

cummeRbund

March 24, 2012

CuffData-class *Class "CuffData"*

Description

A 'pointer' class for all information (FPKM, annotation, differential expression) for a given feature type (genes, isoforms, TSS, CDS). The methods for this function communicate directly with the SQL backend to present data to the user.

Objects from the Class

Objects can be created by calls of the form `new("CuffData", DB, tables, filters, type, idField, ...)`.

Slots

`DB`: Object of class "SQLiteConnection" ~~
`tables`: Object of class "list" ~~
`filters`: Object of class "list" ~~
`type`: Object of class "character" ~~
`idField`: Object of class "character" ~~

Methods

`dim` signature(x = "CuffData"): ...
`getFeatures` signature(object = "CuffData"): ...

Note

None

Author(s)

Loyal A. Goff

References

None

See Also

None

Examples

```
showClass("CuffData")
```

CuffDist-class *Class "CuffDist"*

Description

A 'pointer' class to information relative to the distribution-level tests (promoters, splicing, and relative CDS usage)

Objects from the Class

Objects can be created by calls of the form `new("CuffDist", DB, table, type, testId, ...)`.

Slots

DB: Object of class "SQLiteConnection" ~~

table: Object of class "character" ~~

type: Object of class "character" ~~

testId: Object of class "character" ~~

Methods

dim signature(x = "CuffDist"):...

Note

None

Author(s)

Loyal A. Goff

References

None

See Also

None

Examples

```
showClass("CuffDist")
```

CuffFeature-class *Class "CuffFeature"*

Description

A 'data' container class for all FPKM, annotation, and differential expression data for a single feature (gene, isoform, TSS, or CDS).

Objects from the Class

Objects can be created by calls of the form `new("CuffFeature", annotation, fpkm, diff, ...)`.

Slots

`annotation`: Object of class "data.frame" ~~
`fpkm`: Object of class "data.frame" ~~
`diff`: Object of class "data.frame" ~~

Methods

`fpkmMatrix` signature (object="CuffFeature"): ...
`length` signature (x = "CuffFeature"): ...

Accessors

`annotation` signature (object="CuffFeature"): Access @annotation slot

Note

'CuffGene' is a superclass of 'CuffFeature' that links gene information for a given gene with all isoform-, TSS-, and CDS-level data for the given gene.

Author(s)

Loyal A. Goff

References

None

See Also

[CuffGene](#)

Examples

```
showClass("CuffFeature")
```

CuffFeatureSet-class

Class "CuffFeatureSet"

Description

A 'data' container class for all FPKM, annotation, and differential expression data for a set of features (genes, isoforms, TSS, CDS).

Objects from the Class

Objects can be created by calls of the form `new("CuffFeatureSet", annotation, fpkm, diff, ...)`.

Slots

annotation: Object of class "data.frame" ~~

fpkm: Object of class "data.frame" ~~

diff: Object of class "data.frame" ~~

Methods

diffData signature(object = "CuffFeatureSet"): ...

featureNames signature(object = "CuffFeatureSet"): ...

features signature(object = "CuffFeatureSet"): ...

fpkmMatrix signature(object = "CuffFeatureSet"): ...

samples signature(object = "CuffFeatureSet"): ...

length signature(object = "CuffFeatureSet"): ...

Accessors

annotation signature(object="CuffFeatureSet"): Access @annotation slot

Note

None.

Author(s)

Loyal A. Goff

References

None.

See Also

[CuffGeneSet](#)

Examples

```
showClass("CuffFeatureSet")
```

CuffGene-class *Class "CuffGene"*

Description

A 'data' container class for all FPKM, annotation, and differential expression Data (as well as for all linked features) for a given gene.

Objects from the Class

Objects can be created by calls of the form `new("CuffGene", annotation, fpkm, diff, ...)`.

Slots

`id`: Object of class "character" ~~
`isoforms`: Object of class "CuffFeature" ~~
`TSS`: Object of class "CuffFeature" ~~
`CDS`: Object of class "CuffFeature" ~~
`annotation`: Object of class "data.frame" ~~
`fpkm`: Object of class "data.frame" ~~
`diff`: Object of class "data.frame" ~~

Extends

Class "[CuffFeature](#)", directly.

Methods

No methods defined with class "CuffGene" in the signature.

Accessors

genes signature(object = "CuffGene"): Access @genes slot
isoforms signature(object = "CuffGene"): Access @isoforms slot
TSS signature(object = "CuffGene"): Access @TSS slot
CDS signature(object = "CuffGene"): Access @CDS slot

Note

None.

Author(s)

Loyal A. Goff

References

None.

See Also

[CuffFeature](#)

Examples

```
showClass("CuffGene")
```

CuffGeneSet-class *Class "CuffGeneSet"*

Description

A 'data' container class for all FPKM, annotation, and differential expression data (an associated features) for a given set of genes.

Objects from the Class

Objects can be created by calls of the form `new("CuffGeneSet", annotation, fpkm, diff, ...)`.

Slots

`ids`: Object of class "character" ~~
`isoforms`: Object of class "CuffFeatureSet" ~~
`TSS`: Object of class "CuffFeatureSet" ~~
`CDS`: Object of class "CuffFeatureSet" ~~
`annotation`: Object of class "data.frame" ~~
`fpkm`: Object of class "data.frame" ~~
`diff`: Object of class "data.frame" ~~

Extends

Class "[CuffFeatureSet](#)", directly.

Methods

No methods defined with class "CuffGeneSet" in the signature.

Accessors

genes signature(object = "CuffGeneSet"): Access @genes slot
isoforms signature(object = "CuffGeneSet"): Access @isoforms slot
TSS signature(object = "CuffGeneSet"): Access @TSS slot
CDS signature(object = "CuffGeneSet"): Access @CDS slot

Note

None.

Author(s)

Loyal A. Goff

References

None.

See Also

[CuffFeatureSet](#)

Examples

```
showClass("CuffGeneSet")
```

CuffSet-class *Class "CuffSet"*

Description

A 'pointer' class to connect to, and retrieve data from the SQLite backend database.

Objects from the Class

Objects can be created by calls of the form `new("CuffSet", DB, conditions, genes, isoforms, TSS, CDS, promoters, splicing, relCDS, ...)`. Available methods are primary accessors to retrieve `CuffGeneSet` or `CuffGene` objects for manipulation.

Slots

DB: Object of class "SQLiteConnection" ~~
conditions: Object of class "data.frame" ~~
genes: Object of class "CuffData" ~~
isoforms: Object of class "CuffData" ~~
TSS: Object of class "CuffData" ~~
CDS: Object of class "CuffData" ~~
promoters: Object of class "CuffDist" ~~
splicing: Object of class "CuffDist" ~~
relCDS: Object of class "CuffDist" ~~

Methods

[signature(x = "CuffSet"):...

Accessors

genes signature(object = "CuffSet"): Access @genes slot
isoforms signature(object = "CuffSet"): Access @isoforms slot
TSS signature(object = "CuffSet"): Access @TSS slot
CDS signature(object = "CuffSet"): Access @CDS slot
promoters signature(object = "CuffSet"): Access @promoters slot
splicing signature(object = "CuffSet"): Access @splicing slot
relCDS signature(object = "CuffSet"): Access @relCDS slot

Note

None.

Author(s)

Loyal A. Goff

References

None.

See Also

None.

Examples

```
showClass("CuffSet")
```

JSdist

Jensen-Shannon distance on columns

Description

JSdist takes a matrix of expression probabilities (calculated directly or output from makeprobs()) and returns a dist object of the pairwise Jensen-Shannon distances between columns

Usage

```
JSdist(mat)
```

Arguments

mat A matrix of expression probabilities (e.g. from makeprobs())

Details

Returns pairwise Jensen-Shannon distance (in the form of a dist object) for a matrix of probabilities (by column)

Value

A dist object of pairwise J-S distances between columns.

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
mat<-matrix(sample(1:50, 50), 10)
probs<-makeprobs(mat)
js.distance<-JSdist(probs)
```

JSdistVec

JSdistVec

Description

Returns the Jensen-Shannon Distance (square root of JS divergence) between two probability vectors.

Usage

```
JSdistVec(p, q)
```

Arguments

p	A vector of probabilities
q	A vector of probabilities

Details

Should not be called directly by user.

Value

Returns the JS distance as a numeric

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
p<-sample(1:5000,20)
q<-sample(1:5000,20)
p<-makeprobsvec(p)
q<-makeprobsvec(q)
JSdistVec(p,q)
```

PINK1

PINK1

Description

A sample 'CuffGene' dataset

Usage

```
data(sampleData)
```

Format

PINK1 is a CuffGene object (extends CuffFeature) with all sample gene-, isoform-, TSS-, and CDS-level data for the gene 'PINK1'.

Details

Sample CuffGene data for gene 'PINK1'

Source

None

References

None

Examples

```
data(sampleData)
PINK1
```

addFeatures	<i>addFeatures</i>
-------------	--------------------

Description

Adds a data.frame of features to a the SQLite backend database.

Usage

```
## S4 method for signature 'CuffSet'  
addFeatures(object, features, level="genes", ...)
```

Arguments

object	An object of class ('CuffSet' or 'CuffData')
features	A data.frame of features to add. 1st column MUST contain ids (ie. gene_id for 'gene' features, isoform_id for 'isoform' features, etc)
level	One of c('genes','isoforms','TSS','CDS') to indicate which type of features you are being added, and to what data-level.
...	Additional arguments.

Details

None

Value

None

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
#None yet.
```

 createDB

createDB

Description

This should not be called directly by the user.

Usage

```
createDB(dbFname = "cuffData.db", driver = "SQLite")
```

Arguments

dbFname	File name for backend database (by default this is 'cuffData.db'). If you change this value, be sure to point to the new file with every call to 'readCufflinks'.
driver	DB driver for backend database (only SQLite supported at this time.)

Details

Should not be called directly

Value

Creates database backend file

Note

None

Author(s)

Loyal A. Goff

References

None

 csBoxplot

csBoxplot

Description

Creates a ggplot2 plot object with a geom_box layer displaying summary statistics for FPKM values across samples (x).

Usage

```
## S4 method for signature 'CuffData'
csBoxplot(object, logMode=TRUE, ...)
```

Arguments

object	An object of class CuffData.
logMode	A logical argument to log10 -transform FPKM values.
...	Additional arguments to csBoxplot

Details

None

Value

A ggplot2 plot object with a geom_box layer.

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
a<-readCufflinks(system.file("extdata", package="cummeRbund")) #Read cufflinks data and
genes<-a@genes #CuffData object for all genes
csBoxplot(genes)
```

csCluster

csCluster

Description

Returns a ggplot2 plot object with geom_line layer plotting FPKM values over conditions faceted by k-means clustering clusters. (Euclidean). This is very crude at this point. This does not return any of the clustering information directly, but if you want it, you can retrieve it from the ggplot object returned.

Usage

```
## S4 method for signature 'CuffFeatureSet'
csCluster(object, k, iter.max=100, ...)
```

Arguments

object	An object of class CuffFeatureSet.
k	Number of pre-defined clusters to attempt to find.
iter.max	Max iterations
...	Additional arguments

Details

Uses 'kmeans' function.

Author(s)

Loyal A. Goff

Source

None

References

None.

Examples

```
data(sampleData)
csCluster(sampleGeneSet, 4)
```

csDensity

Density plot of CuffData

Description

Creates a smoothed density plot, by sample, for log10 FPKM values from a cuffdiff run.

Usage

```
## S4 method for signature 'CuffData'
csDensity(object, logMode=TRUE, pseudocount=1.0, labels, features=FALSE, ...)
```

Arguments

object	An object of class CuffData.
logMode	A logical value of whether or not to log10-transform FPKM values. By default this is TRUE.
pseudocount	Pseudocount value added to FPKM to avoid errors in log-transformation of true zero values.
labels	A list of tracking_id values or gene_short_name values used for 'callout' points on the density plot for reference. (Not implemented yet).
features	Will include all fields from 'features' slot in returned ggplot object. Useful for further manipulations of plot object using feature-level attributes (e.g. gene_type, class_code, etc)
...	Additional arguments

Details

Creates a density plot, by sample, for log10-transformed FPKM values from a cuffdiff run.

Value

A ggplot2 plot object

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
a<-readCufflinks(system.file("extdata", package="cummeRbund")) #Create CuffSet object from
genes<-a@genes #Create CuffData object for all 'genes'
d<-csDensity(genes) #Create csDensity plot
d #Render plot
```

csHeatmap

csHeatmap

Description

Creates a ggplot plot object with a geom_tile layer of FPKM values per feature and sample.

Usage

```
## S4 method for signature 'CuffFeatureSet'
csHeatmap(object, rescaling='none', clustering='none', labCol=T, labRow=T, logMode=
border=FALSE, heatscale= c(low='darkred',mid='orange',high='white'), heatMidpoint=)
```

Arguments

object	An object of class 'CuffFeatureSet' or 'CuffGeneSet'
rescaling	Rescaling can either be 'row' or 'column' OR you can pass rescale a function that operates on a matrix to do your own rescaling. Default is 'none'.
clustering	Clustering can either be 'row','column','none', or 'both', in which case the appropriate indices are re-ordered based on the pairwise Jensen-Shannon distance of FPKM values. Alternatively you can pass your own clustering function so long as the returned value is a re-ordered matrix.
labCol	A logical argument to display column labels.
labRow	A logical argument to display row labels.
logMode	A logical argument to log10-transform FPKM values prior to plotting.
pseudocount	Value to be added to FPKM for appropriate log transformation and clustering. (Avoids zero-based errors)
border	A logical argument to draw border around plot.

heatscale A list with min length=2, max length=3 that detail the low,mid,and high colors to build the color scale.

heatMidpoint Value for midpoint of color scale.

... Additional arguments to csHeatmap

Details

None

Value

A ggplot2 plot object with a geom_tile layer to display FPKM values by sample (x) and feature (y)

Note

None

Author(s)

Loyal A. Goff and Cole Trapnell

References

None.

Examples

```
data(sampleData)
csHeatmap(sampleGeneSet)
```

csScatter

Scatter Plot

Description

A scatter plot comparing the FPKM values from two samples in a cuffdiff run.

Usage

```
## S4 method for signature 'CuffData'
csScatter(object, x, y, logMode=TRUE, pseudocount=1.0, labels, smooth=FALSE, col)
```

Arguments

object An object of class ('CuffData','CuffFeatureSet')

x Sample name for x axis

y Sample name for y axis

logMode Logical argument to log2-transform data (default: T)

pseudocount Value to add to zero FPKM values for log transformation (default: 0.0001)

smooth Logical argument to add a smooth-fit regression line

`labels` A list of `tracking_ids` or `gene_short_names` that will be 'callout' points in the plot for reference. Useful for finding genes of interest in the field. Not implemented yet.

`colorByStatus` A logical argument whether or not to color the points by 'significant' Y or N. [Default = FALSE]

`...` Additional arguments to `csScatter`

Details

None

Value

ggplot object with `geom_point` and `geom_rug` layers

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```

a<-readCufflinks(system.file("extdata", package="cummeRbund")) #Create CuffSet object from
genes<-a@genes #Create CuffData object for all genes
s<-csScatter(genes,'hESC','Fibroblasts',smooth=TRUE) #Create plot object
s #render plot object

```

csVolcano

Volcano Plot

Description

Creates a volcano plot of log fold change in expression vs $-\log(pval)$ for a pair of samples (x,y)

Usage

```

## S4 method for signature 'CuffData'
csVolcano(object, x, y, features=FALSE, ...)

```

Arguments

object	An object of class CuffData, CuffFeatureSet, or CuffGeneSet
x	Sample name from 'samples' table for comparison
y	Sample name from 'samples' table for comparison
features	Will include all fields from 'features' slot in returned ggplot object. Useful for further manipulations of plot object using feature-level attributes (e.g. gene_type, class_code, etc)
...	Additional arguments

Details

This creates a 'volcano' plot of fold change vs. significance for a pairwise comparison of genes or features across two different samples.

Value

A ggplot2 plot object

Note

None

Author(s)

Loyal A. Goff

References

None.

Examples

```
a<-readCufflinks(system.file("extdata", package="cummeRbund")) #Create CuffSet object
genes<-a@genes #Create cuffData object for all genes
v<-csVolcano(genes,"hESC","Fibroblasts") # Volcano plot of all genes for conditions x='hESC'
v #print plot
```

cummeRbund-package *cummeRbund: The finishing touch on your Tuxedo workflow. Analysis, manipulation, and visualization of Cufflinks HTS data. ~ package title ~*

Description

Allows for persistent storage, access, and manipulation of Cufflinks high-throughput sequencing data. In addition, provides numerous plotting functions for commonly used visualizations. ~ A concise (1-5 lines) description of the package ~

Details

Package: cummeRbund
 Version: 0.1.3
 Suggests:
 Depends: R (>= 2.7.0), RSQLite, reshape, ggplot2, methods
 License: MIT License
 Collate: AllGenerics.R AllClasses.R database-setup.R methods-CuffSet.R methods-CuffData.R methods-CuffDist.R
 LazyLoad: yes
 biocViews: HighThroughputSequencing, HighThroughputSequencingData, RNAseq, RNAseqData, GeneExpression, D
 Packaged: 2011-08-05 18:03:50 UTC; lgoff
 Built: R 2.12.1; ; 2011-08-05 18:03:57 UTC; unix

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```

Further information is available in the following vignettes:

`cummeRbund-manual` An R package for visualization and analysis of Cufflinks high-throughput sequencing data (so

~~ An overview of how to use the package, including the most important ~~ functions ~~

Author(s)

L. Goff, C. Trapnell

Maintainer: Loyal A. Goff <lgoff@csail.mit.edu>

References

~~ Literature or other references for background information ~~

diffData *Differential comparison data*

Description

An accessor method to retrieve differential expression data from a 'CuffData', 'CuffFeatureSet', or 'CuffFeature' object

Usage

```
## S4 method for signature 'CuffData'  
diffData(object, x, y, features=FALSE, lnFcCutoff=20)
```

Arguments

object	An object of class ('CuffData' or 'CuffFeatureSet')
x	Optional, if x and y are both missing, data for all pairwise differential comparisons are returned, otherwise if x and y are sample names from the 'samples' table, then only differential data pertaining to those two samples are returned.
y	See 'x'
features	A logical value that returns all feature-level data as part of data.frame when true. object must be of class 'CuffData'.
lnFcCutoff	For plotting purposes, extreme values of ln_fold_change are removed from view. This is the cutoff for where these should be trimmed.
...	Additional arguments.

Details

None

Value

A data.frame object

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
data(sampleData)  
diff<-diffData(sampleGeneSet) #returns a dataframe of differential expression data from s
```

`distValues`*distValues*

Description

Returns a data.frame of distribution-level test values from a CuffDist object (@promoters, @splicing, @relCDS)

Usage

```
## S4 method for signature 'CuffDist'  
distValues(object)
```

Arguments

<code>object</code>	An object of class 'CuffDist'
<code>...</code>	Additional arguments to distValues

Details

None

Value

Returns a data.frame of distribution-level test values.

Note

None

Author(s)

Loyal A. Goff

References

None

See Also

None

Examples

```
a<-readCufflinks(system.file("extdata", package="cummeRbund")) # Read cufflinks data and  
distValues(a@promoters) # returns data.frame of values from CuffDist object in slot 'prom'
```

expressionBarplot *Barplot*

Description

A barplot of FPKM values with confidence intervals for a given gene, set of genes, or features of a gene (e.g. isoforms, TSS, CDS, etc).

Usage

```
## S4 method for signature 'CuffFeatureSet'  
expressionBarplot(object, logMode=TRUE, pseudocount=1.0, showErrorbars=TRUE, ...)
```

Arguments

object	An object of class ('CuffFeatureSet','CuffGeneSet','CuffFeature','CuffGene')
logMode	A logical value whether or not to draw y-axis on log10 scale. Default = FALSE.
pseudocount	Numerical value added to each FPKM during log-transformation to avoid errors.
showErrorbars	A logical value whether or not to draw error bars. Default = TRUE
...	Additional arguments.

Details

None

Value

A ggplot2 plot object

Note

Need to implement logMode and features for this plotting method.

Author(s)

Loyal A. Goff

References

None

Examples

```
data(sampleData)  
PINK1 # sample CuffFeature object  
expressionBarplot(PINK1) #Barplot of PINK1 FPKM values  
expressionBarplot(PINK1@isoforms) #Barplot of PINK1 FPKM values faceted by isoforms
```

expressionPlot *Expression Plot*

Description

A line plot (optionally with confidence intervals) detailing FPKM expression levels across conditions for a given gene(s) or feature(s)

Usage

```
## S4 method for signature 'CuffFeature'
expressionPlot(object, logMode=FALSE, pseudocount=1.0, drawSummary=FALSE, sumFun
```

Arguments

object	An object of class ('CuffFeature' or 'CuffGene')
logMode	A logical value to draw y-axis (FPKM) on log-10 scale. Default = FALSE.
pseudocount	A numeric value added to FPKM to avoid errors on log-10 transformation.
drawSummary	A logical value. Draws a 'summary' line with mean FPKM values for each condition.
sumFun	Function used to determine values for summary line. Default = mean_cl_boot
showErrorbars	A logical value whether or not to draw error bars.
...	Additional arguments

Details

None

Value

A ggplot2 plot object

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
data(sampleData)
PINK1 # sample CuffFeature object
expressionPlot(PINK1) #Line plot of PINK1 FPKM values
expressionPlot(PINK1@isoforms) #Line plot of PINK1 FPKM values faceted by isoforms
```

featureNames	<i>Feature names</i>
--------------	----------------------

Description

Retrieve a vector of feature names from a 'CuffData' or 'CuffFeatureSet' object

Usage

```
## S4 method for signature 'CuffData'  
featureNames(object)
```

Arguments

object An object of class ('CuffData' or 'CuffFeatureSet')

Details

None

Value

A list of feature names

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
data(sampleData)  
featureNames(sampleGeneSet)
```

`features`*Features*

Description

Returns a data frame of features from a `CuffData`, `CuffFeatureSet`, or `CuffFeature` object

Usage

```
## S4 method for signature 'CuffData'  
features(object)
```

Arguments

`object` An object of class ('`CuffData`', '`CuffFeatureSet`', or '`CuffFeature`')

Details

If features have been added to `cuffData` via `addFeatures()` then these will be presented as well.

Value

A `data.frame` of feature-level information

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
data(sampleData)  
features(sampleGeneSet)
```

findSimilar *findSimilar*

Description

Returns a CuffGeneSet containing n genes with the most similar expression profiles to gene/profile x.

Usage

```
## S4 method for signature 'CuffSet'  
findSimilar(object, x, n)
```

Arguments

object	A object of class 'CuffSet'
x	A 'gene_id' or 'gene_short_name' from which to look up an expression profile OR a vector of expression values to compare all genes (vector must have same length and order of 'samples')
n	Number of similar genes to return

Details

By default, returns a CuffGeneSet object with n similar genes. This may change in the future.

Value

A CuffGeneSet object of n most similar genes to x.

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
a<-readCufflinks(system.file("extdata", package="cummeRbund"))  
mySimilarGenes<-findSimilar(a, "PINK1", 10)
```

fpkm-methods

Retrieve FPKM values

Description

Returns a data.frame from @FPKM slot

Details

Returns a data.frame of FPKM values.

Value

A data.frame of FPKM-level values for a set of features.

Methods

```
signature(object = "CuffData")  
signature(object = "CuffFeature")  
signature(object = "CuffFeatureSet")
```

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
data(sampleData)  
fpkm(PINK1)
```

fpkmMatrix*fpkmMatrix*

Description

Retrieve FPKM values as gene by condition matrix

Usage

```
## S4 method for signature 'CuffData'  
fpkmMatrix(object)
```

Arguments

object An object of class ('CuffData', 'CuffFeatureSet', 'CuffGeneSet', 'CuffGene', or 'Cuff-Feature')

Details

None.

Value

A feature x condition matrix of FPKM values.

Note

None

Author(s)

Loyal A. Goff

References

None.

Examples

```
data(sampleData)
fpkmMatrix(sampleGeneSet)
```

getGene

getGene

Description

Primary accessor from a CuffSet object to retrieve all related information for 1 (one) given gene, indexed by gene_id or gene_short_name.

Usage

```
## S4 method for signature 'CuffSet'
getGene(object, geneId, sampleIdList=NULL)
```

Arguments

object An object of class 'CuffSet' (Primary 'pointer' object for Cufflinks data).

geneId A character string to identify which gene for which you would like to retrieve all information.

sampleIdList A vector of sample names used to subset or re-order samples in returned object

Details

None.

Value

Returns a CuffGene object containing all related information for a given gene_id or gene_short_name

Note

Right now, this does not return an error if it cannot find a gene. (this is probably a bad thing...)

Author(s)

Loyal A. Goff

References

None.

Examples

```
a<-readCufflinks(system.file("extdata", package="cummeRbund")) #Read cufflinks data and c
myGene<-getGene(a,"PINK1") # Retrieve all information for gene "PINK1"
```

getGenes

getGenes

Description

Primary accessor from a CuffSet object to retrieve all related information for >1 (MANY) given genes, indexed by gene_id or gene_short_name.

Usage

```
## S4 method for signature 'CuffSet'
getGenes(object, geneIdList, sampleIdList=NULL)
```

Arguments

`object` An object of class 'CuffSet' (Primary 'pointer' object for Cufflinks data).

`geneIdList` A vector of gene_ids or gene_short_namesto identify which genes for which you would like to retrieve all information.

`sampleIdList` A vector of sample names used to subset or re-order samples in returned object

Details

None.

Value

Returns a CuffGeneSet object containing all related information for a given set of gene_id or gene_short_name values

Note

Right now, this does not return an error if it cannot find a gene. (this is probably a bad thing...)

Author(s)

Loyal A. Goff

References

None.

Examples

```
a<-readCufflinks(system.file("extdata", package="cummeRbund")) #Read cufflinks data and c
data(sampleData)
sampleIDs
myGene<-getGenes(a,sampleIDs) # Retrieve all information for a set of 20 'sample' genes.
```

getLevels

getLevels

Description

Returns a list of samples as levels. This should not be called directly by user.

Usage

```
## S4 method for signature 'CuffData'
getLevels(object)
```

Arguments

object An object of class 'CuffData' or 'CuffFeatureSet' or 'CuffFeature'

Details

For internal usage only.

Value

A vector of sample names as factors.

Note

None.

Author(s)

Loyal A. Goff

References

None.

`makeprobs`*Transform a matrix into probabilities by columns*

Description

This function takes a matrix of expression values (must be greater than 0) and returns a matrix of probabilities by column. This is a required transformation for the Jensen-Shannon distance which is a metric that operates on probabilities.

Usage

```
makeprobs(a)
```

Arguments

`a` A matrix of expression values (values must be greater than 0).

Details

To make a matrix of probabilities by row, use `t()` to transpose prior to calling `makeprobs`.

Value

A matrix of expression probabilities by column.

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
myMat<-matrix(sample(1:50, 50), 10)
probs<-makeprobs(myMat)
```

makeprobsvec	<i>makeprobsvec</i>
--------------	---------------------

Description

Sums a vector of numerics and divides by the sum

Usage

```
makeprobsvec(p)
```

Arguments

`p` A vector of numerics

Details

None

Value

A vector of probabilities

Note

Should not be called directly by user.

Author(s)

Loyal A. Goff

References

None

Examples

```
p<-sample(1:5000,20)
makeprobsvec(p)
```

readCufflinks	<i>readCufflinks</i>
---------------	----------------------

Description

This initializes the backend SQLite table and provides a DB connection for all downstream data analysis.

Usage

```
readCufflinks(dir = getwd(), dbFile = "cuffData.db", geneFPKM = "genes.fpkm_tracking", isoformFPKM = "isoforms.fpkm_tracking", tssFPKM = "tss_groups.fpkm_tracking", cdsFPKM = "cds.fpkm_tracking", promoterFile = "promoters.diff", splicingFile = "splicing.diff", driver = "SQLite", rebuild = FALSE, ...)
```

Arguments

<code>dir</code>	Directory in which all CuffDiff output files can be located. Defaults to current working directory.
<code>dbFile</code>	Name of backend database. Default is 'cuffData.db'
<code>geneFPKM</code>	genes.fpkm_tracking file
<code>geneDiff</code>	gene_exp.diff file
<code>isoformFPKM</code>	isoforms.fpkm_tracking file
<code>isoformDiff</code>	isoform_exp.diff file
<code>TSSFPKM</code>	tss_groups.fpkm_tracking file
<code>TSSDiff</code>	tss_group_exp.diff file
<code>CDSFPKM</code>	cds.fpkm_tracking file
<code>CDSExpDiff</code>	cds_exp.diff file
<code>CDSDiff</code>	cds.diff file (distribution tests on CDS)
<code>promoterFile</code>	promoters.diff file (distribution tests on promoters)
<code>splicingFile</code>	splicing.diff (distribution tests on isoforms)
<code>driver</code>	Driver for backend database. (Currently only "SQLite" is supported).
<code>rebuild</code>	A logical argument to rebuild database backend.
<code>...</code>	Additional arguments to readCufflinks

Details

This is the initialization function for the cummeRbund package. It creates the SQLite backend database, populates the data, and provides a connection object for all future interactions with the dataset. Once the initial build is complete, this function will default to using the database for all future sessions. **IMPORTANT:** - Each R session should begin with a call to readCufflinks to re-open the connection to the database. - Should any connectivity issues to the database arise, another call to readCufflinks should create a new connection object and repair any issue. - The database can always be rebuild (using rebuild=TRUE) from the original CuffDiff output files.

Value

A CuffSet object. A 'pointer' class that allows interaction with cufflinks/cuffdiff data via a SQLite database backend.

Note

None.

Author(s)

Loyal A. Goff

References

None.

Examples

```
a<-readCufflinks(system.file("extdata", package="cummeRbund")) #Read cufflinks data in sa
```

sampleGeneSet	<i>sampleGeneSet</i>
---------------	----------------------

Description

A sample CuffGeneSet data set for 20 genes.

Usage

```
data(sampleData)
```

Format

sampleGeneSet is a CuffGeneSet (extends CuffFeatureSet) object containing all sample gene-, isoform-, TSS-, and CDS-level data for 20 different genes. These data were derived from a toy set of hESC-vs-iPSC-vs-Fibroblast RNA-Seq expression data.

Details

None

Source

None

References

None

Examples

```
data(sampleData)
```

 sampleIDs

sampleIDs

Description

A vector of gene_ids used to create 'sampleGeneSet' example

Usage

```
data(sampleData)
```

Format

The format is: chr "sampleIDs"

Details

None

Source

None

References

None

Examples

```
data(sampleData)
```

 samples

Get sample list from CuffData object

Description

Returns a list of sample names from a CuffData or CuffFeatureSet object

Usage

```
## S4 method for signature 'CuffData'
samples(object)
```

Arguments

object An object of class ('CuffData','CuffFeatureSet','CuffFeature')

Details

None

Value

A list of sample names

Note

None

Author(s)

Loyal A. Goff

References

None

See Also

None

Examples

```
a<-readCufflinks(system.file("extdata", package="cummeRbund")) #Create CuffSet object
samples(a@genes)
```

shannon.entropy *Shannon entropy*

Description

Calculates the Shannon entropy for a probability distribution

Usage

```
shannon.entropy(p)
```

Arguments

p A vector of probabilities (must sum to ~1)

Details

None

Value

Returns a numeric value for the Shannon entropy of the supplied probability distribution

Note

None

Author(s)

Loyal A. Goff

References

None

Examples

```
x<-sample(1:500,50)
p<-x/sum(x)
shannon.entropy(p)
```

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