

# Package: moultmcmcExtra (via r-universe)

August 27, 2024

**Title** Add-on Functions for Moult Models

**Version** 0.0.0.9000

**Description** Add-on functions for the moultmcmc package for modelling avian primary moult phenology.

**License** MIT + file LICENSE

**Encoding** UTF-8

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**Biarch** true

**Depends** R (>= 3.4.0)

**Imports** cowplot, dplyr, fuzzyjoin, ggplot2, grDevices, magrittr, MASS, matrixStats, methods, moultmcmc, nlme, RColorBrewer, Rcpp (>= 0.12.0), RcppParallel (>= 5.0.1), rlang, rstan (>= 2.18.1), rstantools (>= 2.2.0), stats, stringr, tidyr

**LinkingTo** BH (>= 1.66.0), Rcpp (>= 0.12.0), RcppEigen (>= 0.3.3.3.0), RcppParallel (>= 5.0.1), rstan (>= 2.18.1), StanHeaders (>= 2.18.0)

**SystemRequirements** GNU make

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Remotes** pboesu/moultmcmc

**LazyData** true

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

**RemoteUrl** <https://github.com/pboesu/moultmcmcExtra>

**RemoteRef** HEAD

**RemoteSha** 3a67f0d32775e713d59085492d7bdb13948a7db9

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moultmcmcExtra-package

*The 'moultmcmcExtra' package.*

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### Description

A DESCRIPTION OF THE PACKAGE

### References

Stan Development Team (NA). RStan: the R interface to Stan. R package version 2.26.11. <https://mc-stan.org>

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compairs\_plot

*Pairwise plots of posterior draws*

---

### Description

Plots pairwise scatter/density plots of posterior draws

### Usage

```
compairs_plot(
  x,
  y = NULL,
  pars = NULL,
  scatter = TRUE,
  overlay = TRUE,
  names = NULL,
  col = NULL,
  ...
)
```

**Arguments**

x	a moultmcmc object
y	an optional second moultmcmc object
pars	An optional character vector of parameter names. If pars is not specified then the default is to use the first 4 parameters of x.
scatter	logical, draw scatterplot of posterior samples if overlay = FALSE, else draw contours
overlay	logical, plot scatterplots and density contours of both models in each triangle, else draw one model per triangle
names	optional character vector of model names
col	optional vectors of colours (length 2)
...	further arguments to plot.default (the call that draws the scatter/contour plot)

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 compare\_plot\_annual\_raneff

*Compare plot that handles random effect models*

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**Description**

Compare plot that handles random effect models

**Usage**

```
compare_plot_annual_raneff(..., names = NULL)
```

**Arguments**

...	two or a moult or moultmcmc model
names	optional character vector of model names

**Value**

a plot comparing parameter estimates and their uncertainties

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moultmcmc_ranef	<i>Bayesian inference for Underhill-Zucchini moult models and expansions</i>
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### Description

Bayesian inference for Underhill-Zucchini moult models and expansions

### Usage

```
moultmcmc_ranef(
  moult_column,
  date_column,
  id_column = NULL,
  start_formula = ~1,
  duration_formula = ~1,
  sigma_formula = ~1,
  year_factor_column,
  type = 2,
  lump_non_moult = FALSE,
  data,
  init = "auto",
  flat_prior = TRUE,
  beta_sd = 0,
  log_lik = FALSE,
  use_phi_approx = FALSE,
  active_moult_recaps_only = TRUE,
  same_sigma = FALSE,
  ...
)
```

### Arguments

moult_column	the name the column in data containing moult indices, i.e. a numeric vector of (linearized) moult scores in [0,1] (0 = old plumage, 1 = new plumage; for model types 1-5), numerical moult codes (1 = old plumage, 2 = moulting, 3 = new plumage; for model type 1), or a mixed column created by <a href="#">consolidate_moult_records</a> for model type 12.
date_column	the name the column in data containing sampling dates, encoded as days since an arbitrary reference date, i.e. a numeric vector
id_column	(optional) factor identifier. Usually a season-individual combination to encode within-season recaptures, defaults to NULL. When provided moultmcmc will attempt to fit the relevant recaptures model.
start_formula	model formula for start date
duration_formula	model formula for duration

<code>sigma_formula</code>	model formula for start date sigma
<code>year_factor_column</code>	the name of a factor column in data that contains <code>year_factor</code> values
<code>type</code>	integer (one of 1,2,3,4,5,12) referring to type of moult data and consequently model to be fitted (see details)
<code>lump_non_moult</code>	logical; should pre- and post-moult observations be treated as indistinguishable? if TRUE and type <code>%in% c(1,2,12)</code> , the relevant lumped model will be fitted (see details).
<code>data</code>	Input data frame must contain a numeric column "date" and a column "moult_cat" which is a numeric vector of categorical moult codes (1 = old plumage, 2 = moulting, 3 = new plumage).
<code>init</code>	Specification of initial values for all or some parameters. Can be the string "auto" for an automatic guess based on the data, or any of the permitted <code>rstan</code> options: the digit 0, the strings "0" or "random", or a function. See the detailed documentation for the <code>init</code> argument in <code>rstan::stan</code> .
<code>flat_prior</code>	use uniform prior on start date and duration (TRUE) or vaguely informative truncated normal prior (FALSE). Defaults to TRUE.
<code>beta_sd</code>	use zero-centred normal priors for regression coefficients other than intercepts? If <code>&lt;= 0</code> the stan default of improper flat priors is used.
<code>log_lik</code>	boolean retain pointwise log-likelihood in output? This enables model assessment and selection via the loo package. Defaults to FALSE, can lead to very large output arrays when sample size is large.
<code>use_phi_approx</code>	logical flag whether to use stan's <code>Phi_approx</code> function to calculate the "old" likelihoods
<code>active_moult_recaps_only</code>	logical flag whether to ignore repeated observations outside the active moult phase
<code>same_sigma</code>	logical flag, currently unused
<code>...</code>	Arguments passed to <code>rstan::sampling</code> (e.g. <code>iter</code> , <code>chains</code> ).

## Details

`type` refers to the type of moult data available (see Underhill and Zucchini (1998) and Underhill, Zucchini and Summers (1990)).

`type = 1` sample is representative of entire population (not yet moulting, in moult, and birds which have completed moult). For `type 1` data, any value between 0 and 1 ( $> 0$  and  $< 1$ ) can be used as the moult index for birds in active moult. The value used does not matter, only the fact that they are in moult. `type = 2` (default) sample is representative of entire population (not yet moulting, in moult, and birds which have completed moult). Moult scores are required.

`type = 3` sample is representative only of birds in moult. Individuals with moult scores 0 or 1 are ignored.

`type = 4` sample is representative only of birds in moult and those that have completed moult. Individuals with moult scores 0 are ignored.

`type = 5` sample is representative only of birds that have not started moult or that are in moult. Individuals with moult scores 1 are ignored.

**Value**

An object of class stanfit returned by `rstan::sampling`

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predict_ranef	<i>Predict method for moultmcmc models with non-individual random effects</i>
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**Description**

Predict method for moultmcmc models with non-individual random effects

**Usage**

```
predict_ranef(
  object,
  newdata = NULL,
  predict.type = "parameters",
  summary = TRUE,
  intervals = 0.1,
  prob = 0.95,
  ...
)
```

**Arguments**

object	a fitted moultmcmc model
newdata	data.frame with explanatory variables for which to make predictions
predict.type	specifies form of predictions, see details.
summary	logical, if TRUE (default) return a data.frame of posterior means, otherwise return a list of arrays of the full posterior sample of the predicted quantity (with one list element per predicted quantity and array dimensions <code>nrow(newdata) * number of posterior draws</code> )
intervals	not currently used
prob	nominal coverage probability of credible interval
...	further arguments

**Value**

a data.frame or list, depending on input arguments

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siskin_capture	<i>Empirical moult dependent capture probabilities</i>
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**Description**

A lookup dataset containing empirical capture probabilities for siskins

**Usage**

```
siskin_capture
```

**Format**

A data frame with 1000 rows and 2 variables:

**pfmg** pfmg

**p\_cap** capture probability

**Source**

P. Boersch-Supan / Hugh Insley

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uz5_linpred_recap_annual_raneff
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*Bayesian inference for the Type 5 moult model with repeat measures and an additional annual random intercept*

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**Description**

Bayesian inference for the Type 5 moult model with repeat measures and an additional annual random intercept

**Usage**

```
uz5_linpred_recap_annual_raneff(
  moult_index_column,
  date_column,
  id_column,
  start_formula = ~1,
  duration_formula = ~1,
  sigma_formula = ~1,
  year_factor_column,
  beta_sd = 0,
  data,
  init = "auto",
  log_lik = TRUE,
  ...
)
```

**Arguments**

<code>moult_index_column</code>	the name the column in data containing moult indices, i.e. a numeric vector of (linearized) moult scores (0 = old plumage, 1 = new plumage).
<code>date_column</code>	the name the column in data containing sampling dates, encoded as days since an arbitrary reference date, i.e. a numeric vector
<code>id_column</code>	factor identifier. Usually a season-individual combination to encode within-season recaptures
<code>start_formula</code>	model formula for start date
<code>duration_formula</code>	model formula for duration
<code>sigma_formula</code>	model formula for start date sigma
<code>year_factor_column</code>	the name of a factor column in data that contains <code>year_factor</code> values
<code>beta_sd</code>	use zero-centred normal priors for regression coefficients other than intercepts? If $\leq 0$ the stan default of improper flat priors is used.
<code>data</code>	Input data frame
<code>init</code>	Specification of initial values for all or some parameters. Can be the string "auto" for an automatic guess based on the data, or any of the permitted rstan options: the digit 0, the strings "0" or "random", or a function. See the detailed documentation for the <code>init</code> argument in <code>?rstan::stan</code> .
<code>log_lik</code>	boolean retain pointwise log-likelihood in output? This enables model assessment and selection via the loo package. Defaults to true, can lead to very large output arrays if sample size is large.
<code>...</code>	Arguments passed to <code>rstan::sampling</code> (e.g. <code>iter</code> , <code>chains</code> ).

**Value**

An object of class `stanfit` returned by `rstan::sampling`



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