

Package ‘OptM’

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Title Estimating the Optimal Number of Migration Edges from 'Treemix'

Version 0.1.8

Description The popular population genetic software 'Treemix' by 'Pickrell and Pritchard' (2012) <[DOI:10.1371/journal.pgen.1002967](https://doi.org/10.1371/journal.pgen.1002967)> estimates the number of migration edges on a population tree. However, it can be difficult to determine the number of migration edges to include. Previously, it was customary to stop adding migration edges when 99.8% of variation in the data was explained, but 'OptM' automates this process using an ad hoc statistic based on the second-order rate of change in the log likelihood. 'OptM' also has added functionality for various threshold modeling to compare with the ad hoc statistic.

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License GPL (>= 2)

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 optM

optM function

Description

Load a folder of .llik files from the program Treemix and determine the optimal number of migration edges to include

Usage

```
optM(
  folder,
  orientagraph = F,
  tsv = NULL,
  method = "Evanno",
  ignore = NULL,
  thresh = 0.05,
  ...
)
```

Arguments

folder	A character string of the path to a directory containing .llik, .cov.gz and .model-cov.gz files produced by Treemix
orientagraph	A logical indicating whether the files were produced from Treemix (FALSE) or OrientAGraph (TRUE). Default = F
tsv	a string defining the name of the tab-delimited output file. If NULL (default), then no data file is produced.
method	a string containing the method to use, either "Evanno", "linear", or "SiZer". Default is "Evanno".
ignore	a numeric vector of whole numbers indicating migration edges to ignore. Useful when running Treemix on a prebuilt tree (ignore = 0). Default is NULL.
thresh	a numeric value between 0 and 1 for the threshold to use for the proportion of increase in likelihood that defines when a plateau is reached. Default is 0.05 (5%), only applicable for method = "linear".
...	other options sent to the function "SiZer" - see the R package 'SiZer'

Value

If method = "Evanno": A data frame with 17 columns summarizing the results for each migration edge (rows).

The columns are: "m" - number of migration edges from the model; "runs" = number of iterations for "m"; "mean(Lm)" - mean log likelihood across runs; "sd(Lm)" - standard deviation of log likelihood across runs; "min(Lm)" - minimum log likelihood across runs; "max(Lm)" - maximum log likelihood across runs; "L'(m)" - first-order rate of change in log likelihood; "sdL'(m)"

- standard deviation of first-order rate of change in log likelihood; "minL'(m)" - minimum first-order rate of change in log likelihood; "maxL'(m)" - maximum first-order rate of change in log likelihood; "L"(m) - second-order rate of change in log likelihood; "sdL"(m) - standard deviation of the second-order rate of change in log likelihood; "minL"(m) - minimum second-order rate of change in log likelihood; "maxL"(m) - maximum second-order rate of change in log likelihood; "Deltam" - the ad hoc deltaM statistic (second order rate of change in log likelihood); "mean(f)" - mean proportion of variation explained by the models; "sd(f)" - standard deviation of the proportion of variation explained by the models

If method = "linear": A list containing 5 elements:

\$out - a data frame with the name of each model, the degrees of freedom (df), the Akaike information criterion (AIC), the deltaAIC, and the optimal estimate for m based on the model.

\$PiecewiseLinear - the piecewise linear model object

\$BentCable - the bent cable model object

\$SimpleExponential - the simple exponential model object

\$NonLinearLeastSquares - the NLS model object

If method = "SiZer": an object of class "SiZer" (see the R package 'SiZer' for more information)

Examples

```
# Load a folder of simulated test data for m = 3
folder <- system.file("extdata", package = "OptM")
test.optM = optM(folder)

# To view the various linear modeling estimates:
# test.linear = optM(folder, method = "linear")

# To view the results from the SiZer package:
# test.sizer = optM(folder, method = "SiZer")
```

plot_optM

plot_optM function

Description

Plotting the optM results. This function visualizes the output of optM, including the amount of total variation explained across each value of the migration rate

Usage

```
plot_optM(input, method = "Evanno", plot = TRUE, pdf = NULL)
```

Arguments

input	an object produced by the function 'optM'
method	a string containing the method to use, either "Evanno", "linear", or "SiZer". Default is "Evanno", but needs to match that used in 'optM'
plot	logical of whether or not to display the plot
pdf	string of the file name to save the resulting pdf plot. If NULL, no file is saved. Default is NULL

Value

a plot or pdf of a plot

Examples

```
# Load a folder of simulated test data for m = 3
folder <- system.file("extdata", package = "OptM")
# Run the Evanno method and plot the results
test.optM = optM(folder)
plot_optM(test.optM, method = "Evanno")

# To view the various linear modeling estimates and plot:
# test.linear = optM(folder, method = "linear")
# plot_optM(test.linear, method = "linear")

# To view the results from the SiZer package:
# test.sizer = optM(folder, method = "SiZer")
# plot_optM(test.sizer, method = "SiZer")
```

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