

Package ‘spqn’

January 23, 2026

Title Spatial quantile normalization

Version 1.22.0

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 RELEASE_3_22

git_last_commit 1495b7b

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2026-01-22

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

Maintainer Yi Wang <yiwangthu5@gmail.com>

Contents

spqn-package	2
normalize_correlation	2
plot_IQR_condition_exp	3
plot_signal_condition_exp	4
qqplot_condition_exp	4
Index	6

 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](https://doi.org/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

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

<code>cor_mat</code>	correlation matrix, generated by gene expression matrix, with genes sorted by average expression levels.
<code>ave_exp</code>	vector, average expression level of each gene for the normalized gene expression matrix.
<code>IQR_list</code>	List, output of <code>get_IQR_condition_exp</code> .

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 examining 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

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

* **package**

spqn-package, [2](#)

get_IQR_condition_exp
(plot_IQR_condition_exp), [3](#)

normalize_correlation, [2](#)

plot_IQR_condition_exp, [3](#)
plot_signal_condition_exp, [4](#)

qqplot_condition_exp, [4](#)

spqn (spqn-package), [2](#)
spqn-package, [2](#)