Package 'gomms'

May 14, 2017

Type Package

Title GLM-Based Ordination Method

Version 1.0

Date 2017-05-13

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Description A zero-inflated quasi-Poisson factor model to display similarity between samples visually in a low (2 or 3) dimensional space.

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NeedsCompilation no

Repository CRAN

Date/Publication 2017-05-14 17:30:27 UTC

R topics documented:

`gomms-package` *GLM-Based Ordination Method*

Description

preliminary analysis of similarity between samples in a low (2 or 3) dimensional display.

Author(s)

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References

Sohn, M.B. and Li, H. (2017). A GLM-Based Latent Variable Ordination Method for Microbiome Samples (Submitted).

Examples

```
## Not run:
# load test data

data(gomms_test_data);

# estimate factor scores
cdat <- as.matrix(gomms_test_data[,-ncol(gomms_test_data)]);
rslt <- gomms(cdat);

# plot estimated factor scores
y <- as.matrix(gomms_test_data$group);
gomms.plot(rslt, y);

## End(Not run)
```

`gomms` *GLM-Based Ordination Method for Microbiome Samples*

Description

estimate factor loadings and scores.

Usage

```
gomms(X, n.factors = 2, min.prop.nonzeros = 0.05, show.max.delta = FALSE)
```

Arguments

`X`	raw count data.
`n.factors`	number of factors. Default value is 2.
`min.prop.nonzeros`	minimum proportion of nonzeros allowed in analysis.
`show.max.delta`	display the maximum different between jth and (j+1)th iterations.

Value

estimated factor scores.

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`gomms.plot` *Plot Factor Loadings*

Description

plot estimated factor loadings for each sample.

Usage

```
gomms.plot(X, Y, col.markers = NULL, pch.markers = NULL, ...)
```

Arguments

`X`	two dimnsional matrix of factor scores.
`Y`	one or two dimensional matrix of classification.
`col.markers`	user specified colors for classification.
`pch.markers`	user specified plot symbols for classification.
`...`	optional graphical parameters to be passed.

`gomms_test_data` *Test Data*

Description

70 samples and 83 features. The last column contains the population identification for each sample.

Usage

```
data(gomms_test_data)
```

`Qqpois` *Probability of a Zero from a Zero State*

Description

estimate the probability of a zero from a zero state.

Usage

```
Qqpois(cdat, eta.hat, mu.hat, dispersion)
```

Arguments

`cdat`	count Data.
`eta.hat`	estimated proportion of zeros from a zero state.
`mu.hat`	estimated mean count.
`dispersion`	estimated values for dispersion.

Value

estimated probability of a zero from a zero state.

Index