

# Package: lhreg (via r-universe)

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**Type** Package

**Title** Phylogeny and Species Trait Effects on Detectability

**Version** 0.2-1

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**Description** Phylogeny and species trait effects on detectability, supporting material for the manuscript entitled 'Phylogeny and species traits predict songbird detectability' by Solymos, Matsuoka, Stralberg, Bayne, and Barker.

**URL** <https://github.com/borealbirds/lhreg>

**BugReports** <https://github.com/borealbirds/lhreg/issues>

**Depends** Matrix, DEoptim, mvtnorm, pbapply

**Suggests** knitr, rmarkdown, ape, parallel, plotrix, phytools, intrval

**VignetteBuilder** knitr

**License** GPL-2

**LazyLoad** yes

**LazyData** true

**Repository** <https://psolymos.r-universe.dev>

**RemoteUrl** <https://github.com/borealbirds/lhreg>

**RemoteRef** HEAD

**RemoteSha** f26788efb8e366782b688d04de4d633f2f4bcfd2

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cor_matrix	<i>Phylogenetic Correlation Matrix</i>
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**Description**

Phylogenetic correlation matrix.

**Usage**

```
data("cor_matrix")
```

**Format**

A matrix.

**Source**

See manuscript.

**References**

Manuscript.

**Examples**

```
data(cor_matrix)
str(cor_matrix)
```

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lhreg	<i>Phylogeny and Species Trait Effects on Detectability</i>
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**Description**

Functions used in the manuscript.

**Usage**

```
lhreg(Y, X, SE, V, init=NULL, lambda=NA, method="Nelder-Mead",
      hessian=FALSE, DELimit=10, eval=FALSE)
```

```
## S3 method for class 'lhreg'
logLik(object, ...)
## S3 method for class 'lhreg'
summary(object, ...)
## S3 method for class 'lhreg'
simulate(object, nsim = 1, seed = NULL,
```

```

    lambda = NA, obs_error = FALSE, ...)
profile_lambda1(object, value, ...)

loo1(i, object, return_coefs=TRUE)
loo2(i, object, return_coefs=TRUE, method=NULL)

parametric_bootstrap(object, nsim=1, seed = NULL, method, cl=NULL, ...)
pred_int(object, boot, cl=NULL)

```

### Arguments

Y	response vector.
X	model matrix for the mean.
SE	standard error estimate (observation error) for the response.
V	correlation matrix.
init	initial values or NULL.
lambda	phylogeny strength, non-negative, NA means it is not fixed value but estimated.
method	method argument accepted by <a href="#">optim</a> , or "DE" when DEoptim is called. Method for loo2 is same as for the input object\$method by default (method=NULL).
hessian	logical, if the Hessian needs to be estimated at MLE.
DElimit	limit for DEoptim search (used as [-DElimit, +DElimit]) when method = "DE".
eval	logical, the negative log-likelihood is evaluated at <code>init</code> given the data arguments without optimization.
object	a fitted object returned by <code>lhreg</code> .
value	fixed value for lambda in profile likelihood calculations.
i	index of observations to drop for cross-validation.
nsim	number of response vectors to simulate. Defaults to 1.
seed	an object specifying if and how the random number generator should be initialized as described in <a href="#">simulate</a> .
obs_error	logical, if observation error is to be taken into account.
cl	number of parallel processes or cluster object.
return_coefs	logical, if (re)estimated coefficients are to be returned.
boot	an object with <code>parametric_bootstrap</code> results.
...	other arguments passed to underlying functions.

### Details

See Examples and Vignettes for details.

**Value**

lhreg returns an object of lhreg, that is a list.

The summary method returns a summary for the input object. The logLik method returns the log-likelihood. The simulate method returns the random deviates under a multivariate normal model.

profile\_lambda1 returns log-likelihood based on fixed lambda profile likelihood.

loo1 returns the observed value for the held-out data point and the corresponding prediction based on multiple linear regression. Also returns coefficients based on the training data when return\_coefs=TRUE.

loo2 returns the observed value for the held-out data point and the corresponding prediction based on correlated mixed-effects model. Also returns coefficients based on the training data when return\_coefs=TRUE.

parametric\_bootstrap uses the simulate method to simulate observations from a Multivariate Normal distribution according to the input object (without the observation error) to refit the model and returns simulated values and estimates.

pred\_int calculates the prediction interval for an observation conditional on the other species and the known tree (this one and the other species included), and returns the bootstrap distribution of the prediction that can be used to calculate quantile based prediction intervals.

**Author(s)**

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**See Also**

[optim](#), [DEoptim](#)

**Examples**

```
## see examples in the vignette
## Not run:
vignette(topic = "lhreg", package = "lhreg")

## End(Not run)
```

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 lhreg\_data

*Life History Traits*


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**Description**

Life history traits.

**Usage**

```
data("lhreg_data")
```

**Format**

A data frame.

**Source**

See manuscript.

**References**

Manuscript.

**Examples**

```
data(lhreg_data)
str(lhreg_data)
```

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