## Package ‘fishmove’

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**Description** Functions to predict fish movement parameters plotting leptokurtic fish dispersal kernels (see Radinger and Wolter, 2014: Patterns and predictors of fish dispersal in rivers. Fish and Fisheries. 15:456-473.)  
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Description

Functions to predict fish movement parameters based on multiple regression and plotting leptokurtic fish dispersal kernels.

Package: fishmove
Version: 0.3-1
Date: 2015-03-23
Depends: ggplot2, plyr, MASS, boot
License: GPL (>= 2)
Depends: ggplot2
URL: http://dx.doi.org/10.1111/faf.12028

Details

The package fishmove consists of two main functions: fishmove and pdk:

fishmove predicts movement parameters of leptokurtic fish dispersal. The prediction is based on multiple regression on four variables (fish length, aspect ratio of the caudal fin (Pauly, 1989), stream order (Strahler, 1957) and time).

The package 'fishmove' is based on a meta-analysis of heterogeneous fish movement in rivers (see Radinger and Wolter, 2014)

The movement parameters are calculated for a stationary ($\sigma_{stat}$) and for a mobile component ($\sigma_{mob}$) of a fish population. These parameters in combination with a value for the share of each component can be used to describe and display leptokurtic dispersal kernels according to:

$$F(x) = p \times \frac{1}{\sqrt{2\pi\sigma_{stat}^2}} \times e^{-\frac{(x-\mu)^2}{2\sigma_{stat}^2}} + (1 - p) \times \frac{1}{\sqrt{2\pi\sigma_{mob}^2}} \times e^{-\frac{(x-\mu)^2}{2\sigma_{mob}^2}}$$

In addition, common fish length and aspect ratio, are already provided for 40 different species from fishbase.org (Froese and Pauly, 2011).

The pdk function provides plots (based on ggplot2) of probability density kernels (pdk) for leptokurtic fish dispersal. For each plot the fitted mean as well as the upper and the lower bound (based on confidence or prediction interval) are displayed.

The fishmove.query function provides a tool to query a dispersal kernel (predicted by fishmove) where (distance from source) a certain probability can be found. Also the reverse is possible to query what probability of occurrence is found in a certain distance on the dispersal kernel.

Improvements, bug fixes and constructive criticism are welcome.
datafishmove

Author(s)

Johannes Radinger
Maintainer: Johannes Radinger <jradinger@igb-berlin.de>

References


Examples

# Prediction for a selected fish species with time=365 days
trout <- fishmove(species="Salmo trutta fario", T=365)

# Plot of a leptokurtic dispersal kernel
# (density plot for fitted mean, lower and upper limit)
pdk(trout)

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<th>Basic Data for fishmove</th>
</tr>
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Description

Data for performing multiple regression to calculate movement parameters of leptokurtic fish dispersal. Underlying dataset for function fishmove.

Usage

datafishmove

Format

This dataframe contains following columns:

- **FAMILY** scientific name of fish family
- **SPECIES** scientific name of fish species
- **STREAM.ORDER** stream order (Strahler, 1957)
- **LENGTH** fish length in mm
- **ASPECT.RATIO** aspect ratio of the caudal fin (Pauly, 1989)
TIME  Time of study
SIGMA_STAT  movement parameter of stationary component
SIGMA_MOB  movement parameter of mobile component
p  share of stationary component
REP  indication of replicates

Author(s)
Johannes Radinger

Source

References

fishmove  Prediction of Fish Movement Parameters based on Multiple Regression

Description
Functions to predict fish movement parameters of leptokurtic fish dispersal, based on multiple regression.

Usage
fishmove(species=NA,L=NA,AR=NA,SO=6,T=30,interval="confidence",rep=50,seed=NA,...)

Arguments
species  Fish species (scientific name) from speciesfishmove, used for prediction of movement parameters. If species is set, then values for length and the aspect ratio are taken from speciesfishmove and must not be provided by the user. Any additional argument on fish length and/or aspect ratio overwrites these settings. speciesfishmove originates in fishbase.org (Froese and Pauly, 2011).
L  Fish length (mm), used for prediction of movement parameters. Also a vector of several fish lengths can be provided.
AR  Aspect ratio of the caudal fin, used for prediction of movement parameters (Pauly, 1989). A vector of several aspect ratios can be provided.
**fishmove**

S0 Stream order (Strahler, 1957), used for prediction of movement parameters. The default value for S0 is 6. A vector of several stream orders can be provided.

T Time step (days), used for prediction of movement parameters. The default value for new.time is 30 (days). A vector of several times can be provided.

interval Type of interval calculation. Can be either "confidence" or "prediction". The default for interval is "confidence". See `predict.lm`.

rep Number of regression runs to correct for replicates in datafishmove. The default value for rep is 50.

seed Number (integer) specifying a fixed seed for the random subsampling process (replicates of regression runs). By default this value is set random.

... do not use.

Details

`fishmove` predicts movement parameters of leptokurtic fish dispersal. The prediction is based on multiple regression on four variables (fish length, aspect ratio of the caudal fin (Pauly, 1989), stream order (Strahler, 1957) and time).

The package 'fishmove' is based on a meta-analyis of heterogeneous fish movement in rivers (see Radinger and Wolter, 2013)

The movement parameters are calculated for a stationary ($\sigma_{stat}$) and for a mobile component ($\sigma_{mob}$) of a fish population. These parameters in combination with a value for the share of each component can be used to describe and display leptokurtic dispersal kernels according to:

\[
F(x) = p \star \frac{1}{\sqrt{2\pi\sigma_{stat}^2}} \star e^{-\frac{(x-\mu)^2}{2\sigma_{stat}^2}} + (1-p) \star \frac{1}{\sqrt{2\pi\sigma_{mob}^2}} \star e^{-\frac{(x-\mu)^2}{2\sigma_{mob}^2}}
\]

New values are calculated for a fitted mean and its upper and lower bound (confidence or prediction interval) based on a set of new input variables. In addition, common fish length and aspect ratio, are already provided for appr. 40 different species from fishbase.org (Froese and Pauly, 2011).

Value

- `coef.fishmove` Array of regression parameters of the original multiple regression
- `pred.fishmove` predicted value, upper and lower bound for $\sigma_{stat}$ (movement parameter of stationary component) and $\sigma_{mob}$ (movement parameter of mobile component)

Author(s)

Johannes Radinger

References


See Also

pdk, lm, predict.lm

Examples

```r
# Prediction for a selected fish species with time=365 daysishmove(species="Salmo trutta fario", T=365)

# Prediction with fish length=350 mm, aspect ratio=2, stream order=4 and prediction interval
# fishmove(L=350, AR=2, SO=4, T=365, interval="prediction")
```

### fishmove.estimate

*Estimation of fish movement parameters (\(\sigma_{\text{stat}}, \sigma_{\text{mob}}\) and \(p\)) from field data*

#### Description

Function to estimate the three fish movement parameters \(\sigma_{\text{stat}}, \sigma_{\text{mob}}\) and \(p\) describing the leptokurtic shape of fish dispersal kernels from field data.

#### Usage

```
fishmove.estimate(data=NA, start=NA, ci=FALSE, rep=100, conf=0.95, ...)
```

#### Arguments

- `data` Single numeric vector of movement distances (field measurements) which should be used to estimate movement parameters. Here, only absolute movement distances are considered and differences in up- or downstream movement are ignored (symmetrical dispersal kernel assumed).
- `start` Named list of starting values used for the internal optimization process. If nothing is provided the 10% and 90% quantile of the input data are used as starting values for \(\sigma_{\text{stat}}\) and \(\sigma_{\text{mob}}\) and 0.67 is used as the starting value for \(p\).
- `ci` Logical. If true confidence intervals (method=bca) are calculated. This feature is under current development and still unstable. The default value for `ci` is FALSE.
- `rep` Number of bootstrap replicates to calculate the confidence interval of the obtained parameters. The default value for `rep` is 100.
- `conf` Confidence interval used for parameter estimates. The default value for `conf` is 0.95.
- `...` do not use.
fishmove.estimate

Details

fishmove.estimate estimates the three fish movement parameters $\sigma_{\text{stat}}$, $\sigma_{\text{mob}}$ and $p$ describing the leptokurtic shape of fish dispersal kernels from field data. Here, a symmetrical dispersal kernel is assumed and only absolute movement distances are considered and differences in up- or downstream movement are ignored. The parameters are obtained by optimizing a double normal distribution with $\sigma_{\text{stat}}$ as dispersion (standard deviation) parameter for the first distribution, $\sigma_{\text{mob}}$ as dispersion (standard deviation) parameter for the second distribution, and $p$ the weighing factor for the distributions (share of the stationary component):

$$F(x) = p \cdot \frac{1}{\sqrt{2\pi \sigma_{\text{stat}}^2}} e^{-\frac{(x-\mu)^2}{2\sigma_{\text{stat}}^2}} + (1-p) \cdot \frac{1}{\sqrt{2\pi \sigma_{\text{mob}}^2}} e^{-\frac{(x-\mu)^2}{2\sigma_{\text{mob}}^2}}$$

The optimization is based on a maximum likelihood approach ("L-BFGS-B") using the underlying fitdistr() and optim() functions.

Under development: Based on non-parametric bootstrapping approach the 95%-confidence interval (method="bca") is calculated for the three extracted parameters. The default number of bootstrap replicates (rep) is set to 100.

Value

If no confidence intervals are calculated (default), the return object is of class "fitdistr". The three estimated movement parameters $\sigma_{\text{stat}}$ (movement parameter of stationary component), $\sigma_{\text{mob}}$ (movement parameter of mobile component) and $p$ (share of the stationary component) and their corresponding standard errors are provided. If bootstrapped confidence interval are calculated the fit, the lower and the upper bound of $\sigma_{\text{stat}}$, $\sigma_{\text{mob}}$ and $p$ are provided.

Author(s)

Johannes Radinger

References


See Also

fishmove, pdk, fitdistr

Examples

# Fictive fish movement data e.g. from a telemetry study (displacement distances)
set.seed(42)
fielddata <- c(rnorm(mean=0,sd=50,300),rnorm(mean=0,sd=700,200))

# extracting parameters using code(fishmove.estimate)
parameters <- fishmove.estimate(fielddata)
parameters
```r
# Plot
hist(fielddata,breaks=30,freq=FALSE)

# Definition of probability density function based on two superimposed normal distributions
# ddoublenorm <- function(x,sigma_stat,sigma_mob,p){
# dnorm(x,mean=0,sd=sigma_stat)*p +
# dnorm(x,mean=0,sd=sigma_mob)*(1-p)}

# x <- seq(min(fielddata),max(fielddata),length.out=1000)

#lines(x,
# ddoublenorm(x,
# parameters$estimate["sigma_stat"],
# parameters$estimate["sigma_mob"],
# parameters$estimate["p"],
# col="red")
```

## fishmove.query

**Prediction of Probabilities of Fish Movement/Occurrence based on Leptokurtic Dispersal Kernels**

### Description

Function to predict probabilities of fish movement/occurrence based on leptokurtic dispersal kernels fitted via multiple regression.

### Usage

```r
fishmove.query(fishmove,p=0.67,dist=NA,fromto=NA,prob=NA,reach=NA,w=1,level="fit",...)
```

### Arguments

- **fishmove**: Output object (predicted dispersal kernel) from `fishmove`. If `fishmove`-kernel is predicted for multiple values e.g. of stream order, only first values are used for subsequent query.
- **p**: Share of stationary component on the population (0-1). The default value for `p` is 0.67.
- **dist**: Optional argument for distance (distance from source) where the user wants to know the kernel probability (height of the dispersal density kernel).
- **fromto**: Optional argument for a segment (defined by from distance - to distance) where the user wants to know the cumulative kernel probability (Integral: area under dispersal density kernel between from and to.)
**fishmove.query**

prob  
Optional argument: Reverse argument of distance/from to. Probability is provided and distance from source is calculated. Argument used in combination with reachlength.

reach  
Optional argument: Length of receiving reach. Argument used in combination with prob.

w  
Optional argument: Weighting factor for the dispersal kernel e.g. weight by source population size. When weight is used area under dispersal kernel (and thus the overall cumulative probability) equals the weighting factor. The default value for weight is 1.

level  
If statistical interval is calculated with fishmove, level defines if upper ("upr") or lower ("lwr") level of the calculated interval is used. The default value for level is "fit".

...  
do not use.

**Details**

fishmove.query allows querying the dispersal kernel (predicted from fishmove) for several questions e.g.:

(i) what is the probability of occurrence in a distance x (distance) from the source population

(ii) what is the cumulative probability of occurrence in a target reach between from/to distance (fromto) from the source population. (Integral: area under dispersal density kernel between from and to)

(iii) where (distance, with a given reach length) is a certain probability (prob) of occurrence on the dispersal kernel. So output here is a distance.

The movement parameters are calculated by fishmove for a stationary ($\sigma_{stat}$) and for a mobile component ($\sigma_{mob}$) of a fish population.

The queried probabilities and distances depend on the parameters defined during the prediction of fishmove e.g. fishlength, aspect ratio, stream order etc. as well as on the share of the stationary component ($p$) the kernel weighting factor (weight) and the level (level).

**Value**

out  
distance (in m) or probability depending on the input

**Author(s)**

Johannes Radinger

**References**


**See Also**

fishmove, pdk
Examples

# Prediction for a selected fish species
fm <- fishmove(L=100, AR=1.5, T=365, rep=20)

# Query using fishmove.query
# at which distance is the cumulative probability (area under kernel) of a 50 m reach 0.06
# fishmove.query(fm, prob=0.06, reachlength=50)
# what is the probability of occurrence in a reach between 0 and 50 m from the source population
fishmove.query(fm, from=0, to=50)

pdk

Plotting Probability Dispersal Kernel (pdk) of Fish Movement

Description
Plotting probability dispersal Kernel (pdk) of fish movement based on multiple regression

Usage
pdk(fishmove, p = 0.67,...)

Arguments

fishmove Output from fishmove, containing the movement parameters \( \sigma_{stat} \) and \( \sigma_{mob} \).
p Share of stationary component on the population (0-1). The default value for \( p \) is 0.67.
.
Details

pdk provides graphs (based on ggplot2) displaying probability density kernels (pdk) for leptokurtic fish dispersal. For each plot the fitted mean as well as the upper and the lower bound (based on confidence or prediction interval, see predict.lm) are displayed.

\( p \) is the share of the stationary component in the population resp. \( 1-p \) is the share of the mobile component. An average value for \( p \) is 0.66 (66% stationary) (Radinger and Wolter, 2013).

The underlying leptokurtic density function is:

\[
F(x) = p \times \frac{1}{\sqrt{2\pi \sigma_{stat}^2}} e^{-\frac{(x-\mu)^2}{2\sigma_{stat}^2}} + (1 - p) \times \frac{1}{\sqrt{2\pi \sigma_{mob}^2}} e^{-\frac{(x-\mu)^2}{2\sigma_{mob}^2}}
\]

Author(s)
Johannes Radinger
speciesfishmove

References

See Also
fishmove.lm, predict.lm, ggplot

Examples
# Plotting dispersal kernel for selected fish species with time=365 days
pdk(fishmove(species="Salmo trutta fario",T=365))

---

**speciesfishmove**  Morphological Data for various Fish Species

**Description**
Data of length and aspect ratio of the caudal fin (Pauly, 1989) for various fish species (appr. 40 species). Accompanying dataset for function fishmove originating from fishbase.org (Froese and Pauly, 2011).

**Usage**
speciesfishmove

**Format**
This dataframe contains following columns:
- **FAMILY**  scientific name of fish family
- **SPECIES**  scientific name of fish species
- **LENGTH**  common fish length in mm
- **ASPECT.RATIO**  aspect ratio of the caudal fin (Pauly, 1989)

**Author(s)**
Johannes Radinger

**Source**

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