Package ‘DeconRNASeq’
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Type Package
Title Deconvolution of Heterogeneous Tissue Samples for mRNA-Seq data
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Depends R (>= 2.14.0), limSolve, pcaMethods, ggplot2, grid
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Description DeconSeq is an R package for deconvolution of heterogeneous tissues based on mRNA-Seq data. It modeled expression levels from heterogeneous cell populations in mRNA-Seq as the weighted average of expression from different constituting cell types and predicted cell type proportions of single expression profiles.
License GPL-2
biocViews DifferentialExpression
NeedsCompilation no

R topics documented:

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package DeconRNASeq contains function "DeconRNASeq", implementing the decomposition of RNA-Seq expression profilings of heterogeneous tissues into cell/tissue type specific expression and cell type concentration based on cell-type-specific reference measurements.

Description

Main function "DeconRNASeq" implements an nonnegative decomposition by quadratic programming as datasets = signature*A, where "datasets" are the originally measured data matrix (e.g. genes by samples), "signature" is the signature matrix (genes by cell types) and "A" the cell type concentration matrix (cell types by samples)

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DeconRNASeq(datasets, signature)

Author(s)

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

References


Description

A data frame providing the expression profilings of GSE19830 microarray samples.

Usage

all.datasets
Array proportions

**Format**

A matrix with expression studies in the GSE19830 microarray samples: the first three columns are corresponding to the liver, while the last three samples are corresponding to the brain.

**Author(s)**

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

**Examples**

```r
data(rat_liver_brain)
```

---

**Description**

array.proportions: a data frame providing the fractions for liver and brain from the microarray GSE 19830 study

**Usage**

```r
array.proportions
```

**Format**

A matrix whose rows are mixing samples’ name and columns are fractions from pure liver and brain tissues

**Author(s)**

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

**Examples**

```r
data(rat_liver_brain)
```

---

**Description**

array.signatures: a data frame providing the expression values from rat pure liver and brain samples, each has three replicates

**Usage**

```r
array.signatures
```
Format
a data matrix with 30 expressions from rat pure liver and brain tissues

Author(s)
Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

Examples
data(rat_liver_brain)

condplot (step, cond)

Arguments
step an array with the number of genes used to calculate the condition numbers of signature matrices, default stepwise = 20
cond an array with the condition numbers of signature matrices

Value
a plot for the condition numbers of signature matrices

Author(s)
Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

References
Examples

```r
library(DeconRNASeq)

# toy data example:

step <- seq(20, 1000, by=20) # every 20 genes

## cell type-specific gene expression matrix:

x.signature <- matrix(rexp(2000), ncol=2)

sig.cond <- sapply(step, function(x) kappa(scale(x.signature[1:x,])))

function (step, cond)
```

datasets  

Data objects for liver and kidney mixing samples

Description

A data frame providing the RPKM of seven mixing samples.

Usage

datasets

Format

A data frame with 31979 genes’ expression on the 7 mixing samples: reads.1, reads.2, reads.3, reads.4, reads.5, reads.6, reads.7

Author(s)

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

Examples

data(liver_kidney)

decon.bootstrap  

Estimate the confidence interval for the proportions predicted by deconvolution

Description

A function is used to estimate the the confidence interval for the proportions predicted by deconvolution through bootstrapping.

Usage

decon.bootstrap(data.set, possible.signatures, n.sig, n.iter)
DeconRNASeq

Arguments

data.set the data object for mixing samples
possible.signatures a data frame providing the expression values from pure tissue samples
n.sig the number of genes/transcripts used for estimation of proportions from our deconvolution
n.iter the number of bootstraps for our deconvolution

Value

A three-dimensional array to store means and 95% confidence interval

Author(s)

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

References


DeconRNASeq Function for Deconvolution of Complex Samples from RNA-Seq.

Description

This function predicts proportions of constituting cell types from gene expression data generated from RNA-Seq data. Perform nonnegative quadratic programming to get per-sample based globally optimized solutions for constituting cell types.

Usage

DeconRNASeq(datasets, signatures, proportions = NULL, checksig = FALSE, known.prop = FALSE, use.scale = TRUE, fig = TRUE)

Arguments

datasets measured mixture data matrix, genes (transcripts) e.g. gene counts by samples. The user can choose the appropriate counts, RPKM, FPKM etc.

signatures signature matrix from different tissue/cell types, genes (transcripts) by cell types. For gene counts, the user can choose the appropriate counts, RPKM, FPKM etc.

proportions proportion matrix from different tissue/cell types.

checksig whether the condition number of signature matrix should be checked, default = FALSE

known.prop whether the proportions of cell types have been known in advanced for proof of concept, default = FALSE

use.scale whether the data should be centered or scaled, default = TRUE

fig whether to generate the scatter plots of the estimated cell fractions vs. the true proportions of cell types, default = TRUE
Fraction

Details
Data in the originally measured mixture sample matrix: datasets and reference matrix: signatures, need to be non-negative. We recommend to deconvolute without log-scale.

Value
Function DeconRNA-Seq returns a list of results
- `out.all`: estimated cell type fraction matrix for all the mixture samples
- `out.pca`: svd calculated PCA on the mixture samples to estimate the number of pure sources according to the cumulative R2
- `out.rmse`: averaged root mean square error (RMSE)) measuring the differences between fractions predicted by our model and the truth fraction matrix for all the tissue types

Author(s)
Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

References

Examples
```r
## Please refer our demo
##source("DeconRNASeq.R")
### multi_tissue: expression profiles for 10 mixing samples from multiple tissues
#data(multi_tissue.rda)
#datasets <- x.data[,2:11]
#signatures <- x.signature.filtered.optimal[,2:6]
#proportions <- fraction

#DeconRNASeq(datasets, signatures, proportions, checksig=FALSE, known.prop = TRUE, use.scale = TRUE) 
```

fraction

mixing fractions for multi-tissues mixing samples

Description
A data frame providing the fractions from multiple tissues in the mixing samples

Usage
fraction

Format
A matrix whose rows are mixing samples’ name and columns are fractions from pure tissues including brain, muscle, lung, liver and heart
Author(s)

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

Examples

data(multi_tissue)

---

liver_kidney  

data objects for liver and kidney mixing samples

Description

A list containing:
1) datasets: a data frame providing the RPKM of seven mixing samples.
2) proportions: a data frame providing the fractions for liver and kidney in the mixing samples
3) signatures: a data frame providing the expression values from pure liver and kidney samples

Usage

liver_kidney

Format

A list 1) a data frame with 31979 genes’ expression on the 7 mixing samples: reads.1, reads.2, reads.3, reads.4, reads.5, reads.6, reads.7
2) a matrix whose rows are mixing samples’ name and columns are fractions from pure live and kidney tissues
3) a data matrix with 630 expressions from pure liver and kidney tissues

Author(s)

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

Examples

data(liver_kidney)
multiplot

Draw the plots of proportions of cells determined from deconvolution vs. proportions of the cells actually mixed (when available) with RMSE.

Description

A function is used to draw the multiple plots of proportions of cells determined from deconvolution vs. proportions of the cells actually mixed. Each plot corresponds to one tissue/cell.

Usage

multiplot(..., plotlist = NULL, cols)

Arguments

... any number of the plot objects that store the scatter plots for all the cells/tissue types
plotlist any other plot objects
cols columns of the plots, default = 1

Value

A pdf file with the plots of proportions of cells determined from deconvolution vs. proportions of the cells actually mixed with RMSE

Author(s)

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

References


Examples

## The function is currently defined as
function (..., plotlist = NULL, cols) {
  pdf("scatterplots.pdf")
  require(grid)
  plots <- c(list(...), plotlist)
  numPlots = length(plots)
  plotCols = cols
  plotRows = ceiling(numPlots/plotCols)
  grid.newpage()
  pushViewport(viewport(layout = grid.layout(plotRows, plotCols)))
  vplayout <- function(x, y) viewport(layout.pos.row = x, layout.pos.col = y)
  for (i in 1:numPlots) {
    curRow = ceiling(i/plotCols)
    curCol = (i - 1)%/%plotCols + 1
}
multi_tissue

```r
print(plots[[i]], vp = vplayout(curRow, curCol))
}
dev.off()
```

**data objects for multi-tissues mixing samples**

**Description**

a list containing:

1) `x.data`: a data frame providing the RPKM of nine mixing samples.
2) `x.signatures`: a data frame providing the expression values from pure brain, muscle, lung, liver and heart samples.
3) `x.signatures.filtered`: a data frame providing the expression values from pure brain, muscle, lung, liver and heart samples after filtering.
4) `x.signatures.filtered.optimal`: a data frame providing the expression values from pure brain, muscle, lung, liver and heart samples used for the example in DeconRNA-Seq.
5) `fraction`: a data frame providing the fractions from 5 tissues in the mixing samples

**Usage**

`multi_tissue`

**Format**

A list

1) a matrix with all the genes’ expression in the mixing samples: the first two columns are corresponding to the RefSeq accession numbers and gene symbols
2) a matrix whose rows are gene symbols and columns are RPKM expressions from pure tissues.
3) a matrix whose rows are gene symbols and columns are RPKM expressions from pure tissues: the genes with RPKM less than 200 within any of the five tissues have been filtered.
4) a matrix whose rows are gene symbols and columns are RPKM expressions from pure tissues: based on the filtered signature matrix, the optimal number of genes have been selected for the deconvolution according to the condition numbers
5) a matrix whose rows are mixing samples’ name and columns are fractions from pure tissues including brain, muscle, lung, liver and heart

**Author(s)**

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

**Examples**

```r
data(multi_tissue)
```
proportions

proportions for liver and kidney mixing samples

Description
proportions: a data frame providing the fractions for liver and kidney in the mixing samples

Usage
proportions

Format
a matrix whose rows are mixing samples’ name and columns are fractions from pure live and kidney tissues

Author(s)
Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

Examples
data(liver_kidney)

rmse

Calculate the differences between proportions predicted by deconvolution and the values actually measured

Description
A function is used to calculate the root-mean-square error (RMSE) for the accuracy of estimated proportions.

Usage
rmse(x, y)

Arguments
x proportions from the actual measurement
y estimated proportions from our deconvolution

Value
A number for RMSE

Author(s)
Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>
References


signatures

data objects for liver and kidney pure samples

Description

signatures: a data frame providing the expression values from pure liver and kidney samples

Usage

signatures

Format

a data matrix with 630 expressions from pure liver and kidney tissues

Author(s)

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

Examples

data(liver_kidney)

x.data

data objects for multi-tissues mixing samples

Description

A data frame providing the RPKM of nine mixing samples.

Usage

x.data

Format

A matrix with all the genes’ expression in the mixing samples: the first two columns are corresponding to the RefSeq accession numbers and gene symbols

Author(s)

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

Examples

data(multi_tissue)
x.signature

data objects for multi-tissues pure samples

Description
A data frame providing the expression values from pure brain, muscle, lung, liver and heart samples.

Usage
x.signature

Format
A matrix whose rows are gene symbols and columns are RPKM expressions from pure tissues.

Author(s)
Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

Examples
data(multi_tissue)

x.signature.filtered  filtered signatures for multi-tissues pure samples

Description
A data frame providing the expression values from pure brain, muscle, lung, liver and heart samples after filtering.

Usage
x.signature.filtered

Format
A matrix whose rows are gene symbols and columns are RPKM expressions from pure tissues: the genes with RPKM less than 200 within any of the five tissues have been filtered.

Author(s)
Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

Examples
data(multi_tissue)
Description

A data frame providing the expression values from pure brain, muscle, lung, liver and heart samples used for the example in DeconRNA-Seq.

Usage

x.signature.filtered.optimal

Format

A matrix whose rows are gene symbols and columns are RPKM expressions from pure tissues: based on the filtered signature matrix, the optimal number of genes have been selected for the deconvolution according to the condition numbers

Author(s)

Ting Gong <tinggong@gmail.com> Joseph D. Szustakowski <joseph.szustakowski@novartis.com>

Examples

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