Package ‘patternator’

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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

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**anole**

*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*).

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**clean_patterns**

*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  

Extract quantitative features from the continuous dorsal pattern of a female brown anole lizard

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

data  a data.table or data.frame object with three columns x, y, and loc 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 clean_patterns. The xy-coordinates should be of type "numeric", whereas the location should be of type "character" and capitalized.

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**

```r
# 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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