

# Package ‘fishmove’

May 7, 2015

**Type** Package

**Title** Prediction of Fish Movement Parameters

**Version** 0.3-3

**Date/Publication** 2015-05-07 17:11:01

**Author** Johannes Radinger

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

**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.)

**License** GPL (>= 2)

**Depends** ggplot2, plyr, MASS, boot

**LazyLoad** yes

**LazyData** yes

**URL** <http://dx.doi.org/10.1111/faf.12028>

**NeedsCompilation** no

**Repository** CRAN

## R topics documented:

|                             |           |
|-----------------------------|-----------|
| fishmove-package . . . . .  | 2         |
| datafishmove . . . . .      | 3         |
| fishmove . . . . .          | 4         |
| fishmove.estimate . . . . . | 6         |
| fishmove.query . . . . .    | 8         |
| pdk . . . . .               | 10        |
| speciesfishmove . . . . .   | 11        |
| <b>Index</b>                | <b>12</b> |

---

|                  |  |
|------------------|--|
| fishmove-package | <i>Prediction of Fish Movement Parameters based on Multiple Regression</i> |
|------------------|--|

---

## Description

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

Package: fishmove  
 Version: 0.3-3  
 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:

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

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.

**Author(s)**

Johannes Radinger

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

**References**

Froese, R. and Pauly D. (2011) *FishBase*. World Wide Web electronic publication. [www.fishbase.org](http://www.fishbase.org), version (12/2011).

Pauly, D. (1989) A simple index of metabolic level in fishes. *Fishbyte, Newsletter of the Network of Tropical Fisheries Scientists* 7, 22.

Radinger, J. and Wolter C. (2014) Patterns and predictors of fish dispersal in rivers. *Fish and Fisheries*. 15:456-473. DOI: <http://dx.doi.org/10.1111/faf.12028>.

Strahler, A. N. (1957) Quantitative analysis of watershed geomorphology. *Transactions of the American Geophysical Union* 8, 913-920.

**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)
```

---

datafishmove

*Basic Data for fishmove*

---

**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

Radinger, J. and Wolter C. (2014) Patterns and predictors of fish dispersal in rivers. *Fish and Fisheries*. 15:456-473. DOI: <http://dx.doi.org/10.1111/faf.12028>.

#### References

Pauly, D. (1989) A simple index of metabolic level in fishes. *Fishbyte, Newsletter of the Network of Tropical Fisheries Scientists* 7, 22.  
 Strahler, A.N. (1957) Quantitative analysis of watershed geomorphology. *Transactions of the American Geophysical Union* 8, 913-920.

---

|          |  |
|----------|--|
| fishmove | <i>Prediction of Fish Movement Parameters based on Multiple Regression</i> |
|----------|--|

---

#### 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.  |

|          |   |
|----------|---|
| SO       | Stream order ( <i>Strahler, 1957</i> ), used for prediction of movement parameters. The default value for SO 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 <a href="#">predict.lm</a> .                  |
| 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-analysis 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:

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

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

- Froese, R. and Pauly D. (2011) *FishBase*. World Wide Web electronic publication. [www.fishbase.org](http://www.fishbase.org), version (12/2011).
- Pauly, D. (1989) A simple index of metabolic level in fishes. *Fishbyte, Newsletter of the Network of Tropical Fisheries Scientists* 7, 22.

Radinger, J. and Wolter C. (2014) Patterns and predictors of fish dispersal in rivers. *Fish and Fisheries*. 15:456-473. DOI: <http://dx.doi.org/10.1111/faf.12028>.

Strahler, A. N. (1957) Quantitative analysis of watershed geomorphology. *Transactions of the American Geophysical Union* 8, 913-920.

### See Also

[pdk](#), [lm](#), [predict.lm](#)

### Examples

```
# Prediction for a selected fish species with time=365 days
fishmove(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,S0=4,T=365,interval="prediction")
```

---

|                   |  |
|-------------------|--|
| fishmove.estimate | <i>Estimation of fish movement parameters (<math>\sigma_{stat}</math>, <math>\sigma_{mob}</math> and <math>p</math>) from field data</i> |
|-------------------|--|

---

### Description

Function to estimate the three fish movement parameters  $\sigma_{stat}$ ,  $\sigma_{mob}$  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 $\sigma_{stat}$ and $\sigma_{mob}$ 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.  |

## Details

fishmove.estimate estimates the three fish movement parameters  $\sigma_{stat}$ ,  $\sigma_{mob}$  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  $\sigma_{stat}$  as dispersion (standard deviation) parameter for the first distribution,  $\sigma_{mob}$  as dispersion (standard deviation) parameter for the second distribution, and  $p$  the weighing factor for the distributions (share of the stationary component):

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

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

out If no confidence intervals are calculated (default), the return object is of class "fitdistr". The three estimated movement parameters  $\sigma_{stat}$  (movement parameter of stationary component),  $\sigma_{mob}$  (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  $\sigma_{stat}$ ,  $\sigma_{mob}$  and  $p$  are provided.

## Author(s)

Johannes Radinger

## References

Radinger, J. and Wolter C. (2014) Patterns and predictors of fish dispersal in rivers. *Fish and Fisheries*. 15:456-473. DOI: <http://dx.doi.org/10.1111/faf.12028>.

## 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
```

```

# 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

```
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.) |



|       |   |
|-------|---|
| 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 use area under dispersal kernel (and thus the overall cumulative probability) equals the weighing 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

Radinger, J. and Wolter C. (2014) Patterns and predictors of fish dispersal in rivers. *Fish and Fisheries*. 15:456-473. DOI: <http://dx.doi.org/10.1111/faf.12028>.

### 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.       |
| ...      | do not use.   |

## 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:

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

## Author(s)

Johannes Radinger

## References

Radinger, J. and Wolter C. (2014) Patterns and predictors of fish dispersal in rivers. *Fish and Fisheries*. 15:456-473. DOI: <http://dx.doi.org/10.1111/faf.12028>.

## 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 | <i>Morphological Data for various Fish Species</i> |
|-----------------|--|

---

## 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](http://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

Froese, R. and Pauly D. (2011) *FishBase*. World Wide Web electronic publication. [www.fishbase.org](http://www.fishbase.org), version (12/2011).

## References

Pauly, D. (1989) A simple index of metabolic level in fishes. *Fishbyte, Newsletter of the Network of Tropical Fisheries Scientists* 7, 22.

# Index

## \*Topic **package**

fishmove-package, 2

datafishmove, 3

fishmove, 4, 7, 9, 11

fishmove-package, 2

fishmove.estimate, 6

fishmove.query, 8

fitdistr, 7

ggplot, 11

lm, 6, 11

pdk, 6, 7, 9, 10

predict.lm, 5, 6, 10, 11

print.fishmove (fishmove), 4

speciesfishmove, 11

summary.fishmove (fishmove), 4