

Package ‘CoGAPS’

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Title Coordinated Gene Activity in Pattern Sets

Author Thomas Sherman, Wai-shing Lee, Conor Kelton, Ondrej Maxian, Jacob Carey, Genevieve Stein-O'Brien, Michael Considine, Maggie Wodicka, John Stansfield, Shawn Sivy, Carlo Colantuoni, Alexander Favorov, Mike Ochs, Elana Fertig

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.

Maintainer Elana J. Fertig <ejfertig@jhmi.edu>, Thomas D. Sherman <tomsherman159@gmail.com>

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LinkingTo Rcpp, BH

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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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Maintainer: Elana J. Fertig <ejfertig@jhmi.edu>, Michael F. Ochs <ochsm@tcnj.edu>

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(SimpSim)
result <- CoGAPS(SimpSim.data)
binMatrix <- binaryA(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 gene set statistics

Description

calculates the gene set statistics for each column of A using a Z-score from the elements of the A matrix, the input gene set, and permutation tests

Usage

```
calcCoGAPSStat(object, GStoGenes, numPerm = 500)
```

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

```
calcCoGAPSStat(object, GStoGenes, numPerm = 500)
```

Arguments

object	an object of type CogapsResult
GStoGenes	data.frame or list with gene sets
numPerm	number of permutations for null

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 similarity 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, which = "feature")

## S4 method for signature 'CogapsResult'
calcZ(object, which = "feature")
```

Arguments

object an object of type CogapsResult
 which either "feature" or "sample" indicating which matrix to calculate the z-score for

Value

matrix of z-scores

Examples

```
data(SimpSim)
result <- CoGAPS(SimpSim.data)
feature_zscore <- calcZ(result)
```

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 = 500, uncertainty = NULL,
  checkpointOutFile = "gaps_checkpoint.out", checkpointInterval = 1000,
  checkpointInFile = NULL, transposeData = FALSE, BPPARAM = NULL,
  geneNames = NULL, sampleNames = NULL, matchedPatterns = NULL,
  outputToFile = NULL, ...)
```

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
geneNames	vector of names of genes in data
sampleNames	vector of names of samples in data
matchedPatterns	manually matched patterns for distributed CoGAPS
outputToFile	name of a file to save the output to, will create 4 files of the form "filename_nPatterns_[Amean, Asd, Pmean, Psd].extension"
...	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=250)

# Running from file name
gist_path <- system.file("extdata/GIST.mtx", package="CoGAPS")
resultB <- CoGAPS(gist_path, nIterations=250)

# Setting Parameters
params <- new("CogapsParams")
params <- setParam(params, "nPatterns", 5)
resultC <- CoGAPS(GIST.data_frame, params, nIterations=250)
```

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

singleCell is the data single cell?
 sparseOptimization speeds up performance with sparse data, note this can only be used with the 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

CogapsResult-class *CogapsResult*

Description

Contains all output from Cogaps run

Slots

sampleStdDev std dev of the sampled P matrices
 featureStdDev std dev of the sampled A matrices

computeGeneGSProb *compute gene probability*

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.

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(SimpSim)
result <- CoGAPS(SimpSim.data)
getClusteredPatterns(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(SimpSim)
result <- CoGAPS(SimpSim.data)
getCorrelationToMeanPattern(result)
```

```
getMeanChiSq
```

return chi-sq of final matrices

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(SimpSim)
result <- CoGAPS(SimpSim.data)
getMeanChiSq(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(SimpSim)
result <- CoGAPS(SimpSim.data)
getOriginalParameters(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")
```

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(SimpSim)
result <- CoGAPS(SimpSim.data)
getSubsets(result)
```

getUnmatchedPatterns	<i>return unmatched patterns from each subset</i>
----------------------	---

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(SimpSim)
result <- CoGAPS(SimpSim.data)
getUnmatchedPatterns(result)
```

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(SimpSim)
result <- CoGAPS(SimpSim.data)
getVersion(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)

Usage

```
GIST.data_frame
```

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

Description

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

Usage

GIST.matrix

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

Description

CoGAPS result from running on GIST dataset

Usage

GIST.result

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)

Usage

GIST.uncertainty

GWCoGAPS

*Genome Wide CoGAPS***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,
  geneNames = NULL, sampleNames = NULL, matchedPatterns = NULL, ...)
```

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
geneNames	vector of names of genes in data
sampleNames	vector of names of samples in data
matchedPatterns	manually matched patterns for distributed CoGAPS
...	allows for overwriting parameters in params

Value

CogapsResult object

Examples

```
data(SimpSim)
result <- GWCoGAPS(SimpSim.data, BPPARAM=BiocParallel::SerialParam(), nIterations=250)
```

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

Description

constructor for CogapsParams

Usage

```
## S4 method for signature 'CogapsParams'
initialize(.Object, ...)
```

Arguments

```
.Object      CogapsParams object
...          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

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

Description

calculate the most associated pattern for each gene

Usage

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

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

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.

Value

By default a non-overlapping list of genes associated with each lp. If full=TRUE a data.frame of genes rankings with a column for each lp will also be returned.

plotPatternMarkers	<i>heatmap of original data clustered by pattern markers statistic</i>
--------------------	--

Description

heatmap of original data clustered by pattern markers statistic

Usage

```
plotPatternMarkers(object, data, patternPalette, sampleNames,
  samplePalette = NULL, heatmapCol = blured, colDenogram = TRUE,
  scale = "row", ...)
```

Arguments

object	an object of type CogapsResult
data	the original data as a matrix
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
colDenogram	logical indicating whether to display sample denogram
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(SimpSim)
result <- CoGAPS(SimpSim.data)
plotResiduals(result, SimpSim.data)
```

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(SimpSim)
result <- CoGAPS(SimpSim.data)
D_estimate <- reconstructGene(result)
```

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,
  geneNames = NULL, sampleNames = NULL, matchedPatterns = NULL, ...)
```

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
geneNames	vector of names of genes in data
sampleNames	vector of names of samples in data
matchedPatterns	manually matched patterns for distributed CoGAPS
...	allows for overwriting parameters in params

Value

CogapsResult object

Examples

```
data(SimpSim)
result <- scCoGAPS(t(SimpSim.data), BPPARAM=BiocParallel::SerialParam(), nIterations=250)
```

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, cut = NULL, minNS = NULL,
  maxNS = NULL)

## S4 method for signature 'CogapsParams'
setDistributedParams(object, nSets, 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)
```

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)
```

SimpSim.data	<i>Simulated data</i>
--------------	-----------------------

Description

Simulated data

Usage

```
SimpSim.data
```

SimpSim.result	<i>CoGAPS result from running on simulated data</i>
----------------	---

Description

CoGAPS result from running on simulated data

Usage

```
SimpSim.result
```

tf2ugFC

Gene sets defined by transcription factors defined from TRANSFAC.

Description

Gene sets defined by transcription factors defined from TRANSFAC.

Usage

tf2ugFC

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