

Graph matching results with precision matrices

alpha = 0.0125

```
In [346... 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 [347... # alphas 0, 1, 2, 3 correspond to: alpha parameter = 0, 0.0025, 0.0075, 0.0125
alpha = 3

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 [348... 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 [349... 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:
        if isinstance(dict[key], 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

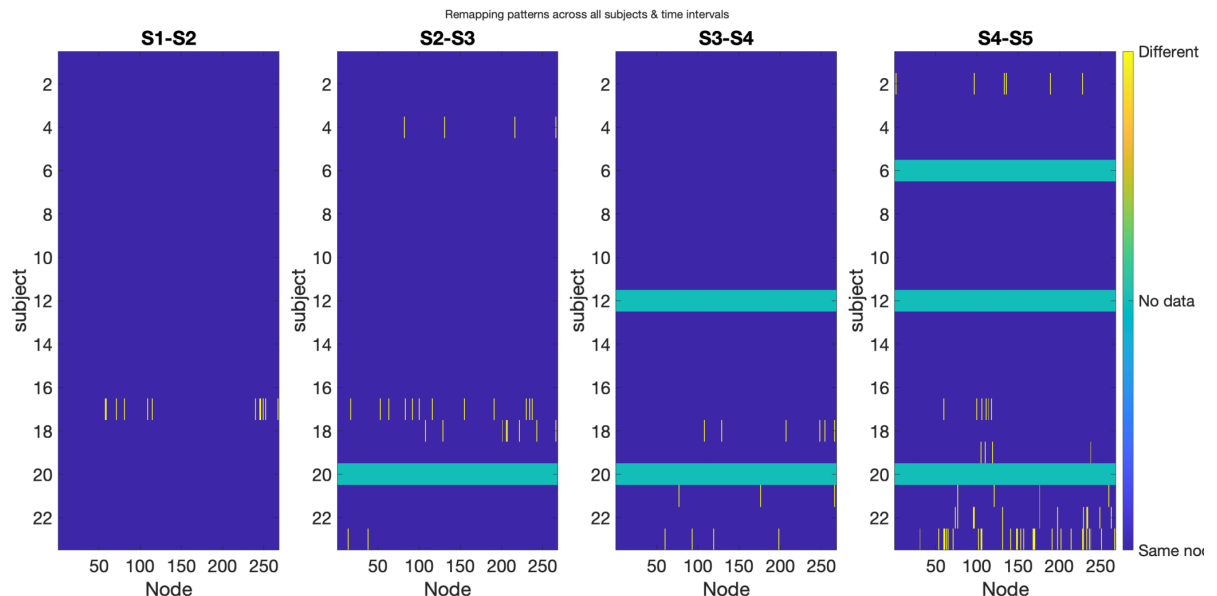
```

In [350...] 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[350...] (-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 [351... # Analysis 1
a1=results['corr_w_chaco']
als1=a1['s1s2']
als2=a1['s2s3']
als3=a1['s3s4']
als4=a1['s4s5']

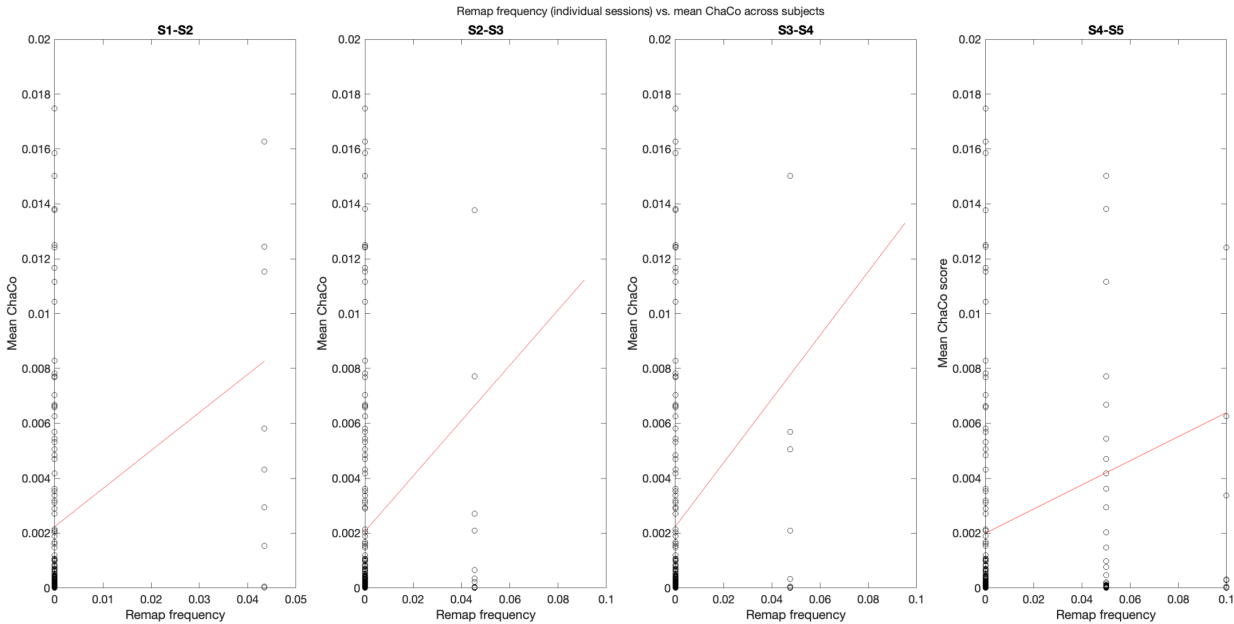
dict = {'Stat' : ['Pearson p', 'Pearson rho'],
        'S1-S2' : [als1['p'], als1['rho']] ,
        'S2-S3' : [als2['p'], als2['rho']] ,
        'S3-S4' : [als3['p'], als3['rho']] ,
        'S4-S5' : [als4['p'], als4['rho']] }

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				
	S1-S2	S2-S3	S3-S4	S4-S5
Stat				
Pearson p	0.008617	0.002855	0.006975	0.016791
Pearson rho	0.160175	0.181546	0.164455	0.145969

Out[351... (-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 [352... # 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')
```

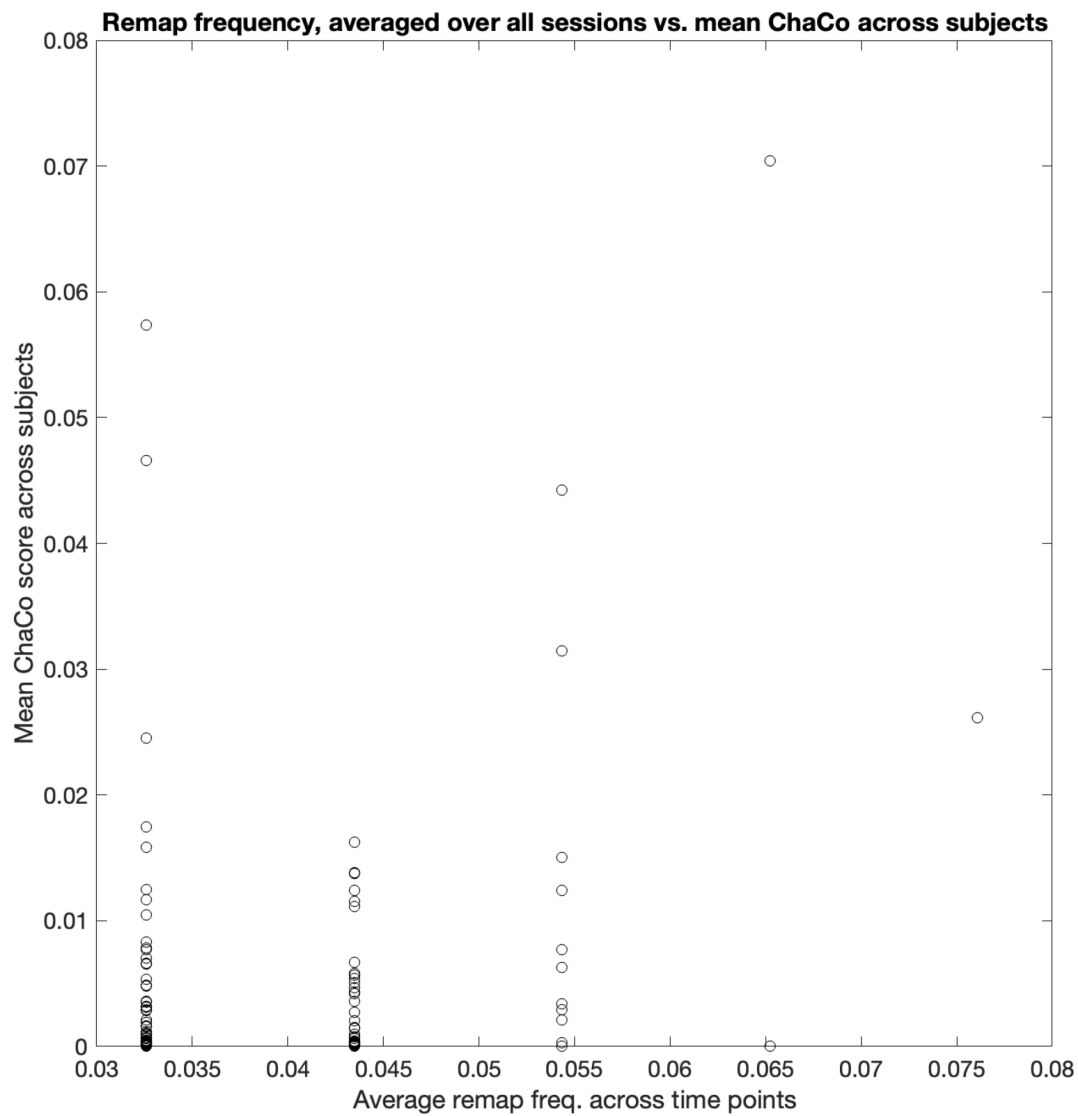
Analysis 2a

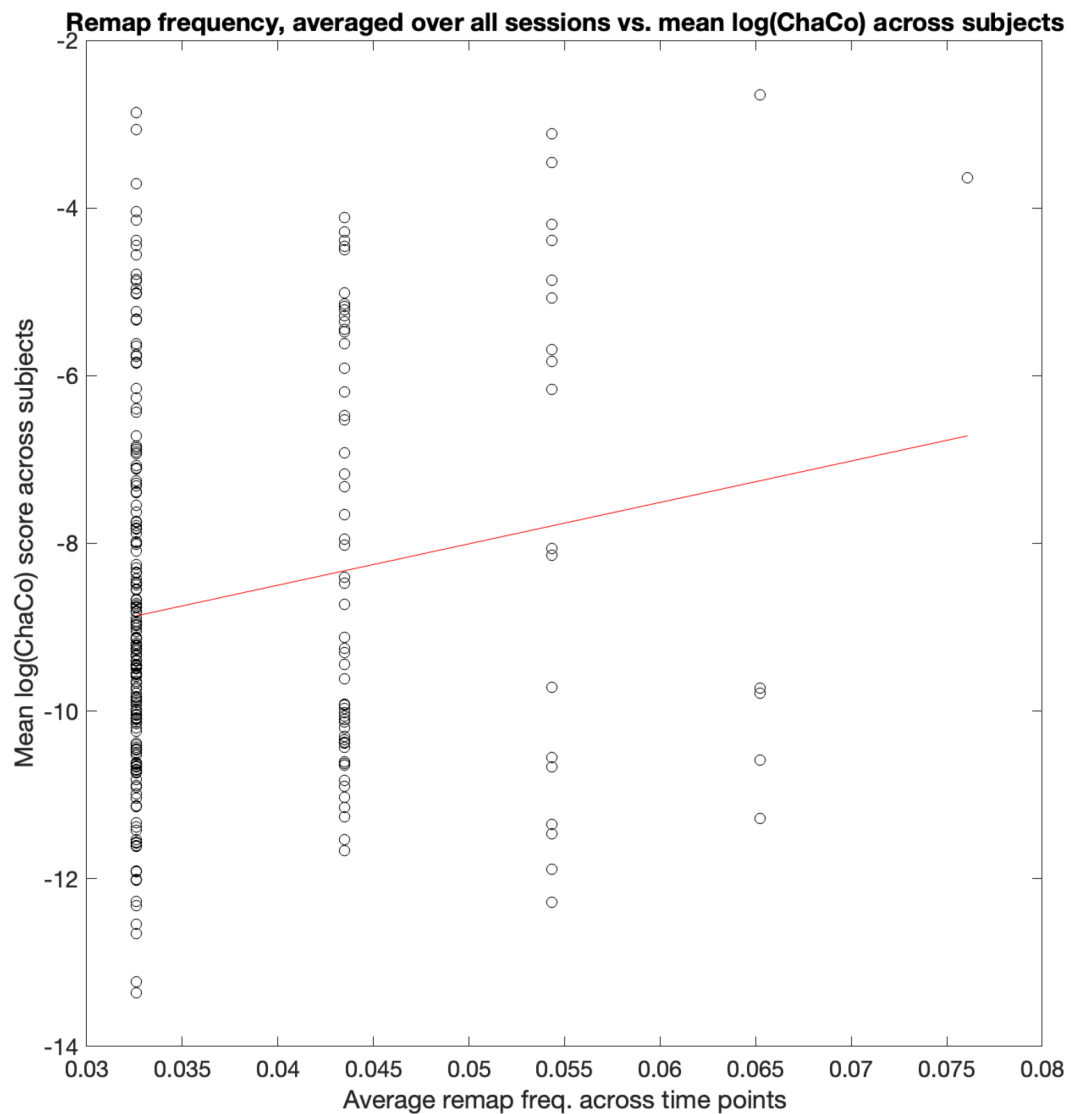
Value	
Stat	
Spearman p	0.000004
Spearman rho	0.277096
Pearson p	0.100647
Pearson rho	0.100500

Analysis 2b - log
transformed data

Value	
Stat	
Pearson p	0.100647

Out[352... (-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 [353... # 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

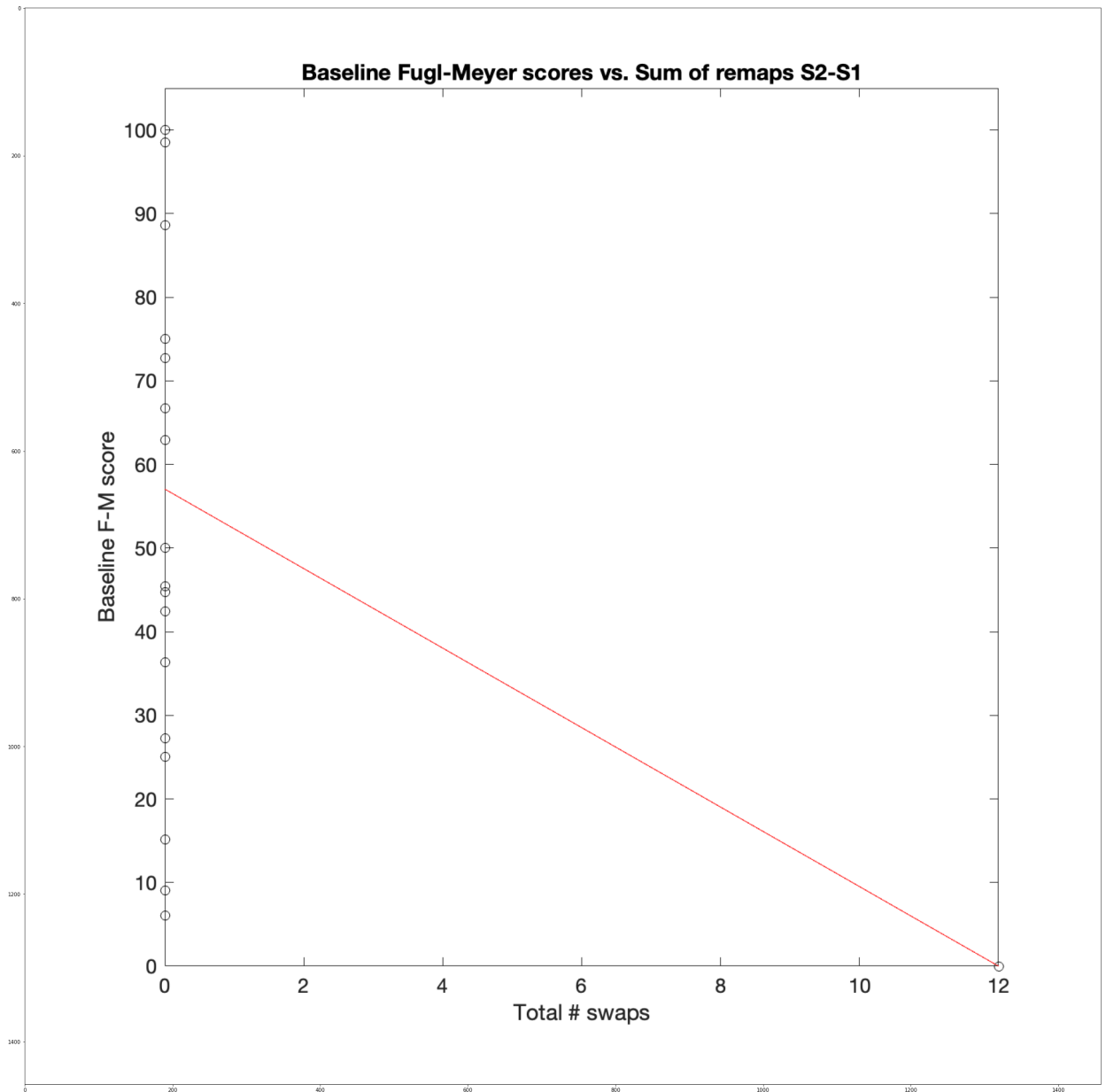
Value

Stat

Pearson p 0.092916

Pearson rho -0.376078

Out[353... <matplotlib.image.AxesImage at 0x7fac38298790>



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

Loading [MathJax]/jax/output/CommonHTML/fonts/TeX/fontdata.js Pearson rho'],

```

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

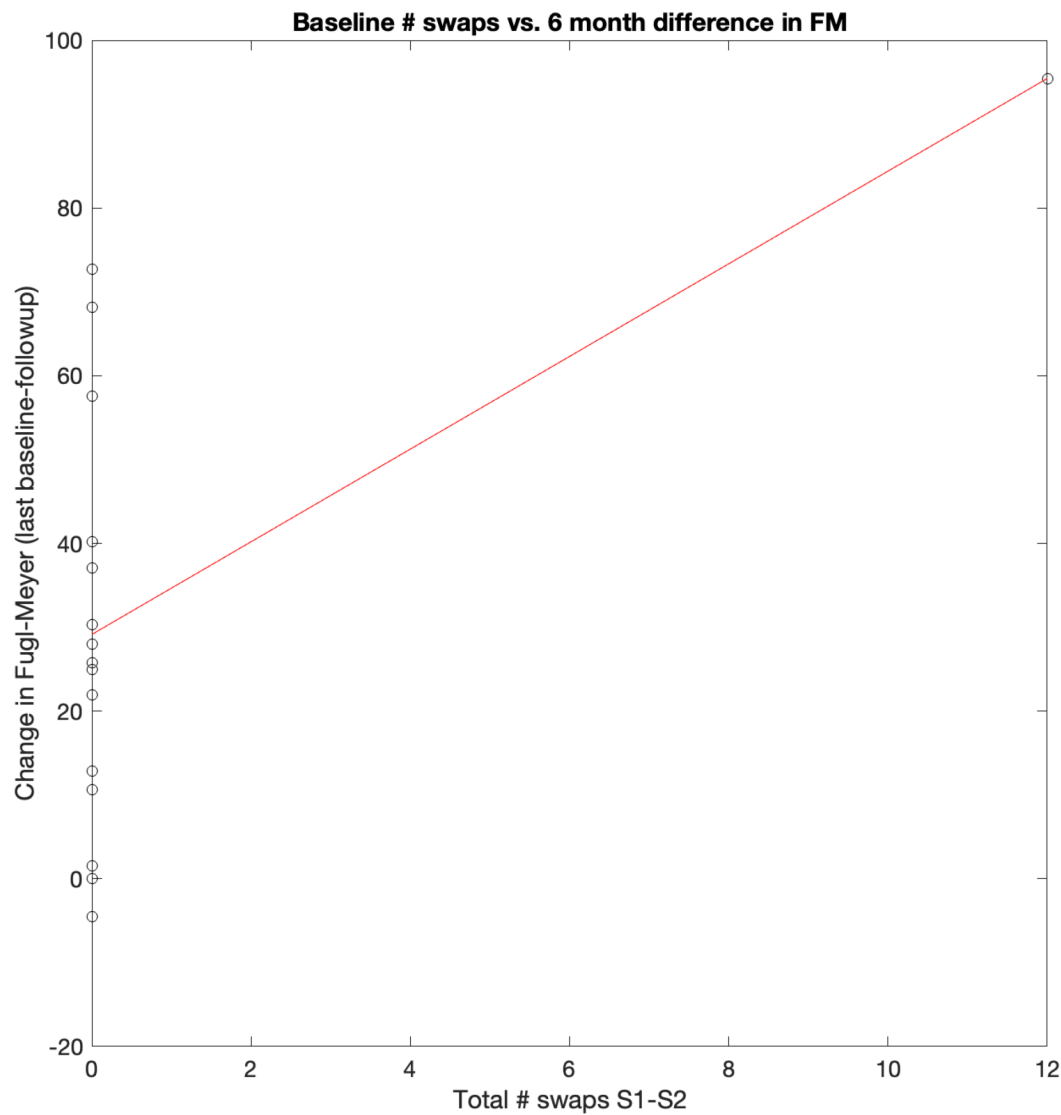
df4 = pd.DataFrame(dict)
df4=df4.set_index('Stat')
df4=df4.style.applymap(color_negative_red).set_caption("Analysis 4")
display(df4)
img1 = mpimg.imread(str(figures_dir+'baselineswaps_6monthFM.png'))
fig = plt.figure(constrained_layout=True,figsize=(30,30))
ax1 = fig.add_subplot(1,1,1)
ax1.imshow(img1)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

```

Analysis 4

Value	
Stat	
Pearson p	0.021470
Pearson rho	0.537326

Out[354...] (-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 [355... # 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

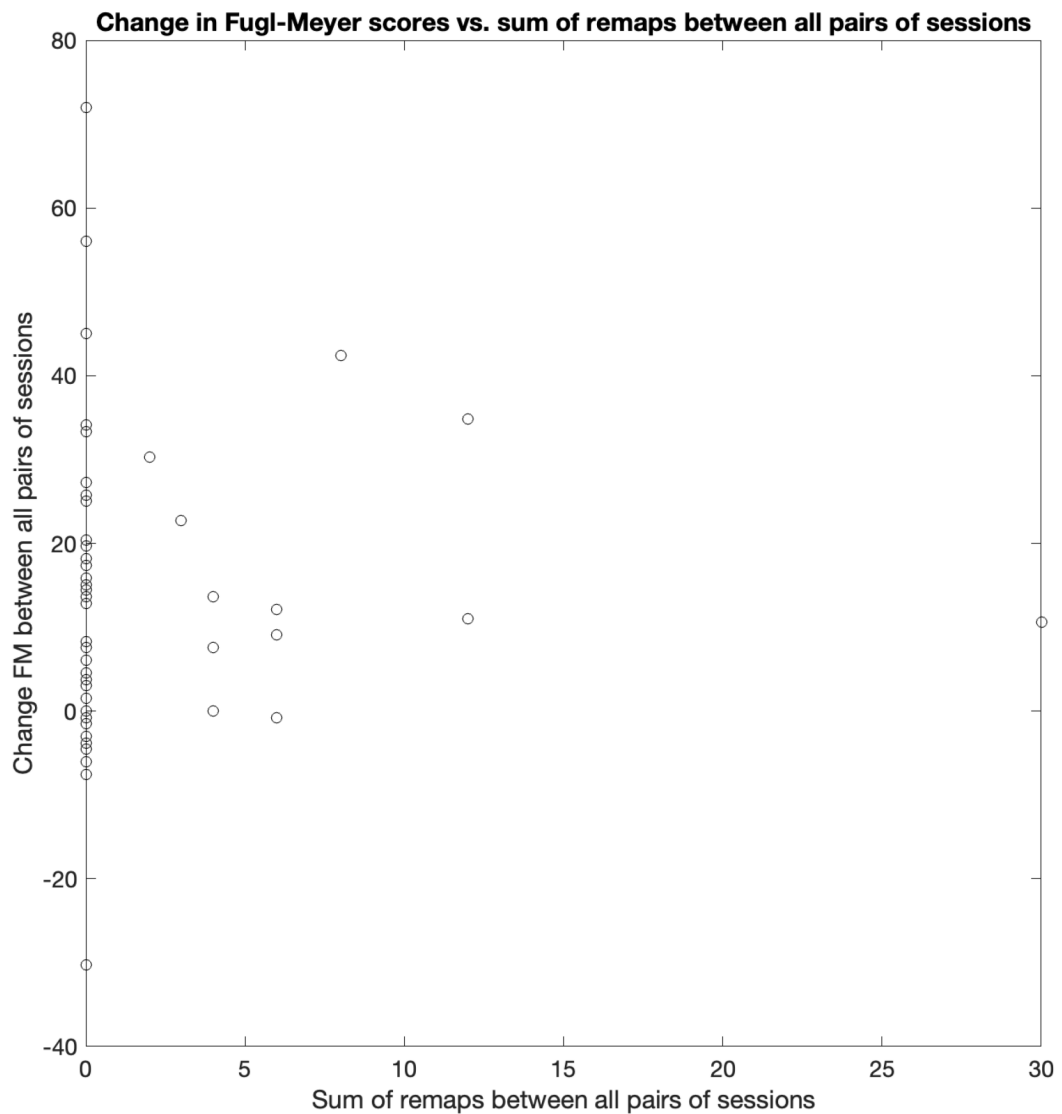
Value

Stat

Spearman p 0.029898

Spearman rho 0.238512

Out [355... (-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 [356... # 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")
display(df6)
```

Analysis 6				
	Sum remaps	Recovery	Age	Sex
p-values				
Sum remaps	0.000000	0.040928	0.910708	0.160645
Recovery	0.040928	0.000000	0.460306	0.587612
Age	0.910708	0.460306	0.000000	0.108752
Sex	0.160645	0.587612	0.108752	0.000000

Analysis 7

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

```
In [357... # 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']]}

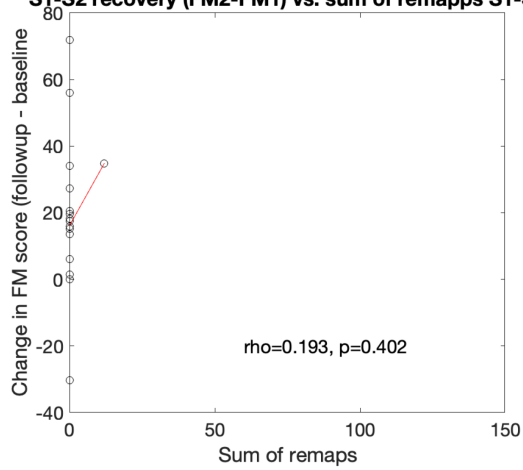
df7 = pd.DataFrame(dict)
df7=df7.set_index('Stat')
df7=df7.style.applymap(color_negative_red).set_caption("Analysis 7")
display(df7)
img1 = mpimg.imread(str(figures_dir+'remaps_recovery_sessionspecific.png'))
fig = plt.figure(constrained_layout=True,figsize=(40,40))
ax1 = fig.add_subplot(1,1,1)
ax1.imshow(img1)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

Analysis 7				
	S1-S2	S2-S3	S3-S4	S4-S5
Stat				
Pearson p	0.402271	0.004884	0.730768	0.068117
Pearson rho	0.192857	0.589876	0.079860	0.415980

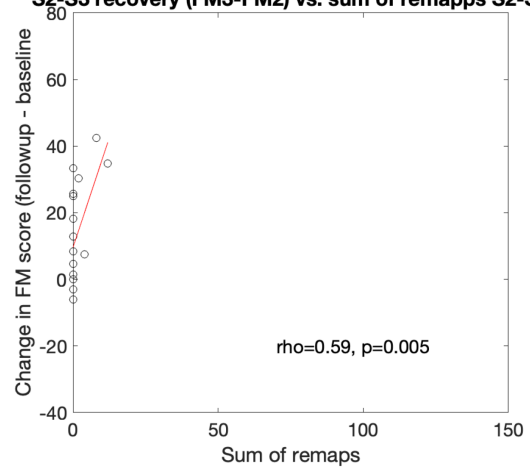
```
Out[357... (-0.5, 2082.5, 1905.5, -0.5)
```

Session-specific change in Fugl-Meyer scores vs. sum of remaps

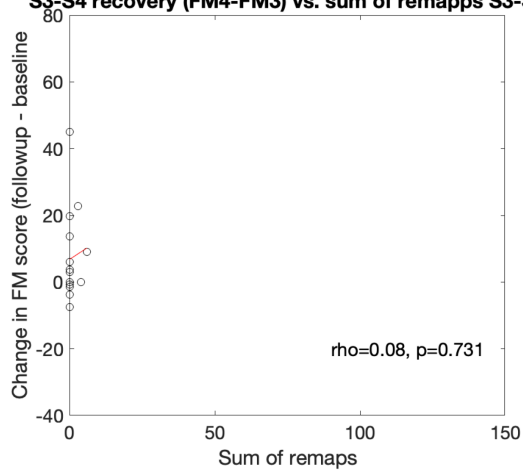
S1-S2 recovery (FM2-FM1) vs. sum of remapps S1-S2



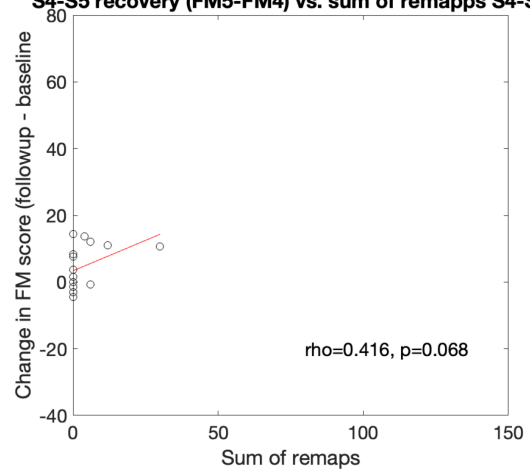
S2-S3 recovery (FM3-FM2) vs. sum of remapps S2-S3



S3-S4 recovery (FM4-FM3) vs. sum of remapps S3-S4



S4-S5 recovery (FM5-FM4) vs. sum of remapps S4-S5



In []:

In []: