Package ‘opa’

Type Package
Title An Implementation of Ordinal Pattern Analysis
Version 0.3.6
Description Quantifies hypothesis to data fit for repeated measures
and longitudinal data, as described by Thorngate (1987)
<doi:10.1177/2158244015604192>. Hypothesis and data are encoded as
pairwise relative orderings which are then compared to determine the
percentage of orderings in the data that are matched by the hypothesis.
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Author Timothy Beechey [aut, cre](<https://orcid.org/0000-0001-8858-946X>)
Maintainer Timothy Beechey <tim.beechey@protonmail.com>
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group_results

Description

Group-level PCC and chance values.

Usage

group_results(m, digits)

## Default S3 method:
group_results(m, digits)

## S3 method for class 'opafit'
group_results(m, digits = 2)

Arguments

m an object of class "opafit" produced by \texttt{opa}().
digits a positive integer.

Details

If the model was fitted with no grouping variable, a single PCC and c-value are returned. If a grouping variable was specified in the call to \texttt{opa} then PCCs and c-values are returned for each factor level of the grouping variable.

Value

a matrix with 1 row per group.

Examples

dat <- data.frame(t1 = c(9, 4, 8, 10),
                  t2 = c(8, 8, 12, 10),
                  t3 = c(8, 5, 10, 11))
opamod <- \texttt{opa}(dat, 1:3)
group_results(opamod)
individual_results

Individual-level PCC and chance values.

Description

Individual-level PCC and chance values.

Usage

individual_results(m, digits)

## Default S3 method:
individual_results(m, digits)

## S3 method for class 'opafit'
individual_results(m, digits = 2)

Arguments

- m: an object of class "opafit" produced by opa()
- digits: an integer

Details

If the model was fitted with no grouping variable, a matrix of PCCs and c-values are returned corresponding to the order of rows in the data. If the opa model was fitted with a grouping variable specified, a table of PCCs and c-values is returned ordered by factor level of the grouping variable.

Value

a matrix containing a column of PCC values and a column of c-values with 1 row per row of data.

Examples

dat <- data.frame(t1 = c(9, 4, 8, 10),
                  t2 = c(8, 8, 12, 10),
                  t3 = c(8, 5, 10, 11))
opamod <- opa(dat, 1:3)
individual_results(opamod)
Fit an ordinal pattern analysis model

**Description**

`opa` is used to fit ordinal pattern analysis models by computing the percentage of pair orderings in each row of data which are matched by corresponding pair orderings in an hypothesis, in addition the chance of a permutation of the data producing a percentage match as great.

**Usage**

```r
opa(
  dat, 
  hypothesis, 
  group = NULL, 
  pairing_type = "pairwise", 
  diff_threshold = 0, 
  cval_method = "stochastic", 
  nreps = 1000L, 
  progress = FALSE 
)
```

**Arguments**

- **dat**: a data frame
- **hypothesis**: a numeric vector
- **group**: an optional factor vector
- **pairing_type**: a string
- **diff_threshold**: a positive integer or floating point number
- **cval_method**: a string, either "exact" or "stochastic"
- **nreps**: an integer, ignored if `cval_method = "exact"
- **progress**: a boolean indicating whether to display a progress bar

**Details**

Data is expected in **wide** format with 1 row per individual and 1 column per measurement condition. Data must contain only columns consisting of numerical values of the **dependent** variable.

The length of the hypothesis must be equal to the number of columns in the dependent variable data.frame `dat`.

Any **independent** variable must be passed separately as a vector with the *group* keyword. The grouping vector must be a **factor**.

**pairing_type** must be either "pairwise" or "adjacent". The "pairwise" option considered the relative ordering of every pair of observations in the data and every pair of elements of the hypothesis.
The "adjacent" option considered the ordering of adjacent pairs only. If unspecified, the default is "pairwise".

diff_threshold may be a positive integer or double. If unspecified a default zero threshold is used. The diff_threshold is never applied to the hypothesis.

cval_method is either "stochastic" or "exact". The "stochastic" option generates random reorderings of each data row. The "exact" method generates every possible permutation of each data row. Care must be taken using the "exact" method since the number of permutations is the factorial of the number of columns in the data. For large numbers of data columns it is best to use the default "stochastic" method to sample orderings.

nreps specifies the number of random reorderings to generate when using the "stochastic" method for computing chance values. The default value of nreps is 1000. If the cval_method = "exact" option is specified, nreps is ignored.

Value

opa returns an object of class "opafit".

An object of class "opafit" is a list containing the following components:

group_pcc the percentage of pairwise orderings from all pooled data rows which were correctly classified by the hypothesis.

individual_pccs a vector containing the percentage of pairwise orderings that were correctly classified by the hypothesis for each data row.

condition_pccs a matrix containing PCCs for each pair of conditions, or a list containing such a matrix for each group level if a grouping variable is passed to opa
correct_pairs an integer representing the number of pairwise orderings pooled across all data rows that were correctly classified by the hypothesis.
total_pairs an integer, the number of pair orderings contained in the data.
group_cval the group-level chance value.

individual_cvals a vector containing chance values for each data row

n_permutations an integer, the number of permutations of the data used to compute chance values.

pccs_geq_observed an integer, the number of permutations which generated PCC values at least as great as the PCC of the observed data.

pcc_replicates a matrix containing PCC values, one column per data row, computed from all permutations used to compute chance values.
call the matched call

References


Examples

```r
dat <- data.frame(group = c("a", "b", "a", "b"),
    t1 = c(9, 4, 8, 10),
    t2 = c(8, 8, 12, 10),
    t3 = c(8, 5, 10, 11))

dat$group <- factor(dat$group, levels = c("a", "b"))
opamod <- opa(dat[,2:4], 1:3)
opamod <- opa(dat[,2:4], 1:3, nreps = 500)
opamod <- opa(dat[,2:4], 1:3, cval_method = "exact")
opamod <- opa(dat[,2:4], 1:3, pairing_type = "adjacent")
opamod <- opa(dat[,2:4], 1:3, diff_threshold = 1)
opamod <- opa(dat[,2:4], 1:3, group = dat$group)
```

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**pcc_threshold_plot**  
Plots individual PCCs relative to a user-supplied PCC threshold value.

Description

Plots individual PCCs relative to a user-supplied PCC threshold value.

Usage

```r
pcc_threshold_plot(m, pcc_threshold = 75)
```

Arguments

- `m` an object of class "opafit"
- `pcc_threshold` a numeric scalar

Value

an object of class "ggplot"

Examples

```r
dat <- data.frame(t1 = c(9, 4, 8, 10),
    t2 = c(8, 8, 12, 10),
    t3 = c(8, 5, 10, 11))

opamod <- opa(dat, 1:3)
pcc_threshold_plot(opamod)
pcc_threshold_plot(opamod, pcc_threshold = 85)
```
plot.opafit

Plots individual-level PCCs and chance-values.

Description

Plots individual-level PCCs and chance-values.

Usage

## S3 method for class 'opafit'
plot(x, ...)

Arguments

x

an object of class "opafit" produced by opa()

... ignored

Value

an object of class "ggplot"

Examples

dat <- data.frame(t1 = c(9, 4, 8, 10),
 t2 = c(8, 8, 12, 10),
 t3 = c(8, 5, 10, 11))
opamod <- opa(dat, 1:3)
plot(opamod)

plot_hypothesis

Plot a hypothesis.

Description

Plot a hypothesis.

Usage

plot_hypothesis(h)

Arguments

h

a numeric vector

Value

an object of class "ggplot"
### Examples

```r
h <- c(1, 2, 3, 3, 3)
plot_hypothesis(h)
```

```r
summary.opafit
Prints a summary of results from a fitted ordinal pattern analysis model.
```

### Description

Prints a summary of results from a fitted ordinal pattern analysis model.

### Usage

```r
## S3 method for class 'opafit'
summary(object, ..., digits = 2L)
```

### Arguments

- `object`: an object of class "opafit".
- `...`: ignored
- `digits`: an integer used for rounding values in the output.

### Value

No return value, called for side effects.

### Examples

```r
dat <- data.frame(t1 = c(9, 4, 8, 10),
                  t2 = c(8, 8, 12, 10),
                  t3 = c(8, 5, 10, 11))
opamod <- opa(dat, 1:3)
summary(opamod)
summary(opamod, digits = 3)
```
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