Package 'ZIBseq'

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Type Package

Title Differential Abundance Analysis for Metagenomic Data via Zero-Inflated Beta Regression

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Description Detects abundance differences across clinical conditions. Besides, it takes the sparse nature of metagenomic data into account and handles compositional data efficiently.

License GPL (>= 2)

LazyLoad yes

Depends R (>= 3.3.1), gamlss, nlme

Imports stats, gamlss.dist

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NeedsCompilation no

R topics documented:

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ZIBseq-package *Identify differentially abundant features*

Description

Detects abundance differences across clinical conditions. Besides, it takes the sparse nature of metagenomic data into account and handles compositional data efficiently.

Index of help topics:

ZIBseq	Conducts the zero-inflated beta regression based on the general count 'data' and categorical vector 'outcome'.
ZIBseq-package	Identify differentially abundant features
calc_qvalues	a function used to calculate q values
testdata	Real metagenomic data

~~ An overview of how to use the package, including the most important functions ~~

Author(s)

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References

Peng Xiaoling, Li Gang, and Liu Zhenqiu. Journal of Computational Biology. January 2016, 23(2): 102-110. doi:10.1089/cmb.2015.0157.

See Also

~~ Optional links to other man pages, e.g. ~~ ~~ ZIBseq ~~

Examples

```
## Not run:
data(testdata)
x=testdata[,9:248]
p=dim(x)[2]
for (i in 1:p){x[,i]=as.numeric(as.character(x[,i]))}
gr=testdata[,2]
gr=as.numeric(gr)
gr[which(gr<4)]=0
gr[which(gr==4)]=1
result=ZIBseq(data=x,outcome=gr)

## End(Not run)
```

`calc_qvalues` *a function used to calculate q values*

Description

Estimates their q-values based on a list of p-values resulting from the simultaneous testing of many hypothesis.

Usage

```
calc_qvalues(pvalues)
```

Arguments

`pvalues`	input the p value

Details

To control the false discovery rate(FDR), q-value has been widely accepted as an alternative approach for multiple hypothesis testing correction in recent years.

Value

qvalues

Author(s)

chen hongliang

References

http://bioconductor.org/packages/release/bioc/html/qvalue.html

Examples

```
##---- Should be DIRECTLY executable !! ----
##-- ==>  Define data, use random,
##--or do  help(data=index)  for the standard data sets.

## The function is currently defined as
function (pvalues)
{
    nrows = length(pvalues)
    lambdas <- seq(0, 0.95, 0.01)
    pi0_hat <- array(0, dim = c(length(lambdas)))
    for (l in 1:length(lambdas)) {
        count = 0
        for (i in 1:nrows) {
            if (pvalues[i] > lambdas[l]) {
```

```
            count = count + 1
        }
        pi0_hat[l] = count/(nrows * (1 - lambdas[l]))
    }
  }
  f <- unclass(smooth.spline(lambdas, pi0_hat, df = 3))
  f_spline <- f$y
  pi0 = f_spline[length(lambdas)]
  ordered_ps <- order(pvalues)
  pvalues <- pvalues
  qvalues <- array(0, dim = c(nrows))
  ordered_qs <- array(0, dim = c(nrows))
  ordered_qs[nrows] <- min(pvalues[ordered_ps[nrows]] * pi0,
      1)
  for (i in (nrows - 1):1) {
      p = pvalues[ordered_ps[i]]
      new = p * nrows * pi0/i
      ordered_qs[i] <- min(new, ordered_qs[i + 1], 1)
  }
  for (i in 1:nrows) {
      qvalues[ordered_ps[i]] = ordered_qs[i]
  }
  return(qvalues)
}
```

`testdata` *Real metagenomic data*

Description

The metagenomic dataset was downloaded from dbGaP under study ID phs000258. The data and analytical results were first reported by Zupancic et al. (2012). There were a total of 310 Amish adult samples with 112 males and 198 females. And there were a total of 240 taxa at the genus level.

Usage

```
data(testdata)
```

Format

testdata is a data frame with 310 cases(rows) and 248 variables(columns). Among 248 variables, 240 of them are taxa at the genus level and 8 of them are clinical phenotypes.

ZIBseq *Conducts the zero-inflated beta regression based on the general count* data *and categorical vector* outcome.

Description

zero-inflated beta regression

Usage

```
ZIBseq(data, outcome, transform = F, alpha = 0.05)
```

Arguments

data	a matrix records the count data
outcome	a categorical vector of a specific kind of clinical condition
transform	square-root transform of the compositional matrix
alpha	customized threshold while calculating q values

Details

The function takes the sparse nature of metagenomics data into account and handle the compositional data efficiently.

Value

sigFeature	output the significant feature
useFeature	features being concerned
qvalue	qvalue
pvalue	pvalue

Author(s)

Hongliang Chen

References

Peng Xiaoling, Li Gang, and Liu Zhenqiu. Journal of Computational Biology. January 2016, 23(2): 102-110. doi:10.1089/cmb.2015.0157.

See Also

calc_qvalues

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