
```

clear all;
close all;

cd ('/Users/Aurina/Documents/Genetics_connectome/Gen_Cog/Data/
Connectomes/WithACT/'); %choose the folder
Parcellation = {'aparcaseg'}; % choose parcellation
Tract = {'iFOD2_'}; % choose tract method

Name = strcat(Tract{1}, Parcellation{1});
load (sprintf('%s.mat', Name));

Density = zeros(size(density,2),1);

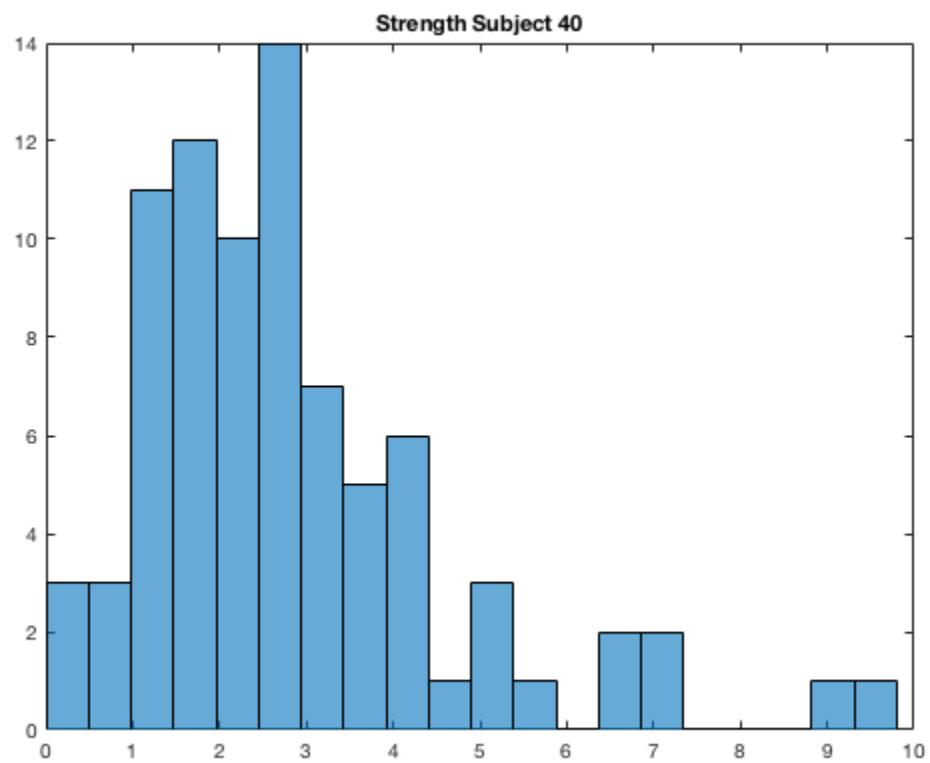
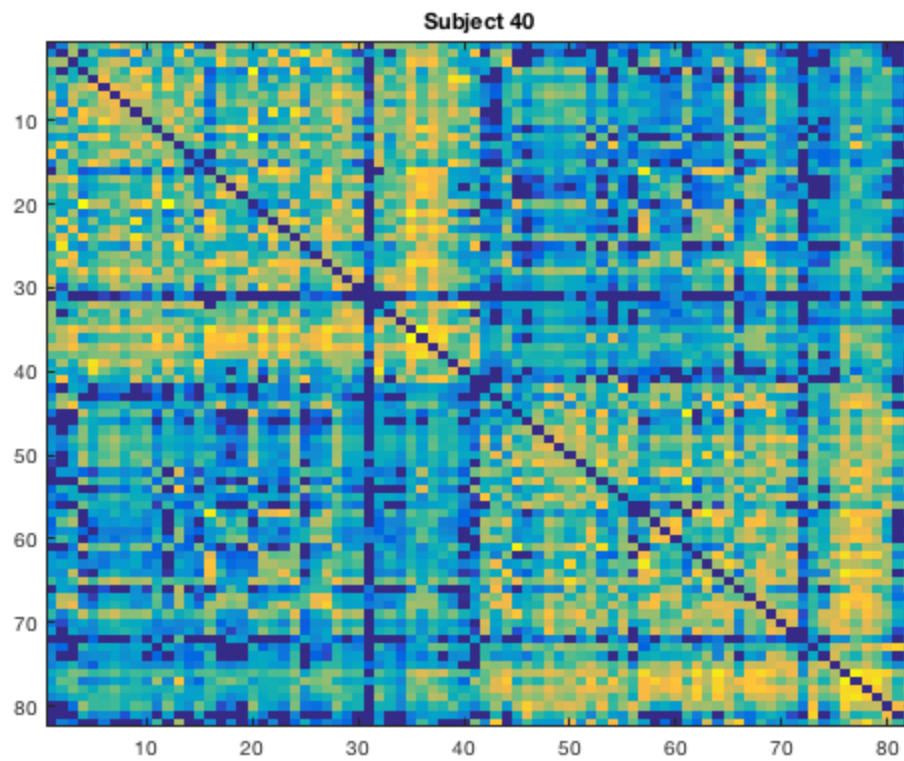
for i=1:size(density,2)
    figure; imagesc(log(density{i})); title(sprintf('Subject %d',
sub_id{i}));

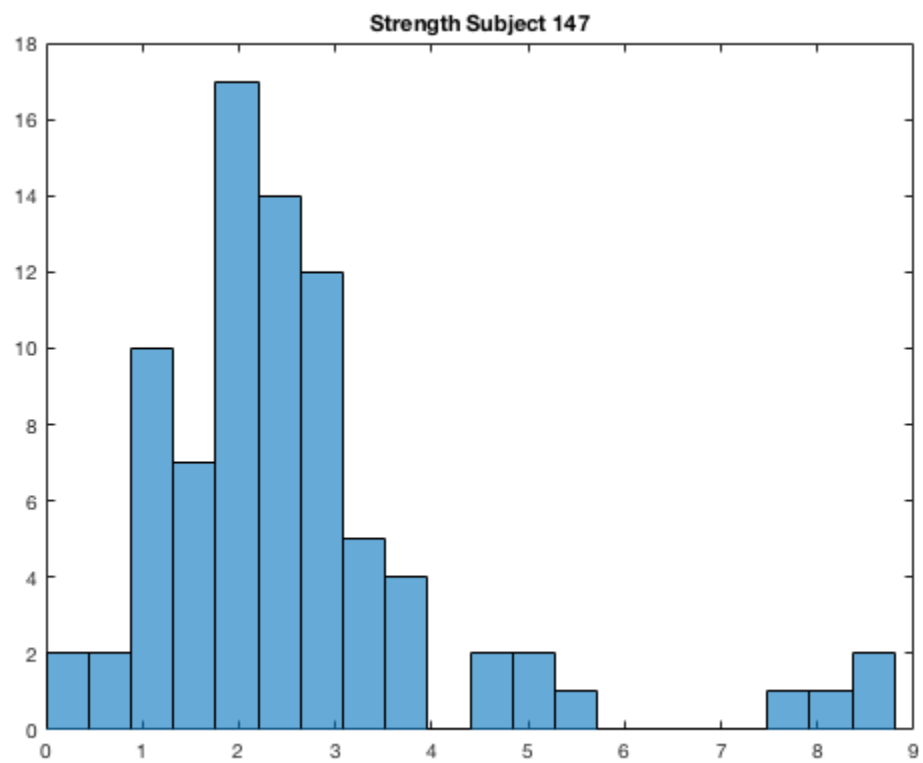
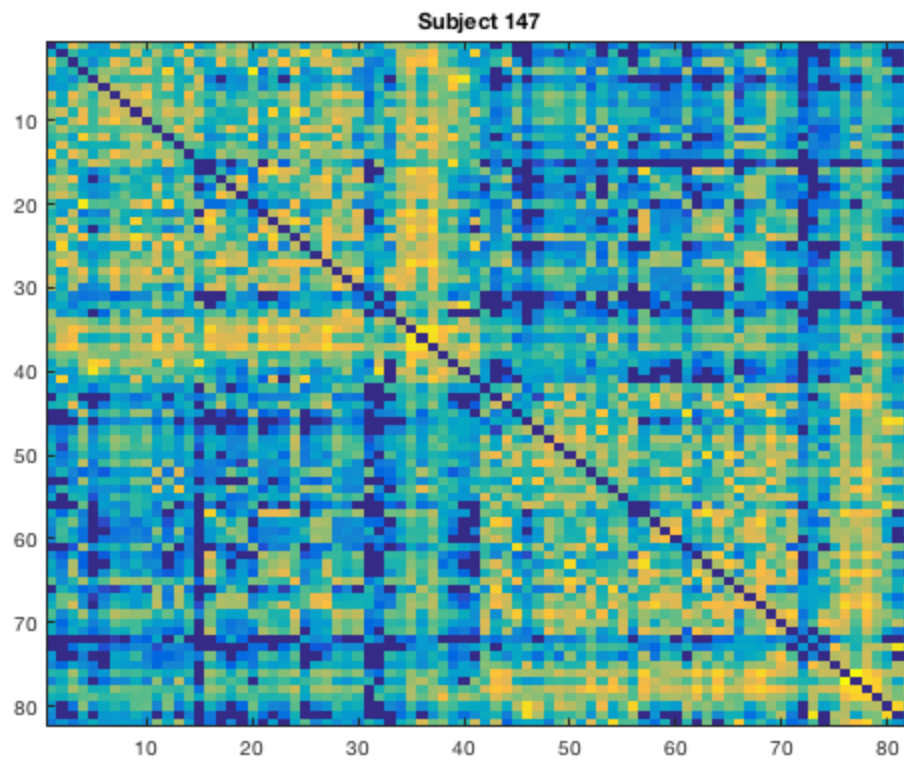
    Strength = sum(density{i});

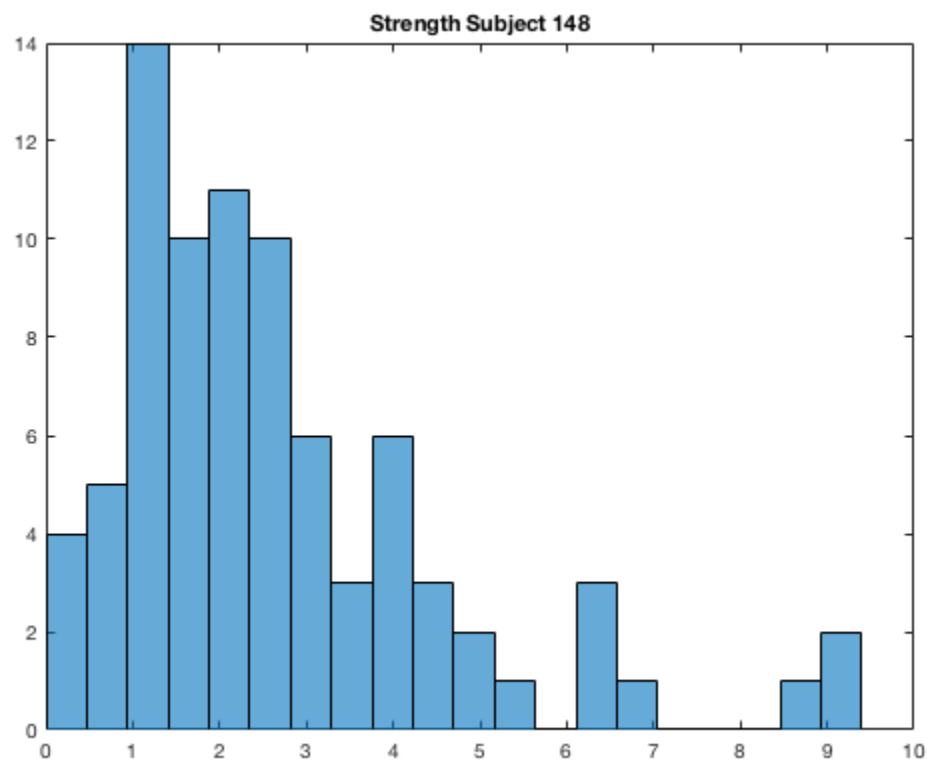
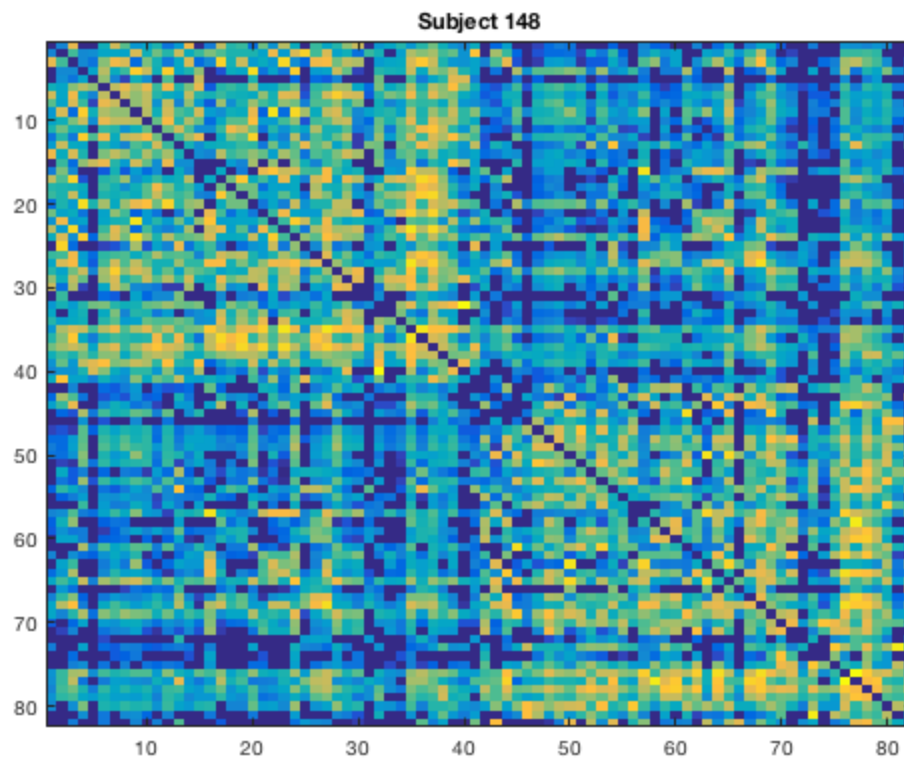
    figure; histogram(Strength, 20); title(sprintf('Strength Subject
%d', sub_id{i}));

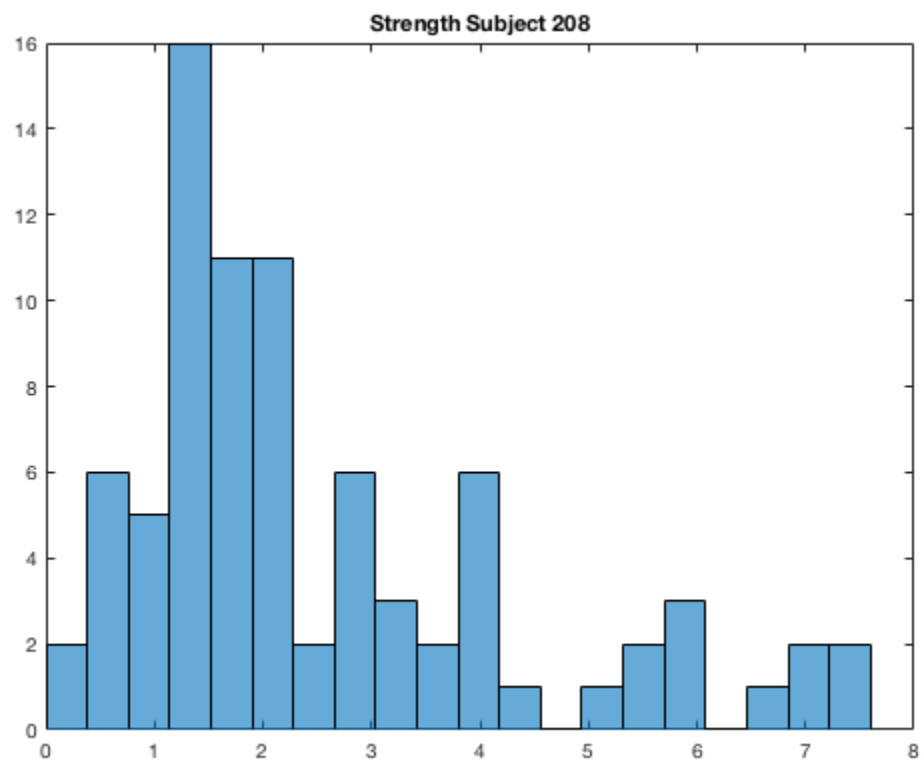
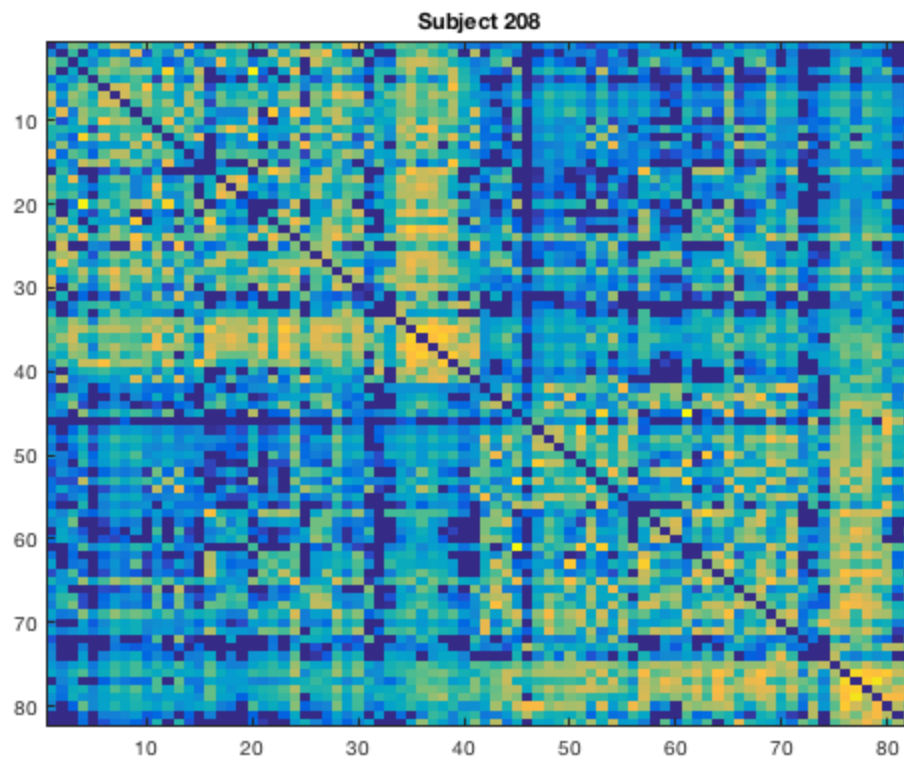
end
% clear all;
% close all;
%
% cd ('/Users/Aurina/Documents/Genetics_connectome/Gen_Cog/Data/
Connectomes/WithACT/'); %choose the folder
% Parcellation = {'aparcaseg'}; % choose parcellation
% Tract = {'iFOD2_'}; % choose tract method
%
% Name = strcat(Tract{1}, Parcellation{1});
% load (sprintf('%s.mat', Name));
%
% Density = zeros(size(density,2),1);
%
% for i=1:size(density,2)
%     figure; imagesc(log(density{i})); title(sprintf('Subject %d',
sub_id{i}));
%
%     Strength = sum(density{i});
%
%     figure; histogram(Strength, 20); title(sprintf('Strength Subject
%d', sub_id{i}));
%
% end

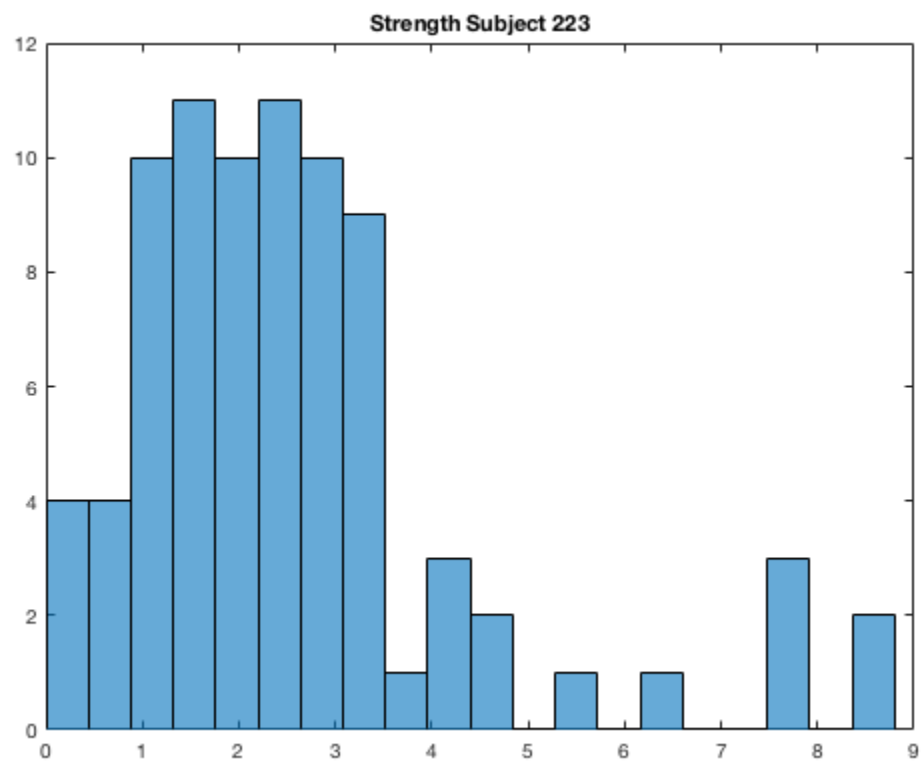
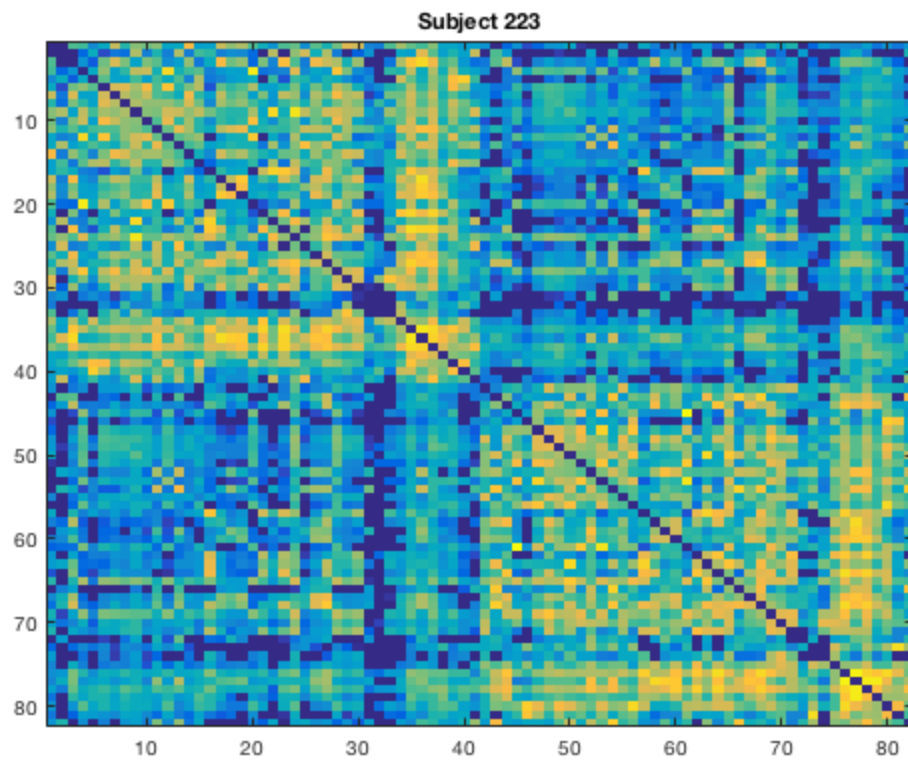
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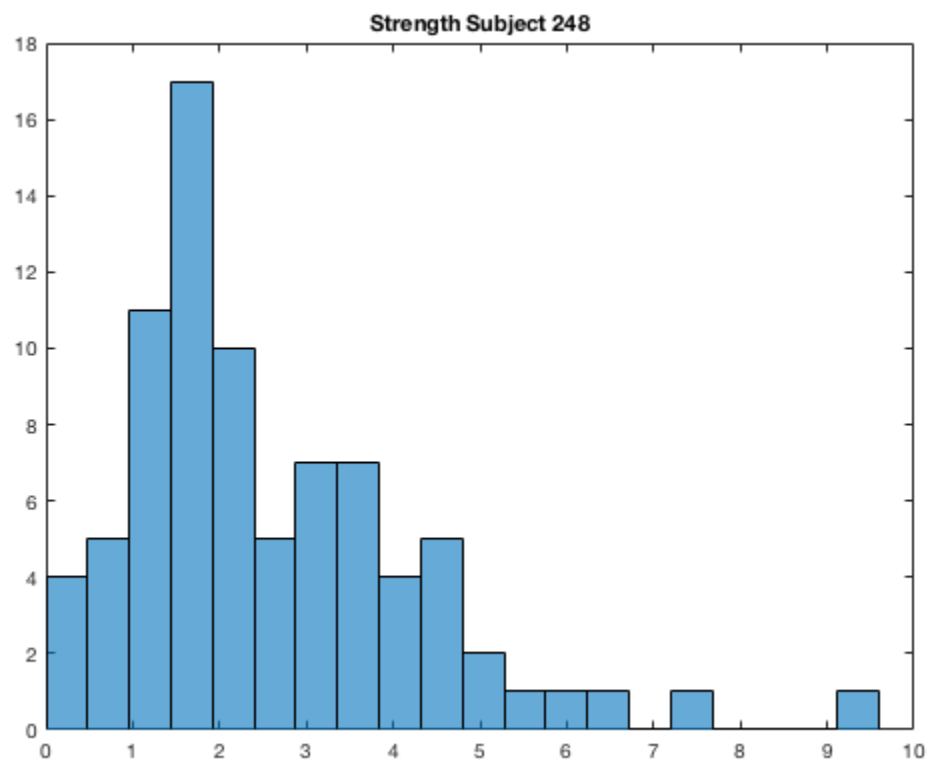
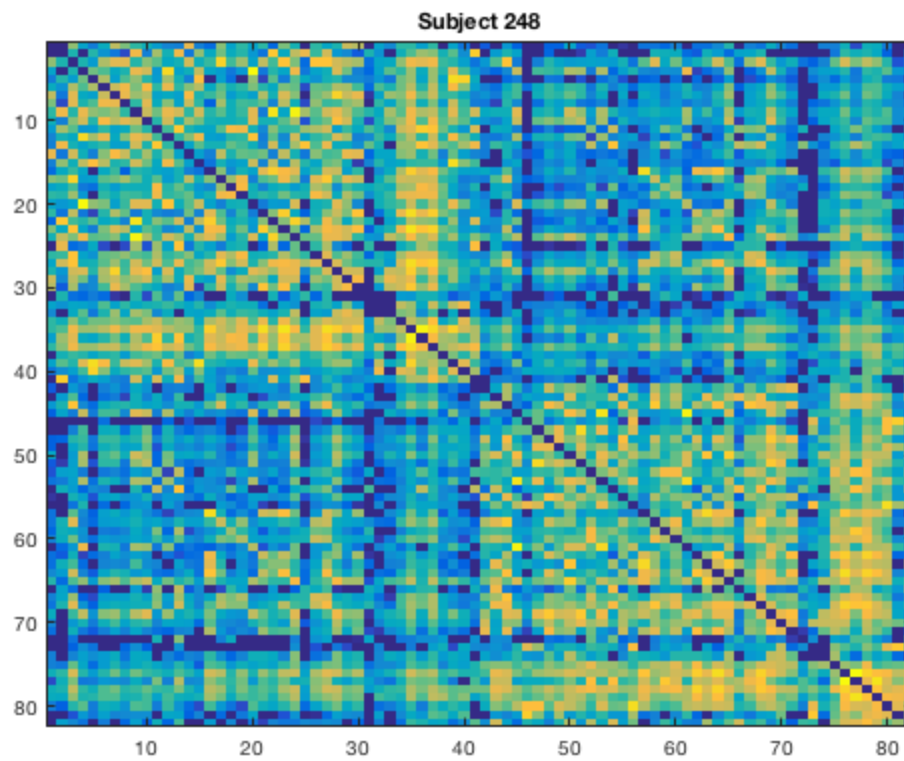


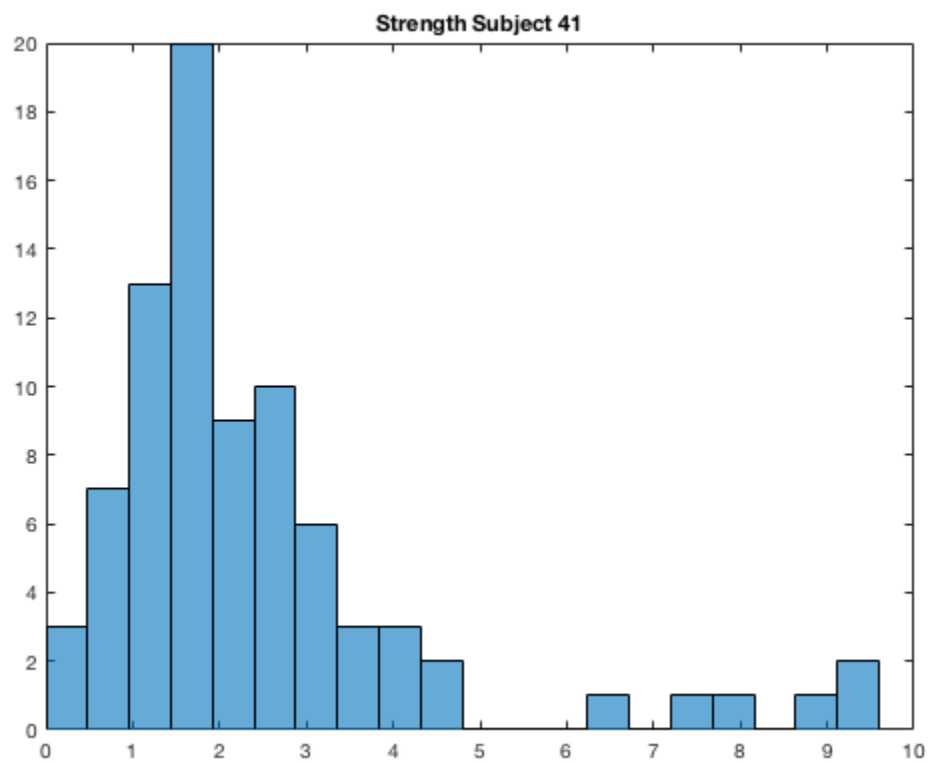
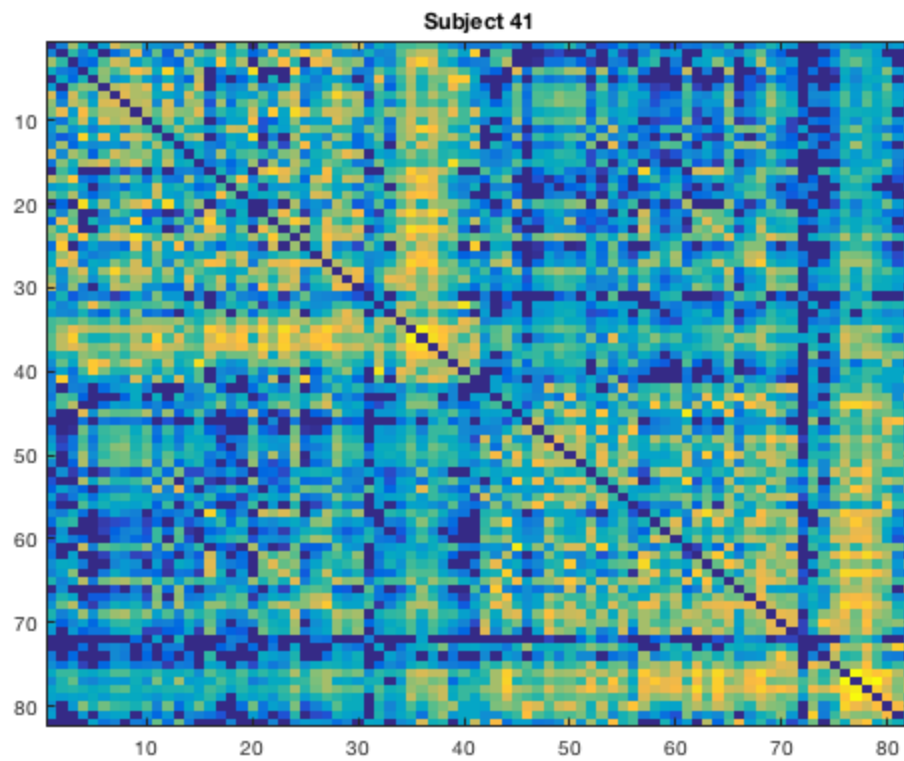


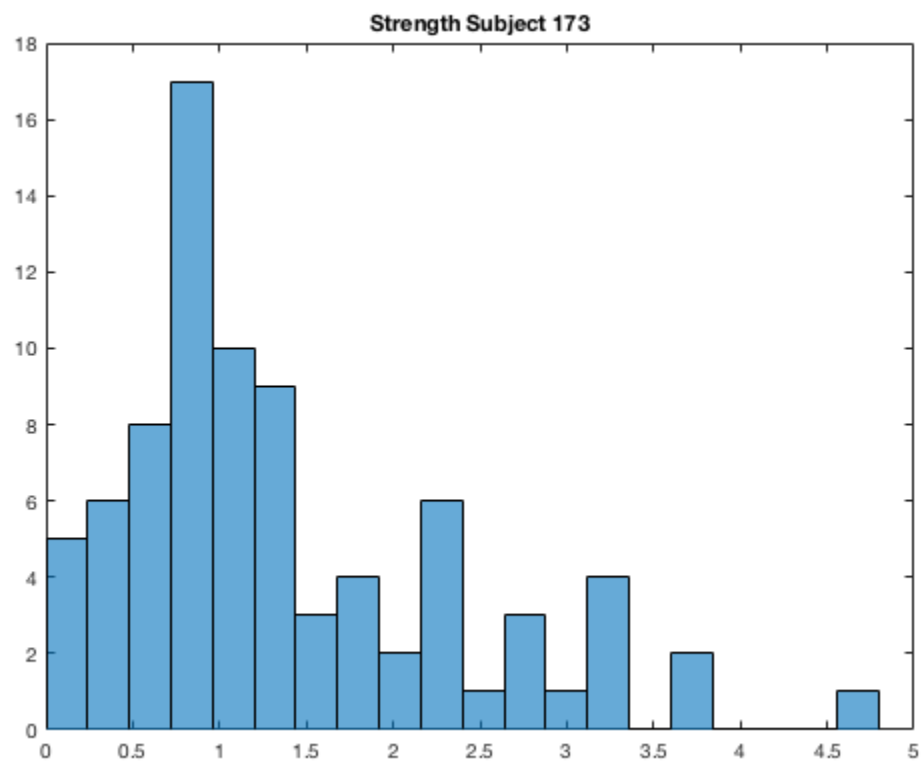
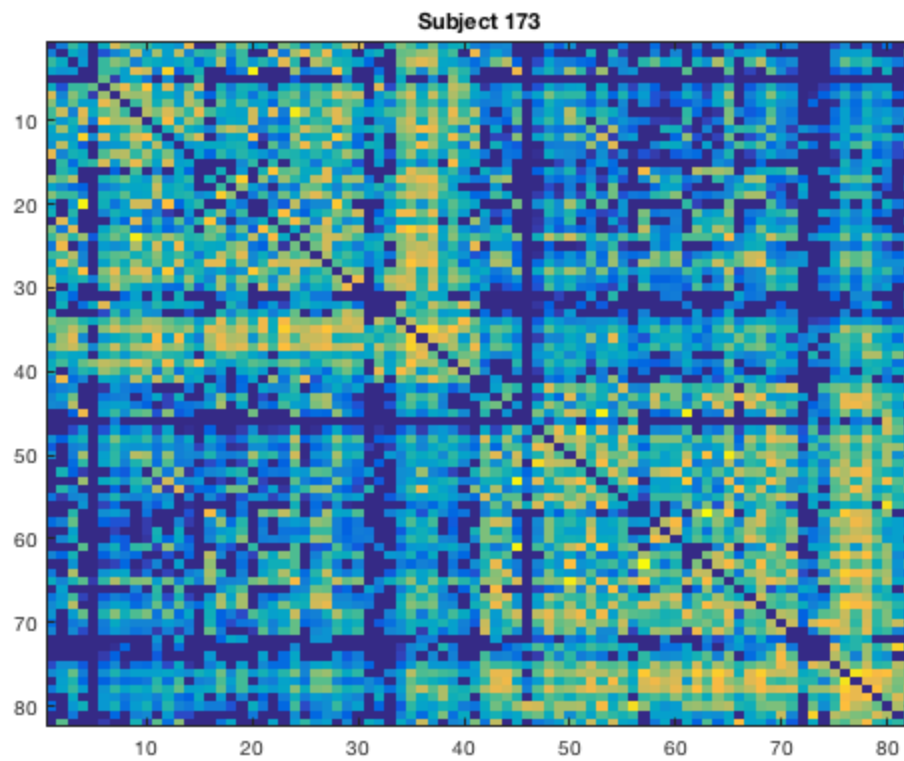


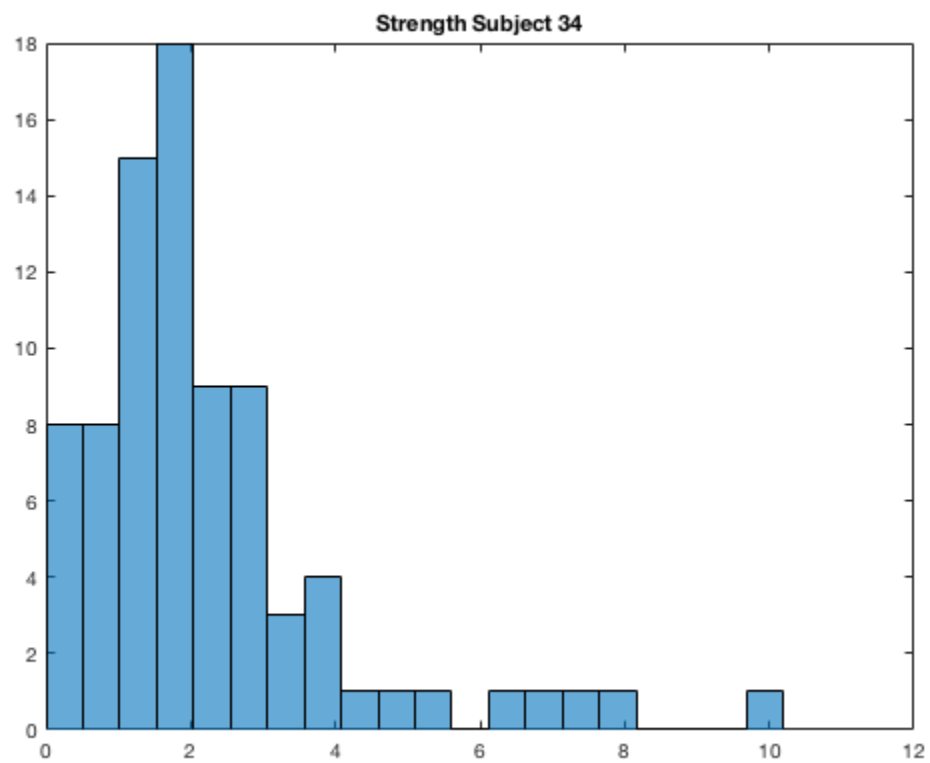
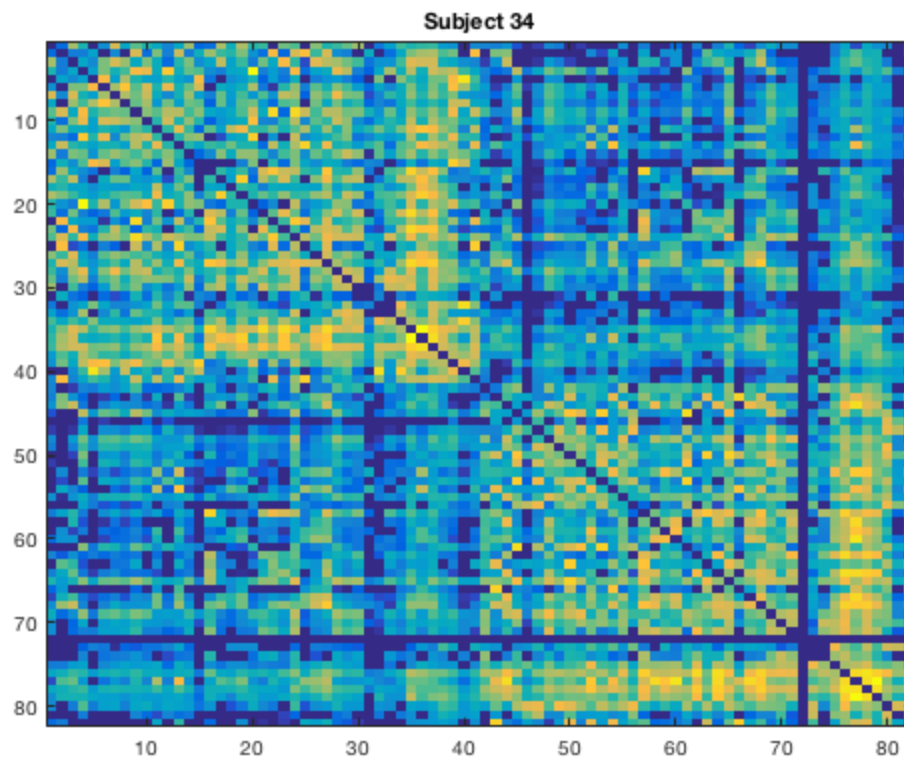


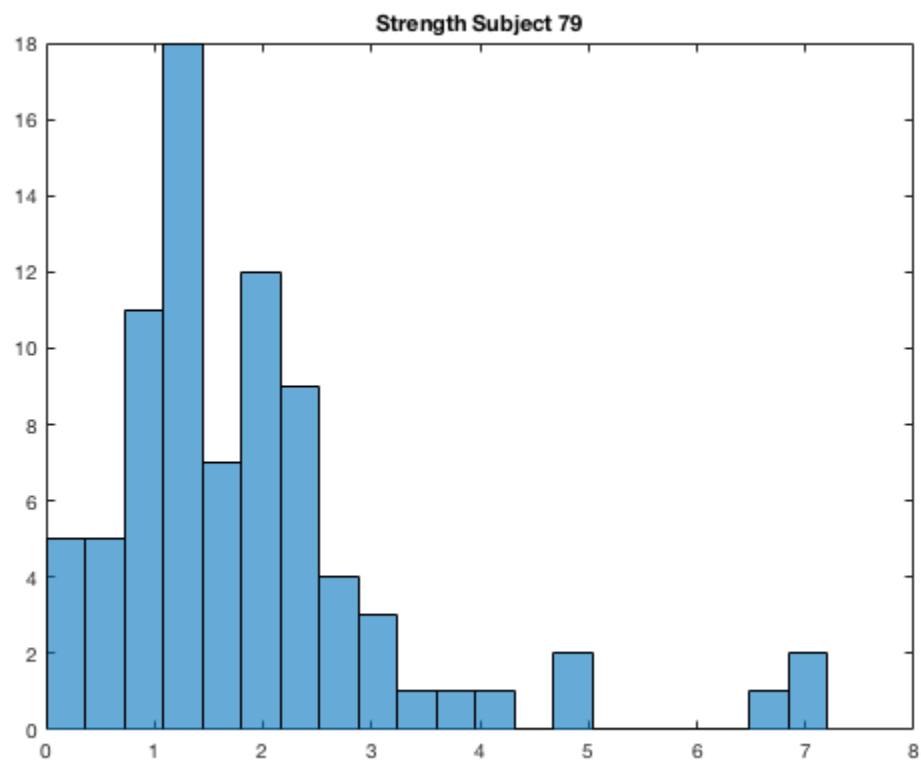
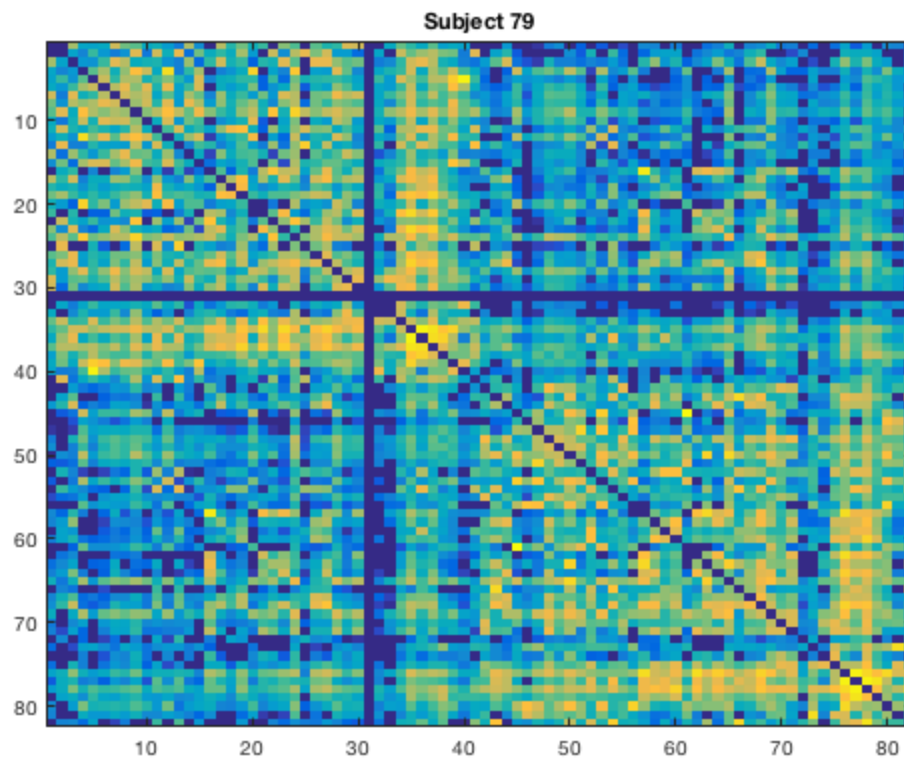


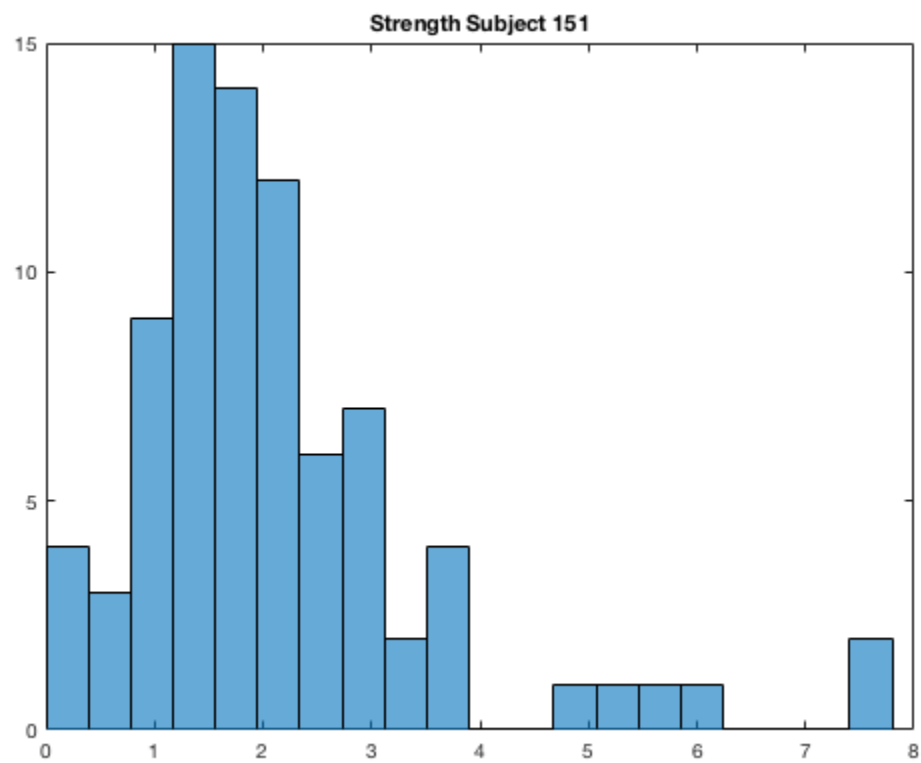
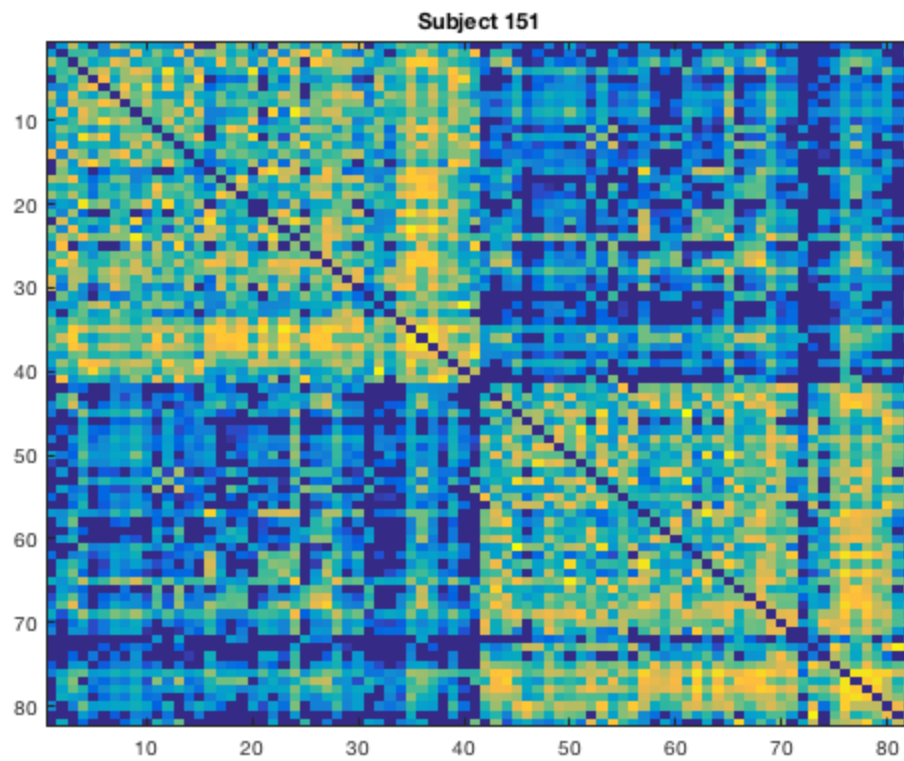


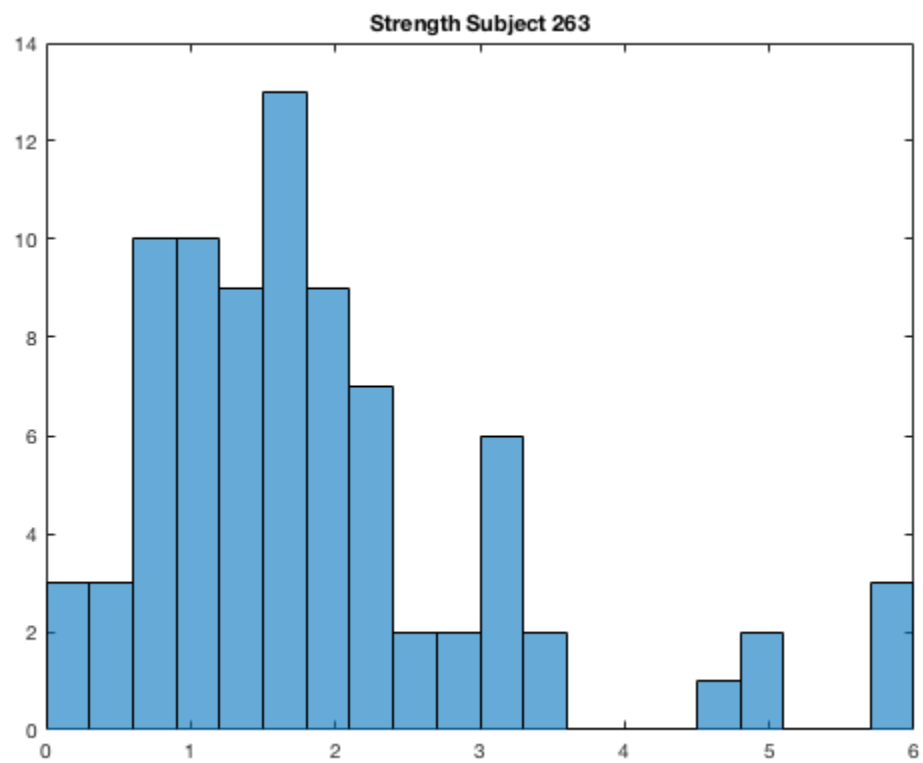
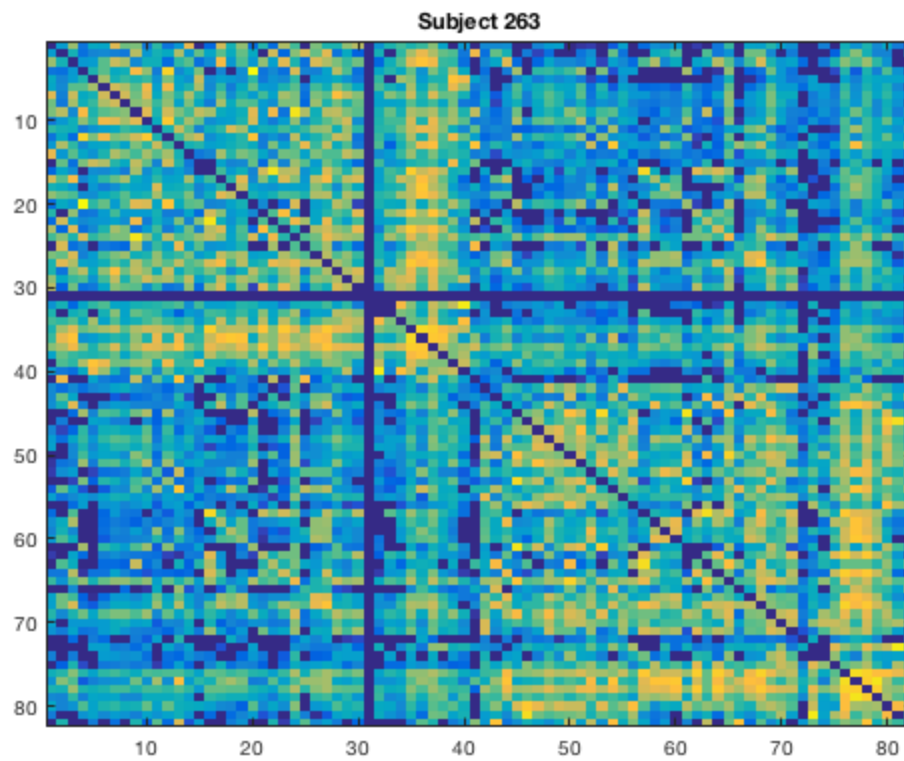


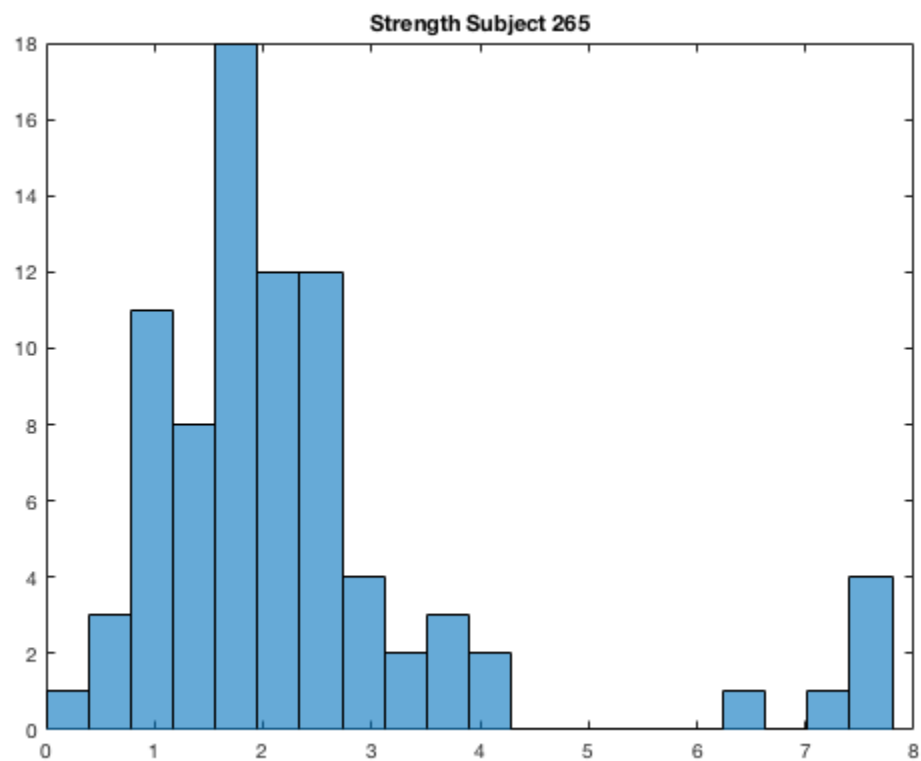
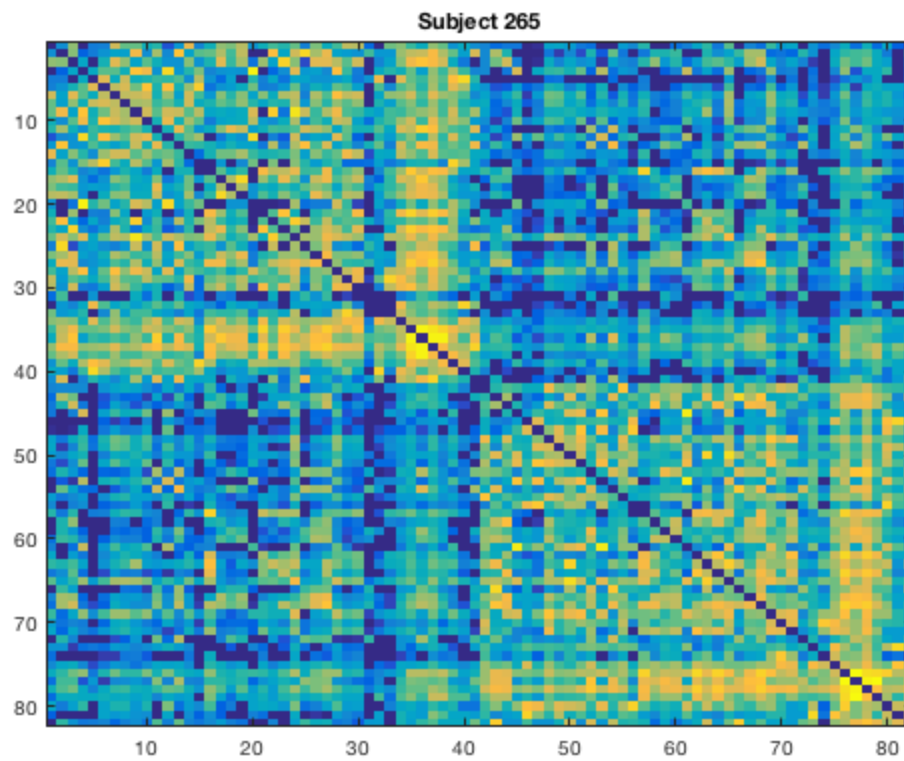


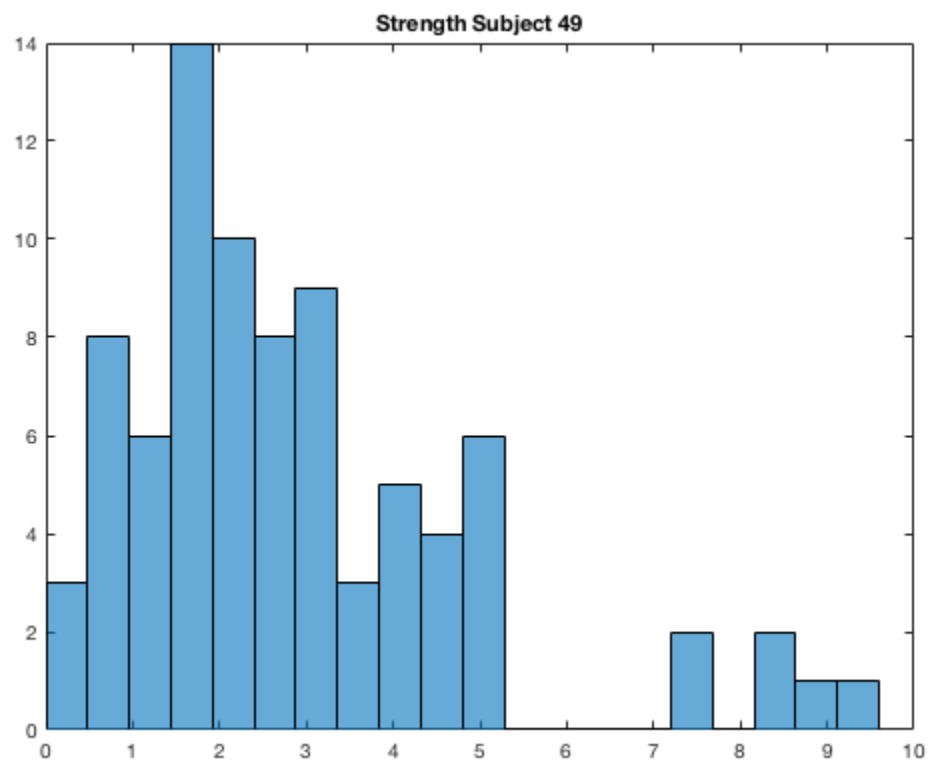
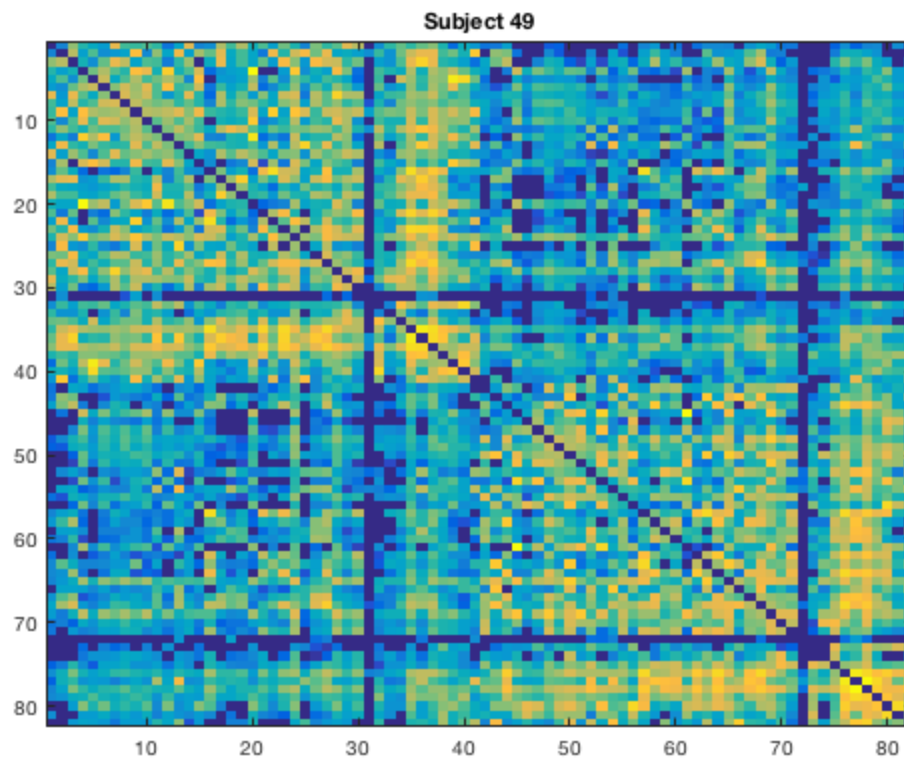


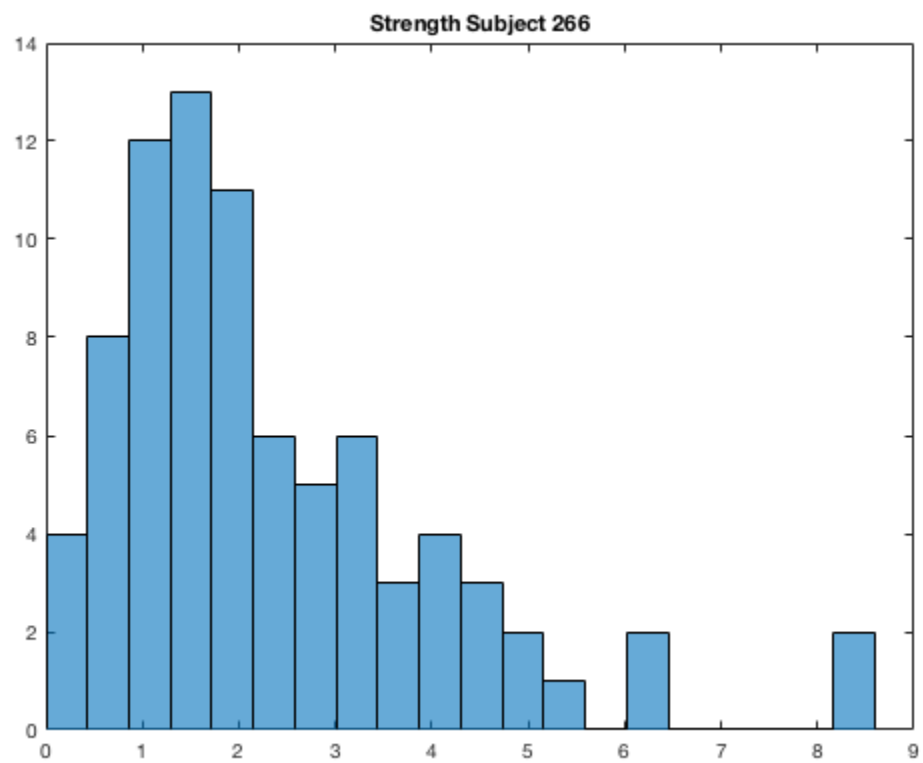
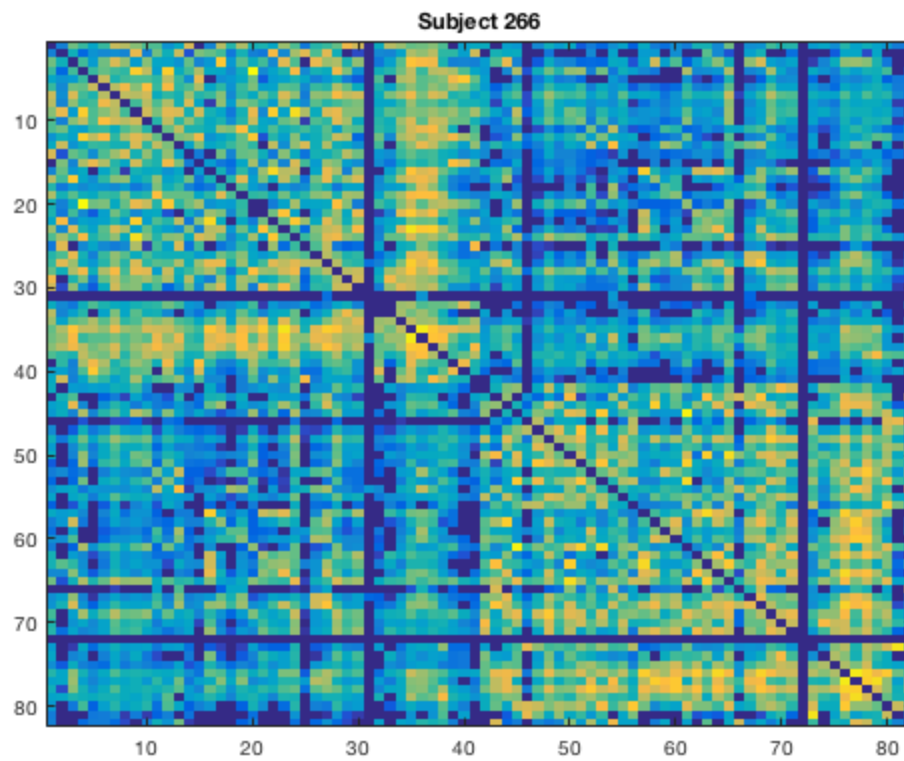


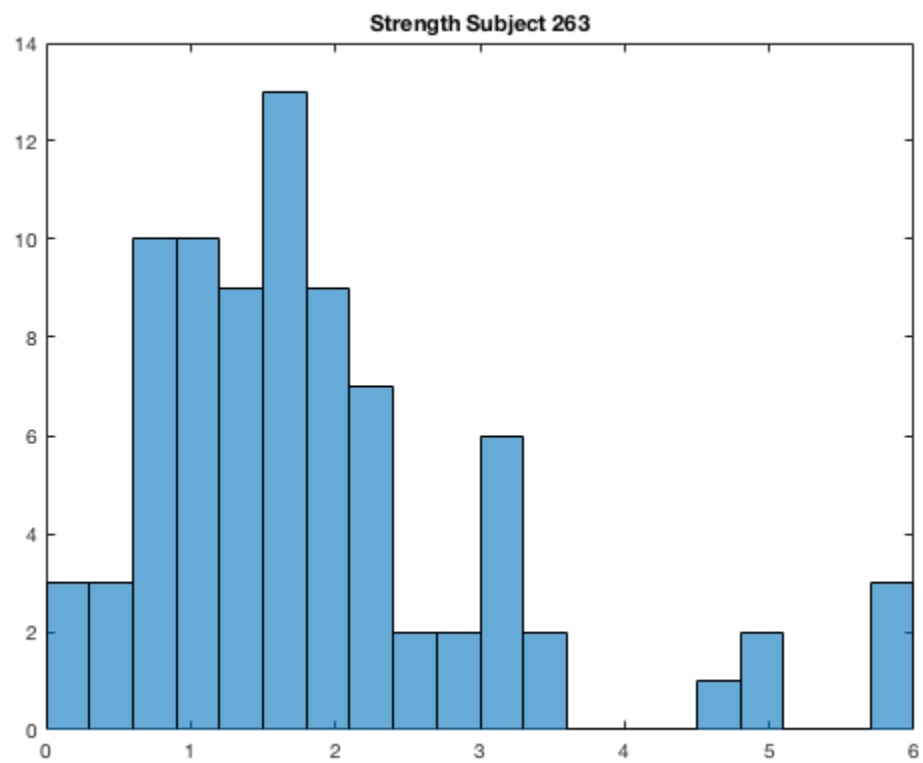
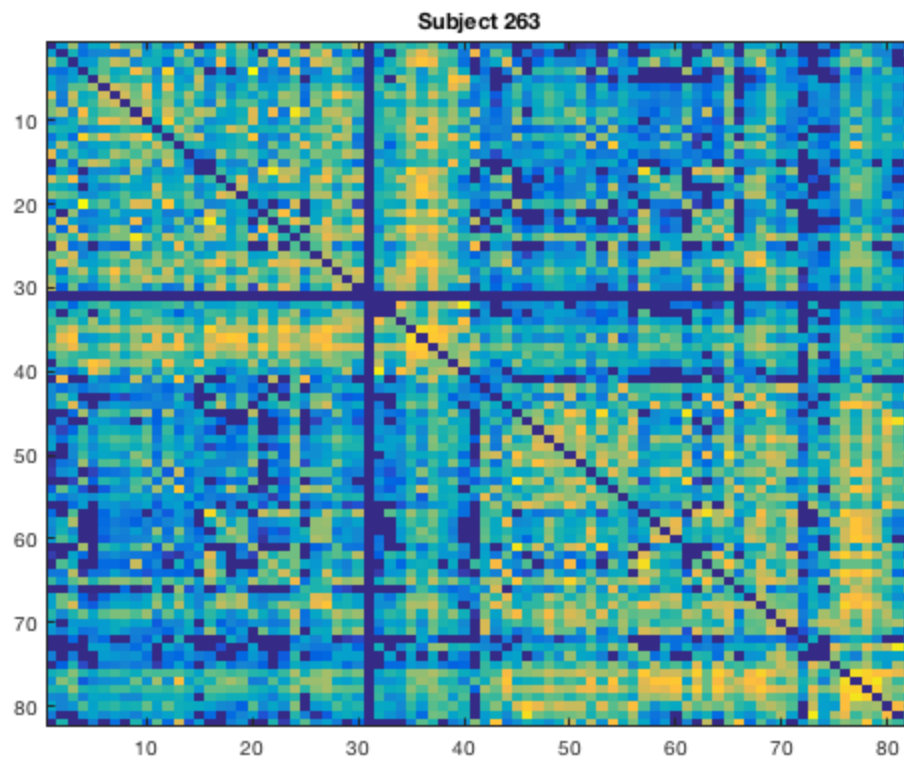


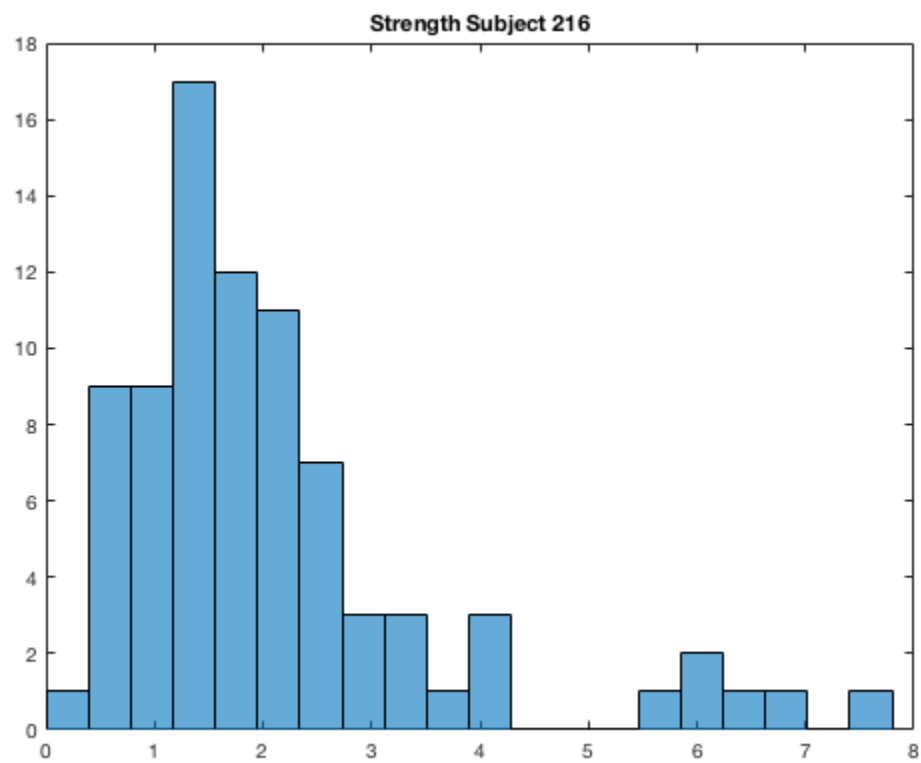
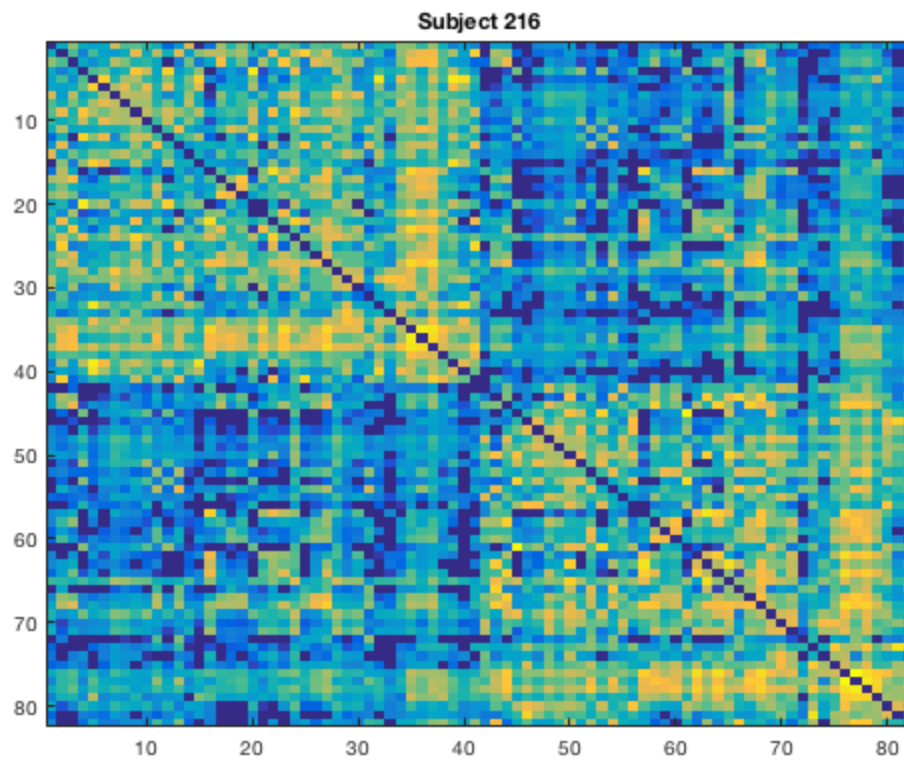












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