

Package: patternator (via r-universe)

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Type Package

Title Feature Extraction from Female Brown Anole Lizard Dorsal Patterns

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Author Seong Hyun Hwang, Rachel Myoung Moon

Maintainer Seong Hyun Hwang <krshh1412@gmail.com>

Description Provides a set of functions to efficiently recognize and clean the continuous dorsal pattern of a female brown anole lizard (*Anolis sagrei*) traced from 'ImageJ', an open platform for scientific image analysis (see <<https://imagej.net>> for more information), and extract common features such as the pattern sinuosity indices, coefficient of variation, and max-min width.

Depends R (>= 3.3.0)

Imports data.table (>= 1.10.0), graphics

Suggests plyr (>= 1.8.0)

License GPL (>= 2)

URL <https://github.com/stathwang/patternator>

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LazyData true

RoxygenNote 6.0.1

NeedsCompilation no

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

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anole	<i>Dorsal pattern image of a female brown anole lizard</i>
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Description

A sample dorsal pattern pixel image of a female brown anole lizard traced from the ImageJ software.

Usage

anole

Format

A data.table with 1675 rows and 2 variables:

x x-coordinate of a pixel

y y-coordinate of a pixel

References

Moon and Kamath (2016), Examining the Ecological, Morphological, and Behavioral Correlates of Dorsal Pattern Variations in Female Brown Anole Lizards (*Anolis sagrei*).

clean_patterns	<i>Automatically recognize, clean and label the pixels of a dorsal pattern image traced from ImageJ</i>
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Description

The function clean_patterns implements a k-means clustering-based automatic cleaning of the continuous dorsal pattern of a female brown anole lizard traced from the ImageJ software.

Usage

```
clean_patterns(data, kmeans = TRUE, seed = 123, outliers = TRUE)
```

Arguments

data	a data.table or data.frame: an input data should have two columns x and y in that order, indicating the x-coordinates and the y-coordinates, respectively. The columns should be of type "numeric".
kmeans	logical, whether to use k-means clustering to eliminate a reference pixel, if any. Defaults to TRUE. See the details below.
seed	a single value, interpreted as an integer with the default set to 123.
outliers	logical, whether to eliminate potential outliers in the x-coordinate even after removing the 1cm reference line with k-means clustering. Defaults to TRUE.

Details

clean_patterns implements a k-means clustering-based automatic cleaning of the continuous dorsal pattern of a female brown anole lizard, *Anolis sagrei*, traced from ImageJ, an open source image processing program designed for scientific multidimensional images. The function efficiently

- eliminates the 1cm reference pixel and possible outliers in the x direction,
- randomly chooses a mid-dorsal axis if there exist more than one,
- chooses the largest x-coordinate if multiple x-coordinates are given per y-coordinate,
- manages left or right dorsal pattern that heavily crosses over the mid-dorsal axis by first removing the mid-dorsal axis and then regrouping left and right pattern,
- removes pixels through which left or right pattern crosses over since empirically it has little impact on the values of the extracted features, see extract_features function,
- handles left or right dorsal pattern broken with a gap

Value

Returns a data.table object with the following three columns:

x, y the xy-coordinate of a pixel; type "numeric"

loc the location label of a pixel, one of LEFT, RIGHT, MID; type "character"

Author(s)

Seong Hyun Hwang, Rachel Myoung Moon

Examples

```
# load the sample dorsal pattern image
data(anole)

# plot of the pattern shows it contains the reference pixel
plot(anole$x, anole$y)

# remove the reference pixel, possible outliers and ambiguities
cleaned <- clean_patterns(anole)

# check the plot again
```

```
plot(cleaned$x, cleaned$y)
```

extract_features	<i>Extract quantitative features from the continuous dorsal pattern of a female brown anole lizard</i>
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Description

The function `extract_features` efficiently extracts various features such as the pattern sinuosity indices, coefficient of variation, and max-min width from the output of `clean_patterns`.

Usage

```
extract_features(data)
```

Arguments

<code>data</code>	a <code>data.table</code> or <code>data.frame</code> object with three columns <code>x</code> , <code>y</code> , and <code>loc</code> in that order, indicating the x-coordinate, the y-coordinate, and the location of a pixel (LEFT, RIGHT, or MID), respectively, preferably from an output of <code>clean_patterns</code> . The xy-coordinates should be of type "numeric", whereas the location should be of type "character" and capitalized.
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Details

`extract_features` efficiently extracts common features from the continuous dorsal pattern of a female brown anole lizard, *Anolis sagrei*, such as the pattern sinuosity indices, coefficient of variation, and max-min width. The input data should either be a `data.table` or `data.frame` object with the columns indicating the xy-coordinates and the location of the pixels.

Value

Returns a `data.table` object with the following columns:

`lt_psi`, `rt_psi` left/right pattern sinuosity index (PSI), computed as lt_len / md_len and rt_len / md_len , respectively

`av_psi` average pattern sinuosity index (PSI), $(ls_ind + rs_ind) / 2$

`lt_pcv`, `rt_pcv` left/right pattern coefficient of variation (PCV), computed by dividing the standard deviation of the distance values between mid-dorsal axis and left/right pattern by the average distance.

`av_pcv` average pattern coefficient of variation (PCV), $(lt_pcv + rt_pcv) / 2$

`max_width`, `min_width` the maximum and the minimum width between the left and the right pattern

`av_width` average width between the left and the right pattern

`pmm` pattern max-min width (PMM), $(max_width - min_width) / av_width$

`pasy` pattern asymmetry index (PASY), computed by first subtracting the distance between mid-dorsal axis and left pattern from the corresponding distance between mid-dorsal axis and right pattern and then taking the average of the resulting differences; the closer to zero it is, the more symmetric the dorsal pattern is on average

`lt_len`, `rt_len`, `md_len` the length (the count of pixels) of the left pattern, the right pattern, and the mid-dorsal axis, respectively

Author(s)

Seong Hyun Hwang, Rachel Myoung Moon

Examples

```
# load the sample dorsal pattern image
data(anole)

# clean the dorsal pattern and extract quantitative features
features <- extract_features(clean_patterns(anole))
```

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