Package ‘ternarynet’

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R topics documented:

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attractorSummary

Summarize Attractors

Description

This function summarizes the posterior probability of possible attractors.

Usage

attractorSummary(tpost, post.prob.limit = 0.01, wildtype = TRUE)

Arguments

tpost a ternaryPost object
post.prob.limit the minimum posterior probability for an attractor to be listed
wildtype if TRUE, the wildtype attractors are summarized; if FALSE, the perturbed attractors are summarized.

Value

The function returns a matrix of attractors and posterior probabilities for each perturbation.

Author(s)

Matthew N. McCall and Anthony Almudevar

See Also


Examples

ssObj <- matrix(c(1,1,1,0,1,0,1,0,1),nrow=3)
pObj <- matrix(c(1,0,0,1,0,0,0,0,1),nrow=3)
rownames(ssObj) <- rownames(pObj) <- colnames(ssObj) <- colnames(pObj) <- c("Gene1","Gene2","Gene3")
tnfitObj <- tnetfit(ssObj, pObj)
tnpostObj <- tnetpost(tnfitObj, mdelta=10, msample=10)
attractorSummary(tnpostObj)
**graphPosterior**

**Network Topology**

**Description**

This function summarizes the topology of the ternary network using marginal edge probabilities.

**Usage**

```r
graphPosterior(tpost)
```

**Arguments**

- `tpost`: a ternaryPost object

**Value**

The function returns a matrix of marginal posterior probabilities of each possible network edge – rows are children and columns are parents. The first column represents no parents.

**Author(s)**

Matthew N. McCall and Anthony Almudevar

**See Also**


**Examples**

```r
ssObj <- matrix(c(1,1,1,1,1,0,0,0,1),nrow=3)
pObj <- matrix(c(1,0,0,0,1,0,0,0,1),nrow=3)
rownames(ssObj) <- rownames(pObj) <- colnames(ssObj) <- colnames(pObj) <- c("Gene1","Gene2","Gene3")
tnfitObj <- tnetfit(ssObj, pObj)
tnpostObj <- tnetpost(tnfitObj, mdelta=10, msample=10)
graphPosterior(tnpostObj)
```

---

**plotFit**

**Network Fit Plot**

**Description**

This function plots the graph corresponding to the minimum scoring network.

**Usage**

```r
plotFit(ternaryFit, type="interactive", ...)
```
Arguments

- ternaryFit: a ternaryFit object
- type: the type of plot to produce. "interactive" produces a plot that can be altered in the plotting window using the tkplot function from the igraph package. "static" produces a standard plot in any R graphics device.
- ...: additional parameters passed to the plotting function

Value

A plot of the network corresponding to the minimum score (stored in the graphObjMin slot) is plotted.

Author(s)

Matthew N. McCall and Anthony Almudevar

See Also


Examples

```r
ssObj <- matrix(c(1,1,1,0,1,0,0,1),nrow=3)
pObj <- matrix(c(1,0,0,1,0,0,0,1),nrow=3)
tnfitObj <- tnetfit(ssObj, pObj)
plotFit(tnfitObj, type="static")
```

plotPost

Network Posterior Plot

Description

This function plots the graph consisting of all edges with a marginal posterior probability greater than the selected threshold.

Usage

```r
plotPost(ternaryPost, threshold=0.5, type="interactive", ...)
```

Arguments

- ternaryPost: a ternaryPost object
- type: the type of plot to produce. "interactive" produces a plot that can be altered in the plotting window using the tkplot function from the igraph package. "static" produces a standard plot in any R graphics device.
- threshold: the marginal posterior probability required for an edge to be included in the plot.
- ...: additional parameters passed to the plotting function
**Value**

A plot of the network consisting of all edges with a marginal posterior probability greater than the selected threshold.

**Author(s)**

Matthew N. McCall and Anthony Almudevar

**See Also**


**Examples**

```r
ssObj <- matrix(c(1,1,1,1,0,1,0,1,0),nrow=3)
pObj <- matrix(c(1,0,0,1,0,0,0,0,0),nrow=3)
tnfitObj <- tnetfit(ssObj, pObj)
tnpostObj <- tnetpost(tnfitObj, mdelta=10, msample=10)
plotPost(tnpostObj, type="static")
```

---

**plotTraces**

This function plots the trace of four model parameters.

**Usage**

```r
plotTraces(tfit)
```

**Arguments**

- `tfit` a ternaryFit object

**Value**

The function creates a 2x2 grid of the four trace plots.

**Author(s)**

Matthew N. McCall and Anthony Almudevar

**See Also**

Examples

```r
ssObj <- matrix(c(1,1,1,0,1,0,0,1),nrow=3)
pObj <- matrix(c(1,0,0,1,0,0,0,1),nrow=3)
tnfitObj <- tnetfit(ssObj, pObj)
plotTraces(tnfitObj)
```

predictAttractor

**Predict the attractor(s) resulting from a given perturbation**

Description

This function computes the posterior probabilities of attractors reached for a given perturbation using the networks from a ternaryPost object.

Usage

```r
predictAttractor(tpost, perturbations, wildtype = TRUE, verbose = FALSE)
```

Arguments

- `tpost`: a ternaryPost object
- `perturbations`: a list with two elements: `perturbed.genes` and `forced.states`
- `wildtype`: if `TRUE`, the wildtype attractors are summarized; if `FALSE`, the perturbed attractors are summarized.
- `verbose`: if `TRUE`, periodic reports on progress are printed.

Value

The function returns a list with two elements: `post.prob`: the posterior probability of each attractor `attractor.summary`: a single vector of steady states based on the resulting attractor

Author(s)

Matthew N. McCall and Anthony Almudevar

See Also


Examples

```r
ssObj <- matrix(c(1,1,1,0,1,0,0,1),nrow=3)
pObj <- matrix(c(1,0,0,1,0,0,0,1),nrow=3)
rownames(ssObj) <- rownames(pObj) <- colnames(ssObj) <- colnames(pObj) <- c("Gene1","Gene2","Gene3")
tnfitObj <- tnetfit(ssObj, pObj)
tnpostObj <- tnetpost(tnfitObj, mdelta=10, msample=10)
predictAttractor(tnpostObj, list(perturbed.genes=c(1,2),forced.states=c(1,1)))
```
simulateSteadyState    Simulate Steady State Data

Description
This function generates simulated steady state data from a given network.

Usage
simulateSteadyState(perturbationObj, tableObj, graphObj, degreeObj, wildtype=FALSE)

Arguments
perturbationObj
  a matrix of perturbation experiments. Rows are genes and columns are experiments.
tableObj
  a matrix containing the transition function tables
graphObj
  a matrix containing the parents of each node
degreeObj
  a vector containing the in-degree of each node
wildtype
  if TRUE, the perturbations are assumed to be transient; if FALSE, the perturbations are assumed to be persistent.

Value
The function creates a steadyStateObj.

Author(s)
Matthew N. McCall and Anthony Almudevar

See Also

Examples
pObj <- matrix(c(1,0,0,0,1,0,0,0,1),nrow=3)
degreeObj <- c(0,1,1)
graphObj <- matrix(nrow=1,ncol=3)
graphObj[1,1] <- 0
graphObj[1,2] <- 1
graphObj[1,3] <- 2
tableObj <- matrix(nrow=3,ncol=3)
tableObj[1,] <- rep(0,3)
tableObj[2,] <- c(-1,0,1)
tableObj[3,] <- c(-1,0,1)
ssObj <- simulateSteadyState(pObj, tableObj, graphObj, degreeObj)
Description

This is a class representation of the output of the ternary network fitting algorithm implemented in the function `tnetfit()`.

Creating Objects

While one can create their own objects using the function `ternaryFit()`, this is highly discouraged. Typically this class is created by running the `tnetfit` function.

Slots

- `perturbationObj`: a matrix of perturbation experiments. Rows are genes and columns are experiments.
- `steadyStateObj`: a matrix of steady gene expression observations from a perturbation experiment. Rows are genes and columns are experiments.
- `geneNames`: a vector of gene names corresponding to the rows of the `perturbationObj` and `steadyStateObj`.
- `experimentNames`: a vector of experiment names corresponding to the columns of the `perturbationObj` and `steadyStateObj`.
- `degreeObjMin`: a vector containing the in-degree of each node in the fit achieving the minimum score.
- `graphObjMin`: a matrix containing the parents of each node in the fit achieving the minimum score.
- `tableObjMin`: a matrix containing the table in the fit achieving the minimum score.
- `newScore`: the most recent score.
- `minScore`: the minimum score.
- `finalTemperature`: the final value of the temperature parameter.
- `traces`: a dataframe containing traces for 4 parameters.
- `stageCount`: the number of stages.
- `xSeed`: the random seed.
- `inputParams`: the `ternaryFitParameters` object used.

Methods

All named elements can be accessed and set in the standard way (e.g. `xSeed(object)` and `xSeed(object)<-`).

Author(s)

Matthew N. McCall and Anthony Almudevar

See Also

ternaryFitParameters-class

Examples

```r
ssObj <- matrix(c(1,1,1,0,1,1,0,0,1),nrow=3)
pObj <- matrix(c(1,0,0,0,1,0,0,0,1),nrow=3)
tnfitObj <- tnetfit(ssObj, pObj)
class(tnfitObj)
```

ternaryFitParameters-class

Ternary Network Fitting Parameters

Description

This is a class representation of the input parameters for the ternary network fitting algorithm implemented in the function `tnetfit`.

Creating Objects

```r
ternaryFitParameters()
```

This creates a `ternaryFitParameters` object with the default fitting parameters.

Slots

- `perturbationType`: this parameter currently can only be set to 1
- `scoreType`: the method to score networks. Can be set to either 1 or 2, corresponding the the score types in Almudevar et al. (2011).
- `backupStage`: current fit is output periodically according to this parameter
- `maxStage`: the maximum number of stages permitted. Ideally, the actual number of stages required until convergence should be much less than this value.
- `maxTransition`: This parameter provides an adaptive truncation of the stage sample size. The stage terminates before the specified fixed sample size if the number of transitions resulting in a strict increase of the score reaches this value. If the sampler is in steady state, then this count should be approximately half the number of transitions in which the score changes value.
- `epsilon`: Convergence tolerance.
- `beta0`: Algorithm terminates when this number of consecutive convergence events have occurred.
- `chi0`: The target initial acceptance rate. This should be close to 1, although setting it too close will increase computation time.
- `delta`: The increment change in steady state distribution between stages (as variational distance). Larger values tend to decrease computation time, but too large a value will result in spurious convergence.
- `ne`: The fixed sample size (number of MCMC transitions) per stage.
- `m0`: The sample size (number of transitions) used to determine the initial temperature.
- `maxDegree`: Maximum number of parents per node permitted in model topology.
- `pAddParent`: This is the probability of adding a parent to a randomly selected node in the proposal function.
- `pExchangeParent`: This parameter gives the probability of a parent exchange in the proposal function. The AddParent operation takes precedence, so this probability should be interpreted as being conditional on the rejection of the AddParent operation.
neighborDegree: Number of applications of the proposal function.

pNeighborhood: Vector of probabilities denoted, which generates the random number of proposal function iterations. The length is one less than neighborDegree. If neighborDegree equals 1 then no iteration is performed, and this vector is ignored.

rho: Weight parameter for the exponential smoothing of the variance estimate. For no smoothing set to 1.

degree: This parameter provides a complexity penalty. This number times the number of edges is added to the score. To apply no penalty set this parameter to 0.

Methods

All named elements can be accessed and set in the standard way (e.g. scoreType(object) and scoreType(object)<-).

Author(s)

Matthew N. McCall and Anthony Almudevar

See Also


Examples

# create an instance
ternaryFitParameters()

---

**ternaryPost-class**  
*Ternary Network Posterior*

**Description**

This is a class representation of the output of the ternary network posterior sampling algorithm implemented in the function tnetpost.

**Creating Objects**

While one can create their own objects using the function ternaryPost(), this is highly discouraged. Typically this class is created by running the tnetpost function.

**Slots**

- perturbationObj: a matrix of perturbation experiments. Rows are genes and columns are experiments.
- steadyStateObj: a matrix of steady gene expression observations from a perturbation experiment. Rows are genes and columns are experiments.
- geneNames: a vector of gene names corresponding to the rows of the perturbationObj and steadyStateObj.
experimentNames: a vector of experiment names corresponding to the columns of the perturbationObj and steadyStateObj.
scores: the score of each sample
degreeObjs: the in-degree vector for each sample
graphObjs: the graph matrix for each sample
tableObjs: the table matrix for each sample
inputParams: the ternaryFitParameters object used

Methods
All named elements can be accessed and set in the standard way (e.g. scores(object) and scores(object)<-).

Author(s)
Matthew N. McCall and Anthony Almudevar

See Also

Examples
ssObj <- matrix(c(1,1,1,0,1,1,0,0,1),nrow=3)
pObj <- matrix(c(1,0,0,0,1,0,0,0,1),nrow=3)
tnfitObj <- tnetfit(ssObj, pObj)
tnpostObj <- tnetpost(tnfitObj, mdelta=10, msample=10)
class(tnpostObj)

---

tnetfit  
Ternary Network Fitting

Description
This function fits a ternary network based on perturbation experiments.

Usage
tnetfit(steadyStateObj, perturbationObj, params=ternaryFitParameters(), xSeed=NA)

Arguments
steadyStateObj  a matrix of steady gene expression observations from a perturbation experiment. Rows are genes and columns are experiments.
perturbationObj  a matrix of perturbation experiments. Rows are genes and columns are experiments.
params  a ternaryFitParameters object
xSeed  an integer random seed. If NA, a random seed is generated.
tnetpost

Description

This function samples from the posterior density of a ternary network based on perturbation experiments.

Usage

tnetpost(tfit, mdelta=as.integer(10000), msample=as.integer(2000), temperatureScale=1.0, xSeed=NA)

Arguments

- **tfit**: a ternaryFit object
- **mdelta**: number of transitions between samples
- **msample**: number of samples
- **temperatureScale**: the final temperature is multiplied by this value for sampling
- **xSeed**: an integer random seed. If NA, a random seed is generated.

Value

The function returns a ternaryPost object.

Author(s)

Matthew N. McCall and Anthony Almudevar
See Also


Examples

```r
ssObj <- matrix(c(1,1,1,0,1,1,0,0,1),nrow=3)
pObj <- matrix(c(1,0,0,0,1,0,0,0,1),nrow=3)
rownames(ssObj) <- rownames(pObj) <- colnames(ssObj) <- colnames(pObj) <- c("Gene1","Gene2","Gene3")
tnfitObj <- tnetfit(ssObj, pObj)
tnpostObj <- tnetpost(tnfitObj, mdelta=10, msample=10)
```
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