MatClassRSA

User Manual

Version 2.0

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1. Introduction

In recent years, repeated trials of M/EEG responses have come to be analyzed in the framework of Representational Similarity Analysis (RSA, Kriegeskorte et al., 2008). RSA abstracts modality-specific response activations to Representational Dissimilarity Matrices (RDMs), which summarize pairwise response dissimilarities across all stimuli. This enables disparate response modalities, such as neural responses and computational models, to be compared quantitatively.

The MatClassRSA toolbox provides multiple functionalities for computing RDMs from M/EEG response data. First, matrices can be computed by classifying the data – that is, using machine learning to predict categorical labels of data from a trained statistical model. The classifier output can be treated as a similarity matrix (in the case of multicategory confusion matrices) or a distance matrix (in the case of a matrix of pairwise classification accuracies). As alternatives to classification, RDMs can be computed using Pearson correlation or Euclidean distance (Guggenmos et al., 2018). In addition to computing RDMs, MatClassRSA includes functions for assessing data quality; optionally preprocessing the data; and visualizing RDMs.

The purpose of MatClassRSA is to facilitate cognitive neuroscience research for researchers who wish to perform classification and RSA. Our target end users are those who already work with repeated-trials M/EEG data in Matlab (e.g., for ERP analyses), and who wish to perform new types of analyses with these data. By removing the burden of implementing standard machine-learning and other analysis procedures by hand, we hope that the toolbox makes these computationally focused analyses accessible to a wider range of researchers.

Users should, however, be mindful of the following:

- MatClassRSA is a collection of functions and does not have a GUI. Users should be comfortable loading/saving data and calling functions either using scripts or from the command line in Matlab.
- The toolbox does not perform data cleaning, but it is designed to work with data in the form that is commonly output by the EEGLAB toolbox after preprocessing (REF).

1.1. Overview

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When **MatClassRSA** is used for research, please cite the publication describing the software package:

> Bernard C. Wang, Anthony M. Norcia, and Blair Kaneshiro (2017). MatClassRSA: A Matlab Toolbox for M/EEG Classification and Visualization of Proximity Matrices. bioRxiv preprint 194563; doi: https://doi.org/10.1101/194563.

For commercial use of **MatClassRSA** please contact Bernard C. Wang: bernardcwang@gmail.com.

Support

For questions, comments, suggestions, feature requests, and bug reports, please contact bernardcwang@gmail.com.

The EEG data for the example analyses presented here are from the Object Category EEG Dataset and can be downloaded from the Stanford Digital Repository:

> Blair Kaneshiro, Steinunn Arnardóttir, Anthony M. Norcia, and Patrick Suppes (2015). Object Category EEG Dataset (OCED). Stanford Digital Repository. Available at: https://purl.stanford.edu/tc919dd5388

Software Background

This software was originally developed for members of the Stanford Vision and Neuro-Development Lab, Stanford Translational Auditory Research Lab, and Music Engagement Research Initiative to perform EEG classification in conjunction with visualizations related to Representational Similarity Analysis. Based on the level of interest in the software and development of code to for related analyses, we eventually packaged the functionalities into a toolbox for greater benefit to the general research community.

Related Work

1.2. Setup and Installation

The software was tested on the following operating systems:

- Linux Fedora 24 (Twenty Four)
- OS X El Capitan (10.11.6) and higher

Software may encounter bugs if run on other versions of Matlab or operating systems than those listed above. Please report any bugs to bernardcwang@gmail.com

Dependencies

The software is compatible with Matlab 2016b and above. Some functions may be usable on earlier versions of Matlab, but the toolbox has not been fully tested on previous versions.

The software requires two Matlab toolboxes: The Statistics and Machine Learning Toolbox and the Image Processing Toolbox.

The sole external dependency for MatClassRSA is LIBSVM, which is included in the download of MatClassRSA:

> Chih-Chung Chang and Chih-Jen Lin, LIBSVM : A library for support vector machines. ACM Transactions on Intelligent Systems and Technology, 2:27:1--27:27, 2011. Software available at http://www.csie.ntu.edu.tw/~cjlin/libsvm

Installation

Download the latest version of this package at https://github.com/berneezy3/MatClassRSA/

The external dependency, LIBSVM, must be set up first. Once inside the MatClassRSA main directory, please navigate to '`src/Classification/libsvm-3.21/matlab`' and refer to the README file for LIBSVM installation instructions.

After setting up LIBSVM, run the following in the Matlab IDE to add the MatClassRSA functions into your search path:

```
> downloadPath = <Your download directory here, in char array format>;
> addpath([downloadPath 'src/Classification/libsvm-3.21/matlab']);
> addpath([downloadPath 'src/Classification/']);
> addpath([downloadPath 'src/RDM_Computation/']);
> addpath([downloadPath 'src/Visualization']);
> addpath([downloadPath 'src/Classification/libsvm-3.21/matlab']);
```

MatClassRSA functions will be runnable from this point. To automatically import MatClassRSA upon Matlab startup, please create a 'startup.m' somewhere in your Matlab search path (this can be found using the command "path"), and add the above lines into it.

1.3. Main Functions

The main MatClassRSA functions that users will call fall into five categories:

1. **Data Quality Assessments**: Computes split-half reliability of the data (Reliability/ directory, two main functions).
2. **Data Preprocessing**: Optional operations to prepare data for RDM computations (Preprocessing/ directory, three main functions).
3. **Classification**: Classifies the M/EEG data in multicategory or pairwise schemes using LDA, SVD, or Random Forest. Users can input all data and labels for cross validation, or can partition the data outside the function for separate training and testing (Classification/ directory, three main functions).
4. **Computing RDMs**: Converts multicategory confusion (similarity) matrices to RDMs Computes non-classification RDMs directly from response data matrices. Converts existing RDMs (distance matrices) to ranked representations (RDM_Computation directory, three main functions).
5. **Visualizing RDMs**: Creates RDM visualizations including matrix image, multidimensional scaling plot, dendrogram, and minimum spanning tree (Visualization/ directory, four main functions).

Underlying these main functions and the illustrative analyses are a number of helper functions. Users do not need to interact directly with the helper functions in order to access the above functionalities of the toolbox, but may do so for advanced or custom analyses.

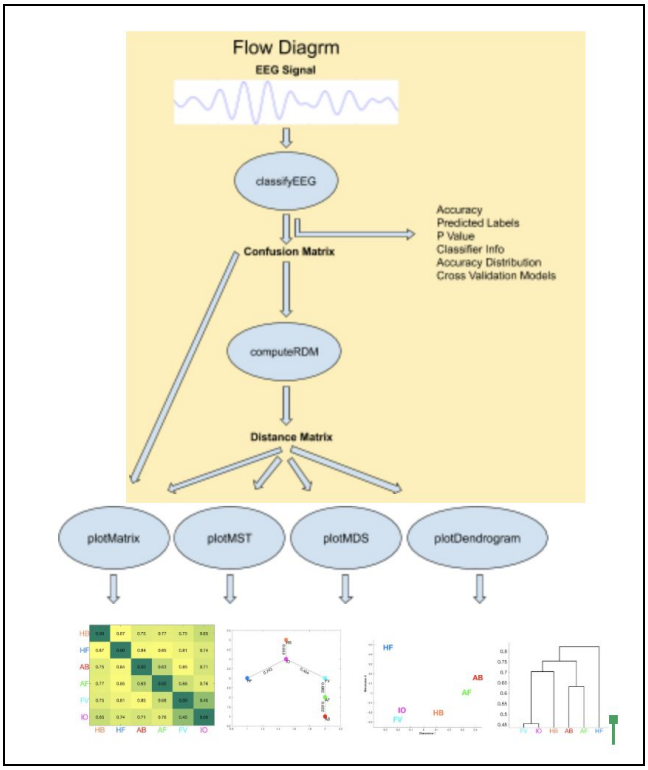


Figure: Overview of toolbox functions.

1.4. Input Data Specifications

It is the responsibility of the user to have loaded the data to be analyzed so that the required variables are present in the workspace, are correctly formatted, and can be passed in as MatClassRSA function inputs.

Response Data Matrices, Labels Vectors, Participant Vectors

Functions that perform data quality assessments, data preprocessing, classification, and computation of RDMs directly from response data require at minimum an M/EEG data matrix and vector of trial labels as inputs.

The functions included in the toolbox expect **data matrices** to contain repeated-trials data (ranging from tens to thousands of trials per stimulus) from at least two categories (i.e., at least two unique values in the labels vector). Nearly all functions operating on data will accept a 3D matrix of dimensions space-by-time-by-trial (as output by EEGLAB) or a 2D matrix of dimensions trial-by-feature, in cases where data from single electrodes or single time points are analyzed. The data matrix should contain *all* trials to be analyzed – aggregated across stimuli and, if desired, across participants. In function implementation, the matrix of response data is usually referred to as `X`.

MatClassRSA functions were developed with the primary use case of data matrices containing time-domain evoked responses from multiple electrodes. Consequently the docstrings, manual entries, and illustrative analyses reflect this usage (i.e., references to data from different sensors/electrodes and time samples). It is, however, possible to input response data of other formats. For example, data matrices can contain spatial-filtering components (such as principal components or independent components) along the space dimension, and oscillatory band power or Fourier coefficients as alternative features to time samples. In these cases, users should be mindful to interpret the structure and features of the output data accordingly.

Figure: Acceptable input data formats. X, Y, and P.

The **vector of trial labels** is referred to here as `Y`. Since the labels vector provides stimulus identifiers corresponding to each trial of response data, it should correspond in length to the trial dimension of the corresponding 2D or 3D input data matrix, and its ordering should match the ordering of the data trials. MatClassRSA expects `Y` to be a numeric row or column vector (e.g., not a cell array of strings); the values need not start at 1 nor be continuous. When matrices of size nStimuli-by-nStimuli (such as classifier confusion matrices or RDMs) are output by MatClassRSA functions, these matrices' rows and columns will be ordered by the sorted unique elements of the labels vector.

Certain preprocessing functions also accept as input a **vector of participant identifiers**. This vector, which we refer to as `P`, must be the same length as the trial labels vector `Y` and is used to specify, in cases where the input data matrix contains data from multiple participants, which participant is associated with each trial of data.

RDMs as Inputs

Users wishing to transform (i.e., convert values to ranks) or visualize existing RDMs may pass these directly into the respective functions. RDMs are assumed to be square, symmetric matrices of size num_stimuli-by-num_stimuli.

1.5. Illustrative Examples

MatClassRSA comes with a collection of illustrative examples to demonstrate the most common expected use cases of the software. They are contained in the **examples/** folder in the main directory of the toolbox and are described in the Illustrative Examples section of this User Manual.

2. Assessing Data Quality

The reliability of the data affects any further downstream data analyses and also places an upper bound on how well any model can explain the data. Thus, it is important to assess how reliable the data are.

TODO

MatClassRSA includes two functions to compute the reliability of the data. First, `computeSpaceTimeReliability`, computes reliability using all available data at each response feature (typically electrode and/or time sample). Next, `computeSampleSizeReliability`, computes reliability for a single electrode or time point over a varying trial sample size.

Figure: Flowchart of this section's functions.

2.1. `computeSpaceTimeReliability`

This function computes the reliability of the response data matrix on a per-electrode (component) basis across time. This computation is performed across a specified number of permutations. A typical use case would be to average the output reliabilites across the electrodes (components) dimension and the permutations dimension to obtain a time course of average electrode reliability.

Syntax

```
[reliabilities] = computeSpaceTimeReliability(X, Y, numPermutations, rngType);
```

Required inputs

The function has two required inputs: Response data matrix `X` and labels vector `Y`.

`X` — M/EEG data matrix.

The `X` matrix contains the response data. The `X` matrix can be passed into the function in the following shapes:

- A 3D electrode-by-time-by-trial matrix.
- A 2D trial-by-feature matrix. For example, this matrix could contain response activations at a single time sample recorded from multiple electrodes, or across time from a single electrode. In the function code, 2D data matrices are effectively treated as trial-by-time (single electrode) matrices.

`Y` — Labels vector.

The `Y` vector contains the numeric labels corresponding to each trial in the M/EEG data matrix `X`. Both row and column vectors will be accepted. The length of `Y` must correspond to the size of `X` along the trial dimension.

Optional inputs

`numPermutations` — Number of random permutations along the trial dimension to perform split-half reliability calculation.

The `numPermutations` argument contains an integer greater than 0 that describes the number of times to randomly sample the trials. If this is not specified or is empty, the default number of permutations is 10.

`rngType` — Random seed for reproducibility.

The `rngType` argument allows the user to set the random number generator (`rng`) in order to control the reproducibility of the computed reliabilities, or to avoid identical randomizations at each launch of Matlab. Options for `rngType` are as follows:

- Single acceptable rng specification input (e.g., 1, `'default'`, `'shuffle'`); in these cases, the generator will be set to `'twister'`.
    - If `'default'` is entered, the seed will be set to 0.
    - If `'shuffle'` is entered, the seed will based on the current time.

- Dual-argument (seed, generator) specifications as either a 2-element cell array (e.g., `{'shuffle', 'twister'}`) or string array (e.g., `["shuffle", "twister"]`).
- rng struct as assigned by `rngType = rng`.

If this input is not specified or is empty, rng will be assigned as `{'shuffle', 'twister'}`. For more information, see the documentation for MatClassRSA helper function **`setUserSpecifiedRng`** and Matlab function **`rng`**.

Outputs

`reliabilities` — Matrix of electrode reliabilities across time. If the input data matrix was 3D, the dimensions of this matrix are space-by-time-by-permutation. If the input data matrix was 2D, the dimensions of this matrix are time-by-permutation.

The output matrix contains the reliability of each electrode across time if a 3D data matrix was provided. One would typically average across the permutations and electrodes dimensions in order to obtain a time course of average reliability across electrodes. If a 2D matrix was entered, the data are assumed to contain only one electrode (component) and one would average across the permutations dimension to obtain a time course of average reliability.

Example function calls

In the following calls, the function will use default specifications for `numPermutations` and `rngType`:

```
reliabilities = computeSpaceTimeReliability(X, Y);
reliabilities = computeSpaceTimeReliability(X, Y, [], []);
```

If the user wishes to use a custom specification for `rngType` (the fourth input), all four inputs must be provided in the function call (whether or not the optional third input `numPermutations` is specified). If wanting to use the default specification for the third input `numPermutations` in this case, it can be entered as an empty input while the fourth input is specified:

```
reliabilities = computeSpaceTimeReliability(X, Y, [], {5, 'philox'});
```

Alternatively, the user can specify all four inputs as follows (e.g., with 100 permutations):

```
reliabilities = computeSpaceTimeReliability(X, Y, 100, {5, 'philox'});
```

2.2. `computeSampleSizeReliability`

Reliability is known to vary according to the size (number of trials per stimulus) of the data. This function computes the reliability of a single time sample across varying trial subset sizes. A

typical use case would be to average, for each trial subset size, the output reliabilities across the electrode (components) or time dimension and also across the permutations dimension. This produces a vector whose entries indicate the average reliability across electrodes or time for each trial subset size.

Syntax

```
[reliabilities] = computeSpaceTimeReliability(X, Y, featureIdx,
numTrialsPerHalf, numPermutations, numTrialPermutations, rngType);
```

Required inputs

The function has two required inputs: Response data matrix `X` and labels vector `Y`.

`X` — M/EEG data matrix.

The `X` matrix contains the response data. The `X` matrix can be passed into the function in the following shapes:

- A 3D electrode-by-time-by-trial matrix.
- A 2D trial-by-feature matrix. For example, this matrix could contain response activations at a single time sample recorded from multiple electrodes, or across time from a single electrode. In the function code, 2D data matrices are effectively treated as trial-by-time (single electrode) matrices.

`Y` — Labels vector.

The `Y` vector contains the numeric labels corresponding to each trial in the M/EEG data matrix `X`. Both row and column vectors will be accepted. The length of `Y` must correspond to the size of `X` along the trial dimension.

`featureIdx` — Index of time point at which reliability for each electrode (component) is desired.

The `featureIdx` argument is an integer that indicates the feature index (e.g., time sample) at which to compute the reliability across electrodes and across different sizes of trial subsets.

- `featureIdx` should be between 1 and the number of time points in the data inclusive for a trial-by-time input matrix, or between 1 and the number of electrodes in the data for a trial-by-electrode input matrix.
- If a 3D matrix is input, `featureIdx` specifies the index at which the data are subset *along the second (time) dimension*. If a 2D matrix is input, it is the index at which the data are subset *along the second (feature) dimension*.

Optional inputs

`numTrialsPerHalf` — This is a vector of integers which determines the number of trials to use in each reliability calculation.

The fourth input is an optional `numTrialsPerHalf` argument, which allows the user to determine how reliable the data would be if different numbers of trials were used or collected in the experiment.

- For example, if the user wanted to determine how reliable the data are if each condition had 16 and 20 trials, the user would input `[8, 10]` for this argument.
- If a requested number of trials exceeds the number of available trials, `NaN` reliability is returned for that entry.

If this input is not provided or is empty, this argument defaults to 1, meaning that the function will use two trials to compute reliability across electrodes.

`numPermutations` — Number of random permutations along the trial dimension to perform split-half reliability calculation.

Given a set of trials, the fifth input `numPermutations` is an optional argument that determines how many times to randomly shuffle the trials to compute the split-half reliability. If this is not specified or is empty, `numPermutations` defaults to 10.

`numTrialPermutations` — Number of randomly chosen trials for a given trial subset size.

For each trial subset size, the sixth input `numTrialPermutations` is an optional argument that determines how many times the trial subset should be randomly sampled. For example, if we want to compute how reliable the data are with a trial subset size of 10, this argument determines how many times to randomly choose 10 trials from the provided data.

`rand_seed` — Random seed for reproducibility

The seventh input is an optional `rngType` argument, which allows the user to set the random number generator (`rng`) in order to control the reproducibility of the computed reliabilities, or to avoid identical randomizations at each launch of Matlab. Options for `rand_seed` are as follows:

- Single acceptable rng specification input (e.g., 1, `'default'`, `'shuffle'`); in these cases, the generator will be set to `'twister'`.
  - If `'default'` is entered, the seed will be set to 0.
  - If `'shuffle'` is entered, the seed will based on the current time.
- Dual-argument specifications as either a 2-element cell array (e.g., `{'shuffle', 'twister'}`) or string array (e.g., `["shuffle", "twister"]`).
- rng struct as assigned by `rand_seed = rng`.

If not specified, rng will be assigned as `{'shuffle', 'twister'}`.

Outputs

`reliabilities` — This matrix contains the reliability of a single electrode (component) or time point for different sizes of trial subsets.

If a 3D data matrix was provided, then the dimensions of the `reliabilities` matrix are: `numTrialPermutations` x length(`numTrialsPerHalf`) x space. One would typically average across the first and third dimension to obtain a curve that describes how average electrode reliability varies as a function of number of trials used.

Example function calls

Call the function with 2D or 3D input data matrix, feature / time point 5, and default specifications for optional inputs:

```
reliabilities = computeSpaceTimeReliability(X, Y, 5);
reliabilities = computeSpaceTimeReliability(X, Y, 5, [], [], [], []);
```

To compute reliabilities at a single *electrode* (rather than time point) when calling the function, permute the first two dimensions of the input data matrix so that its dimensions are *time-by-space*-by-trial:

```
reliabilities = computeSpaceTimeReliability(permute(X, [2, 1, 3]),
                                            Y, 5);
```

Call the function with 2D or 3D input data matrix, time point 5, an increasing number of trials to use, from 1 to 10 in each split-half partition, and otherwise default inputs:

```
reliabilities = computeSpaceTimeReliability(X, Y, 5, 1:10);
```

If the user wishes to specify the fifth, sixth, or seventh input, all prior inputs must be present. In this case, if the user wishes to use default values for inputs preceding a specified input, the preceding inputs can be empty ([ ]) inputs. For example, to call the function with a 2D or 3D input data matrix, time point 5, and specifying non-default values for only the last optional input (rng specification):

```
reliabilities = computeSpaceTimeReliability(X, Y, 5, [], [], [],
                                            {5, 'philox'});
```

3. Data Preprocessing

Users may wish to perform additional, optional preprocessing procedures to prepare cleaned data for downstream MatClassRSA analyses.

Figure: Flowchart of this section's functions.

3.1. `shuffleData`

This function computes the reliability of the ... 9/27 START HERE AND ALSO CLEAN UP FUNCTION DOCSTRING

Syntax

```
[randX, randY, randP, randIdx] = shuffleData(X, Y, P, r)
```

Required inputs

The function has two required inputs: Response data matrix `X` and labels vector `Y`.

`X` — M/EEG data matrix.

The `X` matrix contains the response ...

`Y` — Labels vector.

The `Y` vector contains the numeric labels corresponding...

Optional inputs

`num_permutations` — Number of random permutations along the trial dimension to perform split-half reliability calculation.

The `num_permutations` argument ...

`rand_seed` — Random seed for reproducibility.

The `rand_seed` argument allows ...

Outputs

`reliabilities` — Matrix of electrode reliabilities across time.

The output matrix contains the reliability of each electrode across time if a 3D data matrix was provided...

Example function calls

In the following calls, the function will use default specifications for `num_permutations` and `rand_seed`:

```
reliabilities = computeSpaceTimeReliability(X, Y);
reliabilities = computeSpaceTimeReliability(X, Y, [], []);
```

If the user wishes to use

```
reliabilities = computeSpaceTimeReliability(X, Y, [], {5, 'philox'});
```

noiseNormalization

When recording brain responses using EEG or MEG, data from individual electrodes typically vary in terms of signal-to-noise ratio (SNR). The `noiseNormalization` function “downweights” electrodes that have low SNR and “upweights” electrodes that have high SNR.

TODO

Usage

```
[norm_data, sigma_inv] = noiseNormalization(X, Y);
```

Required Inputs

The function has two required inputs: Response data matrix `X` and labels vector `Y`.

`X` — M/EEG data matrix.

The `X` matrix contains the response data. The `X` matrix can be passed into the function as the following shapes:

- A 3D space-by-time-by-trial matrix
- A 2D trial-by-time matrix

If a 2D data matrix is provided, it is assumed that it is the data matrix associated with a single electrode (component).

`Y` — Labels vector.

The `Y` vector contains the numeric labels corresponding to each trial in the M/EEG data matrix `X`. Both row and column vectors will be accepted. The length of `Y` must correspond to the size of `X` along the trial dimension.

Outputs

`norm_data` — Matrix of data that have been normalized by the covariance matrix.

This matrix is the same size as the input data matrix.

`sigma_inv` — This matrix contains the inverse of the square root of covariance matrix, $\Sigma^{-\frac{1}{2}}$, that was used to normalize the data.

The size of this matrix is `num_components x num_components`.

Example function calls

TODO

EEG Classification and RDM Construction

General intro paragraph about what is going on in this section

`classifyCrossValidate`

The first functionality of MatClassRSA is the classification of EEG trials. The classification procedure produces a confusion matrix, which can then be transformed and used for RSA-style visualizations. The `classifyEEG` function handles all classification and cross-validation tasks, and supports numerous related configurations, as described in the below section.

EEG data can be passed in directly to the function, as MatClassRSA supports multiple shapes of data. In addition, the package provides numerous configurable features and options when conducting cross validation,

Correct classifications of each class are plotted on the diagonal, while the off diagonal squares represent misclassifications.

Usage

```
[CM, accuracy, predY, pVal, classifierInfo, varargout] =
     classifyEEG(X, Y, Name, Value);
```

Required Inputs

The classification function has two required inputs: EEG data matrix `X` and labels vector `Y`.

`X` — EEG data matrix

The `X` matrix contains the EEG data used for training and testing during classification. The `X` matrix can be passed into the function as the following shapes:

- A 3D space-by-time-by-trials matrix
- A 2D trials-by-features matrix

The input data matrix can be subsetted along the space/time (3D matrix) or features (2D matrix) dimensions using the '`spaceUse`', '`timeUse`', and '`featureUse`' name-value pairs described below. 3D input matrices will be reshaped as 2D matrices by the classification function prior to cross validation.

`Y` — Labels vector

The `Y` vector contains the numeric labels corresponding to each trial in the EEG data matrix `X`. Both row and column vectors will be accepted. The length of `Y` must correspond to the size of `X` along the trial dimension. Note that classification is the assignment of discrete (category) labels

to data observations. The prediction of continuous values, which is a regression task, is not currently implemented in this toolbox.

Optional Inputs (name-value pair arguments)

'`spaceUse`', '`timeUse`', '`featureUse`' — Data subsetting (default none)

For 3D EEG input `X` matrices, the user can specify additional name-value parameters '`spaceUse`' and '`timeUse`'. These should be vectors that contain the indices in the space or feature dimension which the user wants to subset. For example, given a 128*500*200 (space * time * trials) input matrix `X`, the command

```
classifyEEG(X, Y, 'spaceUse', 50:59)
```

would return a 10*500*200 matrix, with the x dimension representing the 50th to 59th space dimension of the original matrix.

Similarly, with 2D input data matrices, users can pass in the name-value parameter '`featureUse`', such that, given a 4000*5000 input matrix `X`, the command

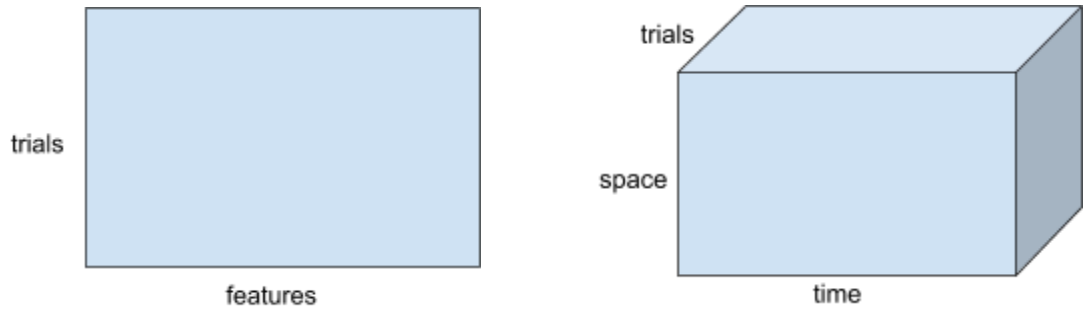
```
classifyEEG(X, Y, 'featureUse', 1:10)
```

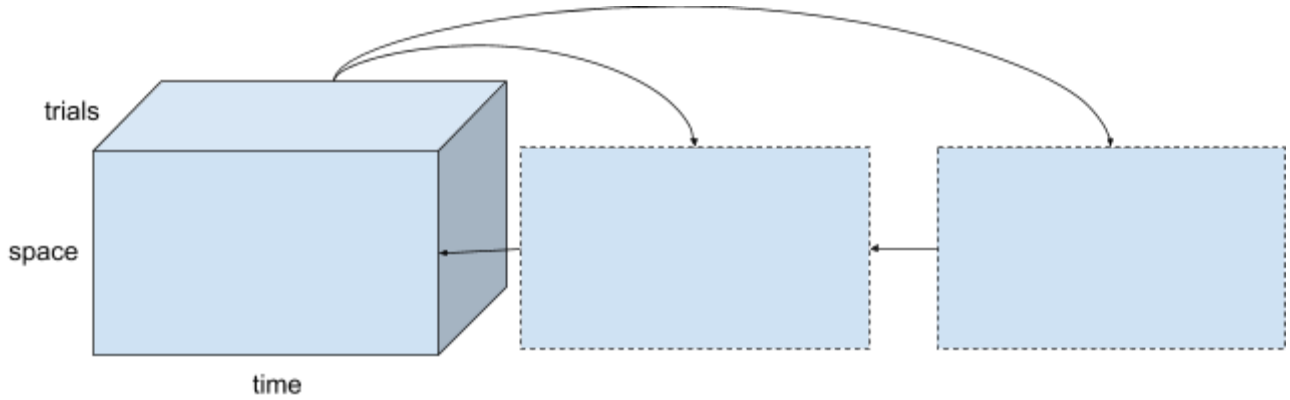
would return a 4000*10 size matrix, for which the columns now contain the first 10 features of the original input matrix `X`.

The default is to not subset the data.

After the optional step of subsetting the matrix, 3D matrices will be converted to 2D matrices by concatenating each trial along the time dimension of the matrix, then passed onto the next step.

EEG Input data representations





'`randomSeed`' — Control randomization (default 'shuffle')

This parameter controls randomization seeding within the package. The default value, '`shuffle`', seeds the random number generator based on current time, which causes execution of the function to return slightly different results each time it is run. If the user wants to obtain replicable results, '`default`' should be passed in as the input value, as such

```
classifyEEG(X, Y, 'randomSeed', 'default');
```

'`shuffleData`' — Data shuffling (default 1)

Once the EEG matrix `X` is in the 2D format as input to classification, MatClassRSA by default shuffles the rows in the `X` matrix in conjunction with their labels in `Y`, such that each row in `X` still corresponds to the same label in `Y`. The motivation for this operation is to remove possible ordering effects from the classification results when performing cross validation. In cases where the data were collected in blocks, each containing responses to only one stimulus, randomized data shuffling additionally ensures that trials of each class will be evenly distributed throughout folds. However, if input data are already ordered in such a way that the user wants to maintain (e.g., train on data from 9 participants, test on data from the 10th), data shuffling can be turned off.

To turn off data shuffling, add the '`shuffleData`' name-value pair as follows:

```
classifyEEG(X, Y, 'shuffleData', 0);
```

'`averageTrials`' — Trial averaging (default none)
'`averageTrialsHandleRemainder`' — Handle remainder trials (if any) from trial averaging (default 'discard')

Trial averaging, or signal averaging, is a technique applied to the EEG trials from the same category to improve the signal to noise ratio. This technique will often improve classification accuracy and produce more distinct structure in visualizations of corresponding confusion

matrices. This is done by grouping trials of the same class together, then replacing each group with their signal average, across the trial dimension.

For example, if we had 50 trials of class 1 and 50 trials of class 2 and decided to average in groups of 5, we would call the function as follows:

```
classifyEEG(X, Y, 'averageTrials', 5);
```

This will split class 1 and class 2 trials each into groups 5 (10 groups), and then average each group across trials, resulting in 10 trials of each class. Cross validation and classification would be performed with these averaged trials.

Sometimes the number of trials of a certain class will not be integer-divisible by the group size that the user specifies. For these cases, MatClassRSA includes an additional parameter, '`averageTrialsHandleRemainder`', which accepts these four options to handle remainder cases:

- '`discard`': (default) Discard remainder trials.
- '`newGroup`': Create new groups using remainder data, even if the groups do not satisfy the user specified number of groups.
- '`append`': Append all remainder trials to a group with the same label.
- '`Distribute`': Distribute remainder trials among groups with the same label as evenly as possible.

Notes:

- If the '`averageTrialsHandleRemainder`' parameter is passed in without a specification for '`averageTrials`', the program should output a warning and continue calculations without averaging trials.
- As a final step in this function, shuffleData is called. This because xx

'`PCA`' — Principal Component Analysis (default 0.9)
'`PCAinFold`' — Perform Principal Component Analysis separately for each cross-validation training partition (default 1)

MatClassRSA supports feature dimensionality using Principal Component Analysis (PCA). Here, PCA is performed across the columns (features) of the 2D trials-by-feature EEG matrix `X` that is passed into the classifier, transforming the matrix to a trials-by-PC-feature matrix X_{PC}. Based on the number of PCs retained (*K*), only the first *K* columns of X_{PC} will be input to the classifier.

The number of principal components (PCs) can be selected in two ways. First, the user can specify the exact number of PCs to retain. In this case, an integer value greater than 1 specifies the desired number of PCs. For example, to retain 20 PCs for classification, the function will be called as

```
classifyEEG(X, Y, 'PCA', 20);
```

Alternatively, the user can specify a desired proportion of variance explained, and the corresponding number of PCs (in descending order of variance explained) will be retained for classification. In this case, a decimal value greater than 0 and less than 1 that represents the proportion of variance the user wants explained should be passed in. For example, to retain as many PCs as are needed to explain 75% of the variance in the data, the user would call

```
classifyEEG(X, Y, 'PCA', 0.75);
```

The default value for '`PCA`' is .9, which selects the most important features that explain 90% of the variance. PCA is performed after data subsetting, if subsetting has been specified.

An additional parameter that can be specified is '`PCAinFold`'. This parameter allows users to choose whether to conduct PCA on the entire 2D `X` matrix (prior to partitioning for cross validation), or separately for each cross-validation training partition. Technically, the correct way to implement PCA would be to compute it separately for every training partition, so that the training observations are not involved in the computation of PCs. However, computing PCA only once on the entire data set is much faster, and in practice often results in similar results as conducting PCA within each separate fold, so we provide that as an option for the user.

'`PCAinFold`' by default is set to 1 (on), meaning that PCA will be computed separately for every training partition. To compute PCA just once over the entire dataset, call the function as

```
classifyEEG(X, Y, 'PCAinFold', 0);
```

'`nFolds`' — Number of cross-validation folds (default 10)

Cross validation is a technique that can be used to assess how a machine learning model trained on a particular dataset will generalize to the population. Cross validation achieves this by splitting the data along N-folds; then, from n = 1:N, all the data *except* the observations in fold *n* are used to train the model, which is then used to predict the labels of observations in fold *n*. The accuracies for each fold are aggregated at the end to produce the estimated accuracy for the classification.

The '`nFolds`' parameter must be an integer greater than or equal to 2, and must be less than or equal to the number of trials. The default number of folds is 10. For classifications with very few observations (e.g., less than 100 observations total), it may be wise to increase the number of folds so that more observations can be used for training in each fold. At the most extreme, the user can specify leave-one-out cross validation, where only one observation is withheld for testing in each fold, and therefore the number of folds is equal to the number of observations:

```
classifyEEG(X, Y, 'nFolds', length(Y));
```

'`classify`' — Specify classifier type (default 'SVM')
'`kernel`' — Specify decision function kernel for SVM classifier (default 'rbf')
'`numTrees`' - Specify number of decision trees in random Forest classifier (default is 128)

'minTreeLeaf' - Specify minimum number of observations per tree leaf (default is 1)
MatClassRSA currently supports three different classifiers:

- 'SVM': Support Vector Machine (default)
- 'LDA': Linear Discriminant Analysis
- 'RF', 'RandomForest': Random forest

SVM. Multi-class classification via Support Vector Machine (SVM) is performed using the LIBSVM library (Chang & Lin, 2011). SVM is the default classifier of MatClassRSA. When SVM is called, the user may additionally specify the input parameter 'kernel', which is a hyperparameter that determines the kernel to use for the decision function in SVM. 'kernel' will not do anything if a classifier other than SVM is used for the classification.

Below are the acceptable kernels:

- 'linear'
- 'polynomial'
- 'rbf' (radial basis function — default)
- 'sigmoid'

For example, to call the SVM classifier with a linear kernel:

```
classifyEEG(X, Y, 'classify', 'SVM', 'kernel', 'linear');
```

LDA. Multiclass Linear Discriminant Analysis (LDA) is computed using the fitcdiscr function in Matlab. For example,

```
classifyEEG(X, Y, 'classify', 'LDA');
```

Random Forest. MatclassRSA uses the Treebagger function in Matlab for Random Forest classification. Our classifyEEG function allows for the tuning of the following hyperparameters:

- 'numTrees': Number of bagged classification trees to use in the ensemble (default 128).
- 'minLeafSize': Minimum number of observations per tree leaf (default 1).

For example, to use the Random Forest classifier with 50 trees and minimum 2 observations per tree leaf, the user would call the classifier as

```
classifyEEG(X, Y, 'classify', 'RandomForest',...
      'numTrees', 50, 'minLeafSize', 2);
```

'pValueMethod' — Specify which method to calculate p-value (default 'binomcdf')
'permutations' — Specify how many permutation iterations to perform if doing a permutation test (default 1000).

We provide 3 ways to compute the p-value of the classification:

- 'binomcdf' (default)

- 'permuteTestLabels'
- 'permuteFullModel'

Binomial distribution. The default 'binomcdf' option uses the classification accuracy and number of test trials per fold to estimate the probability of attaining the mean classifier accuracy under the null hypothesis of the binomial distribution (number of successes *n* in *k* attempts). Since 'binomcdf' requires results from only one classification attempt, this is the fastest way to compute p-value. However, this method is not recommended if there exists a high imbalance of observations for each class, or if each test fold contains an insufficient number of observations. Therefore, as a rule of thumb we recommend using this approach with at least 100 observations total, which are split among no more than 10 cross-validation folds (i.e., at least 10 observations in each test partition).

The latter two options conduct permutation testing, in which the number of permutations is determined by the value passed in for the 'permutations' parameter, *N*. This parameter is ignored if the 'binomcdf' option is used.

Permute test labels only. With the 'permuteTestLabels' option, we perform *k*-fold cross validation only once. In each fold, the classification model is trained on the intact data and labels, but predictions are made on test observations whose labels have been shuffled. The prediction is repeated *N* times, with the test labels re-randomized for each attempt. The 'permuteTestLabels' option is the second fastest method, since it requires training the *k* models only once, but a total of *k***N* prediction operations are performed. So that there are enough test labels to randomize in each fold, here we also recommend having at least 100 observations total, and no more than 10 cross-validation folds.

Permute full classifier models. With the 'permuteFullModel' option, we perform the entire 10-fold cross validation *N* times. For each of the *N* permutation iterations, the entire labels vector (training and test observations) is shuffled, and in each fold, the classifier model is both trained and tested using the shuffled labels. As the full classification procedure is performed *N* times, the 'permuteFullModel' option is the slowest, but is suitable to use with any classifier configuration, including settings with unbalanced classes, few observations, and up to *N*-fold cross validation.

Outputs

'CM' — Classifier confusion matrix

The confusion matrix summarizes the performance of the classifier. For MatClassRSA confusion matrices, rows represent actual labels while columns represent predicted labels. Element *i*, *j* in the confusion matrix therefore represents the number of observations belonging to class *i* that the classifier labeled as belonging to class *j*. The sum of the values of the confusion matrix

represents the total number of observations classified. Values along the diagonal (*i*=*j*) represent correct classifications.

'accuracy' — Classifier accuracy

The classifier accuracy is the proportion of classification attempts that were correct. Accuracies are returned as values between 0 and 1 (1 representing 100% accuracy). The accuracy is computed as the total proportion of classifications that were correct (i.e., sum of the diagonal of the confusion matrix divided by the sum of the confusion matrix). Note that for classifications involving unbalanced classes, this manner of computation may not be ideal, and the user may rather prefer to compute a per-class accuracy by normalizing each row of the confusion matrix by the total observations belonging to that class (sum of the row).

'predY' — Predicted labels

This is a vector of predicted labels, in the same order as the input vector `Y`. This vector may be useful for further analyses comparing performance of different classifiers.

'pVal' — *p*-value of the classification

Scalar value of the p-value computed according to parameters '`pValueMethod`' and '`permutations`', as specified above.

'classifierInfo' — Configuration option checklist

This is a struct containing all of the parameters and their respective values that were used for classification.

'accDist' - permutation test accuracy distribution

This is a vector containing all the accuracies computed in the permutation test. Therefore, this output argument only has a valid value if either '`permuteTestLabels`' or '`permuteFullModel`' is passed in for the parameter '`pValueMethod`'. If '`binomcdf`' is passed in, then this output will be NaN.

'modelsConcat' - Vectorized classification models

For *k*-fold cross validation, the *k* number of classification models are saved and output in this struct variable. Note that the models will be different objects depending on the classifier chosen, for example, SVM saves its model into a struct, LDA saves its model into a *ClassificationDiscriminant* object, and RF saves its model into a *TreeBagger* object.

Computing Representational Dissimilarity Matrices: `computeRDM`

Classifier confusions can be thought of as measures of similarity among the brain responses, which can then be related to similarities among the stimuli. That is, similar stimuli may bring about similarities in certain features of the EEG responses; and more similar responses will be more difficult for the classifier to differentiate. Along these lines, the confusion matrix output by a classifier can be treated as a similarity matrix, which can then be converted to a distance matrix, or Representational Dissimilarity Matrix (RDM), and subsequently used in RSA-style analyses.

Usage

```
RDM = computeRDM(CM, Name, Value);
```

Required Input

Computation of the RDM requires only one input, the matrix `CM`. We anticipate that for users of this toolbox, the input matrix will typically be the confusion matrix from a classification; however, as documented below, users can input any generalized proximity matrix (including correlation matrices, pairwise classifier accuracies, and pairwise similarity/distance ratings), and use the optional name-value pair arguments to customize the RDM computation procedure.

'`CM`' — Input matrix

The `CM` matrix is a square matrix for which element *i*, *j* contains a pairwise similarity or distance measure of *i* and *j*. As input, the matrix need not be symmetric and need not contain values on the diagonal. If inputting a confusion matrix from outside of MatClassRSA, the user should ensure that the format is consistent with this toolbox, with rows representing actual class, and columns the predicted class.

Optional Inputs (name-value pair arguments)

The following optional name-value pair arguments reflect the order of operations for computing the RDM: Normalization, then symmetrization, conversion to distance, and finally conversion to rank or percentile rank distance.

'`normalize`' — Normalization of matrix rows (default 'diagonal')

This function normalizes a matrix by dividing each row of the matrix by its sum (giving an estimated conditional probability matrix; element *i*, *j* becoming interpretable as P(*j*|*i*)), by the value of the respective diagonal element in that row (scaling every element in relation to a unity self-similarity measure for every class), or with no normalization. Normalization options are as follows:

- ‘`diagonal`’: Divide every row of the matrix by the respective diagonal element for that row (e.g., element *2,2* for row 2; element *9,9* for row 9) (default).
- ‘`sum`’: Divide every row of the matrix by the sum of that row.
- ‘`none`’: Do not normalize the matrix.

Note: In the present version of the software, specifying ‘`diagonal`’ or ‘`sum`’ when the operation will produce a divisor of zero (e.g., zero on the diagonal or sum of row being zero) will currently produce an error. The user might consider adding a small offset to avoid these errors. A fix will be introduced in a future version of the software.

‘`symmetrize`’ — Symmetrize the matrix (default ‘average’)

As input matrices need not be symmetric, this operation provides several options for doing so. The result is that element *i,j* of the matrix will be equal to element *j,i*. The following symmetrization options are supported:

- ‘`average`’: Compute arithmetic mean, x_out = (x_in + x_in^T) / 2. This is the default.
- ‘`geometric`’: Compute geometric mean, x_out = sqrt(x_in .* x_in^T).
- ‘`harmonic`’: Compute harmonic mean, x_out = 2 * x_in .* x_in^T ./ (x_in + x_in^T).
- ‘`none`’: Do not symmetrize the matrix.

‘`distance`’ — Convert similarities to distances (default ‘linear’)
‘`distpower`’ — Additional input parameter for ‘power’ or ‘log’ distance calculation (default 1)

After normalization and symmetrization, the matrix of similarities can be converted to distances. MatClassRSA currently offers four options for computing distances:

- ‘`linear`’: Compute linear distance, x_out = 1 - x_in. This is the default.
- ‘`power`’: Compute power distance, x_out= 1- x_in.^`distpower`**
- ‘`logarithmic`’: Compute log distance,
  x_out = 1 - log2(`distPower` * xIn + 1) ./ log2(`distPower` + 1)**
- ‘`none`’: Do not convert matrix values from similarities to differences.

**If using the ‘`power`’ or ‘`logarithmic`’ parameters, the user can additionally specify the power parameter with the name-value pair ‘`distpower`’ (the value is an integer, default 1). For example, to use power distance with a power of 2, call the function as follows:

```
RDM = computeRDM(CM, 'distance', 'power', 'distpower', 2);
```

‘`rankdistances`’ — Compute rank or percentile rank of distances (default ‘none’)

Ranked correlations are sometimes preferred for comparing multiple RDMs. Therefore, this function offers three options for converting distances to ranked distances.

- ‘`none`’: Do not convert distances to rank distances. This is the default.

- ‘rank’: Convert distances to rank distances (uses tied ranks).
- ‘percentrank’: Convert distances to percentile rank distances.

Examples

Compute RDM from MatClassRSA confusion matrix, using all default parameters (normalize using diagonal; symmetrize with arithmetic mean; linear distance computation; no ranks):

```
RDM = computeRDM(CM);
```

Compute RDM with no normalization, symmetrize with geometric mean, power 2 distance computation, and rank distance (e.g., input matrix is pairwise similarity ratings):

```
RDM = computeRDM(CM, ‘normalize’, ‘none’, ‘symmetrize’,...
      ‘geometric’, ‘distance’, ‘power’, ‘distpower’, 2,...
      ‘rankdistances’, ‘rank’);
```

Compute RDM with no normalization or symmetrization; linear distance computation, and percent rank (e.g., input matrix is pairwise correlation matrix):

```
RDM = computeRDM(CM, ‘normalize’, ‘none’,...
      ‘symmetrize’, ‘none’, ‘rankdistances’, ‘percentrank’);
```

computeEuclideanRDM

Compute an RDM using the cross-validated Euclidean distance similarity metric.

Usage

```
RDM = computeEuclideanRDM(X, Y, num_permutations, rand_seed);
```

Required Input

'X' — Input data matrix
The `X` matrix contains the EEG data used for training and testing during classification. The `X` matrix is passed into the function as a 2D feature-by-trials matrix. A typical use case would be to provide a 2D matrix with dimensions of: nSpace-by-nTrials.

'Y' — Labels vector
The `Y` vector contains the numeric labels corresponding to each trial in the EEG data matrix `X`. Both row and column vectors will be accepted. The length of `Y` must correspond to the size of `X` along the trial dimension.

'num_permutations' — Number of random permutations along the trial dimension to acquire train and test partitions
The `num_permutations` argument contains an integer that describes the number of times to randomly sample the trials for the train and test set. If this is not entered, the default number of permutations is 10.

Optional Inputs

'rand_seed' — Random seed for reproducibility
The `rand_seed` argument is an integer that allows the user to control the reproducibility of the computed reliabilities.

computePearsonRDM

Compute an RDM using the cross-validated Pearson correlation similarity metric.

Usage

```
RDM = computePearsonRDM(X, Y, num_permutations, rand_seed);
```

Required Input

'X' — Input data matrix
The `X` matrix contains the EEG data used for training and testing during classification. The `X` matrix is passed into the function as a 2D feature-by-trials matrix. A typical use case would be to provide a 2D matrix with dimensions of: nSpace-by-nTrials.

'Y' — Labels vector
The `Y` vector contains the numeric labels corresponding to each trial in the EEG data matrix `X`. Both row and column vectors will be accepted. The length of `Y` must correspond to the size of `X` along the trial dimension.

'num_permutations' — Number of random permutations along the trial dimension to acquire train and test partitions
The `num_permutations` argument contains an integer that describes the number of times to randomly sample the trials for the train and test set. If this is not entered, the default number of permutations is 10.

Optional Inputs

'rand_seed' — Random seed for reproducibility
The `rand_seed` argument is an integer that allows the user to control the reproducibility of the computed reliabilities.

Visualization Functions: `plotMatrix`, `plotMDS`, `plotDendrogram`, `plotMST`

Visualizations of the distance matrices computed in the previous section can reveal information about the structure of the stimuli as they are represented in the brain response. MatClassRSA offers four such visualizations: Visualization of a confusion matrix/RDM, dendrogram plot, multidimensional scaling (MDS), and minimum spanning tree (MST). The latter three visualizations in particular may bring to light stimulus clusters that are not immediately evident from visualization of the confusion matrix alone.

Plot Distance Matrix/Confusion Matrix

To visualize distance matrices or confusion matrices, we use the `plotMatrix()` function.

Usage

```
img = plotMatrix(matrix, varargin)
plotMatrix(matrix, varargin)
```

Required Input

'`RDM`' — Input matrix

RDM - a relational dissimilarity matrix, either computed from the MatClassRSA `computeRDM` function or acquired externally.

Optional Inputs (name-value pair arguments)

'`axisColors`' — Label each class using colored squares (default 'black')

This parameter can be used in conjunction with '`axisLabels`' (below) to display color-coded labels. Colors should be passed in via a cell array of either color abbreviations, full-length color names, or RGB color triplets.

For example, to set node colors with standard Matlab color abbreviations:

```
plotMatrix(RDM, 'axisColors', {'y' 'm' 'c' 'r'})
```

To set node colors using full-length color names:

```
plotMatrix(RDM, 'axisColors', {'yellow' 'magenta' 'cyan'
'red'})
```

To set node colors using RGB triplets:

```
plotMatrix(RDM, 'axisColors',...
     {'[1 1 0]' '[1 0 1]' '[0 1 1]' '[1 0 0]'})
```

'axisLabels' — Label each class using text (default class numbers)

This parameter, used in conjunction with 'axisColors' (above), will display color-coded labels. Labels should be passed in via a cell array, where each element in the cell array is a char array representing the string label. For example,

```
plotMatrix(RDM, 'axisLabels', {'a', 'b', 'c', 'd'})
```

'iconPath' - Label each class using .jpeg or .png files.

This parameter specifies a directory location in which category labels are stored, *in the same order in which the classes are ordered*. The path should be passed in as the relative or absolute location of the file containing the images. Images will be automatically resized to a square shape. For example,

```
plotMatrix(RDM, 'iconPath', '../Figs/')
```

'colorMap' - Overall color scheme of the plot

This parameter can be used to call a default Matlab colormap, or one specified by the user, to change the overall look of the plot. For example,

```
plotMatrix(RDM, 'colorMap', 'hsv')
```

'colorBar' - Choose whether to display colorbar or not (default 0)

Set this parameter to 0 to hide, or 1 to show.

'matrixLabels' - Print matrix values in cells (default 1)

Use this parameter to choose whether or not to display values for each square in the matrix. Ignore parameter to turn off, enter any value to turn on.

'FontSize' - Font size of matrix and axis labels

Enter a numeric value to specify the font size of the matrix labels and the axis labels.

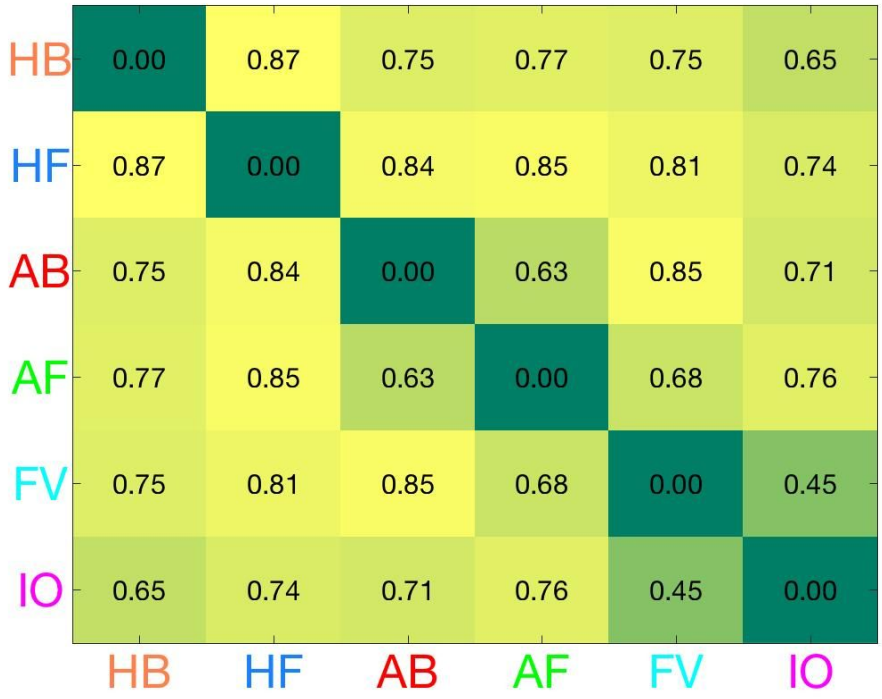


Figure: Example RDM visualization.

Plot Dendrogram

Dendrograms are commonly used to illustrate the hierarchical clustering of a dataset. MatClassRSA supports agglomerative clustering, the “bottom-up” approach in which each observation (or class, in this case), starts as a cluster, and each pair of clusters are subsequently merged in each level until all the observations form one cluster altogether.

Usage

```
img = plotDendrogram(matrix, varargin)
plotDendrogram(matrix, varargin)
```

Required Input

‘RDM’ — Input matrix

RDM - a relational dissimilarity matrix, either computed from the MatClassRSA `computeRDM` function or acquired externally.

Optional Inputs (name-value pair arguments)

‘distMethod’ - Cluster distance computation (default ‘average’)

Choose algorithm to compute distance between clusters. The toolbox currently offers the following options:

- 'average': Unweighted average distance (UPGMA). This is the default.
- 'centroid': Centroid distance (UPGMC), appropriate for Euclidean distances only
- 'complete': Furthest distance
- 'median': Weighted center of mass distance (WPGMC), appropriate for Euclidean distances only
- 'single': Shortest distance
- 'ward': Inner squared distance (minimum variance algorithm), appropriate for Euclidean distances only
- 'weighted': Weighted average distance (WPGMA)

‘nodeColors’ — Label each class using colored squares (default ‘black’)

This parameter can be used in conjunction with ‘nodeLabels’ (below) to display color-coded labels. Colors should be passed in via a cell array of either color abbreviations, full-length color names, or RGB color triplets.

For example, to set node colors with standard Matlab color abbreviations:

```
plotDendrogram(RDM, ‘nodeColors’, {‘y’ ‘m’ ‘c’ ‘r’})
```

To set node colors using full-length color names:

```
plotDendrogram(RDM, ‘nodeColors’,...
     {‘yellow’ ‘magenta’ ‘cyan’ ‘red’})
```

To set node colors using RGB triplets:

```
plotDendrogram(RDM, ‘nodeColors’,...
     {‘[1 1 0]’ ‘[1 0 1]’ ‘[0 1 1]’ ‘[1 0 0]’})
```

‘nodeLabels’ — Label each class using text (default class number)

This parameter, used in conjunction with ‘nodeColors’ (above), will display color-coded labels. Labels should be passed in via a cell array, where each element in the cell array is a char array representing the string label. For example,

```
plotDendrogram(RDM, ‘nodeLabels’, {‘a’, ‘b’, ‘c’, ‘d’})
```

‘iconPath’ - Label each class using .jpeg or .png files.

This parameter specifies a directory location in which category labels are stored, *in the same order in which the classes are ordered*. The path should be passed in as the relative or absolute

location of the file containing the images. Images will be automatically resized to a square shape. For example,

```
plotDendrogram(RDM, 'iconPath', '../Figs/')
```

'orientation' - Dendrogram orientation (default 'down')

This parameter lets the user specify which direction to point the dendrogram (orientation defined here as the side that contains the dendrogram leaves).

- 'down' (default)
- 'up'
- 'left'
- 'right'

'reorder' - Specify order of classes in the dendrogram

This parameter allows the user to pass in an array that contains the preferred order of classes in the dendrogram display. This may cause overlapping dendrograph lines.

'yLim' - Set range of the Y-axis.

Pass in as an array of length 2, `[yMin yMax]`.

'textRotation' - Rotate text (default 0)

Set this parameter to an amount in degrees to rotate the text.

'lineWidth' - Line width

Use this parameter to set the width of the lines in the dendrogram.

'lineColor' - Line color

Use this parameter to set the color of the lines in the dendrogram. Similar to 'nodeColors', we can either pass in color abbreviations, full-length color names, or RGB color triplets.

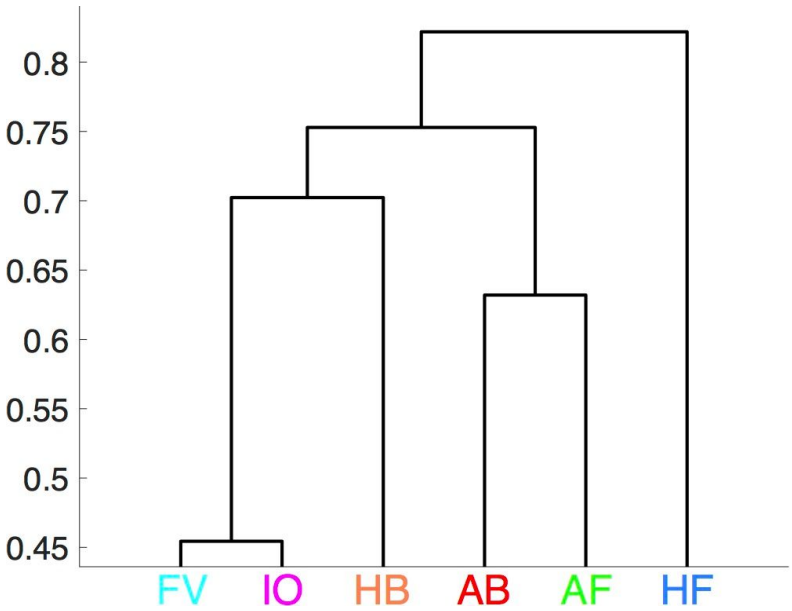


Figure: Example dendrogram.

Multidimensional Scaling (MDS) Plot

Multidimensional scaling is a visualization technique that projects the distances among items in a set to a lower-dimensional subspace for visualization. In the context of MatClassRSA, MDS will be used to visualize similarity between stimulus categories, as represented by the classifier confusions of the brain response.

Usage

```
img = plotMDS(matrix, varargin)
plotMDS(matrix, varargin)
```

Required Input

'`RDM`' — Input matrix

RDM - a relational dissimilarity matrix, either computed from the MatClassRSA `computeRDM` function or acquired externally.

Optional Inputs (name-value pair arguments)

'`nodeColors`' — Label each class using colored squares (default black)

This parameter can be used in conjunction with 'nodeLabels' (below) to display color-coded labels. Colors should be passed in via a cell array of either color abbreviations, full-length color names, or RGB color triplets.

For example, to set node colors with standard Matlab color abbreviations:

```
plotMDS(RDM, 'nodeColors', {'y' 'm' 'c' 'r'})
```

To set node colors using full-length color names:

```
plotMDS(RDM, 'nodeColors',...
     {'yellow' 'magenta' 'cyan' 'red'})
```

To set node colors using RGB triplets:

```
plotMDS(RDM, 'nodeColors',...
     {'[1 1 0]' '[1 0 1]' '[0 1 1]' '[1 0 0]'})
```

'nodeLabels' — Label each class using text (default class number)

This parameter, used in conjunction with 'nodeColors' (above), will display color-coded labels. Labels should be passed in via a cell array, where each element in the cell array is a char array representing the string label. For example,

```
plotMDS(RDM, 'nodeLabels', {'a', 'b', 'c', 'd'})
```

'iconPath' - Label each class using .jpeg or .png files.

This parameter specifies a directory location in which category labels are stored, *in the same order in which the classes are ordered*. The path should be passed in as the relative or absolute location of the file containing the images. Images will be automatically resized to a square shape. For example,

```
plotMDS(RDM, 'iconPath', '../Figs/')
```

'dimensions' - Choose which MDS dimensions to display (default [1 2])

This parameter takes in a vector of length 2, with the first value being the x-axis dimension, the second being the y-axis dimension. There will be *n* number of dimensions, with *n* being the number of classes (or the number of rows in RDM). Dimension 1 provides the highest-variance separation of data, with n providing the lowest.

'xLim' - Set range of the X-axis

This parameter takes in an array of length 2, `[xMin xMax]`.

'yLim' - Set range of the Y-axis

This parameter takes in an array of length 2, `[yMin yMax]`.

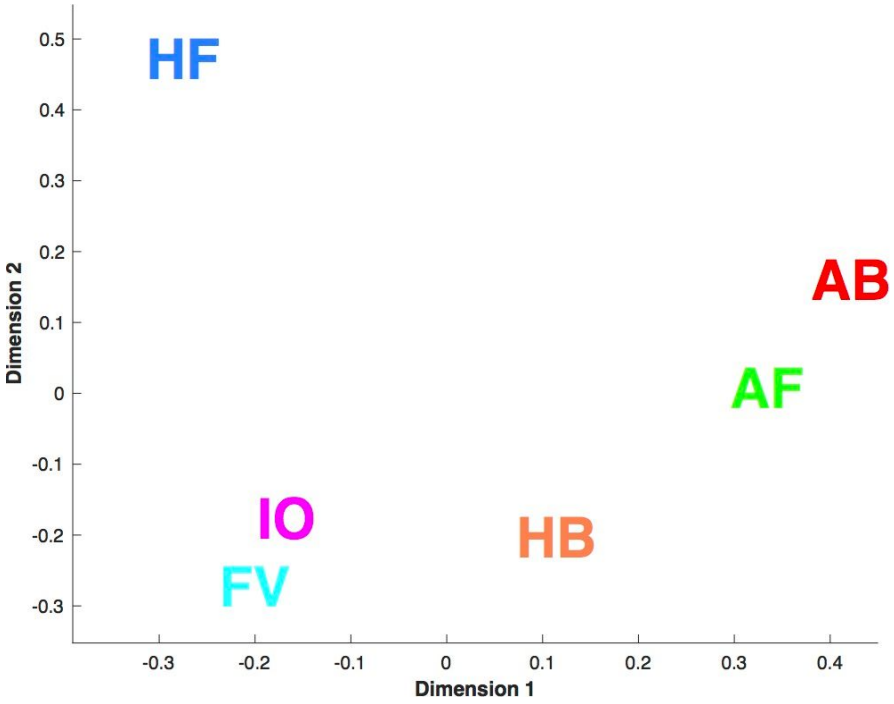


Figure: Example MDS plot.

Minimum Spanning Tree (MST) Plot

Minimum Spanning Trees are graphs that contain nodes representing each instance of a dataset, with the edges that have the shortest possible cumulative distance with all of the nodes in the graph being connected.

Usage

```
img = plotMST(matrix, varargin)
plotMST(matrix, varargin)
```

Required Input

'RDM' — Input matrix

RDM - a relational dissimilarity matrix, either computed from the MatClassRSA `computeRDM` function or acquired externally.

Optional Inputs (name-value pair arguments)

'nodeColors' — Label each class using colored squares (default black)

This parameter can be used in conjunction with 'nodeLabels' (below) to display color-coded labels. Colors should be passed in via a cell array of either color abbreviations, full-length color names, or RGB color triplets.

For example, to set node colors with standard Matlab color abbreviations:

```
plotMST(RDM, 'nodeColors', {'y' 'm' 'c' 'r'})
```

To set node colors using full-length color names:

```
plotMST(RDM, 'nodeColors',...
     {'yellow' 'magenta' 'cyan' 'red'})
```

To set node colors using RGB triplets:

```
plotMST(RDM, 'nodeColors',...
     {'[1 1 0]' '[1 0 1]' '[0 1 1]' '[1 0 0]'})
```

'nodeLabels' — Label each class using text (default class number)

This parameter, used in conjunction with 'nodeColors' (above), will display color-coded labels. Labels should be passed in via a cell array, where each element in the cell array is a char array representing the string label. For example,

```
plotMST(RDM, 'nodeLabels', {'a', 'b', 'c', 'd'})
```

'iconPath' - Label each class using .jpeg or .png files.

This parameter specifies a directory location in which category labels are stored, *in the same order in which the classes are ordered*. The path should be passed in as the relative or absolute location of the file containing the images. Images will be automatically resized to a square shape. For example,

```
plotMST(RDM, 'iconPath', '../Figs/')
```

'edgeLabelSize' - Size of labels on each edge (default 15)

Use this parameter to adjust the text size of the labels on each edge of the minimum spanning tree.

'nodeLabelSize' - Size of labels on each node (default 15)

Use this parameter to adjust the text size of the labels on each node of the minimum spanning tree.

‘`nodeLabelRotation`’ - Degrees of rotation for node labels (default 50)

Use this parameter to specify text rotation, in degrees, of the node labels.

‘`roundEdgeLabel`’ - Number of significant figures for edge label display (default 4)

Use this parameter to specify the number of significant figures by which edge labels should be rounded.

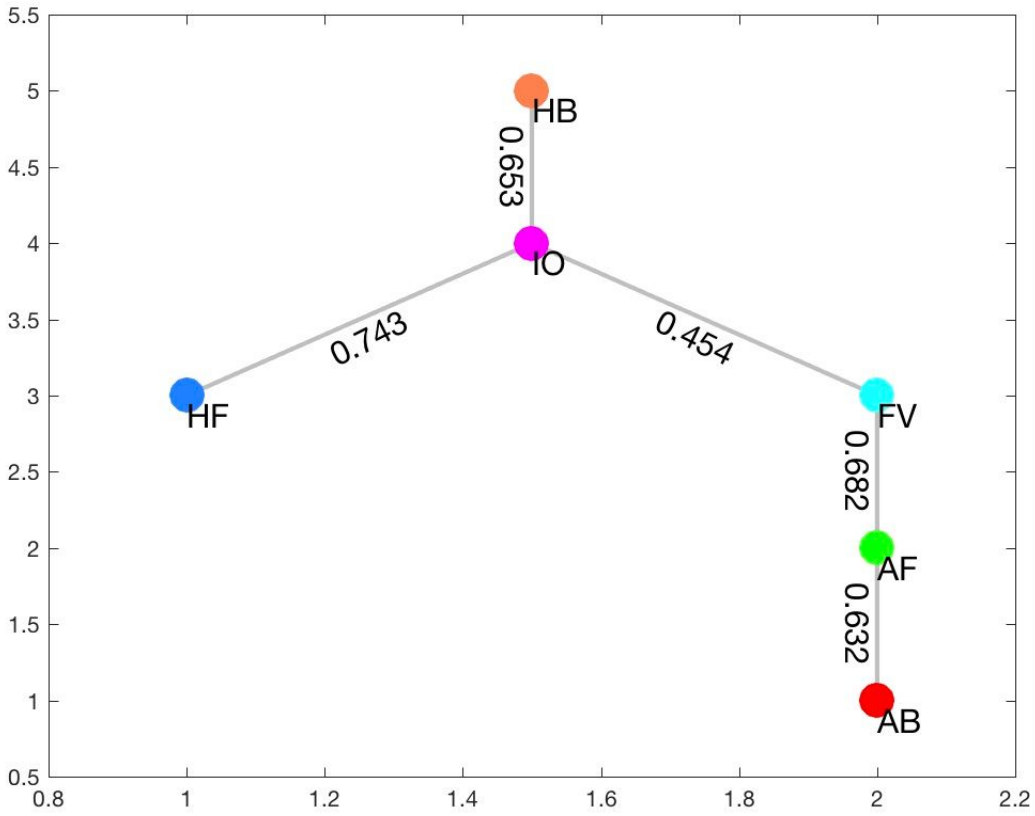


Figure: Example minimum spanning tree.

Selected References

M/EEG classification in cognitive neuroscience

Carlson, T., Tovar, D. A., Alink, A., & Kriegeskorte, N. (2013). Representational dynamics of object vision: the first 1000 ms. Journal of vision, 13(10), 1-1.

Cichy, R. M., Pantazis, D., & Oliva, A. (2014). Resolving human object recognition in space and time. Nature neuroscience, 17(3), 455-462.

Kaneshiro, B., Guimaraes, M. P., Kim, H. S., Norcia, A. M., & Suppes, P. (2015). A representational similarity analysis of the dynamics of object processing using single-trial EEG classification. PloS one, 10(8), e0135697.

Perreau Guimaraes, M., Wong, D. K., Uy, E. T., Grosenick, L., & Suppes, P. (2007). Single-trial classification of MEG recordings. *IEEE Transactions on Biomedical Engineering*, *54*(3), 436-443.

Philiastides, M. G., & Sajda, P. (2006). Temporal characterization of the neural correlates of perceptual decision making in the human brain. *Cerebral cortex*, *16*(4), 509-518.

Schaefer, R. S., Farquhar, J., Blokland, Y., Sadakata, M., & Desain, P. (2011). Name that tune: decoding music from the listening brain. *NeuroImage*, *56*(2), 843-849.

Stober, S., Cameron, D. J., & Grahn, J. A. (2014). Classifying EEG Recordings of Rhythm Perception. *Proceedings of the 15th International Society for Music Information Retrieval Conference (ISMIR)*, 649-654.

Classification

Breiman, L. (2001). Random forests. *Machine learning*, *45*(1), 5-32.

Chang, C. C., & Lin, C. J. (2011). LIBSVM: a library for support vector machines. *ACM transactions on intelligent systems and technology (TIST)*, *2*(3), 27.

Cortes, C., & Vapnik, V. (1995). Support-vector networks. *Machine learning*, *20*(3), 273-297.

Fisher, R. A. (1936). The use of multiple measurements in taxonomic problems. *Annals of human genetics*, *7*(2), 179-188.

Representational Similarity Analysis

Kriegeskorte, N., Mur, M., Ruff, D. A., Kiani, R., Bodurka, J., Esteky, H., Tanaka, T., & Bandettini, P. A. (2008). Matching categorical object representations in inferior temporal cortex of man and monkey. *Neuron*, *60*(6), 1126-1141.

Kriegeskorte, N., Mur, M., & Bandettini, P. (2008). Representational similarity analysis–connecting the branches of systems neuroscience. *Frontiers in systems neuroscience*, *2*.

Nili, H., Wingfield, C., Walther, A., Su, L., Marslen-Wilson, W., & Kriegeskorte, N. (2014). A toolbox for representational similarity analysis. *PLoS computational biology*, *10*(4), e1003553.