# 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](https://github.com/ScialdoneLab/WOTPLY).

**License** GPL-3  
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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")
rownames(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

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

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

Arguments

- `path`: Character string with the path to the folder with the output of 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/](https://broadinstitute.github.io/wot/)
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)

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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 probabilities from the clusters at time t (on the columns) towards the clusters at time t+1 (on the rows). The matrices can be obtained 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)

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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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