Package: RateViz (via r-universe)

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Type Package

Title Visualizations for instantaneous rate matrices

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Description This package uses an instantaneous rate matrix (such as is
used for models of DNA evolution, morphological character
change over evolutionary history, and other areas) and
summarizes it in various ways. These could include bubble
plots, a network showing transitions, or calculations to figure
out likely paths between two states.

Depends expm, miscTools, igraph

License GPL (>= 2)

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

RemoteUrl https://github.com/bomeara/RateViz

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Description

This package uses an instantaneous rate matrix (such as is used for models of DNA evolution, morphological character change over evolutionary history, and other areas) and summarizes it in various ways. These could include bubble plots, a network showing transitions, or calculations to figure out likely paths between two states.

Details

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License:	GPL (>=2)

Author(s)

Brian C. O'Meara and Jeremy M. Beaulieu

Maintainer: Brian C. O'Meara <omeara.brian@gmail.com>

Examples

```
#A random sample transition matrix
Q <- matrix(runif(9), 3, 3)
diag(Q) <- 0
diag(Q) <- -rowSums(Q)
colnames(Q) <- c("A", "B", "C")
rownames(Q) <- c("A", "B", "C")
print(Q)
ComputePathwayProbability(Q, from=1, to=3)
PlotTransitionNetwork(Q)
```

ComputePathwayProbability

ComputePathwayProbability

Description

This implements the rate summary used in Zanne et al. 2014. Using the rate matrix, one can calculate

Usage

```
ComputePathwayProbability(Q, from, to, correct.diag = TRUE, total.time = 1e+06)
```

Arguments

Q	Instantaneous rate matrix
from	Index (position) of start state in the matrix (i.e., the second character)
to	Index (position) of end state in the matrix
correct.diag	Normally the diagonal is the negative sum of the non-diagonal elements in a row. If TRUE, this verifies that this is so
total.time	A large enough time such that there is essentially no chance of remaining unchanged

Value

A vector with the probability of each path into the final state.

Author(s)

Brian C. O'Meara

References

Zanne et al. 2014

Examples

```
#A random sample transition matrix
Q <- matrix(runif(9), 3, 3)
diag(Q) <- 0
diag(Q) <- -rowSums(Q)
colnames(Q) <- c("A", "B", "C")
rownames(Q) <- c("A", "B", "C")
print(Q)
ComputePathwayProbability(Q, from=1, to=3)
```

PlotBubbleMatrix   *PlotBubbleMatrix*

Description

Plots a rate matrix such that circle area correlates with the rate

Usage

```
PlotBubbleMatrix(Q, main = "", special = Inf, cex = 1)
```

Arguments

Q	Instantaneous rate matrix
main	Optional plot title
special	If you want to highlight a particular element, input its number here
cex	Adjustment for text size

Value

None

Author(s)

Brian C. O'Meara

Examples

```
#A random sample transition matrix
Q <- matrix(runif(9), 3, 3)
diag(Q) <- 0
diag(Q) <- -rowSums(Q)
colnames(Q) <- c("A", "B", "C")
rownames(Q) <- c("A", "B", "C")
print(Q)
PlotBubbleMatrix(Q)
```

PlotTransitionNetwork *PlotTransitionNetwork*

Description

This plots a network showing transition rates between given states. It uses igraph for plotting.

Usage

```
PlotTransitionNetwork(Q, main = "", layout.fn = layout.circle, ...)
```

Arguments

Q	Instantaneous rate matrix
main	Title for plot (optional)
layout.fn	Layout function from igraph. By default this uses a circle layout, but you may use other igraph functions. layout.fruchterman.reingold may generate a good looking graph.
...	Other arguments to pass to plot.igraph()

Value

No return

Author(s)

Brian C. O'Meara

Examples

```
#A random sample transition matrix
Q <- matrix(runif(9), 3, 3)
diag(Q) <- 0
diag(Q) <- -rowSums(Q)
colnames(Q) <- c("A", "B", "C")
rownames(Q) <- c("A", "B", "C")
print(Q)
PlotTransitionNetwork(Q)
```

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