

Package ‘HMLET’

December 6, 2023

Type Package

Title What the Package Does (Title Case)

Version 0.1

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Description MLET uses machine learning algorithm to analyze Eye-Tracking data.

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Imports combinat,

dplyr,
ggplot2,
miceadds,
purrr,
reshape2,
rray,
stats,
tidyr,
vdiff

Suggests testthat (>= 3.0.0)

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Config/testthat/edition 3

Encoding UTF-8

LazyData true

RoxygenNote 7.2.3

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ClusterStats_HMLET	<i>Adds cluster statistics to t value dataframe, includes all info for all tests.</i>
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Description

Adds cluster statistics to t value dataframe, includes all info for all tests.

Usage

```
ClusterStats_HMLET(data, paired = T, detailed = F, threshold_t = NULL)
```

Arguments

data	data frame with temporal data for permutation tests routine, output from PermutationTestDataPrep_HMLET.R.
paired	optional boolean to control T-tests. True is for statistical comparisons in paired mode, False for a two-sample T-Test; defaults to True.
detailed	optional boolean to include cluster statistics and t value statistics within one dataframe. Defaults to False to populate dataframe only with cluster statistics.
threshold_t	optional probability threshold for statistical comparison computed based on number of subjects. alpha = 0.025.

Value

returns data frame with cluster statistics

`ComputeSubjectLevelPerm_HMLET`*Provides unique permutation indices within each subject.*

Description

Provides unique permutation indices within each subject.

Usage

```
ComputeSubjectLevelPerm_HMLET(labels, n = 1)
```

Arguments

<code>labels</code>	labels from the data frame.
<code>n</code>	optional integer for number of permutations to resample data.

Value

labels of unique permutation indices to use for subject level permutation test.

`ComputeTValues_HMLET` *Compute t values for permutation tests.*

Description

Compute t values for permutation tests.

Usage

```
ComputeTValues_HMLET(respTime, paired = TRUE)
```

Arguments

<code>respTime</code>	dataframe for responses in temporal order.
<code>paired</code>	optional boolean to control T-tests. True is for statistical comparisons in paired mode, False for a two-sample T-Test; defaults to True.

Value

t values in the format of a data frame.

CreateTimeBinData_HMLET

Collapse time points in specified time bins.

Description

Collapse time points in specified time bins.

Usage

```
CreateTimeBinData_HMLET(
  data,
  groupingColumns = NULL,
  timeBinWidth = 250,
  timeMax = 3000,
  FixatedOn,
  timePoint = "timeStamp",
  AOIs = NULL,
  timeForward = T,
  aggregateFun = mean
)
```

Arguments

data	dataframe containing temporal data.
groupingColumns	optional array of strings for column names of variables to be grouped, defaults to NULL.
timeBinWidth	optional integer specified time interval for time bins, defaults to 250.
timeMax	optional integer for maximum time in temporal order, samples are left out if duration is longer. Defaults to 3000.
FixatedOn	string for column name of specific AOI in dataframe to be fixated on.
timePoint	optional string representing column name for time Stamps, defaults to "timeStamp".
AOIs	optional array of strings representing column names for areas of interest, defaults to NULL.
timeForward	optional boolean to sort timebins, defaults to True for ascending order.
aggregateFun	optional function for aggregation, defaults to mean.

Value

temporal data with sorted time points into time bins.

ExportDataForGUI_HMLET

ExportDataForGUI_HMLET Export samples of trial with maximum time point to CSV file for MATLAB GUI.

Description

ExportDataForGUI_HMLET Export samples of trial with maximum time point to CSV file for MATLAB GUI.

Usage

```
ExportDataForGUI_HMLET(
    data,
    ID = "ID",
    trial = "trial",
    timePoint = "timePoint",
    timeMax = NULL,
    dataPointDuration,
    response,
    fixation,
    condition,
    testName = NULL,
    gazeX,
    gazeY,
    gazeXRelative = NULL,
    gazeYRelative = NULL,
    miscVars = NULL,
    fileName = "HMLET_DataforGUI.csv",
    path = getwd()
)
```

Arguments

data	dataframe containing temporal data.
ID	optional string for column name that represents IDs within data frame, defaults to "ID."
trial	string for column name that represents trials within data frame, for example "TrialNum."
timePoint	string for column name that represents time intervals, for example "timeStamp."
timeMax	optional integer for maximum time in temporal order, samples are left out if duration is longer. Default is NULL
dataPointDuration	optional integer or character for specified duration of samples, used for time bins in CreateTimeBinData_HMLET.
response	the column in which participants' responses are stored e.g., HIT, Miss, FA, and CR.
fixation	data for specific AOI in dataframe to be fixated on. #TODO: ASK
condition	string for column name that specifies a condition within the data frame.

testName	optional string for name of data – used as condition name or test names to compare permutation test results between different tests/conditions later, defaults to NULL.
gazeX	integer X-coordinate of gaze point on the screen according to top left corner.
gazeY	integer Y-coordinate of gaze point on the screen according to top left corner.
gazeXRelative	optional integer X-coordinate of gaze point relative to an arbitrary center.
gazeYRelative	optional integer Y-coordinate of gaze point relative to an arbitrary center.
miscVars	optional list of strings containing column names of additional variables to be included in exported file
fileName	optional string for output csv file, defaults to "HMLET_DataforGUI.csv."
Path	optional path to identify the destination location default: current working directory

FindClusters_HMLET	<i>Cluster all samples whose t value is greater than threshold value by temporal adjacency.</i>
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Description

Cluster all samples whose t value is greater than threshold value by temporal adjacency.

Usage

```
FindClusters_HMLET(tValues, threshold_t = threshold_t)
```

Arguments

tValues	dataframe of t values calculated from ComputeTValues_HMLET.
threshold_t	optional probability threshold for statistical comparison, defaults to NA and will be computed based on number of trials when "between trials permutation" is called or will be computed based on number of subjects when "between subjects permutation" is called. Alpha = 0.025.

Value

t value dataframe with appended cluster information.

GenerateRandomData_HMLET

Generate unique random permutations To be completed

Description

Generate unique random permutations To be completed

Usage

```
GenerateRandomData_HMLET(
  tMax = 20,
  effectOffset = 5,
  trialNum = 40,
  subjNum = 20,
  effectSize = 0.2
)
```

PermutationTestDataPrep_HMLET

Return a data frame compatible for permutation tests routine.

Description

Return a data frame compatible for permutation tests routine.

Usage

```
PermutationTestDataPrep_HMLET(
  data,
  ID = "ID",
  trial,
  timePoint,
  condition,
  gazeMeasure,
  conditionLevels = NULL,
  targetAOI = NULL,
  testName = NULL,
  timeBinName = NULL
)
```

Arguments

data	data frame with temporal data for permutation tests routine.
ID	optional string for column name that represents IDs within data frame, defaults to "ID".
trial	string for column name that represents trials within data frame.
timePoint	string for column name that represents time intervals.

condition	string for column name that specifies a condition within the data frame.
gazeMeasure	string for column name which includes numerical value of the gaze measure at each time point such as gaze proportion.
conditionLevels	optional array of string column names to denote all the values of conditions, defaults to NULL.
targetAOI	optional string for column name to focus on specific AOI, defaults to NULL.
testName	optional string for name of data – used as condition name or test names to compare permutation test results between different tests/conditions later, defaults to NULL.

Value

data frame compatible for permutation tests and other HMLET modules

PermutationTest_HMLET *Permutation Tests General Routine.*

Description

Permutation Tests General Routine.

Usage

```
PermutationTest_HMLET(
  data,
  samples = 2000,
  paired = T,
  permuteTrialsWithinSubject = F,
  threshold_t = NA
)
```

Arguments

data	data frame with temporal data for permutation tests routine, output from PermutationTestDataPrep_HMLET.R.
samples	optional integer for number of samples, defaults to 2000.
paired	optional boolean to control T-tests. True is for statistical comparisons in paired mode, False for a two-sample T-Test; defaults to True.
permuteTrialsWithinSubject	optional boolean to run permutation test pipeline for conducting permutation tests between trials or between subjects, defaults to False.
threshold_t	optional probability threshold for statistical comparison, defaults to NA and will be computed based on number of trials when "between trials permutation" is called or will be computed based on number of subjects when "between subjects permutation" is called. Alpha = 0.025.

Value

a list of permutation tests in which distribution of desired statistic under the null hypothesis is estimated in a large number of permutations of the original data

PlotNullDistribution_HMLET
Plot Null Distribution.

Description

Plot Null Distribution.

Usage

PlotNullDistribution_HMLET(resultList)

Arguments

resultList list of the dataframes that is already prepared by PrepareMLETData_HMLET or a list that is the result of PermutationTest_HMLET.

Value

null distribution plot handle.

PlotTemporalGazeTrends_HMLET
Plot temporal gaze trends.

Description

Plot temporal gaze trends.

Usage

```
PlotTemporalGazeTrends_HMLET(
  resultList,
  showDataPointProp = T,
  showOverallMean = "Point",
  gazePropRibbonAlpha = 0.1,
  clusterFillColor = "#CC9933",
  clusterFillAlpha = 0.5,
  pointSize = 1,
  pointAlpha = 0.7,
  pointFatten = 3,
  testNameOrder = NULL,
  conditionOrder = NULL,
  onlySignificantClusters = T,
  clusterData = NULL,
  yLabel = "Gaze Proportion",
  dataAxisLabel = "Data Points (%)",
  xLabel = "Time (ms)",
  lineWidthGazeProp = 1,
  lineWidthDataPointProp = 1,
```

```

        lineWidthOverallMean = 1,
        lineTypeOverallMean = "dotted",
        alphaOverallMean = 0.5,
        shapeCodeOverallMean = 1,
        tickSizeOverallMean = NULL
    )

```

Arguments

<code>resultList</code>	dataframe of the data that is already prepared by <code>PrepareMLETData_HMLET</code> or a list that is the result of <code>PermutationTest_HMLET</code> .
<code>showDataPointProp</code>	optional boolean to display data points on the axes, defaults to <code>True</code> .
<code>showOverallMean</code>	optional string to specify the overall mean. "Line" = to display a horizontal line on the y = average. "Point" to display overall average and range in a pointRange format. "none" to not display it, defaults to "Point".
<code>gazePropRibbonAlpha</code>	optional float to change opacity of gaze ribbon, defaults to 0.1.
<code>clusterFillColor</code>	optional string to change fill color of clustered data points, defaults to "#CC9933".
<code>clusterFillAlpha</code>	optional float to change opacity of clustered data points, defaults to 0.5.
<code>pointSize</code>	optional integer to change size of points on plot, defaults to 1.
<code>pointAlpha</code>	optional float to change opacity of points on plot, defaults to 0.7.
<code>pointFatten</code>	optional integer to change size of lines on plot, defaults to 3.
<code>testNameOrder</code>	specify order of test name labels, defaults to <code>NULL</code> .
<code>conditionOrder</code>	specify order of condition levels, defaults to <code>NULL</code> .
<code>onlySignificantClusters</code>	optional Boolean to plot only the significant clusters, defaults to <code>True</code> .
<code>clusterData</code>	data containing all clusters generated from <code>ClusterStats_HMLET</code> to display on plot, defaults to <code>NULL</code> .
<code>yLabel</code>	"Proportion" specify label for the y axis, defaults to "Gaze"
<code>dataAxisLabel</code>	Specify label for the second y axis on the right, defaults to "Data Points \(%\)".
<code>xLabel</code>	Specify label for the x axis, defaults to "Time \(\text{ms}\)"
<code>lineWidthGazeProp</code>	Specify line width for gaze proportion, defaults to 1.
<code>lineWidthDataPointProp</code>	Specify line width for data point numbers, defaults to 1.
<code>lineWidthOverallMean</code>	Specify line width for overall mean, defaults to 1.
<code>lineTypeOverallMean</code>	Specify line type for overall mean, defaults to "dotted".
<code>alphaOverallMean</code>	Specify alpha for overall mean, defaults to 0.5.
<code>shapeCodeOverallMean</code>	Specify the shape of the overall mean points when <code>showOverallMean = "Point"</code> , defaults to 1 \(\text{circle}\).

tickSizeOverallMean

Optional to specify where to plot the overall means when showOverallMean = "Point", defaults to NULL.

Value

a plot handle that visualizes the data from PrepareMLETData_HMLET or the list from Permutation-Test_HMLET.

PreprocessRawData_HMLET

*Pre-Process data to extract AOIs.
Creates a csv file that formats all data into a table.
Should be Completed later*

Description

Pre-Process data to extract AOIs.
Creates a csv file that formats all data into a table.
Should be Completed later

Usage

```
PreprocessRawData_HMLET(
  data,
  ID = "ID",
  trial = "trial",
  timePoint = "timePoint",
  GazeX = "GazeX_Relative",
  GazeY = "GazeY_Relative",
  AOINames = NULL,
  fileName = "ETDataforMATLAB.csv",
  path = getwd()
)
```

Arguments

data	dataframe containing temporal data.
ID	optional string for column name that represents IDs within data frame, defaults to "ID."
trial	string for column name that represents trials within data frame, for example "TrialNum."
timePoint	string for column name that represents time intervals, for example "timeStamp."
GazeX	# TODO: ASK
GazeY	# TODO: ASK
fileName	optional string for output csv file, defaults to "ETDataforMATLAB.csv."
path	specifies working directory of project.

RelativeViewingProportionLabels_HMLET

Label trials whether participant was disproportionately or equally looking toward items

Description

Label trials whether participant was disproportionately or equally looking toward items

Usage

```
RelativeViewingProportionLabels_HMLET(
  data,
  ID = "ID",
  trial,
  AOIName,
  comparingAOI = c("Target", "Lure"),
  targetAOI = "Target",
  dispropotionCriterion = 10
)
```

Arguments

data	data frame with temporal data for permutation tests routine.
ID	optional string for column name that represents IDs within data frame, defaults to "ID".
trial	string for column name that represents trials within data frame.
AOIName	string for column name which includes name of the AOI that the subject is looking at each timePoint.
comparingAOI	names of the two AOIs that are their looking proportion should be compared.
targetAOI	names of the two AOIs that are their looking proportion should be compared.
dispropotionCriterion	optional string for column name to focus on specific AOI, defaults to NULL.
testName	Name of this data – can be used as condition name or test names to compare permutation test results between different tests/conditions later

Value

data frame as original data with an extracolumn with labels

SubjectLevelPermutationTestWithin_HMLET

Conduct subject level permutation tests between trials.

Description

Conduct subject level permutation tests between trials.

Usage

```
SubjectLevelPermutationTestWithin_HMLET(
  data,
  samples = 2000,
  paired = T,
  threshold_t = NA
)
```

Arguments

data	data frame with temporal data for permutation tests routine, output from PermutationTestDataPrep_HMLET.R.
samples	optional number of resampling data, how many permutations needed.
paired	optional boolean to control T-tests. True is for statistical comparisons in paired mode, False for a two-sample T-Test; defaults to True.
threshold_t	optional probability threshold for statistical comparison computed based on number of subjects. alpha = 0.025.

Value

returns t value distribution presented in a data frame.

TrialLevelPermutationTestWithin_HMLET

Conduct trial level permutation tests between trials.

Description

Conduct trial level permutation tests between trials.

Usage

```
TrialLevelPermutationTestWithin_HMLET(
  data,
  samples = 2000,
  paired = T,
  threshold_t = NA
)
```

Arguments

data	data frame with temporal data for permutation tests routine, output from PermutationTestDataPrep_HMLET.R.
samples	optional number of resampling data, how many permutations needed.
paired	optional boolean to control T-tests. True is for statistical comparisons in paired mode, False for a two-sample T-Test; defaults to True.
threshold_t	optional probability threshold for statistical comparison computed based on number of trials. $\alpha = 0.025$.

Value

returns t value distribution presented in a data frame.

UniquePermutations_HMLET

Generate unique random permutations.

Description

Generate unique random permutations.

Usage

```
UniquePermutations_HMLET(listInput, n = 1)
```

Arguments

listInput	Arbitrary list.
n	An integer number indicating the number of permutations.

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