

Package: ijAnalysis (via r-universe)

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Title Miscellaneous tools for image analysis tasks

Version 0.0.4

Description A miscellaneous toolbox for various image analysis tasks.
Initially contains tools for downstream analysis of my ImageJ
plugin Puncta Tracker and hence the ij name. Part of the y3628
analysis suite.

License GPL (>= 3)

Encoding UTF-8

Roxygen list(markdown = TRUE)

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Imports y3628 (>= 0.0.3), dplyr, purrr, reticulate, rlang, vctrs,
stringr, jsonlite, tibble, readr, utils, ggplot2, readxl, damr,
ggetho, behavr, data.table, stats

Depends R (>= 4.1)

Suggests knitr, rmarkdown

VignetteBuilder knitr

Config/pak/sysreqs libicu-dev libpng-dev python3 libx11-dev

Repository <https://yeyuan98.r-universe.dev>

RemoteUrl <https://github.com/yeyuan98/ijAnalysis>

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.parse_meta	<i>Parse spot array JSON data to metaRcd.</i>
-------------	---

Description

Parse spot array JSON data to metaRcd.

Usage

```
.parse_meta(ser.coord, ser.dist)
```

Arguments

ser.coord	Serialized coord.
ser.dist	Serialized dist.

Value

A y3628::metaRcd object.

Examples

```
# Does not apply. Internal use only.
```

`.selectNCT.index` *Get index for spotInRoi nuclear/full-cell data subsetting.*

Description

Get index for spotInRoi nuclear/full-cell data subsetting.

Usage

```
.selectNCT.index(dfNucCyt, what)
```

Arguments

<code>dfNucCyt</code>	Parsed spotInRoi nuclear/full-cell data.
<code>what</code>	What to subset. must be nuclear, cytoplasm, or full.

Value

Indices for subsetting.

Examples

```
# Does not apply. Internal use only.
```

`actogram_loadFromMetadata`
Load behavior activity data from metadata

Description

Load behavior activity data from metadata

Usage

```
actogram_loadFromMetadata(path, data_dir = "./", ...)
```

Arguments

<code>path</code>	Path to metadata, must be commonly used delimited or excel.
<code>data_dir</code>	Path to the behavior data dir.
<code>...</code>	These dots are for future extensions and must be empty.

Value

`behavr:::behavr` behavior data table.

Examples

```
# TODO
```

actogram_plot	<i>Plotting actogram</i>
---------------	--------------------------

Description

Plotting actogram

Usage

```
actogram_plot(
  behavr,
  file = NULL,
  file.options = list(device = tools::file_ext(file), height = 9.14, width = 10.6)
)
```

Arguments

behavr	behavr::behavr behavior data table.
file	Optional path to save the plot. Backend is ggplot2::ggsave().
file.options	List to specify options for saving the plot.

Value

ggplot plot object.

Examples

```
# TODO
```

behavior_loadMetadata	<i>Load behavior metadata</i>
-----------------------	-------------------------------

Description

Load behavior metadata

Usage

```
behavior_loadMetadata(path)
```

Arguments

path	Path to metadata file. See body for column spec.
------	--

Value

Metadata tibble.

Examples

```
# Not exported.
```

ctcf_plot

Standardized plotting of CTCF data

Description

Standardized plotting of CTCF data

Usage

```
ctcf_plot(data, x, y, fill = NA)
```

Arguments

data	tibble of CTCF data
x	x-axis variable for plotting
y	y-axis variable for plotting
fill	fill variable for plotting

Value

ggplot object

Examples

```
# TODO
```

ctcf_read_csv	<i>Read CTCF results table</i>
---------------	--------------------------------

Description

Read CTCF results table

Usage

```
ctcf_read_csv(path, ...)
```

Arguments

path	Path to the CTCF analysis csv
...	Forwarded to readr::read_csv

Value

tibble of CTCF table

Examples

```
#TODO
```

ij_nnd.compute	<i>Compute NND metrics for a pair of spot sets.</i>
----------------	---

Description

Compute NND metrics for a pair of spot sets.

Usage

```
ij_nnd.compute(foreach, to, z.proximal)
```

Arguments

foreach	For each spot in foreach,
to	compute its distance to the nearest neighbor in to spot set.
z.proximal	Only spots in close enough z-proximity is computed.

Value

y3628::metaRcrd object storing the NND results. For spots that have no Z-proximal spots in the to spot set, NAs are returned.

Examples

```
# TODO
```

ij_RoiPointsSaver	<i>Initialize an ImageJ ROI point set saver function</i>
-------------------	--

Description

Initialize an ImageJ ROI point set saver function

Usage

```
ij_RoiPointsSaver(use_python)
```

Arguments

use_python Path to the Python binary to use.

Value

A ROI saver function.

Examples

```
# TODO
```

jtk.init	<i>JTK Cycle V3.1 Adaptation jtk.init</i>
----------	---

Description

Initialize the JTK environment for all periods

Usage

```
jtk.init(periods, interval = 1)
```

Arguments

periods Periods to test on (in units of spacing interval).

interval Spacing of time points (in physical unit like hours).

For example, `jtk.init(9:15, 2)` means that data time point spacing is 2-hour and possible periods would be 18-hour to 30-hour (2-hour spacing).

Value

None; Run only for side effects on JTK_env.

Examples

```
# Refer to the JTK Cycle guide.
```

jtkdist	<i>JTK Cycle V3.1 Adaptation</i> jtkdist
---------	--

Description

JTK Cycle V3.1 Adaptation jtkdist

Usage

```
jtkdist(timepoints, reps = 1, normal = FALSE, alt = FALSE)
```

Arguments

timepoints	Number of time points in the data.
reps	Number of replicates for each time point.
normal	Not used. Refer to JTK Cycle paper.
alt	Not used. Refer to JTK Cycle paper.

Value

Not used. Refer to JTK Cycle paper.

Examples

```
# Refer to the JTK Cycle guide.
```

`jtkget`*JTK Cycle V3.1 Adaptation*

Description

This is getter function to fetch computation results of `jtkx`.

Usage

```
jtkget(get.AMP.CI = FALSE)
```

Arguments

`get.AMP.CI` Bool, whether to get amplitude confidence interval, which will be length=2 numeric vector.

Details

In this adaptation, `jtkx` results are stored internally in a package environment `JTK_env`. This function is a getter of the environment.

Value

Named numeric vector of current `jtkx` results stored in `JTK_env`. If `get.AMP.CI==TRUE`, only return the amplitude confidence interval.

Examples

```
# Refer to the JTK Cycle guide.
```

`jtkstat`*JTK Cycle V3.1 Adaptation* `jtkstat`

Description

`jtkstat`: calculate the p-values for all (period,phase) combos. v3.1 modified to analyze data with missing values.

Usage

```
jtkstat(z)
```

Arguments

`z` Numeric vector of data at each time point.

Value

None; Run only for side effects on JTK_env.

Examples

```
# Internal use by `jtkx` only.
```

<code>jtkx</code>	<i>JTK Cycle V3.1 Adaptation jtkx</i>
-------------------	---------------------------------------

Description

`jtkx`: integration of `jtkstat` and `jtkdist` for repeated use.

Usage

```
jtkx(z, ampci = FALSE, conf = 0.8)
```

Arguments

<code>z</code>	Numeric vector of data at each time point.
<code>ampci</code>	Boolean, whether to compute amplitude CI and p-value.
<code>conf</code>	Confidence level of amplitude. Only useful if <code>ampci == TRUE</code> .

Value

None; Run only for side effects on JTK_env.

Examples

```
# Refer to the JTK Cycle guide.
```

<code>nlsGroup</code>	<i>nls() fitting of multiple groups</i>
-----------------------	---

Description

`nls()` fitting of multiple groups

Usage

```
nlsGroup(.data, var.group, formula, ...)
```

Arguments

.data data.frame with variables to fit with additional group variables.
var.group group variables. Follow `y3628::grouper()`.
formula Formula to run `nls()`
... Additional parameters forwarded to `nls()`. Most notably, you need to provide start values unless you are using self-starting models. See `stats::nls()`.

Value

Data frame of fitting parameters, with group variables.

Examples

```
# Puromycin, self-starting SSmicmen kinetics
nlsGroup(Puromycin, state, rate~SSmicmen(conc,Vm,K))
# Custom formula. Must provide start values.
michaelis_menten <- rate ~ (Vm)*conc/(K+conc)
nlsGroup(Puromycin, state, michaelis_menten, start=list(Vm=100,K=0.01))
```

nnd.order

Order permutation for a NND result record

Description

Order permutation for a NND result record

Usage

```
nnd.order(nnd.results, ...)
```

Arguments

nnd.results y3628::metaRcrd of NND result.
... Passed to `base::order`

Value

Order permutation using the nnd field.

Examples

```
# Does not apply. Internal use only.
```

```
periodogram_loadClocklab
    Load Clocklab periodogram batch export table
```

Description

Load Clocklab periodogram batch export table

Usage

```
periodogram_loadClocklab(data, meta, ...)
```

Arguments

data	Path to the Clocklab periodogram csv export file.
meta	Path to the metadata file.
...	These dots are for future extensions and must be empty.

Value

Periodogram table with metadata columns

Examples

```
# TODO
```

```
plot.boxPoint    Boxplot with data points, viridis_d color filled
```

Description

Boxplot with data points, viridis_d color filled

Usage

```
## S3 method for class 'boxPoint'
plot(data, x, y, fill)
```

Arguments

data	Data
x	x, must be already quoted
y	y, must be already quoted
fill	fill, must be already quoted

Value

ggplot object

Examples

```
# Internal use
```

plot_ggsave	<i>Simple wrapper of ggsave for saving plots.</i>
-------------	---

Description

Simple wrapper of ggsave for saving plots.

Usage

```
plot_ggsave(  
  plots = list(),  
  widths,  
  heights,  
  units = "in",  
  dir = "plots_eps",  
  ...  
)
```

Arguments

plots	Named list of plots to save.
widths	Width of the plots. Either length one or same as plots.
heights	Height of the plots. Either length one or same as plots.
units	Unit of width and height
dir	Directory under which to save the plot
...	These dots are for future extensions and must be empty.

Examples

```
# TODO
```

rfish_count	<i>Count number of dots per cell</i>
-------------	--------------------------------------

Description

Count number of dots per cell

Usage

```
rfish_count(samples, dots, by = c("sample", "image"), ...)
```

Arguments

samples	tibble of samples table, rfish_read_samples()
dots	tibble of dots table, rfish_read_dots()
by	group by which variables before counting
...	<tidy-select> extra columns (from samples table) to retain

Value

Count table (number of dots per cell).

Examples

```
# TODO
```

rfish_read_dots	<i>Read dots table from snakemake pipeline output</i>
-----------------	---

Description

Read dots table from snakemake pipeline output

Usage

```
rfish_read_dots(path, ...)
```

Arguments

path	Path to the dots csv
...	Forwarded to readr::read_csv

Value

tibble of dots table

Examples

```
#TODO
```

rfish_read_samples *Read samples table from snakemake pipeline output*

Description

Read samples table from snakemake pipeline output

Usage

```
rfish_read_samples(path, ...)
```

Arguments

path	Path to the samples excel.
...	Forwarded to readxl::read_excel

Value

tibble of samples table

Examples

```
#TODO
```

spotInRoi_addMeta *Add metadata column to spotInRoi data*

Description

Add metadata column to spotInRoi data

Usage

```
spotInRoi_addMeta(df, idMap, meta, ...)
```

Arguments

df	spotInRoi table, see details.
idMap	identifier map table, see details.
meta	metadata table.
...	<tidy-select> columns to select from the metadata table.

Details

spotInRoi data here takes a generalized meaning - a data frame with two id columns \$tp, \$meas, plus any number of additional columns.

The identifier map table must contain two id columns \$tp, \$meas, plus additional columns that are identifiers in the metadata table.

Value

spotInRoi data with the specified metadata columns.

Examples

```
# TODO
```

```
spotInRoi_as.data.frame.df.nnd
```

Expand NND results as data frame entries

Description

Expand NND results as data frame entries

Usage

```
spotInRoi_as.data.frame.df.nnd(df.nnd, nnd.column = "result")
```

Arguments

df.nnd	Data frame with a NND result column
nnd.column	Character name of the column that stores NND results.

Value

Expanded data frame with each NND value as one row

Examples

```
# TODO
```

spotInRoi_joinMeta *Join spotInRoi data with metadata columns*

Description

Join spotInRoi data with metadata columns

Usage

```
spotInRoi_joinMeta(df, df.meta, by, ...)
```

Arguments

df	spotInRoi data frame.
df.meta	metadata data frame.
by	columns to perform join
...	<tidy-select> columns to select from the metadata data frame.

Value

spotInRoi data frame joined with metadata.

Examples

```
# Not exported
```

spotInRoi_nnd.sort *Sort spotInRoi data based on NND results*

Description

Sort spotInRoi data based on NND results

Usage

```
spotInRoi_nnd.sort(df.nnd, nnd.column = "result", ...)
```

Arguments

df.nnd	spotInRoi data with NND results.
nnd.column	Character name of the column that stores NND results.
...	Passed to base::order for order permutation.

Value

Sorted spotInRoi results.

Examples

```
# TODO
```

spotInRoi_read_csv *Read data for spotInRoi analysis of the Puncta Tracker ImageJ plugin.*

Description

Read data for spotInRoi analysis of the Puncta Tracker ImageJ plugin.

Usage

```
spotInRoi_read_csv(file, parse.spotOut = FALSE, ...)
```

Arguments

file File passed to readr::read_csv.
parse.spotOut Whether to parse spotOut array data.
... Other parameters passed to readr::read_csv.

Value

tibble of the spotInRoi analysis result.

Examples

```
# TODO
```

spotInRoi_selectNCT *Predefined subsetting of spotInRoi nuclear/full-cell data.*

Description

Predefined subsetting of spotInRoi nuclear/full-cell data.

Usage

```
spotInRoi_selectNCT(dfNucCyt, what)
```

Arguments

dfNucCyt Parsed spotInRoi nuclear/full-cell data.
 what What to subset. must be nuclear, cytoplasm, or full.

Value

Subsetted spotInRoi nuclear/full-cell data.

Subset defaults

Predefined subsetting rules are as follows:

nuclear - for each cell select the ROI with the smallest equi.D
 full - for each cell select the ROI with the largest equi.D
 cytoplasm - currently not implemented and will error.

Examples

```
# TODO
```

subset_behavr *Simple subset of behavr : : behavr behavior tables*

Description

Simple subset of behavr : : behavr behavior tables

Usage

```
subset_behavr(behavr, expr)
```

Arguments

behavr Behavior table to subset
 expr An expression that evaluates to logical. See details.

Details

Right now the subsetting creates an intermediate logical vector, which can be very large.

Value

Subsetted behavior table.

Examples

```
# Not exported
```

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