%% Step 1: Initialization and Setup

% Define the number of subjects and regions

n\_subjects = 10; % Number of subjects

n\_regions = 90; % Number of brain regions

% Initialize a cell array to hold the datasets for each subject

tractography\_data = cell(1, n\_subjects);

% Directory path for the data (adjust if necessary)

data\_dir = './';

% Initialize a 3D matrix to store all subjects' connection matrices

all\_subjects\_data = zeros(n\_regions, n\_regions, n\_subjects);

%% Step 2: Read the Data from CSV Files

for i = 1:n\_subjects

% Construct the filename for each subject

filename = fullfile(data\_dir, sprintf('subject\_%d\_tractography.csv', i));

% Read the CSV file into a table

data\_table = readtable(filename, 'ReadVariableNames', true);

% Convert the table to a matrix (ignore the region labels)

data\_matrix = table2array(data\_table(:, 2:end)); % skip the region name column

% Store the data matrix in the cell array and 3D matrix

tractography\_data{i} = data\_matrix;

all\_subjects\_data(:, :, i) = data\_matrix;

% Print a message indicating successful data loading

fprintf('Loaded data for subject %d\n', i);

end

%% Step 3: Compute Average Connection Matrix

% Compute the mean connection matrix across all subjects

mean\_matrix = mean(all\_subjects\_data, 3);

% Display the average connection matrix

figure;

imagesc(mean\_matrix);

colorbar;

title('Mean Connection Matrix Across 10 Subjects');

xlabel('Brain Region');

ylabel('Brain Region');

axis square;

%% Step 4: Compute Standard Deviation and Variability

% Compute the standard deviation across subjects for each connection

std\_matrix = std(all\_subjects\_data, 0, 3);

% Display the standard deviation matrix

figure;

imagesc(std\_matrix);

colorbar;

title('Standard Deviation of Connections Across Subjects');

xlabel('Brain Region');

ylabel('Brain Region');

axis square;

%% Step 5: Thresholding the Mean Matrix

% Apply a threshold to the mean matrix (retain only connections > threshold)

threshold = 0.5; % Example threshold

thresholded\_matrix = mean\_matrix;

thresholded\_matrix(mean\_matrix < threshold) = 0;

% Display the thresholded matrix

figure;

imagesc(thresholded\_matrix);

colorbar;

title(sprintf('Thresholded Mean Connection Matrix (Threshold = %.2f)', threshold));

xlabel('Brain Region');

ylabel('Brain Region');

axis square;

%% Step 6: Identify Strongest Connections

% Identify the top N strongest connections in the mean matrix

N = 10; % Number of top connections to identify

[sorted\_vals, sorted\_idx] = sort(mean\_matrix(:), 'descend');

% Get the row and column indices of the top N connections

[top\_rows, top\_cols] = ind2sub([n\_regions, n\_regions], sorted\_idx(1:N));

% Display the top N connections and their values

fprintf('Top %d Strongest Connections:\n', N);

for i = 1:N

fprintf('Connection between Region %d and Region %d: %.4f\n', top\_rows(i), top\_cols(i), sorted\_vals(i));

end

%% Step 7: Compute and Display Correlations Between Subjects

% Initialize a matrix to hold correlations between subjects

subject\_correlations = zeros(n\_subjects, n\_subjects);

% Loop through each pair of subjects and compute correlations

for i = 1:n\_subjects

for j = 1:n\_subjects

% Flatten the connection matrices for correlation calculation

subj1\_data = all\_subjects\_data(:, :, i);

subj2\_data = all\_subjects\_data(:, :, j);

subj1\_flat = subj1\_data(:);

subj2\_flat = subj2\_data(:);

% Compute the correlation coefficient between subjects i and j

subject\_correlations(i, j) = corr(subj1\_flat, subj2\_flat);

end

end

% Display the correlation matrix

figure;

imagesc(subject\_correlations);

colorbar;

title('Correlation Between Subjects');

xlabel('Subject');

ylabel('Subject');

axis square;

%% Step 8: Statistical Comparison of Connections Between Groups

% Suppose we want to compare two groups of subjects (e.g., first 5 vs last 5)

% Group 1: Subjects 1 to 5

group1\_data = all\_subjects\_data(:, :, 1:5);

% Group 2: Subjects 6 to 10

group2\_data = all\_subjects\_data(:, :, 6:10);

% Compute the mean connection matrices for both groups

group1\_mean = mean(group1\_data, 3);

group2\_mean = mean(group2\_data, 3);

% Perform a t-test for each connection between the two groups

p\_values = zeros(n\_regions, n\_regions);

for r1 = 1:n\_regions

for r2 = 1:n\_regions

% Extract connection values for both groups

group1\_conn = squeeze(group1\_data(r1, r2, :));

group2\_conn = squeeze(group2\_data(r1, r2, :));

% Perform a two-sample t-test

[~, p] = ttest2(group1\_conn, group2\_conn);

p\_values(r1, r2) = p;

end

end

% Display the p-value matrix

figure;

imagesc(p\_values);

colorbar;

title('P-Values for Group Comparison (T-Test)');

xlabel('Brain Region');

ylabel('Brain Region');

axis square;

%% Step 9: Visualization of Significant Differences

% Threshold the p-value matrix to retain significant differences

alpha = 0.05; % Significance level

significant\_diff\_matrix = p\_values < alpha;

% Display the significant differences

figure;

imagesc(significant\_diff\_matrix);

colorbar;

title(sprintf('Significant Differences (p < %.2f)', alpha));

xlabel('Brain Region');

ylabel('Brain Region');

axis square;

%% Step 10: Save Results for Further Analysis

% Save the mean connection matrix to a CSV file

csvwrite('mean\_connection\_matrix.csv', mean\_matrix);

% Save the thresholded matrix

csvwrite('thresholded\_connection\_matrix.csv', thresholded\_matrix);

% Save the standard deviation matrix

csvwrite('std\_connection\_matrix.csv', std\_matrix);

% Save the p-value matrix for group comparison

csvwrite('p\_value\_matrix.csv', p\_values);

% Save the significant differences matrix

csvwrite('significant\_differences.csv', significant\_diff\_matrix);

fprintf('Analysis completed and results saved.\n');