

# 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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|                   |   |
|-------------------|---|
| affyImGUI-package | <i>The affyImGUI Package: Graphical User Interface for limma analysis of Affymetrix microarrays</i> |
|-------------------|---|

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## Description

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

## Details

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

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 affyImGUI 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 affyImGUI 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, affyImGUI 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. affyImGUI has been tested successfully on Windows, Red Hat Linux, and on Mac OSX with X11.

Please cite Wettenhall et al (2006) if you use results from affyImGUI 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). affyImGUI: 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 `affyImGUI()`.

More documentation is available from <http://bioinf.wehi.edu.au/affyImGUI>.

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

See [limma-package](#) for help about the limma package.

**Examples**

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

---

affyImGUI

*Graphical User Interface for the limma microarray package*

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**Description**

Graphical User Interface for limma package analysis of Affymetrix microarrays.

**Usage**

```
affyImGUI(BigfontsForaffyImGUIpresentation=FALSE)
```

**Arguments**

`BigfontsForaffyImGUIpresentation`

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

**Details**

The `affyImGUI` 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 `affyImGUI()`. The use of `affyImGUI(Bigfonts=TRUE)` is only intended for the preparation of a talk about the affyImGUI 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**

[affyImGUI-package](#), [internal](#)

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internal

*Internal Functions*

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## 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 = ".", GraphAbsoluteDir
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 = NULL)
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:GetContrast: |
| 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:SaveGraphAsPNG:arg1                            |
| 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:arg2:and:SaveGraphAsPDF:arg1     |
| 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:SimpleHeatDiagramDialog:arg1 |
| 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)**

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**

[affyImGUI](#)



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