# Package 'gomms'

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**Type** Package

**Title** GLM-Based Ordination Method

**Version** 1.0

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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.

**License** GPL (>= 2)

**NeedsCompilation** no

**Repository** CRAN

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

## R topics documented:

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gomms-package         *GLM-Based Ordination Method*

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### Description

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

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## 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)
```

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gomms                           *GLM-Based Ordination Method for Microbiome Samples*

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## 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* |
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## 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. |

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| gomms_test_data | *Test Data* |
| --- | --- |

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## 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.

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