Package ‘juicr’

July 22, 2025

Version 0.1

Date 2021-04-29

Title Automated and Manual Extraction of Numerical Data from Scientific Images

Description Provides a GUI interface for automating data extraction from multiple images containing scatter and bar plots, semi-automated tools to tinker with extraction attempts, and a fully-loaded point-and-click manual extractor with image zoom, calibrator, and classifier. Also provides detailed and R-independent extraction reports as fully-embedded .html records.

Type Package

Depends R (>= 3.3.2)

Imports XML, RCurl

SystemRequirements Tcl/Tk toolkit (X11 Quarts for Mac)

VignetteBuilder R.rsp

License GPL (>= 2)

URL `http://lajeunesse.myweb.usf.edu/` `https://github.com/mjlajeunesse/` `https://www.youtube.com/c/LajeunesseLab/`

Encoding UTF-8

RoxygenNote 7.1.1

Suggests EBImage, R.rsp

NeedsCompilation no

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Repository CRAN

Date/Publication 2021-04-30 07:10:02 UTC

Contents

`juicr-package` *Automated, semi-automated, and manual extraction of numerical data from scientific images, plot, charts, and figures*

Description

juicr is a GUI interface for automating data extraction from multiple images containing scatter and bar plots, semi-automated tools to tinker with extraction attempts, and a fully-loaded point-and-click manual extractor with image zoom, calibrator, and classifier. Also provides detailed and R-independent extraction reports as fully-embedded .html records. More information about **juicr** can be found at `http://lajeunesse.myweb.usf.edu/`.

Details

What to cite?

Lajeunesse, M.J. (2021) Automated, semi-automated, and manual extraction of numerical data from scientific images, plot, charts, and figures. *R package, v.0.1*

Installation and Dependencies.

juicr has one external dependency that need to be installed and loaded prior to use in R. This is the EBImage R package (Pau et al. 2010) available only from the Bioconductor repository: `https://www.bioconductor.org/`.

To properly install **juicr**, start with the following R script that loads the Bioconductor resources needed to install the EBImage (also accept all of its dependencies):

```
install.packages("BiocManager");
BiocManager::install("EBImage"))
library(metagear)
```

Finally for Mac OS users, installation is sometimes not straighforward as the GUI_juicr() requires the Tcl/Tk GUI toolkit to be installed. You can get this toolkit by making sure the latest X11 application (xQuartz) is installed from here: `https://www.xquartz.org/`.

Author(s)

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References

Pau, G., Fuchs, F., Sklyar, O., Boutros, M. and Huber, W. (2010) EBImage: an R package for image processing with applications to cellular phenotypes. Bioinformatics 26: 979-981.

`file_getJuicr_Extractions` *Reads a *_juicr.html report and retrieves data extractions and history.*

Description

Reads a juicr generated report of image extractions contained within the .html file.

Usage

```
file_getJuicr_Extractions(aFileName = file.choose(), quiet = FALSE)
```

Arguments

`aFileName`	The file name and location of a *_juicr.html report. Prompts for file name if none is explicitly called. Must be .html format.
`quiet`	When `"TRUE"`, does not display all extraction tables.

Value

A list of tables including all extractions, coordinates, image file names, and `juicr` GUI parameters.

See Also

file_getJuicr_Images

Examples

```
## Not run:

theExtraction <- file_getJuicr_Extractions("pretend_image_juicr.html")
print(theExtraction$points)


## End(Not run)
```

`file_getJuicr_Images` *Reads a *_juicr.html report and extracts images into working directory.*

Description

Reads a juicr generated report of image extractions contained within the .html file, and saves all images (e.g., original, standardized, and standardized with painted extractions).

Usage

```
file_getJuicr_Images(aFileName = file.choose(), quiet = FALSE)
```

Arguments

`aFileName`	The file name and location of a *_juicr.html report. Prompts for file name if none is explicitly called. Must be .html format.
`quiet`	When `"TRUE"`, does not display the file names of all images extracted and saved to the working directory.

Value

A vector of file names of each image extracted from the .html file.

See Also

file_getJuicr_Extractions

Examples

```
## Not run:

file_getJuicr_Images("pretend_image_juicr.html")


## End(Not run)
```

`GUI_juicr` *A GUI screener to quickly code candidate studies for inclusion/exclusion into a systematic review or meta-analysis.*

Description

A GUI screener to help scan and evaluate the title and abstract of studies to be included in a systematic review or meta-analysis. A description of GUI options and layout is found here: `http://lajeunesse.myweb.usf.edu/juicr/juicr_basic_vignette_v0.1.html`.

Usage

```
GUI_juicr(
  theFigureFile = "",
  theJuicrFile = "",
  standardizeTheImage = TRUE,
  standardSize = 1000,
  figureWindowSize = c(800, 600),
  pointSize = 6,
  animateDelay = TRUE,
  groupNames = c("orangeGrp", "berryGrp", "cherryGrp", "plumGrp", "kiwiGrp",
    "bananaGrp", "grapeGrp", "pruneGrp"),
 groupColors = c("dark orange", "turquoise3", "tomato3", "orchid", "yellow green",
    "goldenrod2", "plum4", "saddle brown")
)
```

Arguments

`theFigureFile`	An optional file name and location of a .jpg, .png, or .tiff file containing the scientific image/plot/chart/figure to pre-load in the GUI. Within the GUI there is also a button to select the image file. Images in other formats should be converted to .png prior to using juicr.
`theJuicrFile`	An optional file name and location of a *_juicr.html report containing extractions and images from a previous juicr session to pre-load into the GUI. Within the GUI there is also a button to select an .html file.
`standardizeTheImage`	When `"TRUE"`, all large images are standardized to a common size with a width specified by `"standardSize"`. When `"FALSE"`, the image is unaltered in size.
`standardSize`	The common width in pixels for standardizing large images; default is a width of 1000 pixels.
`figureWindowSize`	Specifies the window size containing the image. By default, this image-viewer window will be 800 (width) by 600 (height) pixels, larger images will be scrollable to fit this window.
`pointSize`	Changes the default size of a clickable data-point on the image. Size is the radius in pixels (default is 6).

`animateDelay`	When `"TRUE"`, creates a very small pause when plotting individual automated extractions – giving an animated effect.
`groupNames`	A vector of the default eight names specifying the labels of each group. Default labels are fruit themed. Can be any size, but GUI will only print first 9 characters.
`groupColors`	A vector of the default eight color names specifying the coloring of each group. Are in color-names format, but can also be HEX.

Value

A console message of where saved .csv or *_juicr.html files are located.

Note

Installation and troubleshooting

For Mac OS users, installation is sometimes not straighforward as this GUI requires the Tcl/Tk GUI toolkit to be installed. You can get this toolkit by making sure the latest X11 application (xQuartz) is installed, see here: `https://www.xquartz.org/`. More information on installation is found in `juicrs`'s vignette.

Examples

```
## Not run:

GUI_juicr(system.file("images", "Kortum_and_Acymyan_2013_Fig4.jpg", package = "juicr"))


## End(Not run)
```

`Kam_et_al_2003_Fig2.jpg` *An example image of a scatterplot figure*

Description

A jpg image of a scatterplot from Figure 2 of Kam, M., Cohen-Gross, S., Khokhlova, I.S., Degen, A.A. and Geffen, E. 2003. Average daily metabolic rate, reproduction and energy allocation during lactation in the Sundevall Jird Meriones crassus. Functional Ecology 17:496-503.

Format

A raw jpg-formated image

Note

How to use

```
readImage(system.file("images", "Kam_et_al_2003_Fig2.jpg", package = "juicr"))
```

`Kortum_and_Acymyan_2013_Fig4.jpg`

An example image of a bar plot figure

Description

A jpg image of a bar plot from Figure 4 of Kortum, P., and Acymyan, C.Z. 2013. How low can you go? Is the System Usability Scale range restricted? Journal of Usability Studies 9:14-24.

Format

A raw jpg-formated image

Note

How to use

```
readImage(system.file("images", "Kortum_and_Acymyan_2013_Fig4.jpg", package = "juicr"))
```

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