```
clear all;
close all;
cd ('/Users/Aurina/Documents/Genetics_connectome/Gen_Cog/Data/
Connectomes/FinalCorrections/');
Parcellation = {'aparcaseg'}; % choose parcellation
Tract = {'FACT_'}; % choose tract method
Name = strcat(Tract{1}, Parcellation{1});
load (sprintf('%s.mat', Name));
Density = zeros(size(density,2),1);
for i=1:size(density,2)
    Mask = count{i};
    density{i}(Mask<10) = 0;
    figure; imagesc(log(density{i})); title(sprintf('Subject %d',
 sub id{i}));
    Deg = degrees_und(density{i});
    Density(i) = density_und(density{i});
    Strength = sum(density{i});
    Len = len{i};
     figure;
     subplot(2,1,1);histogram(Deg, 20); title(sprintf('Degree Subject
 %d', sub_id{i}));
     subplot(2,1,2);histogram(nonzeros(Len(:)), 20);
 title(sprintf('length Subject %d', sub_id{i}));
end
% cd ('/Users/Aurina/Documents/Genetics_connectome/Gen_Cog/Data/
Connectomes/WithACT/');
% Parcellation = {'aparcaseg'};
% Tract = {'FACT_'};
% Name = strcat(Tract{1}, Parcellation{1});
% load (sprintf('%s.mat', Name));
% for i=1:size(density,2)
      figure; imagesc(log(density{i})); title(sprintf('Subject %d',
sub_id{i}));
%
      Deg = degrees_und(density{i});
응
      Len = length{i};
응
      figure;
      subplot(2,1,1);histogram(Deg, 20); title(sprintf('degrees
 Subject %d', sub id{i}));
      subplot(2,1,2);histogram(nonzeros(Len(:)), 20);
title(sprintf('length Subject %d', sub_id{i}));
% end
```



























































































