Package 'CINID'

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Type Package

Title Curculionidae INstar IDentification

Version 1.3-0

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Description Method for identifying the instar of Curculionid larvae from the observed distribution of the headcapsule size of mature larvae.

License GPL (>= 2.0)

Imports graphics, utils, stats

Collate cinid.table.R cinid.plot.R

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CINID-package   *Package on the Curculionidae INstar IDentification*

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Description

This package provides a function computing the Gaussian distributions of the headcapsule width of the first three larval instars of any given Curculionid species from the observed distribution of headcapsule sizes of mature larvae from the same species.

Any larva of this species is assigned to the most probable instar, only using its own headcapsule width and the size distribution of the last larval instar, i.e. the mature instar, of the considered species.

The regular usage in this package is to use firstly the `cinid.table` function and secondly the `cinid.plot` function.

Author(s)

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References

Merville A., Vallier A., Venner S., Siberchicot A., Fouchet D., Heddi A. and Bel-Venner M.-C. (2014). Determining the instar of a weevil larva (Coleoptera:Curculionidae) using a parsimonious method. European Journal of Entomology. 111(4): 567-573. doi: 10.14411/eje.2014.056

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cinid.plot   *Print the observed distribution and the estimated one*

Description

This function computes a histogram of the observed headcapsule widths and the Gaussian curves of the probability densities of the four larval instars, defined formerly by the `cinid.table` function (you must use `cinid.table` before to use `cinid.plot`).

Usage

```
cinid.plot(cinid.out, breaks = 50, xlab = "Headcapsules width", ylab1 = "Density",
ylab2 = "Number of Larvae", main = "", ...)
```

Arguments

cinid.out	the returned two-sized list by cinid.table function.
breaks	the breakpoints or the number of cells for the histogramm. See 'breaks' in 'hist'. See also 'Details'.
xlab	the X axis label. The default value is 'Headcapsule width'.
ylab1	the left Y axis label. The default value is 'Density'.
ylab2	the right Y axis label. The default value is 'Number of Larvae'.
main	the main title. The field is empty by default.
...	further arguments and graphical parameters passed to 'hist'

Details

The default for 'breaks' is '50' because it is usually the best way to cluster HCW data.

Value

An object of class 'histogram'. See 'hist'.

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See Also

'hist'

Examples

```
data(s.oryzae)
soryzae <- s.oryzae$data
mu4.soryzae <- s.oryzae$mu4
sd4.soryzae <- s.oryzae$sd4

HCW.soryzae <- cinid.table(soryzae, mu4 = mu4.soryzae, sd4 = sd4.soryzae)
HCW.soryzae.plot <- cinid.plot(HCW.soryzae, breaks = 50)
```

| cinid.table | *Compute the larvae instar in an individual and a population approach.* |

Description

This function assigns any larva with a known headcapsule width to the most probable instar among four possible ones in the focused Curculionid species. Estimating the larval instar is achieved by means of two distinct methods so-called "deterministic" and "stochastic", respectively.

Furthermore, from the population of larvae to be assigned to the most probable instar, both mean and standard deviation of the headcapsule width are estimated for each of the four larval instars, together with the relative frequency of the four instars in the original population.

Usage

```
cinid.table(HCW, mu4, sd4, threshold = 0.95, file = NULL, w = c(1, 1, 1, 1))
```

Arguments

HCW	vector of individual HeadCapsule Width (HCW). The measures must be in micrometers. The 'NA' values are dismissed by the function.
mu4	estimated mean of the fourth instar. This parameter must be in micrometers. See 'Details'.
sd4	estimated standard deviation of the fourth instar. This parameter must be in micrometers. See 'Details'.
threshold	determination criterion. The value has to be set between 0.25 and 1. The default criterion is set as 0.95. See 'Details'.
file	a character string giving the name of the file where outputs are recorded. Two files are then created, a first one named file_indiv.txt and a second one named file_pop.txt. The NULL value set by default means that the outputs are not recorded
w	vector of instars' weight. By default, the hypothesis is that each instar has the same weight. If any knowledge about relative abundance of each instar is available, instar's weights can be adapted.

Details

The quality of the estimated mu4 and sd4 passed to the function is not controlled. Therefore, these two values must be estimated from a quite large sample, and on larvae that ideally do not belong to the dataset.

The larval instar is considered to be correctly assigned to an individual whenever the greatest value of the four relative probabilities computed is higher than the threshold. A threshold equal to 0.25 corresponds to a randomly assigned instar. A threshold equal to 0.95 means that the relative probability of the assigned instar must be higher or equal than 0.95.

Value

The returned value is a list of two elements :

indiv	data.frame with eleven values (in column) for each Curculionid individual larva (in row). The columns are the observed headcapsule width (HCW), the larval instar estimated with the deterministic method (instar_determ) and with the stochastic one (instar_stoch), the probability (p) and relative density (rd) to belong to the first, second, third and fourth larval instar.
pop	matrix with six parameters (in row) for the first, second, third, fourth and indetermined larval instar (in column). The rows are the estimated mean (mu) and standard deviation (sd) of the headcapsule width distribution, the number of individuals and frequency estimated with both the deterministic method (N_determin and F_determ) and the stochastic one (N_stoch and F_stoch).

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Examples

```
data(s.oryzae)
soryzae <- s.oryzae$data
mu4.soryzae <- s.oryzae$mu4
sd4.soryzae <- s.oryzae$sd4

HCW.soryzae <- cinid.table(soryzae, mu4 = mu4.soryzae, sd4 = sd4.soryzae)
head(HCW.soryzae$indiv)
HCW.soryzae$pop
```

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s.oryzae   *Data on Sitophilus orizae*

Description

s.oryzae is a list of three elements:

- $data: 97 measures (in micrometers) of the headcapsule width of rice weevil larvae (*Sitophilus orizae*) belonging to any of four possible instars.
- $mu4: the mean headcapsule width (in micrometers) estimated from 40 fourth-instar *S. oryzae* larvae. These 40 larvae doesn't belong to the data set s.oryzae$data as stated previously.
- $sd4: the standard deviation of headcapsule width (in micrometers) estimated from 40 fourth-instar *S. oryzae* larvae. These 40 larvae doesn't belong to the data set s.oryzae$data as stated previously.

Usage

```
data(s.oryzae)
```

Format

The format is a list of three elements:

- $data: a vector of 97 numerical values
- $mu4 : a single numerical value
- $sd4 : a single numerical value

References

Merville A., Vallier A., Venner S., Siberchicot A., Fouchet D., Heddi A. and Bel-Venner M.-C. (2014). Determining the instar of a weevil larva (Coleoptera:Curculionidae) using a parsimonious method. European Journal of Entomology. 111(4): 567-573. doi: 10.14411/eje.2014.056

Examples

```
data(s.oryzae)
hcw <- s.oryzae$data
length(hcw)   # 97
mu4.soryzae <- s.oryzae$mu4   # 589
sd4.soryzae <- s.oryzae$sd4   # 24.43
```

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