Package 'spqn'

May 25, 2024

Title Spatial quantile normalization

Version 1.17.0

Description The spqn package implements spatial quantile normalization (SpQN). This method was developed to remove a mean-correlation relationship in correlation matrices built from gene expression data. It can serve as pre-processing step prior to a co-expression analysis.

License Artistic-2.0

Imports graphics, stats, utils, matrixStats

Depends R (>= 4.0), ggplot2, ggridges, SummarizedExperiment, BiocGenerics

Suggests BiocStyle, knitr, rmarkdown, tools, spqnData (>= 0.99.3), RUnit

VignetteBuilder knitr

URL <https://github.com/hansenlab/spqn>

BugReports <https://github.com/hansenlab/spqn/issues>

biocViews NetworkInference, GraphAndNetwork, Normalization

git_url https://git.bioconductor.org/packages/spqn

git_branch devel

git_last_commit 6e3843d

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-05-24

Author Yi Wang [cre, aut],
Kasper Daniel Hansen [aut]

Maintainer Yi Wang <yiwangthu5@gmail.com>

Contents

---

spqn-package   *Spatial quantile normalization*

Description

The spqn package implements spatial quantile normalization (SpQN). This method was developed to remove a mean-correlation relationship in correlation matrices built from gene expression data. It can serve as pre-processing step prior to a co-expression analysis.

Details

See references for details on spatial quantile normalization.

The main function is normalize_correlation. We include a number of plotting functions for examining the mean-correlation relationship, see the vignette for examples.

References

Y Wang, SC Hicks, KD Hansen (2020). *Co-expression analysis is biased by a mean-correlation relationship.* bioRxiv 2020.02.13.944777. doi:10.1101/2020.02.13.944777

---

normalize_correlation   *Spatial quantile normalization (SpQN)*

Description

This method was developed to remove a mean-correlation relationship in correlation matrices built from gene expression data. It can serve as pre-processing step prior to a co-expression analysis.

Usage

```
normalize_correlation(cor_mat, ave_exp, ngrp, size_grp, ref_grp)
```

Arguments

cor_mat	A (square and symmetrix) correlation matrix.
ave_exp	A vector of expression levels, same length as the number of rows of the correlation matrix in cor_mat. For other types of data, ave_exp can be the vector corresponding to the row/column of the correlation matrix, whose dependency with the distribution of correlations need to be removed.
ngrp	Number of bins in each row/column to be used to partition the correlation matrix, integer.
size_grp	Size of the outer bins to be used to appriximate the distribution of the inner bins, in order to smooth the normalization. Note that the product of size_grp and ngrp must be equal or larger than than the row/column number of cor_mat, and there is no smoothness in the normalization when they are equal.
ref_grp	Location of the reference bin on the diagonal, whose distribution will be used as target distribution in the normalization, an integer.

Value

A normalized correlation matrix.

Examples

```
if(require(spqnData)){
  data(gtex.4k)
  cor_ori <- cor(t(assay(gtex.4k)))
  ave_logrpkm <- rowData(gtex.4k)$ave_logrpkm
  normalize_correlation(cor_ori, ave_exp = ave_logrpkm,
                        ngrp=10, size_grp=15, ref_grp=9)}
```

---

plot_IQR_condition_exp

Get and plot the IQRs of submatrices of the correlation matrix.

Description

The get_IQR_condition_exp function computes the IQRs of a set of 10 by 10 same-size bins that partition the correlation matrix, ordered according to expression level.

The plot_IQR_condition_exp function plots the IQR for each bin among a set of 10 by 10 same-size bins that partition the correlation matrix, with IQR denoted by the width of boxes in the plot.

Usage

```
get_IQR_condition_exp(cor_mat, ave_exp)
plot_IQR_condition_exp(IQR_list)
```

Arguments

cor_mat   correlation matrix, generated by gene expression matrix, with genes sorted by average expression levels.

ave_exp   vector, average expression level of each gene for the normalized gene expression matrix.

IQR_list   List, output of `get_IQR_condition_exp`.

Value

A plot with boxes that shows the IQR of each bin

Note

The mnemonic for `condition_exp` is 'conditional on expression'.

Examples

```
if(require(spqnData)) {
    data(gtex.4k)
    cor_mat <- cor(t(assay(gtex.4k)))
    ave_logrpkm <- rowData(gtex.4k)$ave_logrpkm
    IQR_list <- get_IQR_condition_exp(cor_mat, ave_exp = ave_logrpkm)
    plot_IQR_condition_exp(IQR_list)
    }
```

---

plot_signal_condition_exp

Plot the signal and background distribution of a correlation matrix.

Description

This function allows users to visualize the distributions of (assumed) signal and background, conditional on expression levels. The predicted signals are defined by the 0.1% highest correlations in each bin.

Usage

```
plot_signal_condition_exp(cor_mat, ave_exp, signal)
```

Arguments

cor_mat   Matrix, correlation matrix, generated by gene expression matrix

ave_exp   Vector, average expression level of each gene for the normalized expression matrix

signal   a value between 0 and 1 giving the fraction of correlations which should be considered signal. We often use a value of `0.001`.

Value

Invoked for the side effect of producing a plot.

Note

The mnemonic for `condition_exp` is 'conditional on expression'.

Examples

```
if(require(spqnData)) {
  data(gtex.4k)
  cor_mat <- cor(t(assay(gtex.4k)))
  ave_logrpkm <- rowData(gtex.4k)$ave_logrpkm
  plot_signal_condition_exp(cor_mat, ave_exp=ave_logrpkm, signal=0.05)}
```

---

qqplot_condition_exp	*Q-Q plot for examing the distributions across submatrices of a correlation matrix.*

Description

We partition the correlation matrix into 10x10 bins of equal size, with genes ordered according to expression level. As reference bin, we choose the (9,9) bin (ie. the almost-highest expressed genes). We then make a QQ-plot of the (i,j)'th submatrix vs. the (9,9) submatrix. See the SpQN paper for detail on these choices.

Usage

```
qqplot_condition_exp(cor_mat,ave_exp, i,j)
```

Arguments

cor_mat	Matrix, correlation matrix, generated by gene expression matrix.
ave_exp	Vector, average expression level of each gene for the normalized expression matrix.
i	Integer, row number of the submatrix (see details).
j	Integer, column number of the submatrix (see details).

Value

Invoked for the side effect of producing a plot.

Note

The mnemonic for `condition_exp` is 'conditional on expression'.

Examples

```
if(require(spqnData)) {
  data(gtex.4k)
  cor_mat <- cor(t(assay(gtex.4k)))
  ave_logrpkm <- rowData(gtex.4k)$ave_logrpkm
  qqplot_condition_exp(cor_mat, ave_exp=ave_logrpkm, 1, 1)
}
```

Index