

# Package ‘spqn’

June 30, 2025

**Title** Spatial quantile normalization

**Version** 1.20.0

**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>

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spqn-package	<i>Spatial quantile normalization</i>
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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)

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normalize_correlation	<i>Spatial quantile normalization (SpQN)</i>
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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 approximate 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 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)}
```

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plot\_IQR\_condition\_exp

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

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**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)
}
```

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plot\_signal\_condition\_exp

*Plot the signal and background distribution of a correlation matrix.*

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**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)}
```

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qqplot_condition_exp	<i>Q-Q plot for examing the distributions across submatrices of a correlation matrix.</i>
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**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)  
}
```

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