Package 'WOTPLY'

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Type Package

Title Plot Connectivity Between Cells from Different Time Points

Version 0.1.0

Description It shows the connections between selected clusters from the latest time point and the clusters from all the previous time points. The transition matrices between time point t and t+1 are obtained from Waddington-OT analysis <https://github.com/ScialdoneLab/WOTPLY>.

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Depends R (>= 4.0)

Imports network, GGally, sna

Suggests testthat, knitr

VignetteBuilder knitr

biocViews software

Encoding UTF-8

RoxygenNote 7.1.1

NeedsCompilation no

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Repository CRAN

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Contents

`convert_names` *convert_names*

Description

convert_names

Usage

```
convert_names(new_row, new_col, transition_matrix)
```

Arguments

`new_row`	Vector with the new row names to assign to *transition_matrix*
`new_col`	Vector with the new column names to assign to *transition_matrix*
`transition_matrix`	Output from *get_transition_matrix*.

Value

A matrix with row names equal to *new_row* and column names equal to *new_col*.

Author(s)

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Examples

```
transition_1 <- matrix(1, ncol = 2, nrow = 2)
colnames(transition_1) <- c("Stage1", "Stage2")
row.names(transition_1) <- c("Stage1", "Stage2")
col_name_new <- c("Stage1_new", "Stage2_new")
row_name_new <- c("Stage1_new", "Stage2_new")
transition_1 <- convert_names(row_name_new, col_name_new, transition_1)
```

`get_transition_matrix` *get_transition_matrix*

Description

The output of *compute_all_transport_maps* from pythonpackage *WOT* is a matrix. Each entry (i,j) describes the transition probability of cell i at time t towards cluster j at time t+1. From this matrix, the average of the transition probability for all the cells at time t belonging to the same cluster is computed. Finally only the entries of the resulting matrix with above *threshold* are kept. The row names of the final matrix are equal to *level_t_plus*, while the column names are equal to the levels of *cluster_t*.

Usage

```
get_transition_matrix(path, cluster_t, threshold, cells_t)
```

Arguments

`path`	Character string with the path to the folder with the outputof the function compute_all_transport_maps from pythonpackage WOT.
`cluster_t`	Vector with cluster assignment for cells at time t. The length is equal to the length of *cells_t*.
`threshold`	Numeric value. Only entry of the transition matrix with weight equal or above *threshold* are kept.
`cells_t`	Character vector with the name of cells at time t for which we want to obtain the transition matrix.

Value

A matrix with row names equal to *level_t_plus* and column names equal to the levels of *cluster_t*.

Author(s)

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See Also

`https://broadinstitute.github.io/wot/`

`select_top_weights` *select_top_weights*

Description

select_top_weights

Usage

```
select_top_weights(transition_matrix, top_link = NULL)
```

Arguments

`transition_matrix`	Output from *get_transition_matrix*.
`top_link`	Integer.Maximum number of links to select between clusters at time t and clusters at time t+1. Links are sorted according to the weight and then only the *top_link* are kept. If *NULL* (default), all the links are kept.

Value

A matrix

Author(s)

Gabriele Lubatti `<gabriele.lubatti@helmholtz-muenchen.de>`

`WOTPLY` *WOTPLY*

Description

A ggnet2 plot is generated showing the connections between *selected_stages* from the latest time point and the clusters from previous time points . The number of columns is equal to the numbers of time points. In each column, the cluster of the corresponding time point is shown as network node. The weight of the links between clusters at time points t and t+1 reflect the weight of the transition probabilities from *list_transition_matrices*.

Usage

```
WOTPLY(
  list_transition_matrices,
  selected_stages,
  cluster_label,
  legend_time,
  customize_color,
  top_link = NULL
)
```

Arguments

`list_transition_matrices`	List of transition matrices. Each matrix contains the transition probabilitiesfrom the clusters at time t (on the columns) towards the clusters at time t+1 (on the rows). The matrices can be obtain from function *get_transition_matrix*
`selected_stages`	Vector with the name of the clusters related to the latest time point for which we want to know the connection to clusters at previous time points.
`cluster_label`	Vector with the cluster information for all the cells from all time points.
`legend_time`	Vector with time information with length equal to the number of time points.
`customize_color`	Character vector with the name of the colour for each cluster (node) in each time point.
`top_link`	Integer.Maximum number of links to select between clusters at time t and clusters at time t+1. Links are sorted according to the weight and then only the *top_link* are kept. If *NULL* (default), all the links are kept.

Value

A ggnet2 plot

Author(s)

Gabriele Lubatti <`gabriele.lubatti@helmholtz-muenchen.de`>

See Also

`https://CRAN.R-project.org/package=GGally`

Examples

```
transition_1 <- matrix(1,ncol = 2,nrow = 2)
colnames(transition_1) <- c("Stage1", "Stage2")
row.names(transition_1) <- c("Stage1", "Stage2")
l_t <- list((transition_1))
selected_stages <- c("Stage1")
cluster_label <- c("Stage1", "Stage2")
legend_time <- c("Day1", "Day2")
customize_color <- c("#F8766D", "#00BFC4")
WOTPLY(l_t, selected_stages, cluster_label, legend_time, customize_color)
```

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