

Package ‘correlatedtraits’

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Title Data and Analyses for [paper title]

Version 0.0.0.900

Description A package that contains the data and analyses used for the paper [paper].

Depends R (>= 3.4.0)

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LazyData true

Imports dplyr,
ggplot2,
tidyr

RoxygenNote 6.0.1

R topics documented:

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fit_Bev_Holt	<i>Fit raw beetle data to a Beverton-Holt recruitment curve.</i>
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Description

This code takes data returned from [wrangle_beetle_data](#), fits a Beverton-Holt recruitment curve, plots the resulting curve, and returns relevant parameter values as well as a transformed dataset. `fit_Bev_Holt` transforms the data – which has constant female density but variable bean density – to have constant bean density and variable female density.

Usage

```
fit_Bev_Holt(clean_data, show_plot = TRUE, xmax = 30)
```

Arguments

<code>clean_data</code>	the cleaned and compiled data returned from wrangle_beetle_data .
<code>show_plot</code>	Should the plot be drawn? Default is TRUE.
<code>xmax</code>	The maximum x-axis value for the plot.

Details

The form of the Beverton-Holt equation is taken from Otto and Day (2007):

$$N_{t+1} = \frac{\lambda N_t}{1 + \alpha N_t}$$

Data were originally collected by varying resource density (i.e., number of beans) and keeping female density constant (one female per trial). Thus, fecundity was measured at the following female-to-bean ratios:

$$\frac{1}{1}, \frac{1}{3}, \frac{1}{5}, \frac{1}{10}$$

Assuming the relationship that drives density dependence is this ratio of females-to-beans (and not the absolute number of females or beans), we can re-scale these fractions to yield a common denominator (bean density) among all fecundity trials. For female density F and bean density B , the fraction $\frac{F}{B}$ can be re-scaled to have any denominator by multiplying by some proportion equal to 1:

$$\frac{\rho}{\rho} \times \frac{F}{B} = \frac{F}{B}$$

We can choose a proportion ρ such that the observed bean density B is scaled to some desired bean density, B_{new} :

$$\rho = \frac{\frac{B_{new}}{B}}{\frac{B_{new}}{B}} = 1$$

For example, when $B_{new} = 10$ and $B = 5$, $\rho = 2/2$.

In this analysis $B_{new} = 10$, which gives the following female-to-bean ratios at constant resource densities:

$$\frac{10}{10}, \frac{3.33}{10}, \frac{2}{10}, \frac{1}{10}$$

Value

A plot of the cleaned data and the fitted Beverton-Holt function, the result of the model fit, Beverton-Holt parameters lambda, K, and alpha, and the transformed data set.

References

Otto and Day (2007). A Biologist's Guide to Mathematical Modeling in Ecology and Evolution. Princeton University Press. Page 185.

wrangle_beetle_data	<i>Wrangle raw data into a form amenable to analysis.</i>
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Description

Wrangle raw data into a form amenable to analysis.

Usage

```
wrangle_beetle_data(female_fd_path, female_f_path, male_d_path, dates_path)
```

Arguments

<code>female_fd_path</code>	A string that provides the path to the file that contains data for female fecundity and dispersal.
<code>female_f_path</code>	A string that provides the path to the file that contains data for female fecundity data ONLY. These beetles did not disperse.
<code>male_d_path</code>	A string that provides the path to the file that contains data for male dispersal. This file also contains information on dispersal arrays.
<code>dates_path</code>	A string that provides the path to the file that contains data for mating, dispersal, and freezing dates.

Value

A data frame of all the data, cleaned and compiled.

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