

# Package ‘OsteoBioR’

November 15, 2018

**Version** 0.1.1

**Title** Temporal Estimation of Isotopic Values

**Description**

Estimates the temporal changes of isotopic values of bone and teeth data solely based on the renewal rate of different bones/teeth and given measurements. The package furthermore provides plotting and exporting functionalities.

**License** GPL (>= 3)

**Encoding** UTF-8

**LazyData** true

**ByteCompile** true

**Depends** R (>= 3.4.0), Rcpp (>= 0.12.0)

**Imports** rstan (>= 2.18.1), rstantools (>= 1.5.0), ggplot2 (>= 2.2.1),  
methods

**LinkingTo** StanHeaders (>= 2.18.0), rstan (>= 2.18.1), BH (>= 1.66.0),  
Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.3.0)

**Suggests** lintr, testthat

**SystemRequirements** GNU make

**NeedsCompilation** yes

**RoxygenNote** 6.1.0

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**Date/Publication** 2018-11-15 17:40:15 UTC

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OsteoBioR-package	<i>The 'OsteoBioR' package.</i>
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## Description

A DESCRIPTION OF THE PACKAGE

## References

Stan Development Team (NA). RStan: the R interface to Stan. R package version NA. <http://mc-stan.org>

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computeResult	<i>Function to compute resulting isotopic values out of historic ones</i>
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## Description

Given renewal rates for different isotopic probes over time and normal distributions of isotopic values over time, resulting normal distributions of the isotopic probes are calculated.

## Usage

```
computeResult(data, timeVars, boneVars = NULL, meanVar, sdVar,
  cor = 0.5)
```

## Arguments

data	A dataframe specifying the renewal rates of different probes for each time interval. The renewal rates should be between 0 and 100 (percentages). The dataframe should include a column specifying a time-index (e.g. 1, 2, 3, ...) as well as columns for the different bones. Furthermore, the dataframe should contain the mean and sd values for each time interval.
timeVars	A character string specifying the name of the column indicating the time.
boneVars	A vector of character strings indicating the relevant variables containing the renewal rates of bones and teeth.

meanVar	A character string specifying the name of the column indicating the mean values of the isotopic probes over time.
sdVar	A character string specifying the name of the column indicating the standard deviation of the isotopic probes over time.
cor	The temporal correlation between neighbouring time points. Defaults to 0.5

### Value

A data.frame containing the resulting mean and standard deviation for each bone/tooth as well as the covariances.

### See Also

[estimateIntervals](#)

### Examples

```
testDat <- data.frame(
  t = 1:3,
  bone = c(100, 50, 0),
  mean = c(1, 3, 50),
  sd = c(1, 3, 50)
)
computeResult(
  data = testDat,
  timeVars = "t",
  boneVars = "bone",
  meanVar = "mean",
  sdVar = "sd"
)
```

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estimateIntervals

*Function to estimate temporal changes in isotopic values*

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### Description

Given renewal rates for different isotopic probes over time, a model estimates a normal distribution of the isotopic values for each time interval. Out of the given rates of renewal, first the influence of each time interval on the final isotopic value is calculated. This proportion is used as a regressor in a fully Bayesian linear model. The variance is estimated as rbf-Kernel-Matrix, where the hyper-parameters are chosen such that the correlation between time intervals close to each other is about 0.5. The estimation is implemented using `link[rstan]{rstan}`.

**Usage**

```
estimateIntervals(renewalRates, timeVars, boneVars = NULL, isoMean,
  isoSigma, mu_df = 1, mu_mean = 0, mu_sd = 10, rho_mean = 1,
  rho_sd = 0.25, alpha_mean = 2, alpha_sd = 0.5, mc = TRUE,
  adapt_delta = 0.9999, max_treedepth = 25, chains = 4,
  iter = 2000, ...)
```

**Arguments**

renewalRates	A dataframe specifying the renewal rates of different probes for each time interval. The renewalRates should be between 0 and 100 (percentages). The dataframe should include a column specifying a time-index (e.g. 1, 2, 3, ...) as well as columns for the different bones. The renewal rates should contain the times of origin, containing 100.
timeVars	A character string specifying the name of the column indicating the time.
boneVars	A vector of character strings indicating the relevant variables containing the renewal rates of bones and teeth. If not given, the variables with bones are all variables of the dataframe apart from the time variables.
isoMean	A numeric number indicating the mean of the isotopic values measured.
isoSigma	A numeric, positive number indicating the standard deviation of the isotopic values measured.
mu_df	Hyperparameter for the mean of the interval estimates: degrees of freedom of a non-standardized t-Student distribution. Defaults to 1.
mu_mean	Hyperparameter for the mean of the interval estimates: mean of a non-standardized t-Student distribution. Defaults to 0.
mu_sd	Hyperparameter for the mean of the interval estimates: standard deviation of a non-standardized t-Student distribution. Defaults to 10.
rho_mean	Hyperparameter for the length scale of the rbf-kernel: mean of a normal. Defaults to 1.
rho_sd	Hyperparameter for the length scale of the rbf-kernel: standard deviation of a normal. Defaults to 0.25.
alpha_mean	Hyperparameter for the signal variance of the rbf-kernel: mean of a normal. Defaults to 2.
alpha_sd	Hyperparameter for the signal variance of the rbf-kernel: standard deviation of a normal. Defaults to 0.5.
mc	A boolean indicating if multiple cores should be used. If TRUE, which is the default, 4 cores are used.
adapt_delta	A numeric value between 0 and 1 controlling the samplers behavior. Defaults to 0.9999. See <a href="#">stan</a> for more details.
max_treedepth	A numeric, positive value controlling the NUTS sampler. Defaults to 25. See <a href="#">stan</a> for more details.
chains	Number of chains for mcmc. Defaults to 4
iter	Number of iterations per chain for mcmc. Defaults to 2000
...	Arguments passed to rstand <a href="#">sampling</a>

**Value**

A fitted object of class `TemporalIso`.

**See Also**

[sampling](#)

**Examples**

```
## Not run:
data <- data.frame(
  intStart = 0:5,
  intEnd = 1:6,
  bone1 = c(100, 50, 20, 10, 5, 2),
  bone2 = c(100, 10, 5, 1, 1, 1),
  tooth1 = c(0, 100, 0, 0, 0, 0),
  tooth2 = c(0, 0, 100, 0, 0, 0)
)
y_mean <- c(-10, -7, -12, -9)
y_sigma <- c(2, 1.5, 2.5, 2.5)
fit <- estimateIntervals(renewalRates = data,
  timeVars = "intStart",
  boneVars = c("bone1", "bone2", "tooth1", "tooth2"),
  isoMean = y_mean,
  isoSigma = y_sigma)

print(fit)
plot(fit)
plotTime(fit)

# get estimates for specific time points
estimateTimePoint(fit, time = seq(0,5, by = 0.5))

# shift point estimation
plotTime(fit, plotShifts = TRUE, threshold = 0.5)
getShiftTime(fit, threshold = 0.5)

#Staying time estimation
estimatedStayTimes <- getSiteStayTimes(object = fit,
  siteMeans = c(-8, -10),
  siteSigma = c(1, 1.5))

## End(Not run)
```

**Description**

Once the isotopic values in time course are estimated along with `estimateIntervals()`, this function provides an interface to extract the mean, standard deviation and quantiles for a specific point in time

**Usage**

```
estimateTimePoint(object, time, intervalProb = 0.95)
```

**Arguments**

<code>object</code>	An object of class <a href="#">TemporalIso</a> fitted with <code>estimateIntervals()</code>
<code>time</code>	A vector of numerics, indicating the point in time to extract estimates
<code>intervalProb</code>	A numeric between 0 and 1 indicating the coverage of the credible interval

**Value**

A data.frame with time points and their means, standard deviations and credible intervals

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<code>export</code>	<i>Export of TemporalIso samples as csv</i>
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**Description**

Writes the interval samples of a `TemporalIso`-object to a .csv-File.

**Usage**

```
## S4 method for signature 'TemporalIso'
export(fit, file, interval = NULL, ...)
```

**Arguments**

<code>fit</code>	<code>TemporalIso</code> : An instance of class <code>TemporalIso</code> , generated from <a href="#">estimateIntervals</a>
<code>file</code>	character: a character string specifying the path to a .csv-file.
<code>interval</code>	numeric values which are part of the specified time intervals. Defaults to all intervals being exported
<code>...</code>	Optional arguments to <a href="#">write.csv</a> . #'

**See Also**

[write.csv](#)

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getShiftTime	<i>Calculate time points of shifted isotopic values</i>
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**Description**

The function calculates points in time where large changes happen in the isotopic values. It uses the posterior distributions to estimate the probability of changes to be (absolutely or relatively) large.

**Usage**

```
getShiftTime(object, absolute = TRUE, threshold = NULL,  
             probability = 0.5)
```

**Arguments**

object	model of class <a href="#">TemporalIso</a>
absolute	boolean. If the calculation shall be based on absolute or relative differences. Defaults to TRUE.
threshold	numeric. The threshold for a shift to be considered "large". Defaults to 1.5 for absolute isotopic values and 15 percent for relative changes.
probability	the probability for the differences to be larger than the threshold. Defaults to 50 percent.

**Value**

a data.frame containing the interval starts (intStart) and ends (intEnd) of changes.

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getSiteStayTimes	<i>Calculate estimated stay times for locations given isotopic values</i>
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**Description**

The function calculates points in time where large changes happen in the isotopic values. It uses the posterior distributions to estimate the probability of changes to be (absolutely or relatively) large.

**Usage**

```
getSiteStayTimes(object, siteMeans, siteSigma, intervalLengths = NULL,  
                 print = TRUE)
```

**Arguments**

object	model of class <a href="#">TemporalIso</a>
siteMeans	numeric vector. Isotopic mean values of sites/locations.
siteSigma	numeric vector. Isotopic standard deviation values of sites/locations..
intervalLengths	numeric vector. Vector of time interval lengths. Optional (if not given equal length intervals are assumed)
print	boolean. If output should be printed. Defaults to TRUE.

**Value**

a data.frame containing the interval starts (intStart) and ends (intEnd) of changes.

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plot, TemporalIso, missing-method

*Plots for TemporalIso objects*

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**Description**

Inherited from [rstan-plotting-functions](#), the default plot shows posterior uncertainty intervals and point estimates of isotopic values for each interval. The plot method can also regress to standard rstan methods.

**Usage**

```
## S4 method for signature 'TemporalIso,missing'
plot(x, ..., plotfun = "isotopic")
```

**Arguments**

x	TemporalIso: An instance of class TemporalIso, generated from <a href="#">estimateIntervals</a>
...	Optional arguments to the plotting functions.
plotfun	character: a character string specifying which plotting function is to be used. The default is "isotopic", which is a <a href="#">stan_plot</a> only for the interval values. "stan_plot", "stan_trace", "stan_dens" etc regress to the functionality of rstan.

**Value**

a ggplot object which can be further customized using the ggplot2 package.

**See Also**

[rstan-plotting-functions](#), [rstan\\_gg\\_options](#)



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plotTime	<i>Plot of credibility intervals for each time interval, plotted as timeseries</i>
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**Description**

The function plots the credibility intervals for each time interval and returns a ggplot object, which is further customizable.

**Usage**

```
plotTime(object, prop = 0.8, plotShifts = FALSE, ...)
```

**Arguments**

object	model of class <a href="#">TemporalIso</a>
prop	double between 0 and 1: length of credibility interval. The default value is 80 percent.
plotShifts	boolean if shifts shall be marked or not. Defaults to False.
...	arguments handed to <a href="#">getShiftTime</a>

**Value**

a [ggplot](#) object.

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TemporalIso-class	<i>S4 class for temporal estimation of isotopic values</i>
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**Description**

Inherits from [stanfit](#)

**Slots**

regressor	regressor used for estimation (class matrix)
time	timesteps (class vector)

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