Package 'gauseR'

July 22, 2025

Title Lotka-Volterra Models for Gause's 'Struggle for Existence'

Version 1.3

Description A collection of tools and data for analyzing the Gause microcosm experiments, and for fitting Lotka-Volterra models to time series data. Includes methods for fitting single-species logistic growth, and multi-species interaction models, e.g. of competition, predator/prey relationships, or mutualism. See documentation for individual functions for examples. In general, see the lv_optim() function for examples of how to fit parameter values in multi-species systems. Note that the general methods applied here, as well as the form of the differential equations that we use, are described in detail in the Quantitative Ecology textbook by Lehman et al., available at <http://hdl.handle.net/11299/204551>, and in Lina K. Mühlbauer, Maximilienne Schulze, W. Stanley Harpole, and Adam T. Clark. 'gauseR': Simple methods for fitting Lotka-Volterra models describing Gause's 'Struggle for Existence' in the journal Ecology and Evolution.

Imports deSolve, stats, graphics

Suggests knitr, rmarkdown

VignetteBuilder knitr

License GPL-3

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NeedsCompilation no

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Depends R (>= 3.5.0)

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Contents

`gause_1931_AmN_f01` *Growth of population of the flour beetle Tribolium confusum in 16 and 64 grams of flour*

Description

A dataset containing the abundance of Tribolium confusum, grown in monoculture with different quantities of food (flour). Gause's goal was to determine the influence of ecological factors on population growth.

Usage

```
gause_1931_AmN_f01
```

Format

A data frame with 18 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Tribolium confusum

Time Day of experiment

Individuals Number of Individuals

Treatment Treatments:16 and 64g flour per starting beetle pair

Source

Gause (1931) The influence of ecological factors on the size of population. The American Naturalist 65:696, 70-76

`gause_1931_AmN_f02` *The influence of quantity of food on the asymptotic population of Triboliurn confusum.*

Description

A dataset containing the population size of Tribolium confusum at the upper asymptote, as a characteristic for the population beeing in equilibrium, under different quantities of food (flour). Gause's goal was to determine the influence of ecological factors on population growth.

Usage

```
gause_1931_AmN_f02
```

Format

A data frame with 4 rows and 5 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Tribolium confusum

Individuals Number of Individuals at population equlibrium

Treatment Treatments:16, 32, 64 and 128g flour per starting beetle pair

Source

Gause (1931) The influence of ecological factors on the size of population. The American Naturalist 65:696, 70-76

`gause_1931_AmN_f03` *The influence of temperature on the asymptotic population of Moina macrocopa.*

Description

A dataset containing the population size of Moina macrocopa at the upper asymptote, as a characteristic for the population beeing in equilibrium, under different temperatures. Gause's goal was to determine the influence of ecological factors on population growth.

Usage

```
gause_1931_AmN_f03
```

Format

A data frame with 3 rows and 5 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Tribolium confusum

Individuals Number of Individuals at population equlibrium

Treatment Treatments:20, 25 and 35 degrees Celcius

Source

Gause (1931) The influence of ecological factors on the size of population. The American Naturalist 65:696, 70-76

`gause_1932_QR_t05` *The influence of temperature on the growth of the yeast Saccharomyces cerevisiae*

Description

A dataset containing the abundance of Saccharomyces cerevisiae, grown in different temperatures (5.7 to 41 degrees C). The Volume is measured in "Amount of yeast", which refers to a standardized index, based on the alcohol production per Unit of Yeast.

Usage

```
gause_1932_QR_t05
```

Format

A data frame with 102 rows and 7 variables:

Paper Paper from which data are drawn

Table Table number in paper

Experiment Number of series: 1,2 or 3

Species Name of Species: Saccharomyces cerevisiae

Time Hour of experiment

Volume "Amount of Yeast" of Species

Treatment Treatments: Temperatures (5.7 to 41 degrees C)

Source

Gause (1932) Ecology of Populations. The Quarterly Review of Biology 7, vol. 1, pp. 27-46

`gause_1934_book_app_t01`

Raw data on the abundances and volumes of Saccharomyces cerevisiae and Schizosaccharomyces kephir

---

Description

A dataset containing the abundances (number of cells) and volumes of Saccharomyces cerevisiae and Schizosaccharomyces kephir grown in monoculture and in mixture. The data for two experiments with differnet time periods is reported.

Usage

```
gause_1934_book_app_t01
```

Format

A data frame with 60 rows and 10 variables:

Paper Paper from which data are drawn

Table Table number in paper

Experiment Number of experiment: 1 or 2

Species Name of Species: Saccharomyces cerevisiae and Schizosaccharomyces kephir

Time Day of experiment

Volume_Species Volume of yeast species in the mixture, estimated from counted cells

Squares Number of Squares counted

Individuals_Square Average Number of cells per Square

Volume_Total Total volume of yeast

Treatment Treatments: Monoculture and Mixture

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_app_t02` *Alcohol production of Saccharomyces cerevisiae and Schizosaccharomyces kephir*

Description

A dataset containing the alcohol production of Saccharomyces cerevisiae and Schizosaccharomyces kephir cultivated under anaerobic and aerobic conditions, in percent and per unit of yeast volume.

Usage

```
gause_1934_book_app_t02
```

Format

A data frame with 28 rows and 7 variables:

Paper Paper from which data are drawn

Table Table number in paper

Species Name of Species: Saccharomyces cerevisiae, Schizosaccharomyces kephir

Time Hour of experiment

Alcohol Alcohol production in percent

Alcohol.Yeast_Volume Alcohol production per unit of yeast volume

Treatment Treatments: Anaerobic and Aerobic

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_app_t03` *Raw data of Paramecium caudatum and Paramecium aurelia grown in Monoculture and Mixture*

Description

A dataset containing the mean abundances of Paramecium caudatum and Paramecium aurelia, grown in mixture and monoculture. This dataset contains the mean abundances of three experiments. Note, that for day 20, single values are missing and only the mean is reported.

Usage

```
gause_1934_book_app_t03
```

Format

A data frame with 104 rows and 6 variables:

Paper Paper from which data are drawn

Table Table number in paper

Species Name of Species: Paramecium caudatum and Paramecium aurelia

Time Day of experiment

Individuals Number of Individuals

Treatment Treatments: Monoculture and Mixture

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_app_t04` *Raw data of Paramecium caudatum and Paramecium aurelia grown on different media*

Description

A dataset containing the abundance of Paramecium caudatum and Paramecium aurelia, grown in monoculture and in mixture on buffered medium with high wild bacteria concentration ("one loop" medium) and low wild bacteria concentration ("half loop" medium). The number of individuals is reported for monoculture and the number of individuals of the species in the mixture.

Usage

```
gause_1934_book_app_t04
```

Format

A data frame with 68 rows and 7 variables:

Paper Paper from which data are drawn

Table Table number in paper

Species Name of Species: Paramecium caudatum and Paramecium aurelia

Time Day of experiment

Individuals Number of Individuals

Individuals_Mixture Number of Individuals per Species in Mixture

Treatment Treatments: One Loop and Half Loop

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_app_t05`

Raw data of Stylonychia pustulata in monoculture and mixture with and Paramecium aurelia and P. caudatum

---

Description

A dataset containing the abundances of Stylonychia pustulata grown in monoculture and mixture with P. aurelia and P. caudatum and the abundances of P. aurelia and P. caudautum in this mixtures on the medium of Osterhout. This dataset contains the raw data of three different experiments: Stylonychia pustulata grown in monoculture, in mixture with P.aurelia and in mixture wit P.caudatum. The abundances of three to five cultures per experiment and the calculated mean abundances of the experiments are reported. Note, that for day 20 - 25, single values are missing and only the mean is reported.

Usage

```
gause_1934_book_app_t05
```

Format

A data frame with 575 rows and 8 variables:

Paper Paper from which data are drawn

Table Table number in paper

Time Day of experiment

Experiment Number of experiment: 1,2 or 3

Culture Number of culture: 1,2,3,4,5 or Mean

Species Name of Species: Stylonychia pustulata, Paramecium caudatum and Paramecium aurelia

Individuals Number of Individuals

Treatment Treatments: Monoculture and Mixture P.aurelia and Mixture P.caudatum

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f04` *Growth of Paramecium caudatum*

Description

A dataset containing the growth in abundance of Paramecium caudatum over six days.

Usage

`gause_1934_book_f04`

Format

A data frame with 8 rows and 5 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Paramecium caudatum

Time Day of experiment

Individuals Number of Individuals

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f09` *Growth of Saccharomyces cerevisiae*

Description

A dataset containing the growth in volume of Saccharomyces cerevisiae under anaerobic conditions. The Volume is measured in "Amount of yeast", which refers to a standardized index, based on the alcohol production per Unit of Yeast.

Usage

`gause_1934_book_f09`

Format

A data frame with 9 rows and 5 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Saccharomyces cerevisiae

Time Hour of experiment

Volume "Amount of Yeast" of Species

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f10` *Growth of Saccharomyces cerevisiae with medium change*

Description

A dataset containing the abundance of Saccharomyces cerevisiae cultivated in monoculture with a medium change in different time periods under anaerobic conditions. The Number of Individuals is measured in Number of cells per 1/250 mm3.

Usage

```
gause_1934_book_f10
```

Format

A data frame with 29 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Saccharomyces cerevisiae

Time Hour of experiment

Individuals Number of cells per 1/250 mm3

Treatment Treatments: medium change every 3, 12, 24 hours and control

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f11` *Gause Yeast Data*

Description

A dataset containing yeast volume and alcohol concentration for two replicates of S. cerevisiae grown in monoculture.

Usage

```
gause_1934_book_f11
```

Format

A data frame with 11 rows and 7 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Species name

Time Experiment time in hours

Alcohol_Percent Alcohol concentration, in percent

Yeast_Volume Yeast volume, listed in papers as 'amount'

Treatment Experiment replicate, under two 'somewhat different' growth medium concentrations

Source

Huffaker (1958) Experimental Studies on Predation: Dispersion Factors and Predator-Prey Oscillations. Hilgardia 27: 343-83.

`gause_1934_book_f12` *Growth of Saccharomyces cerevisiae with additional alcohol*

Description

A dataset containing the growth in volume of Saccharomyces cerevisiae cultivated under anaerobic conditions with added alcohol.Gause measured the effect of alcohol on reaching a saturated population. The saturation is measured in percent of the satured population grown without additional alcohol.

Usage

```
gause_1934_book_f12
```

Format

A data frame with 6 rows and 5 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Saccharomyces cerevisiae

Alcohol Additional alcohol in percent

Population Percentage of saturated population reached

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f13` *Growth of Saccharomyces cerevisiae and Schizosaccaromyces kephir in mixed population*

Description

A dataset containing the the growth in volume of Saccharomyces cerevisiae and Schizosaccaromyces kephir cultivated in the mixed population (two series of experiments) under anaerobic conditions. Gause also measured the volume of the mixed population. The Volume is measured in "Amount of yeast", which refers to a standardized index, based on the alcohol production per Unit of Yeast.

Usage

```
gause_1934_book_f13
```

Format

A data frame with 47 rows and 5 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Saccharomyces cerevisiae, Schizosaccaromyces kephi and Mixed Population

Time Hour of experiment

Volume "Amount of Yeast" of Species

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f14` *Growth of Saccharomyces cerevisiae in mixed population*

Description

A dataset containing the the growth in volume of Saccharomyces cerevisiae cultivated separately and in the mixed population (two series of experiments) with Schizosaccaromyces kephir under anaerobic conditions. The Volume is measured in "Amount of yeast", which refers to a standardized index, based on the alcohol production per Unit of Yeast.

Usage

```
gause_1934_book_f14
```

Format

A data frame with 32 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Saccharomyces cerevisiae

Time Hour of experiment

Volume "Amount of Yeast" of Species

Treatment Treatments: Monoculture and Mixture

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f15` *Growth of Schizosaccaromyces kephir in mixed population - anaerobic*

Description

A dataset containing the the growth in volume of Schizosaccaromyces kephir cultivated separately and in the mixed population (two series of experiments) with Saccharomyces cerevisiae under anaerobic conditions. The Volume is measured in "Amount of yeast", which refers to a standardized index, based on the alcohol production per Unit of Yeast.

Usage

```
gause_1934_book_f15
```

Format

A data frame with 24 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Schizosaccaromyces kephir

Time Hour of experiment

Volume "Amount of Yeast" of Species

Treatment Treatments: Monoculture and Mixture

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f16` *Growth of Schizosaccaromyces kephir and Saccharomyces cerevisiae in mixed population -aerobic*

Description

A dataset containing the the growth in volume of Schizosaccaromyces kephir cultivated separately and in the mixed population with Saccharomyces cerevisiae under aerobic conditions. The Volume is measured in "Amount of yeast", which refers to a standardized index, based on the alcohol production per Unit of Yeast.

Usage

`gause_1934_book_f16`

Format

A data frame with 27 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Schizosaccaromyces kephir, Saccharomyces cerevisiae and Total_Yeast

Time Hour of experiment

Volume "Amount of Yeast" of Species

Treatment Treatments: Monoculture and Mixture

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f18` *Growth of Paramecium caudatum and Stylonychia mytilis in Mixture*

Description

A dataset containing the abundance of Paramecium caudatum and Stylonychia mytilis, grown in monoculture and in mixture on buffered medium without wild bacteria.

Usage

`gause_1934_book_f18`

Format

A data frame with 28 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Paramecium caudatum and Stylonychia mytilis

Time Day of experiment

Individuals Number of Individuals

Treatment Treatments: Monoculture and Mixture

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f19` *Growth of Paramecium caudatum and Stylonychia mytilis in Mixture with Wild bacteria*

Description

A dataset containing the abundance of Paramecium caudatum and Stylonychia mytilis, grown in monoculture and in mixture on buffered medium containing wild bacteria.

Usage

```
gause_1934_book_f19
```

Format

A data frame with 17 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Paramecium caudatum and Stylonychia mytilis

Time Day of experiment

Individuals Number of Individuals

Treatment Treatments: Monoculture and Mixture

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f21` *Growth of Paramecium caudatum and Paramecium aurelia in Monoculture*

Description

A dataset containing the abundances and the volume of Paramecium caudatum and Paramecium aurelia, to determine the differences in reaching the saturating population regarding Volume and Number of individuals. "Volume" refers to a standardized index, meant to make the abundances of species comparable based on their relative sizes.

Usage

```
gause_1934_book_f21
```

Format

A data frame with 87 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Paramecium caudatum and Paramecium aurelia

Time Day of experiment

Volume "Volume" of Species

Individuals Number of Individuals

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f22` *Paramecium competition experiment*

Description

A dataset containing the abundances of two Paramecium species grown in monoculture and mixture. Note, is for the same experiment as gause_1934_science_f02_03, except that data were digitized separately, and therefore have small variations. These might be useful for estimating observation error in the data digitization process. "Volume" refers to a standardized index, meant to make the abundances of species comparable based on their relative sizes.

Usage

```
gause_1934_book_f22
```

Format

A data frame with 72 rows and 4 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Day Day of experiment

Species1 Name of Species 1

Volume_Species1 Volume of Paramecium caudatum

Species2 Name of Species 2

Volume_Species2 Volume of Paramecium aurelia

Treatment Treatments: Pa and Pc moncultures, or mixture

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f23` *Growth of Paramecium caudatum and Paramecium aurelia with wild bacteria*

Description

A dataset containing the volume of Paramecium caudatum and Paramecium aurelia, grown in monoculture on buffered medium with two different wild bacteria concentrations ("one" and "half loop"). "Volume" refers to a standardized index, meant to make the abundances of species comparable based on their relative sizes.

Usage

```
gause_1934_book_f23
```

Format

A data frame with 61 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Paramecium caudatum and Paramecium aurelia

Time Day of experiment

Volume "Volume" of Species

Treatment Treatments: One Loop and Half Loop

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f24` *Growth of Paramecium caudatum and Paramecium aurelia in Mixture on Half Loop Medium*

Description

A dataset containing the volume of Paramecium caudatum and Paramecium aurelia, grown in monoculture and in mixture on buffered medium with low wild bacteria concentration ("half loop" medium). "Volume" refers to a standardized index, meant to make the abundances of species comparable based on their relative sizes.

Usage

`gause_1934_book_f24`

Format

A data frame with 56 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Paramecium caudatum and Paramecium aurelia

Time Day of experiment

Volume "Volume" of Species

Treatment Treatments: Monoculture and Mixture

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f25` *Growth of Paramecium caudatum and Paramecium aurelia in Mixture on One Loop Medium*

Description

A dataset containing the volume of Paramecium caudatum and Paramecium aurelia, grown in monoculture and in mixture on buffered medium with high wild bacteria concentration ("one loop" medium). "Volume" refers to a standardized index, meant to make the abundances of species comparable based on their relative sizes.

Usage

`gause_1934_book_f25`

Format

A data frame with 57 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Paramecium caudatum and Paramecium aurelia

Time Day of experiment

Volume "Volume" of Species

Treatment Treatments: Monoculture and Mixture

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f26` *Growth of Stylorzychia pustulata in Monoculture and in Mixture*

Description

A dataset containing the abundances of Stylorzychia pustulata cultivated separately, and in the mixed populations with Paramecium caudatum and Paramecium aurelia and the abundances of P. caudatum and P. aurelia grown in mixture with S. pustulata.

Usage

```
gause_1934_book_f26
```

Format

A data frame with 104 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species:Paramecium caudatum, Paramecium aurelia and Stylorzychia pustulata

Time Day of experiment

Individuals Number of Individuals

Treatment Treatments: Monoculture and Mixture(with Species)

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f28` *Elementary interaction between Didinium nasutum and Paramecium caudatum*

Description

A dataset containing the abundances of Paramecium caudatum and Didinium nasutum grown in mixture. Didinium was introduced at day two. "Individuals" refers to the number of individuals pro 0.5 c.c..

Usage

```
gause_1934_book_f28
```

Format

A data frame with 12 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Paramecium caudatum and Didinium nasutum

Time Day of experiment

Individuals Number of Individuals

Treatment Treatments: Monoculture and Mixture

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f29` *Paramecium/Didinium predator-prey experiment*

Description

A dataset containing the abundances of Paramecium caudatum and Didinium nasutum grown in mixture. Didinium was introduced at different days. "Volume" refers to a standardized index, meant to make the abundances of species comparable based on their relative sizes.

Usage

```
gause_1934_book_f29
```

Format

A data frame with 62 rows and 7 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Name of Species: Didinium nasutum and Paramecium caudatum

Time Day of experiment

Volume Volume of Didinium

Individuals Number of Individuals

Treatment Treatments: D. nasutum introduced after 0, 24, 36 and 48 hrs

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f30` *The elementary interaction between Didinium nasutum and Paramecium caudatum*

Description

A dataset containing the abundances of Didinium nasutum and Paramecium caudatum grown in mixture on the medium of Osterhout.

Usage

```
gause_1934_book_f30
```

Format

A data frame with 16 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Time Day of experiment

Species Name of Species: Didinium nasutum and Paramecium caudatum

Individuals Number of Individuals

Treatment Treatment: Osterhout medium

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f31` *The interaction between Didinium nasutum and Paramecium caudatum on oat medium*

Description

A dataset containing the abundances of Didinium nasutum and Paramecium caudatum grown in mixture on oat medium with sediment.

Usage

```
gause_1934_book_f31
```

Format

A data frame with 12 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Time Day of experiment

Species Name of Species: Didinium nasutum and Paramecium caudatum

Individuals Number of Individuals

Treatment Treatment: Oat medium

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f32` *Didinium/Paramecium predator/prey experiment*

Description

A dataset containing the abundances of Paramecium caudatum and Didinium nasutum grown in mixture. Note, is for the same experiment as gause_1934_science_f01, except that data were digitized separately, and therefore have small variations. These might be useful for estimating observation error in the data digitization process.

Usage

```
gause_1934_book_f32
```

Format

A data frame with 17 rows and 8 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Day Day of experiment

Prey Name of Prey Species

Individuals_Prey Number of Prey Individuals

Predator Name of Predator Species

Individuals_Predator Number of Predator Individuals

Immigration Is immigration occurring in this time-step? (yes or no)

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_book_f39.1` *The interaction between Paramecium bursaria and Schizosaccharomyces pombe*

Description

A dataset containing the abundances of Paramecium bursaria and Schizosaccharomyces pombe grown in mixture.

Usage

```
gause_1934_book_f39.1
```

Format

A data frame with 36 rows and 5 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Time Day of experiment

Species Name of Species: Paramecium bursaria and Schizosaccharomyces pombe

Individuals Number of Individuals

Source

Gause (1934) The Struggle for Existence. Dover Publications; Reprint edition.

`gause_1934_science_f01`

Didinium/Paramecium predator/prey experiment

Description

A dataset containing the abundances of Paramecium caudatum and Didinium nasutum grown in mixture. Note, is for the same experiment as gause_1934_book_f32, except that data were digitized separately, and therefore have small variations. These might be useful for estimating observation error in the data digitization process.

Usage

`gause_1934_science_f01`

Format

A data frame with 17 rows and 3 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Day Day of experiment

Prey Name of Prey Species

Individuals_Prey Number of Prey Individuals

Predator Name of Predator Species

Individuals_Predator Number of Predator Individuals

Immigration Is immigration occurring in this time-step? (yes or no)

Source

Gause (1934) Experimental Analysis of Vito Volterra's Mathematical Theory of the Struggle for Existence. Science 79:16-17.

`gause_1934_science_f02_03`

Paramecium competition experiment

Description

A dataset containing the abundances of two Paramecium species grown in monoculture and mixture. Note, is for the same experiment as gause_book_1934_f22, except that data were digitized separately, and therefore have small variations. These might be useful for estimating observation error in the data digitization process. "Volume" refers to a standardized index, meant to make the abundances of species comparable based on their relative sizes.

Usage

```
gause_1934_science_f02_03
```

Format

A data frame with 63 rows and 4 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Day Day of experiment

Species1 Name of Species 1

Volume_Species1 Volume of Paramecium caudatum

Species2 Name of Species 2

Volume_Species2 Volume of Paramecium aurelia

Treatment Treatments: Pa and Pc moncultures, or mixture

Source

Gause (1934) Experimental Analysis of Vito Volterra's Mathematical Theory of the Struggle for Existence. Science 79:16-17.

`gause_1936_AnE_f01` *Interaction between predators (Cheyletus eruditus) and prey (Aleuiroglyphus agilis) on millet, wheat flour and a mixture of these substances.*

Description

A dataset containing the abundance of Cheyletus eruditus and Aleuiroglyphus agilis, as apredator-prey system under different food conditions for the prey (wheat and millet). Gause's goal was to determine the influence of ecological factors on predator-prey dynamics. The number of individuals is reported as Individuals per 0.2 g prey food.

Usage

```
gause_1936_AnE_f01
```

Format

A data frame with 34 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Time Day of experiment

Species Name of Species: Cheyletus eruditus and Aleuiroglyphus agilis

Individuals Number of Individuals per 0.2 g

Treatment Treatments: Wheat, Millet, Wheat+Millet

Source

Gause (1936) Further Studies of Interaction between Predators and Prey. Journal of Animal Ecology, vol. 5, pp. 1-18.

`gause_1936_AnE_f03.1` *Interaction between predators (Cheyletus eruditus) and prey (Aleuroglyphus agilis) with occasional immigration*

Description

A dataset containing the abundance of Cheyletus eruditus and Aleuiroglyphus agilis, as apredator-prey system with an occasional immigration of the prey on the 63rd day. The number of individuals is reported as Individuals per 0.2 g prey food. Wheat flour was used as food.

Usage

```
gause_1936_AnE_f03.1
```

Format

A data frame with 22 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Time Day of experiment

Species Name of Species: Cheyletus eruditus and Aleuiroglyphus agilis

Individuals Number of Individuals per 0.2 g

Treatment Treatments: Immigration or NA

Source

Gause (1936) Further Studies of Interaction between Predators and Prey. Journal of Animal Ecology, vol. 5, pp. 1-18.

`gause_1936_AnE_f03.3a` *Interaction between predators (Cheyletus eruditus) and prey (Aleuroglyphus agilis) with artifical immigration*

Description

A dataset containing the abundance of Cheyletus eruditus and Aleuiroglyphus agilis, as apredator-prey system with an artificial everyday immigration of predator and prey . The number of individuals is reported as Individuals per 0.2 g prey food. Wheat flour was used as food.

Usage

`gause_1936_AnE_f03.3a`

Format

A data frame with 24 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Time Day of experiment

Species Name of Species: Cheyletus eruditus and Aleuiroglyphus agilis

Individuals Number of Individuals per 0.2 g

Treatment Treatment: Immigration

Source

Gause (1936) Further Studies of Interaction between Predators and Prey. Journal of Animal Ecology, vol. 5, pp. 1-18.

`gause_1936_AnE_f03.3b` *Interaction between predators (Cheyletus eruditus) and prey (Aleuroglyphus agilis) with artifical immigration*

Description

A dataset containing the abundance of Cheyletus eruditus and Aleuiroglyphus agilis, as apredator-prey system with an artificial immigration of predator and prey every 8th day. The number of individuals is reported as Individuals per 0.2 g prey food. Wheat flour was used as food.

Usage

`gause_1936_AnE_f03.3b`

Format

A data frame with 26 rows and 6 variables:

Paper Paper from which data are drawn
Figure Figure number in paper
Time Day of experiment
Species Name of Species: Cheyletus eruditus and Aleuiroglyphus agilis
Individuals Number of Individuals per 0.2 g
Treatment Treatment: Immigration

Source

Gause (1936) Further Studies of Interaction between Predators and Prey. Journal of Animal Ecology, vol. 5, pp. 1-18.

`gause_1936_AnE_t02` *Interaction between predators (Cheyletus eruditus) and prey (Aleuroglyphus agilis)-Raw data*

Description

A dataset containing the abundance of Cheyletus eruditus and Aleuiroglyphus agilis, as a predator-prey system on semoletta and wheat flour. A fraction at the beginning of each experiment shows the initial relation between predators and prey; e.g. 10/5 means 10 prey and 5 predators (reported in variable "Treatment"). Dataset includes age structured population abundances. The number of individuals is reported as Individuals per 0.2 g prey food. Wheat flour was used as food.

Usage

```
gause_1936_AnE_t02
```

Format

A data frame with 191 rows and 12 variables:

Paper Paper from which data are drawn
Table Table number in paper
Time Day of experiment
Species Name of Species: Cheyletus eruditus and Aleuiroglyphus agilis
Total_Individuals Number of all Individuals of Species per 0.2 g
Female Number of female individuals per 0.2 g
Male Number of male individuals per 0.2 g
Imago Number of adult Individuals per 0.2 g
Hexapod Number of hexapod larvae stage Individuals per 0.2 g
Octapod Number of octapod larvae stage Individuals per 0.2 g
Initial_Fraction Initial Number of prey/predator
Treatment Treatments: Wheat and Semoletta

Source

Gause (1936) Further Studies of Interaction between Predators and Prey. Journal of Animal Ecology, vol. 5, pp. 1-18.

`gause_1936_AnE_t03` *Interaction between predators (Paramecium bursaria) and prey (Saccharomyces exiguus)*

Description

A dataset containing the abundance of Paramecium bursaria and Saccharomyces exiguus, as a predator-prey system. The primary difference among experimental replicates is the initial abundance of the two species. The number of individuals is reported as Individuals per 0.5 cm3 for Paramecium, and as number of individuals per 0.1 cm3 for Saccharomyces.

Usage

```
gause_1936_AnE_t03
```

Format

A data frame with 266 rows and 6 variables:

Paper Paper from which data are drawn

Table Table number in paper

Experiment Experimental replicate number

Time Day of experiment

Species Name of Species: Cheyletus eruditus and Aleuiroglyphus agilis

Individuals Number of all Individuals of Species per 0.2 g

Source

Gause (1936) Further Studies of Interaction between Predators and Prey. Journal of Animal Ecology, vol. 5, pp. 1-18.

`gause_wrapper` *Automated wrapper for Gause fitting functions*

Description

Automatically runs routine for finding starting values and optimal parameter values for a Lotka-Volterra interaction system. Using the default functions, species dynamics follow the form dni/dt = ni * (ri + aii * ni + sum_j(aij * nj)) where ri are the elements of vector r, and aij are the elements of matrix A.

Usage

```
gause_wrapper(
  time,
  species,
  N_starting = NULL,
  r_starting = NULL,
  A_starting = NULL,
  doplot = TRUE,
  keeptimes = FALSE,
  parm_signs = NULL,
  doopt = TRUE,
  ...
)
```

Arguments

`time`	Vector of time steps corresponding to observations in species data.frame.
`species`	A data.frame with one column per species to be fitted. Note - column names cannot include white spaces or non-standard special characters.
`N_starting`	Optional starting values for initial abundances.
`r_starting`	Optional starting values for species growth rates. If a value is set to zero, it #forces that parameter to zero in the fitting. Values of NA are ignored. Defaults to NULL (no starting values).
`A_starting`	Optional starting values for species interaction coefficients. If a value is set to zero, it #forces that parameter to zero in the fitting. Values of NA are ignored. Defaults to NULL (no starting values).
`doplot`	Logical. Should the resulting model be plotted? Defaults to TRUE.
`keeptimes`	Should predictions be given for the points in the "time" vector, or for a list of 100 evenly spaced time points? Defaults to FALSE.
`parm_signs`	Optional variable specifying signs for parameters. Defaults to NULL (automatically selected).
`doopt`	Should optimizer be used (if TRUE), or should the initial linearized estimates by applied (if FALSE)? Defaults to TRUE.
`...`	Optional additional arguments to be passed to ode and optim functions.

Value

A list with simulated time series (out), paramter estimates (parameter_intervals), optimizer output (optout), and raw data used for fitting (rawdata).

Examples

```
#load competition data
data("gause_1934_science_f02_03")

#subset out data from species grown in mixture
mixturedat<-gause_1934_science_f02_03[gause_1934_science_f02_03$Treatment=="Mixture",]

#extract time and species data
time<-mixturedat$Day
species<-data.frame(mixturedat$Volume_Species1, mixturedat$Volume_Species2)
colnames(species)<-c("P_caudatum", "P_aurelia")

#run wrapper
gause_out<-gause_wrapper(time=time, species=species)
```

`get_lag` *Get timelag*

Description

Calculates time-lagged observations for variable x, separated by treatment.

Usage

```
get_lag(x, time, tau = 1, treatment = NULL, mindt = 0, maxdt = Inf)
```

Arguments

`x`	The time series from which time lagged observations are desired (e.g. population sizes)
`time`	The time steps corresponding to each observation
`tau`	Number of time steps to use between lagged components - defaults to 1
`treatment`	An optional vector of treatment conditions - time lags will only be computed separately within treatments - defaults to NULL (i.e. no treatments)
`mindt`	Minimum dt allowed between observations - defaults to 0
`maxdt`	Maximum dt allowed between observations - defaults to Inf

Value

Returns a data.frame with 7 columns: x (unlagged time series data); laggedx (lagged time series data); xmid (average of time series and lagged time series values); dt (time lag between x and laggedx); time (time for observation x); laggedtime (time for observation laggedx); treatment (treatment for observation)

Examples

```
data(gause_1934_science_f02_03)
lagged_data <- get_lag(x=gause_1934_science_f02_03$Volume_Species1,
               time = gause_1934_science_f02_03$Day,
               treatment = gause_1934_science_f02_03$Treatment)
```

`get_logistic` *Logistic Growth*

Description

Calculates logistic growth for population based on formula Nt=K*(N0*exp(r*time))/(K+N0*(exp(r*time)-1)

Usage

```
get_logistic(time, N0, r, K)
```

Arguments

`time`	The time steps corresponding to each observation
`N0`	Initial Population Size
`r`	Growth rate
`K`	Carying Capacity

Value

population size N for each time steps as a vector

Examples

```
# load Gause competition data
data(gause_1934_science_f02_03)
# extract monoculture data for P.c.
Pcmono<-gause_1934_science_f02_03[gause_1934_science_f02_03$Treatment=="Pc",]

# calculate lag and per-capita growth
lagged_data_Pc <- get_lag(x=Pcmono$Volume_Species1,
                          time = Pcmono$Day)
Pcmono$dNNdt_Pc <- percap_growth(x=lagged_data_Pc$x, laggedx=lagged_data_Pc$laggedx,
                                 dt=lagged_data_Pc$dt)

# fit linear model to get dNNdt ~ r + s*N
mod_Pc<-lm(dNNdt_Pc~Volume_Species1, Pcmono)
rsn_pars<-coef(mod_Pc)

# transform into logistic growth parameters
logistic_pars<-c(r=unname(rsn_pars["(Intercept)"]),
```

```
     K=unname(-rsn_pars["(Intercept)"]/rsn_pars["Volume_Species1"]))

#fit with nls, using linear model estimates as starting values for parameters
nls_mod<-nls(Volume_Species1~get_logistic(time = Day, N0, r, K),
             data=Pcmono,
             start=c(N0=unname(Pcmono$Volume_Species1[which.min(Pcmono$Day)]),
             r=unname(logistic_pars["r"]), K=unname(logistic_pars["K"])))
summary(nls_mod)

# plot results
plot(Volume_Species1~Day, Pcmono, type="b", ylab="P. caudatum Volume")
timesq<-seq(0, 30, length=100)
Ntest<-get_logistic(time = timesq, N0=coef(nls_mod)["N0"], r=coef(nls_mod)["r"],
       K=coef(nls_mod)["K"])

lines(timesq, Ntest, col="red")
```

`huffaker_1963` *Huffaker Mite Data*

Description

A dataset containing the abundances mite species from some of the Huffaker experiments.

Usage

`huffaker_1963`

Format

A data frame with 168 rows and 6 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

Species Species name

Weeks Experiment week

Individuals Number of individuals

Treatment 60 vs. 24-week experiments

Source

Huffaker (1958) Experimental Studies on Predation: Dispersion Factors and Predator-Prey Oscillations. Hilgardia 27: 343-83.

`lv_interaction` *Lotka-Volterra Interactions*

Description

Calculates dn/dt for n species in a Lokta-Volterra system, following the form: dni/dt = ni * (ri + aii * ni + sum_j(aij * nj)) Note that aii coefficients can be positive or negative, although positive coefficients risk having the system run to infinite population sizes, which will crash the function.

Usage

```
lv_interaction(time, n, parms)
```

Arguments

`time`	The time steps corresponding to each observation - exists to interface with ode function, but should be left blank.
`n`	A vector of species abundances
`parms`	A vector of parameters - the first n elements should be the growth rates r1, r2, ... rn for all n species. The remaining terms should be the elements of the interaction matrix A, listed in the order a11, a12, ... a1n, a21, a22, ... a2n, ... an1, an2, ... ann.

Value

vector of growth rates for each species

Examples

```
# load data from competition experiment
data(gause_1934_science_f02_03)

# subset data to include just mixtures
mixturedata<-gause_1934_science_f02_03[gause_1934_science_f02_03$Treatment=="Mixture",]

# get time-lagged observations for each species
Pc_lagged<-get_lag(x = mixturedata$Volume_Species1, time = mixturedata$Day)
Pa_lagged<-get_lag(x = mixturedata$Volume_Species2, time = mixturedata$Day)

# calculate per-capita growth rates
Pc_dNNdt<-percap_growth(x = Pc_lagged$x, laggedx = Pc_lagged$laggedx, dt = Pc_lagged$dt)
Pa_dNNdt<-percap_growth(x = Pa_lagged$x, laggedx = Pa_lagged$laggedx, dt = Pa_lagged$dt)

# fit linear models to dNNdt, based on average
# abundances between current and lagged time steps
Pc_mod_dat<-data.frame(Pc_dNNdt=Pc_dNNdt, Pc=Pc_lagged$laggedx, Pa=Pa_lagged$laggedx)
mod_comp_Pc<-lm(Pc_dNNdt~Pc+Pa, data=Pc_mod_dat)
```

```
Pa_mod_dat<-data.frame(Pa_dNNdt=Pa_dNNdt, Pa=Pa_lagged$laggedx, Pc=Pc_lagged$laggedx)
mod_comp_Pa<-lm(Pa_dNNdt~Pa+Pc, data=Pa_mod_dat)

# model summaries
summary(mod_comp_Pc)
summary(mod_comp_Pa)

# extract parameters
# note - linear regressions give us dynamics in the form:
# dni/nidt ~ (Intercept) + (n1_slope) * n1 + (n2_slope) n2
# and thus:
# dni/dt = n1*((Intercept) + (n1_slope) * n1 + (n2_slope) n2)

# growth rates
r1 <- unname(coef(mod_comp_Pc)["(Intercept)"])
r2 <- unname(coef(mod_comp_Pa)["(Intercept)"])

# self-limitation
a11 <- unname(coef(mod_comp_Pc)["Pc"])
a22 <- unname(coef(mod_comp_Pa)["Pa"])

# effect of Pa on Pc
a12 <- unname(coef(mod_comp_Pc)["Pa"])
# effect of Pc on Pa
a21 <- unname(coef(mod_comp_Pa)["Pc"])

# run ODE:
# make paramter vector:
parms <- c(r1, r2, a11, a12, a21, a22)
initialN <- c(1, 1)
out <- deSolve::ode(y=initialN, times=1:25, func=lv_interaction, parms=parms)
matplot(out[,1], out[,-1], type="l",
   xlab="time", ylab="N", col=c("black","red"), lty=c(1,3), lwd=2, ylim=c(0, 150))
legend("topleft", c("Pc", "Pa"), col=c(1,2), lwd=2, lty=c(1,3))

# now, plot in points from data
points(mixturedata$Day, mixturedata$Volume_Species1, col=1)
points(mixturedata$Day, mixturedata$Volume_Species2, col=2)
```

`lv_interaction_log` *Lotka-Volterra Interactions in Log Space*

Description

Calculates dn/dt for n species in a Lokta-Volterra system, in log space, following the form: dlog(ni)/dt = (ri + aii * ni + sum_j(aij * nj)) This form can be helpful for optimization routines where species abundances are close to zero.

Usage

```
lv_interaction_log(time, n_log, parms)
```

Arguments

`time`	The time steps corresponding to each observation - exists to interface with ode function, but should be left blank.
`n_log`	A vector of species abundances, in log space
`parms`	A vector of parameters - the first n elements should be the growth rates r1, r2, ... rn for all n species. The remaining terms should be the elements of the interaction matrix A, listed in the order a11, a12, ... a1n, a21, a22, ... a2n, ... an1, an2, ... ann.

Value

vector of growth rates for each species in log space

`lv_optim` *Optimizer for Lotka-Volterra Interactions*

Description

Identifies optimal parameter values for a Lotka-Volterra interaction system.

Usage

```
lv_optim(
  pars,
  opt_data,
  parm_signs,
  standardize = TRUE,
  odefun = lv_interaction_log
)
```

Arguments

`pars`	A vector of parameter values in log space to be optimized. Must include a logged starting abundance for each species, followed by the logged absolute values of the growth rates, followed by the logged absolute value of the elements of the interaction matrix.
`opt_data`	Abundance data for optimization. Must include one column labeled 'time' with time steps, and a column for each species abundance.
`parm_signs`	A vector that provides the desired sign of each parameter (i.e. -1 or 1). If value is zero, then the term is held at zero (but should be left out of the pars vector).
`standardize`	A logical, defaulting to TRUE - should error be calculated based on standardized values of outputs? Allows for more equal weighting of observed variabels.
`odefun`	The function to use to simulate the ODE - defaults to lv_interaction_log

Value

squared error between model fits for given parameter values, and observations

Examples

```
# load data from competition experiment
data(gause_1934_book_f32)

# keep all data - no separate treatments exist for this experiment
predatorpreydata<-gause_1934_book_f32

# get time-lagged observations for each species
prey_lagged<-get_lag(x = predatorpreydata$Individuals_Prey, time = predatorpreydata$Day)
predator_lagged<-get_lag(x = predatorpreydata$Individuals_Predator, time = predatorpreydata$Day)

# calculate per-capita growth rates
prey_dNNdt<-percap_growth(x = prey_lagged$x, laggedx = prey_lagged$laggedx, dt = prey_lagged$dt)
predator_dNNdt<-percap_growth(x = predator_lagged$x,
      laggedx = predator_lagged$laggedx, dt = predator_lagged$dt)

# fit linear models to dNNdt, based on average
# abundances between current and lagged time steps
prey_mod_dat<-data.frame(prey_dNNdt=prey_dNNdt, prey=prey_lagged$laggedx,
      predator=predator_lagged$laggedx)
mod_prey<-lm(prey_dNNdt~prey+predator, data=prey_mod_dat)

predator_mod_dat<-data.frame(predator_dNNdt=predator_dNNdt,
      predator=predator_lagged$laggedx, prey=prey_lagged$laggedx)
mod_predator<-lm(predator_dNNdt~predator+prey, data=predator_mod_dat)

# model summaries
summary(mod_prey)
summary(mod_predator)

# extract parameters
# growth rates
r1 <- unname(coef(mod_prey)["(Intercept)"])
r2 <- unname(coef(mod_predator)["(Intercept)"])

# self-limitation
a11 <- unname(coef(mod_prey)["prey"])
a22 <- unname(coef(mod_predator)["predator"])

# effect of Pa on Pc
a12 <- unname(coef(mod_prey)["predator"])
# effect of Pc on Pa
a21 <- unname(coef(mod_predator)["prey"])

# run ODE:
# make parameter vector:
parms <- c(r1, r2, a11, a12, a21, a22)
initialN <- c(4, 0.1)
```

```
out <- deSolve::ode(y=initialN, times=seq(1, 17, length=100), func=lv_interaction, parms=parms)
matplot(out[,1], out[,-1], type="l",
        xlab="time", ylab="N", col=c("black","red"), lty=c(1,3), lwd=2, ylim=c(0, 60))
legend("topright", c("Pc", "Dn"), col=c(1,2), lwd=2, lty=c(1,3))

# now, plot in points from data
points(predatorpreydata$Day, predatorpreydata$Individuals_Predator , col=2)
points(predatorpreydata$Day, predatorpreydata$Individuals_Prey, col=1)

# uh-oh - This is a bad fit. This suggests that our linear model
# approximation isn't very good. Instead, we should try optimizing
# directly using the ode solver

# Re-run using an optimizer
# Data for the optimizer:
# Must have a column with time steps labeled 'time', and
# columns for each species in the community.
opt_data<-data.frame(time=predatorpreydata$Day, Prey=predatorpreydata$Individuals_Prey,
    Predator=predatorpreydata$Individuals_Predator)

# Save the signs of the parameters -
# optimizer works in log space, so these
# must be specified separately
parm_signs<-sign(parms)

# parameter vector for optimizer -
# must be a vector with, first, the
# starting abundances in log space,
# and second, the parameter values,
# again in log space
pars<-c(log(initialN), log(abs(parms)))

# run optimizer
optout<-optim(par = pars, fn = lv_optim, hessian = TRUE,
             opt_data=opt_data, parm_signs=parm_signs)

# extract parameter vector:
parms <- exp(optout$par[-c(1:2)])*parm_signs
initialN <- exp(optout$par[1:2])

out <- deSolve::ode(y=initialN, times=seq(1, 17, length=100), func=lv_interaction, parms=parms)
matplot(out[,1], out[,-1], type="l",
        xlab="time", ylab="N", col=c("black","red"), lty=c(1,3), lwd=2, ylim=c(0, 60))
legend("topright", c("Pc", "Dn"), col=c(1,2), lwd=2, lty=c(1,3))

# now, plot in points from data
points(predatorpreydata$Day, predatorpreydata$Individuals_Predator , col=2)
points(predatorpreydata$Day, predatorpreydata$Individuals_Prey, col=1)

# get rough estimate of confidence intervals
fisher_info<-solve(-optout$hessian)
optout$par_sd<-sqrt(abs(diag(fisher_info)))
```

```
parm_signs_sp<-c(rep(1, ncol(opt_data)-1), parm_signs)
parameter_intervals<-data.frame(lower_sd=exp(optout$par-optout$par_sd)*parm_signs_sp,
                                mu=exp(optout$par)*parm_signs_sp,
                                upper_sd=exp(optout$par+optout$par_sd)*parm_signs_sp)

rownames(parameter_intervals)<-c("prey", "predator", "r1", "r2", "a11", "a12", "a21", "a22")
parameter_intervals
```

`mclaren_1994_f03` *Wolf, Moose, and Fir dynamics from Isle Royale*

Description

A dataset containing the abundances of wolves, moose, and fir trees from the Isle Royale study of McLaren et al.

Usage

```
mclaren_1994_f03
```

Format

A data frame with 140 rows and 7 variables:

Paper Paper from which data are drawn

Figure Figure number in paper

year Year of measurements

Species Species name

width Width of tree rings

individuals Number of wolf or moose individuals

AET..mm. AET water availablility index

Source

McLaren & Peterson (1994) Wolves, Moose, and Tree Rings on Isle Royale. Science 266:1555-1558.

---

ode_prediction *Optimizer extension*

Description

Takes in paramter values in the form returned by the gause_wrapper function, and calculates expected abundances for all n species, returned as a single vector. This function is potentially useful in combination with other optimizer software, e.g. as might be used for hypothesis testing.

Usage

```
ode_prediction(pars_full, time, N)
```

Arguments

`pars_full`	Initial Population Size
`time`	A vector of times. Must be repeated once per species.
`N`	Number of species. Can be either a number, or a vector the same length as time.

Value

a stacked vector with predicted abundances for all species

Examples

```
#load competition data
data("gause_1934_science_f02_03")

#subset out data from species grown in mixture
mixturedat<-gause_1934_science_f02_03[gause_1934_science_f02_03$Treatment=="Mixture",]

#extract time and species data
time<-mixturedat$Day
species<-data.frame(mixturedat$Volume_Species1, mixturedat$Volume_Species2)
colnames(species)<-c("P_caudatum", "P_aurelia")


#run wrapper
gause_out<-gause_wrapper(time=time, species=species)

# number of species
N<-ncol(gause_out$rawdata)-1
# parameters
pars_full<-c(gause_out$parameter_intervals$mu)
# data.frame for optimization
fittigdata<-data.frame(y=unlist(gause_out$rawdata[,-1]),
                        time=gause_out$rawdata$time,
                       N=N)
```

```
yest<-ode_prediction(pars_full, time=fittigdata$time, N=fittigdata$N)
plot(fittigdata$y, yest, xlab="observation", ylab="prediction")
abline(a=0, b=1, lty=2)

#example of how to apply function, using nls()
mod<-nls(y~ode_prediction(pars_full, time, N),
           start = list(pars_full=pars_full),
           data=fittigdata)
summary(mod)
```

`percap_growth` *Per-capita growth rate*

Description

Calculates per-capita growth rate, using log ratios following the formula dN/Ndt = log(N(t)/N0)/dt.

Usage

```
percap_growth(x, laggedx, dt)
```

Arguments

`x`	Abundance
`laggedx`	Lagged abundance
`dt`	Time lag between observations

Value

Per-capita growth rate

Examples

```
data(gause_1934_science_f02_03)
lagged_data <- get_lag(x=gause_1934_science_f02_03$Volume_Species1,
               time = gause_1934_science_f02_03$Day,
               treatment = gause_1934_science_f02_03$Treatment)
dNNdt <- percap_growth(x=lagged_data$x, laggedx=lagged_data$laggedx,
               dt=lagged_data$dt)
```

`test_goodness_of_fit` *Test goodness of fit*

Description

Tests goodness of fit for predictions vs. observations. This statistic can be though of in the same way as a classic "R2", except that it measures scatter around the 1-1 line, rather than around a fitted regresson line of observed vs. predicted values. Value close to 1 indicate a that predictions match observations closely. Values at or below zero indicate that predictions do not match observations any better than the grand mean taken across all observations.

Usage

```
test_goodness_of_fit(observed, predicted, bycolumn = FALSE, droptimecol = TRUE)
```

Arguments

`observed`	A vector or matrix of observed values.
`predicted`	A vector or matrix of predicted values.
`bycolumn`	If TRUE, then separate values are calculated for each column in observed and predicted.
`droptimecol`	If TRUE, will automatically remove the column labeled "time" in the predicted variable. This is useful for dealing with the default output of the gause_wrapper function. Defaults to FALSE.

Examples

```
#load competition data
data("gause_1934_science_f02_03")

#subset out data from species grown in mixture
mixturedat<-gause_1934_science_f02_03[gause_1934_science_f02_03$Treatment=="Mixture",]

#extract time and species data
time<-mixturedat$Day
species<-data.frame(mixturedat$Volume_Species1, mixturedat$Volume_Species2)
colnames(species)<-c("P_caudatum", "P_aurelia")

#run wrapper
#note - keeptimes=TRUE is needed, so that predicted time steps match
#observed time steps
gause_out<-gause_wrapper(time=time, species=species, keeptimes = TRUE)

#calculate goodness of fit
test_goodness_of_fit(observed=species, predicted=gause_out)

# > 0.9 for both time series - these are good fits!
```

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