

Package ‘gitter’

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Type Package

Title An R Package for Quantification of Pinned Microbial Culture

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Description The goal of this package is to allow users to robustly and quickly grid and quantify sizes of pinned colonies in plate images. gitter works by first finding the grid of colonies from a preprocessed image and then locating the bounds of each colony separately. It includes several image pre-processing techniques, such as autorotation of plates, noise removal, contrast adjustment and image resizing.

License LGPL

Imports jpeg, tiff, logging, PET, ggplot2, EBImage

NeedsCompilation no

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gitter	<i>Process a single plate image</i>
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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

<code>image.file</code>	The path to the image. Defaults to a file choosing dialog.
<code>plate.format</code>	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 <code>c(32,48)</code> . Default is 1536.
<code>remove.noise</code>	Logical indicating noise/speckles should be remove from the thresholded image prior to analysis. Default is FALSE.
<code>autorotate</code>	Logical indicating if image should be auto-rotated prior to processing. Only select this option if image is extremely rotated. <code>gitter</code> is able to handle small variations in rotations (1-2 degrees) without auto-rotating. Default is FALSE.
<code>inverse</code>	Logical indicating if input image is inverted, meaning colonies are darker compared to their background. Default is FALSE.
<code>verbose</code>	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".
<code>contrast</code>	Integer between 1 and 100 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.
<code>fast</code>	If set to integer value, the image will be resized to this width in pixels to speed up computation. This is useful for very large images that otherwise take a long time to process. We do not recommend resizing to fewer than 1500 pixels or greater than 4000 pixels in width. Default is NULL.
<code>plot</code>	Logical indicating whether intensity profiles should be plotted. Default is FALSE.
<code>grid.save</code>	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.
<code>dat.save</code>	Directory path to save resulting data files. Set to NULL if you do not want resulting data saved to disk. Default is the current working directory.
<code>.is.ref</code>	Specifies if a reference property list is supplied. Warning: NOT for use by casual users.
<code>.params</code>	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 colonies with small size or low 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

Examples

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

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 = "1", ...)
```

Arguments

image.files Directory containing 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.

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
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Description

This function will run a demo of gitter.

Usage

```
gitter.demo(eg = 1)
```

Arguments

eg	Type of demo. 1 for a single image demo, 1 for a single image demo using a reference image. Default is 1.
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Examples

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

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

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
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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.

Examples

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

plot.gitter	Plot a gitter dat file
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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.

Examples

```
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.

Examples

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

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