

# Package ‘scLink’

March 5, 2020

**Title** Inferring functional gene co-expression networks from single cell gene expression data

**Version** 0.0.1

**Description** The scLink method uses statistical network modeling to understand the co-expression relationships among genes and to construct functional gene networks from single-cell gene expression data.

**License** GPL-2

**Depends** parallel

**Imports** QUIC

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.0.2

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scLink_cor	<i>Calculate scLink’s correlation matrix</i>
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## Description

Calculate scLink’s correlation matrix

## Usage

```
scLink_cor(expr, ncores, nthre = 20, dthre = 0.9)
```

**Arguments**

expr	A gene expression matrix with rows representing cells and columns representing genes. Gene names are given as column names. Can be the output of <code>sclink_norm</code> or user constructed gene expression matrices.
ncores	Number of cores if using parallel computation.
nthre	An integer specifying a threshold on the number of complete observations. Defaults to 20.
dthre	A number specifying the threshold on dropout probabilities. Defaults to 0.9.

**Value**

A correlation matrix for gene co-expression relationships.

**Author(s)**

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sclink_net	<i>Infer gene co-expression networks</i>
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**Description**

Infer gene co-expression networks

**Usage**

```
sclink_net(expr, ncores, lda = seq(1, 0.1, -0.05), nthre = 20, dthre = 0.9)
```

**Arguments**

expr	A gene expression matrix with rows representing cells and columns representing genes. Gene names are given as column names. Can be the output of <code>sclink_norm</code> or user constructed gene expression matrices.
ncores	Number of cores if using parallel computation.
lda	A vector specifying a sequence of lambda values to be used in the penalized likelihood.
nthre	An integer specifying a threshold on the number of complete observations. Defaults to 20.
dthre	A number specifying the threshold on dropout probabilities. Defaults to 0.9.

**Value**

A list for gene co-expression relationships. The list contains a `cor` element for `scLink`'s correlation matrix and a `summary` element for the gene networks. `summary` is a list with each element corresponding to the result of one lambda value. Each element of `summary` contains the following information:

**adj:** the adjacency matrix specifying the gene-gene edges;

**Sigma:** the estimated concentration matrix;

**nedge:** number of edges in the gene network;

**bic:** BIC score;

**lambda:** value of lambda in the penalty.

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sclink\_norm

*Pre-process data for scLink*


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#### Description

Pre-process data for scLink

#### Usage

```
sclink_norm(
  count,
  scale.factor = 1e+06,
  filter.genes = FALSE,
  gene.names = NULL,
  n = 500
)
```

#### Arguments

count	A full gene count matrix with rows representing cells and columns representing genes. Gene names are given as column names.
scale.factor	A number specifying the scale factor used for library size normalization. Defaults to 1e6.
filter.genes	A Boolean specifying whether scLink should select genes based on mean expression. When set to FALSE, users need to specify a set of genes to be used for network construction with gene.names. When set to TRUE, scLink will select genes based on their mean expression, and users need to specify the number of genes to be selected with n.
gene.names	A character vector specifying the genes used for network construction. Only needed when filter.genes = FALSE.
n	An integer specifying the number of genes to be selected by scLink (defaults to 500). Only needed when filter.genes = TRUE.

#### Value

A transformed and normalized gene expression matrix that can be used for correlation calculation and network construction.

#### Author(s)

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