Package 'CBN2Path'

November 10, 2026

Title CBN2Path: an R/Bioconductor package for the analysis of cancer progression pathways using Conjunctive Bayesian Networks

Version 1.2.0

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Description CBN2Path package provides a unifying interface to facilitate CBN-based quantification, analysis and visualization of cancer progression pathways.

URL https://github.com/rockwillck/CBN2Path,
http://dx.doi.org/10.1093/biomet/asp023,
http://dx.doi.org/10.1093/bioinformatics/btp505

BugReports https://github.com/rockwillck/CBN2Path/issues

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Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Imports R6, ggraph, tidygraph, ggplot2, patchwork, cowplot, magrittr, igraph, rlang, grDevices, coda, graphics, stats, TCGAbiolinks, BiocParallel

Suggests testthat (>= 3.0.0), BiocStyle, knitr, rmarkdown

Depends R (>= 4.1.0)

Config/testthat/edition 3

biocViews Software, StatisticalMethod, GraphAndNetwork, Bayesian, Pathways

VignetteBuilder knitr

SystemRequirements GNU Scientific Library (GSL)

OS_type unix

Config/Bioconductor/UnsupportedPlatforms windows

git_url https://git.bioconductor.org/packages/CBN2Path

git_branch RELEASE_3_23

git_last_commit 5c11e25

git_last_commit_date 2026-04-28

Repository Bioconductor 3.23

Date/Publication 2026-11-10

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`CBN2Path-package` *CBN2Path: "CBN2Path: an R/Bioconductor package for the analysis of cancer progression pathways using Conjunctive Bayesian Networks*

Description

CBN2Path package provides a unifying interface to facilitate CBN-based quantification, analysis and visualization of cancer progression pathways.

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See Also

Useful links:

- https://github.com/rockwillck/CBN2Path
- http://dx.doi.org/10.1093/biomet/asp023
- http://dx.doi.org/10.1093/bioinformatics/btp505
- Report bugs at https://github.com/rockwillck/CBN2Path/issues

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base2Indexing *base2Indexing*

Description

base2Indexing

Usage

```
base2Indexing(mat)
```

Arguments

mat	A given poset represented by a binary matrix (in B-CBN)

Value

#Poset weight vectors based on the frequency of occurrence in the BCBN MCMC-sampling scheme.

Examples

```
set.seed(100)
mat <- matrix(sample(c(0, 1), 16, replace = TRUE), 4, 4)
base2Indexing(mat)
```

base2IndVec *base2IndVec*

Description

base2IndVec

Usage

```
base2IndVec(vec)
```

Arguments

vec	a binary genotype vector

Value

a number used for indexing a given genotype

Examples

```
vec <- c(0, 1, 0, 1)
base2IndVec(vec)
```

bcbn *B-CBN*

Description

B-CBN

Usage

```
bcbn(
  data = defaultData(),
  nSamples = 25000,
  theta = 0,
  epsilon = 0.05,
  nChains = 4,
  thin = 10,
  maxL = 1000,
  nCores = 1,
  progressBar = FALSE
)
```

Arguments

data	Generated data
nSamples	Number of samples <def: 25000>
theta	Theta <def: 0>
epsilon	Epsilon <def: 0.05>
nChains	N-Chains <def: 4>
thin	Thin <def: 10>
maxL	The maximum number of iteration <def: 1000>
nCores	Number of parallelized cores <def: 1>
progressBar	Print out progress bar; default is FALSE

Value

A matrix

Examples

```
bcbn()
```

ctcbn *CT-CBN*

Description

CT-CBN

Usage

```
ctcbn(
  datasets,
  bootstrapSamples = 0,
  randomSeed = 1,
  samplingRate = 1,
  epsilon = 2,
  numDrawnSamples = 0,
  numEmRuns = 1,
  nCores = 1,
  progressBar = FALSE
)
```

Arguments

datasets	Vector of Spock objects with poset and pattern/lambda data or a Spock object (alias of ctcbnSingle).
bootstrapSamples	Number of bootstrap samples (requires epsilon > 0, numDrawnSamples = 0)
randomSeed	Random seed.
samplingRate	Sampling rate.
epsilon	If between 0 and 1, the fraction of violations allowed per edge. If negative, the interval 0 to 0.5 will be sampled equidistantly with N points and the output Spock will include multiple resulting posets.
numDrawnSamples	If > 0, the number of samples to draw from the model. If zero (default), the model will be learned from data.
numEmRuns	Number of em runs.
nCores	Maximum number of threads to use to parallelize.
progressBar	Print out progress bar; default is FALSE

Value

A matrix of results.

Examples

```
examplePath <- getExamples()[3]
bc <- Spock$new(
    poset = readPoset(examplePath)$sets,
    numMutations = readPoset(examplePath)$mutations,
    genotypeMatrix = readPattern(examplePath)
)
ctcbn(bc)
ctcbn(c(bc, bc, bc))
```

---

ctcbnSingle *CT-CBN Single Batch*

Description

CT-CBN Single Batch

Usage

```
ctcbnSingle(
  dataset,
  bootstrapSamples = 0,
  randomSeed = 1,
  samplingRate = 1,
  epsilon = 2,
  numDrawnSamples = 0,
  numEmRuns = 1
)
```

Arguments

`dataset`	Spock object with poset and pattern/lambda data.
`bootstrapSamples`	Number of bootstrap samples (requires `epsilon` > 0, `numDrawnSamples` = 0)
`randomSeed`	Random seed.
`samplingRate`	Sampling rate.
`epsilon`	If between 0 and 1, the fraction of violations allowed per edge. If negative, the interval 0 to 0.5 will be sampled equidistantly with N points and the output Spock will include multiple resulting posets.
`numDrawnSamples`	If > 0, the number of samples to draw from the model. If zero (default), the model will be learned from data.
`numEmRuns`	Number of em runs.

Value

A list of output data.

Examples

```
examplePath <- getExamples()[1]
bc <- Spock$new(
    poset = readPoset(examplePath)$sets,
    numMutations = readPoset(examplePath)$mutations,
    genotypeMatrix = readPattern(examplePath)
)
ctcbnSingle(bc)
```

---

edgeMarginalized *edgeMarginalized*

Description

edgeMarginalized

Usage

```
edgeMarginalized(pathProb, x)
```

Arguments

pathProb	The pathway probabilities returned in the step 3 of the R-CBN algorithm
x	The number of mutations to consider

Value

returns the marginal probability of all the potential edges

Examples

```
dag <- matrix(c(2, 2, 4, 1, 3, 3), 3, 2)
lambda <- c(1, 4, 3, 2.5, 2)
x <- 4
pathP <- pathProbCBN(dag, lambda, x)
edgeMarginalized(pathP, x)
```

generateData *Generate Data*

Description

Generate Data

Usage

```
generateData(poset, theta, eps, n)
```

Arguments

poset	Poset matrix
theta	Vector of theta values
eps	Epsilon
n	N

Value

A matrix

Examples

```
poset <- matrix(0, 10, 10)
poset[1, 2] <- 1
poset[2, 3] <- 1
poset[3, 4] <- 1
poset[5, 4] <- 1
poset[6, 7] <- 1
poset[8, 9] <- 1
poset[8, 10] <- 1
poset[6, 9] <- 1
tr <- transitiveClosure(poset)
theta <- c(0.8, 0.7, 0.6, 0.7, 0.4, 0.25, 0.6, 0.75, 0.5, 0.2)
eps <- 0.1
n <- 400
generateData(tr, theta, eps, n)
```

generateMatrixGenotypes *generateMatrixGenotypes*

Description

generateMatrixGenotypes

Usage

```
generateMatrixGenotypes(g)
```

Arguments

g	genotype length

Value

a genotype matrix with ncol=g and nrow=2^g

Examples

```
generateMatrixGenotypes(4)
```

generateTCGAMatrix *Generate TCGA Genotype Matrix*

Description

Generate TCGA Genotype Matrix

Usage

```
generateTCGAMatrix(
  rawData = suppressMessages(getRawTCGAData("TCGA-BLCA")),
 genes = c("TP53", "ARID1A", "KDM6A", "PIK3CA", "RB1", "EP300", "FGFR3", "CREBBP",
    "STAG2", "ATM")
)
```

Arguments

rawData	Raw TCGA data generated using getRawTCGAData
genes	Genes to generate genotype matrix on

Value

A genotype matrix where each row is a patient and each column is a gene

Examples

```
generateTCGAMatrix(rawData = data.frame())
# generateTCGAMatrix()
```

---

genotypeFeasibility *genotypeFeasibility*

Description

genotypeFeasibility

Usage

```
genotypeFeasibility(genotypes, dag, x)
```

Arguments

genotypes	the full set of potential binary genotypes of a given length.
dag	matrix representing the DAG of restrictions.
x	the number of mutations considered.

Value

a binary vector, which indicates feasibility or infeasibility of a set of genotypes

Examples

```
geno4 <- generateMatrixGenotypes(4)
dag <- matrix(c(4, 4, 4, 1, 2, 3), 3, 2)
x <- 4
genoF4 <- genotypeFeasibility(geno4, dag, x)
```

---

genotypeMatrixMutator *genotypeMatrixMutator*

Description

genotypeMatrixMutator

Usage

```
genotypeMatrixMutator(mat, fp, fn)
```

Arguments

mat	The genotype matrix including sampled genotypes, which need to be mutated.
fp	False positive rate
fn	False negative rate

Value

The mutated version of the genotype matrix

Examples

```
set.seed(100)
gMat <- matrix(sample(c(0, 1), 800, replace = TRUE), 200, 4)
gMatMut <- genotypeMatrixMutator(gMat, 0.2, 0.2)
```

---

getExamples *Get paths to examples*

Description

Get paths to examples

Usage

```
getExamples()
```

Value

A vector of paths

Examples

```
getExamples()
```

getRawTCGAData *Get Raw TCGA Data*

Description

Get Raw TCGA Data

Usage

```
getRawTCGAData(project)
```

Arguments

project	TCGA project ID; pass "help" to see list of all project IDs

Value

data frame of TCGA data for given project

Examples

```
getRawTCGAData("help")
```

hcbn *H-CBN*

Description

H-CBN

Usage

```
hcbn(
  datasets,
  anneal = FALSE,
  temp = 0,
  annealingSteps = 0,
  epsilon = 2,
  nCores = 1,
  progressBar = FALSE
)
```

Arguments

datasets	Vector of Spock objects with poset and pattern/lambda data or a Spock object (alias of hcbnSingle).
anneal	If TRUE, performes a simulated annealing run starting from the poset
temp	Temperature of simulated annealing.
annealingSteps	Number of simulated annealing steps.
epsilon	Value of eps for CT-CBN model selection. Requires both pattern and lambda data in input Spock.
nCores	Maximum number of threads to use to parallelize.
progressBar	Print out progress bar; default is FALSE

Value

A matrix of results.

Examples

```
examplePath <- getExamples()[3]
bc <- Spock$new(
    poset = readPoset(examplePath)$sets,
    numMutations = readPoset(examplePath)$mutations,
    genotypeMatrix = readPattern(examplePath)
)
hcbn(bc)
hcbn(c(bc, bc, bc))
```

---

hcbnSingle *H-CBN Single Batch*

Description

H-CBN Single Batch

Usage

```
hcbnSingle(
  datasetObj,
  anneal = FALSE,
  temp = 0,
  annealingSteps = 0,
  epsilon = 2
)
```

Arguments

datasetObj	Spock object with poset and pattern/lambda data.
anneal	If TRUE, performes a simulated annealing run starting from the poset
temp	Temperature of simulated annealing.
annealingSteps	Number of simulated annealing steps.
epsilon	Value of eps for CT-CBN model selection. Requires both pattern and lambda data in input Spock.

Value

A list of output data.

Examples

```
examplePath <- getExamples()[1]
bc <- Spock$new(
    poset = readPoset(examplePath)$sets,
    numMutations = readPoset(examplePath)$mutations,
    genotypeMatrix = readPattern(examplePath)
)
hcbnSingle(bc)
```

---

jensenShannonDivergence *jensenShannonDivergence*

Description

jensenShannonDivergence

Usage

```
jensenShannonDivergence(prob1, prob2)
```

Arguments

prob1	The first (discrete) probability distribution (vector)
prob2	The second (discrete) probability distribution (vector)

Value

Jensen Shannon Divergence between the two (discrete) probability distributions

Examples

```
set.seed(100)
gMat <- matrix(sample(c(0, 1), 12, replace = TRUE), 3, 4)
pathCT <- pathProbQuartetCTCBN(gMat)
pathH <- pathProbQuartetHCBN(gMat)
jensenShannonDivergence(pathCT, pathH)
```

`pathEdgeMapper` *pathEdgeMapper*

Description

pathEdgeMapper

Usage

```
pathEdgeMapper(x)
```

Arguments

x	number of mutations to consider

Value

Pathway to edge compatibility matrix, each element of which indicates whether a given edge is included in the transitive closure of a given pathway (1) or not (0).

Examples

```
peMap <- pathEdgeMapper(4)
```

`pathNormalization` *pathNormalization*

Description

pathNormalization

Usage

```
pathNormalization(pathProb, x)
```

Arguments

pathProb	The pathway probabilities returned in the step 3 of the R-CBN algorithm
x	The number of mutations to consider

Value

The updated pathway probabilities (the step 5 of the R-CBN algorithm)

Examples

```
dag <- matrix(c(2, 2, 4, 1, 3, 3), 3, 2)
lambda <- c(1, 4, 3, 2.5, 2)
x <- 4
pathP <- pathProbCBN(dag, lambda, x)
pathN <- pathNormalization(pathP, x)
```

---

pathProbCBN *pathProbCBN: quantifies pathway probabilities using the output of CT-CBN or H-CBN*

Description

pathProbCBN: quantifies pathway probabilities using the output of CT-CBN or H-CBN

Usage

```
pathProbCBN(dag, lambda, x)
```

Arguments

dag	matrix representing the DAG of restrictions.
lambda	the lambda values, which are produced by the CBN model.
x	the number of mutations considered.

Value

vector of probabilities assigned to all potential pathways of length x

Examples

```
dag <- matrix(c(2, 2, 4, 1, 3, 3), 3, 2)
lambda <- c(1, 4, 3, 2.5, 2)
x <- 4
pathP <- pathProbCBN(dag, lambda, x)
```

pathProbQuartetBCBN *pathProbQuartetBCBN*

Description

pathProbQuartetBCBN

Usage

```
pathProbQuartetBCBN(gMat)
```

Arguments

gMat	The n by 4 binary genotype matrix representing a given quartet for a sample of n genotypes.

Value

The probability distribution (returned by the B-CBN model), which is represented as a vector of length 24.

Examples

```
set.seed(100)
gMat <- matrix(sample(c(0, 1), 12, replace = TRUE), 3, 4)
pathProbQuartetBCBN(gMat)
```

pathProbQuartetCTCBN *pathProbQuartetCTCBN*

Description

pathProbQuartetCTCBN

Usage

```
pathProbQuartetCTCBN(gMat)
```

Arguments

gMat	The n by 4 binary genotype matrix representing a given quartet for a sample of n genotypes.

Value

The probability distribution (returned by the CT-CBN model), which is represented as a vector of length 24.

Examples

```
set.seed(100)
gMat <- matrix(sample(c(0, 1), 12, replace = TRUE), 3, 4)
pathProbQuartetCTCBN(gMat)
```

---

pathProbQuartetHCBN *pathProbQuartetHCBN*

Description

pathProbQuartetHCBN

Usage

```
pathProbQuartetHCBN(gMat)
```

Arguments

gMat	The n by 4 binary genotype matrix representing a given quartet for a sample of n genotypes.

Value

The probability distribution (returned by the H-CBN model), which is represented as a vector of length 24.

Examples

```
set.seed(100)
gMat <- matrix(sample(c(0, 1), 12, replace = TRUE), 3, 4)
pathProbQuartetHCBN(gMat)
```

---

pathProbQuartetRCBN *pathProbQuartetRCBN*

Description

pathProbQuartetRCBN

Usage

```
pathProbQuartetRCBN(gMat)
```

Arguments

gMat	The n by 4 binary genotype matrix representing a given quartet for a sample of n genotypes.

Value

The probability distribution (returned by the R-CBN model), which is represented as a vector of length 24

Examples

```
set.seed(100)
gMat <- matrix(sample(c(0, 1), 12, replace = TRUE), 3, 4)
pathProbQuartetRCBN(gMat)
```

`pathProbSSWM` *pathProbSSWM*

Description

pathProbSSWM

Usage

```
pathProbSSWM(fitness, x)
```

Arguments

`fitness`	A vector of length 2^x, each element of which representing the fitness assigned to one of the 2^x genotypes.
`x`	The number of mutations considered.

Value

vector of probabilities assigned to all potential pathways of length x

Examples

```
f <- c(0, 0.1, 0.2, 0.1, 0.2, 0.4, 0.3, 0.2, 0.2, 0.1, 0, 0.6, 0.4, 0.3, 0.2, 1)
x <- 4
pathP <- pathProbSSWM(f, x)
```

pathwayCompatibilityQuartet *pathwayCompatibilityQuartet*

Description

pathwayCompatibilityQuartet

Usage

```
pathwayCompatibilityQuartet(gMat)
```

Arguments

gMat	The n by 4 binary genotype matrix representing a given quartet for a sample of n genotypes.

Value

The compatibility score, which is represented as a vector of length 24, each element of which corresponds to one of the 24 pathways of length 4.

Examples

```
set.seed(100)
gMat <- matrix(sample(c(0, 1), 800, replace = TRUE), 200, 4)
pathwayCompatibilityQuartet(gMat)
```

pathwayFeasibility *pathwayFeasibility*

Description

pathwayFeasibility

Usage

```
pathwayFeasibility(dag, x)
```

Arguments

dag	matrix representing the DAG of restrictions.
x	the number of mutations considered.

Value

a binary vector, which indicates feasibility or infeasibility of a set of pathways

Examples

```
dag <- matrix(c(4, 4, 4, 1, 2, 3), 3, 2)
x <- 4
pathwayFeasibility(dag, x)
```

---

pathwayGenotypeCompatibility *pathwayGenotypeCompatibility*

Description

pathwayGenotypeCompatibility

Usage

```
pathwayGenotypeCompatibility(pathway, genotype)
```

Arguments

pathway	a vector representing the given pathway.
genotype	a binary vector representing the given genotype.

Value

returns 1 (if the given genotype is compatible with the given pathway), and 0 otherwise

Examples

```
geno1 <- c(1, 0, 1, 0)
geno2 <- c(1, 1, 0, 0)
path <- c(1, 2, 3, 4)
pathwayGenotypeCompatibility(path, geno1)
pathwayGenotypeCompatibility(path, geno2)
```

---

pathwayWeightingRCBN *pathwayWeightingRCBN*

Description

pathwayWeightingRCBN

Usage

```
pathwayWeightingRCBN(edgeProb, peMap)
```

Arguments

edgeProb	Marginal edge probabilities
peMap	Pathway-edge compatibility matrix

Value

The pathway weights (step 4 of the R-CBN algorithm)

Examples

```
dag <- matrix(c(2, 2, 4, 1, 3, 3), 3, 2)
lambda <- c(1, 4, 3, 2.5, 2)
x <- 4
pathP <- pathProbCBN(dag, lambda, x)
edgeProb <- edgeMarginalized(pathP, x)
peMap <- pathEdgeMapper(4)
pathwayWeightingRCBN(edgeProb, peMap)
```

---

permutations *permutations*

Description

permutations

Usage

```
permutations(n, r, v = 1:n, set = TRUE, repeatsAllowed = FALSE)
```

Arguments

n	total number of elements in the set
r	subset size
v	1:n
set	Logical flag indicating whether duplicates should be removed from the source vector v. Defaults to TRUE.
repeatsAllowed	Logical flag indicating whether the constructed vectors may include duplicated values. Defaults to FALSE.

Value

a matrix with (n!/(n-r)!) rows and r columns

Examples

```
perm <- permutations(4, 4)
```

posetWeightingRCBN *posetWeightingRCBN*

Description

posetWeightingRCBN

Usage

```
posetWeightingRCBN(vec)
```

Arguments

vec	The likelihood vector corresponding to a given set of posets

Value

The poset weight vector determined using the reciprocal ranking method

Examples

```
set.seed(100)
logLik <- runif(219)
w1 <- posetWeightingRCBN(logLik)
```

predictability *predictability*

Description

predictability

Usage

```
predictability(prob, x)
```

Arguments

prob	Pathway probability vector
x	The length of genotype vectors

Value

predictability

Examples

```
set.seed(100)
gMat <- matrix(sample(c(0, 1), 12, replace = TRUE), 3, 4)
pathCT <- pathProbQuartetCTCBN(gMat)
pathH <- pathProbQuartetHCBN(gMat)
predC <- predictability(pathCT, 4)
predictability(pathH, 4)
```

---

readLambda *Read a .lambda file*

Description

Read a .lambda file

Usage

```
readLambda(fileStem)
```

Arguments

fileStem	The filename of the .lambda file without the .lambda suffix.

Value

A matrix.

Examples

```
bcPath <- getExamples()[1]
readLambda(bcPath)
```

---

readPattern *Read a .pat file*

Description

Read a .pat file

Usage

```
readPattern(fileStem)
```

Arguments

fileStem	The filename of the .pat file without the .pat suffix.

Value

A matrix.

Examples

```
bcPath <- getExamples()[1]
readPattern(bcPath)
```

`readPoset` *Read a .poset file*

Description

Read a .poset file

Usage

```
readPoset(fileStem)
```

Arguments

`fileStem`	The filename of the .poset file without the .poset suffix.

Value

A list containing the number of mutations and a matrix.

Examples

```
bcPath <- getExamples()[1]
readPoset(bcPath)
```

`readTime` *Read a .time file*

Description

Read a .time file

Usage

```
readTime(fileStem)
```

Arguments

`fileStem`	The filename of the .time file without the .time suffix.

Value

A matrix.

Examples

```
bcPath <- getExamples()[1]
readPattern(bcPath)
```

Spock *Poset and pattern/lambda data*

Description

A data class containing poset and pattern/lambda matrices.

Details

Use the read_ methods to feed data from files.

Value

a Spock object

Public fields

`poset` Poset matrix.

`numMutations` Number of mutations.

`genotypeMatrix` Genotype matrix.

`lambda` Lambda list.

Methods

Public methods:

- `Spock$new()`
- `Spock$getSize()`
- `Spock$getPoset()`
- `Spock$getSecond()`
- `Spock$getPattern()`
- `Spock$getLambda()`
- `Spock$show()`
- `Spock$clone()`

Method `new()`**:** Create a new Spock object.

Usage:

```
Spock$new(poset, numMutations, genotypeMatrix, lambda = NULL)
```

Arguments:

`poset` Poset matrix or list of poset matrices.

`numMutations` Number of mutations.

`genotypeMatrix` Genotype matrix.

`lambda` Lambda list.

Returns: A new `Spock` object.

Method `getSize()`**:** Get the number of posets.

Usage:

```
Spock$getSize()
```

Returns: Number of posets.

Method `getPoset()`**:** Write poset data to a tempfile.

Usage:

```
Spock$getPoset(index = 1)
```

Arguments:

`index` Index of poset.

Returns: File path to tempfile.

Method `getSecond()`**:** Write pattern/lambda data to a tempfile.

Usage:

```
Spock$getSecond(n)
```

Arguments:

`n` Number of drawn samples.

Returns: File path to tempfile.

Method `getPattern()`**:** Write pattern data to a tempfile.

Usage:

```
Spock$getPattern()
```

Returns: File path to tempfile.

Method `getLambda()`**:** Write lambda data to a tempfile.

Usage:

```
Spock$getLambda()
```

Returns: File path to tempfile.

Method `show()`**:** Print summary information to console.

Usage:

```
Spock$show(verbose = FALSE)
```

Arguments:

`verbose` Method prints contents as well as dimensions to console if `TRUE`.

Returns: Nothing.

Method `clone()`**:** The objects of this class are cloneable with this method.

Usage:

```
Spock$clone(deep = FALSE)
```

Arguments:

`deep` Whether to make a deep clone.

Examples

```
examplePath <- getExamples()[1]
bc <- Spock$new(
    poset = readPoset(examplePath)$sets,
    numMutations = readPoset(examplePath)$mutations,
    genotypeMatrix = readPattern(examplePath)
)
```

`transitiveClosure` *Transitive Closure*

Description

Transitive Closure

Usage

```
transitiveClosure(poset)
```

Arguments

`poset`	Poset matrix

Value

Poset matrix

Examples

```
poset <- matrix(0, 10, 10)
poset[1, 2] <- 1
poset[2, 3] <- 1
poset[3, 4] <- 1
poset[5, 4] <- 1
poset[6, 7] <- 1
poset[8, 9] <- 1
poset[8, 10] <- 1
poset[6, 9] <- 1
transitiveClosure(poset)
```

visualizeCBNModel *Visualize CBN Model*

Description

Visualize CBN Model

Usage

```
visualizeCBNModel(
  poset,
  nodeColor = "darkgreen",
  numNodes = max(4, max(poset))
)
```

Arguments

poset	Poset object to visualize
nodeColor	Color of nodes in resulting graph
numNodes	Number of nodes (default is the larger number between 4 and the largest index given in the poset)

Value

Plot (gg object) visualization of CBN model

Examples

```
poset <- readPoset(getExamples()[1])
visualizeCBNModel(poset$sets)
```

visualizeFitnessLandscape *Visualize Fitness Landscape*

Description

Visualize Fitness Landscape

Usage

```
visualizeFitnessLandscape(
  fitness,
  selectNodes = NULL,
  nGenes = 4,
  lowColor = "white",
  highColor = "blue"
)
```

Arguments

fitness	Fitness vectors for each genotype provided in selectNodes or for all genotypes if none selected
selectNodes	Select genotypes to visualize
nGenes	Length of each genotype
lowColor	Color for wild type genotype
highColor	Color for fully mutated genotype

Value

Plot (gg object) visualization of fitness landscape

Examples

```
genotypes <- c(
    "0000",
    "1000",
    "0100",
    "0010",
    "0001",
    "1100",
    "1010",
    "1001",
    "0110",
    "0101",
    "0011",
    "1110",
    "1101",
    "1011",
    "0111",
    "1111"
)
#
colIntensity <- c(0, rep(0.25, 4), rep(0.5, 6), rep(0.75, 4), 1)
visualizeFitnessLandscape(colIntensity)
```

---

visualizeProbabilities

Visualize Pathway Probabilities

Description

Visualize Pathway Probabilities

Usage

```
visualizeProbabilities(
  probabilities,
  outputFile = NULL,
  geneNames = as.character(1:inverseFactorial(length(probabilities))),
  geneColors = rainbow(length(geneNames), v = 0.5),
  columnTitles = TRUE
)
```

Arguments

probabilities	List or matrix of probabilities for each pathway (matrix if multiple models)
outputFile	File to output to; if none provided, a plot will be returned
geneNames	Gene names; if single character, rendered in circles
geneColors	Gene colors
columnTitles	Include column titles

Value

Plot or file name

Examples

```
visualizeProbabilities(c(0.05, 0.03, 0.12, 0.04, 0.02, 0, 0.05, 0.04, 0.05, 0.06, 0.04, 0.02, 0.03, 0.02, 0.05, 0.0

visualizeProbabilities(c(0.05, 0.03, 0.12, 0.04, 0.02, 0, 0.05, 0.04, 0.05, 0.06, 0.04, 0.02, 0.03, 0.02, 0.05, 0.0

mat <- matrix(c(0.1, 0.3, 0, 0.2, 0.4, 0, 0.2, 0.2, 0.1, 0, 0.2, 0.3), ncol = 2)
visualizeProbabilities(mat, columnTitles = TRUE)
```

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