

Package: SCENT (via r-universe)

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Title Single Cell Entropy for Estimating Differentiation Potency

Version 2.0.0

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Description Estimates differentiation potency of single cells from scRNA-Seq data using signaling entropy on protein interaction networks. Implements both the full Signaling Entropy Rate (SR) and the fast CCAT approximation. Based on the method described in Teschendorff AE, Enver T (2017) <doi:10.1038/ncomms15599>.

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Depends R (>= 4.0.0)

Imports Matrix, igraph, stats, Rcpp (>= 1.0.0)

LinkingTo Rcpp, RcppArmadillo

Suggests testthat (>= 3.0.0), knitr, rmarkdown, ggplot2, Seurat, dplyr, tidyr, viridis, pheatmap

VignetteBuilder knitr

URL <https://github.com/Zaoqu-Liu/SCENT>,
<https://zaoqu-liu.github.io/SCENT/>

BugReports <https://github.com/Zaoqu-Liu/SCENT/issues>

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Repository <https://zaoqu-liu.r-universe.dev>

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CompCCAT	<i>Correlation of Connectome And Transcriptome (CCAT)</i>
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Description

Estimates signaling entropy via correlation between gene expression and network connectivity.

Usage

```
CompCCAT(exp.m, ppiA.m)
```

Arguments

exp.m	Gene expression matrix (genes x cells). Supports dense or sparse.
ppiA.m	PPI network adjacency matrix (genes x genes).

Details

CCAT computes the Pearson correlation between gene expression and network degree (number of interaction partners) for each cell. This approximation is based on the observation that pluripotent cells express hub genes at higher levels.

The method automatically applies $\log_2(x+1)$ transformation if the input appears to be raw counts ($\max > 50$).

Value

Numeric vector of CCAT scores (one per cell). Higher values indicate higher differentiation potency.

Author(s)

Andrew E Teschendorff, Zaoqu Liu

References

Teschendorff AE, Enver T. Nat Commun. 2017;8:15599.

Examples

```
## Not run:
data(net13Jun12.m)
exp <- matrix(rpois(5000 * 100, 5), nrow = 5000)
rownames(exp) <- head(rownames(net13Jun12.m), 5000)
ccat <- CompCCAT(exp, net13Jun12.m)

## End(Not run)
```

CompSRana

*Compute Signaling Entropy Rate (SR)***Description**

Computes single-cell differentiation potency using the signaling entropy rate on a protein interaction network.

Usage

```
CompSRana(integ.l, local = FALSE)
```

Arguments

`integ.l` Output from [DoIntegPPI](#), containing expMC and adjMC.
`local` Logical. If TRUE, returns normalized local entropies. Default FALSE.

Details

The signaling entropy rate is defined as:

$$SR = \sum_j \pi_j S_j / SR_{max}$$

where π_j is the stationary distribution and S_j is the local entropy at gene j . SR_{max} is the maximum entropy rate of the network, computed from the largest eigenvalue of the adjacency matrix.

Value

List with elements:

SR Signaling entropy rate (0-1). Higher = higher potency.

inv Stationary distribution matrix (genes x cells).

locS Local entropy matrix (genes x cells).

nlocS Normalized local entropies, or NULL if local = FALSE.

Author(s)

Andrew E Teschendorff, Zaoqu Liu

References

Teschendorff AE, Enver T. Nat Commun. 2017;8:15599.

Examples

```
## Not run:
data(net13Jun12.m)
exp <- matrix(rpois(5000 * 50, 5), nrow = 5000)
rownames(exp) <- head(rownames(net13Jun12.m), 5000)
integ <- DoIntegPPI(exp, net13Jun12.m)
sr <- CompSRana(integ)

## End(Not run)
```

DoIntegPPI

Integrate Expression Data with PPI Network

Description

Finds common genes between expression data and PPI network, then extracts the maximally connected subnetwork.

Usage

```
DoIntegPPI(exp.m, ppiA.m)
```

Arguments

exp.m	Gene expression matrix (genes x cells). Should be library-size normalized. Raw counts will be log2-transformed automatically.
ppiA.m	PPI network adjacency matrix (genes x genes).

Details

The function:

1. Identifies genes present in both expression data and PPI network
2. Extracts the induced subnetwork
3. Finds the largest connected component
4. Returns matched expression and adjacency matrices

Value

List with elements:

expMC Expression matrix for genes in the maximal component.

adjMC Adjacency matrix of the maximal connected component.

Author(s)

Andrew E Teschendorff, Zaoqu Liu

References

Teschendorff AE, Enver T. Nat Commun. 2017;8:15599.

Examples

```
## Not run:
data(net13Jun12.m)
exp <- matrix(rpois(5000 * 100, 5), nrow = 5000)
rownames(exp) <- head(rownames(net13Jun12.m), 5000)
integ <- DoIntegPPI(exp, net13Jun12.m)

## End(Not run)
```

net13Jun12.m

Protein-Protein Interaction Network

Description

Protein-protein interaction network adjacency matrix compiled from multiple public databases. Contains 8434 genes.

Usage

```
net13Jun12.m
```

Format

A symmetric binary matrix (8434 x 8434):

Rows/Columns Gene Entrez IDs

Values 1 = interaction, 0 = no interaction

Source

Compiled from public PPI databases (June 2012).

References

Teschendorff AE, Enver T. Nat Commun. 2017;8:15599.

Examples

```
data(net13Jun12.m)
dim(net13Jun12.m)
sum(net13Jun12.m) / 2 # Number of interactions
```

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