Package ‘TOAST’

May 16, 2024

Type Package
Title Tools for the analysis of heterogeneous tissues
Version 1.18.0
Description This package is devoted to analyzing high-throughput data (e.g. gene expression microarray, DNA methylation microarray, RNA-seq) from complex tissues. Current functionalities include 1. detect cell-type specific or cross-cell type differential signals 2. tree-based differential analysis 3. improve variable selection in reference-free deconvolution 4. partial reference-free deconvolution with prior knowledge.
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BugReports https://github.com/ziyili20/TOAST/issues
Imports stats, methods, SummarizedExperiment, corpcor, doParallel, parallel, ggplot2, tidyr, GGally
Suggests BiocStyle, knitr, rmarkdown, gplots, matrixStats, Matrix
VignetteBuilder knitr
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assignCellType

Align cell types when reference proportions are known

Description

Align target proportions with reference proportions by pearson correlation coefficients.

Usage

assignCellType(input, reference)

Arguments

- **input**: Input proportiona matrix of dimension N by K.
- **reference**: Reference proportion matrix of dimension N by K.

Value

The aligned proportion matrix, following the cell type ordering of reference proportion matrix.

Author(s)

Ziyi Li <zli16@mdanderson.org>
References

Ziyi Li, Zhijin Wu, Peng Jin, Hao Wu. "Dissecting differential signals in high-throughput data from complex tissues."

Examples

```r
## generate estimated proportion matrix
estProp <- matrix(abs(runif(50*4,0,1)), 50, 4)
estProp <- sweep(estProp, 1, rowSums(estProp), "/")

## generate reference proportion matrix
refProp <- matrix(abs(runif(50*4,0,1)), 50, 4)
refProp <- sweep(refProp, 1, rowSums(refProp), "/")

estProp_aligned = assignCellType(input = estProp, reference = refProp)
```

Description

This dataset is a list containing two matrices, one of which is methylation 450K array data of 3000 CpG sites on 50 samples, the other is methylation 450K array data of 3000 matched CpG sites on three immune cell types. The first dataset is generated by simulation. It originally has 459226 features and 50 samples. We reduce it to 3000 CpGs by random selection.

Usage

```r
data("beta_emp")
```

Format

The format is: List of 2 $Y.raw$: num [1:3000, 1:50] 0.7661 0.0968 0.8882 0.0286 0.6956 ... 
attr(*, "dimnames")=List of 2 ..$ : chr [1:3000] "cg08752431" "cg14555682" "cg23086843" 
"cg20308511" ... ..$ : NULL 
$ref.m$: num [1:3000, 1:3] 0.7712 0.0996 0.9065 0.037 0.7242 ... 
attr(*, "dimnames")=List of 2 ..$ : chr [1:3000] "cg08752431" "cg14555682" "cg23086843" 
"cg20308511" ... ..$ : chr [1:3] "CD4T" "CD8T" "BCell"

Examples

```r
data(beta_emp)
```
CBS_PBMC_array  An example dataset for partial reference-free cell composition estimation from tissue gene expression

Description
The dataset contains 511 microarray gene expressions for 20 PBMC samples (mixed_all) and PBMC microarray reference for the matched 511 genes from 5 immune cell types (LM_5). It also contains the true cell compositions from cell sorting experiment (trueProp) and prior knowledge of cell compositions for 5 cell types in PBMC (prior_alpha and prior_sigma).

Usage
data("CBS_PBMC_array")

References

Examples
data("CBS_PBMC_array")
CBS_PBMC_array$mixed_all[1:5,1:5]
head(CBS_PBMC_array$LM_5,3)
head(CBS_PBMC_array$trueProp,3)
CBS_PBMC_array$prior_alpha
CBS_PBMC_array$prior_sigma

cedar  Testing cell type specific differential signals for specified phenotype by considering DE/DM state correlation between cell types.

Description
This function provides posterior probability of whether a feature is DE/DM in certain cell type given observed bulk data.
cedar

Usage
cedar(Y_raw, prop, design.1, design.2=NULL, factor.to.test=NULL, pval = NULL, p.adj = NULL, tree = NULL, p.matrix.input = NULL, de.state = NULL, cutoff.tree = c('fdr', 0.01), cutoff.prior.prob = c('pval', 0.01), similarity.function = NULL, parallel.core = NULL, corr.fig = FALSE, run.time = TRUE, tree.type = c('single', 'full'))

Arguments
Y_raw: matrix of observed bulk data, with rows representing features and columns representing samples
prop: matrix of cell type composition of samples, with rows representing samples and columns representing cell types
design.1: covariates with cell type specific effect, with rows representing samples and columns representing covariates
design.2: covariates without cell type specific effect, with rows representing samples and columns representing covariates
factor.to.test: A phenotype name, e.g. "disease", or a vector of contrast terms, e.g. c("disease", "case", "control")
pval: matrix of p-values, with rows representing features and columns representing cell types. colnames must be same as input of prop
p.adj: matrix of adjusted p-values, with rows representing features and columns representing cell types. colnames must be same as input of prop
tree: tree structure between cell types, a matrix with row representing layers and column representing cell types (column name is required)
p.matrix.input: prior probability on each node of the tree structure. only work when tree structure has been specified. the dimension must be same as tree input.
de.state: DE/DM state of each feature in each cell type, with row representing features and column representing cell types (1:DE/DM, 0:non-DE/DM)
cutoff.tree: cut off used to define DE state to estimate tree could be 'fdr' or 'pval' default it 'fdr'=0.01. suggest to start with restrictive cut off and change to relative loose value when the restrictive cut off is failed
cutoff.prior.prob: cut off used to define DE state to estimate prior probs of nodes on tree could be 'fdr' or 'pval' default it 'fdr'=0.01. suggest to start with restrictive cut off and change to relative loose value when the restrictive cut off is failed
similarity.function: custom function used to calculate similarity between cell types that used for tree structure estimation. the input of the custom is assumed to be a matrix of log transformed p-value. dimension is: selected gene number * cell number
parallel.core: number of cores for parallel running, default is NULL
corr.fig: a boolean value, whether to plot correlation between cell types use function plotCorr()
run.time: a boolean value, whether to report running time in seconds
tree.type: tree type for inference, default is c('single', 'full')
Value

A list

toast_res If pval is NULL, then TOAST result by function csTest() is returned

tree_res matrix of posterior probability of each feature for each cell type

fig If corr.fig = TRUE, then figure show DE/DM state correlation between cell types will be returned

time_used If run.time = TRUE, then running time (seconds) of CeDAR will be returned

Author(s)

Luxiao Chen <luxiao.chen@emory.edu>

Examples

N <- 300 # simulation a dataset with 300 samples
K <- 3 # 3 cell types
P <- 500 # 500 features

### simulate proportion matrix
Prop <- matrix(runif(N*K, 10, 60), ncol = K)
Prop <- sweep(Prop, 1, rowSums(Prop), FUN = "/")
colnames(Prop) <- c("Neuron", "Astrocyte", "Microglia")

### simulate phenotype names
design <- data.frame(disease = factor(sample(0:1, size = N, replace = TRUE)),
                      age = round(runif(N, 30, 50)),
                      race = factor(sample(1:3, size = N, replace = TRUE)))
Y <- matrix(rnorm(N*P, N, P), ncol = N)
rownames(Y) <- paste0("gene", 1:nrow(Y))
d1 <- data.frame('disease' = factor(sample(0:1, size = N, replace = TRUE)))

### Only provide bulk data, proportion
res <- cedar(Y_raw = Y, prop = Prop,
              design.1 = design[, 1:2],
              design.2 = design[, 3],
              factor.to.test = 'disease',
              cutoff.tree = c('pval', 0.1),
              corr.fig = TRUE,
              cutoff.prior.prob = c('pval', 0.1))

### result of toast (independent test)
str(res$toast_res)

### posterior probability of DE/DM of cedar with single layer tree structure
head(res$tree_res$single$pp)

### posterior probability of DE/DM of cedar with multiple layer tree structure
head(res$tree_res$full$pp)

### estimated tree structure of three cell types
head(res$tree_res$full$tree_structure)

### scatter plot of -log10(pval) showing DE/DM state correlation between cell types
res$fig
### Using custom similarity function to estimate tree structure
### In CeDAR, the input is assumed to be a matrix of log transformed p-values
### with row representing genes and columns representing cell types

```r
sim.fun <- function(log.pval){
  similarity.res <- sqrt((1 - cor(log.pval, method = 'spearman'))/2)
  return(similarity.res)
}
```

```r
res <- cedar(Y_raw = Y, prop = Prop,
  design.1 = design[,1:2],
  design.2 = design[,3],
  factor.to.test = 'disease',
  cutoff.tree = c('pval',0.1),
  similarity.function = sim.fun,
  corr.fig = FALSE,
  cutoff.prior.prob = c('pval',0.1) )
```

### posterior probability of DE/DM of cedar with multiple layer tree structure

```r
head(res$tree_res$full$pp)
```

### Using custom tree structure as input
### cell type 1 and cell type 3 are more similar
```r
tree.input <- rbind(c(1,1,1),c(1,2,1),c(1,2,3))
```

### If column name is provided for the matrix; make sure it is same as variable Prop
colnames(tree.input) <- c("Neuron", "Astrocyte", "Microglia")

```r
res <- cedar(Y_raw = Y, prop = Prop,
  design.1 = design[,1:2],
  design.2 = design[,3],
  factor.to.test = 'disease',
  cutoff.tree = c('pval',0.1),
  tree = tree.input,
  corr.fig = FALSE,
  cutoff.prior.prob = c('pval',0.1) )
```

### posterior probability of DE/DM of cedar with multiple layer tree structure

```r
head(res$tree_res$custom$pp)
```

### Using custom tree structure and prior probability of each node as input
### cell type 1 and cell type 3 are more similar
tree.input <- rbind(c(1,1,1),c(1,2,1),c(1,2,3))
colnames(tree.input) <- c("Neuron", "Astrocyte", "Microglia")

```r
p.matrix.input <- rbind(c(0.2,0.2,0.2), c(0.5,0.25,0.5), c(0.5,1,0.5))
```

# marginally, each cell type has 0.05 (cell 1: 0.2 * 0.5 * 0.5, cell 2: 0.2 * 0.25 * 1)
# probability to be DE for a randomly picked gene
# there will be about 50% DE genes in cell type 1 overlapped with cell type 3;
ChooseMarker

ChooseMarker(pure_all, CellType, nMarkCT = 10, chooseSig = FALSE, verbose = TRUE)

Description

Choose cell type-specific markers from pure cell type profiles generated by microarray or RNA-seq, or from single cell RNA-seq data by differential analysis.

Usage

ChooseMarker(pure_all, CellType, nMarkCT = 10, chooseSig = FALSE, verbose = TRUE)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>pure_all</td>
<td>Input pure cell type profile matrix or single cell data matrix. Rows are for genes, columns are for cell types or cells.</td>
</tr>
<tr>
<td>CellType</td>
<td>A list object consisting of cell type information for columns in pure_all. Each element is a cell type, and contains the corresponding column number in pure_all matrix. For example, CellType = list(BCell = 1:3, CD4T = 4:5).</td>
</tr>
<tr>
<td>nMarkCT</td>
<td>Number of markers chosen per cell type. Default is 10.</td>
</tr>
<tr>
<td>chooseSig</td>
<td>A boolean variable representing whether to consider the significance of selected markers. When chooseSig = FALSE, all nMarkerCT number of markers will be chosen per cell type. Otherwise the non-significant (p value &gt; 0.05) markers will be filtered out.</td>
</tr>
<tr>
<td>verbose</td>
<td>A boolean variable of whether to output messages.</td>
</tr>
</tbody>
</table>
Details

Here we provide more details for CellType variable. This variable should be a list, with each element being the corresponding column numbers in pure_all for each cell type. For example, suppose pure_all is a 1000 by 300 matrix with row being genes and column being cells (or cell types). The first 1 to 100 columns are cell A, 101 to 200 columns are cell B, and 201 to 300 columns are cell C. Then CellType should be assigned as CellType = list(A = 1:100, B = 101:200, C = 201:300). If pure_all only has three columns for three cell types A, B and C, then CellType = list(A = 1, B = 2, C = 3).

Value

A list variable, including the selected variables for all cell types.

Author(s)

Ziyi Li <zli16@mdanderson.org>

References

Ziyi Li, Zhenxing Guo, Ying Cheng, Peng Jin, Hao Wu. "Robust partial reference-free cell composition estimation from tissue expression profiles."

Examples

```r
## randomly simulate pure cell type profiles
pure_all <- matrix(abs(rnorm(1000*9)), 1000, 9)
CellType <- list(CellA = 1:3,
                 CellB = 4:6,
                 CellC = 7:9)

## choose significant markers
SelMarker <- ChooseMarker(pure_all, CellType,
nMarkCT = 30,
chooseSig = TRUE,
verbose = FALSE)
```

Description

This function improve the feature selection in reference-free deconvolution through cross-cell type differential analysis

Usage

```r
csDeconv(Y_raw, K, FUN, nMarker = 1000,
InitMarker = NULL, TotalIter = 30, bound_negative = FALSE)
```
Arguments

Y_raw A G*N matrix, G is the number of features, N is the number of subjects; or a SummarizedExperiment object.

K The number of cell types. Need to be specified a priori.

FUN The reference-free deconvolution function, this function should take Y_raw and K, and the return values should be a N by K proportion matrix. N is the number of samples and K is the number of cell types. Default function is a wrapper of the RefFreeCellMix() function from CRAN package RefFreeEWAS.

nMarker The number of markers used in the deconvolution. Default is 1000.

InitMarker A vector of length L to represent the selection of initial markers. L should be equal or smaller than G. If G is large, it is recommended that L is much smaller than G. If not specified, the most variable nMarker features will be used.

TotalIter The total number of iterations of applying cross-cell type differential analysis. Default is 30.

bound_negative Whether to bound all negative parameter estimators to zero.

Value

allProp A list of estimated proportions from all iterations.

allRMSE A vector of root mean squared errors (RMSE) from all iterations.

estProp A N*K matrix representing the mixture proportions of K cell types in N subjects, chosen from allProp with the smallest RMSE.

updatedAtInx Selected variable index from the algorithm.

Author(s)

Ziyi Li <zli16@mdanderson.org>

References

Ziyi Li and Hao Wu. "Improving reference-free cell composition estimation by cross-cell type differential analysis".

Examples

Y_raw <- abs(matrix(runif(10000*20, 0,1),10000,20))
K <- 3

## wrap your reference-free deconvolution method into a function
## this function should take Y and K as input
## and output a N by K proportion matrix
## here we use RefFreeCellMix() as an example
outT <- csDeconv(Y_raw, K)

RefFreeCellMix_wrapper <- function(Y, K){
  outY = myRefFreeCellMix(Y,
mu0=myRefFreeCellMixInitialize(Y, K = K)
Prop0 = outY$Omega
return(Prop0)
}

outT <- csDeconv(Y_raw, K, FUN = RefFreeCellMix_wrapper)

---

**csTest**  
*Testing differential signals for specified phenotype and cell type(s).*

**Description**

This function conducts statistical tests for specified phenotype and cell type(s).

**Usage**

```r
csTest(fitted_model, coef = NULL, cell_type = NULL, contrast_matrix = NULL, var_shrinkage = TRUE, verbose = TRUE, sort = TRUE)
```

**Arguments**

- `fitted_model` The output from fitModel() function.
- `coef` A phenotype name, e.g. "disease", or a vector of contrast terms, e.g. c("disease", "case", "control").
- `cell_type` A cell type name, e.g. "celltype1", or "neuron". If cell_type is NULL or specified as "ALL", compound effect of coef in all cell types will be tested.
- `contrast_matrix` If contrast_matrix is specified, coef and cell_type will be ignored! A matrix (or a vector) to specify contrast, e.g., cmat <- matrix(0, 2, 6); cmat[1,3] <- 1; cmat[2,4] <- 1 is to test whether the 3rd parameter and 4th parameter are zero simultaneously i.e. beta3 = beta4 = 0.
- `var_shrinkage` Whether to apply shrinkage on estimated MSE or not. Applying shrinkage helps remove extremely small variance estimation and stabilise statistics.
- `verbose` A boolean parameter. Testing information will be printed if verbose = TRUE.
- `sort` A boolean parameter. The output results will be sorted by p value if sort = TRUE.

**Value**

A matrix including the results from testing the phenotype in specified cell type(s).

**Author(s)**

Ziyi Li <zli16@mdanderson.org>
References

Ziyi Li, Zhijin Wu, Peng Jin, Hao Wu. "Dissecting differential signals in high-throughput data from complex tissues."

Examples

N <- 300 # simulation a dataset with 300 samples
K <- 3 # 3 cell types
P <- 500 # 500 features

### simulate proportion matrix
Prop <- matrix(runif(N*K, 10,60), ncol=K)
Prop <- sweep(Prop, 1, rowSums(Prop), FUN="/")
colnames(Prop) <- c("Neuron", "Astrocyte", "Microglia")

### simulate phenotype names
design <- data.frame(disease=factor(sample(0:1, size = N,replace=TRUE)),
                      age=round(runif(N, 30,50)),
                      race=factor(sample(1:3, size = N,replace=TRUE)))
Y <- matrix(rnorm(N*P, N, P), ncol = N)

### generate design matrix and fit model
Design_out <- makeDesign(design, Prop)
fitted_model <- fitModel(Design_out, Y)

### check the names of cell types and phenotypes
fitted_model$all_cell_types
fitted_model$all_coefs

test <- csTest(fitted_model, coef = "age",
cell_type = "Neuron", contrast_matrix = NULL)

### detect age effect in neuron
test <- csTest(fitted_model, coef = "age",
cell_type = "Astrocyte", contrast_matrix = NULL)

test <- csTest(fitted_model, coef = "age",
cell_type = "Microglia", contrast_matrix = NULL)

## coef can be specified in different ways:
### jointly test a phenotype:
test <- csTest(fitted_model, coef = "age",
cell_type = "joint", contrast_matrix = NULL)

### if I do not specify cell_type
test <- csTest(fitted_model, coef = "age",
cell_type = NULL, contrast_matrix = NULL)

## this is exactly the same as
test <- csTest(fitted_model, coef = "age",
contrast_matrix = NULL)

### other examples
test <- csTest(fitted_model, coef = "race",
cell_type = "Astrocyte", contrast_matrix = NULL)
test <- csTest(fitted_model, coef = "age",
cell_type = "Microglia", contrast_matrix = NULL)
### DEVarSelect

DEVarSelect is a function for selecting cross-cell type differential features for reference-free deconvolution. It takes a data matrix containing P features and N samples; or a SummarizedExperiment object. The function is used to specify contrast levels and select features that are differentially expressed across different cell types.

#### Description

This function selects cross-cell type differential features for reference-free deconvolution.

#### Usage

```r
DEVarSelect(Y_raw, Prop0, nMarker, bound_negative)
```

#### Arguments

- **Y_raw**: A data matrix containing P features and N samples; or a SummarizedExperiment object.
- **Prop0**: A N by K proportion matrix with K as number of cell types.
- **nMarker**: Number of markers selected.
- **bound_negative**: Whether to bound all negative parameter estimators to zero.
Selected markers using cross-cell type differential analysis.

Ziyi Li <zli16@mdanderson.org>

Ziyi Li, Zhijin Wu, Peng Jin, Hao Wu. "Dissecting differential signals in high-throughput data from complex tissues."

Y_raw <- matrix(runif(5000*20, 0, 1), 5000, 20)
tmp <- matrix(runif(20*4), 20, 4)
Prop0 <- sweep(tmp, 1, rowSums(tmp), "/")
varlist <- DEVarSelect(Y_raw, Prop0,
nMarker=1000,
bound_negative=FALSE)

findRefinx

Description
Find index for marker genes with largest coefficient of variation based on raw data.

Usage
findRefinx(rawdata, nmarker=1000, sortBy = "var")

Arguments
rawdata A data matrix with rows representing features and columns representing samples; or a SummarizedExperiment object.
nmarker Desired number of markers after selection. Default is 1000.
sortBy Desired method to select features. "var" represents selecting by largest variance. "cv" represents selecting by largest coefficients of variation. Default is "var".

Value
A vector of index for the selected markers.

Ziyi Li <zli16@mdanderson.org>
References

Ziyi Li, Zhijin Wu, Peng Jin, Hao Wu. "Dissecting differential signals in high-throughput data from complex tissues."

Examples

```r
Y_raw <- matrix(runif(5000*20, 0, 1), 5000, 20)
idx <- findRefinX(Y_raw, nmarker=500)
idx2 <- findRefinX(Y_raw, nmarker=500, sortBy = "cv")
```

---

fitModel  

**Fit model with proportions and phenotypes.**

Description

This function receives design matrix from makeDesign() and fits the model including all cell types and phenotypes.

Usage

```r
fitModel(Design_out, Y)
```

Arguments

- `Design_out`: The output from function makeDesign().
- `Y`: A G*N matrix, G is the number of features, N is the number of subjects; or a SummarizedExperiment object.

Value

- `Design_out`: The input Design_out object.
- `N`: Number of samples from matrix Y.
- `coefs`: Estimated coefficients (beta) in the model.
- `coefs_var`: Estimated variance of the coefficients (beta variance) in the model.
- `Y`: Observation Y matrix.
- `Ypred`: Predicted Y from the fitted model.
- `all_coefs`: The names of all phenotypes.
- `all_cell_types`: The names of all cell types.
- `MSE`: Estimated mean squared error.
- `model_names`: The names of all terms in the fitted model.

Author(s)

Ziyi Li <zli16@mdanderson.org>
References

Ziyi Li, Zhijin Wu, Peng Jin, Hao Wu. "Dissecting differential signals in high-throughput data from complex tissues."

Examples

\[
N = 300 \quad \# \text{simulation a dataset with 300 samples} \\
K = 3 \quad \# \text{3 cell types} \\
P \leftarrow 500 \quad \# \text{500 features}
\]

### simulate proportion matrix
\[
\text{Prop} = \text{matrix(\text{runif}(N*K, 10, 60), ncol=K)} \\
\text{Prop} = \text{sweep(Prop, 1, rowSums(Prop), FUN="/")} \\
\text{colnames(Prop) = c("Neuron", "Astrocyte", "Microglia")} \\
\text{Y \leftarrow matrix(\text{rnorm}(N*P, N, P), ncol = N)}
\]

### simulate phenotype names
\[
\text{design <- data.frame(disease=factor(sample(0:1, size = N, replace=TRUE)),} \\
\text{age=round(\text{runif}(N, 30, 50)),} \\
\text{race=factor(sample(1:3, size = N, replace=TRUE)))} \\
\text{Design_out \leftarrow \text{makeDesign(design, Prop)}}
\]

### fit model
\[
\text{fitted_model \leftarrow \text{fitModel(Design_out, Y)}}
\]

GetPrior

**Get prior knowledge for supported tissue types**

Description

Users can use this function to get priors provided in this package. Users can also directly specify tissue type in MDeconv function.

Usage

\[
\text{GetPrior(alpha = NULL, sigma = NULL)}
\]

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>sigma</td>
<td>Keep it as NULL for supported tissues. Otherwise a numeric vector for manually specified sigma.</td>
</tr>
</tbody>
</table>
**makeDesign**

**Value**

- **alpha_prior**: Prior knowledge for the mean of proportions.
- **sigma_prior**: Prior knowledge for the sigma of proportions.

**Author(s)**

Ziyi Li <zli16@mdanderson.org>

**References**

Ziyi Li, Zhenxing Guo, Ying Cheng, Peng Jin, Hao Wu. "Robust partial reference-free cell composition estimation from tissue expression profiles."

**Examples**

- `GetPrior("human pbmc")`
- `GetPrior("human liver")`
- `GetPrior("human brain")`
- `GetPrior("human skin")`
- `GetPrior("human pancreas")`

```r
makeDesign
Generate design matrix from input phenotypes and proportions.
```

**Description**

This function generates a design matrix and prepares for following `fitModel` and `csTest`.

**Usage**

`makeDesign(design, Prop)`

**Arguments**

- **design**: A N by P phenotype matrix, with rows as samples and columns as phenotypes (e.g., age, gender, disease, etc.).
- **Prop**: A N by K proportion matrix, with rows as samples and columns as cell types.

**Value**

- **design_matrix**: A comprehensive design matrix incorporated phenotype and proportion information.
- **Prop**: The input proportion matrix.
- **design**: The input design/phenotype matrix.
- **all_coefs**: The names of all phenotypes.
- **all_cell_types**: The names of all cell types.
- **formula**: The formula of the tested model, including all phenotypes, cell types and interaction terms.
Author(s)
Ziyi Li <zli16@mdanderson.org>

References
Ziyi Li, Zhijin Wu, Peng Jin, Hao Wu. "Dissecting differential signals in high-throughput data from complex tissues."

Examples
N = 300 # simulation a dataset with 300 samples
K = 3 # 3 cell types

### simulate proportion matrix
Prop = matrix(runif(N*K, 10, 60), ncol=K)
Prop = sweep(Prop, 1, rowSums(Prop), FUN="/")
colnames(Prop) = c("Neuron", "Astrocyte", "Microglia")

### simulate phenotype names
design <- data.frame(disease=factor(sample(0:1, size = N,replace=TRUE)),
                      age=round(runif(N, 30, 50)),
                      race=factor(sample(1:3, size = N,replace=TRUE)))
Design_out <- makeDesign(design, Prop)

MDeconv
Estimate cell compositions via partial reference-free deconvolution.

Description
This function is the wrapper for TOAST/-P (partial reference-free deconvolution without prior) and TOAST/+P (with prior). It guides cell composition estimation through extra biological information, including cell type specific markers and prior knowledge of compositions.

Usage
MDeconv(Ymat, SelMarker, 
alpha = NULL, sigma = NULL,
epsilon = 0.001, maxIter = 1000,
verbose = TRUE)

Arguments
Ymat A gene expression data matrix from complex tissues. Rows represent genes and columns represent samples. Row names (e.g. gene symbol or ID) are needed. There is no need to filter data matrix by marker genes.

SelMarker A list variable with each element includes cell type-specific markers for this cell type. The marker list can be selected from pure cell type profiles or single cell data using ChooseMarker(). It can also be easily created manually. Please see details section below and example for more information.
alpha  A vector including the prior mean for all cell types.
sigma  A vector including the prior standard deviation for all cell types.
epsilon  A numeric variable to control the level of convergence. With a large epsilon, it converges quickly and the algorithm may not converge well. With a small epsilon, it converges slower and the algorithm may converge "too much". The default value is 1e-3, which we find is a reasonable threshold.
maxIter  Number of maximum iterations.
verbose  A boolean variable of whether to output messages.

Details

More about SelMarker: in addition to selecting markers using ChooseMarker(), we can manually specific marker list. For example, if we know there are two cell type-specific markers for cell type A "Gene1" and "Gene2", and two cell type-specific markers for cell type B "Gene3" and "Gene4", we can create marker list by SelMarker = list(CellA = c("Gene1","Gene2"), CellB = c("Gene3","Gene4")).

One thing to note is that, the genes in marker list should have matches in row names of Ymat. If not, the unmatched markers will be removed during analysis.

Value

A list including

H  Estimated proportion matrix, rows for cell types and columns for samples.
W  Estimated pure cell type profile matrix, rows for genes and columns for cell types

Author(s)

Ziyi Li <zli16@mdanderson.org>

References

Ziyi Li, Zhenxing Guo, Ying Cheng, Peng Jin, Hao Wu. "Robust partial reference-free cell composition estimation from tissue expression profiles."

Examples

# simulate mixed data from complex tissue
# without prior
Wmat <- matrix(abs(rnorm(60*3, 4, 4)), 60, 3)
SelMarker <- list(CellA = 1:20,
                  CellB = 21:40,
                  CellC = 41:60)
for(i in 1:3) {
  Wmat[SelMarker[[i]], i] <- abs(rnorm(20, 50, 10))
}
Hmat <- matrix(rnorm(3*25), 3, 25)
Hmat <- sweep(Hmat, 2, colSums(Hmat), "/")
myprojectMix

Ymat <- Wmat %*% Hmat + abs(rnorm(60*25))
rownames(Ymat) <- 1:60

# deconvolution with TOAST/-P (TOAST without prior)
res <- MDeconv(Ymat, SelMarker, verbose = FALSE)
print(dim(Ymat))
cor(t(res$H), t(Hmat))

# suppose we observe the proportions
# for the same tissue from another study
alpha_prior <- rep(0.33, 3)
sigma_prior <- rep(1, 3)

# deconvolution with TOAST/+P (TOAST with prior)
res2 <- MDeconv(Ymat, SelMarker,
                 alpha = alpha_prior, sigma = sigma_prior,
                 verbose = FALSE)
cor(t(res2$H), t(Hmat))

myprojectMix

Replicate the function myprojectMix() from RefFreeEWAS package

Description

Replicate the function myprojectMix() from RefFreeEWAS package (https://cran.r-project.org/web/packages/RefFreeEWAS/index.html) as that package is not in CRAN anymore

Usage

myprojectMix(Y, Xmat, nonnegative=TRUE, sumLessThanOne=TRUE, lessThanOne=!sumLessThanOne)

Arguments

Y Matrix (m CpGs x n Subjects) of DNA methylation beta values
Xmat Matrix (m CpGs x K cell types) of cell-type specific methylomes
nonnegative All coefficients >=0?
sumLessThanOne Coefficient rows should sum to less than one?
lessThanOne Every value should be less than one (but possibly sum to value greater than one)?

Details

Function for projecting methylation values (Y) onto space of methyomes (Xmat), with various constraints. This is the reference-based method described in Houseman et al. (2012) and also appearing in the minfi package.

Value

Projection coefficients resulting from constrained projection
myRefFreeCellMix

Description

Replicate the function RefFreeCellMix() from RefFreeEWAS package (https://cran.r-project.org/web/packages/RefFreeEWAS/index.html) as that package is not in CRAN anymore.

Usage

myRefFreeCellMix(Y,mu0=NULL,K=NULL,iters=10,Yfinal=NULL,verbose=TRUE)

Arguments

Y Matrix (m CpGs x n Subjects) of DNA methylation beta values
mu0 Matrix (m CpGs x K cell types) of *initial* cell-type specific methylomes
K Number of cell types (ignored if mu0 is provided)
iters Number of iterations to execute
Yfinal Matrix (m* CpGs x n Subjects) of DNA methylation beta values on which to base final methylomes
verbose Report summary of errors after each iteration?

Details

Reference-free decomposition of DNA methylation matrix into cell-type distributions and cell-type methylomes, Y = Mu Omega^T. Either an initial estimate of Mu must be provided, or else the number of cell types K, in which case RefFreeCellMixInitialize will be used to initialize. Note that the decomposition will be based on Y, but Yfinal (=Y by default) will be used to determine the final value of Mu based on the last iterated value of Omega.

Value

Object of S3 class RefFreeCellMix, containing the last iteration of Mu and Omega.

Author(s)

E. Andres Houseman

References

Replicate the function `RefFreeCellMixInitialize()` from RefFreeEWAS package (https://cran.r-project.org/web/packages/RefFreeEWAS/index.html) as that package is not in CRAN anymore.

```r
myRefFreeCellMixInitialize(Y,K=2,Y.Distance=NULL, Y.Cluster=NULL,
                           largeOK=FALSE, dist.method = "euclidean", ...)
```

**Arguments**

- `Y`: Matrix (m CpGs x n Subjects) of DNA methylation beta values
- `K`: Number of cell types
- `Y.Distance`: Distance matrix (object of class "dist") to use for clustering.
- `Y.Cluster`: Hierarchical clustering object (from hclust function)
- `largeOK`: OK to calculate distance matrix for large number of subjects? (See details.)
- `dist.method`: Method for calculating distance matrix
- `...`: Additional parameters for hclust function

**Details**

Initializes the methylome matrix "Mu" for RefFreeCellMix by computing the mean methylation (from Y) over K clusters of Y, determined by the Y.Cluster object. If Y.Cluster object does not exist, it will be created from Y.Distance (using additional clustering parameters if supplied). If Y.Distance does not exist, it will be created from t(Y). As a protection against attempting to fit a very large distance matrix, the program will stop if the number of columns of Y is > 2500, unless largeOK is explicitly set to TRUE.

**Value**

An m x K matrix of mean methylation values.

**Author(s)**

E. Andres Houseman
**plotCorr**

*Show DE/DM state correlation between cell types*

**Description**

This function generates -log10 transformed p-values for each pair of cell types and calculate corresponding Pearson correlation and odds ratio - a modification of function 'ggpairs' in package 'GGally'.

**Usage**

```r
plotCorr(pval, de.state=NULL, pval.thres=NULL, fdr.thres=NULL, p.size = 0.2,
        p.color = grDevices::adjustcolor("black", alpha.f = 0.2),
        fig.margin = c(1,1,1,1),
        fig.margin.unit = 'in', line.type = 'dashed', line.color = 'blue')
```

**Arguments**

- `pval`: matrix of p-values, with rows representing features and columns representing cell types.
- `de.state`: (optional) matrix of DE/DM states (1: DE/DM, 0:non-DE/DM), with rows representing features and columns representing cell types.
- `pval.thres`: threshold of p-value to define DE/DM, required if de.state not provided.
- `fdr.thres`: threshold of FDR to define DE/DM, required if de.state not provided and FDR is preferred than p-value.
- `p.size`: point size for scatter plot
- `p.color`: point color for scatter plot
- `fig.margin`: figure margin
- `fig.margin.unit`: unit of figure margin
- `line.type`: line type in scatter plot
- `line.color`: line color in scatter plot

**Value**

A figure contains scatter plots, Pearson correlation and odds ratio of -log10 transformed p-values for each pair of cell types.

**Author(s)**

Luxiao Chen <luxiao.chen@emory.edu>
Examples

```r
pval.1 <- runif(1000,0,1)
pval.2 <- pval.1 + rnorm(1000,0,0.01)
pval.2[pval.2 < 0] = 0
pval.3 <- runif(1000,0,1)

pval.input <- data.frame('cell.1'=pval.1, 'cell.2'=pval.2, 'cell.3'=pval.3)

plotCorr(pval = pval.input, pval.thres = 0.05)
```

Description

The dataset contains normalized beta values for 3000 CpGs from 100 samples (50 Rheumatoid arthritis patients and 50 controls) and their phenotypes (disease status, age, and gender). The dataset also contains a sub-setted blood reference matrix for the matched 3000 CpGs. This data was obtained and processed based on GSE42861.

Usage

```r
data("RA_100samples")
```

References


Examples

```r
data(RA_100samples)
RA_100samples$Y_raw[1:5,1:5]
head(RA_100samples$Pheno)
head(RA_100samples$Blood_ref)
```
Tsisal

Complete Deconvolution of DNA methylation data based on TOAST and SISAL

Description

A function to conduct complete reference-free deconvolution on DNA methylation data. If a full reference or a partial reference panel is provided, this function also automatically annotate the solved proportions to known cell types.

Usage

Tsisal(Y_raw, K = NULL, knowRef = NULL, possibleCellNumber = 3:15)

Arguments

Y_raw  The DNA methylation 450K array data from complex tissues, rows for CpG sites and columns for samples.
K  The number of pure cell types, we allow users to pre-specify or use our method to estimate.
knowRef  The external reference panel for cell type label assignment.
possibleCellNumber  Range of possible number of cell types. Default is 3:15.

Value

estProp  Estimated proportions.
selMarker  Selected cell type-specific markers.
K  Optional number of cell types.

Author(s)

Weiwei Zhang <wwzhangly@163.com>

References

Complete deconvolution of DNA methylation signals from complex tissues: a geometric approach. Weiwei Zhang, Hao Wu and Ziyi Li.

Examples

### generate a simulation data
knowRef <- matrix(runif(5000*5), 5000, 5)
colnames(knowRef) <- paste0("CellType", 1:5)
Y_raw <- matrix(runif(5000*20), 5000, 20)
rownames(Y_raw) <- paste0("CpG", 1:5000)
colnames(Y_raw) <- paste0("Sample", 1:20)
Tsise(Y_raw = Y_raw, K = 5, knowRef = knowRef)

## if cell type number is unknown
# Tsise(Y.raw = Y_raw, K = NULL, knowRef = knowRef, possibleCellNumber = 4:10)
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