Package: WOTPLY (via r-universe)

September 15, 2024

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>.

License GPL-3

Depends R (>= 4.0)

Imports network, GGally, sna

Suggests testthat, knitr

VignetteBuilder knitr

biocViews software

Encoding UTF-8

RoxygenNote 7.1.1

NeedsCompilation no

Author Gabriele Lubatti [aut, cre, cph]

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

Date/Publication 2022-09-12 07:43:01 UTC

Repository https://gabrielelubatti.r-universe.dev

RemoteUrl https://github.com/cran/WOTPLY

RemoteRef HEAD

RemoteSha 4ee0b1ae45d9716919d7e4900011ceb7c5a1c372

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)

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

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)

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

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 clus-
ters 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)
```

Index