Package: birdsize (via r-universe)

August 29, 2024

Title Estimate Avian Body Size Distributions

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Description Generate estimated body size distributions for populations or communities of birds, given either species ID or species' mean body size. Designed to work naturally with the North American Breeding Bird Survey, or with any dataset of bird species, abundance, and/or mean size data.

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URL https://github.com/diazrenata/birdsize

BugReports https://github.com/diazrenata/birdsize/issues

Depends R (>= 2.10)

Imports stats, truncnorm

Suggests covr, dplyr, ggplot2, knitr, purrr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Encoding UTF-8

LazyData true

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

Repository https://ropensci.r-universe.dev

RemoteUrl https://github.com/ropensci/birdsize

RemoteRef main

RemoteSha 78d7840018d750a5917547e71843da953a3a89cb

Contents

`community_generate` *Simulate individual measurements for many populations*

Description

For a community (i.e. a collection of populations of different species, or of the same species at different points in time or locations, etc), simulate individual-level size and metabolic rate measurements.

Usage

```
community_generate(
  community_data_table,
  abundance_column_name = "speciestotal"
)
```

Arguments

`community_data_table`
: dataframe containing at least one of `AOU`, `scientific_name`, or `mean_size` and a column for species abundances

`abundance_column_name`
: character, the name of the column with species abundances. Defaults to "speciestotal".

Value

a dataframe one row per individual, all columns from `community_data_table`, and additional columns for species attributes.

Specifically:

- AOU: the AOU, if provided
- sim_species_id: the sim_species_id if provided
- genus: the genus associated with the AOU if provided, or the genus if provided
- species: the species associated with the AOU if provided, or the species if provided
- individual_mass: the simulated body mass (in grams) for this individual
- individual_bmr: the simulated basal metabolic rate for this individual
- mean_size: the mean body mass for this species (i.e. the parameter used for simulation)
- sd_size: the standard deviation of body mass for this species (i.e. the parameter used for simulation)
- abundance: the number of individuals simulated of this species (i.e. parameter used for simulation)
- sd_method: the method for finding the standard deviation for body mass for this species
- scientific_name: the scientific name

Examples

```
demo_community <- community_generate(demo_route_clean)
head(demo_community)
```

---

demo_route_clean *Cleaned data for a hypothetical Breeding Bird Survey route.*

Description

This is the cleaned version of demo_route_raw, a toy dataset for use in vignettes and function testing. It contains all the same column names as would be expected for a Breeding Bird survey route dataset downloaded, e.g. from ScienceBase or the Data Retriever (Pardieck et al. 2019). However, the actual data values are simulated data.

Usage

```
demo_route_clean
```

Format

A data frame with 27 rows and 15 variables:

record_id inherited from data downloaded through the Data Retriever

routedataid inherited from Pardieck et al. 2018 (as are all following fields). Unique data identification number.

countrynum inherited. Three-digit numerical code for country. In these data, the toy countrynum is 900.

statenum inherited. Two-digit numerical code for state, province, or territory. For these data, the toy number is 99.

route inherited. Three-digit code identifying the route, unique within states. For this dataset, 1.

rpid inherited. Three-digit run protocol identifier. Here, set to 101.

year inherited. Four-digit year of the survey.

AOU inherited. Five-digit species identification number.

count10 inherited. Total individuals of the species recorded on stops 1-10.

count20 inherited. Total individuals of the species recorded on stops 11-20.

count30 inherited. Total individuals of the species recorded on stops 21-30.

count40 inherited. Total individuals of the species recorded on stops 31-40.

count50 inherited. Total individuals of the species recorded on stops 40-50.

stoptotal inherited. Total number of stops (of 50), where the species was recorded.

speciestotal inherited. Total individuals of the species recorded across the entire run of the route (sum of stops).

Details

Nearly all column names are inherited from Pardieck et al. (2019) and are further explained in the Files and Fields Definitions document included as part of the Breeding Bird Survey data release.

The cleaning process removes unidentified species and those poorly sampled by Breeding Bird Survey methods (using the filter_bbs_survey function) and, for these data, filters the `year` to `1994` for rapid testing.

References

- Pardieck, K. L., Ziolkowski, D. J., Lutmerding, M., Aponte, V., & Hudson, M.-A. (2019). North American Breeding Bird Survey Dataset 1966—2018, version 2018.0. U.S. Geological Survey. https://doi.org/10.5066/P9HE8XYJ

`demo_route_raw` *Raw data for a hypothetical Breeding Bird Survey route.*

Description

A toy dataset for use in vignettes and function testing. It contains all the same column names as would be expected for a Breeding Bird survey route dataset downloaded, e.g. from ScienceBase or the Data Retriever (Pardieck et al. 2019). However, the actual data values are simulated data.

Usage

```
demo_route_raw
```

Format

A data frame with 1160 rows and 15 variables:

record_id inherited from data downloaded through the Data Retriever

routedataid inherited from Pardieck et al. 2018 (as are all following fields). Unique data identification number.

countrynum inherited. Three-digit numerical code for country. In these data, the toy countrynum is 900.

statenum inherited. Two-digit numerical code for state, province, or territory. For these data, the toy number is 99.

route inherited. Three-digit code identifying the route, unique within states. For this dataset, 1.

rpid inherited. Three-digit run protocol identifier. Here, set to 101.

year inherited. Four-digit year of the survey.

AOU inherited. Five-digit species identification number.

count10 inherited. Total individuals of the species recorded on stops 1-10.

count20 inherited. Total individuals of the species recorded on stops 11-20.

count30 inherited. Total individuals of the species recorded on stops 21-30.

count40 inherited. Total individuals of the species recorded on stops 31-40.

count50 inherited. Total individuals of the species recorded on stops 40-50.

stoptotal inherited. Total number of stops (of 50), where the species was recorded.

speciestotal inherited. Total individuals of the species recorded across the entire run of the route (sum of stops).

Details

Nearly all column names are inherited from Pardieck et al. (2019) and are further explained in the Files and Fields Definitions document included as part of the Breeding Bird Survey data release.

References

- Pardieck, K. L., Ziolkowski, D. J., Lutmerding, M., Aponte, V., & Hudson, M.-A. (2019). North American Breeding Bird Survey Dataset 1966—2018, version 2018.0. U.S. Geological Survey. https://doi.org/10.5066/P9HE8XYJ

`filter_bbs_survey` *Clean raw Breeding Bird Survey survey data*

Description

The raw data for the Breeding Bird Survey includes unidentified species and some species that are not well-sampled by the BBS methods. This function filters a dataframe to remove those species.

Usage

```
filter_bbs_survey(bbs_survey_data)
```

Arguments

`bbs_survey_data` data frame with columns for species and AOU

Value

bbs_survey_data with unidentified species, nightbirds, waterbirds, non-targets removed

Examples

```
head(filter_bbs_survey(demo_route_raw))
```

---

individual_metabolic_rate *Estimate individual-level BMR*

Description

Given an individual's body mass (in grams), use allometric scaling (Fristoe 2015) to estimate basal metabolic rate.

Usage

```
individual_metabolic_rate(mass)
```

Arguments

`mass` mass in grams

Value

estimated basal metabolic rate

References

- Fristoe, T. S. (2015). Energy use by migrants and residents in North American breeding bird communities. Global Ecology and Biogeography, 24(4), 406–415. https://doi.org/10.1111/geb.12262

Examples

```
individual_metabolic_rate(10)
```

known_species — *List of species known to* `birdsize`

Description

A table of the AOU (Pardieck et al 2019), genus, and species of the 443 species with species-specific data built in to `birdsize`.

Usage

```
known_species
```

Format

A data frame with 443 rows and 6 variables:

AOU AOU used in Paradieck et al. (2019)

genus genus, from Paradieck et al. (2019)

species species, from Paradieck et al. (2019)

References

- Pardieck, K.L., Ziolkowski Jr., D.J., Lutmerding, M., Aponte, V., and Hudson, M-A.R., 2019, North American Breeding Bird Survey Dataset 1966 - 2018 (ver. 2018.0): U.S. Geological Survey, Patuxent Wildlife Research Center, https://doi.org/10.5066/P9HE8XYJ.

pop_generate — *Simulate body masses for a population*

Description

Draws body mass measurements for a population of birds (of all the same species) given the population size and either (1) the species AOU or (2) the mean and potentially standard deviation of body mass for that species.

Usage

```
pop_generate(
  abundance = NA_integer_,
  AOU = NA_integer_,
  scientific_name = NA_character_,
  mean_size = NA_real_,
  sd_size = NA_real_,
  sim_species_id = 1
)
```

Arguments

`abundance`	integer number of individuals to draw. *Required*.
`AOU`	the numeric AOU code used for this species in the Breeding Bird Survey
`scientific_name`	as "Genus species"
`mean_size`	numeric, mean body mass (in grams) for this species.
`sd_size`	numeric, standard deviation of body mass for this species.
`sim_species_id`	defaults AOU or 1

Details

`abundance` is required, as well as *one of*: `AOU`, `scientific_name`, or `mean_size`.

Value

a dataframe with `abundance` rows - one record per individual - and columns for species attributes.

Specifically:

- `AOU`: the AOU, if provided
- `sim_species_id`: the `sim_species_id` if provided
- `scientific_name`: the scientific name if provided
- `individual_mass`: the simulated body mass (in grams) for this individual
- `individual_bmr`: the simulated basal metabolic rate for this individual
- `mean_size`: the mean body mass for this species (i.e. the parameter used for simulation)
- `sd_size`: the standard deviation of body mass for this species (i.e. the parameter used for simulation)
- `abundance`: the number of individuals simulated of this species (i.e. parameter used for simulation)
- `sd_method`: the method for finding the standard deviation for body mass for this species

Examples

```
pop_generate(abundance = 5, AOU = 2881)
pop_generate(abundance = 5, scientific_name = "Selasphorus calliope")
pop_generate(abundance = 5, mean_size = 20, sd_size = 3)
```

species_define *Define a species*

Description

Creates a list with taxonomic/identifying information and parameters for mean and standard deviation of body mass.

Usage

```
species_define(
  AOU = NA_integer_,
  scientific_name = NA_character_,
  mean_size = NA_real_,
  sd_size = NA_real_,
  sim_species_id = 1
)
```

Arguments

AOU	the numeric AOU code used for this species in the Breeding Bird Survey
scientific_name	the species' scientific name, as "Genus species"
mean_size	mean body size
sd_size	sd of body size
sim_species_id	identifier; if using taxonomic info, defaults to AOU. If not, defaults to 1. Supplying other values can be useful for simulation models.

Details

The identifying information used depends on which parameters are provided, with the following order of preference: AOU > scientific name > user provided mean and sd > user provided mean and estimated sd.

Value

list with species parameter information

Examples

```
species_define(AOU = 2881)
species_define(scientific_name = "Perdix perdix")
species_define(mean_size = 400, sd_size = 30)
species_define(mean_size = 400)
```

species_lookup *Species lookup*

Description

Given either AOU or scientific name, looks up a species' taxonomic information and mean and standard deviation of body size in sd_table.

Usage

```
species_lookup(AOU = NA_integer_, scientific_name = NA_character_)
```

Arguments

AOU	the numeric AOU code used for this species in the Breeding Bird Survey
scientific_name	the species' scientific name, as "Genus species"

Value

data frame with columns AOU, genus, species, mean_mass, mean_sd, contains_estimates, scientific_name

Examples

```
species_lookup(AOU = 2881)
species_lookup(scientific_name = "Selasphorus calliope")
```

toy_aou_community *Toy data frame of abundances and AOUs (for vignettes)*

Description

This data table is a toy data frame for the vignettes. It has abundances and AOU codes for 5 species to make up a hypothetical community.

Usage

```
toy_aou_community
```

Format

A data frame with 5 rows and 2 variables:

AOU AOU

abundance Number of individuals to simulate masses for

toy_size_community *Toy data frame of abundances and species mean sizes (for vignettes)*

Description

This data table is a toy data frame for the vignettes. It has abundances and mean body sizes for 5 species to make up a hypothetical community.

Usage

```
toy_size_community
```

Format

A data frame with 5 rows and 3 variables:

mean_size Mean mass, in g

abundance Number of individuals to simulate masses for

sim_species_id ID

toy_species_name_community *Toy data frame of abundances and species names (for vignettes)*

Description

This data table is a toy data frame for the vignettes. It has abundances and scientific names for 5 species to make up a hypothetical community.

Usage

```
toy_species_name_community
```

Format

A data frame with 5 rows and 2 variables:

scientific_name Scientific name

abundance Number of individuals to simulate masses for

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