# Package 'correlatedtraits'

May 19, 2017

**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)

**License** MIT

**LazyData** true

**Imports** dplyr,
    ggplot2,
    tidyr

**RoxygenNote** 6.0.1

## R topics documented:

---

fit_Bev_Holt                *Fit raw beetle data to a Beverton-Holt recruitment curve.*

---

### Description

This code takes data returned from `wrangle_beetle_data`, fits a Beverton-Holt recruitement 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)
```

1

## Arguments

| | |
|---|---|
| `clean_data` | The cleaned and compiled data returned from `wrangle_beetle_data`. |
| `show_plot` | Should the plot be drawn? Default is `TRUE`. |
| `xmax` | 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 $\rho$ 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 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.

---

test_kernel_fits         *Test multiple kernel fits to dispersal data.*

---

### 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)
```

### Arguments

clean_data        The cleaned and compiled data returned from wrangle_beetle_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 $dist, where <distribution> is either poisson, nbinom, pig, or sichel. The structure of these results exaclty follows the output from optim. For example, to get parameter estimates for fits to the Poisson distribution, using data from female beetles, use output$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       *Wrangle raw data into a form amenable to analysis.*

---

### 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 disperal. 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.

# Index