Package ‘affylmGUI’

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Title GUI for limma Package with Affymetrix Microarrays

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Imports grDevices, graphics, stats, utils, tcltk, tkrplot, limma, affy, affyio, affyPLM, gcrma, BiocGenerics, AnnotationDbi, BiocManager, R2HTML, xtable

Description A Graphical User Interface (GUI) for analysis of Affymetrix microarray gene expression data using the affy and limma packages.

License GPL (>=2)

URL `http://bioinf.wehi.edu.au/affylmGUI/`

biocViews GUI, GeneExpression, Transcription, DifferentialExpression, DataImport, Bayesian, Regression, TimeCourse, Microarray, mRNAMicroarray, OneChannel, ProprietaryPlatforms, BatchEffect, MultipleComparison, Normalization, Preprocessing, QualityControl

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Contents

`affylmGUI-package` *The affylmGUI Package: Graphical User Interface for limma analysis of Affymetrix microarrays*

Description

The affylmGUI package provides a Graphical User Interface (GUI) for analysis of Affymetrix microarray data using the limma package (Linear Modes for MicroArray data).

Details

The GUI is launched by typing `affylmGUI()` at the R prompt. For detailed help, including example sesssions, see the affylmGUI home page at `http://bioinf.wehi.edu.au/affylmGUI`.

The limma package offers R users a command-line interface to state-of-the-art techniques for linear modelling of microarray data and for identifying differentially expressed genes (Ritchie et al, 2015). The affylmGUI package, while not as powerful as limma to the expert user, offers a simple point-and-click interface to many of the commonly-used limma and affy functions.

To use the affylmGUI package, you need to have R 1.8.1 or later, Tcl/Tk 8.3 or later (ActiveTcl for Windows/Linux or Fink Tcl/Tk for MacOSX (X11)) and the limma, affylmGUI and tkrplot R packages. At least one of the affy, gcrma or affyPLM Bioconductor packages are also required for normalization and probe-set summarization. The R2HTML (CRAN) and xtable (CRAN) packages are recommended. affylmGUI has been tested succesfully on Windows, Red Hat Linux, and on Mac OSX with X11.

Please cite Wettenhall et al (2006) if you use results from affylmGUI in a publication. Also consider citing Irizarry et al (2003) if RMA normalization is used for Wu et al (2004) if gcrma normalization is used.

Author(s)

Created by James Wettenhall between 2003 and September 2006. Maintained by Keith Satterley between September 2006 and July 2015. Currently maintained by Gordon Smyth.

References

Wettenhall, JM, Simpson, KM, Satterley, K, Smyth, GK (2006). affylmGUI: a graphical user interface for linear modeling of single channel microarray data. *Bioinformatics* 22, 897-899.

Ritchie, ME, Phipson, B, Wu, D, Hu, Y, Law, CW, Shi, W, and Smyth, GK (2015). limma powers differential expression analyses for RNA-sequencing and microarray studies. *Nucleic Acids Research* 43, e47. `http://nar.oxfordjournals.org/content/43/7/e47`

Irizarry, RA, Hobbs, B, Collin, F, Beazer-Barclay, YD, Antonellis, KJ, Scherf, U, Speed, TP (2003). Exploration, normalization, and summaries of high density oligonucleotide array probe level data. Biostatistics 4(2), 249-264.

Wu, Z, Irizarry, RA, Gentleman, R, Martinez-Murillo, F, Spencer, F. (2004). A model based background adjustment for oligonucleotide expression arrays. Journal of the American Statistical Association 99(468), 909-917.

See Also

The GUI is launched by `affylmGUI()`.

More documentation is available from `http://bioinf.wehi.edu.au/affylmGUI`.

`showChangeLog()` shows the most recent lines from the affylmGUI package changeLog.

See `limma-package` for help about the limma package.

Examples

```
library(limma)
changeLog(package="affylmGUI")
```

`affylmGUI` *Graphical User Interface for the limma microarray package*

Description

Graphical User Interface for limma package analysis of Affymetrix microarrays.

Usage

```
affylmGUI(BigfontsForaffylmGUIpresentation=FALSE)
```

Arguments

`BigfontsForaffylmGUIpresentation`	logical, if `TRUE` then larger fonts are used. However, some font sizes are not controlled by affylmGUI and so must be adjusted in the operating system, e.g., in the Control Panel in Windows under Display, Appearance.

Details

The `affylmGUI` function launches a Graphical User Interface for the affy, gcrma, affyPLM and limma packages. The GUI uses Tk widgets (via the R TclTk interface by Peter Dalgaard) in order to provide a simple interface to limma functions for linear modelling of Affymetrix microarrays and identification of differentially expressed genes.

Almost all users will type `affylmGUI()`. The use of `affylmGUI(Bigfonts=TRUE)` is only intended for the preparation of a talk about the affylmGUI package.

Author(s)

Created by James Wettenhall between 2003 and September 2006. Maintained by Keith Satterley between September 2006 and July 2015. Currently maintained by Gordon Smyth.

See Also

`affylmGUI-package`, `internal`

`internal` *Internal Functions*

Description

Internal functions defined by the affylmGUI package.

Usage

```
AboutaffylmGUI()
affyHelp()
affylmGUIhelp()
affyPlotMA()
affyPlotMAcontrast()
ChooseCDF()
ChooseContrastParameterization()
chooseDir()
ChooseEbayesStatistic()
ComputeContrasts()
ComputeLinearModelFit()
CopyGraph(img)
DeleteContrastParameterization()
DensityPlot()
DensityPlotAll()
evalRcode()
ExportHTMLreport()
ExportNormalizedExpressionValues()
ExportTopTable()
fixSeps(string)
generalPlotFunction(code="",WindowTitle="")
GetComponentsToExportInHTMLreport(contrastParameterizationIndex=NULL)
GetContrast(contrastParameterizationIndex)
GetContrastNamesForHeatDiagram(numContrasts=2,ContrastNames=c("Contrast 1","Contrast 2"))
GetContrastParameterizationName()
GetContrasts(NumContrasts=0)
GetDEcutoff()
GetGeneLabelsOptions()
GetJpegOrPngParams(graphFileType)
GetJpegOrPngX11Params(graphFileType)
GetlimmaDataSetName()
GetLogPLMDataChoice()
GetMultipleContrasts(contrastParameterizationIndex)
GetNormalizationMethod()
getPackageVersion(pkgName)
GetParameterizationName()
GetPlotLabels(plottitle="",xlabel="",ylabel="")
GetPlotSize()
GetPlotTitle(plottitle="")
GetPValueCutoff(p.value=0.01)
GetResidualTypeChoice()
GetRNATypesFrom.ContrastsFromDropDowns.String(string)
```

```
GetSetNames(numSets=2,set1="",set2="",set3="")
GetSlideNum(all=FALSE)
GetSlideNums()
GetWhichProbes(includeBoth=FALSE)
GetWtAreaParams()
GetWtFlagParams()
HeatDiagramDialog(parameterName)
HeatDiagramPlot()
HTMLplotUsingFunction(Caption = "", File = "plot.html", GraphRelativeDirectory = ".", GraphAbsolute
ImageArrayPlot()
ImageQualityResidualPlot()
ImageQualityWeightPlot()
initGlobals()
IntensityHistogram()
IntensityHistogramAll()
limmaHelp()
LogOddsPlot()
NewLimmaFile()
NormalizedIntensityBoxPlot()
NormalizeNow()
nstrstr(haystack,needle)
NUSEPlotAll()
onDestroy()
onExit()
OpenALimmaFile(FileName)
OpenCDFandTargetsfiles()
OpenCDFFile()
OpenLimmaFile()
OpenTargetsFile()
PlotOptions()
QQTplot()
RawIntensityBoxPlot()
Require(pkg)
Resize(img,plotFunction)
RLEPlotAll()
RNADegradationPlotAll()
SaveAsLimmaFile()
SaveGraphAsJpeg(initialfile, plotFunction)
SaveGraphAsPDF(initialfile, plotFunction)
SaveGraphAsPNG(initialfile, plotFunction)
SaveGraphAsPostscript(initialfile, plotFunction)
SaveLimmaFile()
SetupPlotKeyBindings(tt,img)
SetupPlotMenus(tt,initialfile,plotFunction,img)
SetWD()
showChangeLog()
showCitations()
showTopTable(...,export=FALSE)
SimplifyContrastsExpression(string)
strstr(haystack, needle)
tclArrayVar()
TclRequire(tclPkg)
```

```
Try(expr)
TryReadImgProcFile(expr)
UpDownOrBoth()
vennDiagramaffylmGUI(object, include = "both", names, cex = 1.5, mar = rep(1, 4), ...)
VennDiagramPlot()
ViewContrastsMatrixAsPairs(contrastsMatrix, contrastsMatrixList,contrastParameterizationIndex = N
ViewContrastsMatrixInTable(contrastsMatrixList, contrastParameterizationIndex = NULL)
ViewExistingContrastParameterization()
ViewRNATargets()
```

Arguments

`...`	HTMLplotUsingFunction:arg14:and:showTopTable:arg1:and:vennDiagramaffylmGUI:arg6
`Align`	HTMLplotUsingFunction:arg8
`all`	GetSlideNum:arg1
`BG`	HTMLplotUsingFunction:arg12
`Caption`	HTMLplotUsingFunction:arg1
`code`	generalPlotFunction: arg1: a code
`ContrastNames`	GetContrastNamesForHeatDiagram:arg2
`contrastParameterizationIndex`	GetComponentsToExportInHTMLreport:arg1:and:contrastParameterizationIndex:arg1:and:GetContr
`export`	showTopTable:arg2
`expr`	Try:arg1:and:TryReadImgProcFile:arg1
`File`	HTMLplotUsingFunction:arg2
`FileName`	OpenALimmaFile:arg1
`GraphAbsoluteDirectory`	HTMLplotUsingFunction:arg4
`GraphBorder`	HTMLplotUsingFunction:arg7
`GraphFileName`	HTMLplotUsingFunction:arg5
`graphFileType`	GetJpegOrPngParams:arg1:and:GetJpegOrPngX11Params:arg1
`GraphRelativeDirectory`	HTMLplotUsingFunction:arg3
`GraphSaveAs`	HTMLplotUsingFunction:arg6
`haystack`	nstrstr:arg1:and:strstr:arg1
`Height`	HTMLplotUsingFunction:arg11
`img`	Resize:arg1:and:SetupPlotMenus:arg4:and:CopyGraph:arg1:and:SetupPlotKeyBindings:arg2
`includeBoth`	GetWhichProbes:arg1
`initialfile`	SetupPlotMenus:arg2:and:SaveGraphAsJpeg:arg1:and:SaveGraphAsPDF:arg1:and:SaveGraphAsPN
`needle`	nstrstr:arg2:and:strstr:arg2
`NumContrasts`	GetContrasts:arg1
`numContrasts`	GetContrastNamesForHeatDiagram:arg1
`numSets`	GetSetNames:arg1
`p.value`	GetPValueCutoff:arg1:A p-value cutoff.
`parameterName`	HeatDiagramDialog:arg1

`pkgName`	getPackageVersion:arg1
`pkg`	Require:arg1
`plotFunction`	Resize:arg2:and:HTMLplotUsingFunction:arg9:and:SetupPlotMenus:arg3:and:SaveGraphAsJpeg:ar
`plottitle`	GetPlotLabels:arg1:and:GetPlotTitle:arg1
`res`	HTMLplotUsingFunction:arg13
`set1`	GetSetNames:arg2
`set2`	GetSetNames:arg3
`set3`	GetSetNames:arg4
`string`	fixSeps:arg1:A character string:and:GetRNATypesFrom.ContrastsFromDropDowns.String:arg1:and:
`tclPkg`	TclRequire:arg1
`tt`	SetupPlotMenus:arg1:and:SetupPlotKeyBindings:arg1
`Width`	HTMLplotUsingFunction:arg10
`WindowTitle`	generalPlotFunction: arg2: a title
`xlabel`	GetPlotLabels:arg2
`ylabel`	GetPlotLabels:arg3
`object`	vennDiagramaffylmGUI:arg1
`include`	vennDiagramaffylmGUI:arg2
`names`	vennDiagramaffylmGUI:arg3
`cex`	vennDiagramaffylmGUI:arg4
`mar`	vennDiagramaffylmGUI:arg5
`contrastsMatrix`	ViewContrastsMatrixAsPairs:arg1
`contrastsMatrixList`	ViewContrastsMatrixAsPairs:arg2:and:ViewContrastsMatrixInTable:arg1
`PointSize`	HTMLplotUsingFunction:arg12

Details

These functions are called by `affylmGUI()` via the GUI and are not intended to be called directly by users.

Author(s)

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See Also

`affylmGUI`

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