

# Package: ladybird (via r-universe)

September 14, 2024

**Type** Package

**Title** Analysis of Ladybird Occurrence Data

**Version** 0.0.2

**Description** Analysis of ladybird occurrence data from Belgium, the Netherlands and the UK since 1990.

**License** GPL-3

**URL** <https://inbo.github.io/ladybird>

**BugReports** <https://github.com/inbo/ladybird/issues>

**Imports** INLA, assertthat, dplyr, git2rdata, leaflet, pROC, readr, rlang, sf, shiny, tidyr

**Suggests** INBOtheme, here, plotly, scales

**Remotes** inbo/inbotheme

**Additional\_repositories** <https://inla.r-inla-download.org/R/stable>

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.1

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

**RemoteUrl** <https://github.com/inbo/ladybird>

**RemoteRef** HEAD

**RemoteSha** eb7459eb063eb704a250a701340c0da9866af555

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base_model	<i>Fit a base model to a species</i>
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**Description**

Fit a base model to a species

**Usage**

```
base_model(
  species = "Harm_axyr",
  min_occurrences = 1000,
  min_species = 3,
  first_order = TRUE,
  center_year = 2001
)
```

**Arguments**

species	Name of the species.
min_occurrences	The minimum number of occurrences per species.
min_species	The minimum number of species recorded at the combination of location and year.
first_order	Use first (TRUE) or second (FALSE) order random walk for the year component. Defaults to TRUE.
center_year	The year to center to. Defaults to 2001.

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cumulative_model	<i>Fit a model to a species using the cumulative predictions for a secondary species</i>
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**Description**

Fit a model to a species using the cumulative predictions for a secondary species

**Usage**

```
cumulative_model(
  species = "Adal_bipu",
  min_occurrences = 1000,
  min_species = 3,
  secondary,
  first_order = TRUE,
  center_year = 2001
)
```

**Arguments**

species	Name of the species.
min_occurrences	The minimum number of occurrences per species.
min_species	The minimum number of species recorded at the combination of location and year.
secondary	The output of base_model() for a different species.
first_order	Use first (TRUE) or second (FALSE) order random walk for the year component. Defaults to TRUE.
center_year	The year to center to. Defaults to 2001.

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fit_model	<i>Fit a model to a species using the predictions for a secondary species</i>
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**Description**

Fit a model to a species using the predictions for a secondary species

**Usage**

```
fit_model(first_order = TRUE, base_data, trend_prediction, base_prediction)
```

**Arguments**

first_order	Use first (TRUE) or second (FALSE) order random walk for the year component. Defaults to TRUE.
base_data	A dataframe with the base data.
trend_prediction	A dataframe with the timestamps to predict the trend.
base_prediction	A dataframe with the locations and timestamps to predict.

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import_data	<i>Import and standardise the raw data</i>
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**Description**

Import and standardise the raw data

**Usage**

```
import_data(belgium, output, strict = TRUE)
```

**Arguments**

belgium	path to the CSV file with the Belgian data.
output	path to the root of the data package
strict	What to do when the metadata changes. <code>strict = FALSE</code> overwrites the data and the metadata with a warning listing the changes, <code>strict = TRUE</code> returns an error and leaves the data and metadata as is. Defaults to <code>TRUE</code> .

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load_relevant	<i>Load the relevant occurrence data</i>
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**Description**

Load the relevant occurrence data

**Usage**

```
load_relevant(min_occurrences = 1000, min_species = 3)
```

**Arguments**

min_occurrences	The minimum number of occurrences per species.
min_species	The minimum number of species recorded at the combination of location and year.

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occurrence_map	<i>Display a leaflet map with the occurrences for a given species</i>
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**Description**

Display a leaflet map with the occurrences for a given species

**Usage**

```
occurrence_map()
```

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probability\_model      *Fit a model to a species using the predictions for a secondary species*

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**Description**

Fit a model to a species using the predictions for a secondary species

**Usage**

```
probability_model(  
  species = "Adal_dece",  
  min_occurrences = 1000,  
  min_species = 3,  
  secondary,  
  first_order = TRUE,  
  center_year = 2001  
)
```

**Arguments**

species	Name of the species.
min_occurrences	The minimum number of occurrences per species.
min_species	The minimum number of species recorded at the combination of location and year.
secondary	The output of base_model() for a different species.
first_order	Use first (TRUE) or second (FALSE) order random walk for the year component. Defaults to TRUE.
center_year	The year to center to. Defaults to 2001.

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