Package: ADAMgui (via r-universe)

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Type Package

Title Activity and Diversity Analysis Module Graphical User Interface

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Depends R(>= 3.6), stats, utils, methods, ADAM

Suggests markdown, BiocStyle

Imports GO.db (>= 3.5.0), dplyr (>= 0.7.6), shiny (>= 1.1.0), stringr (>= 1.3.1), stringi (>= 1.2.4), varhandle (>= 2.0.3), ggplot2 (>= 3.0.0), ggrepel (>= 0.8.0), ggpubr (>= 0.1.8), ggsignif (>= 0.4.0), reshape2 (>= 1.4.3), RColorBrewer (>= 1.1-2), colorRamps (>= 2.3), DT (>= 0.4), data.table (>= 1.11.4), gridExtra (>= 2.3), shinyjs (>= 1.0), knitr, testthat

Description ADAMgui is a Graphical User Interface for the ADAM package. The ADAMgui package provides 2 shiny-based applications that allows the user to study the output of the ADAM package files through different plots. It's possible, for example, to choose a specific GFAG and observe the gene expression behavior with the plots created with the GFAGtargetUi function. Features such as differential expression and foldchange can be easily seen with aid of the plots made with GFAGpathUi function.

biocViews GeneSetEnrichment, Pathways, KEGG

VignetteBuilder knitr

LazyLoad yes

NeedsCompilation no

Encoding UTF-8

RoxygenNote 6.1.1

License GPL (>= 2)

URL TBA

BugReports https://github.com/jrybarczyk/ADAMgui/issues

Config/pak/sysreqs cmake make libicu-dev libpng-dev libuv1-dev libssl-dev zlib1g-dev

Repository Bioconductor 3.24

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RemoteUrl https://github.com/bioc/ADAMgui

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`DiffAedes` *Aedes aegypti RNA-seq differential expression data example*

Description

A sample fragment of differential gene expression from an RNA-seq experiment of Aedes aegypti mosquito.

Format

A data.frame with 1973 rows and 3 variables

References

AKBARI, O. S. et al. The developmental transcriptome of the mosquito aedes aegypti, an invasive species and major arbovirus vector. G3: Genes— Genomes— Genetics, Genetics Society of America, v. 3, n. 9, p. 1493–1509, 2013.

Examples

```
data(DiffAedes)
```

GeneFunctionAedes *Relation between Aedes aegypti genes and KEGG pathways*

Description

A relation between the GFAGs present in ResultAnalysisAedes and their respective genes.

Format

A data.frame with 782 rows and 2 variables

References

Molan, A. L. 2018. "Construction of a Tool for Multispecies Genic Functional Enrichment Analysis Among Comparative Samples." Master's thesis, Institute of Biosciences of Botucatu – Univ. Estadual Paulista. http://hdl.handle.net/11449/157105.

Examples

```
data(GeneFunctionAedes)
```

GFAGpathUi *GFAGpathUi*

Description

Launch GFAGpathUi Graphical User Interface (GUI) in local machine or default browser.

Usage

```
GFAGpathUi(browser)
```

Arguments

browser	is a logical variable necessary to run the app. When x=TRUE the app is launched in your default web browser. When x=FALSE the app is launched in your local machine.

Details

This shiny (GUI) enables the visualization and plotting of P.value distribution of the Paths in the GFAG output file. The plots were optimized for a maximun of 50 Paths, you can still plot more than 50 paths but the graphs tend to get rather long.

Value

return a shiny Graphical User Interface (GUI).

Author(s)

Giordano Bruno Sanches Seco <giordano.bruno@unesp.br>

Examples

```
#Creating input files
data(DiffAedes)
data(GeneFunctionAedes)
data(ResultAnalysisAedes)
## Not run:
#Input file 1
write.table(DiffAedes,file = "DiffAedes.txt",sep = "\t", col.names = TRUE,
row.names = FALSE, quote = FALSE)
#Input file 2
write.table(GeneFunctionAedes,file = "GeneFunctionAedes.txt",sep = "\t",
col.names = TRUE, row.names = FALSE, quote = FALSE)
#Input file 3
write.table(ResultAnalysisAedes,file = "ResultAnalysisAedes.txt",sep = "\t",
col.names = TRUE, row.names = FALSE, quote = FALSE)
#Grahphical analysis
GFAGpathUi(browser = TRUE) # Launch the app in your default web browser.
GFAGpathUi(browser = FALSE) # Launch the app in your local machine.

## End(Not run)
```

`GFAGtargetUi` *GFAGtargetUi*

Description

Launch Launch GFAGtargetUi Graphical User Interface (GUI) in local machine or default browser

Usage

```
GFAGtargetUi(browser)
```

Arguments

`browser`	is a logical variable necessary to run the app. When browser=TRUE the app is launched in your default web browser. When browser=FALSE the app is launched in your local machine.

Details

This shiny (GUI) enables the creation of a plot that shows the expression of the targets in a selected path between control and case. See the vignette for more information.

Value

return a shiny Graphical User Interface (GUI).

Author(s)

Giordano Bruno Sanches Seco <giordano.bruno@unesp.br>

Examples

```
#Creating input files
data(DiffAedes)
data(GeneFunctionAedes)
data(ResultAnalysisAedes)
## Not run:
#Input file 1
write.table(DiffHs,file = "DiffAedes.txt",sep = "\t", col.names = TRUE,
row.names = FALSE, quote = FALSE)
#Input file 2
write.table(GeneFunctionHs,file = "GeneFunctionAedes.txt",sep = "\t",
col.names = TRUE, row.names = FALSE, quote = FALSE)
#Input file 3
write.table(ResultAnalysisAedes,file = "ResultAnalysisAedes.txt",sep = "\t",
col.names = TRUE, row.names = FALSE, quote = FALSE)
#Grahphical analysis
GFAGtargetUi(browser = TRUE) # Launch the app in your default web browser.
GFAGtargetUi(browser = FALSE) # Launch the app in your local machine.

## End(Not run)
```

ResultAnalysisAedes *Result from an example of ADAM Aedes aegypti analysis*

Description

Result from ADAM Aedes aegypti analysis according to ExpressionAedes data.

Format

A data.frame with 87 rows and 22 variables

References

Molan, A. L. 2018. "Construction of a Tool for Multispecies Genic Functional Enrichment Analysis Among Comparative Samples." Master's thesis, Institute of Biosciences of Botucatu – Univ. Estadual Paulista. http://hdl.handle.net/11449/157105.

Examples

```
data(ResultAnalysisAedes)
```

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