

Package ‘CoGAPS’

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Title Coordinated Gene Activity in Pattern Sets

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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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Imports BiocParallel, cluster, methods, gplots, graphics, grDevices, RColorBrewer, Rcpp, S4Vectors, SingleCellExperiment, stats, SummarizedExperiment, tools, utils, rhdf5, dplyr, fgsea, forcats, ggplot2

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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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References

Fertig EJ, Ding J, Favorov AV, Parmigiani G, Ochs MF. CoGAPS: an R/C++ package to identify patterns and biological process activity in transcriptomic data. *Bioinformatics*. 2010 Nov 1;26(21):2792-3

 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

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()
```

calcCoGAPStat

calculate statistic on sets of measurements (genes) or samples

Description

calculates a statistic to determine if a pattern is enriched in a a particular set of measurements or samples.

Usage

```

calcCoGAPStat(
  object,
  sets = NULL,
  whichMatrix = "featureLoadings",
  numPerm = 1000,
  ...
)

## S4 method for signature 'CogapsResult'
calcCoGAPStat(
  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 |
| ... | handles old arguments for backwards compatibility |

Value

gene set statistics for each column of A

| | |
|----------------|---|
| calcGeneGSStat | <i>probability gene belongs in gene set</i> |
|----------------|---|

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 similiarity statistic

| | |
|-------|-------------------------------|
| calcZ | <i>compute z-score matrix</i> |
|-------|-------------------------------|

Description

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

Usage

```

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

Examples

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

| | |
|--------------------|---|
| callInternalCoGAPS | <i>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</i> |
|--------------------|---|

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 | <i>check that provided data is valid</i> |
|-----------------|--|

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 | <i>check that all inputs are valid</i> |
|-------------|--|

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 | <i>Check if package was built with checkpoints enabled</i> |
|--------------------|--|

Description

Check if package was built with checkpoints enabled

Usage

```
checkpointsEnabled()
```

Value

true/false if checkpoints are enabled

Examples

```
CoGAPS::checkpointsEnabled()
```

| | |
|--------|--|
| CoGAPS | <i>CoGAPS Matrix Factorization Algorithm</i> |
|--------|--|

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 necessary 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 | <i>compute gene probability</i> |
|-------------------|---------------------------------|

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

```
computeGeneGSProb(  
  object,  
  GStoGenes,  
  numPerm = 500,  
  Pw = rep(1, ncol(object@featureLoadings)),  
  PwNull = FALSE  
)  
  
## S4 method for signature 'CogapsResult'  
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

```
convertDataToMatrix(data)
```

Arguments

`data` data input

Value

data matrix

`corcut` *cluster patterns together*

Description

cluster patterns together

Usage

```
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 *calculate 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 *convert 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

| | |
|------------|---|
| createSets | <i>partition genes/samples into subsets</i> |
|------------|---|

Description

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

Usage

```
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

| | |
|-------------------|--|
| distributedCogaps | <i>CoGAPS Distributed Matrix Factorization Algorithm</i> |
|-------------------|--|

Description

runs CoGAPS over subsets of the data and stitches the results back together

Usage

```
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 = ".")  
  
## S4 method for signature 'character'  
fromCSV(save_location = ".")
```

Arguments

save_location directory to read from

Value

CogapsResult object

gapsCat *wrapper around cat*

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)  
  
## S4 method for signature 'CogapsResult'  
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 | <i>extracts gene/sample names from the data</i> |
|-------------|---|

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 | <i>return featureLoadings matrix from CogapsResult object</i> |
|--------------------|---|

Description

return featureLoadings matrix from CogapsResult object

Usage

```
getFeatureLoadings(object)

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

Arguments

| | |
|--------|--------------------------------|
| object | an object of type CogapsResult |
|--------|--------------------------------|

Value

featureLoadings matrix

Examples

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

| | |
|--------------|-------------------------------------|
| getGeneNames | <i>extract gene names from data</i> |
|--------------|-------------------------------------|

Description

extract gene names from data

Usage

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

Value

vector of gene names

| | |
|--------------|--|
| getMeanChiSq | <i>return chi-sq of final matrices</i> |
|--------------|--|

Description

return chi-sq of final matrices

Usage

```
getMeanChiSq(object)

## S4 method for signature 'CogapsResult'
getMeanChiSq(object)
```

Arguments

object an object of type CogapsResult

Value

chi-sq error

Examples

```
data(GIST)
getMeanChiSq(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

```
getParam(object, whichParam)

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

Arguments

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

Value

the value of the parameter

Examples

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

getPatternGeneSet *generate statistics associating patterns with gene sets*

Description

generate statistics associating patterns with gene sets

Usage

```
getPatternGeneSet(
  object,
  gene.sets,
  method = c("enrichment", "overrepresentation"),
  ...
)

## S4 method for signature 'CogapsResult,list,character'
getPatternGeneSet(
  object,
  gene.sets,
  method = c("enrichment", "overrepresentation"),
  ...
)
```

Arguments

| | |
|-----------|---|
| object | an object of type CogapsResult |
| gene.sets | a list of gene sets to test. List names should be the names of the gene sets |
| method | enrichment or overrepresentation. Conducts a test for gene set enrichment using fgsea::gsea ranking features by pattern amplitude or a test for gene set overrepresentation in pattern markers using fgsea::fora, respectively. |
| ... | additional parameters passed to patternMarkers if using overrepresentation method |

Value

list of dataframes containing gene set enrichment or gene set overrepresentation statistics

Examples

```

data(GIST)
gs.test <- list(
  "gs1" = c("Hs.2", "Hs.4", "Hs.36", "Hs.96", "Hs.202"),
  "gs2" = c("Hs.699463", "Hs.699288", "Hs.699280", "Hs.699154", "Hs.697294")
)
getPatternGeneSet(object = GIST.result, gene.sets = gs.test, method = "enrichment")
getPatternGeneSet(object = GIST.result, gene.sets = gs.test, method = "overrepresentation")

```

getPatternMatrix *return pattern matrix from CogapsResult object*

Description

return pattern matrix from CogapsResult object

Usage

```

getPatternMatrix(object)

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

```

Arguments

object an object of type CogapsResult

Value

pattern matrix

Examples

```

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

```

getRetinaSubset *get specified number of retina subsets*

Description

combines retina subsets from extdata directory

Usage

```

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

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

Arguments

object an object of type CogapsResult

Value

sampleFactors matrix

Examples

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

| | |
|----------------|---------------------------------------|
| getSampleNames | <i>extract sample names from data</i> |
|----------------|---------------------------------------|

Description

extract sample names from data

Usage

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

Value

vector of sample names

| | |
|------------|---|
| getSubsets | <i>return the names of the genes (samples) in each subset</i> |
|------------|---|

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

Value

CogapsParams object

Examples

```
data(GIST)
unmatchedPatterns <- getUnmatchedPatterns(GIST.result)
```

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 | <i>return version number used to generate this result</i> |
|------------|---|

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

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

| | |
|-----------------|--|
| GIST.data_frame | <i>GIST gene expression data from Ochs et al. (2009)</i> |
|-----------------|--|

Description

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

| | |
|-------------|--|
| GIST.matrix | <i>GIST gene expression data from Ochs et al. (2009)</i> |
|-------------|--|

Description

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

| | |
|-------------|---|
| GIST.result | <i>CoGAPS result from running on GIST dataset</i> |
|-------------|---|

Description

CoGAPS result from running on GIST dataset

| | |
|------------------|--|
| GIST.uncertainty | <i>GIST gene expression uncertainty matrix from Ochs et al. (2009)</i> |
|------------------|--|

Description

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

| | |
|----------|---------------------------|
| GWCoGAPS | <i>Genome Wide CoGAPS</i> |
|----------|---------------------------|

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 necessary 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 <- GWCoGAPS(GIST.matrix, params, BPPARAM=BiocParallel::SerialParam())

## End(Not run)
```

```
initialize,CogapsParams-method
      constructor for CogapsParams
```

Description

constructor for CogapsParams

Usage

```
## 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

```
initialize,CogapsResult-method
      Constructor for CogapsResult
```

Description

Constructor for CogapsResult

Usage

```
## S4 method for signature 'CogapsResult'
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 | <i>checks if file is rds format</i> |
|-----------|-------------------------------------|

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 | <i>Result of applying CoGAPS on the Toy example.</i> |
|--------------|--|

Description

Result of applying CoGAPS on the Toy example.

Usage

```
data(modsimresult)
```

Format

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

| | |
|------------|---|
| ncolHelper | <i>get number of columns from supported file name or matrix</i> |
|------------|---|

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 | <i>get number of rows from supported file name or matrix</i> |
|------------|--|

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 | <i>parse parameters passed through the ... variable</i> |
|------------------|---|

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 | <i>compute pattern markers statistic</i> |
|----------------|--|

Description

calculate the most associated pattern for each gene

Usage

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

```
## S4 method for signature 'CogapsResult'
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

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

| | |
|--------------|--|
| patternMatch | <i>Match Patterns Across Multiple Runs</i> |
|--------------|--|

Description

Match Patterns Across Multiple Runs

Usage

```
patternMatch(allPatterns, gapsParams)
```

Arguments

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

Value

a matrix of consensus patterns

plotPatternGeneSet *generate a barchart of most significant hallmark sets for a pattern*

Description

generate a barchart of most significant hallmark sets for a pattern

Usage

```
plotPatternGeneSet(patterngeneset, whichpattern = 1, padj_threshold = 0.05)

## S4 method for signature 'list,numeric,numeric'
plotPatternGeneSet(patterngeneset, whichpattern = 1, padj_threshold = 0.05)
```

Arguments

patterngeneset output from getPatternGeneSet
whichpattern which pattern to generate bar chart for
padj_threshold maximum adjusted p-value of gene sets rendered on the resulting plot

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

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 | pallet 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](#)

plotResiduals

plot of residuals

Description

calculate residuals and produce heatmap

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)
# too expensive to call since it plots
# plotResiduals(GIST.result, GIST.matrix)
```

| | |
|-----------------|-------------------------|
| reconstructGene | <i>reconstruct gene</i> |
|-----------------|-------------------------|

Description

reconstruct gene

Usage

```
reconstructGene(object, genes = NULL)

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

Arguments

| | |
|--------|---|
| object | an object of type CogapsResult |
| genes | 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 | <i>subset data by uniformly partitioning rows (cols)</i> |
|-----------------|--|

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 | <i>subset rows (cols) proportional to the user provided weights</i> |
|-----------------------------|---|

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 *use user provided subsets*

Description

use user provided subsets

Usage

```
sampleWithExplicitSets(allParams)
```

Arguments

| | |
|-----------|--|
| allParams | list of all CoGAPS parameters |
| total | total number of rows (cols) that are being partitioned |

Value

list of subsets

| | |
|----------|---------------------------|
| scCoGAPS | <i>Single Cell CoGAPS</i> |
|----------|---------------------------|

Description

wrapper around single-cell distributed algorithm for CoGAPS

Usage

```
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,
  ...
)
```

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 necessary 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

```
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

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

| | |
|------------------|--|
| setFixedPatterns | <i>set the fixed patterns for either the A or the P matrix</i> |
|------------------|--|

Description

these parameters are interrelated so they must be set together

Usage

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

```
## S4 method for signature 'CogapsParams'
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 |

Value

the modified params object

Examples

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

| | |
|----------|-------------------------------------|
| setParam | <i>set the value of a parameter</i> |
|----------|-------------------------------------|

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")
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 | <i>checks if file is supported</i> |
|-----------|------------------------------------|

Description

checks if file is supported

Usage

supported(file)

Arguments

| | |
|------|--------------|
| file | path to file |
|------|--------------|

Value

TRUE if file is supported, FALSE if not

| | |
|-------|--|
| toCSV | <i>save CoGAPS Result object as a set of csvs to directory see fromCSV</i> |
|-------|--|

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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