

Package ‘BioMVCClass’

April 10, 2023

Title Model-View-Controller (MVC) Classes That Use Biobase

Version 1.66.0

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Description Creates classes used in model-view-controller (MVC) design

Depends R (>= 2.1.0), methods, MVCClass, Biobase, graph, Rgraphviz

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biocViews Visualization, Infrastructure, GraphAndNetwork

git_url <https://git.bioconductor.org/packages/BioMVCClass>

git_branch RELEASE_3_16

git_last_commit 964bec3

git_last_commit_date 2022-11-01

Date/Publication 2023-04-10

R topics documented:

exprModel-class	2
graphModel-class	3
graphView-class	4
GSE-class	5
gseModel-class	6
heatmapView-class	7
Index	8

exprModel-class

Class "exprModel": A class to represent an ExpressionSet model

Description

exprModel is a class to represent an ExpressionSet model. This class inherits from the virtual class, gModel. An object of exprModel is responsible for storing and updating the data.

Objects from the Class

Objects can be created by calls of the form `new("exprModel", ...)`. The initialize method for this class will be created in other packages that use this package (for example, the initialize method will be created in the iSNetwork package).

Slots

modelData: the model data, which is an ExpressionSet

linkData: a list of functions that link this model to its parent and child models (if it has any)

virtualData: the data that is needed by the views of this object

modelName: the name of this model

modelVar: a list of variables that refer to the modelData (for instance this may be t-test values that were calculated from the modelData)

Extends

Class "gModel", directly.

Methods

No methods defined with class "exprModel" in the signature. The methods for this class will be created in other packages that use this package like iSNetwork.

Author(s)

Elizabeth Whalen

See Also

[graphModel-class](#)

`graphModel-class`*Class "graphModel": A class to represent a graph model*

Description

graphModel is a class to represent a graph model. This class inherits from the virtual class, gModel. An object of graphModel is responsible for storing and updating the data.

Objects from the Class

Objects can be created by calls of the form `new("graphModel", ...)`. The initialize method for this class will be created in other packages that use this package (for example, the initialize method will be created in the iSNetwork package).

Slots

`modelData`: the model data, which is a graph object

`linkData`: a list of functions that link this model to its parent and child models (if it has any)

`virtualData`: data that is needed by views of this model

`modelName`: the name of this model

`modelVar`: a list of variables that refer to the modelData (for instance this may be t-test values that were calculated from the modelData)

Extends

Class "gModel", directly.

Methods

No methods defined with class "graphModel" in the signature. The methods for this class will be created in other packages that use this package like iSNetwork.

Author(s)

Elizabeth Whalen

See Also

[exprModel-class](#)

graphView-class *Class "graphView": A class to represent a graph view*

Description

graphView is a class to represent a view that is a graph. graphView inherits from the class, plotView, which inherits from the virtual class, genView.

Objects from the Class

Objects can be created by calls of the form `new("graphView", ...)`. The initialize method for this class will be created in other packages that use this package (for example, the initialize method will be created in the iSNetwork package).

Slots

`plotDevice`: the plot device number

`plotPar`: the parameter list for the plot, see `par()`

`drArea`: an object of class "GtkDrawingArea"

`dataName`: a character string describing what data are shown in the view

`win`: an object of class "GtkWindow" that holds the view

`winNum`: a number that tells what number view this is (for example, the first view created will have `winNum=1`)

`grLayout`: the Ragraph object, which represents the layout for the graph plot

Extends

Class "plotView", directly. Class "genView", by class "plotView".

Methods

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

Author(s)

Elizabeth Whalen

GSE-class

Class "GSE": A class to represent gene set enrichment data

Description

GSE is a class to represent gene set enrichment data and will be used in the modelData slot in the gseModel object. This class will store all of the information that pertains to performing gene set enrichment.

Objects from the Class

Objects can be created by calls of the form `new("GSE", ...)`.

Slots

incidMat: the incidence matrix that shows the relationship between the genes and the gene sets
gTestStat: the test statistic for the genes relationship with the phenotype
gsTestStat: the test statistic for the gene set
expData: the experimental data (here it will be of class ExpressionSet)
descr: a description of the gene set being studied

Methods

incidMat<- Sets the incidMat slot
incidMat Returns the incidMat slot
gTestStat<- Sets the gTestStat slot
gTestStat Returns the gTestStat slot
gsTestStat<- Sets the gsTestStat slot
gsTestStat Returns the gsTestStat slot
expData<- Sets the expData slot
expData Returns the expData slot
descr<- Sets the descr slot
descr Returns the descr slot

Author(s)

Elizabeth Whalen

See Also

[gseModel-class](#)

`gseModel-class`*Class "gseModel": A class to represent a GSE model*

Description

`gseModel` is a class to represent a gene set enrichment (GSE) model. This class inherits from the virtual class, `gModel`.

Objects from the Class

Objects can be created by calls of the form `new("gseModel", ...)`. The initialize method for this class will be created in other packages that use this package (for example, the initialize method will be created in the `iSNetwork` package).

Slots

`modelData`: the model data, which is an object of GSE

`linkData`: a list of functions that link this model to its parent and child models (if it has any)

`virtualData`: the data that is needed by the views of this object

`modelName`: the name of this model

`modelVar`: a list of variables that refer to the `modelData` (for instance this may be t-test values that were calculated from the `modelData`)

Extends

Class `"gModel"`, directly.

Methods

No methods defined with class `"gseModel"` in the signature. The methods for this class will be created in other packages that use this package like `iSNetwork`.

Author(s)

Elizabeth Whalen

See Also

[GSE-class](#), [graphModel-class](#), [exprModel-class](#)

heatmapView-class *Class "heatmapView": A class to represent a heatmap view*

Description

heatmapView is a class to represent a view that is a heatmap. heatmapView inherits from the class, plotView, which inherits from the virtual class, genView.

Objects from the Class

Objects can be created by calls of the form `new("heatmapView", ...)`. The initialize method for this class will be created in other packages that use this package (for example, the initialize method will be created in the iSNetwork package).

Slots

ordering: a list of information returned from the heatmap function

plotDevice: the plot device number

plotPar: the parameter list for the plot, see `par()`

drArea: an object of class "GtkDrawingArea"

dataName: a character string describing what data are shown in the view

win: an object of class "GtkWindow" that holds the view

winNum: a number that tells what number view this is (for example, the first view created will have `winNum=1`)

rNames: the names of the rows to be included in the heatmap (this allows the original data to be subset in the view)

Extends

Class "plotView", directly. Class "genView", by class "plotView".

Methods

ordering<- Sets the ordering slot

ordering Returns the ordering slot

rNames<- Sets the rNames slot

rNames Returns the rNames slot

Author(s)

Elizabeth Whalen

Index

* classes

- exprModel-class, 2
 - graphModel-class, 3
 - graphView-class, 4
 - GSE-class, 5
 - gseModel-class, 6
 - heatmapView-class, 7
- descr (GSE-class), 5
descr, GSE-method (GSE-class), 5
descr<- (GSE-class), 5
descr<-, GSE-method (GSE-class), 5
- expData (GSE-class), 5
expData, GSE-method (GSE-class), 5
expData<- (GSE-class), 5
expData<-, GSE-method (GSE-class), 5
exprModel (exprModel-class), 2
exprModel-class, 2
- graphModel (graphModel-class), 3
graphModel-class, 3
graphView (graphView-class), 4
graphView-class, 4
grLayout (graphView-class), 4
grLayout, graphView-method
 (graphView-class), 4
grLayout<- (graphView-class), 4
grLayout<-, graphView-method
 (graphView-class), 4
- GSE (GSE-class), 5
GSE-class, 5
gseModel (gseModel-class), 6
gseModel-class, 6
gsTestStat (GSE-class), 5
gsTestStat, GSE-method (GSE-class), 5
gsTestStat<- (GSE-class), 5
gsTestStat<-, GSE-method (GSE-class), 5
gTestStat (GSE-class), 5
gTestStat, GSE-method (GSE-class), 5
- gTestStat<- (GSE-class), 5
gTestStat<-, GSE-method (GSE-class), 5
- heatmapView (heatmapView-class), 7
heatmapView-class, 7
- incidMat (GSE-class), 5
incidMat, GSE-method (GSE-class), 5
incidMat<- (GSE-class), 5
incidMat<-, GSE-method (GSE-class), 5
- ordering (heatmapView-class), 7
ordering, heatmapView-method
 (heatmapView-class), 7
ordering<- (heatmapView-class), 7
ordering<-, heatmapView-method
 (heatmapView-class), 7
- rNames (heatmapView-class), 7
rNames, heatmapView-method
 (heatmapView-class), 7
rNames<- (heatmapView-class), 7
rNames<-, heatmapView-method
 (heatmapView-class), 7