

Package ‘permutest’

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Title Permutation Tests for Time Series Data

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Description Helps you determine the analysis window to use when analyzing densely-sampled time-series data, such as EEG data, using permutation testing (Maris & Oostenveld 2007) <doi:10.1016/j.jneumeth.2007.03.024>. These permutation tests can help identify the timepoints where significance of an effect begins and ends, and the results can be plotted in various types of heatmap for reporting.

Depends R (>= 2.10), lmPerm

Imports plyr, ggplot2, viridis

Suggests doParallel, dplyr, tidyr, knitr

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Encoding UTF-8

LazyData true

RoxygenNote 6.1.1

BugReports <https://github.com/cvoeten/permutest/issues>

VignetteBuilder knitr

NeedsCompilation no

Repository CRAN

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MMN	<i>EEG data from Jager (in prep.). See the vignette for details.</i>
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Description

EEG data from Jager (in prep.). See the vignette for details.

Usage

```
data(MMN)
```

Format

A standard data frame.

permu.test	<i>Permutation tests for time series data.</i>
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Description

Permutation tests for time series data.

Usage

```
permu.test(formula, data, subset = NULL, parallel = FALSE,
  progress = "text", ...)
```

Arguments

formula	A formula of the following form: ‘outcome ~ predictors timepoint variables’. Multivariate outcomes (e.g. 32 EEG electrodes) are supported; use ‘cbind(Fp1,Fp2,etc) ~ predictors timepoint’.
data	The dataset referencing these predictors.
subset	If specified, will only analyze the specified subset of the data.
parallel	Whether to parallelize the permutation testing using plyr’s ‘parallel’ option. Needs some additional set-up; see the plyr documentation.
progress	A plyr ‘progress’ bar name, see the plyr documentation. Ignored if parallel=TRUE.
...	Other arguments to be passed to ‘aovp’.

Value

A dataframe of p-values.

Examples

```
# EEG data example using the MMN dataset

# Run permutation tests on all electrodes and timepoints, reporting p-values for the three
# manipulated factors
perms <- permu.test(cbind(Fp1,AF3,F7,F3,FC1,FC5,C3,CP1,CP5,P7,P3,Pz,P03,O1,Oz,O2,P04,P4,P8,CP6,CP2,
                        C4,FC6,FC2,F4,F8,AF4,Fp2,Fz,Cz) ~ dev*session | time,data=MMN)

# Run the tests in parallel on two CPU threads
# first, set up the parallel backend
library(doParallel)
cl <- makeCluster(2)
registerDoParallel(cl)
perms <- permu.test(cbind(Fp1,AF3,F7,F3,FC1,FC5,C3,CP1,CP5,P7,P3,Pz,P03,O1,Oz,O2,P04,P4,P8,CP6,CP2,
                        C4,FC6,FC2,F4,F8,AF4,Fp2,Fz,Cz) ~ dev*session | time,data=MMN,parallel=TRUE)
stopCluster(cl)

# Plot the results
plot(perms)
```

plot.permutes

Create a heatmap of the results of permutation testing.

Description

Create a heatmap of the results of permutation testing.

Usage

```
## S3 method for class 'permutes'
plot(x, type = c("F", "p", "w2"), breaks = NULL,
     ...)
```

Arguments

x	Output of permu.test. You may want to subset it if you want to simulate zooming in.
type	The quantity to plot; one of 'F' (default), 'p', or 'w2' (omega squared).
breaks	The granularity of the labels of the x axis. Pass 'unique(data[,2])' to get a tick for every timepoint. Combine this trick with subsetting of your dataset, and perhaps averaging over all your dependent variables, to 'zoom in' on your data to help you determine precisely where significance begins and stops to occur.
...	Other arguments, which will be ignored (the ellipsis is provided for consistency with the generic plot() method).

Value

A ggplot2 object containing a heatmap of p-values.

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