Package 'coGPS'

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Type Package

Title cancer outlier Gene Profile Sets

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Author Yingying Wei, Michael Ochs

Maintainer Yingying Wei <ywei@jhsph.edu>

Description Gene Set Enrichment Analysis of P-value based statistics for outlier gene detection in dataset merged from multiple studies

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Suggests limma

Imports graphics, grDevices

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Contents

`coGPS-package` *Cancer Outlier Gene Profile Sets*

Description

Gene Set Enrichment Analysis of P-value based statistics for outlier gene detection in dataset merged from multiple studies

Author(s)

Yingying Wei, Michael Ochs Maintainer: Yingying Wei <ywei@jhsph.edu>

References

Wei, Y., Hennessey, P., Gaykalova, D., Califano, J.A., Ochs, M.F., (2011) Cancer Outlier Gene Profile Sets Elucidate Pathways in Head and Neck Squamous Cell Carcinoma.

`coGPS internal` *coGPS package internal function.*

Description

These functions are not part of the package application programming interface and are not recommended to be used by the users.

Usage

```
plotCOPA
```

`PatientSpecificGeneList` *Patient Specific outlier gene list*

Description

Generate an outlier gene list for each patient restricted to the top PCOPA scored genes

Usage

```
PatientSpecificGeneList(exprslist, alpha, side, type,TopGeneNum)
```

Arguments

exprslist	Each element of $exprslist$ is a list with the first element being $exprs$ and the second element being $classlab$. Each row of $exprs$ represents one gene and each column represents one sample. $classlab$ is a zero-one vector indicating the status of samples. We use 0 for the baseline group, usually the normal group, and 1 for the comparison group, usually the tumor group.
alpha	Significance level for P-value.
side	A vector specifying the definition of P-value in each of the study, which could be either up, $down$, or $twosided$.
type	A vector specifying whether the outlier pattern is $subtype$ or $uniform$.
TopGeneNum	a number specifying the top number of outlier genes scored by PCOPA to be included in the generation of individual outlier gene list for each patient.

Value

outliergene_bypatient

a list whose length equals the number of tumor samples (patients). each element of the list is a list of length equaling to the length of $exprslist$, in other words the number of studies(or data type), showing the outlier gene for each patient in each study (or data type)

Author(s)

Yingying Wei

References

Wei, Y., Hennessey, P., Gaykalova, D., Califano, J.A., Ochs, M.F., (2011) Cancer Outlier Gene Profile Sets Elucidate Pathways in Head and Neck Squamous Cell Carcinoma.

Examples

```
#read in data
data(Exon_exprs_matched)
data(Methy_exprs_matched)
data(CNV_exprs_matched)
data(Exon_classlab_matched)
data(Methy_classlab_matched)
data(CNV_classlab_matched)
head(Exon_exprs_matched)

#exprslist[[i]]$exprs should be in matrix format
Exon_exprs<-as.matrix(Exon_exprs_matched)
Methy_exprs<-as.matrix(Methy_exprs_matched)
CNV_exprs<-as.matrix(CNV_exprs_matched)

#exprslist[[i]]$classlab should be in vector format
Exon_classlab<-unlist(Exon_classlab_matched)
Methy_classlab<-unlist(Methy_classlab_matched)
```

```
CNV_classlab<-unlist(CNV_classlab_matched)

#make an exprslist consisting 3 studies
trylist<-list()
trylist[[1]]<-list(exprs=Exon_exprs,classlab=Exon_classlab)
trylist[[2]]<-list(exprs=Methy_exprs,classlab=Methy_classlab)
trylist[[3]]<-list(exprs=CNV_exprs,classlab=CNV_classlab)

#generate an outlier gene list for each patient restricted to the top PCOPA scored genes
IndividualList7<-PatientSpecificGeneList(trylist,0.05,side=c("up","down","up"),type="subtype",TopGeneNum=100)
```

PCOPA *P-value based outlier gene detection*

Description

Calculate P-value based statistics for outlier gene detection in dataset merged from multiple studies and give out outlier gene list for each patient.

Usage

```
PCOPA(exprslist, alpha, side, type)
```

Arguments

exprslist	Each element of $exprslist$ is a list with the first element being $exprs$ and the second element being $classlab$. Each row of $exprs$ represents one gene and each column represents one sample. $classlab$ is a zero-one vector indicating the status of samples. We use 0 for the baseline group, usually the normal group, and 1 for the comparison group, usually the tumor group.
alpha	Significance level for P-value.
side	A vector specifying the definition of P-value in each of the study, which could be either up, $down$, or $twosided$.
type	A vector specifying whether the outlier pattern is $subtype$ or $uniform$.

Value

PCOPAstatistics
: the P-value based outlier gene detection statistics

outliergene_bypatient
: a list whose length equals the number of tumor samples (patients). each element of the list is a list of length equaling to the length of $exprslist$, in other words the number of studies(or data type), showing the outlier gene for each patient in each study (or data type)

Author(s)

Yingying Wei

References

Wei, Y., Hennessey, P., Gaykalova, D., Califano, J.A., Ochs, M.F., (2011) Cancer Outlier Gene Profile Sets Elucidate Pathways in Head and Neck Squamous Cell Carcinoma.

Examples

```
#read in data
data(Exon_exprs_matched)
data(Methy_exprs_matched)
data(CNV_exprs_matched)
data(Exon_classlab_matched)
data(Methy_classlab_matched)
data(CNV_classlab_matched)
head(Exon_exprs_matched)

#exprslist[[i]]$exprs should be in matrix format
Exon_exprs<-as.matrix(Exon_exprs_matched)
Methy_exprs<-as.matrix(Methy_exprs_matched)
CNV_exprs<-as.matrix(CNV_exprs_matched)

#exprslist[[i]]$classlab should be in vector format
Exon_classlab<-unlist(Exon_classlab_matched)
Methy_classlab<-unlist(Methy_classlab_matched)
CNV_classlab<-unlist(CNV_classlab_matched)

#make an exprslist consisting 3 studies
trylist<-list()
trylist[[1]]<-list(exprs=Exon_exprs,classlab=Exon_classlab)
trylist[[2]]<-list(exprs=Methy_exprs,classlab=Methy_classlab)
trylist[[3]]<-list(exprs=CNV_exprs,classlab=CNV_classlab)

#calculate P-value based statistics for outlier gene detection and output the outlier gene list for each patient
a7<-PCOPA(trylist,0.05,side=c("up","down","up"),type="subtype")
```

`permCOPA` *Calculate PCOPA value for permuations*

Description

Run permutations by randomly shuffling the sample class labels and calculate a vector of PCOPA values for each permutation.

Usage

```
permCOPA(exprslist, alpha=0.05, side, type, perms=100)
```

Arguments

exprslist	Each element of $exprslist$ is a list with the first element being $exprs$ and the second element being $classlab$. Each row of $exprs$ represents one gene and each column represents one sample. $classlab$ is a zero-one vector indicating the status of samples. We use 0 for the baseline group, usually the normal group, and 1 for the comparison group, usually the tumor group.
alpha	Significance level for P-value.
side	A vector specifying the definition of P-value in each of the study, which could be either up, $down$, or $twosided$.
type	A vector specifying whether the outlier pattern is $subtype$ or $uniform$.
perms	Number of permutations to run.

Value

permResult	A matrix where each row correspond to a gene and each column correspond to one permutation.

Author(s)

Michael Ochs

References

Wei, Y., Hennessey, P., Gaykalova, D., Califano, J.A., Ochs, M.F., (2011) Cancer Outlier Gene Profile Sets Elucidate Pathways in Head and Neck Squamous Cell Carcinoma.

Examples

```
#read in data
data(Exon_exprs_matched)
data(Methy_exprs_matched)
data(CNV_exprs_matched)
data(Exon_classlab_matched)
data(Methy_classlab_matched)
data(CNV_classlab_matched)
head(Exon_exprs_matched)

#exprslist[[i]]$exprs should be in matrix format
Exon_exprs<-as.matrix(Exon_exprs_matched)
Methy_exprs<-as.matrix(Methy_exprs_matched)
CNV_exprs<-as.matrix(CNV_exprs_matched)

#exprslist[[i]]$classlab should be in vector format
Exon_classlab<-unlist(Exon_classlab_matched)
Methy_classlab<-unlist(Methy_classlab_matched)
CNV_classlab<-unlist(CNV_classlab_matched)

#make an exprslist consisting 3 studies
trylist<-list()
```

```
trylist[[1]]<-list(exprs=Exon_exprs,classlab=Exon_classlab)
trylist[[2]]<-list(exprs=Methy_exprs,classlab=Methy_classlab)
trylist[[3]]<-list(exprs=CNV_exprs,classlab=CNV_classlab)

#run 2 permutations
perma7<-permCOPA(trylist,0.05,side=c("up","down","up"),type="subtype",perms=2)
```

PlotTopPCOPA *Plot expression patterns of top ranked genes.*

Description

It first sorts the expression value $exprslist[[i]]\$exprs[j,]$ among the baseline samples(e.g. normal ones) and comparison group (e.g. tumor ones)seperately for selected gene j, and then plot the sorted expression values. The first argument $exprslist$ should be the same one as for $PCOPA$; the second argument $PCOPAresult$ should be an output of PCOPA; the third argument $topcut$ determines how far we would go down the top ranked list; and the last argument $typelist$ is a vector specifying the titles for each graph corresponds to a specific study.

Usage

```
PlotTopPCOPA(exprslist, PCOPAresult, topcut, typelist)
```

Arguments

exprslist	Each element of $exprslist$ is a list with the first element being $exprs$ and the second element being $classlab$. Each row of $exprs$ represents one gene and each column represents one sample. $classlab$ is a zero-one vector indicating the status of samples. We use 0 for the baseline group, usually the normal group, and 1 for the comparison group, usually the tumor group.
PCOPAresult	Output of PCOPA.
topcut	Cutoff of top ranked gene list.
typelist	A vector specifying the titles for each graph corresponds to a specific study.

Author(s)

Michael Ochs, Yingying Wei

Examples

```
#read in data
data(Exon_exprs_matched)
data(Methy_exprs_matched)
data(CNV_exprs_matched)
data(Exon_classlab_matched)
data(Methy_classlab_matched)
data(CNV_classlab_matched)
head(Exon_exprs_matched)
```

```
#exprslist[[i]]$exprs should be in matrix format
Exon_exprs<-as.matrix(Exon_exprs_matched)
Methy_exprs<-as.matrix(Methy_exprs_matched)
CNV_exprs<-as.matrix(CNV_exprs_matched)

#exprslist[[i]]$classlab should be in vector format
Exon_classlab<-unlist(Exon_classlab_matched)
Methy_classlab<-unlist(Methy_classlab_matched)
CNV_classlab<-unlist(CNV_classlab_matched)

#make an exprslist consisting 3 studies
trylist<-list()
trylist[[1]]<-list(exprs=Exon_exprs,classlab=Exon_classlab)
trylist[[2]]<-list(exprs=Methy_exprs,classlab=Methy_classlab)
trylist[[3]]<-list(exprs=CNV_exprs,classlab=CNV_classlab)

#calculate P-value based statistics for outlier gene detection and output the outlier gene list for each patient
a7<-PCOPA(trylist,0.05,side=c("up","down","up"),type="subtype")

#plot expression patterns of top ranked genes.
PlotTopPCOPA(trylist,a7,topcut=1,typelist=c("Exon","Methy","CNV"))
```

`SampleData` *Sample Data for coGPS*

Description

Here we present an example of coGPS analysis.

Arguments

`Exon_exprs_matched`
: Expression data for 44 tumors and 25 normals. Each row indicates a gene with row name showing gene name and each column indicates a sample with column name showing sample name.

`Exon_class_matched`
: A length 69 vector showing status of corresponding exon samples, 0 for normals and 1 for tumors.

`Methy_exprs_matched`
: Methylation data for 44 tumors and 25 normals.

`Methy_class_matched`
: A length 69 vector showing status of corresponding methylation samples, 0 for normals and 1 for tumors.

`CNV_exprs_matched`
: Copy number data for 44 tumors and 25 normals.

`CNV_class_matched`
: A length 69 vector showing status of corresponding copy number samples, 0 for normals and 1 for tumors.

`Hs.gmtl.c1` Broad Institute C1 Positional Gene Sets.

Details

In this application, the columns of each data type are matched. In other words, the first columns of Exon_exprs_matched, Methy_exprs_matched and CNV_exprs_matched correspond to the same patient. And hence the Exon_class_matched, Methy_class_matched and CNV_class_matched are identical. However, suppose in applications that we are not concerned with the outlier gene list for each patient, we can leave with the samples (columns) unmatched.

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