

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 Rcpp

License MIT

LazyData true

Imports dplyr,
ggplot2,
parallel,
rstan,
tidyr

RoxygenNote 6.0.1

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fit_growth	<i>Fit raw beetle data to a specified growth function..</i>
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Description

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

Usage

```
fit_growth(data, show_plot = TRUE, xmax = 30, model)
```

Arguments

<code>data</code>	The cleaned and compiled data returned from <code>wrangle_beetle_data</code> .
<code>show_plot</code>	Should the plot be drawn? Default is TRUE.
<code>xmax</code>	The maximum x-axis value for the plot.
<code>model</code>	Which model should be used to fit the growth data? Currently, either Beverton-Holt or logistic.

Details

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

$$N_{t+1} = \frac{R_0 N_t}{1 + \alpha N_t}$$

The logistic equation uses the discrete-time logistic formula:

$$N_{t+1} = N_t + N_t r_d \left(1 - \frac{N_t}{K}\right)$$

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:

$$\frac{10}{10}, \frac{3.\overline{33}}{10}, \frac{2}{10}, \frac{1}{10}$$

Value

A plot of the cleaned data and the fitted growth function, the result of the model fit, parameter estimates for the growth rate, carrying capacity, and any other model parameters, 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.
- Gotelli (2001). A Primer of Ecology, Third Edition. Sinauer Associates, Inc. Page 35.

stan_data	<i>a function to transform clean_data into a form that can be passed to Stan.</i>
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Description

a function to transform clean_data into a form that can be passed to Stan.

Usage

```
stan_data(data)
```

test_kernel_fits	<i>Test multiple kernel fits to dispersal data.</i>
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Description

test_kernel_fits takes output from [wrangle_beetle_data](#) and runs tests to determine the best-fitting dispersal kernel for all beetles as a whole, for females independently, and for males independently. The following kernels are tested: the Poisson distribution ([Poisson](#)), the negative binomial distribution ([NegBinomial](#)), the Sichel distribution ([SICHEL](#)), and the Poisson Inverse Gaussian distribution (a special case of the Sichel distribution where $\nu = -0.5$).

Usage

```
test_kernel_fits(clean_data)
```

Value

A list of lists. Each top-level list (\$all, \$females, or \$males) contains the following objects:

- \$dist - A vector of the distances that were measured for each individual in the data subset.
- \$x - A vector of patch distances relevant to the study ($x = 0:40$).
- \$AIC - An AIC table ranking each distribution by its AIC score when fit to the data in \$dist.
- \$frequency - The frequency of each distance measured in \$dist, measured over the patches in \$x.
- \$plot - A [ggplot](#) object showing the data in \$frequency along with the best-fit plot of each candidate distribution.
- \$<distribution> - The results of maximum-likelihood fits of each distribution to the data in \$dist, where <distribution> is either poisson, nbinom, pig, or sichel. The structure of these results exactly follows the output from [optim](#). For example, to get parameter estimates for fits to the Poisson distribution, using data from female beetles, use output\$females\$poisson\$par.
- \$<distribution>\$fit - The mass density function for a given distribution over \$x (i.e., the line drawn in \$plot).

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

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