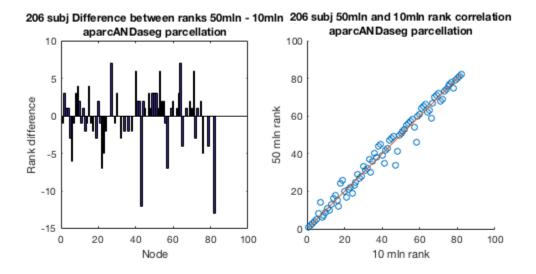
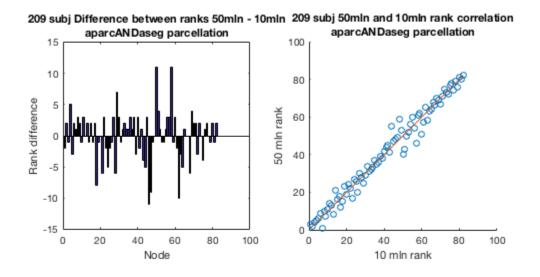
```
% differences between 10 and 50 mln streamlines
clear all; close all;
cd ('/Users/Aurina/GoogleDrive/Genetics_connectome/Gen_Cog/Data/
Connectomes/10_50_mlnStreamlines/');
load('FACT_aparcANDaseg_10_mil.mat');
density10 = density;
deg10 = zeros(length(density10), size(density10{1},1));
NumNodes = size(density{1},1);
for i=1:length(density10)
    deq10(i,:) = degrees und(density10{i});
end
load('FACT aparcANDaseg 50 mil.mat');
density50 = density;
deg50 = zeros(length(density), size(density{1},1));
for i=1:length(density)
    deg50(i,:) = degrees_und(density50{i});
end
0
% dif = deg50-deg10;
% for i=1:length(density)
      FigHandle = figure('Position', [100, 100, 1200, 1200]);
응
      subplot(3,2,5);
응
      scatter(deg10(i,:), deg50(i,:));
응
      xlabel('10 mil streamlines degrees'); ylabel('50 mil streamlines
 degrees');
응
      hold on;
응
      x = linspace(1, size(density\{1\}, 1), size(density\{1\}, 1));
읒
      y = x;
응
      plot(x,y);
%
응
      subplot(3,2,6); bar(x,dif(i,:)); title('Difference between
 degrees (50mln - 10mln streamlines)');
      xlabel('Node');
응
      ylabel('Difference in degrees');
      Matrix10 = fRandom2AnatomicalParcellations_annot('aparc',
 'ANDaseq', density10{i});
      Matrix50 = fRandom2AnatomicalParcellations_annot('aparc',
 'ANDaseg', density50{i});
      subplot(3,2,1); imagesc(log(Matrix10)); axis square; title
 ('Connectome 10 mil streamlines');
      subplot(3,2,2); imagesc(log(Matrix50)); axis square; title
 ('Connectome 50 mil streamlines');
응
      subplot(3,2,3); histogram(deg10(i,:), 20); title('Degree
 distribution 10 mil'); xlabel('Degree');
      subplot(3,2,4); histogram(deg50(i,:), 20); title('Degree
 distribution 50 mil'); xlabel('Degree');
% end
```

```
% A = mean(dif,1);
% figure; bar(x,A);
Ranks10 = zeros(length(density), NumNodes);
Ranks50 = zeros(length(density), NumNodes);
for i=1:length(density)
    [ignore, idx10] = sort( deg10(i,:) , 'descend');
    [ignore, idx50] = sort( deg50(i,:) , 'descend');
    Ranks10(i,idx10) = 1:numel(idx10);
    Ranks50(i,idx50) = 1:numel(idx50);
end
R = zeros(length(density), NumNodes);
for i=1:length(density)
R10 = Ranks10(i,:);
R50 = Ranks50(i,:);
Ra = R50-R10;
R(i,:) = Ra;
figure;
%FigHandle = figure('Position', [100, 100, 1200, 1200]);
subplot(1,2,1); bar(Ra); title(sprintf('%d subj Difference
between ranks 50mln - 10mln\naparcANDaseg parcellation',
 sub id(i))) ;xlabel('Node'); ylabel('Rank difference'); axis square;
subplot(1,2,2); scatter(R10, R50); title(sprintf('%d subj 50mln and
 10mln rank correlation\naparcANDaseq parcellation', sub id(i)));
xlabel('10 mln rank'); ylabel('50 mln rank');axis square;
hold on;
x = linspace(1, size(density\{1\}, 1), size(density\{1\}, 1));
y = x;
plot(x,y);
end
```

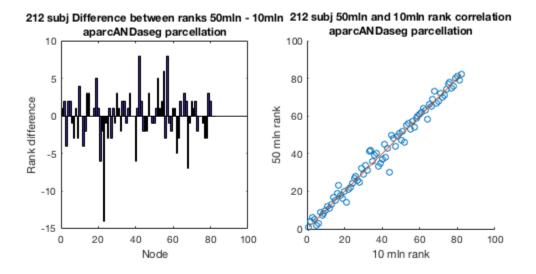
205 subj Difference between ranks 50mln - 10mln 205 subj 50mln and 10mln rank correlation aparcAN Daseg parcellation aparcANDaseg parcellation Rank difference 50 mln rank -5 -10 -15 -20 Node 10 mln rank



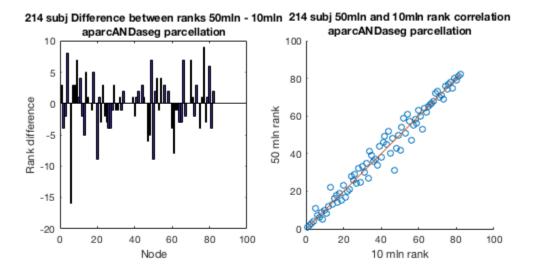
208 subj Difference between ranks 50mln - 10mln 208 subj 50mln and 10mln rank correlation aparcAN Daseg parcellation aparcANDaseg parcellation Rank difference 50 mln rank -5 -10 0 6 Node 10 mln rank



210 subj Difference between ranks 50mln - 10mln 210 subj 50mln and 10mln rank correlation aparcAN Daseg parcellation aparcANDaseg parcellation Rank difference 50 mln rank -10 -15 Node 10 mln rank



213 subj Difference between ranks 50mln - 10mln 213 subj 50mln and 10mln rank correlation aparcAN Daseg parcellation aparcANDaseg parcellation Rank difference 50 mln rank -5 -10 -15 Node 10 mln rank



215 subj Difference between ranks 50mln - 10mln 215 subj 50mln and 10mln rank correlation aparcAN Daseg parcellation aparcANDaseg parcellation Rank difference 50 mln rank -5 -10 -15 Node 10 mln rank

