Package ‘CoGAPS’

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Description Coordinated Gene Activity in Pattern Sets (CoGAPS) implements a Bayesian MCMC matrix factorization algorithm, GAPS, and links it to gene set statistic methods to infer biological process activity. It can be used to perform sparse matrix factorization on any data, and when this data represents biomolecules, to do gene set analysis.
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CoGAPS-package

CoGAPS: Coordinated Gene Activity in Pattern Sets

Description

CoGAPS implements a Bayesian MCMC matrix factorization algorithm, GAPS, and links it to gene set statistic methods to infer biological process activity. It can be used to perform sparse matrix factorization on any data, and when this data represents biomolecules, to do gene set analysis.

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Author(s)

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References


binaryA

binary heatmap for standardized feature matrix

Description

creates a binarized heatmap of the A matrix in which the value is 1 if the value in Amean is greater than threshold * Asd and 0 otherwise

Usage

binaryA(object, threshold = 3)

## S4 method for signature 'CogapsResult'
binaryA(object, threshold = 3)

Arguments

- **object**: an object of type CogapsResult
- **threshold**: the number of standard deviations above zero that an element of Amean must be to get a value of 1
**buildReport**

**Value**

plots a heatmap of the A Matrix

**Examples**

data(GIST)

# to expensive to call since it plots
# binaryA(GIST.result, threshold=3)

---

**buildReport**

*Information About Package Compilation*

**Description**

Information About Package Compilation

**Usage**

buildReport()

**Details**

returns information about how the package was compiled, i.e. which compiler/version was used, which compile time options were enabled, etc...

**Value**

string containing build report

**Examples**

CoGAPS::buildReport()

---

**calcCoGAPSStat**

*calculate statistic on sets of measurements (genes) or samples*

**Description**

calculates a statistic to determine if a pattern is enriched in a particular set of measurements or samples.
Usage
calcCoGAPSStat(
  object,
  sets = NULL,
  whichMatrix = "featureLoadings",
  numPerm = 1000,
  ...
)

## S4 method for signature 'CogapsResult'
calcCoGAPSStat(
  object,
  sets = NULL,
  whichMatrix = "featureLoadings",
  numPerm = 1000,
  ...
)

Arguments

object an object of type CogapsResult
sets list of sets of measurements/samples
whichMatrix either "featureLoadings" or "sampleFactors" indicating which matrix to calculate the statistics for
numPerm number of permutations to use when calculating p-value
...

Value
gene set statistics for each column of A

calcGeneGSStat probability gene belongs in gene set

Description
calculates the probability that a gene listed in a gene set behaves like other genes in the set within the given data set

Usage
calcGeneGSStat(
  object,
  GStoGenes,
  numPerm,
  Pw = rep(1, ncol(object@featureLoadings)),
)
nullGenes = FALSE
)

## S4 method for signature 'CogapsResult'
calcGeneGSStat(
  object,
  GStoGenes,
  numPerm,
  Pw = rep(1, ncol(object@featureLoadings)),
  nullGenes = FALSE
)

### Arguments

- **object**
  - an object of type CogapsResult

- **GStoGenes**
  - data.frame or list with gene sets

- **numPerm**
  - number of permutations for null

- **Pw**
  - weight on genes

- **nullGenes**
  - logical indicating gene adjustment

### Value

gene similarity statistic

calcZ 

```r
> calcZ
```

**compute z-score matrix**

### Description

calculates the Z-score for each element based on input mean and standard deviation matrices

### Usage

calcZ(object, whichMatrix)

```r
> calcZ(object, whichMatrix)
```

**S4 method for signature 'CogapsResult'

calcZ(object, whichMatrix)

### Arguments

- **object**
  - an object of type CogapsResult

- **whichMatrix**
  - either "featureLoadings" or "sampleFactors" indicating which matrix to calculate the z-score for

### Value

matrix of z-scores
callInternalCoGAPS

Examples

data(GIST)
featureZScore <- calcZ(GIST.result, "featureLoadings")

callInternalCoGAPS

make correct call to internal CoGAPS dispatch function. CoGAPS
could be called directly, but to avoid any re-entrant behavior this func-
tion is called instead. It is a light wrapper around cogaps_cpp that
handles setting the distributed parameters

Description

make correct call to internal CoGAPS dispatch function. CoGAPS could be called directly, but to
avoid any re-entrant behavior this function is called instead. It is a light wrapper around cogaps_cpp
that handles setting the distributed parameters

Usage

callInternalCoGAPS(data, allParams, uncertainty, subsetIndices, workerID)

Arguments

data data in a supported format
allParams list of all parameters
uncertainty uncertainty of data in the same format
index index for which subset to run on
sets list of all subsets
geneNames names of all genes
sampleNames names of all samples
fixedMatrix matrix of matched patterns

Value

CogapsResult object
checkDataMatrix

Description
check that provided data is valid

Usage
checkDataMatrix(data, uncertainty, params)

Arguments
- data: data matrix
- uncertainty: uncertainty matrix, can be null
- params: CogapsParams object

Value
throws an error if data has problems

checkInputs

Description
check that all inputs are valid

Usage
checkInputs(data, uncertainty, allParams)

Arguments
- data: data matrix
- uncertainty: uncertainty matrix, can be null
- allParams: list of all parameters

Value
throws an error if inputs are invalid
checkpointsEnabled  
*Check if package was built with checkpoints enabled*

**Description**
Check if package was built with checkpoints enabled

**Usage**
checkpointsEnabled()

**Value**
true/false if checkpoints are enabled

**Examples**
CoGAPS::checkpointsEnabled()

---

**CoGAPS**  
*CoGAPS Matrix Factorization Algorithm*

**Description**
calls the C++ MCMC code and performs Bayesian matrix factorization returning the two matrices that reconstruct the data matrix

**Usage**
CoGAPS(
  data,
  params = new("CogapsParams"),
  nThreads = 1,
  messages = TRUE,
  outputFrequency = 1000,
  uncertainty = NULL,
  checkpointOutFile = "gaps_checkpoint.out",
  checkpointInterval = 0,
  checkpointInFile = NULL,
  transposeData = FALSE,
  BPPARAM = NULL,
  workerID = 1,
  asynchronousUpdates = TRUE,
  nSnapshots = 0,
  snapshotPhase = "sampling",
  ...
)
Arguments

- **data**: File name or R object (see details for supported types)
- **params**: CogapsParams object
- **nThreads**: maximum number of threads to run on
- **messages**: T/F for displaying output
- **outputFrequency**: number of iterations between each output (set to 0 to disable status updates, other output is controlled by @code messages)
- **uncertainty**: uncertainty matrix - either a matrix or a supported file type
- **checkpointOutFile**: name of the checkpoint file to create
- **checkpointInterval**: number of iterations between each checkpoint (set to 0 to disable checkpoints)
- **checkpointInFile**: if this is provided, CoGAPS runs from the checkpoint contained in this file
- **transposeData**: T/F for transposing data while reading it in - useful for data that is stored as samples x genes since CoGAPS requires data to be genes x samples
- **BPPARAM**: BiocParallel backend
- **workerID**: if calling CoGAPS in parallel the worker ID can be specified, only worker 1 prints output and each worker outputs when it finishes, this is not neccesary when using the default parallel methods (i.e. distributed CoGAPS) but only when the user is manually calling CoGAPS in parallel
- **asynchronousUpdates**: enable asynchronous updating which allows for multi-threaded runs
- **nSnapshots**: how many snapshots to take in each phase, setting this to 0 disables snapshots
- **snapshotPhase**: which phase to take snapshots in e.g. "equilibration", "sampling", "all"
- ... allows for overwriting parameters in params

Details

The supported R types are: matrix, data.frame, SummarizedExperiment, SingleCellExperiment. The supported file types are csv, tsv, and mtx.

Value

CogapsResult object

Examples

# Running from R object
data(GIST)
resultA <- CoGAPS(GIST.data_frame, nIterations=25)

# Running from file name
gist_path <- system.file("extdata/GIST.mtx", package="CoGAPS")
resultB <- CoGAPS(gist_path, nIteraTions=25)

# Setting Parameters
params <- new("CogapsParams")
params <- setParam(params, "nPatterns", 3)
resultC <- CoGAPS(GIST.data_frame, params, nIteraTions=25)

---

**CogapsParams**  
_CogapsParams constructor_

**Description**

create a CogapsParams object

**Usage**

CogapsParams(...)

**Arguments**

...  parameters for the initialization method

**Value**

CogapsParams object

**Examples**

params <- CogapsParams(nPatterns=10)
params

---

**CogapsParams-class**  
_CogapsParams_

**Description**

Encapsulates all parameters for the CoGAPS algorithm
Slots

nPatterns  number of patterns CoGAPS will learn
nIterations  number of iterations for each phase of the algorithm
alphaA  sparsity parameter for feature matrix
alphaP  sparsity parameter for sample matrix
maxGibbsMassA  atomic mass restriction for feature matrix
maxGibbsMassP  atomic mass restriction for sample matrix
seed  random number generator seed
sparseOptimization  speeds up performance with sparse data (roughly >80 default uncertainty
distributed  either "genome-wide" or "single-cell" indicating which distributed algorithm should be used
nSets  [distributed parameter] number of sets to break data into
cut  [distributed parameter] number of branches at which to cut dendrogram used in pattern matching
minNS  [distributed parameter] minimum of individual set contributions a cluster must contain
maxNS  [distributed parameter] maximum of individual set contributions a cluster can contain
explicitSets  [distributed parameter] specify subsets by index or name
samplingAnnotation  [distributed parameter] specify categories along the rows (cols) to use for weighted sampling
samplingWeight  [distributed parameter] weights associated with samplingAnnotation
subsetIndices  set of indices to use from the data
subsetDim  which dimension (1=rows, 2=cols) to subset
geneNames  vector of names of genes in data
sampleNames  vector of names of samples in data
fixedPatterns  fix either 'A' or 'P' matrix to these values, in the context of distributed CoGAPS (GWCoGAPS/scCoGAPS), the first phase is skipped and fixedPatterns is used for all sets - allowing manual pattern matching, as well as fixed runs of standard CoGAPS
whichMatrixFixed  either 'A' or 'P', indicating which matrix is fixed
takePumpSamples  whether or not to take PUMP samples
checkpointInterval  how many iterations between each checkpoint (set to 0 to disable)
checkpointInFile  file path to load checkpoint from
checkpointOutFile  file path where checkpoint should be written to
CogapsResult-class  CogapsResult

Description

Contains all output from Cogaps run

Slots

  factorStdDev  std dev of the sampled P matrices
  loadingStdDev  std dev of the sampled A matrices

compiledWithOpenMPSupport

Check if compiler supported OpenMP

Description

Check if compiler supported OpenMP

Usage

  compiledWithOpenMPSupport()

Value

  true/false if OpenMP was supported

Examples

  CoGAPS::compiledWithOpenMPSupport()
**computeGeneGSProb**

### Description

Computes the p-value for gene set membership using the CoGAPS-based statistics developed in Fertig et al. (2012). This statistic refines set membership for each candidate gene in a set specified in GSGenes by comparing the inferred activity of that gene to the average activity of the set.

### Usage

```r
computeGeneGSProb(
  object,
  GStoGenes,
  numPerm = 500,
  Pw = rep(1, ncol(object@featureLoadings)),
  PwNull = FALSE
)
```

#### S4 method for signature 'CogapsResult'

```r
computeGeneGSProb(
  object,
  GStoGenes,
  numPerm = 500,
  Pw = rep(1, ncol(object@featureLoadings)),
  PwNull = FALSE
)
```

### Arguments

- **object**: an object of type CogapsResult
- **GStoGenes**: data.frame or list with gene sets
- **numPerm**: number of permutations for null
- **Pw**: weight on genes
- **PwNull**: logical indicating gene adjustment

### Value

A vector of length GSGenes containing the p-values of set membership for each gene contained in the set specified in GSGenes.
**convertDataToMatrix**  
convert any acceptable data input to a numeric matrix

**Description**  
convert supported R objects containing the data to a numeric matrix, if data is a file name do nothing. Exits with an error if data is not a supported type.

**Usage**  
```r
convertDataToMatrix(data)
```

**Arguments**  
- `data` data input

**Value**  
data matrix

**corcut**  
cluster patterns together

**Description**  
cluster patterns together

**Usage**  
```r
corcut(allPatterns, cut, minNS)
```

**Arguments**  
- `allPatterns` matrix of all patterns across subsets  
- `cut` number of branches at which to cut dendrogram  
- `minNS` minimum of individual set contributions a cluster must contain

**Value**  
patterns listed by which cluster they belong to
**corrToMeanPattern**

CorrToMeanPattern calculates the correlation of each pattern in a cluster to the cluster mean.

**Description**

calculate correlation of each pattern in a cluster to the cluster mean

**Usage**

corrToMeanPattern(cluster)

**Value**
correlation of each pattern

---

**createCogapsResult**

createCogapsResult converts the list output from C++ code to a CogapsResult object.

**Description**

convert list output from C++ code to a CogapsResult object

**Usage**

createCogapsResult(returnList, allParams)

**Arguments**

- **returnList**: list from cogaps_cpp
- **allParams**: list of all parameters

**Value**

CogapsResult object
Create sets to partition genes/samples into subsets.

**Description**

Either genes or samples or partitioned depending on the type of distributed CoGAPS (i.e. genome-wide or single-cell).

**Usage**

```r
createSets(data, allParams)
```

**Arguments**

- `data`: either file name or matrix
- `allParams`: list of all CoGAPS parameters

**Value**

List of sorted subsets of either genes or samples.

**Distributed CoGaps (CoGAPS Distributed Matrix Factorization Algorithm)**

**Description**

Runs CoGAPS over subsets of the data and stitches the results back together.

**Usage**

```r
distributedCogaps(data, allParams, uncertainty)
```

**Arguments**

- `data`: File name or R object (see details for supported types)
- `allParams`: list of all parameters used in computation
- `uncertainty`: uncertainty matrix (same supported types as data)

**Details**

For file types CoGAPS supports csv, tsv, and mtx

**Value**

List
findConsensusMatrix

find the consensus pattern matrix across all subsets

Description
find the consensus pattern matrix across all subsets

Usage
findConsensusMatrix(unmatchedPatterns, gapsParams)

Arguments
unmatchedPatterns
list of all unmatched pattern matrices from initial run of CoGAPS
gapsParams
list of all CoGAPS parameters

Value
matrix of consensus patterns

fromCSV

read CoGAPS Result object from a directory with a set of csvs see toCSV

Description
save as csv

Usage
fromCSV(save_location = ".")

Arguments
save_location
directory to read from

Value
CogapsResult object
Description
cleans up message printing

Usage
gapsCat(allParams, ...)

Arguments
allParams all cogaps parameters
... arguments forwarded to cat

Value
conditionally print message

---

getAmplitudeMatrix
return Amplitude matrix from CogapsResult object

Description
return Amplitude matrix from CogapsResult object

Usage
getAmplitudeMatrix(object)

Arguments
object an object of type CogapsResult

Value
amplitude matrix

Examples
data(GIST)
amplitudeMatrix <- getAmplitudeMatrix(GIST.result)
getClusteredPatterns

return clustered patterns from set of all patterns across all subsets

Description

return clustered patterns from set of all patterns across all subsets

Usage

getClusteredPatterns(object)

## S4 method for signature 'CogapsResult'
getClusteredPatterns(object)

Arguments

object an object of type CogapsResult

Value

CogapsParams object

Examples

data(GIST)
clusteredPatterns <- getClusteredPatterns(GIST.result)

getCorrelationToMeanPattern

return correlation between each pattern and the cluster mean

Description

return correlation between each pattern and the cluster mean

Usage

getCorrelationToMeanPattern(object)

## S4 method for signature 'CogapsResult'
getCorrelationToMeanPattern(object)

Arguments

object an object of type CogapsResult
Value
CogapsParams object

Examples

data(GIST)
corrToMeanPattern <- getCorrelationToMeanPattern(GIST.result)

getDimNames  extracts gene/sample names from the data

Description
extracts gene/sample names from the data

Usage
getDimNames(data, allParams)

Arguments
data data matrix
allParams list of all parameters

Value
list of all parameters with added gene names

getFeatureLoadings  return featureLoadings matrix from CogapsResult object

Description
return featureLoadings matrix from CogapsResult object

Usage
getFeatureLoadings(object)

## S4 method for signature 'CogapsResult'
getFeatureLoadings(object)

Arguments
object an object of type CogapsResult
**getGeneNames**

**Value**

featureLoadings matrix

**Examples**

```r
data(GIST)
fLoadings <- getFeatureLoadings(GIST.result)
```

---

**Description**

extract gene names from data

**Usage**

```r
getGeneNames(data, transpose)
```

**Value**

vector of gene names

---

**getMeanChiSq**

**Description**

return chi-sq of final matrices

**Usage**

```r
getMeanChiSq(object)
```

### S4 method for signature 'CogapsResult'

```r
gMeanChiSq(object)
```

**Arguments**

- `object` an object of type CogapsResult

**Value**

chi-sq error

**Examples**

```r
data(GIST)
gMeanChiSq(GIST.result)
```
getOriginalParameters  return original parameters used to generate this result

Description
return original parameters used to generate this result

Usage
getOriginalParameters(object)

## S4 method for signature 'CogapsResult'
getOriginalParameters(object)

Arguments

object an object of type CogapsResult

Value
CogapsParams object

Examples
data(GIST)
params <- getOriginalParameters(GIST.result)

getParam get the value of a parameter

Description
get the value of a parameter

Usage
ggetParam(object, whichParam)

## S4 method for signature 'CogapsParams'
ggetParam(object, whichParam)

Arguments

object an object of type CogapsParams
whichParam a string with the name of the requested parameter
getPatternHallmarks

**Value**

the value of the parameter

**Examples**

```r
params <- new("CogapsParams")
getParam(params, "seed")
```

generate statistics associating patterns with MSigDB hallmark gene sets

**Description**

generate statistics associating patterns with MSigDB hallmark gene sets

**Usage**

```r
getPatternHallmarks(object)
```

```r
## S4 method for signature 'CogapsResult'
getPatternHallmarks(object)
```

**Arguments**

- `object` an object of type CogapsResult

**Value**

dataframe of hallmark info

getPatternMatrix

**Description**

return pattern matrix from CogapsResult object

**Usage**

```r
getPatternMatrix(object)
```

```r
## S4 method for signature 'CogapsResult'
getPatternMatrix(object)
```
getRetinaSubset

Arguments

object an object of type CogapsResult

Value

pattern matrix

Examples

data(GIST)
patternMatrix <- getPatternMatrix(GIST.result)

getRetinaSubset(n = 1)

Arguments

n number of subsets to use

Value

matrix of RNA counts

Examples

retSubset <- getRetinaSubset()
dim(retSubset)
### getSampleFactors

return sampleFactors matrix from CogapsResult object

**Description**

return sampleFactors matrix from CogapsResult object

**Usage**

```r
getSampleFactors(object)
```

## S4 method for signature 'CogapsResult'
getSampleFactors(object)

**Arguments**

- `object`: an object of type CogapsResult

**Value**

sampleFactors matrix

**Examples**

```r
data(GIST)
sFactors <- getSampleFactors(GIST.result)
```

### getSampleNames

extract sample names from data

**Description**

extract sample names from data

**Usage**

```r
getSampleNames(data, transpose)
```

**Value**

vector of sample names
getSubsets

return the names of the genes (samples) in each subset

Description

return the names of the genes (samples) in each subset

Usage

getSubsets(object)

## S4 method for signature 'CogapsResult'
getSubsets(object)

Arguments

object an object of type CogapsResult

Value

CogapsParams object

Examples

data(GIST)
subsets <- getSubsets(GIST.result)

getUnmatchedPatterns

return unmatched patterns from each subset

Description

return unmatched patterns from each subset

Usage

getUnmatchedPatterns(object)

## S4 method for signature 'CogapsResult'
getUnmatchedPatterns(object)

Arguments

object an object of type CogapsResult
getValueOrRds

table

| getValueOrRds | get input that might be an RDS file |

Description

get input that might be an RDS file

Usage

getValueOrRds(input)

Arguments

input some user input

Value

if input is an RDS file, read it - otherwise return input

getVersion

table

| getVersion | return version number used to generate this result |

Description

return version number used to generate this result

Usage

getVersion(object)

## S4 method for signature 'CogapsResult'
getVersion(object)

Arguments

object an object of type CogapsResult
### Value

version number

### Examples

```r
data(GIST)
getVersion(GIST.result)
```

<table>
<thead>
<tr>
<th>GIST.data_frame</th>
<th>GIST gene expression data from Ochs et al. (2009)</th>
</tr>
</thead>
</table>

### Description

GIST gene expression data from Ochs et al. (2009)

<table>
<thead>
<tr>
<th>GIST.matrix</th>
<th>GIST gene expression data from Ochs et al. (2009)</th>
</tr>
</thead>
</table>

### Description

GIST gene expression data from Ochs et al. (2009)

<table>
<thead>
<tr>
<th>GIST.result</th>
<th>CoGAPS result from running on GIST dataset</th>
</tr>
</thead>
</table>

### Description

CoGAPS result from running on GIST dataset

<table>
<thead>
<tr>
<th>GIST.uncertainty</th>
<th>GIST gene expression uncertainty matrix from Ochs et al. (2009)</th>
</tr>
</thead>
</table>

### Description

GIST gene expression uncertainty matrix from Ochs et al. (2009)
GWCoGAPS  

Description

wrapper around genome-wide distributed algorithm for CoGAPS

Usage

GWCoGAPS(
  data,
  params = new("CogapsParams"),
  nThreads = 1,
  messages = TRUE,
  outputFrequency = 500,
  uncertainty = NULL,
  checkpointOutFile = "gaps_checkpoint.out",
  checkpointInterval = 1000,
  checkpointInFile = NULL,
  transposeData = FALSE,
  BPPARAM = NULL,
  workerID = 1,
  asynchronousUpdates = FALSE,
  ...
)

Arguments

data  File name or R object (see details for supported types)
params  CogapsParams object
nThreads  maximum number of threads to run on
messages  T/F for displaying output
outputFrequency  number of iterations between each output (set to 0 to disable status updates, other output is controlled by @code messages)
uncertainty  uncertainty matrix - either a matrix or a supported file type
checkpointOutFile  name of the checkpoint file to create
checkpointInterval  number of iterations between each checkpoint (set to 0 to disable checkpoints)
checkpointInFile  if this is provided, CoGAPS runs from the checkpoint contained in this file
transposeData  T/F for transposing data while reading it in - useful for data that is stored as samples x genes since CoGAPS requires data to be genes x samples
BPPARAM  BiocParallel backend
workerID

if calling CoGAPS in parallel the worker ID can be specified, only worker 1 prints output and each worker outputs when it finishes, this is not neccessary when using the default parallel methods (i.e. distributed CoGAPS) but only when the user is manually calling CoGAPS in parallel

asynchronousUpdates

enable asynchronous updating which allows for multi-threaded runs

... allows for overwriting parameters in params

Value

CogapsResult object

Examples

```r
## Not run:
data(GIST)
params <- new("CogapsParams")
params <- setDistributedParams(params, nSets=2)
params <- setParam(params, "nIterations", 100)
params <- setParam(params, "nPatterns", 3)
result <- GWCoGAPS(GIST.matrix, params, BPPARAM=BiocParallel::SerialParam())
## End(Not run)
```

initialize,CogapsParams-method

*constructor for CogapsParams*

Description

creator for CogapsParams

Usage

```r
## S4 method for signature 'CogapsParams'
initialize(.Object, distributed = NULL, ...)
```

Arguments

- `.Object`: CogapsParams object
- `distributed`: either "genome-wide" or "single-cell" indicating which distributed algorithm should be used
- `...`: initial values for slots

Value

initialized CogapsParams object
Constructor for CogapsResult

## S4 method for signature 'CogapsResult'

```r
initialize(
  .Object,
  Amean,
  Pmean,
  Asd,
  Psd,
  meanChiSq,
  geneNames,
  sampleNames,
  diagnostics = NULL,
  ...
)
```

### Arguments

- `.Object`: CogapsResult object
- `Amean`: mean of sampled A matrices
- `Pmean`: mean of sampled P matrices
- `Asd`: std dev of sampled A matrices
- `Psd`: std dev of sampled P matrices
- `meanChiSq`: mean value of ChiSq statistic
- `geneNames`: names of genes in data
- `sampleNames`: names of samples in data
- `diagnostics`: assorted diagnostic reports from the run
- `...`: initial values for slots

### Value

initialized CogapsResult object
isRdsFile  
checks if file is rds format

**Description**
checks if file is rds format

**Usage**
isRdsFile(file)

**Arguments**
- file  
  path to file

**Value**
TRUE if file is .rds, FALSE if not

---

**MANOVA**
**MANOVA statistical test for patterns between sample groups**

**Description**
MANOVA statistical test–wraps base R manova

**Usage**
MANOVA(interestedVariables, object)

## S4 method for signature 'matrix,CogapsResult'
MANOVA(interestedVariables, object)

**Arguments**
- interestedVariables  
  study design for manova
- object  
  CogapsResult object

**Value**
list of manova fit results
modsimdata

Toy example to run CoGAPS on.

Description

- V1..V20. some variables, for example levels of gene expression

Usage

data(modsimdata)

Format

'data.frame': 25 obs. of 20 variables.

modsimresult

Result of applying CoGAPS on the Toy example.

Description

Result of applying CoGAPS on the Toy example.

Usage

data(modsimresult)

Format

S4 class ‘CogapsResult’ [package “CoGAPS”] with 7 slots.

ncolHelper

get number of columns from supported file name or matrix

Description

get number of columns from supported file name or matrix

Usage

ncolHelper(data)

Arguments

data either a file name or a matrix

Value

number of columns
nrowHelper

get number of rows from supported file name or matrix

Description
get number of rows from supported file name or matrix

Usage
nrowHelper(data)

Arguments
data either a file name or a matrix

Value
number of rows

parseExtraParams

parse parameters passed through the ... variable

Description
parse parameters passed through the ... variable

Usage
parseExtraParams(allParams, extraParams)

Arguments
allParams list of all parameters
extraParams list of parameters in ...

Value
allParams with any valid parameters in extraParams added

Note
will halt with an error if any parameters in extraParams are invalid
patternMarkers  

*compute pattern markers statistic*

**Description**

calculate the most associated pattern for each gene

**Usage**

```r
patternMarkers(object, threshold = "all", lp = NA, axis = 1)
```

### S4 method for signature 'CogapsResult'

```r
patternMarkers(object, threshold = "all", lp = NA, axis = 1)
```

**Arguments**

- `object` an object of type CogapsResult
- `threshold` the type of threshold to be used. The default "all" will distribute genes into pattern with the lowest ranking. The "cut" thresholds by the first gene to have a lower ranking, i.e. better fit to, a pattern.
- `lp` a vector of weights for each pattern to be used for finding markers. If NA markers for each pattern of the A matrix will be used.
- `axis` either 1 or 2, specifying if pattern markers should be calculated using the rows of the data (1) or the columns of the data (2)

**Value**

By default a non-overlapping list of genes associated with each lp.

**Examples**

```r
data(GIST)
pm <- patternMarkers(GIST.result)
```

---

patternMatch  

*Match Patterns Across Multiple Runs*

**Description**

Match Patterns Across Multiple Runs

**Usage**

```r
patternMatch(allPatterns, gapsParams)
```
### plotPatternMarkers

**Arguments**

- `allPatterns`  matrix of patterns stored in the columns
- `gapsParams`  CoGAPS parameters object

**Value**

- a matrix of consensus patterns

---

### plotPatternHallmarks  generate a barchart of most significant hallmark sets for a pattern

**Description**

generate a barchart of most significant hallmark sets for a pattern

**Usage**

```r
plotPatternHallmarks(object, patternhallmarks, whichpattern = 1)
```

**Arguments**

- `object`  an object of type CogapsResult
- `patternhallmarks`  output from getPatternHallmarks
- `whichpattern`  which pattern to generate bar chart for

**Value**

- image object of barchart

---

### plotPatternMarkers  heatmap of original data clustered by pattern markers statistic

**Description**

heatmap of original data clustered by pattern markers statistic
plotResiduals

Usage

plotPatternMarkers(
  object,
  data,
  patternMarkers,
  patternPalette,
  sampleNames,
  samplePalette = NULL,
  heatmapCol = bluered,
  colDendrogram = TRUE,
  scale = "row",
  ...)

Arguments

object      an object of type CogapsResult
data        the original data as a matrix
patternMarkers pattern markers to be plotted, as generated by the patternMarkers function
patternPalette a vector indicating what color should be used for each pattern
sampleNames names of the samples to use for labeling
samplePalette a vector indicating what color should be used for each sample
heatmapCol  palette giving color scheme for heatmap
colDendrogram logical indicating whether to display sample dendrogram
scale       character indicating if the values should be centered and scaled in either the row
direction or the column direction, or none. The default is "row".
...          additional graphical parameters to be passed to heatmap.2

Value

heatmap of the data values for the patternMarkers

See Also

heatmap.2
Usage
plotResiduals(object, data, uncertainty = NULL)

## S4 method for signature 'CogapsResult'
plotResiduals(object, data, uncertainty = NULL)

Arguments
object an object of type CogapsResult
data original data matrix run through GAPS
uncertainty original standard deviation matrix run through GAPS

Value
creates a residual plot

Examples
data(GIST)
# to expensive to call since it plots
# plotResiduals(GIST.result, GIST.matrix)

---
reconstructGene  reconstruct gene

Description
reconstruct gene

Usage
reconstructGene(object, genes = NULL)

## S4 method for signature 'CogapsResult'
reconstructGene(object, genes = NULL)

Arguments
object an object of type CogapsResult
genesis an index of the gene or genes of interest

Value
the D' estimate of a gene or set of genes

Examples
data(GIST)
estimatedD <- reconstructGene(GIST.result)
sampleUniformly

subset data by uniformly partitioning rows (cols)

Description
subset data by uniformly partitioning rows (cols)

Usage
sampleUniformly(allParams, total, setSize)

Arguments

- allParams: list of all CoGAPS parameters
- total: total number of rows (cols) that are being partitioned
- setSize: the size of each subset of the total

Value
list of subsets

sampleWithAnnotationWeights
subset rows (cols) proportional to the user provided weights

Description
subset rows (cols) proportional to the user provided weights

Usage
sampleWithAnnotationWeights(allParams, setsize)

Arguments

- allParams: list of all CoGAPS parameters
- setSize: the size of each subset of the total

Value
list of subsets
sampleWithExplicitSets  \textit{use user provided subsets}

\textbf{Description}

use user provided subsets

\textbf{Usage}

\texttt{sampleWithExplicitSets(allParams)}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{allParams} \hspace{1em} list of all CoGAPS parameters
  \item \texttt{total} \hspace{1em} total number of rows (cols) that are being partitioned
\end{itemize}

\textbf{Value}

list of subsets

\textit{scCoGAPS} \hspace{1em} \textit{Single Cell CoGAPS}

\textbf{Description}

wrapper around single-cell distributed algorithm for CoGAPS

\textbf{Usage}

\begin{verbatim}
scCoGAPS(
  data,
  params = new("CogapsParams"),
  nThreads = 1,
  messages = TRUE,
  outputFrequency = 500,
  uncertainty = NULL,
  checkpointOutFile = "gaps_checkpoint.out",
  checkpointInterval = 1000,
  checkpointInFile = NULL,
  transposeData = FALSE,
  BPPARAM = NULL,
  workerID = 1,
  asynchronousUpdates = FALSE,
  ...
)
\end{verbatim}
Arguments

data File name or R object (see details for supported types)
params CogapsParams object
nThreads maximum number of threads to run on
messages T/F for displaying output
outputFrequency number of iterations between each output (set to 0 to disable status updates, other output is controlled by @code messages)
uncertainty uncertainty matrix - either a matrix or a supported file type
checkpointOutFile name of the checkpoint file to create
checkpointInterval number of iterations between each checkpoint (set to 0 to disable checkpoints)
checkpointInFile if this is provided, CoGAPS runs from the checkpoint contained in this file
transposeData T/F for transposing data while reading it in - useful for data that is stored as samples x genes since CoGAPS requires data to be genes x samples
BPPARAM BiocParallel backend
workerID if calling CoGAPS in parallel the worker ID can be specified, only worker 1 prints output and each worker outputs when it finishes, this is not necesssary when using the default parallel methods (i.e. distributed CoGAPS) but only when the user is manually calling CoGAPS in parallel
asynchronousUpdates enable asynchronous updating which allows for multi-threaded runs
... allows for overwriting parameters in params

Value
CogapsResult object

Examples

## Not run:
data(GIST)
params <- new("CogapsParams")
params <- setDistributedParams(params, nSets=2)
params <- setParam(params, "nIterations", 100)
params <- setParam(params, "nPatterns", 3)
result <- scCoGAPS(t(GIST.matrix), params, BPPARAM=BiocParallel::SerialParam())

## End(Not run)
setAnnotationWeights  set the annotation labels and weights for subsetting the data

Description

these parameters are interrelated so they must be set together

Usage

setAnnotationWeights(object, annotation, weights)

## S4 method for signature 'CogapsParams'
setAnnotationWeights(object, annotation, weights)

Arguments

- `object`: an object of type CogapsParams
- `annotation`: vector of labels
- `weights`: vector of weights

Value

the modified params object

Examples

```r
params <- new("CogapsParams")
params <- setAnnotationWeights(params, c('a', 'b', 'c'), c(1,2,1))
```

setDistributedParams  set the value of parameters for distributed CoGAPS

Description

these parameters are interrelated so they must be set together

Usage

setDistributedParams(
  object,
  nSets = NULL,
  cut = NULL,
  minNS = NULL,
  maxNS = NULL
)

## S4 method for signature 'CogapsParams'

setDistributedParams(
  object,
  nSets = NULL,
  cut = NULL,
  minNS = NULL,
  maxNS = NULL
)

### Arguments

- **object**: an object of type CogapsParams
- **nSets**: number of sets to break data into
- **cut**: number of branches at which to cut dendrogram used in pattern matching
- **minNS**: minimum of individual set contributions a cluster must contain
- **maxNS**: maximum of individual set contributions a cluster can contain

### Value

the modified params object

### Examples

```r
params <- new("CogapsParams")
params <- setDistributedParams(params, 5)
```

---

## setFixedPatterns

setFixedPatterns(object, fixedPatterns, whichMatrixFixed)

### Arguments

- **object**: an object of type CogapsParams
- **fixedPatterns**: values for either the A or P matrix
- **whichMatrixFixed**: either 'A' or 'P' indicating which matrix is fixed

### Description

these parameters are interrelated so they must be set together

### Usage

```r
setFixedPatterns(object, fixedPatterns, whichMatrixFixed)
```

---

## Description

setFixedPatterns

set the fixed patterns for either the A or the P matrix

these parameters are interrelated so they must be set together

### Usage

```r
setFixedPatterns(object, fixedPatterns, whichMatrixFixed)
```
setParam

set the value of a parameter

Description

set the value of a parameter

Usage

setParam(object, whichParam, value)

## S4 method for signature 'CogapsParams'
setParam(object, whichParam, value)

Arguments

object an object of type CogapsParams
whichParam a string with the name of the parameter to be changed
value the value to set the parameter to

Value

the modified params object

Examples

params <- new("CogapsParams")
data(GIST)
params <- setFixedPatterns(params, getSampleFactors(GIST.result), "P")

params <- setParam(params, "seed", 123)
### startupMessage

**write start up message**

**Description**

write start up message

**Usage**

startupMessage(data, allParams)

**Arguments**

- **data**: data set
- **allParams**: list of all parameters

**Value**

message displayed to screen

### stitchTogether

**concatenate final results across subsets**

**Description**

concatenate final results across subsets

**Usage**

stitchTogether(result, allParams, sets)

**Arguments**

- **result**: list of CogapsResult object from all runs across subsets
- **allParams**: list of all CoGAPS parameters
- **sets**: indices of sets used to break apart data

**Value**

list with all CoGAPS output
**supported**

*checks if file is supported*

**Description**

checks if file is supported

**Usage**

supported(file)

**Arguments**

file: path to file

**Value**

TRUE if file is supported, FALSE if not

---

**toCSV**

*save CoGAPS Result object as a set of csvs to directory see fromCSV*

**Description**

save as csv

**Usage**

toCSV(object, save_location = ".")

## S4 method for signature 'CogapsResult,character'
toCSV(object, save_location = ".")

**Arguments**

object: CogapsResult object

save_location: directory to write to

**Value**

none
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