Contents

Summary: 1. MATLAB demo function - generate sample plots reported in paper

Preprocessing required: * REQUIREMENTS: 1. report.txt files for each modality (see below) 2. twin/sibling pair ids (numeric id's between 1 to number of subjects/images based on the subject ordering/reading list) for example: MZ sub id set and MZ pair id set etc.. 3. Note: The randomized sample includes pairs of MZ; DZ; Full-Siblings (FS); Maternal Half Siblings (MHS) and Paternal Half Siblings (PHS)

```
       NOTE: a sample set of report files and twin/sibling pair ids
       (randomized) have been included in data folder for illustration
       purposes
```

Brief Overview of pre-processing: 1. We assume that Bag-of-features (BoF) have been generated and approximate matching has been performed using the code available at http://www.matthewtoews.com/ THE PRE-PROCESSING involves running: i. featExtract.exe for each image (.nii files): output will be .key files containing 3D SIFT features ii. featMatchMultiple -t 2 -r- -n 20 *.key (for all .key files of a given modality): output will be multiple files including report.txt 2. report.txt generated for each modality will act as a input for the following analysis 3. We have included sample report files (Random permutation applied on our set) 4. Note: cross check the file order read in featMatchMultiple.exe and the sibling/twin pair IDs

```
ADDITIONAL processing/files:
        1. feature match visualization requires 3D SIFT feature files
        (not included here)
        2. Significance values (-log10 pvalues) in paper are based on
        sample size matches using bipartite matching (age-based);
        However, sample illustration uses random sample size matching
        3. Similarly hemisphere asymmetry analysis and
        pairwise feature correspondence analysis requires restricted data
        and thus have been excluded here
```

Reference: Multi-modal brain fingerprinting: a manifold approximation based framework Authors: Kuldeep Kumar (kkumar@livia.etsmtl.ca), Laurent Chauvin Matthew Toews (Matthew.Toews@etsmtl.ca) Olivier Colliot and Christian Desrosiers (christian.desrosiers@etsmtl.ca)

LIVIA, ETS Montreal, Canada January 2018

```
%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%%
```

Standard figure parameters

```
    Line_width = 3 ;
    Marker_size= 14;
    leg_FontSize=13;
    gca_FontSize = 32;

    color_option{1} = 'r' ;
    color_option{2} = 'g' ;
    color_option{3} = 'b' ;
    color_option{4} = 'c' ;
    color_option{5} = 'm' ;
    color_option{6} = 'y' ;
    color_option{7} = 'k' ;
    marker_option{1} = '*' ;
    marker_option{2} = 'o' ;
    marker_option{3} = 'd' ;
    marker_option{4} = 's' ;
    marker_option{5} = 'x' ;
    marker_option{6} = '^' ;
    marker_option{7} = '+' ;
```

Flags and initializations

flag to display figure: 1: yes, 0: no

```
flag_display_figure =1;

% labels for sibling types
cell_sibling_type{1} = 'MZ';
cell_sibling_type{2} = 'DZ';
cell_sibling_type{3} = 'FS';
cell_sibling_type{4} = 'MHS';
cell_sibling_type{5} = 'FHS';

% Define the twin/sibling types to be used for analyses
max_sib_type = 3;                                                          % 3: MZ, DZ, FS;  5: MZ, DZ, FS, MHS and FHS also
```

Load/Read twin/sibling pair info.

```
%load SAMPLE twin/sibling subject id and pair id information
twin_sib_info_file ='../data/SAMPLE_cell_subID_and_sibpairID.mat';
load(twin_sib_info_file);                                                  % output will be variable: 'SAMPLE_cell_subID_and_sibpairID'
                                                                           % variable: a cell array of size 5 x 2
                                                                           % dim 1 correspond to twin/sibling type:
                                                                           %       1. MZ; 2. DZ; 3. FS; 4. MHS; and 5. PHS
                                                                           % dim 2: corresponds to sub ids and pair ids
                                                                           %       1. sub_id_set  2. pair_id_set
                                                                           % NOTE: the SAMPLE info is randomized before sharing
```

Load subject proximity graph:

```
max_modality_combinations= 9;                                              % hard coded for illustration
cell_NxN_data_matrix = cell(max_modality_combinations,1);

% Set of modalities used for illustration
cell_modality{1} = 'FA';
cell_modality{2} = 'T1w 125mm';
cell_modality{3} = 'T2w 125mm';
cell_modality{4} = 'rfMRI';
cell_modality{5} = 'T1w+FA';
cell_modality{6} = 'T1w+rfMRI';
cell_modality{7} = 'FA+rfMRI';
cell_modality{8} = 'T1w+T2w+FA';
cell_modality{9} = 'T1w+T2w+FA+rfMRI';

%DATA: load SAMPLE report files (feature match count) for each modality
 cell_report_filename = { 'SAMPLE_report_FA.mat';
                          'SAMPLE_report_T1w_125mm';
                          'SAMPLE_report_T2w_125mm';
                          'SAMPLE_rfMRI_pairwise_pearson_corr_ICA100';};

% For report.txt files:
% 1. read feature match count files (report.txt)
% 2. Obtain Normalized Jaccard Similarity

cell_report_files = cell(3,1);

for loop_i=1:(length(cell_report_filename)-1)
    load(['../data/'   cell_report_filename{loop_i}]);
    cell_report_files{loop_i,1} = SAMPLE_report_mat ;
    cell_NxN_data_matrix{loop_i} = compute_normalized_jaccard_similarity_matrix(cell_report_files(loop_i,1));
end

% read rfMRI NxN_data_matrix
load(['../data/'   cell_report_filename{length(cell_report_filename)}]);
cell_NxN_data_matrix{length(cell_report_filename)} = SAMPLE_rfMRI_pairwise_pearson_corr_ICA100 ;
```

Create Modality combinations (Hard coded for illustration purpose)

```
 % 1. T1w + FA
 loop_i = 5;
 cell_NxN_data_matrix{loop_i} = compute_normalized_jaccard_similarity_matrix(cell_report_files(1:2));

 % 2. T1w +rfMRI: (linear combination, with combination weights computed using a grid
 % search, to optimize MAP values )
 loop_i = 6;
 lambda = 0.2;
 cell_NxN_data_matrix{loop_i} = lambda*cell_NxN_data_matrix{4}+(1-lambda)*cell_NxN_data_matrix{2} ;

 % 3. FA + rfMRI (linear combination, with combination weights computed using a grid
 % search, to optimize MAP values )
 loop_i = 7;
 lambda = 0.4;
 cell_NxN_data_matrix{loop_i} = lambda*cell_NxN_data_matrix{4}+(1-lambda)*cell_NxN_data_matrix{2} ;

 % 4. T1w + T2w + FA (1.25mm)
 loop_i=8;
 cell_NxN_data_matrix{loop_i} = compute_normalized_jaccard_similarity_matrix(cell_report_files(1:3));

 % 5. T1w + T2w + FA + rfMRI
 loop_i = 9;
 lambda = 0.2;
 cell_NxN_data_matrix{loop_i} = lambda*cell_NxN_data_matrix{4}+(1-lambda)*cell_NxN_data_matrix{8} ;
```

%%%

Example 1: Compact fingerprint generation

%%%

```
array_modality_set = [ 1; 2; 5;];                                       % FA, T1w and T1w + FA
num_spect_component = 150;                                              % number of eigen vectors in fingerprint
cell_compact_fingerprint = cell(length(array_modality_set),1);

 for loop_i=1:length(array_modality_set)

    % compact fingerprint generation
    NxN_data_matrix = cell_NxN_data_matrix{array_modality_set(loop_i),1};
    cell_compact_fingerprint{loop_i,1} = compute_compact_fingerprint(NxN_data_matrix,num_spect_component);

 end
```

%%%

Example 2: Compact fingerprint analysis: d-prime and -log10 p-value MZ vs DZ plots (Fig 2.)

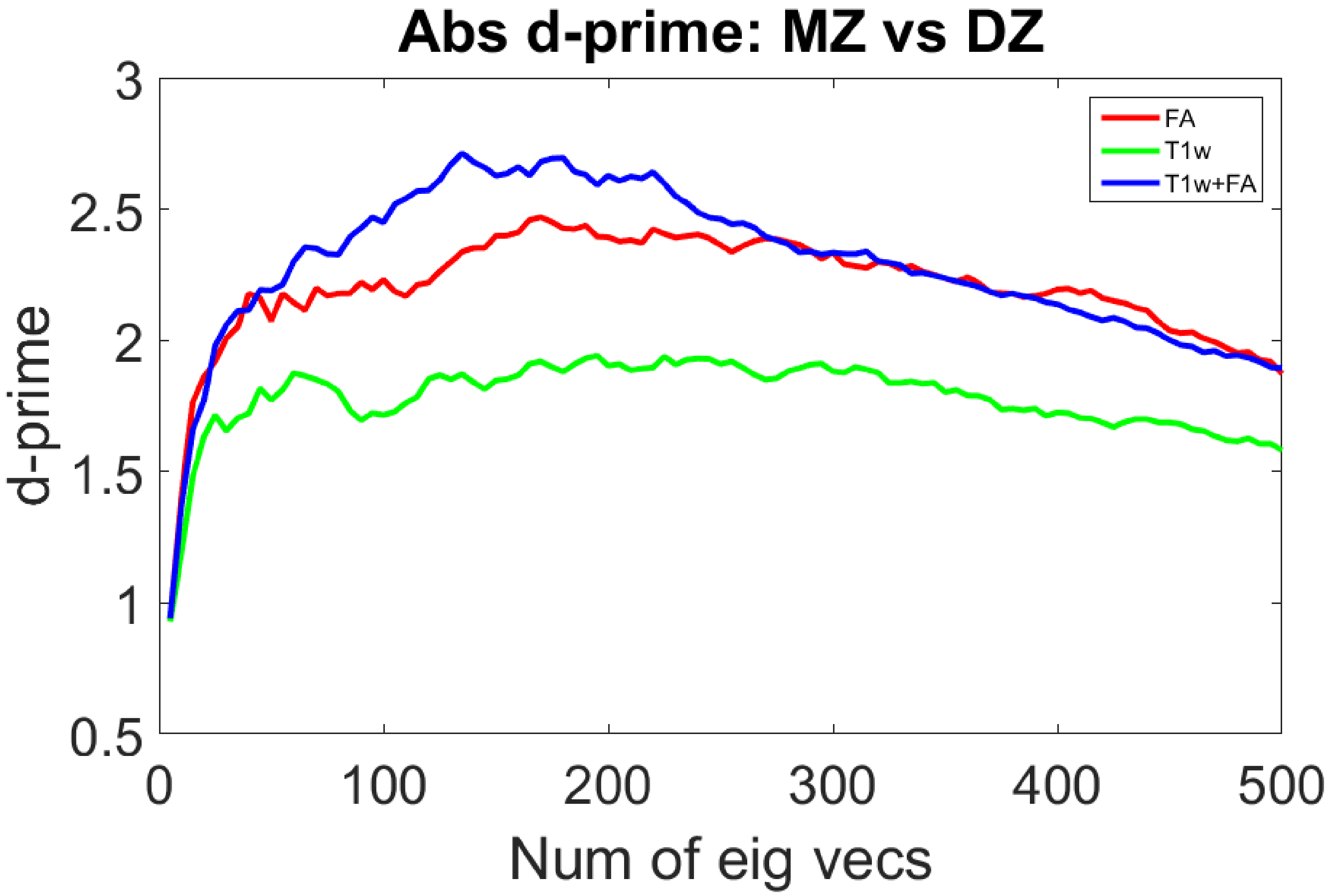
%%%

```
%
% compute d-prime and -log10 p-value for pairwise fingerprint distance: MZ vs DZ
%

 array_num_spect_component = (5:5:500)';
 array_modality_set = [ 1; 2; 5;];                                      % FA, T1w and T1w + FA (all at 1.25mm resolution)

 num_sibtype_comparisons = (max_sib_type*(max_sib_type-1))/2;           % 1. MZ vs DZ, 2: MZ vs FS, 3: DZ vs FS

 cell_d_prime = cell(length(array_num_spect_component),num_sibtype_comparisons,length(array_modality_set));
 cell_pval_ttest2 = cell(length(array_num_spect_component),num_sibtype_comparisons,length(array_modality_set));
 cell_pval_ranksum = cell(length(array_num_spect_component),num_sibtype_comparisons,length(array_modality_set));

for loop_i=1:length(array_modality_set)

    % compact fingerprint generation
    NxN_data_matrix = cell_NxN_data_matrix{array_modality_set(loop_i),1};
    temp_cell_compact_fingerprint = compute_compact_fingerprint_size_impact(NxN_data_matrix,array_num_spect_component);

    for loop_num_spect = 1:length(array_num_spect_component)

       % compute Euclidean Distance between fingerprint pairs for MZ, DZ, FS
       mat_compact_fingerprint = temp_cell_compact_fingerprint{loop_num_spect,1};
       cell_pairwise_distance = cell(max_sib_type,1);

       for loop_sib_type=1:max_sib_type
           sub_id_set = SAMPLE_cell_subID_and_sibpairID{loop_sib_type,1};
           pair_id_set = SAMPLE_cell_subID_and_sibpairID{loop_sib_type,2};
           [cell_pairwise_distance{loop_sib_type,1}] = compute_pairwise_fingerprint_distance_sibling_pairs(sub_id_set,pair_id_set,mat_compac
t_fingerprint);
       end
       % compute d-prime and pval for MZ vs DZ, MZ vs FS, and DZ vs FS
       temp_count_loop_comparison =1;
       for loop_sib_type_1 = 1:(max_sib_type-1)
           array_pairwise_distance_1 = cell_pairwise_distance{loop_sib_type_1,1} ;

           for loop_sib_type_2 = (loop_sib_type_1 + 1):max_sib_type
               array_pairwise_distance_2 = cell_pairwise_distance{loop_sib_type_2,1} ;

               cell_d_prime{loop_num_spect,temp_count_loop_comparison,loop_i} = compute_d_prime(array_pairwise_distance_1,array_pairwise_distance_2);
               [cell_pval_ttest2{loop_num_spect,temp_count_loop_comparison,loop_i},cell_pval_ranksum{loop_num_spect,1,loop_i}] = compute_pval_ttest2_ranksum(array_pairwise_distance_1,array_pairwise_distance_2);
               temp_count_loop_comparison = temp_count_loop_comparison + 1;
           end
       end
    end
end
```

Plot absolute d-prime and p-val for increasing fingerprint length/size

Absolute d-prime: MZ vs DZ

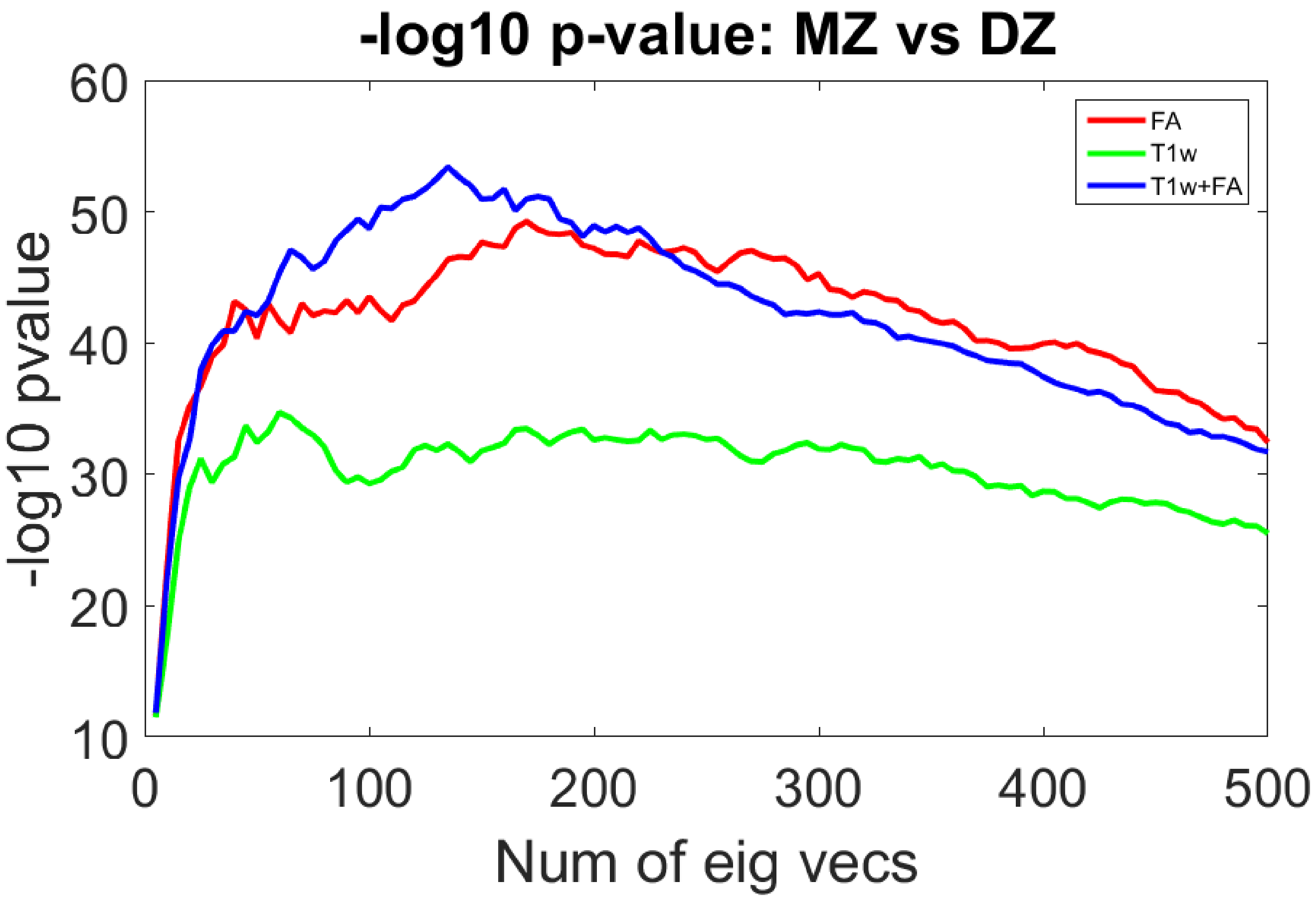
```
temp_count_loop_comparison=1;                                             % 1: MZ vs DZ, 2: MZ vs FS, .....
temp_data = cell_d_prime(:,temp_count_loop_comparison,1:(length(array_modality_set)));
data_mat  = abs((reshape(cell2mat(temp_data),size(temp_data,1),size(temp_data,3))));

figure_title = 'Abs d-prime: MZ vs DZ';
x_tick_array = [ 0; (100:100:500)';];
cell_label{1} = 'Num of eig vecs';
cell_label{2} = 'd-prime';
leg_location =  'northeast';
cell_legend = {'FA'; 'T1w'; 'T1w+FA';};
save_plot_name = [];                                                      % assign filename to save it else empty

plot_compact_fingerprint_analysis(data_mat,x_tick_array,figure_title,cell_legend,leg_location,cell_label,save_plot_name);
```



-log10 p-value (ttest2): MZ vs DZ

```
temp_count_loop_comparison=1;                                             % 1: MZ vs DZ, 2: MZ vs FS, .....
temp_data = cell_pval_ttest2(:,temp_count_loop_comparison,1:(length(array_modality_set)));
```

```
data_mat  = -1*log10((reshape(cell2mat(temp_data),size(temp_data,1),size(temp_data,3))));

figure_title = '-log10 p-value: MZ vs DZ';
x_tick_array = [ 0; (100:100:500)';];
cell_label{1} = 'Num of eig vecs';
cell_label{2} = '-log10 pvalue';
leg_location =  'northeast';
cell_legend = {'FA'; 'T1w'; 'T1w+FA';};
save_plot_name = [];                                                       % assign filename to save it else empty

plot_compact_fingerprint_analysis(data_mat,x_tick_array,figure_title,cell_legend,leg_location,cell_label,save_plot_name);
```

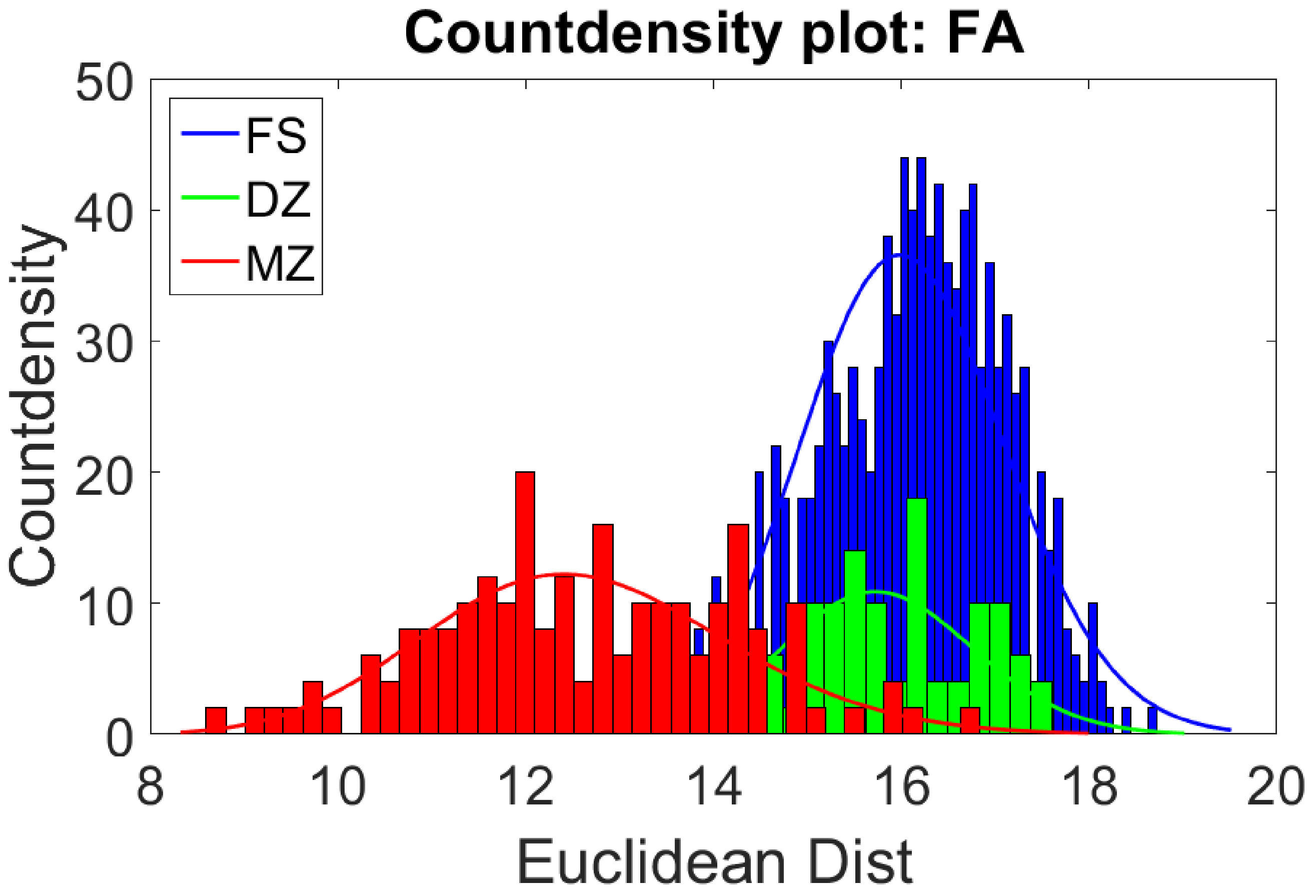


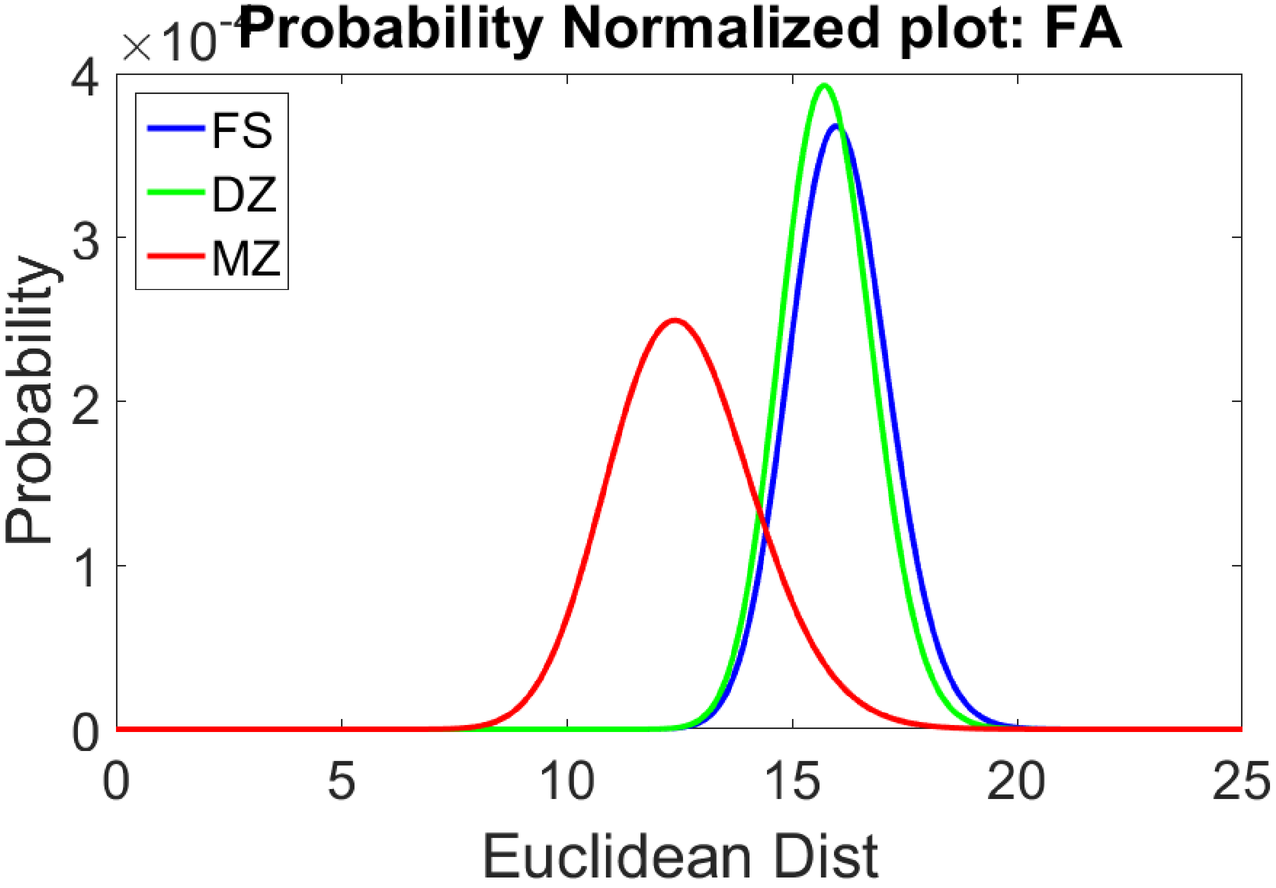
%%

```
     Example 3: Compact fingerprint comparison plots: MZ, DZ, FS pairs (Fig 3.)
```

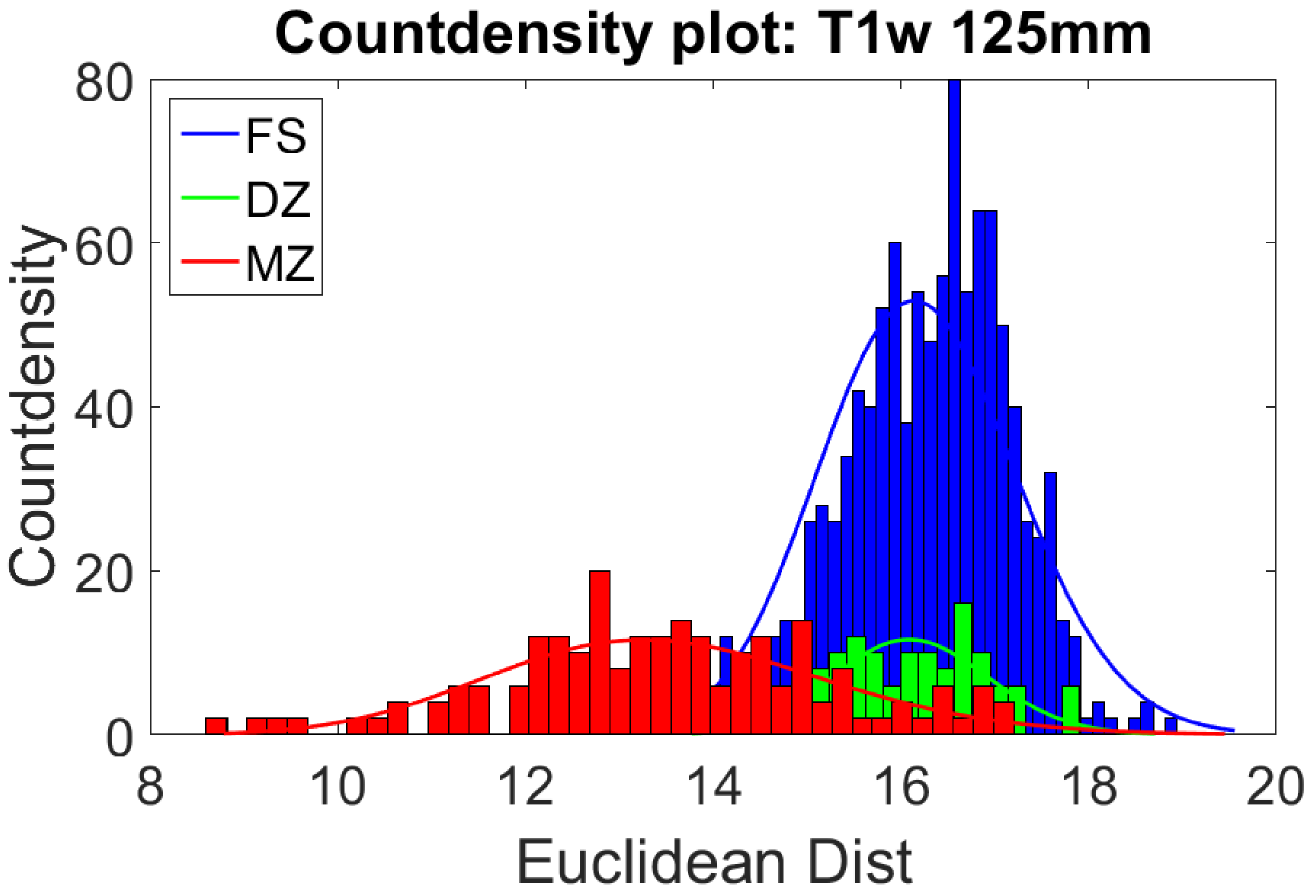
%%

```
array_modality_set = [ 1; 2; 5;];                                          % FA, T1w and T1w + FA
num_spect_component = 150;                                                 % number of eigen vectors in fingerprint
cell_pairwise_distance = cell(max_sib_type,length(array_modality_set));

for loop_i=1:length(array_modality_set)

    % compact fingerprint generation
    NxN_data_matrix = cell_NxN_data_matrix{array_modality_set(loop_i),1};
    mat_compact_fingerprint = compute_compact_fingerprint(NxN_data_matrix,num_spect_component);

    for loop_sib_type=1:max_sib_type
        sub_id_set = SAMPLE_cell_subID_and_sibpairID{loop_sib_type,1};
        pair_id_set = SAMPLE_cell_subID_and_sibpairID{loop_sib_type,2};
        [cell_pairwise_distance{loop_sib_type,loop_i}] = compute_pairwise_fingerprint_distance_sibling_pairs(sub_id_set,pair_id_set,mat_compact_fingerprint);
    end

    % get data for MZ, DZ, FS for a given modality
    cell_data = cell_pairwise_distance(:,loop_i);
    save_plot_name = [];
    modality = cell_modality(array_modality_set(loop_i));

    %count density histogram
    plot_compact_fingerprint_analysis_countdensity_histogram(cell_data,modality,save_plot_name);
    %Plot probability normalized curves (gamma histogram fitting)
    plot_compact_fingerprint_analysis_probability_normalized_curves(cell_data,modality,save_plot_name);

end
```

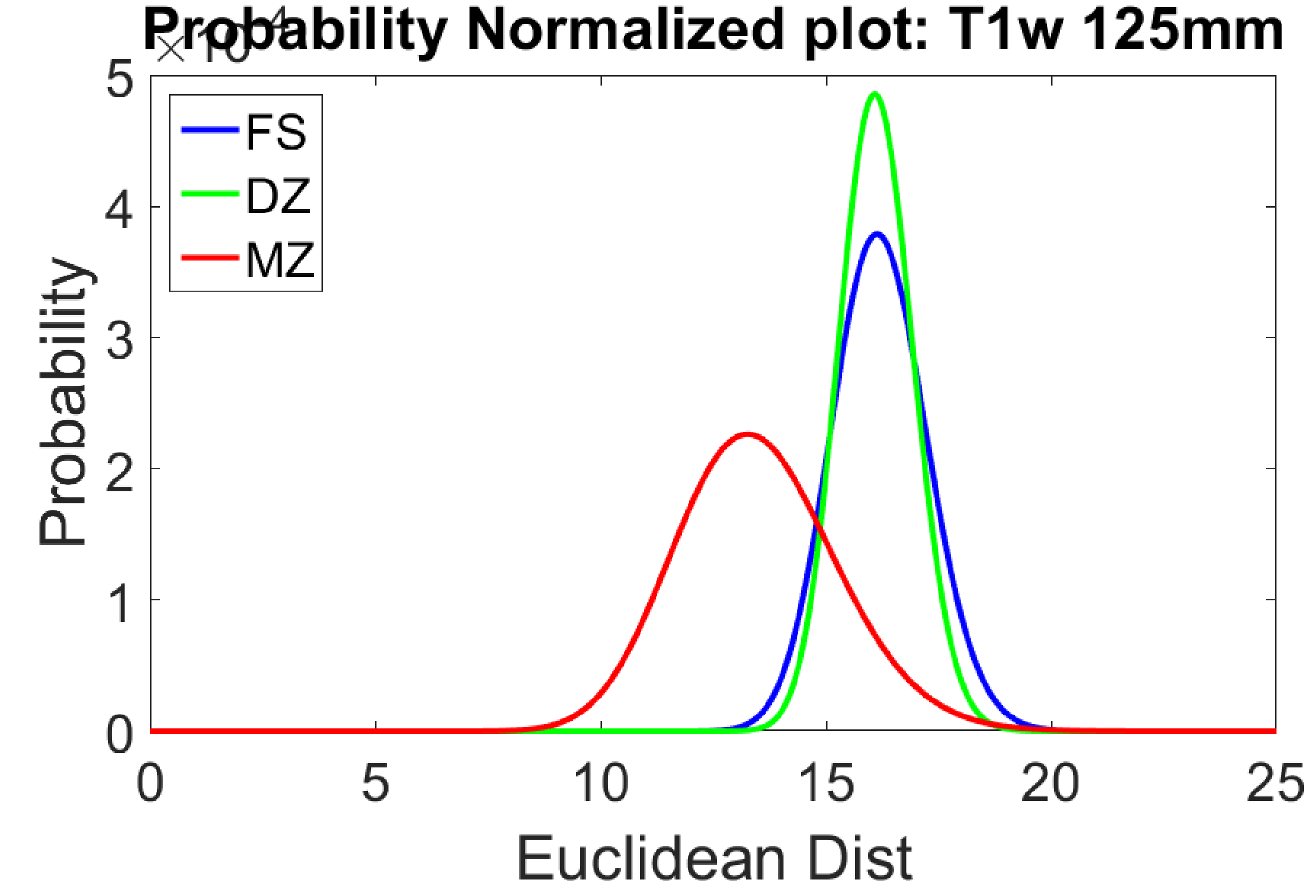


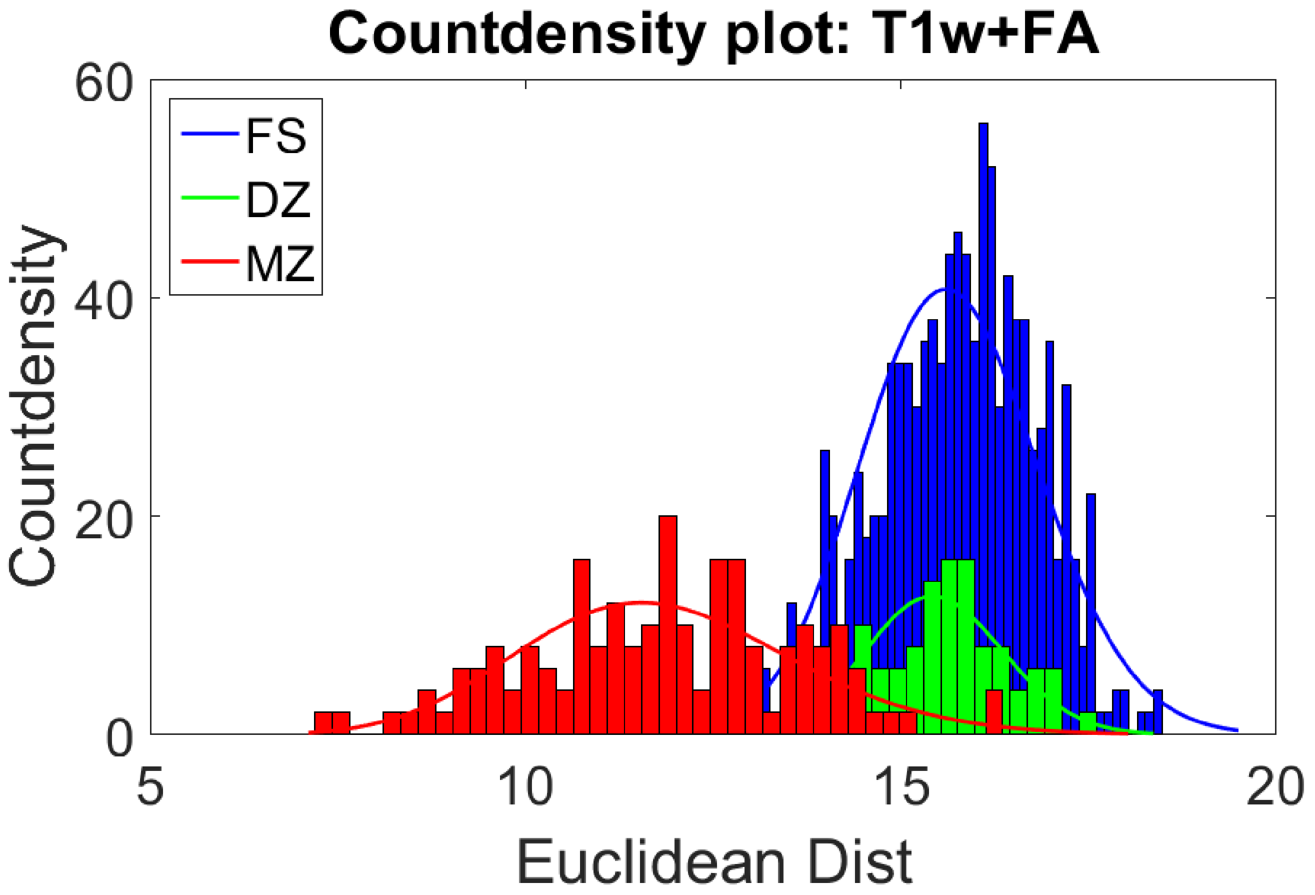


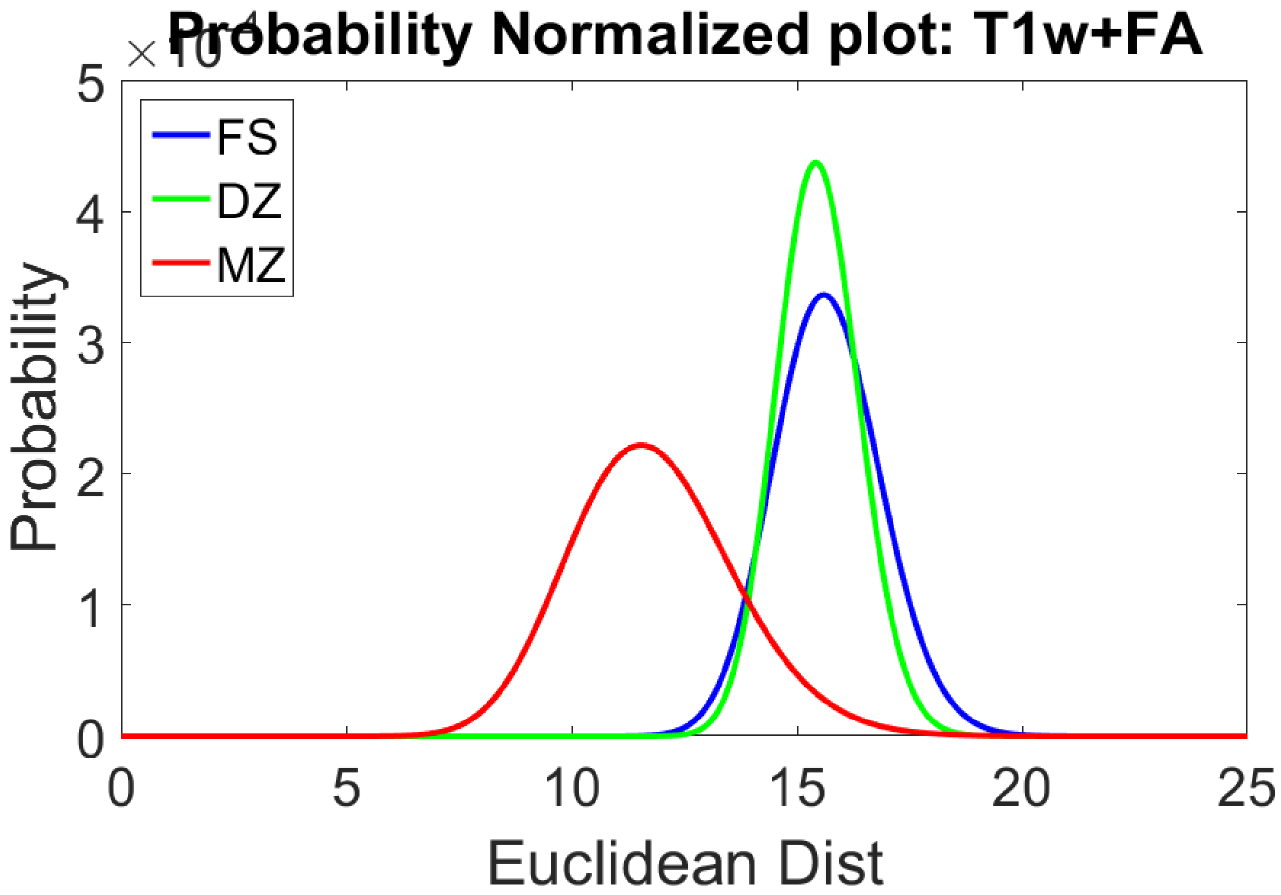
Probability Normalized plot: FA



Countdensity plot: T1w 125mm


Probability Normalized plot: T1w 125mm
×10^-4
FS
DZ
MZ
Probability
0
1
2
3
4
5
0
5
10
15
20
25
Euclidean Dist


Countdensity plot: T1w+FA
FS
DZ
MZ
Countdensity
0
20
40
60
5
10
15
20
Euclidean Dist



%%

Example 4: Rank Reterival Analysis: Mean Average Precision Table (Table 2, partial)

%%

```
%
% compute rank reterival measures for each sibling type and a given modality/combination
%           1. Mean Avg Precision and
%           2. mean recall@10
%
%          Additional outputs include detailed measures:
%                     3. average precision array
%                     4. recall@k   (k=1 to num_sub -1)
%                     5. precision@k  (k=1 to num_sub -1)
%
% Note: We can either use i) the subject proximity graphs directly or
% ii) compute pairwise Euclidean distance for compact fingerprints
%

flag_option_map = 1;                                                       % 1: subject proximity graphs 0: distance
array_modality_set = (1:9)' ;
num_spect_component = 150;                                                 % number of eigen vectors in fingerprint
cell_compact_fingerprint = cell(length(array_modality_set),1);

% rank reterival measures
mat_mean_avg_precision = zeros(length(array_modality_set), max_sib_type);
mat_mean_recall_at_10 = zeros(length(array_modality_set), max_sib_type);

%  additional detailed measures
cell_array_avg_precision = cell(length(array_modality_set), max_sib_type);
cell_mat_recall_at_k = cell(length(array_modality_set), max_sib_type);
cell_mat_precision_at_k = cell(length(array_modality_set), max_sib_type);

 for loop_i=1:length(array_modality_set)

        if(flag_option_map==1)
            % subject proximity graphs: Normalized Jaccard Similarity measures
            NxN_data_matrix = cell_NxN_data_matrix{array_modality_set(loop_i),1};
            flag_distance_or_similarity = 1;                               %: 0-distance; 1-similarity
        else
            % compact fingerprint generation
            NxN_data_matrix = compute_compact_fingerprint(cell_NxN_data_matrix{array_modality_set(loop_i),1},num_spect_component);
            flag_distance_or_similarity = 0;                                %: 0-distance; 1-similarity
        end

        knn_value = size(NxN_data_matrix,2)-1;                              % consider all subjects except self
        [nearest_neighbor_matrix] = compute_nearest_neighbor_matrix(NxN_data_matrix,knn_value,flag_distance_or_similarity);

        for loop_sib_type=1:max_sib_type
           sub_id_set = SAMPLE_cell_subID_and_sibpairID{loop_sib_type,1};
           pair_id_set = SAMPLE_cell_subID_and_sibpairID{loop_sib_type,2};
           [mat_mean_avg_precision(loop_i,loop_sib_type),mat_mean_recall_at_10(loop_i,loop_sib_type),cell_array_avg_precision{loop_i,loop_sib_type},cell_mat_recall_at_k{loop_i,loop_sib_type},cell_mat_precision_at_k{loop_i,loop_sib_type}] = compute_rank_reterival_measures(sub_id_set,pair_id_set,nearest_neighbor_matrix);
        end
 end
```

Display mean average precision (MAP) values

```
data_matrix    = round(mat_mean_avg_precision,3);
cell_column    = cell_sibling_type(1:max_sib_type);
cell_row_label = cell_modality ;

display_table_values(data_matrix, cell_column, cell_row_label);
```

```
sTable =

                         MZ       DZ       FS
                        _____    _____    _____

    FA                  0.964    0.219     0.16
    T1w 125mm           0.831    0.136    0.121
    T2w 125mm           0.879    0.173    0.132
    rfMRI               0.968    0.352    0.205
    T1w+FA              0.977    0.279     0.21
    T1w+rfMRI           0.984    0.352    0.229
    FA+rfMRI             0.99    0.439    0.276
    T1w+T2w+FA          0.991    0.354    0.247
    T1w+T2w+FA+rfMRI    0.997    0.546    0.371
```

%%%

```
      Example 4: Mean Recall@10 values (Supplement material Fig Table 8, partial)
```

%%%

```
% Display mean recall @ 10 values
data_matrix    = round(mat_mean_recall_at_10,3);
cell_column    = cell_sibling_type(1:max_sib_type);
cell_row_label = cell_modality ;

display_table_values(data_matrix, cell_column, cell_row_label);
```

```
sTable =

                         MZ       DZ       FS
                        _____    _____    _____

    FA                  0.992    0.421    0.307
    T1w 125mm           0.903    0.317     0.22
    T2w 125mm           0.954    0.349    0.249
    rfMRI               0.975    0.524    0.369
    T1w+FA              0.996    0.508    0.372
    T1w+rfMRI           0.996    0.635    0.438
    FA+rfMRI            0.996     0.69     0.47
    T1w+T2w+FA              1    0.579    0.429
    T1w+T2w+FA+rfMRI        1    0.817    0.603
```

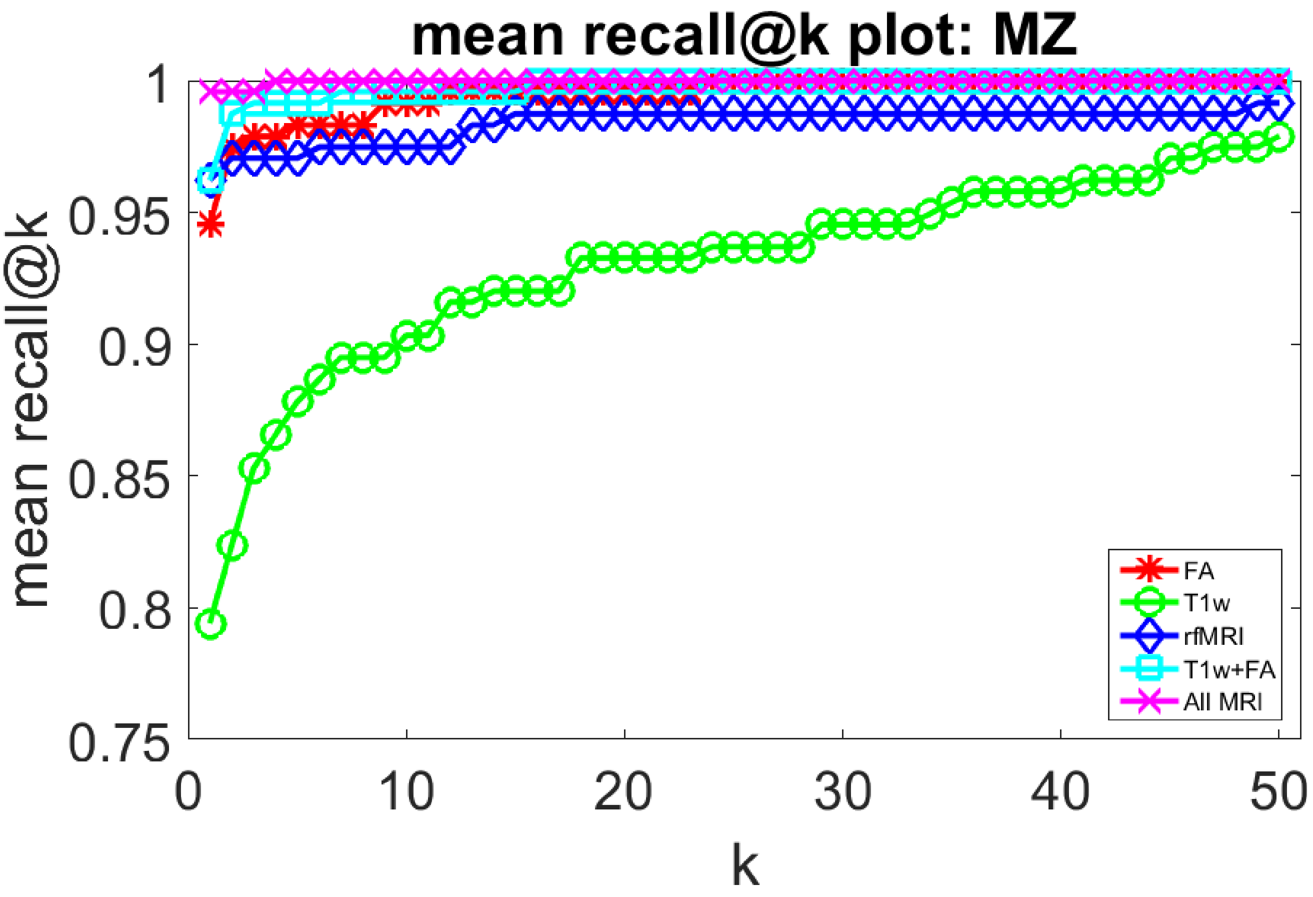
%%%

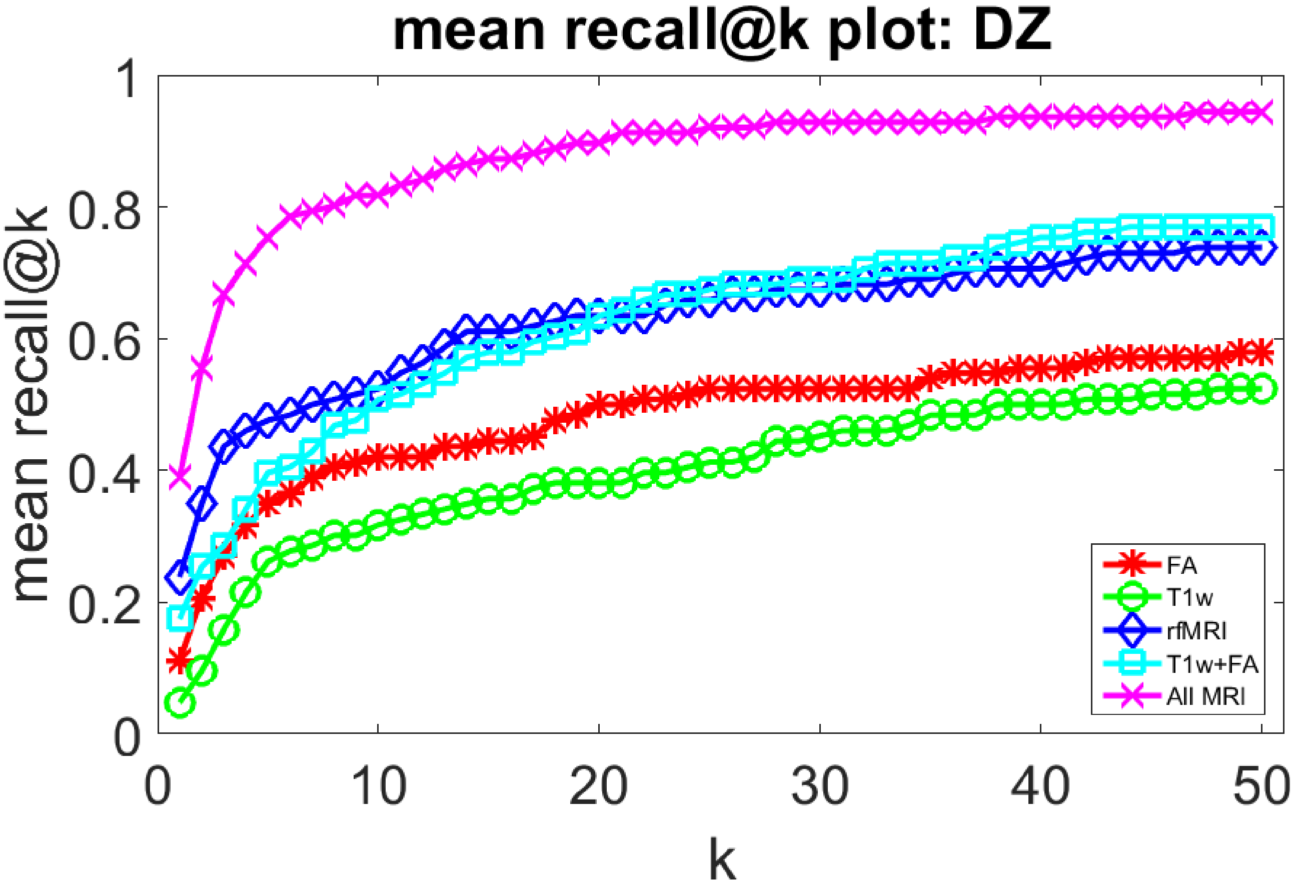
```
      Example 5: Mean Recall@k Plots (Supplement material Fig 1.)
```

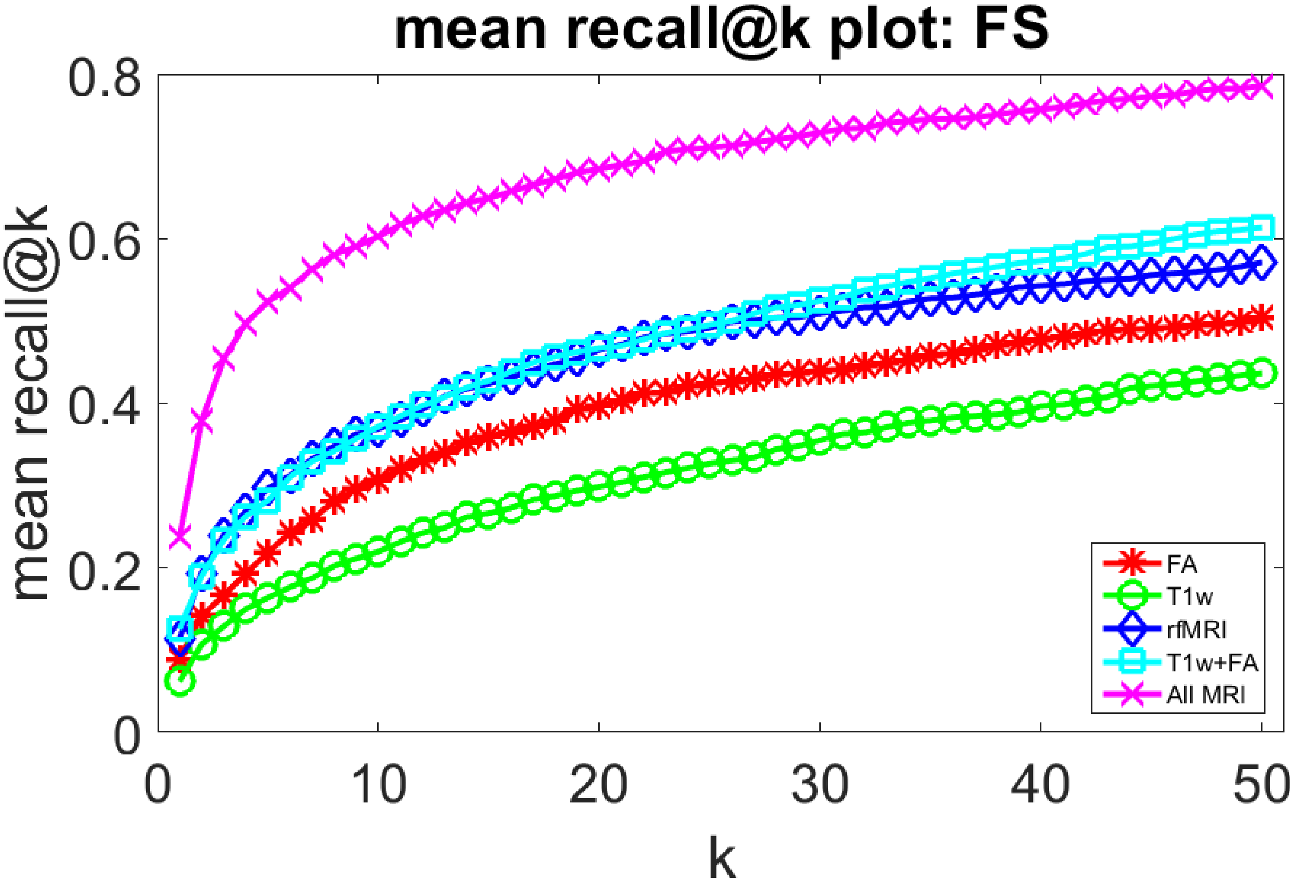
%%%

```
temp_knn_value =50;                                                         % number of nearest neighbors or k value
```

```
% get mean recall@k for k=1,2.....,temp_knn_value
array_modality_set = [ 1; 2; 4; 5; 9;];                                    % see cell_modality for index reference
mat_mean_recall_at_k = zeros(length(array_modality_set),temp_knn_value,max_sib_type);

% compute mean recall@k values using recal@k matrix
for loop_i=1:length(array_modality_set)
    for loop_sib_type =1:max_sib_type
        temp_mat = cell_mat_recall_at_k{array_modality_set(loop_i),loop_sib_type}(:,1:50);
        mat_mean_recall_at_k(loop_i,:,loop_sib_type) = mean(temp_mat);
    end
end

%plot for each twin/sibling type
for loop_sib_type =1:max_sib_type

    data_mat  = mat_mean_recall_at_k(:,:,loop_sib_type);
    x_array   = (1:50)';

    figure_title  = ['mean recall@k plot: ', cell_sibling_type{loop_sib_type}];
    cell_label{1} = 'k';
    cell_label{2} = 'mean recall@k';
    leg_location  =  'southeast';
    cell_legend   = {'FA'; 'T1w'; 'rfMRI'; 'T1w+FA'; 'All MRI';};
    save_plot_name = [];                                                       % assign filename to save it else empty

    plot_mean_recall_at_k(data_mat,x_array,figure_title,cell_legend,leg_location,cell_label,save_plot_name);
end
```







%%

```
Example 6: Relative informativeness Table: MZ, DZ, FS  (Table 3)
```

%%%

```
% Compute relative informativeness

relative_identification_knn_value = 10;                                    % number of nearest neighbors for realtive identification
                                                                           % identification considered success within these many neighbors o
nly

cell_compare_modality1_vs_modality2 = { 'T1w vs T2w';
                                         'T1w vs FA';
                                         'T1w vs rfMRI';
                                         'FA vs rfMRI';
                                         'T1w vs T1w+T2w+FA+rfMRI';
                                         'T2w vs T1w+T2w+FA+rfMRI';
                                         'FA  vs T1w+T2w+FA+rfMRI';
                                         'rfMRI vs T1w+T2w+FA+rfMRI';
                                         };

% hard code the modalities to be compared
% indices are based on cell_modality
array_modality1_index = [ 2; 2; 2; 1; 2; 3; 1; 4; ];
array_modality2_index = [ 3; 1; 4; 4; 9; 9; 9; 9; ];
mat_relative_identification_percent = zeros(length(array_modality1_index),4,max_sib_type);

for loop_i=1:length(array_modality1_index)

     if(flag_option_map==1)
            % subject proximity graphs: Normalized Jaccard Similarity measures
            NxN_data_matrix_1 = cell_NxN_data_matrix{array_modality1_index(loop_i),1};
            NxN_data_matrix_2 = cell_NxN_data_matrix{array_modality2_index(loop_i),1};
            flag_distance_or_similarity = 1;                               %: 0-distance; 1-similarity
     else
            % compact fingerprint generation
            NxN_data_matrix_1 = compute_compact_fingerprint(cell_NxN_data_matrix{array_modality1_index(loop_i),1},num_spect_component);
            NxN_data_matrix_2 = compute_compact_fingerprint(cell_NxN_data_matrix{array_modality2_index(loop_i),1},num_spect_component);
            flag_distance_or_similarity = 0;                               %: 0-distance; 1-similarity
     end

     nearest_neighbor_matrix_mod1= compute_nearest_neighbor_matrix(NxN_data_matrix_1,relative_identification_knn_value,flag_distance_or_simi
larity);
     nearest_neighbor_matrix_mod2= compute_nearest_neighbor_matrix(NxN_data_matrix_2,relative_identification_knn_value,flag_distance_or_simi
larity);

    for loop_sib=1:max_sib_type
            sub_id_set = SAMPLE_cell_subID_and_sibpairID{loop_sib,1};
            pair_id_set = SAMPLE_cell_subID_and_sibpairID{loop_sib,2};
            [mat_relative_identification_percent(loop_i,1:4,loop_sib)] = compute_relative_identification_percentage(sub_id_set,pair_id_set,n
earest_neighbor_matrix_mod1,nearest_neighbor_matrix_mod2);
    end
end
```

Display realtive identification percentages: MZ, DZ, FS tables

```
cell_relative_comparison_order = { 'Both';  'Mod1'; 'Mod2';  'None'; };
cell_column = cell_relative_comparison_order;
cell_row_label = cell_compare_modality1_vs_modality2 ;

for loop_sib=1:max_sib_type
    % display for each twin/sibling type
    disp(['Relative Identification percentage for : ' cell_sibling_type{loop_sib}]);
    data_matrix =round(mat_relative_identification_percent(:,:,loop_sib),2);
    display_table_values(data_matrix, cell_column, cell_row_label);
end
```

```
Relative Identification percentage for : MZ

sTable = 

                                 Both     Mod1    Mod2    None
                                 _____    ____    ____    ____

    T1w vs T2w                   85.71    4.62    9.66       0
    T1w vs FA                    90.34       0    8.82    0.84
    T1w vs rfMRI                 88.24     2.1    9.24    0.42
    FA vs rfMRI                  96.64    2.52    0.84       0
    T1w vs T1w+T2w+FA+rfMRI      90.34       0    9.66       0
    T2w vs T1w+T2w+FA+rfMRI      95.38       0    4.62       0
    FA  vs T1w+T2w+FA+rfMRI      99.16       0    0.84       0
    rfMRI vs T1w+T2w+FA+rfMRI    97.48       0    2.52       0
```

```
Relative Identification percentage for : DZ

sTable = 

                                 Both     Mod1     Mod2     None 
                                 _____    _____    _____    _____

    T1w vs T2w                   15.87    15.87    19.05    49.21
    T1w vs FA                    15.87    15.87    26.19    42.06
    T1w vs rfMRI                 18.25    13.49    34.13    34.13
    FA vs rfMRI                  26.19    15.87    26.19    31.75
    T1w vs T1w+T2w+FA+rfMRI      28.57     3.17    53.17    15.08
    T2w vs T1w+T2w+FA+rfMRI      33.33     1.59    48.41    16.67
    FA  vs T1w+T2w+FA+rfMRI      39.68     2.38    42.06    15.87
    rfMRI vs T1w+T2w+FA+rfMRI    49.21     3.17    32.54    15.08

Relative Identification percentage for : FS

sTable = 

                                 Both     Mod1     Mod2     None 
                                 _____    _____    _____    _____

    T1w vs T2w                   10.26    11.72    14.65    63.37
    T1w vs FA                    10.62    11.36    20.05    57.97
    T1w vs rfMRI                  9.52    12.45    27.38    50.64
    FA vs rfMRI                  12.91    17.77    23.99    45.33
    T1w vs T1w+T2w+FA+rfMRI      18.96     3.02     41.3    36.72
    T2w vs T1w+T2w+FA+rfMRI      21.98     2.93    38.28    36.81
    FA  vs T1w+T2w+FA+rfMRI      25.64     5.04    34.62    34.71
    rfMRI vs T1w+T2w+FA+rfMRI    34.89     2.01    25.37    37.73
```

%%%

%%%

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