

# I will use the following notebook to demonstrate different steps in preprocessing

These steps will include:

- 1) Slice timing correction
- 2) Motion correction
- 3) Coregistration
- 4) Spatial and temporal filtering

In [1]:

```
import os
from glob import glob

# Import new things that we'll need
import pandas as pd
import numpy as np
import nipype.interfaces.afni as afni
import nipype.interfaces.fsl as fsl
from nipype.interfaces.utility import Function
import seaborn as sns
import nibabel as nb
import json
import nipype.interfaces.io as nio
import nipype.pipeline.engine as pe
import matplotlib.pyplot as plt

%matplotlib inline
```

I next want to get a list of all of my functional files

In [2]:

```
sid = ['021']
base_dir = '/Users/hlee/Documents/GitHub/mattfeld_2020'
work_dir = '/Users/hlee/Documents/GitHub'
func_dir = os.path.join(base_dir, f'dset/sub-{sid[0]}/ses-S1/func')
# Get a list of my *localizer* json and nifti converted files
loc_func_json = sorted(glob(func_dir + '/*loc*.json'))
loc_func_files = sorted(glob(func_dir + '/*loc*.nii.gz'))

# Get a list of my *study task* json and nifti converted files
study_func_json = sorted(glob(func_dir + '/*study*.json'))
study_func_files = sorted(glob(func_dir + '/*study*.nii.gz')) #making a list like st
```

Next I want to build and run function to perform slice timing correction. I'm going to have to extract some important information from the .json files like the

**multiband slicetiming.**

In [20]:

```
# Here I am building a function that eliminates the
# mapnode directory structure and assists in saving
# all of the outputs into a single directory
def get_subs(func_files):
    '''Produces Name Substitutions for Each Contrast'''
    subs = []
    for curr_run in range(len(func_files)):
        subs.append(('_tshifter%d' %curr_run, ''))
        subs.append(('_volreg%d' %curr_run, ''))
    return subs

# Here I am building a function that takes in a
# text file that includes the number of outliers
# at each volume and then finds which volume (e.g., index)
# has the minimum number of outliers (e.g., min)
# searching over the first 201 volumes
# If the index function returns a list because there were
# multiple volumes with the same outlier count, pick the first one
def best_vol(outlier_count):
    best_vol_num = outlier_count.index(min(outlier_count[:200]))
    if isinstance(best_vol_num, list):
        best_vol_num = best_vol_num[0]
    return best_vol_num

#####how about min(outlier_count[:more than 200]))???#####
#def best_vol(outlier_count):
#    #best_vol_num = outlier_count.index(min(outlier_count[:400]))
#    #if isinstance(best_vol_num, list):
#        #best_vol_num = best_vol_num[0]
#    #return best_vol_num
#####no difference btw 200 and 400 without other changes#####

# Here I am creating a list of lists containing the slice timing for each study run
slice_timing_list = []
for curr_json in study_func_json:
    curr_json_data = open(curr_json)
    curr_study_func_metadata = json.load(curr_json_data)
    slice_timing_list.append(curr_study_func_metadata['SliceTiming'])

# Here I am establishing a nipype work flow that I will eventually execute
psb6351_wf = pe.Workflow(name='psb6351_wf')

# Create a Function node to substitute names of files created during pipeline
getsubs = pe.Node(Function(input_names=['func_files'],
                           output_names=['subs'],
                           function=get_subs),
                  name='getsubs')
getsubs.inputs.func_files = study_func_files

# Here I am inputting just the first run functional data
# I want to use afni's 3dToutcount to find the number of outliers at each volume.
# I will use this information to later select the earliest volume
# with the least number of outliers
# to serve as the base for the motion correction
id_outliers = pe.Node(afni.OutlierCount(),
                      name = 'id_outliers')

# Mandatory Inputs
id_outliers.inputs.in_file = study_func_files[0] # Input dataset #if the number is 1
```

```

# Optional Inputs
id_outliers.inputs.automask = True # Clip off small voxels
id_outliers.inputs.fraction = True # Write out the fraction of masked voxels which a
id_outliers.inputs.legendre = True # Use Legendre polynomials
id_outliers.inputs.polort = 4 # Detrend each voxel timeseries with polynomials of or
id_outliers.inputs.out_file = 'outlier_file'

#ATM ONLY: Add an unwarping mapnode here using the field maps

# Create a Function node to identify the best volume based
# on the number of outliers at each volume. I'm searching
# for the index in the first 201 volumes that has the
# minimum number of outliers and will use the min() function
# I will use the index function to get the best vol.
getbestvol = pe.Node(Function(input_names=['outlier_count'],
                              output_names=['best_vol_num'],
                              function=best_vol),
                      name='getbestvol')
psb6351_wf.connect(id_outliers, 'out_file', getbestvol, 'outlier_count')

# Extract the earliest volume with the
# the fewest outliers of the first run as the reference
extractref = pe.Node(fsl.ExtractROI(t_size=1),
                     name = "extractref")
extractref.inputs.in_file = study_func_files[0]
extractref.inputs.t_min = int(np.ceil(nb.load(study_func_files[0]).shape[3]/2)) #PIC
psb6351_wf.connect(getbestvol, 'best_vol_num', extractref, 't_min')

## QUESTION: Would I want to do slice timing correction here? Why? Why not?
### I have a question..do I need to do despiking in preprocessing?

# Below is the command that runs AFNI's 3dTshift command
# this is the node that performs the *slice timing correction*
# I input the study func files as a list and the slice timing
# as a list of lists. I'm using a MapNode to iterate over the two.
# this should allow me to parallelize this on the HPC
tshifter = pe.MapNode(afni.TShift(),
                      iterfield=['in_file','slice_timing'],
                      name = 'tshifter')

# Mandatory Input
tshifter.inputs.in_file = study_func_files # Input file to 3dT-shift

# Optional Inputs
tshifter.inputs.tr = str(curr_study_func_metadata['RepetitionTime']) # Manually set
tshifter.inputs.slice_timing = slice_timing_list # Time offsets from the volume acqu
tshifter.inputs.outputtype = 'NIFTI_GZ' # AFNI output filetype
tshifter.inputs.tzero = 0.0 # Align each slice to time offset of given slice
tshifter.inputs.interp = 'quintic' # Different interpolation methods # default = Four

# Below is the command that runs AFNI's 3dvolreg command.
# this is the node that performs the *motion correction*
# I'm iterating over the functional files which I am passing
# functional data from the slice timing correction node before
# I'm using the earliest volume with the least number of outliers
# during the first run as the base file to register to.
volreg = pe.MapNode(afni.Volreg(),
                    iterfield=['in_file'],
                    name = 'volreg')

```

```

# Optional Input
volreg.inputs.outputtype = 'NIFTI_GZ' # AFNI outputtype
volreg.inputs.zpad = 4 # Zeropad around the edges by 'n' voxels during rotations
volreg.inputs.verbose = True # More detailed description of the process
psb6351_wf.connect(tshifter, 'out_file', volreg, 'in_file')
psb6351_wf.connect(extractref, 'roi_file', volreg, 'basefile')

# Below is the code if I wanted to use the FSL McFlirt command
'''
motion_corr = pe.MapNode(fsl.MCFLIRT(),
                        iterfield=['in_file'],
                        name = 'motion_corr')
motion_corr.inputs.output_type = 'NIFTI_GZ'
psb6351_wf.connect(tshifter, 'out_file', motion_corr, 'in_file')
psb6351_wf.connect(extractref, 'roi_file', motion_corr, 'ref_file')
'''

# Below is the node that collects all the data and saves
# the outputs that I am interested in. Here in this node
# I use the substitutions input combined with the earlier
# function to get rid of nesting
datasink = pe.Node(nio.DataSink(), name="datasink")
datasink.inputs.base_directory = os.path.join(base_dir, 'derivatives')
datasink.inputs.container = f'sub-{{sid[0]}}'
psb6351_wf.connect(tshifter, 'out_file', datasink, 'sltime_corr')
psb6351_wf.connect(extractref, 'roi_file', datasink, 'study_ref')
psb6351_wf.connect(volreg, 'out_file', datasink, 'motion.@corrfile')
psb6351_wf.connect(volreg, 'oned_matrix_save', datasink, 'motion.@matrix')
psb6351_wf.connect(volreg, 'oned_file', datasink, 'motion.@par')
psb6351_wf.connect(getsubs, 'subs', datasink, 'substitutions')

# The following two lines set a work directory outside of my
# local git repo and runs the workflow
psb6351_wf.base_dir = work_dir + f'/psb6351workdir/sub-{{sid[0]}}'
psb6351_wf.run()

```

```

201002-19:25:34,885 nipype.interface INFO:
    sub: /Users/hlee/Documents/GitHub/mattfeld_2020/derivatives/s
ub-021/motion/_volreg1/sub-021_ses-S1_task-study_2_bold_tshift.1D -> /
Users/hlee/Documents/GitHub/mattfeld_2020/derivatives/sub-021/motion//
sub-021_ses-S1_task-study_2_bold_tshift.1D
201002-19:25:34,894 nipype.interface INFO:
    sub: /Users/hlee/Documents/GitHub/mattfeld_2020/derivatives/s
ub-021/motion/_volreg2/sub-021_ses-S1_task-study_3_bold_tshift.1D -> /
Users/hlee/Documents/GitHub/mattfeld_2020/derivatives/sub-021/motion//
sub-021_ses-S1_task-study_3_bold_tshift.1D
201002-19:25:34,902 nipype.interface INFO:
    sub: /Users/hlee/Documents/GitHub/mattfeld_2020/derivatives/s
ub-021/motion/_volreg3/sub-021_ses-S1_task-study_4_bold_tshift.1D -> /
Users/hlee/Documents/GitHub/mattfeld_2020/derivatives/sub-021/motion//
sub-021_ses-S1_task-study_4_bold_tshift.1D

201002-19:25:34,913 nipype.workflow INFO:
    [Node] Finished "psb6351_wf.datasink".

```

Out[20]:

**Now I will load and plot the motion files**

In [21]:

```
motion_dir = os.path.join(base_dir, f'derivatives/sub-{sid[0]}/motion')
study_motion_files = sorted(glob(motion_dir + '/*study*_tshift.1D'))

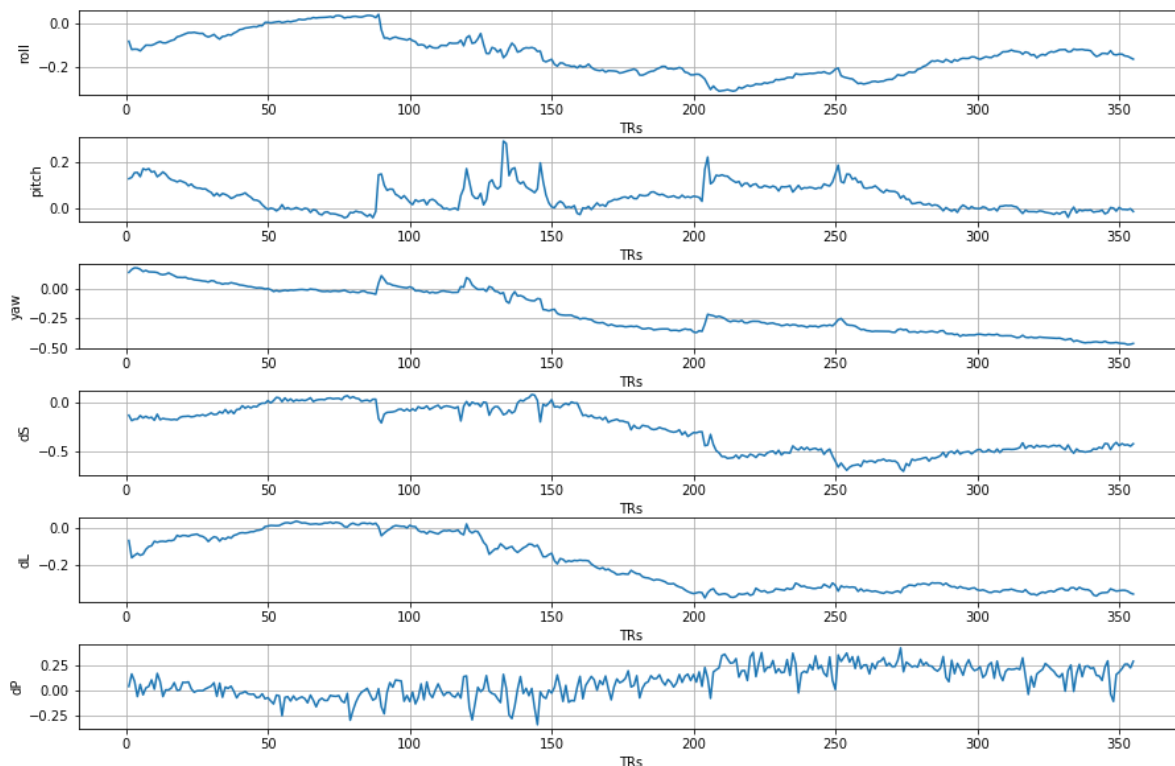
for curr_mot_file in study_motion_files:
    motion_df = pd.read_csv(curr_mot_file, sep=" ", header=None)
    motion_df.columns = ['roll', 'pitch', 'yaw', 'dS', 'dL', 'dP']

    num_vols = range(1, len(motion_df)+1)
    fig, axs = plt.subplots(motion_df.shape[1], 1, figsize = (15, 10))
    # make a little extra space between the subplots
    fig.subplots_adjust(hspace=0.5)

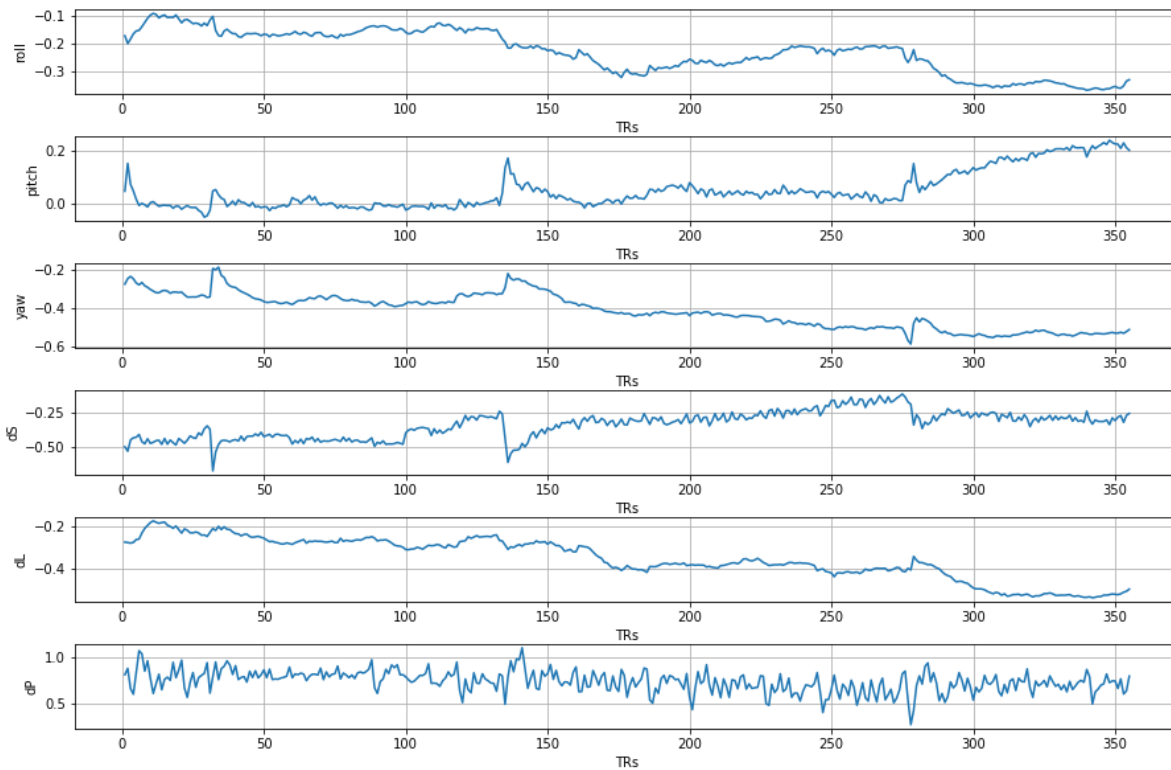
    for idx, curr_col in enumerate(motion_df.keys()):
        axs[idx].plot(num_vols, motion_df[f'{curr_col}'])
        axs[idx].set_xlabel('TRs')
        axs[idx].set_ylabel(f'{curr_col}')
        axs[idx].grid(True)

plt.show()
```

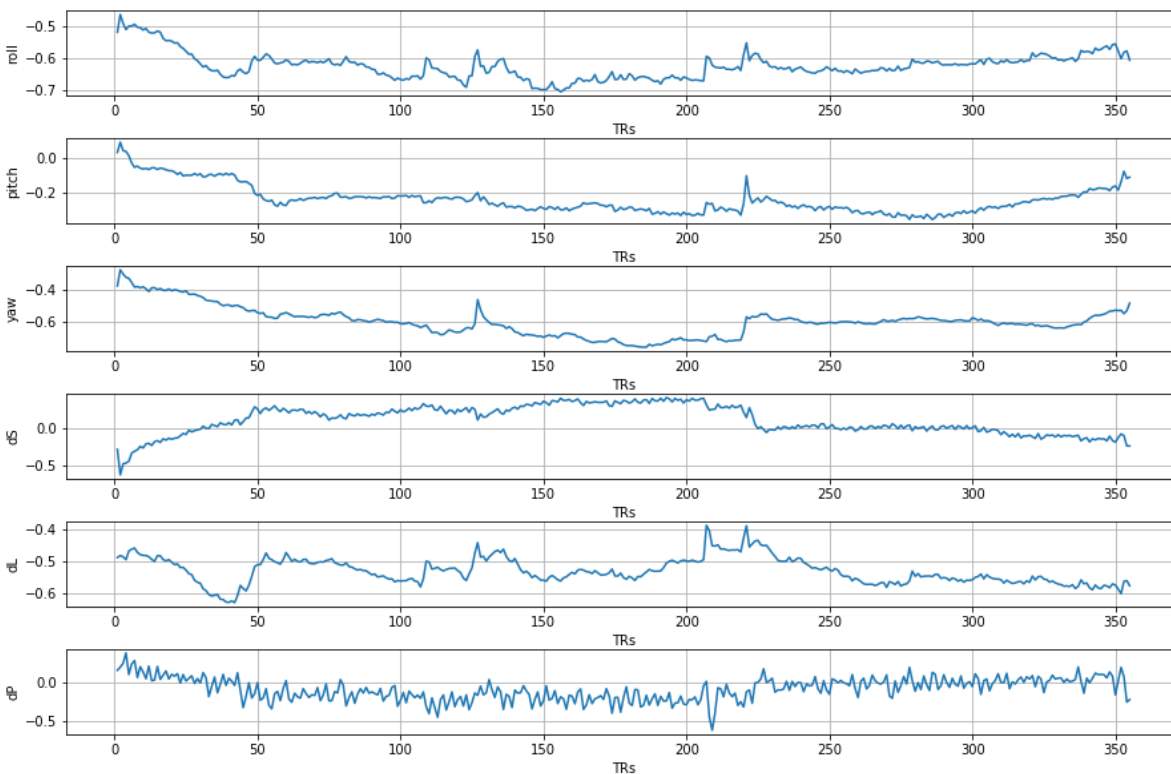
/opt/anaconda3/envs/py376/lib/python3.7/site-packages/ipykernel\_launcher.py:5: ParserWarning: Falling back to the 'python' engine because the 'c' engine does not support regex separators (separators > 1 char and different from '\s+' are interpreted as regex); you can avoid this warning by specifying engine='python'.



/opt/anaconda3/envs/py376/lib/python3.7/site-packages/ipykernel\_launcher.py:5: ParserWarning: Falling back to the 'python' engine because the 'c' engine does not support regex separators (separators > 1 char and different from '\s+' are interpreted as regex); you can avoid this warning by specifying engine='python'.

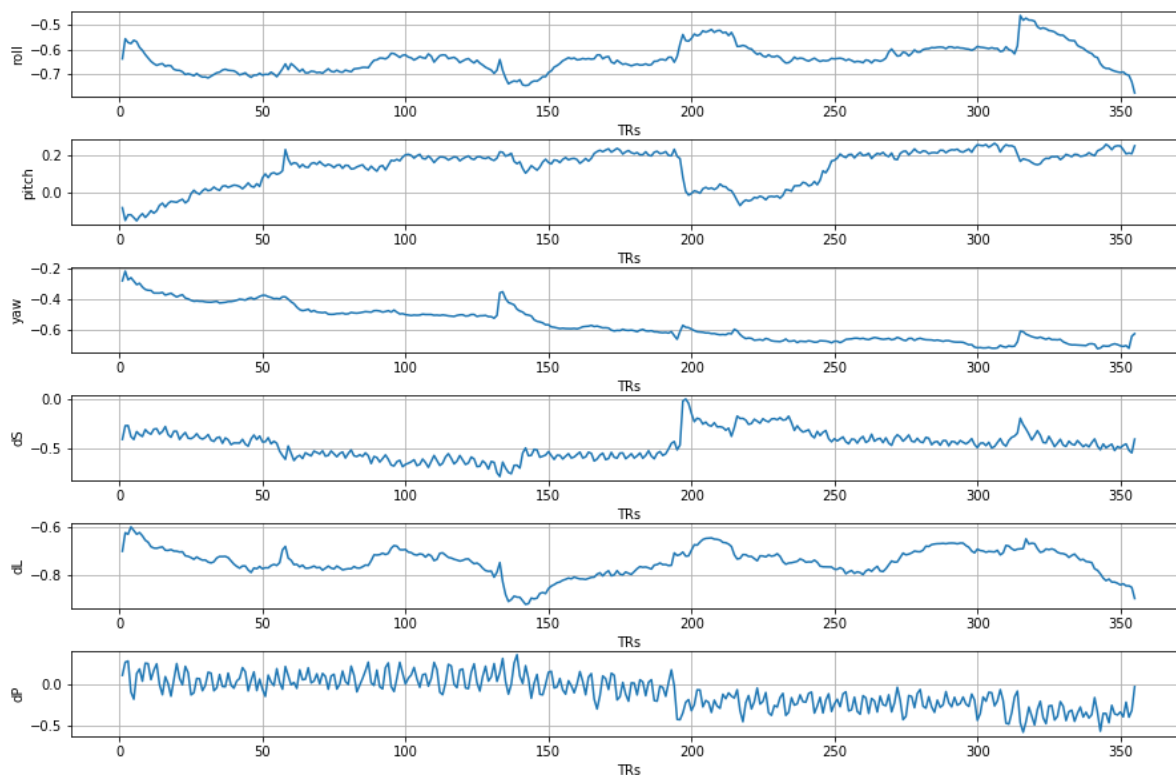


```
/opt/anaconda3/envs/py376/lib/python3.7/site-packages/ipykernel_launcher
er.py:5: ParserWarning: Falling back to the 'python' engine because the 'c'
engine does not support regex separators (separators > 1 char and different
from '\s+' are interpreted as regex); you can avoid this warning by specifying
engine='python'.
```



```
/opt/anaconda3/envs/py376/lib/python3.7/site-packages/ipykernel_launcher
er.py:5: ParserWarning: Falling back to the 'python' engine because the
```

e 'c' engine does not support regex separators (separators > 1 char and different from '\s+' are interpreted as regex); you can avoid this warning by specifying engine='python'.



In [15]:

```
study_motcorr_files = sorted(glob(motion_dir + '/*.nii.gz'))
study_motcorr_img_data = nb.load(study_motcorr_files[0]).get_fdata()
study_orig_img_data = nb.load(study_func_files[0]).get_fdata()

#test_motcorr_img_data.shape

print(test_motcorr_img_data[50,50,32,50])
print(study_orig_img_data[50,50,32,50])
```

-----  
NameError Traceback (most recent call  
last)

```
<ipython-input-15-91c616b1a32b> in <module>
      5 #test_motcorr_img_data.shape
      6
----> 7 print(test_motcorr_img_data[50,50,32,50])
      8 print(study_orig_img_data[50,50,32,50])
```

NameError: name 'test\_motcorr\_img\_data' is not defined

In [ ]:



