

# Package ‘limmaGUI’

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**Version** 1.86.0

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**Title** GUI for limma Package With Two Color Microarrays

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**Imports** methods, grDevices, graphics, limma, R2HTML, tcltk, tkrplot,  
xtable, utils

**Description** A Graphical User Interface for differential expression analysis of two-  
color microarray data using the limma package.

**License** GPL (>=2)

**URL** <http://bioinf.wehi.edu.au/limmaGUI/>

**biocViews** GUI, GeneExpression, DifferentialExpression, DataImport,  
Bayesian, Regression, TimeCourse, Microarray, mRNAMicroarray,  
TwoChannel, BatchEffect, MultipleComparison, Normalization,  
Preprocessing, QualityControl

**git\_url** <https://git.bioconductor.org/packages/limmaGUI>

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## Contents

|                       |   |
|-----------------------|---|
| LGchangeLog . . . . . | 2 |
| limmaGUI . . . . .    | 2 |

|              |          |
|--------------|----------|
| <b>Index</b> | <b>8</b> |
|--------------|----------|

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 LGchangeLog

*LimmaGUI Change Log*


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**Description**

Write as text the most recent changes from the limmaGUI package changelog.

**Usage**

```
LGchangeLog(n=20)
```

**Arguments**

n                    integer, number of lines to write of changelog.

**Value**

No value is produced, but a number of lines of text are written to standard output.

**Author(s)**

Gordon Smyth

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limmaGUI

*Graphical User Interface for the limma microarray package*


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**Description**

Graphical User Interface for the limma microarray package

**Usage**

```
AboutLimmaGUI()
AboutNormalization()
BChelp()
ChooseContrastsParameterization(parameterizationTreeIndex)
ChooseEbayesStatistic()
ChooseParameterization()
ChoosePlotSymbolByClicking(spotType, cex)
ChooseSpotType(parameterizationTreeIndex)
ComputeContrasts()
CopyGraph(img)
CreateNewParameterization()
DeleteContrastsParameterization()
deleteItemFromList(list1, itemName = NULL, index = NULL)
DeleteParameterization()
DupCorBoxPlot()
ebayesBoxPlots()
evalRcode()
ExportHTMLreport()
```

```
ExportTopTable()
fixSeps(string)
GetBackgroundCorrectionMethod()
GetBetweenArrayNormalizationMethod()
GetCoef(parameterizationTreeIndex, whichCoef = "onlyOne")
GetComponentstoExportInHTMLreport(parameterizationIndex = NULL)
GetContrastsParameterizationName()
GetContrastsParameterizationNames(parameterizationTreeIndex)
GetDEcutoff()
GetDesignOrContrasts(Design = FALSE, Contrasts = FALSE, NumContrasts = 0,
                      parameterizationIndex = 0)
GetGeneLabelsOptions()
GetImageAnalysisColumnHeadings()
GetImageProcessingFileType()
GetJpegOrPngParams(graphFileType)
GetJpegOrPngX11Params(graphFileType)
GetlimmaDataSetName()
GetlmFitMethod()
GetLowessType()
GetNEWxlim(xlim)
GetNormexpOffsetValue(CurrentNormexpOffsetValue)
GetNumParametersNoTargets()
getPackageVersion(pkgName)
GetParameterizationName()
GetParameterNames(parameterizationTreeIndex)
GetParametersAndOrContrasts(parameterizationTreeIndex, whatFor = "heat")
GetPlotLabels(plottitle = "", xlabel = "", ylabel = "")
GetPlotSize()
GetPlotTitle(plottitle = "")
GetPValueCutoff(p.value = 0.01)
GetReducedDuplicateSpacing(parameterizationTreeIndex)
GetRNATypesFrom.ContrastsFromDropDowns.String(string)
GetSlideNum()
GetSpotTypesForLinearModel()
GetSpotTypesIncludedNames(parameterizationTreeIndex)
GetWithinArrayNormalizationMethod()
GetWtAreaParams()
HeatDiagramDialog(parameterName)
HeatDiagramPlot()
HowManyDups()
HTMLplotUsingFunction(Caption = "", File = .HTML.file,
                      GraphRelativeDirectory = ".", GraphAbsoluteDirectory =
                      NULL, GraphFileName = "", GraphSaveAs = "png",
                      GraphBorder = 1, Align = "center", plotFunction =
                      NULL, Width = 600, Height = 600, PointSize = 12,
                      BG = "white", res = 72, ...)
ImageArrayPlot()
ImageArrayPlotDialog(slidenum)
ImportMA()
ImportMADialog()
initGlobals()
InitNewParameterization()
```

```
limmaGUI(BigfontsForlimmaGUIpresentation = FALSE)
limmaHelp()
lmFitMethodHelp()
LogOddsPlot()
MAPlot()
MAPlotAvg()
MBoxPlot()
MMPlot()
NewLimmaFile()
NormalizeNow()
nstrstr(haystack, needle)
onDestroy()
onExit()
OpenALimmaFile(FileName)
OpenGALandTargetsandSpotTypesfiles()
OpenGALFile()
OpenLimmaFile()
OpenSpotTypesFile()
OpenTargetsFile()
plotMAColorCoded()
PlotOptions()
PrintTipGroupMAPlot()
QQTplot()
read.marrayTools(MFile,AFile, path, verbose, sep, quote, header, ...)
ReadImageProcessingFiles()
Require(pkg)
Resize(img, plotFunction)
SaveAsLimmaFile()
SaveGraphAsJpeg(initialfile, plotFunction)
SaveGraphAsPDF(initialfile, plotFunction)
SaveGraphAsPNG(initialfile, plotFunction)
SaveGraphAsPostscript(initialfile, plotFunction)
SaveLimmaFile()
SelectPlotSymbols(SpotTypes)
SetLayoutParameters()
SetupPlotKeyBindings(tt, img)
SetupPlotMenus(tt, initialfile, plotFunction, img)
SetWD()
showChangeLog()
showCitations()
showGAL()
showTopTable(..., export = FALSE)
SimplifyContrastsExpression(string)
strstr(haystack, needle)
tclArrayVar()
TclRequire(tclPkg)
TryReadImgProcFile(expr)
UpdateSpotTypesStatus()
UpDownOrBoth()
VennDiagramPlot()
ViewDesignOrContrastsMatrixAsPairs(DesignOrContrasts, designOrContrastsList,
parameterizationIndex, contrastsParameterizationIndex)
```

```

        = NULL)
ViewDesignOrContrastsMatrixInTable(DesignOrContrasts, designOrContrastsList,
        parameterizationIndex, contrastsParameterizationIndex
        = NULL)
ViewExistingContrastsParameterization()
ViewExistingParameterization()
ViewRNATargets()
ViewSpotTypes()

```

## Arguments

BigfontsForlimmaGUIpresentation  
 If set to TRUE, larger fonts are used. However, some font sizes are not controlled by limmaGUI and so must be adjusted in the operating system, e.g. in the Control Panel in Windows under Display, Appearance.

... HTMLplotUsingFunction:arg15, showTopTable:arg1

AFile Flat-file of log-intensities output by marrayTools

Align HTMLplotUsingFunction:arg8

BG HTMLplotUsingFunction:arg13

Caption HTMLplotUsingFunction:arg1

cex ChoosePlotSymbolByClicking:arg2

contrastsParameterizationIndex  
 ViewDesignOrContrastsMatrixInTable:arg4, ViewDesignOrContrastsMatrixAsPairs:arg4

Contrasts GetDesignOrContrasts:arg2

CurrentNormexpOffsetValue  
 GetNormexpOffsetValue:arg1

designOrContrastsList  
 ViewDesignOrContrastsMatrixInTable:arg2, ViewDesignOrContrastsMatrixAsPairs:arg2

DesignOrContrasts  
 ViewDesignOrContrastsMatrixInTable:arg1, ViewDesignOrContrastsMatrixAsPairs:arg1

Design GetDesignOrContrasts:arg1

export showTopTable:arg2

expr TryReadImgProcFile:arg1

FileName A file name.

File HTMLplotUsingFunction:arg2

GraphAbsoluteDirectory  
 HTMLplotUsingFunction:arg4

GraphBorder HTMLplotUsingFunction:arg7

GraphFileName HTMLplotUsingFunction:arg5

graphFileType GetJpegOrPngParams:arg1, GetJpegOrPngX11Params:arg1

GraphRelativeDirectory  
 HTMLplotUsingFunction:arg3

GraphSaveAs HTMLplotUsingFunction:arg6

|                           |  |
|---------------------------|--|
| haystack                  | nstrstr:arg1, strstr:arg1  |
| header                    | See help for read.table  |
| Height                    | HTMLplotUsingFunction:arg11  |
| img                       | SetupPlotMenus:arg1, Resize:arg1, CopyGraph:arg1, SetupPlotKeyBindings:arg2  |
| index                     | deleteItemFromList:arg1  |
| initialfile               | SaveGraphAsJpeg:arg1, SaveGraphAsPDF:arg1, SaveGraphAsPNG:arg1, SaveGraphAsPostscript:arg1, SetupPlotMenus:arg2  |
| itemName                  | deleteItemFromList:arg1  |
| list1                     | deleteItemFromList:arg1  |
| MFile                     | Flat-file of log-ratios output by marrayTools  |
| needle                    | nstrstr:arg2, strstr:arg2  |
| NumContrasts              | GetDesignOrContrasts:arg3  |
| p.value                   | A p-value cutoff.  |
| parameterizationIndex     | GetDesignOrContrasts:arg4, GetComponentsToExportInHTMLreport:arg1, GetDesignOrContrasts:arg4, ViewDesignOrContrastsMatrixInTable:arg3, ViewDesignOrContrastsMatrixAsPairs:arg3   |
| parameterizationTreeIndex | GetParametersAndOrContrasts:arg1, ChooseContrastsParameterization:arg1, ChooseSpotType:arg1, GetCoef:arg1, GetParameterNames:arg1, GetReducedDuplicateSpacing:arg1, GetContrastsParameterizationNames:arg1, GetSpotTypesIncludedNames:arg1 |
| parameterName             | HeatDiagramDialog:arg1   |
| path                      | Path to the directory containing the MFile and AFile   |
| pkgName                   | getPackageVersion:arg1   |
| pkg                       | Require:arg1   |
| plotFunction              | SetupPlotMenus:arg1, HTMLplotUsingFunction:arg9, Resize:arg1, SaveGraphAsJpeg:arg2, SaveGraphAsPDF:arg2, SaveGraphAsPNG:arg2, SaveGraphAsPostscript:arg2   |
| plottitle                 | GetPlotLabels:arg1, GetPlotTitle:arg1  |
| PointSize                 | HTMLplotUsingFunction:arg12  |
| quote                     | See help for read.table  |
| res                       | HTMLplotUsingFunction:arg14  |
| sep                       | Column separator. ("t" for tab-delimited text)   |
| slidenum                  | ImageArrayPlotDialog:arg1  |
| spotType                  | ChoosePlotSymbolByClicking:arg1  |
| SpotTypes                 | SelectPlotSymbols:arg1   |
| string                    | fixSeps:arg1, SimplifyContrastsExpression:arg1, GetRNATypesFrom.ContrastsFromDropDowns.Stri  |
| tc1Pkg                    | TclRequire:arg1  |
| tt                        | SetupPlotKeyBindings:arg1, SetupPlotMenus:arg1   |
| verbose                   | Optional diagnostic messages   |
| whatFor                   | GetParametersAndOrContrasts:arg2   |
| whichCoef                 | GetCoef:arg2   |
| Width                     | HTMLplotUsingFunction:arg10  |
| xlabel                    | GetPlotLabels:arg2   |
| xlim                      | GetNEWxlim:arg1  |
| ylabel                    | GetPlotLabels:arg3   |

**Details**

This function launches a Graphical User Interface for the limma package by Gordon Smyth. The GUI uses Tk widgets (via the R TclTk interface by Peter Dalgaard) in order to provide a simple interface to the limma functions for linear modelling of microarrays and identification of differentially expressed genes.

**Author(s)**

James Wettenhall

# Index

## \* documentation

- LGchangeLog, 2
- AboutLimmaGUI (limmaGUI), 2
- AboutNormalization (limmaGUI), 2
- BChelp (limmaGUI), 2
- ChooseContrastsParameterization (limmaGUI), 2
- chooseDir (limmaGUI), 2
- ChooseEbayesStatistic (limmaGUI), 2
- ChooseParameterization (limmaGUI), 2
- ChoosePlotSymbolByClicking (limmaGUI), 2
- ChooseSpotType (limmaGUI), 2
- ComputeContrasts (limmaGUI), 2
- ComputeLinearModelFit (limmaGUI), 2
- CopyGraph (limmaGUI), 2
- CreateNewParameterization (limmaGUI), 2
- CreateTreeAndList (limmaGUI), 2
- DeleteContrastsParameterization (limmaGUI), 2
- deleteItemFromList (limmaGUI), 2
- DeleteParameterization (limmaGUI), 2
- DupCorBoxPlot (limmaGUI), 2
- ebayesBoxPlots (limmaGUI), 2
- evalRcode (limmaGUI), 2
- ExportAvalues (limmaGUI), 2
- ExportHTMLreport (limmaGUI), 2
- ExportMvalues (limmaGUI), 2
- ExportTopTable (limmaGUI), 2
- fixSeps (limmaGUI), 2
- GetBackgroundCorrectionMethod (limmaGUI), 2
- GetBetweenArrayNormalizationMethod (limmaGUI), 2
- GetCoef (limmaGUI), 2
- GetComponentstoExportInHTMLreport (limmaGUI), 2
- GetContrastsParameterizationName (limmaGUI), 2
- GetContrastsParameterizationNames (limmaGUI), 2
- GetDEcutoff (limmaGUI), 2
- GetDesignOrContrasts (limmaGUI), 2
- GetGeneLabelsOptions (limmaGUI), 2
- GetGenePixFlagWeightings (limmaGUI), 2
- GetImageAnalysisColumnHeadings (limmaGUI), 2
- GetImageProcessingFileType (limmaGUI), 2
- GetJpegOrPngParams (limmaGUI), 2
- GetJpegOrPngX11Params (limmaGUI), 2
- GetlimmaDataSetName (limmaGUI), 2
- GetlmFitMethod (limmaGUI), 2
- GetLowessType (limmaGUI), 2
- GetNEWxlim (limmaGUI), 2
- GetNormexpOffsetValue (limmaGUI), 2
- GetNumParametersNoTargets (limmaGUI), 2
- getPackageVersion (limmaGUI), 2
- GetParameterizationName (limmaGUI), 2
- GetParameterNames (limmaGUI), 2
- GetParametersAndOrContrasts (limmaGUI), 2
- GetPlotLabels (limmaGUI), 2
- GetPlotSize (limmaGUI), 2
- GetPlotTitle (limmaGUI), 2
- GetPValueCutoff (limmaGUI), 2
- GetReducedDuplicateSpacing (limmaGUI), 2
- GetRNATypesFrom.ContrastsFromDropDowns.String (limmaGUI), 2
- GetSlideNum (limmaGUI), 2
- GetSpotTypesForLinearModel (limmaGUI), 2
- GetSpotTypesIncludedNames (limmaGUI), 2
- GetWithinArrayNormalizationMethod (limmaGUI), 2
- GetWtAreaParams (limmaGUI), 2
- HeatDiagramDialog (limmaGUI), 2
- HeatDiagramPlot (limmaGUI), 2
- HowManyDups (limmaGUI), 2
- HTMLplotUsingFunction (limmaGUI), 2
- ImageArrayPlot (limmaGUI), 2
- ImageArrayPlotDialog (limmaGUI), 2
- imageplotlimmaGUI (limmaGUI), 2

ImportMA (limmaGUI), 2  
 ImportMADialog (limmaGUI), 2  
 initGlobals (limmaGUI), 2  
 InitNewParameterization (limmaGUI), 2  
  
 LGchangeLog, 2  
 limmaGUI, 2  
 limmaGUIhelp (limmaGUI), 2  
 limmaHelp (limmaGUI), 2  
 lmFitMethodHelp (limmaGUI), 2  
 LogOddsPlot (limmaGUI), 2  
  
 MAPlot (limmaGUI), 2  
 MAPlotAvg (limmaGUI), 2  
 MBoxPlot (limmaGUI), 2  
 MMPlot (limmaGUI), 2  
  
 NewLimmaFile (limmaGUI), 2  
 NormalizeNow (limmaGUI), 2  
 nstrstr (limmaGUI), 2  
  
 onDestroy (limmaGUI), 2  
 onExit (limmaGUI), 2  
 OpenALimmaFile (limmaGUI), 2  
 OpenGALandTargetsandSpotTypesfiles  
     (limmaGUI), 2  
 OpenGALFile (limmaGUI), 2  
 OpenLimmaFile (limmaGUI), 2  
 OpenSpotTypesFile (limmaGUI), 2  
 OpenTargetsFile (limmaGUI), 2  
  
 plotMAColorCoded (limmaGUI), 2  
 PlotOptions (limmaGUI), 2  
 PrintTipGroupMAPlot (limmaGUI), 2  
  
 QQTplot (limmaGUI), 2  
  
 read.marrayTools (limmaGUI), 2  
 readGALLimmaGUI (limmaGUI), 2  
 ReadImageProcessingFiles (limmaGUI), 2  
 Require (limmaGUI), 2  
 Resize (limmaGUI), 2  
  
 SaveAsLimmaFile (limmaGUI), 2  
 SaveGraphAsJpeg (limmaGUI), 2  
 SaveGraphAsPDF (limmaGUI), 2  
 SaveGraphAsPNG (limmaGUI), 2  
 SaveGraphAsPostscript (limmaGUI), 2  
 SaveLimmaFile (limmaGUI), 2  
 SelectPlotSymbols (limmaGUI), 2  
 SetLayoutParameters (limmaGUI), 2  
 SetupPlotKeyBindings (limmaGUI), 2  
 SetupPlotMenus (limmaGUI), 2  
 SetWD (limmaGUI), 2  
  
 showChangeLog (limmaGUI), 2  
 showCitations (limmaGUI), 2  
 showGAL (limmaGUI), 2  
 showTopTable (limmaGUI), 2  
 SimplifyContrastsExpression (limmaGUI),  
     2  
 strstr (limmaGUI), 2  
  
 tclArrayVar (limmaGUI), 2  
 TclRequire (limmaGUI), 2  
 Try (limmaGUI), 2  
 TryReadImgProcFile (limmaGUI), 2  
  
 UpdateSpotTypesStatus (limmaGUI), 2  
 UpDownOrBoth (limmaGUI), 2  
  
 vennDiagramlimmaGUI (limmaGUI), 2  
 VennDiagramPlot (limmaGUI), 2  
 ViewDesignOrContrastsMatrixAsPairs  
     (limmaGUI), 2  
 ViewDesignOrContrastsMatrixInTable  
     (limmaGUI), 2  
 ViewExistingContrastsParameterization  
     (limmaGUI), 2  
 ViewExistingParameterization  
     (limmaGUI), 2  
 ViewRNATargets (limmaGUI), 2  
 ViewSpotTypes (limmaGUI), 2  
  
 WithinBetweenOrBoth (limmaGUI), 2  
 wtflags2 (limmaGUI), 2