Graph matching results with precision matrices

alpha = 0.0

In [310…
```
import numpy as np
import os
from PIL import Image
import scipy.io as sio
import matplotlib.image as mpimg
from matplotlib import pyplot as plt
from matplotlib.gridspec import GridSpec
import dataframe_image as dfi
from IPython.display import display
import pandas as pd

cwd = os.getcwd()
```

In [311…
```
# alphas 0, 1, 2, 3 correspond to: alpha paramter = 0, 0.0025, 0.0075, 0.0125
alpha = 0

results_dir = str(cwd) + '/results/jupyter/precision/stroke/alpha' + str(alpha
figures_dir = results_dir + 'figures/'

# make results table.
results_dir = str(cwd) + '/results/jupyter/precision/stroke/alpha' + str(alpha
results=loadmat(results_dir  + '/results.mat')
results=results['results']
```

In [312…
```
def color_negative_red(val):
    """
    Takes a scalar and returns a string with
    the css property `'color: red'` for negative
    strings, black otherwise.
    """
    color = 'red' if (val < 0.05 and val > 0) else 'black'
    return 'color: % s' % color
```

In [313…
```
import scipy.io as spio

def loadmat(filename):
    '''
    this function should be called instead of direct spio.loadmat
    as it cures the problem of not properly recovering python dictionaries
    from mat files. It calls the function check keys to cure all entries
    which are still mat-objects
    '''
    data = spio.loadmat(filename, struct_as_record=False, squeeze_me=True)
    return _check_keys(data)

def _check_keys(dict):
    '''
    checks if entries in dictionary are mat-objects. If yes
    todict is called to change them to nested dictionaries
    '''
    for key in dict:
        spio.matlab.mio5_params.mat_struct):
```

```
            dict[key] = _todict(dict[key])
    return dict

def _todict(matobj):
    '''
    A recursive function which constructs from matobjects nested dictionaries
    '''
    dict = {}
    for strg in matobj._fieldnames:
        elem = matobj.__dict__[strg]
        if isinstance(elem, spio.matlab.mio5_params.mat_struct):
            dict[strg] = _todict(elem)
        else:
            dict[strg] = elem
    return dict
```

Analysis 0

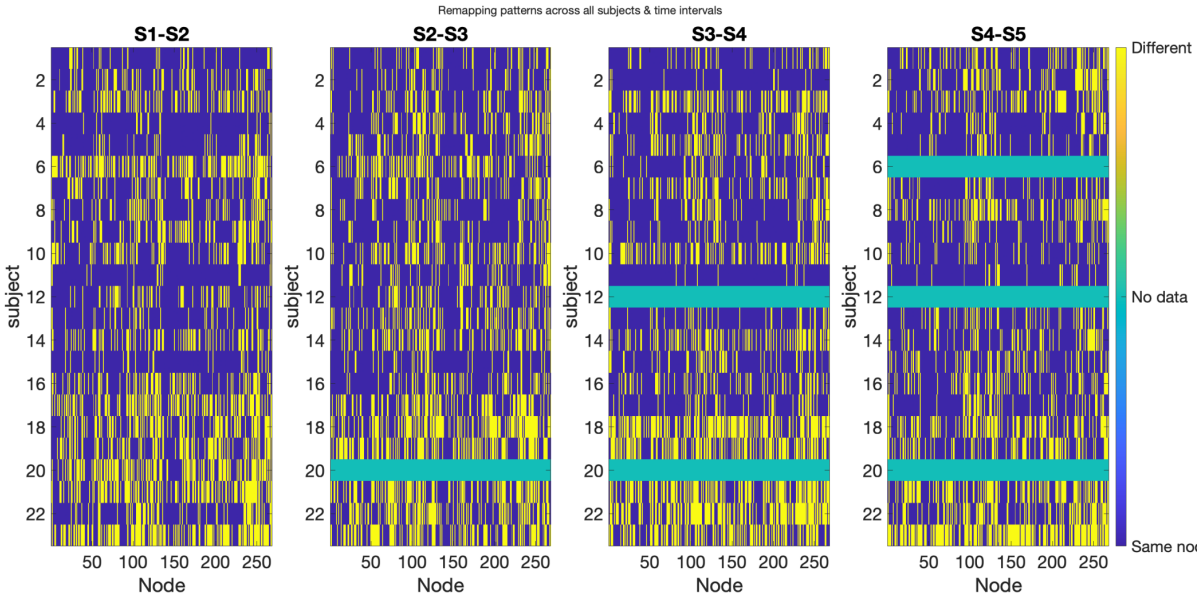
Remapping patterns across all subjects and time points:

- Subjects listed vertically, brain regions listed horizontally (left - right)
- Purple ticks indicate the node was mapped to itself
- Yellow ticks indicate that the node was mapped to a different node (i.e. remapped)
- Turquoise blocks indicate no data for that subject

In [314…

```
img1 = mpimg.imread(str(figures_dir+'remapping_raster_allsubjects_overtime.png
fig = plt.figure(constrained_layout=True,figsize=(30,30))
ax1 = fig.add_subplot(1,1,1)

ax1.imshow(img1)
ax1.axis('off')
```

Out[314… (-0.5, 2916.5, 1457.5, -0.5)



Analysis 1

Correlation between each brain region's remap frequency and mean ChaCo scores across subjects

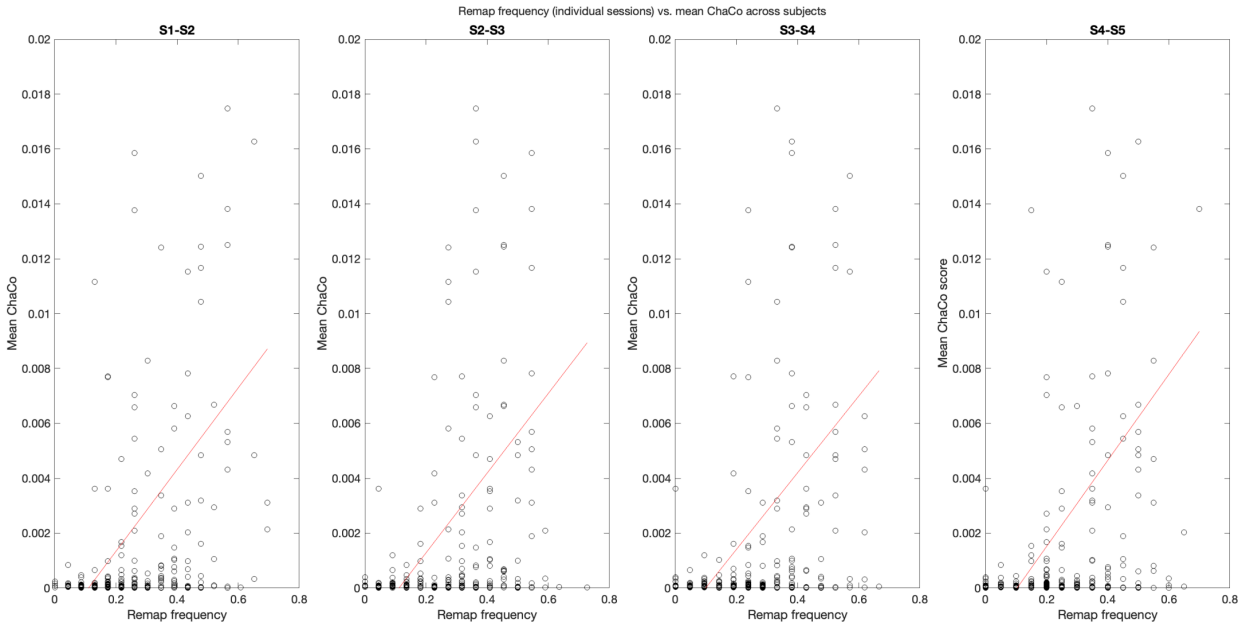
In [315…

```
# Analysis 1
a1=results['corr_w_chaco']
a1s1=a1['s1s2']
a1s2=a1['s2s3']
a1s3=a1['s3s4']
a1s4=a1['s4s5']


dict = {'Stat' : ['Pearson p', 'Pearson rho'],
        'S1-S2' : [a1s1['p'], a1s1['rho']] ,
        'S2-S3' : [a1s2['p'], a1s2['rho']] ,
        'S3-S4' : [a1s3['p'], a1s3['rho']] ,
        'S4-S5' : [a1s4['p'], a1s4['rho']]}

df = pd.DataFrame(dict)
df=df.set_index('Stat')
df=df.style.applymap(color_negative_red).set_caption("Analysis 1")
display(df)

img2 = mpimg.imread(str(figures_dir+'corr_remapping_chaco.png'))
fig = plt.figure(constrained_layout=True,figsize=(30,30))
ax1 = fig.add_subplot(1,1,1)
ax1.imshow(img2)
ax1.axis('off')
```

Analysis 1

Stat	S1-S2	S2-S3	S3-S4	S4-S5
Pearson p	0.000003	0.000001	0.000007	0.000000
Pearson rho	0.280054	0.290009	0.271382	0.307646

Out[315… (-0.5, 2916.5, 1457.5, -0.5)



Top figure: remap frequency of each gray matter region, averaged across all pairs of sessions, versus the mean ChaCo score of that region across subjects. Bottom figure: remap frequency of each gray matter region, averaged across all pairs of sessions, versus the **log-transformed** mean ChaCo score of that region across subjects.

In [316…

```
# Analysis 2 - Correlation between remap frequency and ChaCo scores - all sess
a2=results['corr_w_chaco_allsessions']

dict = {'Stat' : ['Spearman p', 'Spearman rho', 'Pearson p', 'Pearson rho'],
        'Value' : [a2['pearson_p'], a2['pearson_rho'],a2['spearman_p'],a2['spe


df2 = pd.DataFrame(dict)
df2=df2.set_index('Stat')
df2=df2.style.applymap(color_negative_red).set_caption("Analysis 2a")
display(df2)
img1 = mpimg.imread(str(figures_dir+'corr_remapping_chaco_allsessions.png'))
fig = plt.figure(constrained_layout=True,figsize=(30,30))
ax1 = fig.add_subplot(1,1,1)

ax1.imshow(img1)
ax1.axis('off')
a2b=results['corr_w_chaco_allsessions_log']

dict = {'Stat' : ['Pearson p', 'Pearson rho'],
        'Value' : [a2b['pearson_p'], a2b['pearson_rho']]}
df2b = pd.DataFrame(dict)
df2b=df2b.set_index('Stat')
df2b=df2b.style.applymap(color_negative_red).set_caption("Analysis 2b - log tr
display(df2b)


img2 = mpimg.imread(str(figures_dir+'corr_remapping_chaco_allsessions_log.png'
fig = plt.figure(constrained_layout=True,figsize=(30,30))
ax1 = fig.add_subplot(1,1,1)

ax1.imshow(img2)
ax1.axis('off')
```

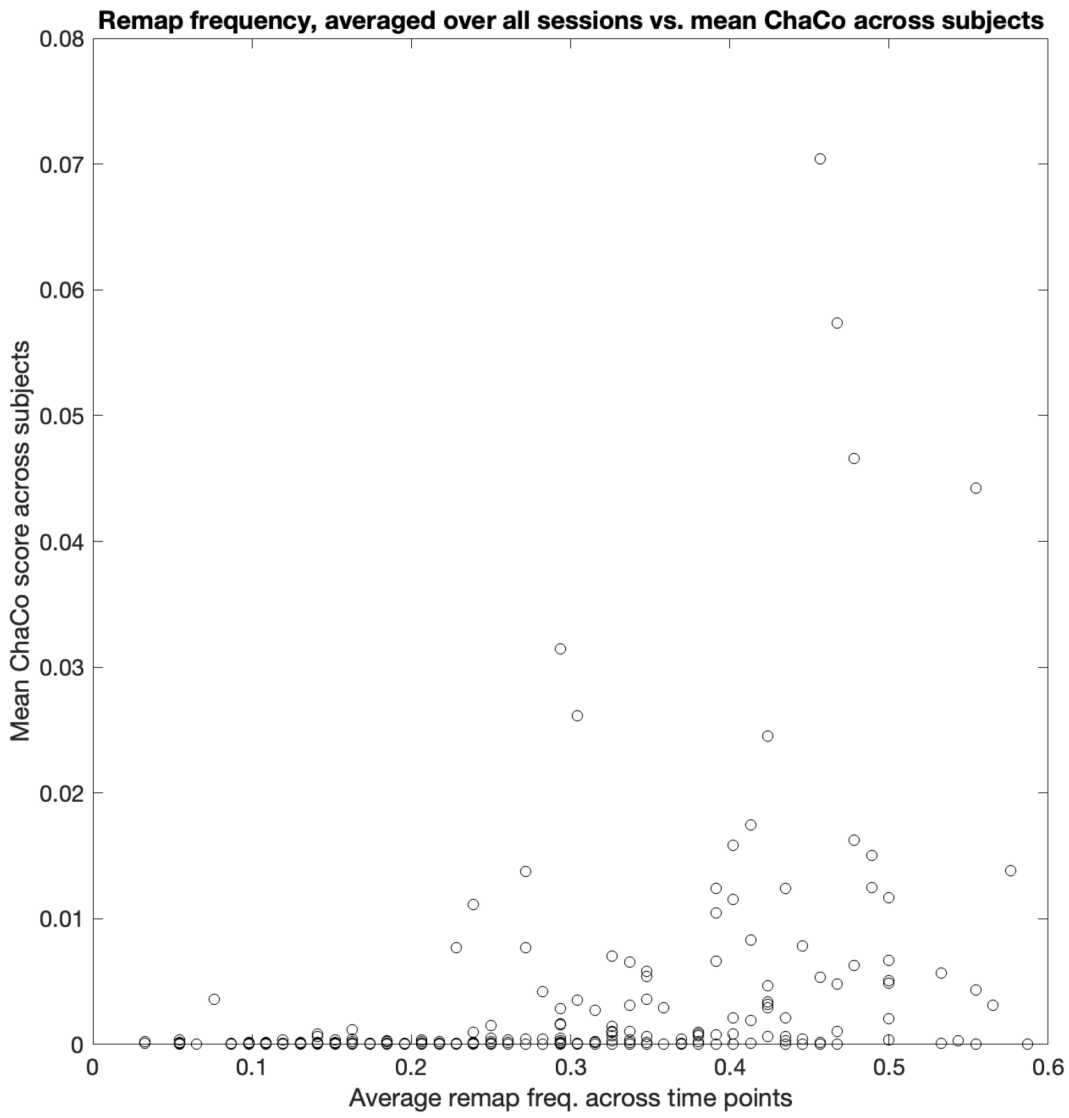
Analysis 2a

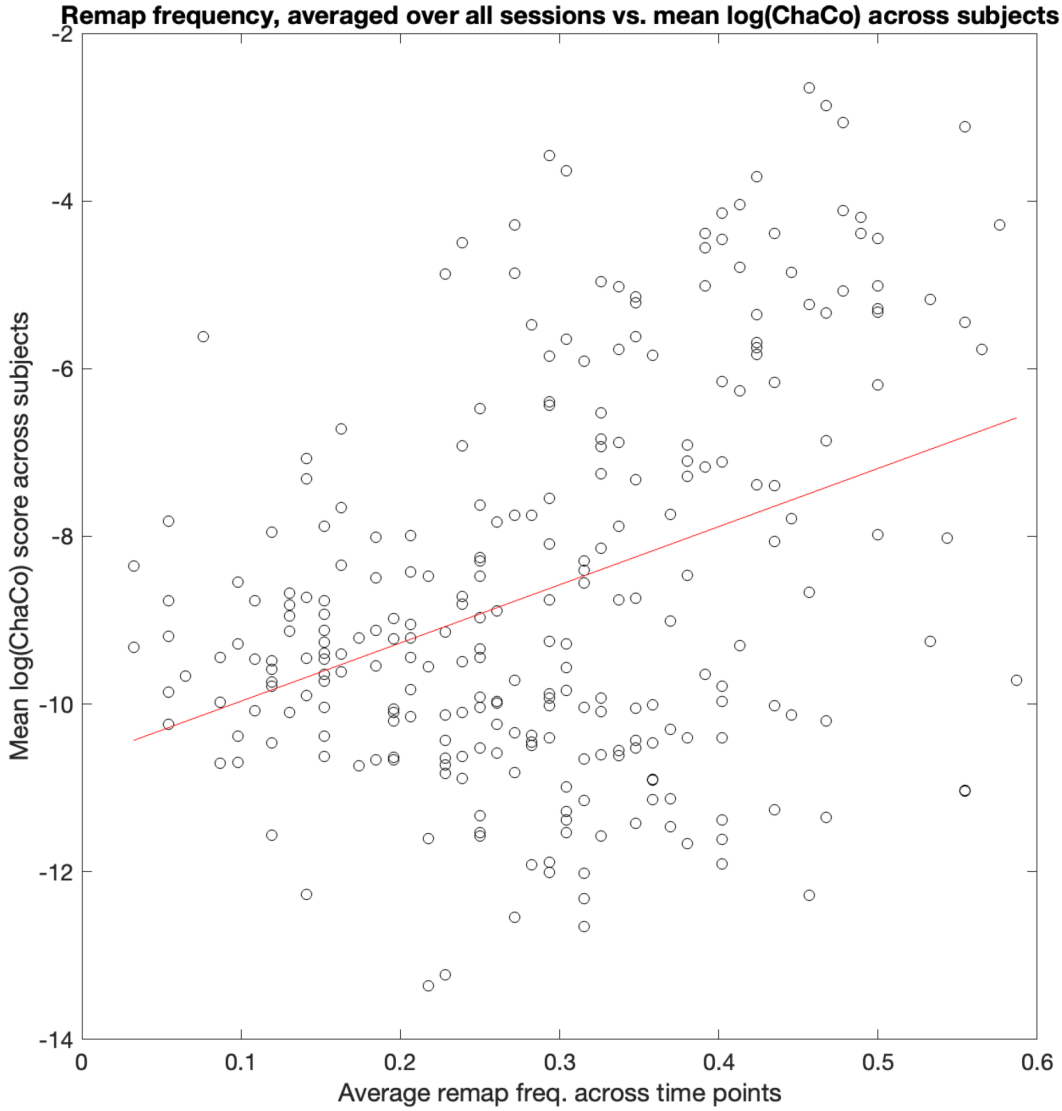
Stat	Value
Spearman p	0.000000
Spearman rho	0.328908
Pearson p	0.000002
Pearson rho	0.285845

Analysis 2b - log transformed data

Stat	Value
Pearson p	0.000002

Out[316… (-0.5, 1457.5, 1457.5, -0.5)





Analysis 3

Correlation between the number of swaps between 7 days and 14 days post-stroke and baseline impairment (day 7 Fugl-Meyer score)

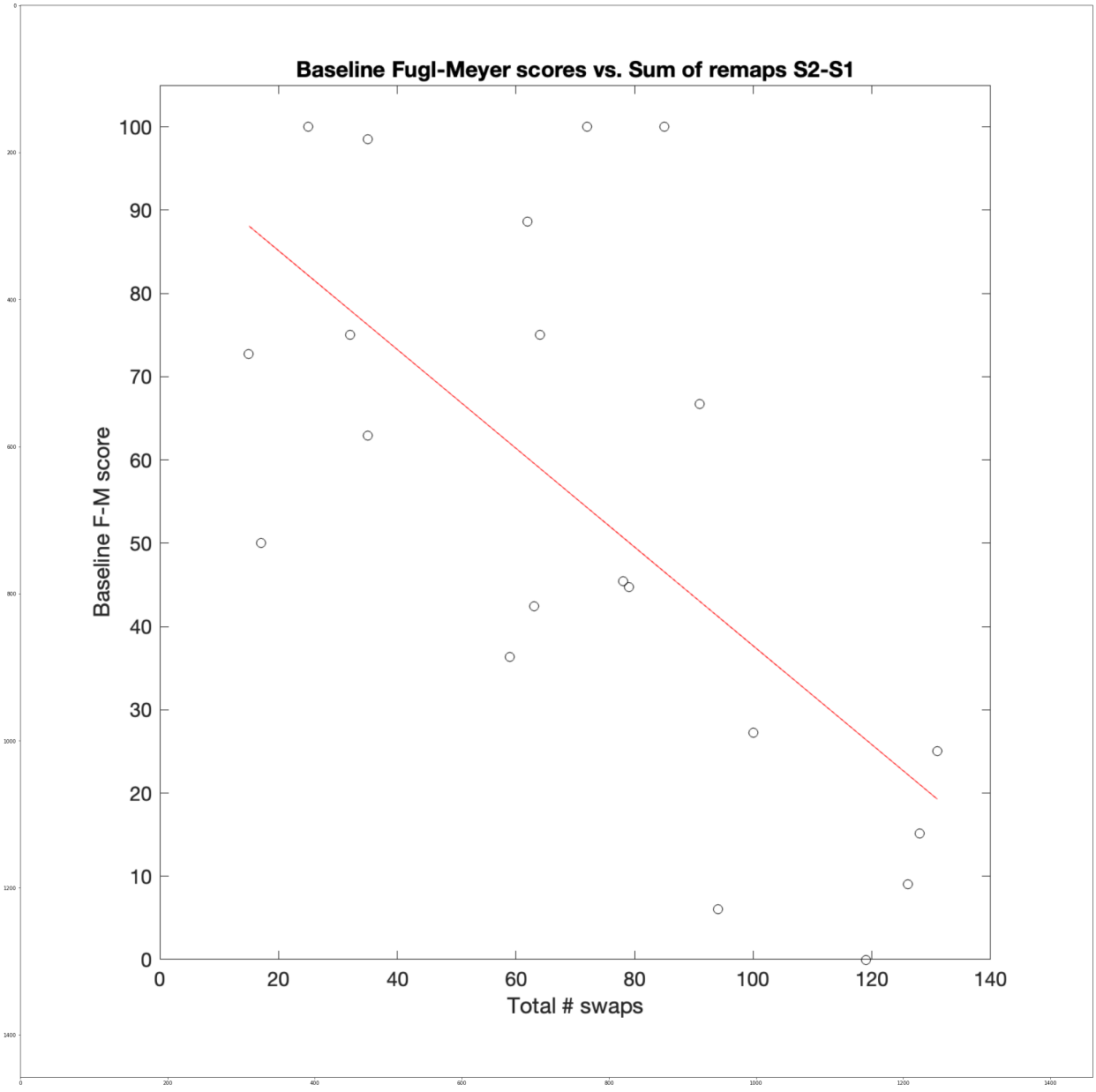
In [317…

```
# Analysis 3 - Baseline FM vs. number of swaps S1-S2
a3=results['baselineFM_remaps_s1s2']

dict = {'Stat' : ['Pearson p', 'Pearson rho'],
        'Value' : [a3['p'], a3['rho']]}

df3 = pd.DataFrame(dict)
df3=df3.set_index('Stat')
df3=df3.style.applymap(color_negative_red).set_caption("Analysis 3")

display(df3)
img1 = mpimg.imread(str(figures_dir+'baselineFM_remaps_s1s2.png'))
fig = plt.figure(constrained_layout=True,figsize=(30,30))
ax1 = fig.add_subplot(1,1,1)
```

Analysis 3

Stat	Value
Pearson p	0.001219
Pearson rho	-0.656796

Out[317… <matplotlib.image.AxesImage at 0x7fac385d8340>



Analysis 4

Correlation between the number of swaps between day 7 and day 14 post-stroke and the degree of motor recovery at 6 months (6 month (S5) FM score - 1 week (S1) FM score)

In [318…

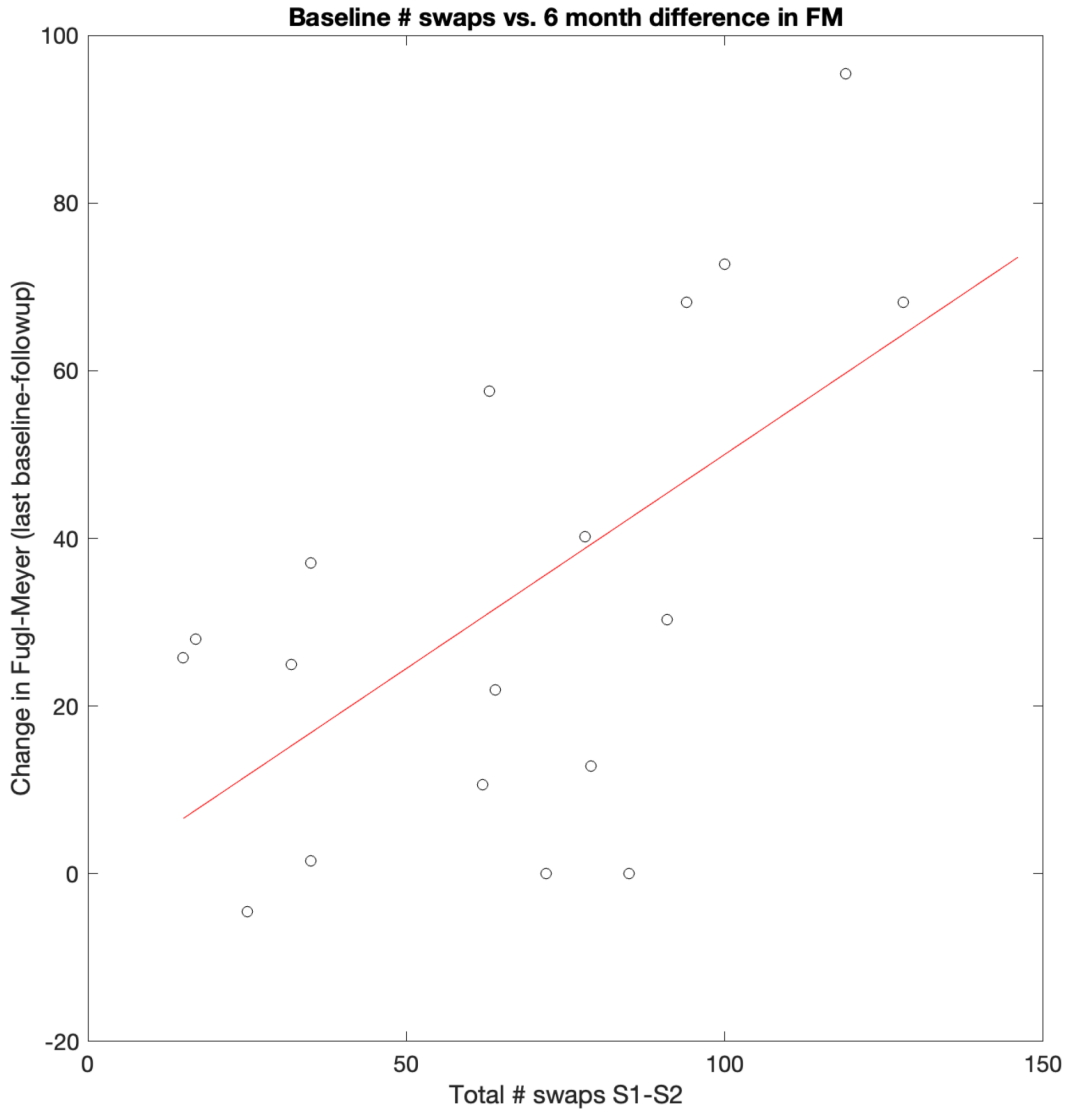
```
# Analysis 4 - Baseline number of swaps vs 6 month FM
a4=results['baselineswaps_6monthFM']

                                    earson rho'],
```

```
        'Value' : [a4['p'], a4['rho']]}

df4 = pd.DataFrame(dict)
df4=df4.set_index('Stat')
df4=df4.style.applymap(color_negative_red).set_caption("Analysis 4")
display(df4)
img1 = mpimg.imread(str(figures_dir+'baselineswaps_6monthFM.png'))
fig = plt.figure(constrained_layout=True,figsize=(30,30))
ax1 = fig.add_subplot(1,1,1)
ax1.imshow(img1)
ax1.axis('off')
```

Analysis 4

Stat	Value
Pearson p	0.008751
Pearson rho	0.598061

Out[318… (-0.5, 1457.5, 1457.5, -0.5)



Analysis 5

Correlation between sum of remaps (across all pairs of sessions) and the change in FM scores (across all pairs of sessions)

In [319…

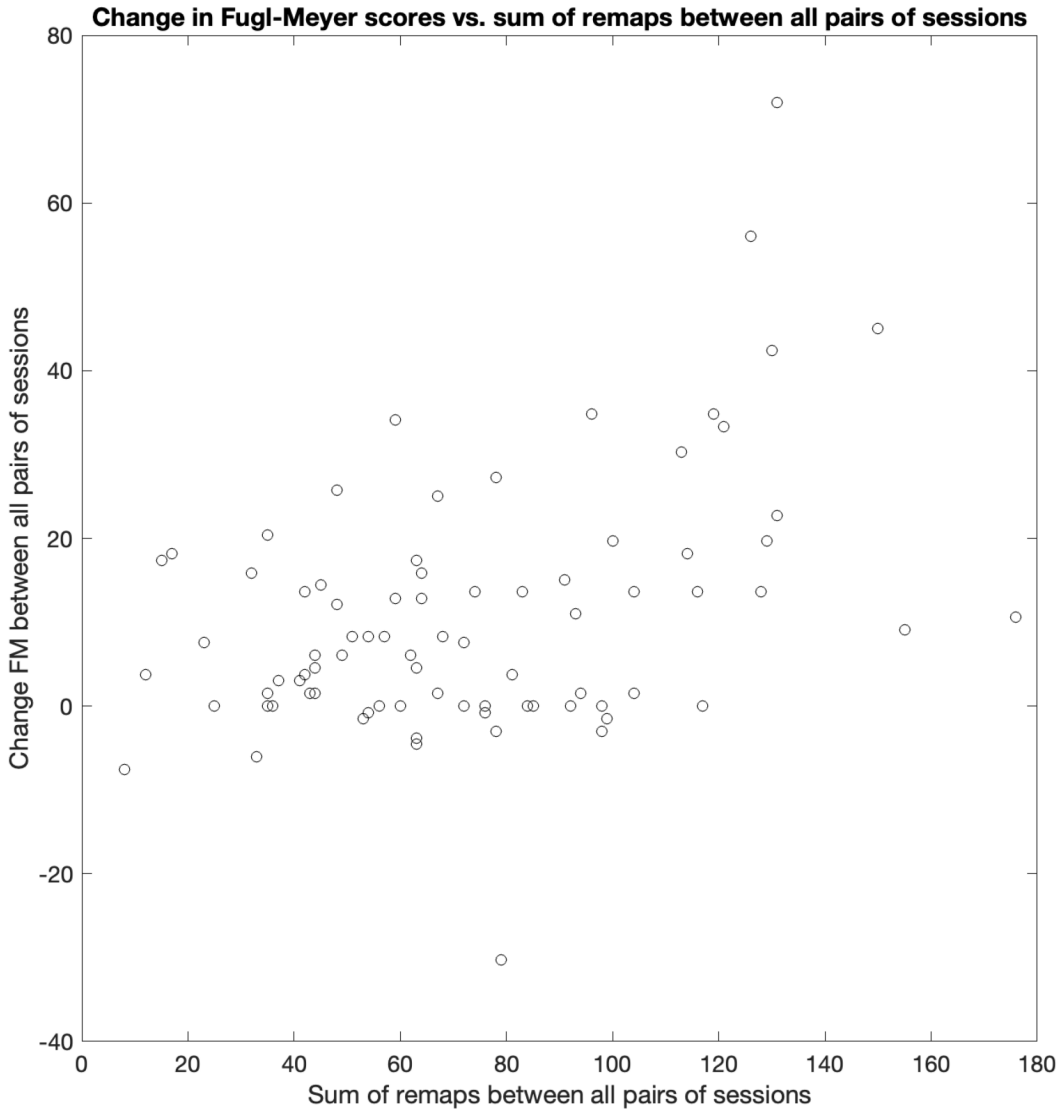
```
# Analysis 5 - corr_recovery_remaps
a5=results['corr_recovery_remaps']

dict = {'Stat' : ['Spearman p', 'Spearman rho'],
        'Value' : [a5['spearman_p'], a5['spearman_rho']]}

df5 = pd.DataFrame(dict)
df5=df5.set_index('Stat')
df5=df5.style.applymap(color_negative_red).set_caption("Analysis 5")
display(df5)
img1 = mpimg.imread(str(figures_dir+'sum_remaps_recovery_allsessions.png'))
fig = plt.figure(constrained_layout=True,figsize=(30,30))
ax1 = fig.add_subplot(1,1,1)
ax1.imshow(img1)
ax1.axis('off')
```

Analysis 5

Stat	Value
Spearman p	0.006081
Spearman rho	0.298744

Out[319…

```
(-0.5, 1457.5, 1457.5, -0.5)
```



Analysis 6

Partial correlation analysis to determine the correlation between sum of remaps (across all pairs of sessions) and the change in FM scores (across all pairs of sessions) while accounting for age and sex.

In [320…

```
# Analysis 6 - corr_recovery_remaps - partial correlation
a6=results['partialcorr_recovery_remaps']

dict = {'p-values' : ['Sum remaps', 'Recovery', 'Age','Sex'],
        'Sum remaps' : [a6['spearman_p'][0][0], a6['spearman_p'][0][1],a6['spe
        'Recovery' : [a6['spearman_p'][1][0], a6['spearman_p'][1][1],a6['spear
        'Age' : [a6['spearman_p'][2][0], a6['spearman_p'][2][1],a6['spearman_p
        'Sex' : [a6['spearman_p'][3][0], a6['spearman_p'][3][1],a6['spearman_p

df6 = pd.DataFrame(dict)
df6=df6.set_index('p-values')
df6=df6.style.applymap(color_negative_red).set_caption("Analysis 6")
```

Analysis 6

p-values	Sum remaps	Recovery	Age	Sex
Sum remaps	0.000000	0.011136	0.380698	0.045664
Recovery	0.011136	0.000000	0.650698	0.777792
Age	0.380698	0.650698	0.000000	0.072949
Sex	0.045664	0.777792	0.072949	0.000000

Analysis 7

Session-specific correlation bewteen amount of motor recovery between sessions, and the number of swaps between sessions

In [321…

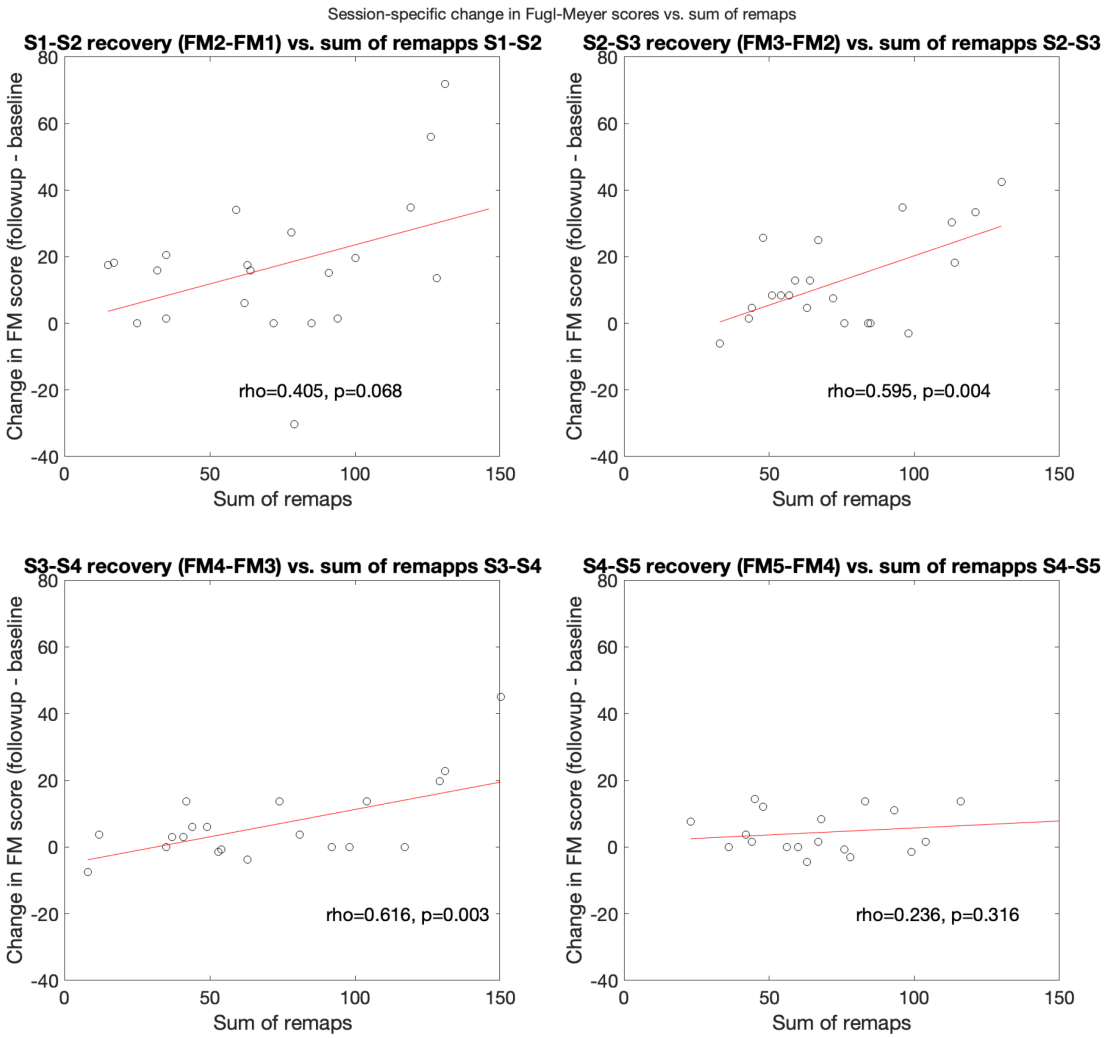
```
# Analysis 7
a7=results['corr_recovery_remap_sessionspecific']
a7s1=a7['s1s2']
a7s2=a7['s2s3']
a7s3=a7['s3s4']
a7s4=a7['s4s5']


dict = {'Stat' : ['Pearson p', 'Pearson rho'],
        'S1-S2' : [a7s1['p'], a7s1['rho']] ,
        'S2-S3' : [a7s2['p'], a7s2['rho']] ,
        'S3-S4' : [a7s3['p'], a7s3['rho']] ,
        'S4-S5' : [a7s4['p'], a7s4['rho']]}

df7 = pd.DataFrame(dict)
df7=df7.set_index('Stat')
df7=df7.style.applymap(color_negative_red).set_caption("Analysis 7")
display(df7)
img1 = mpimg.imread(str(figures_dir+'remaps_recovery_sessionspecific.png'))
fig = plt.figure(constrained_layout=True,figsize=(40,40))
ax1 = fig.add_subplot(1,1,1)
ax1.imshow(img1)
ax1.axis('off')
```

Analysis 7

Stat	S1-S2	S2-S3	S3-S4	S4-S5
Pearson p	0.068384	0.004401	0.002961	0.315800
Pearson rho	0.405249	0.595442	0.615754	0.236324

Out[321…

```
(-0.5, 2082.5, 1905.5, -0.5)
```



In [ ]:

In [ ]: