Package 'SLIDE'

January 20, 2025

Title Single Cell Linkage by Distance Estimation is SLIDE

Version 1.0.0

Description This statistical method uses the nearest neighbor algorithm to estimate absolute distances between single cells
based on a chosen constellation of surface proteins, with these distances being a measure of the similarity between the
two cells being compared. Based on Sen, N., Mukherjee, G., and Arvin, A.M. (2015) <DOI:10.1016/j.ymeth.2015.07.008>.

Depends R (>= 3.4.0)

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 6.0.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

Author Gourab Mukherjee [aut],
Arjun Panda [aut, cre],
Ann Arvin [aut],
Adrish Sen [aut],
Nandini Sen [aut]

Maintainer Arjun Panda <arjunpanda@gwu.edu>

Repository CRAN

Date/Publication 2018-06-15 15:50:12 UTC

Contents

---

bootstrap_cutoff	*Bootstrap Cutoff for SLIDE*

Description

Bootstrap Cutoff for SLIDE

Usage

```
bootstrap_cutoff(uninfected, fraction = 0.1, iter = 20, level = 0.05)
```

Arguments

uninfected	A dataframe of protein expression levels in an uninfected subset of cells. All columns must be numeric expression levels.
fraction	Fraction of uninfected cells used for the SLIDE bootstrap. This value should reflect the size of the infected cell population relative to the uninfected cell population. Must be between >0 and <=0.2. Default is 0.1.
iter	Iterations of the SLIDE bootstrap. Default is 20.
level	Alpha level to determine cutoff for a significant mean distance ratio. Default is 0.05.

Value

This function bootstraps a cutoff for the mean distance ratio from the uninfected cell population by running the SLIDE procedure on a random subset of uninfected cells a specified number of times (default 20x). Only to be used if our pre-determined value of 1.2 is insufficient. Depending on how large the uninfected dataset is, this function may take many hours to complete.

References

Sen, N., Mukherjee, G., Sen, A., Bendall, S. C., Sung, P., Nolan, G. P., & Arvin, A. M. (2014). Single-Cell Mass Cytometry Analysis of Human Tonsil T Cell Remodeling by Varicella Zoster Virus. Cell Reports, 8(2), 633–645. https://doi.org/10.1016/j.celrep.2014.06.024

Examples

```
cutoff <- bootstrap_cutoff(uninfected = UN_sig, fraction = (nrow(I_sig)/nrow(UN_sig)), iter=1)
cutoff
```

I_sig *Protein Expression Levels in an Infected Cell Sample*

Description

Simulated data from an experiment measuring viral reprogramming of lymphocyte surface proteins. These cells demonstrate evidence for significant reprogramming (see vignette for example).

Usage

```
I_sig
```

Format

An object of class `data.frame` with 38 rows and 7 columns.

---

slide *Single Cell Linkage by Distance Estimation is SLIDE*

Description

Single Cell Linkage by Distance Estimation is SLIDE

Usage

```
slide(infected, uninfected, cutoff = 1.2)
```

Arguments

infected	A dataframe of protein expression levels in an infected subset of cells. All columns must be numeric expression levels.
uninfected	A dataframe of protein expression levels in uninfected cells. All columns must be numeric expression levels. This can be interpreted as the population of cells, of which the infected cells are a subset.
cutoff	This is the fold-change in distances being tested from an infected cell to its nearest uninfected and infected cell. The default value is 1.2. Determine an exact value using the `bootstrap_cutoff` function.

Value

A list with containing five items. Non-parametric testing of up or downregulation in protein expression between the `infected` and `uninfected` cells, for both balanced and unbalanced comparisons. Three, it returns a boxplot mirroring these results. Four, the SLIDE Wilcox Rank Sum test results for evidence of cellular remodeling in the infected cells. Fifth, the mean ratio of the distances from each infected cell to its nearest uninfected cell and nearest infected cell.

References

Sen, N., Mukherjee, G., and Arvin, A.M. (2015). Single cell mass cytometry reveals remodeling of human T cell phenotypes by varicella zoster virus. Methods 90, 85–94.

Examples

```
slide(I_sig, UN_sig)
```

UN_sig   *Protein Expression Levels in an Uninfected Cell Population*

Description

Simulated data from an experiment measuring viral reprogramming of lymphocyte surface proteins. These cells represent the uninfected cell population to which the infected cells will be compared to.

Usage

```
UN_sig
```

Format

An object of class `data.frame` with 781 rows and 7 columns.

Index