

# Package ‘permutest’

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**Title** Permutation Tests for Time Series Data

**Version** 1.0

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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)

**Imports** ggplot2, lmPerm, plyr, viridis

**Suggests** doParallel, dplyr, tidyr, knitr, rmarkdown

**License** FreeBSD

**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

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

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

**Usage**

```
data(MMN)
```

**Format**

A standard data frame.

permu.test

*Permutation tests for time series data.***Description**

Permutation tests for time series data.

**Usage**

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

**Arguments**

formula	A formula of the following form: <code>outcome ~ predictors   timepoint variable</code> . Multivariate outcomes (e.g. 32 EEG electrodes) are supported; use <code>cbind(Fp1, Fp2, etc) ~ predictors   timepoint</code> .
data	The dataset referencing these predictors.
subset	If specified, will only analyze the specified subset of the data.
type	One of 'anova' or 'regression'. The former runs an analysis of variance and returns F-values and p-values based on sums of squares. The latter runs a linear-regression analysis and returns t-values and p-values based on individual effects. When running ANOVA, it is advised to use orthogonal predictors, as type III sums of squares are used.
parallel	Whether to parallelize the permutation testing using plyr's <code>parallel</code> option. Needs some additional set-up; see the plyr documentation.
progress	A plyr <code>.progress</code> bar name, see the plyr documentation. Ignored if <code>parallel=TRUE</code> .
...	Other arguments to be passed to <code>aovp</code> .

**Value**

A data frame.

**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,PO3,O1,Oz,O2,PO4,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,PO3,O1,Oz,O2,PO4,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)

# t-values instead of F-values
perms <- permu.test(cbind(Fp1,AF3,F7,F3,FC1,FC5,C3,CP1,CP5,P7,P3,Pz,PO3,O1,Oz,O2,PO4,P4,
                          P8,CP6,CP2,C4,FC6,FC2,F4,F8,AF4,Fp2,Fz,Cz) ~ dev*session | time,data=MMN,
                    type='regression')
```

---

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", "t", "p", "w2", "beta"),
     breaks = NULL, ...)
```

**Arguments**

<code>x</code>	Output of <code>permu.test</code> . You may want to subset it if you want to simulate zooming in.
<code>type</code>	The quantity to plot. For ANOVA, the options are <code>'F'</code> (default), <code>'p'</code> , or <code>'w2'</code> (omega squared). For regression, the options are <code>'t'</code> (default), <code>'beta'</code> , or <code>'p'</code> . If multiple options are presented, only the first option found in the data frame is used.
<code>breaks</code>	The granularity of the labels of the x axis. Pass <code>'unique(data[,2])'</code> 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.
<code>...</code>	Other arguments, which will be ignored (the ellipsis is provided for consistency with the generic <code>plot()</code> method).

**Value**

A `ggplot2` object.