

Package ‘LACE’

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Title Longitudinal Analysis of Cancer Evolution (LACE)

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Depends R (>= 3.6.0)

Imports parallel, Rfast

Suggests BiocGenerics, BiocStyle, testthat, knitr

Name LACE: an R package for the inference of longitudinal cancer evolution models

Description LACE is an algorithmic framework that processes single-cell somatic mutation profiles from cancer samples collected at different time points and in distinct experimental settings, to produce longitudinal models of cancer evolution. The approach solves a Boolean Matrix Factorization problem with phylogenetic constraints, by maximizing a weighed likelihood function computed on multiple time points.

Encoding UTF-8

LazyData TRUE

License file LICENSE

URL <https://github.com/BIMIB-DISCo/LACE>

BugReports <https://github.com/BIMIB-DISCo/LACE>

biocViews BiomedicalInformatics

RoxygenNote 7.0.2

VignetteBuilder knitr

NeedsCompilation no

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data	<i>mutation data from Rambow, Florian, et al. "Toward minimal residual disease-directed therapy in melanoma." Cell 174.4 (2018): 843-855.</i>
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Description

mutation data from Rambow, Florian, et al. "Toward minimal residual disease-directed therapy in melanoma." Cell 174.4 (2018): 843-855.

Usage

data(data)

Format

list of mutation data for four time points

Value

list of mutational data for a total of 674 single cells

Source

Rambow, Florian, et al. "Toward minimal residual disease-directed therapy in melanoma." Cell 174.4 (2018): 843-855.

inference	<i>results obtained with the function LACE on the provided input data from Rambow, Florian, et al. "Toward minimal residual disease-directed therapy in melanoma." Cell 174.4 (2018): 843-855.</i>
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Description

results obtained with the function LACE on the provided input data from Rambow, Florian, et al. "Toward minimal residual disease-directed therapy in melanoma." Cell 174.4 (2018): 843-855.

Usage

data(inference)

Format

results obtained with the function LACE on the provided input data

Value

results obtained with the function LACE on the provided input data

LACE	<i>LACE</i>
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Description

Perform inference of the maximum likelihood clonal tree from longitudinal data.

Usage

```
LACE(
  D,
  lik_w = NULL,
  alpha = NULL,
  beta = NULL,
  initialization = NULL,
  num_rs = 50,
  num_iter = 10000,
  n_try_bs = 500,
  learning_rate = 1,
  marginalize = FALSE,
  num_processes = Inf,
  seed = NULL,
  verbose = TRUE,
  log_file = ""
)
```

Arguments

D	Mutation data from multiple experiments for a list of driver genes.
lik_w	Weight for each data point. If not provided, weights to correct for sample sizes are used.
alpha	False positive error rate provided as list of elements; if a vector of alpha (and beta) is provided, the inference is performed for multiple values and the solution at maximum-likelihood is returned.
beta	False negative error rate provided as list of elements; if a vector of beta (and alpha) is provided, the inference is performed for multiple values and the solution at maximum-likelihood is returned.
initialization	Starting point of the mcmc; if not provided, a random starting point is used.
num_rs	Number of restarts during mcmc inference.
num_iter	Maximum number of mcmc steps to be performed during the inference.
n_try_bs	Number of steps without change in likelihood of best solution after which to stop the mcmc.
learning_rate	Parameter to tune the probability of accepting solutions at lower values during mcmc. Value of learning_rate = 1 (default), set a probability proportional to the difference in likelihood; values of learning_rate greater than 1 increase the chance of accepting solutions at lower likelihood during mcmc while values lower than 1 decrease such probability.
marginalize	Boolean. Shall I marginalize C when computing likelihood?

<code>num_processes</code>	Number of processes to be used during parallel execution. To execute in single process mode, this parameter needs to be set to either NA or NULL.
<code>seed</code>	Seed for reproducibility.
<code>verbose</code>	Boolean. Shall I print to screen information messages during the execution?
<code>log_file</code>	log file where to print outputs when using parallel. If parallel execution is disabled, this parameter is ignored.

Value

A list of 7 elements: B, C, clones_prevalence, relative_likelihoods, joint_likelihood, clones_summary and error_rates. Here, B returns the maximum likelihood longitudinal clonal tree, C the attachment of cells to clones and clones_prevalence clones' prevalence; relative_likelihoods and joint_likelihood are respectively the likelihood of the solutions at each individual time points and the joint likelihood; clones_summary provide a summary of association of mutations to clones. Finally error_rates provides the best values of alpha and beta among the considered ones.

Examples

```
data(data)
inference = LACE(D = data,
  lik_w = c(0.2482690, 0.2566766, 0.2349159, 0.2601385),
  alpha = list(c(0.05, 0.10, 0.05, 0.05)),
  beta = list(c(0.05, 0.10, 0.05, 0.05)),
  num_rs = 5,
  num_iter = 10,
  n_try_bs = 5,
  num_processes = NA,
  seed = 12345,
  verbose = FALSE)
```

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