

# 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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 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.

Package: CoGAPS  
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### Author(s)

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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	<i>calculate correlation of each pattern in a cluster to the cluster mean</i>
-------------------	---

---

**Description**

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

**Usage**

```
corrToMeanPattern(cluster)
```

**Value**

correlation of each pattern

---

createCogapsResult	<i>convert list output from c++ code to a CogapsResult object</i>
--------------------	---

---

**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      *compute pattern markers statistic*

---

## Description

estimate the most associated pattern for each feature

## Usage

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

```
## S4 method for signature 'CogapsResult'
patternMarkers(object, threshold = "all", lp = NULL, axis = 1)
```

## Arguments

object	an object of type CogapsResult
threshold	the type of threshold to be used. The default "all" will distribute features into patterns with the highest ranking as ranked by the increasing Euclidian distance between feature loadings and lp. The alternative "cut" will only keep the features that are ranked higher than the first feature having greater intra-pattern compared to inter-pattern rank. This is useful to limit the number of markers ranked similarly everywhere. Features may be present in multiple patterns for "cut".
lp	list of vectors of weights for each pattern to be used for finding markers. If NULL, list of synthetic one-hot markers for each pattern will be generated and matched against.
axis	controls the matrix to use for ranking. 1 for featureLoadings, 2 for sampleFactors.

## Value

List of: list of marker features for each pattern (best rank first), a matrix of ranks of each feature in each pattern, a matrix of scores for each feature in each pattern.

List of: list of marker features for each pattern (best rank first), and a matrix of ranks of each feature in each pattern.

## 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	<i>generate a barchart of most significant hallmark sets for a pattern</i>
--------------------	--

---

**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	pallelet 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	<i>plot of residuals</i>
---------------	--------------------------

---

**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)
# to 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            *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 *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

*Single Cell CoGAPS***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')
```

---

setParameter	<i>set the value of a parameter</i>
--------------	-------------------------------------

---

**Description**

set the value of a parameter

**Usage**

```
setParameter(object, whichParam, value)
```

```
## S4 method for signature 'CogapsParams'  
setParameter(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	<i>write start up message</i>
----------------	-------------------------------

---

**Description**

write start up message

**Usage**

```
startupMessage(data, allParams)
```

**Arguments**

data	data set
allParams	list of all parameters

**Value**

message displayed to screen



---

stitchTogether	<i>concatenate final results across subsets</i>
----------------	---

---

**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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