Package 'gitter'

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Type Package

Title Robust gridding and quantifying of pinned genetic screens

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Description gitter is a image analysis package for R. Its primary goal is to allow users to robustly and quickly grid and quantify biological images of pinned colonies. It includes several image pre-processing techniques, such as autorotation of plates, noise removal, contrast adjustment and image resizing.

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Depends jpeg, tiff, logging, parallel, PET, ggplot2, EBImage

R topics documented:

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gitter-package   *gitter*

Description

gitter is a image analysis package for R. Its primary goal is to allow users to robustly and quickly grid and quantify biological images of pinned colonies. It includes several image pre-processing techniques, such as autorotation of plates, noise removal, contrast adjustment and image resizing.

Details

Package:	gitter
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Version:	1.0.0
Date:	2013-05-16
License:	LGPL

Author(s)

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gitter   *Process a single plate image*

Description

The following function will grid and quantify a single plate image (for batch processing, see [gitter.batch](#))

Usage

```
gitter(image.file = file.choose(), plate.format = c(32, 48),
       remove.noise = F, autorotate = F, inverse = F, verbose = "l",
       contrast = NULL, fast = NULL, plot = F, grid.save = getwd(),
       dat.save = getwd(), .is.ref = F, .params = NULL)
```

Arguments

image.file	The path to the JPG/JPEG image. Defaults to a file choosing dialog.
plate.format	The plate format, accepted formats: 1536, 768, 384 and 96. Alternatively, you can provide the number of rows and columns on the plate as an integer vector for example "c(32,48)". Default is "1536".
remove.noise	Logical indicating noise/speckles should be remove from the thresholded image prior to analysis. Default is "FALSE".

autorotate	Logical indicating if image should be auto-rotated prior to processing. Only select this option if image is extremely rotated. gitter is able to handle small variations in rotations (1-2 degrees) without auto-rotating. Default is "FALSE".
inverse	Logical indicating if input image is inverted, meaning colonies are darker compared to their background. Default is "FALSE".
verbose	Shows details about the results of running job. For detailed logs "l", for a progress bar "p" or for no output "n". Default is "l".
contrast	Integer indicating how much contrast should be applied to the image, prior to processing. A value of "NULL" will not apply any contrast. Default is "NULL".
fast	Pixel value between 1500-4000 indicating if images should be resized to a certain width to speed up processing. If "NULL", no resizing occurs. Default is "NULL".
plot	Logical indicating whether intensity profiles should be plotted. Default is "FALSE".
grid.save	Directory path to save gridded/thresholded images. Set to "NULL" if you do not want gridded images saved to disk. Default is the current working directory.
dat.save	Directory path to save dat files. Set to "NULL" if you do not want dat files saved to disk. Default is the current working directory.
.is.ref	Specifies if a reference property list is supplied. Warning: NOT for use by casual users.
.params	Reference property list. Warning: NOT for use by casual users.

Value

DAT file	Tab delimited file containing quantified colony sizes. There are two types of flags that can be associated with a data file (1) plate-level flags signify possible misgridding of the plate due to a high number of low colony size or circularity. These flags can be viewed using the [plate.warnings](#) function (2) colony-based flags signify warnings associated with individual colonies. These flags can be viewed in the column named flags of the data file.

row:	row number
col:	column number
size:	quantified colony size
circularity:	circularity of the colony
flags:	colony-based flags: S - Colony spill or edge interference, C- Low colony circularity

Gridded image	
	Thresholded image showing the grid defined over the image

Author(s)

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See Also

[gitter.batch](#)

Examples

```
# Read sample image
```

```
f = system.file("extdata", "sample.jpg", package="gitter")
# Process it
dat = gitter(f)
# View head of the results
head(dat)

# Remember: output files by default are saved to your working directory
```

---

gitter.batch   *Process a batch set of plate images*

Description

This function will process a directory or list of images in a batch. You can also use this function to process images with sparse to empty rows/columns using a reference image.

Usage

```
gitter.batch(image.files, ref.image.file = NULL, verbose = l, ...)
```

Arguments

image.files	Directory containing JPG or JPEG images OR a character vector of image paths.
ref.image.file	Specifies path to a reference image, which will be used to grid images specified in image.files.
verbose	See parameters in [gitter].
...	Additional parameters passed to [gitter].

Value

gitter.batch does not return any values. DAT and gridded files are saved to their respective directories.

Author(s)

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See Also

[gitter]

Examples

```
# Processing image using reference image

# This image would typically fail to process, since its missing several rows
f = system.file("extdata", "sample_dead.jpg", package="gitter")
# We will use this image to successfully process the above image
f.ref = system.file("extdata", "sample.jpg", package="gitter")
# Process
gitter.batch(f, f.ref)

# Remember: output files by default are saved to your working directory
```

---

gitter.demo *Run a demo of gitter*

Description

This function will run a demo of gitter.

Usage

```
gitter.demo(eg=single)
```

Arguments

eg   Type of demo. "single" for a single image demo, "ref" for a single image demo
            using a reference image. Default is "simple".

Value

Summary of the dat file produced is displayed.

Author(s)

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See Also

[gitter](#)

Examples

```
# gitter.demo()
```

---

gitter.read *Read in a data file as a* gitter *data object.*

Description

This function will take a path to a data file generated by [gitter](#) and read it into a [gitter](#) object for
use with plot, summary and warning functions.

Usage

```
gitter.read(path)
```

Arguments

path   Path to the data file generated by [gitter](#).

Value

[gitter](#) data.frame object for use with plot, summary and warning functions.

Author(s)

Omar Wagih <omar.wagih@utoronto.ca>

See Also

gitter

Examples

```
# Get dat file path
f = system.file("extdata", "sample.jpg.dat", package="gitter")
# Read in path as a gitter data object
g = gitter.read(f)
```

---

plate.warnings	*Show any plate-level warnings associated with a* gitter *data object*

Description

This function will show warnings associated with a gitter data object.

Usage

```
plate.warnings(dat)
```

Arguments

dat   The data.frame produced by gitter.

Value

Warnings associated with the gitter data object or NULL if no warnings.

Author(s)

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See Also

gitter

Examples

```
# dat = gitter("/path/to/image")
# plate.warnings(dat)
```

---

plot.gitter   *Plot a gitter dat file*

Description

This function will plot a heatmap or bubble plot of a data.frame produced by gitter or a dat file saved to disk.

Usage

```
## S3 method for class gitter
plot(x, title=, type=heatmap, low=turquoise, mid=black, high=yellow,
             show.text=F, text.color=white, norm=T, show.flags=T,
             flag.color=white, ...)
```

Arguments

x	The data.frame produced by gitter or the path to a dat file saved by gitter.
title	Title of plot. Default is blank.
type	Type of plot. "heatmap" for a heatmap, "bubble" for a bubble plot. Default is "heatmap".
low	Color for the lower bound of colony sizes. Default is "turquoise".
mid	Color of the middle value of colony sizes. Default is "black".
high	Color for the upper bound of colony sizes. Default is "yellow".
show.text	Logical indicating if text representation of colony sizes should be overlaid on the plot. Default is "TRUE".
text.color	Color of text if show.text is "TRUE". Default is "white".
norm	Logical indicating if colony sizes should be normalized by dividing colony sizes the middle mean of values and capping them between 0-2. Default is "TRUE".
show.flags	Logical indicating if dots should be overlaid on the plot for flagged colonies. Default is "TRUE".
flag.color	Color of flag dot if show.flags is "TRUE". Default is "white".
...	Additional arguments. Not used.

Value

a ggplot heatmap or bubble plot.

Author(s)

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See Also

gitter

Examples

```
# Get dat file path
f = system.file("extdata", "sample.jpg.dat", package="gitter")
# Read in path as a gitter data object
g = gitter.read(f)
# Plot a heatmap
plot(g, type=heatmap)
# Show a bubble plot
plot(g, type=bubble, low=black, high=red)
```

---

summary.gitter   *View the summary of a gitter data file*

Description

This function will show a brief summary of a data frame produced by gitter

Usage

```
## S3 method for class gitter
summary(object, ...)
```

Arguments

object   The data.frame produced by gitter.

...   Additional arguments. Not used.

Value

Summary including the call made to gitter, colony size quantiles and more.

Author(s)

Omar Wagih <omar.wagih@utoronto.ca>

See Also

gitter

Examples

```
# dat = gitter("/path/to/image")
# summary(dat)
```

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