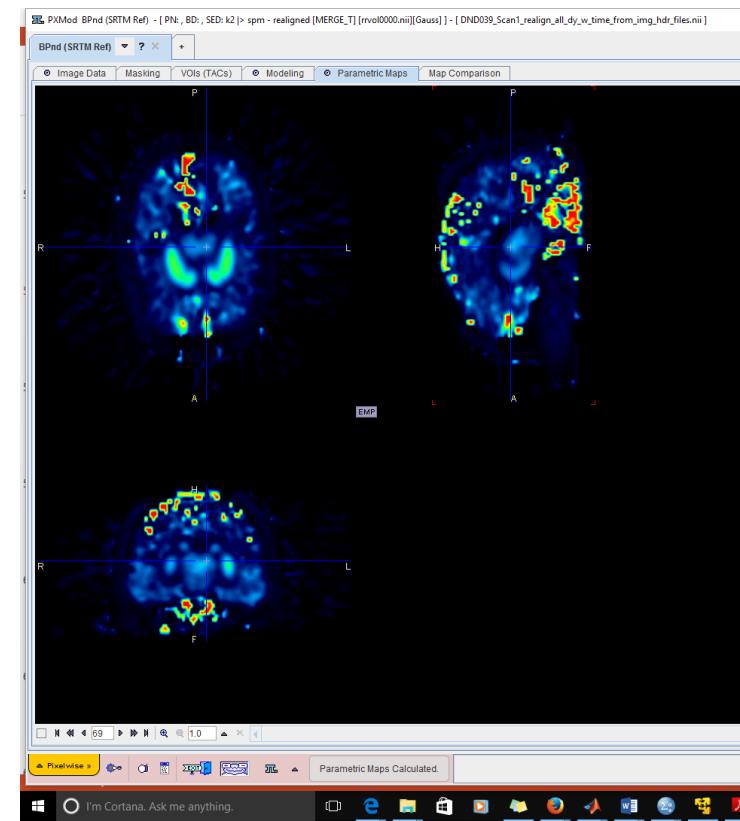
The model will generate the BPnd image, which you can then save as a nifiti file with a name such as “DNDXXX\_SRTM\_BPnd”  
Also, be sure to save the k2 and R1 images, which you can select from the top right drop-down arrow (green circle)



# R1 img (save as DNDXXX\_SRTM\_R1.nii)

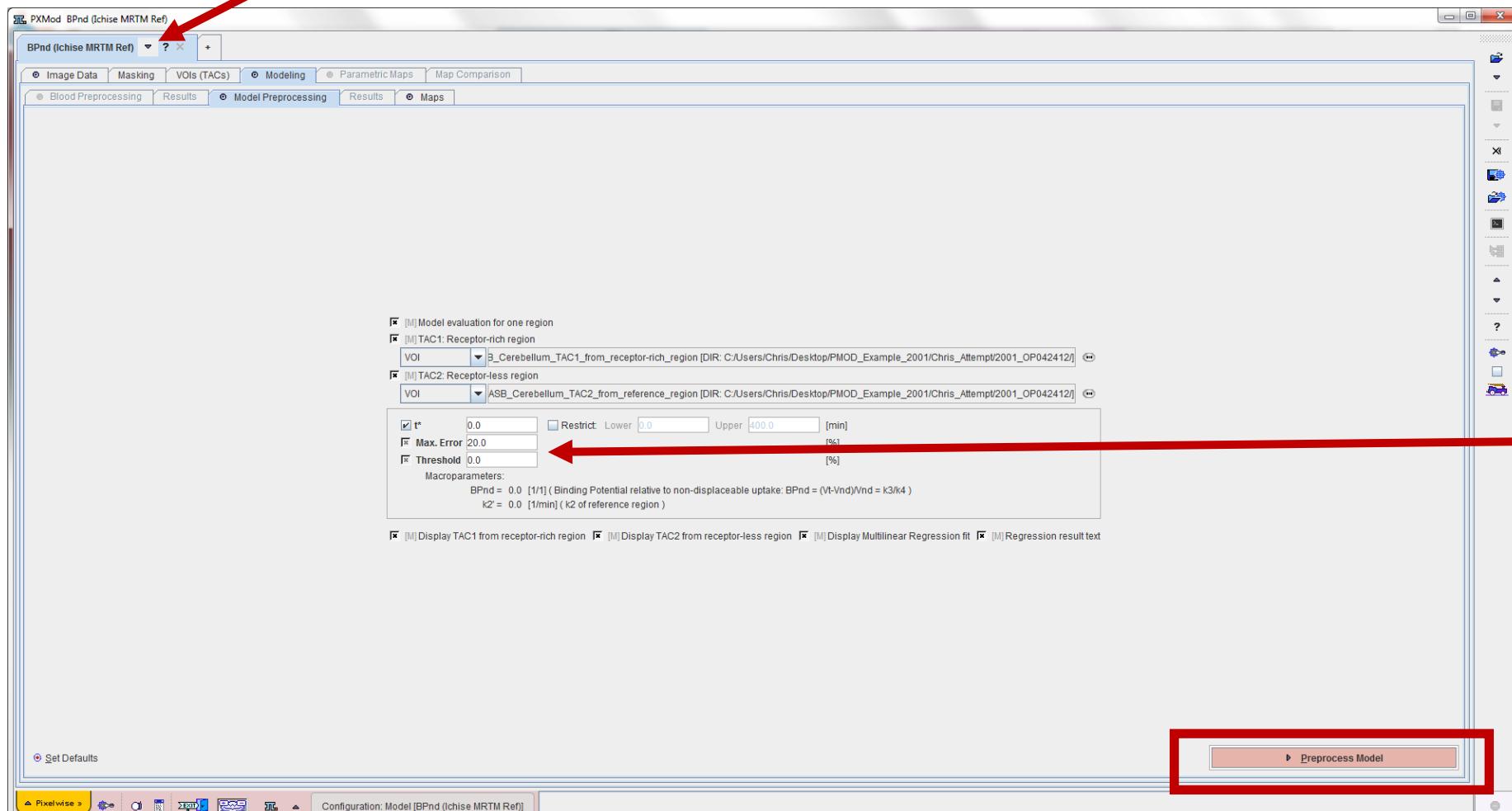


# k2 img (save as DNDXXX\_SRTM\_k2.nii)



# Running additional BPnd models – Ichise MRTM and MRTM2

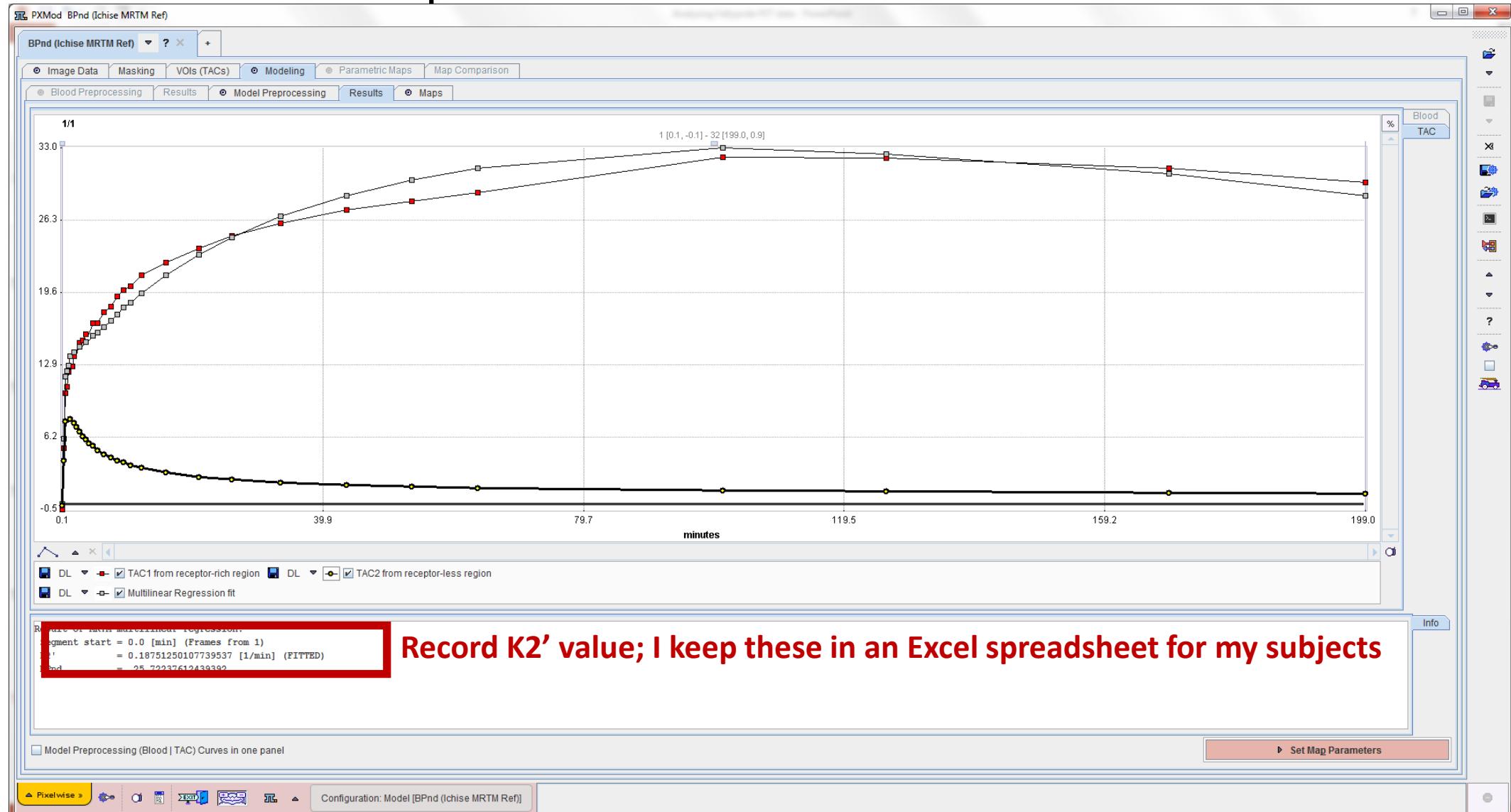
- From the drop down menu at the top left of PXMod, change the model to: BPnd (Ichise MRTM Ref)



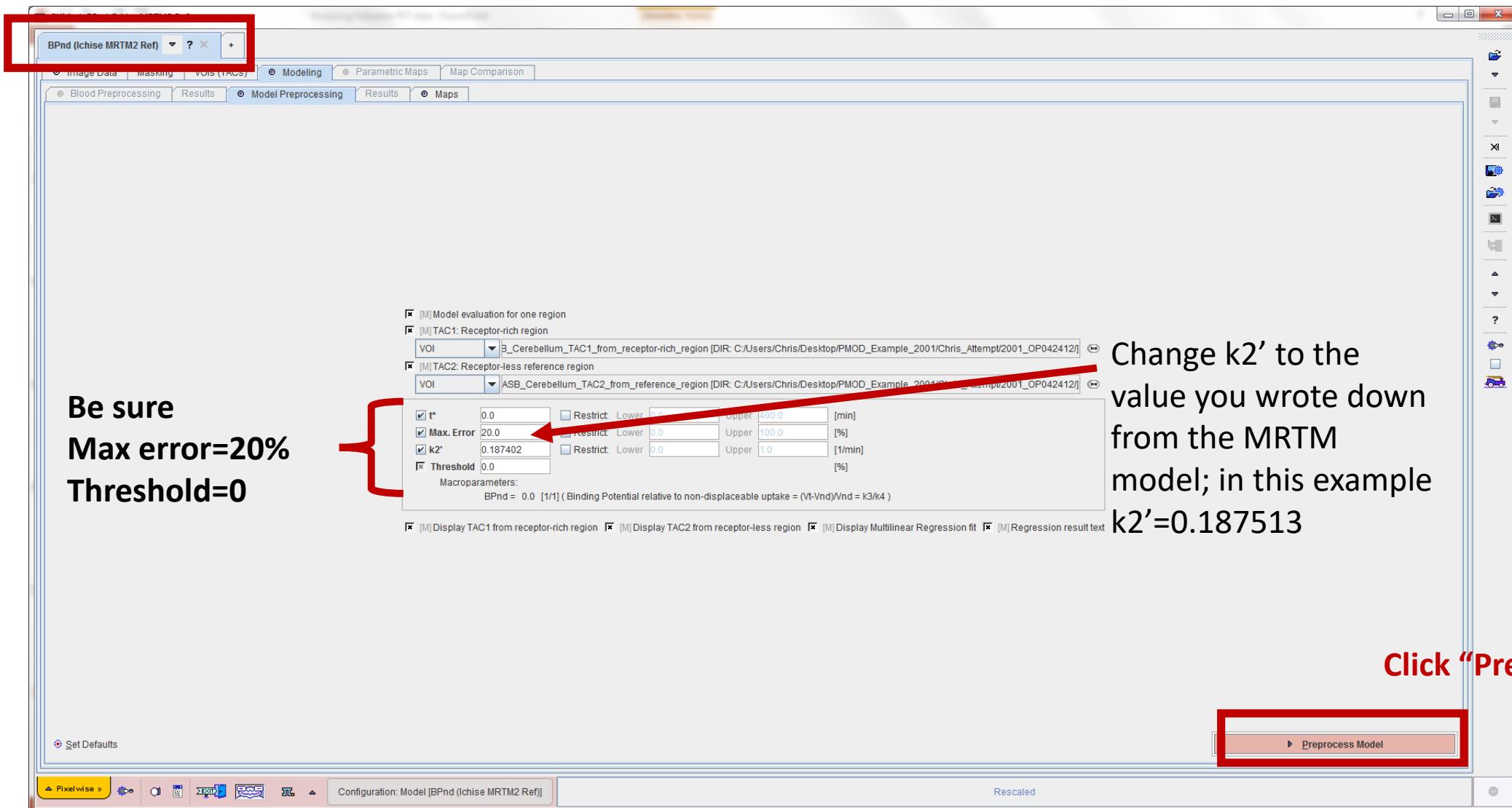
Set Max error to 20%  
Threshold=0

Click “Preprocess Model”

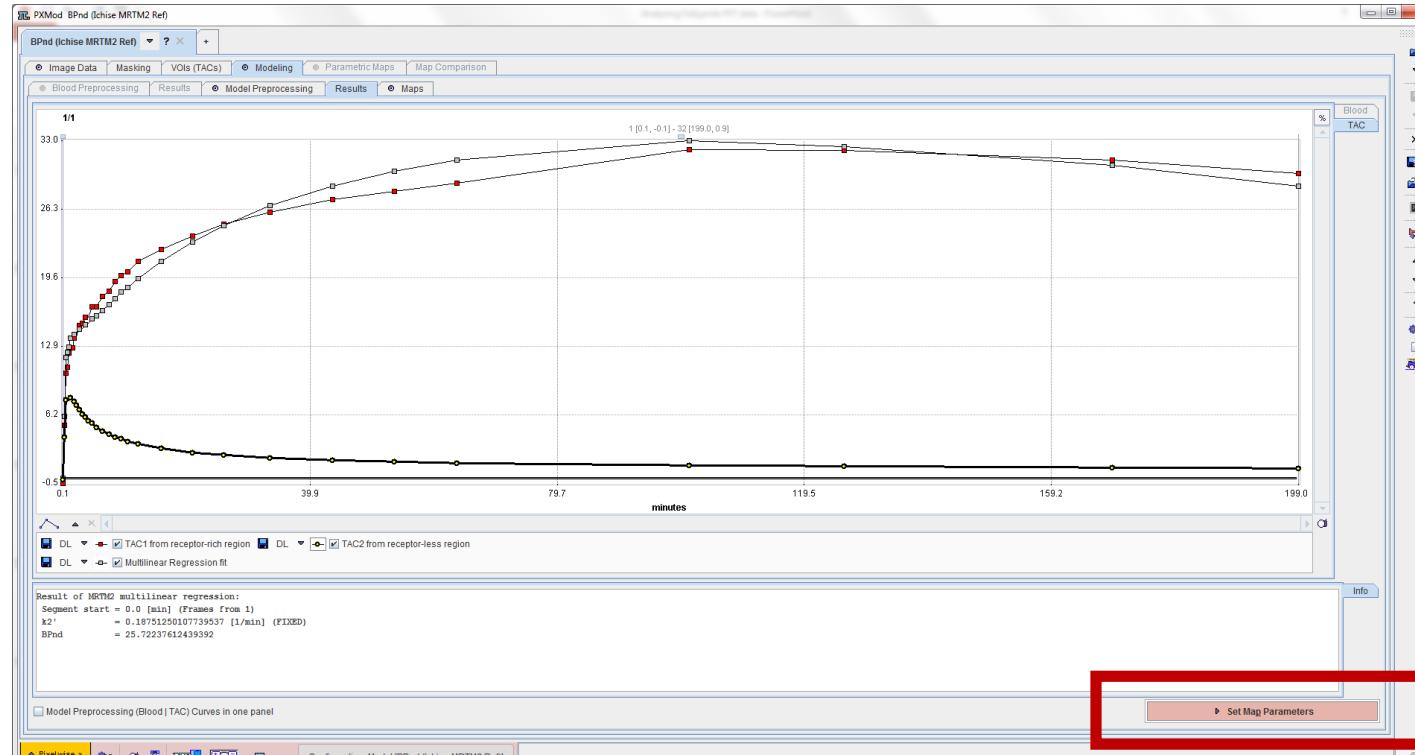
# From Ichise MRTM Ref, we will get the k2' value, which will serve as input for the Ichise MRTM 2 Ref Model



From the drop down menu at the top left of PXMod,  
change the model to: BPnd (Ichise MRTM2 Ref)



When TACs appear with model, select “Set Map Parameters”, get a BPnd image



When prompted, select BPnd, R1, & k2 with BPnd having an upper limit of 60

<input checked="" type="checkbox"/> BPnd	<input checked="" type="checkbox"/> Restrict: Lower 0.0	Upper 60.0	[1/1]
<input checked="" type="checkbox"/> R1	<input type="checkbox"/> Restrict: Lower 0.0	Upper 1.0	[1/1]
<input checked="" type="checkbox"/> k2	<input type="checkbox"/> Restrict: Lower 0.0	Upper 1.0	[1/1]

Then, select “Pixelwise Calculation” at bottom right of screen

When the Ichise MRTM2 BPnd, k2, and R1 images are generated, save them as “subject\_MRTM2\_BPnd”, etc...

