

# Package ‘PopulationGrowthR’

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**Type** Package

**Title** Linear Population Growth Scenarios

**Version** 0.1.1

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**Description**

Fit linear splines to species time series to detect population growth scenarios based on Hyndman, R J and Mesgaran, M B and Cousens, R D (2015) <[doi:10.1007/s10530-015-0962-8](https://doi.org/10.1007/s10530-015-0962-8)>.

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.1.1

**Imports** dplyr

**Depends** R (>= 2.10)

**NeedsCompilation** no

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**Repository** CRAN

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fdata	<i>Frequency and Specimens Data</i>
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**Description**

Example Frequency and Specimens data by year for each species to be used in 'PopulationGrowthR' package

**Usage**

fdata

**Format**

An object of class `data.frame` with 3771 rows and 4 columns.

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freqplot	<i>Frequency plot for a lagphase fit</i>
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**Description**

Frequency plot for a lagphase fit

**Usage**

```
freqplot(
  fit1,
  fit2 = NULL,
  fit3 = NULL,
  fit4 = NULL,
  xlab = "Year",
  ylab = "Frequency",
  main = fit1$name,
  cols = 2:5,
  ...
)
```

**Arguments**

fit1, fit2, fit3, fit4	"lagphase" fit objects to plot
xlab	Label for the $x$ -axis
ylab	Label for the $y$ -axis
main	Title of the plot
cols	Colors to be used to draw the lines
...	(optional) parameters to pass to plot

**Value**

Produces a plot of observed and predicted frequencies for the species against year

**Examples**

```
Species = unique(fdata$Species) #List of all species
fit1 = lagfit(fdata, yeardata, species=Species[1])
freqplot(fit1$fit)
```

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growthplot	<i>Produces plot of the fitted spline function after adjusting for number of Specimens</i>
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**Description**

Produces plot of the fitted spline function after adjusting for number of Specimens

**Usage**

```
growthplot(
  fit,
  ylim = NULL,
  xlab = "Year",
  ylab = "Adjusted Frequency",
  main = fit$name,
  ...
)
```

**Arguments**

fit	a "lagphase" fit object to plot
ylim	vector of size 2 - limits of the \$\$-axis
xlab	Label for the \$\$-axis
ylab	Label for the \$\$-axis
main	Title of the plot
...	(optional) parameters to pass to plot

**Value**

Produces a plot of the fit with confidence bands

**Examples**

```
Species = unique(fdata$Species) #List of all species
fit1 = lagfit(fdata, yeardata, species=Species[1])
growthplot(fit1$fit)
```

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 lagfit

*Fits a piecewise glm model with lags*


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### Description

This function fits a piecewise poisson model to the frequency data of different Species. It assumes that the data contains columns Year, Frequency and Specimens.

### Usage

```
lagfit(
  data,
  yeardata,
  species = NULL,
  knots = NULL,
  zeros = TRUE,
  plotlag = FALSE,
  plotfreq = FALSE
)
```

### Arguments

data	a dataframe containing the columns Species (optional), Year, Frequency and Specimens.
yeardata	a dataframe containing the columns Year and Specimens giving the total number of Specimens for each Year.
species	list of species for which the model is to be fitted. Default is NULL, which fits the model for all species in the data.
knots	a list of knots to be used for the piecewise model. Default is NULL, which chooses the optimal model with 0-4 knots.
zeros	logical. Specifies whether missing year for the species will be filled with zeros. Default is TRUE.
plotlag	logical. If TRUE a plot of the fitted model will be produced for each species.
plotfreq	logical. If TRUE frequency plots will be created for each species.

### Value

If the model is fit for a single species following are returned as a list

- Species - Species name
- Scene - Different scenario of the fit between the knots. A sequence of 0, + or - is returned. A 0 indicates constant, + indicates increasing and a - indicates decreasing.
- Lag - Logical. Is there a lag present or not.
- Laglength - Length of the first lag. Position of the First Knot - the first year for that species

- FirstYear - The first year for that species for which data is available.
- EndYear - The first knot position.
- fit - the fitted model.

If the number of species is more than one, then a list is returned with following items:

- fitdata - dataframe is returned with the items in the above list except for the fitted model.
- fitcoefs - list of coefficients for the piecewise fits for each Species

### Examples

```
#Run lagfit for 1 species only
Species = unique(fdata$Species) #List of all species

fit1 = lagfit(fdata, yeardata, species=Species[1])
#Run lagfit for multiple species
fit2 = lagfit(fdata, yeardata, species=Species[1:3])
fitdata = fit2$fitdata #Dataframe containing fits
fitcoefs = fit2$fitcoefs #List containing slopes of the fitted splines

## Not run:
#Run lagfit for the whole dataset
fitall = lagfit(fdata, yeardata)

## End(Not run)
```

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raw2freqdata

*Extract Frequency and Specimen data from the raw data*


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### Description

Extract Frequency and Specimen data from the raw data

### Usage

```
raw2freqdata(rawdata, species = "species", year = "year")
```

### Arguments

rawdata	a dataframe containing species, year
species	name of the column containing species names
year	name of the column containing year

### Value

Returns a list of two dataframes

- data - a dataframe containing Species, Year, Frequency and Specimens
- yeardata - a dataframe containing Year and Specimens

**Examples**

```
cleandata = raw2freqdata(rawdata)
fdata = cleandata$data
yeardata = cleandata$yeardata
```

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rawdata	<i>Raw GBIF Data</i>
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**Description**

Example raw GBIF data used in ‘PopulationGrowthR’ package

**Usage**

```
rawdata
```

**Format**

An object of class `data.frame` with 34088 rows and 50 columns.

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yeardata	<i>Total Specimens Data</i>
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**Description**

Example total Specimens data by year to be used in ‘PopulationGrowthR’ package

**Usage**

```
yeardata
```

**Format**

An object of class `data.frame` with 60 rows and 2 columns.

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