

Package ‘pollimetry’

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Type Package

Title Estimate pollinator body size and co-varying ecological traits

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Description Tools to estimate pollinator body size and co-varying traits: bee tongue length and foraging distances. This package combines novel (described in Kendall et al. 2018) as well as pre-existing predictive allometries for pollinator body size, bee tongue length and foraging distance. Pre-existing body size equations are implemented for a variety of Diptera, Lepidoptera and Hymenoptera taxa.

Depends R (>= 3.0.0), brms (>= 2.4.0)

Imports stats, repmis

Suggests rstan, pollimetrydata

Additional_repositories <https://github.com/liamkendall/pollimetrydata>

License GPL (>= 2)

LazyData true

RoxygenNote 6.1.0

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bodysize	<i>Converts the intertegular distance (IT) and co-variables to body size in dry weight (mg) for bees or hoverflies.</i>
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Description

Calculates body size in dry weight (mg) from Kendall et al. (2018) using ITD (and co-variate) values.

Usage

```
bodysize(x, taxa, type)
```

Arguments

x	A data frame with columns containing 'IT' values and Sex ('Male' or 'Female'). Optional attributes depending on model choice: Taxonomy ('Family' for bees or 'Subfamily' for hoverflies), 'Region' (Currently only "NorthAmerica", "SouthAmerica", "Australasia" and "Europe" implemented) and 'Species' ("Genus_species" format). Non-implemented regions and/or species are acceptable. See details.
taxa	A vector specifying insect taxa of interest, can be either "bee" for bee models and "hov" for hoverfly models
type	A vector specifying model type to be used: for bees this can be either "taxo" for the full taxonomic model, "phy" for the full phylogenetic model or "IT" for the ITD-only model. In hoverflies: it can either be "taxo" for the full taxonomic model or "IT" for the ITD-only model.

Details

For bees, type option 'taxo' requires IT, sex and taxonomic family. Type option 'phylo' only requires ITD and Sex to run but should be only be used for with Species (and Region) included in model formulation n.b. the function checks for contained species.

For hoverflies, type 'taxo' requires ITD, Subfamily and Sex for each specimen. Type "ITD" for both taxa only requires ITD values (Optional: region and species but check 'setdiff'). If specimens are from included regions or species (see above) we recommend including these as additional columns. Estimates (and variance components) are returned as four additional columns bound to the original dataframe. In the likely case that non-represented taxa and regions are included in inputted datasets, 'allow_new_levels' is set to true for all models. Estimates will then be modelled with group-level uncertainty in the predictions based on the variation of the existing levels.

Value

The original dataframe (x) is returned along with four additional columns: body size (dry weight (mg)), S.E. and 95 percent confidence intervals.

References

Kendall et al. (2018) Pollinator size and its consequences: Predictive allometry for pollinating insects. In prep.

Examples

```
example=cbind.data.frame(IT=c(1.3,2.3),
                          Sex=c("Female","Male"),
                          Family=c("Apidae","Andrenidae"),
                          Region=c("NorthAmerica","Europe"),
                          Species=c("Ceratina_dupla","Andrena_flavipes"))
bodysize(x=example, taxa="bee", type="taxo")
```

foragedist	<i>Converts body weight to measures of foraging distance for bees.</i>
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Description

Calculates foraging distance from Greenleaf et al. (2007) using intertegular distance (ITD) values, van Nieuwstadt and Iraheta (1996) using head width (HW) values for Meliponini (stingless bees) and Guedot et al. (2009) using dry weight (mg) values for Osmia species.

Usage

```
foragedist(x, type = "GreenleafAll")
```

Arguments

x	A vector of either bee intertegular spans (IT) measurements in cm, head width values in mm or dry weight values (mg).
type	The type of foraging distance desired. Options are "GreenleafAll", GrMhd ("Maximum homing distance"), GrThd ("Typical homing distance"), GrMfd ("Maximum feeder training distance"), GrMcd("Maximum communication distance"), "Osmia", "MeliMR", "MeliFT" or "MeliAll". See details in Greenleaf et al. (2007), Guedot et al. (2009) and van Nieuwstadt and Iraheta (1996).

Value

A dataframe with bee and foraging distance (Km) is returned for each bees species.

References

Greenleaf et al. (2007) Bee foraging ranges and their relationship to body size. *Oecologia*, 153, 589-596. <doi:10.1007/s00442-007-0752-9>

Guedot et al. (2009). Relationship between body size and homing ability in the genus *Osmia* (Hymenoptera; Megachilidae). *Ecological Entomology*, 34(1), 158-161. <doi:10.1111/j.1365-2311.2008.01054.x>

van Nieuwstadt, M. G. L., & Iraheta, C. R. (1996). Relation between size and foraging range in stingless bees (Apidae, Meliponinae). *Apidologie*, 27(4), 219-228.

Examples

```
foragedist(c(10,5,2), type = "MeliMR")
```

headwidthsize	<i>Converts pollinator (Diptera, Hymenoptera and Lepidoptera) head width (mm) to body size (dry weight (mg)).</i>
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Description

Calculates dry body weight (mg) using head width (mm) from Hodar (1997).

Usage

```
headwidthsize(HW, Eq = "H97DB")
```

Arguments

HW	A vector of head width measurments (mm).
Eq	a vector of predictive allometries for insect taxa from Hodar (1997). Options implemented are: H97DB (Brachycera), H97DN (Nematocera), H97HA (Hymenoptera), H97LH (Heterocera) and H97LR (Rhopalocera).

Value

A dataframe with pollinator body size as dry weight (mg) is returned for each specimen from selected equation.

References

Kendall et al. (2018) Pollinator size and its consequences: Predictive allometry for pollinating insects.

Hodar, J. A. (1997). The use of regresion equations for the estimation of prey length and biomass in diet studies of insectivore vertebrates. *Miscellania Zoologica*, 20(2), 1-10.

Examples

```
headwidthsize(HW=c(10,5,2), Eq = c("H97DB"))
```

lengthsize	<i>Converts body length to body size (body weight (mg)) for three pollinating insect groups (Diptera, Hymenoptera and Lepidoptera).</i>
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Description

Calculates body size as dry weight (mg) from existing allometries (See 'Details') using body length values (mm).

Usage

```
lengthsize(BL, Eq = "DIP")
```

Arguments

BL	A vector of pollinator body length (BL) measurements (mm).
Eq	A vector specifying which predictive allometry to use. Acronyms denote first (and second author), publication date and taxon. DIP, HYM and LEP options are cases where authors modelled body size across all specimens within each order. Options implemented are: DIP (10 equations): BN06D, G97D, GR84D, JS00DA, R77D, S80DCF, S80DCR, S80DMF, S93DA, W13D) Brachycera (2 equations): S93DB, Sabo02DB Nematocera (3 equations): JS00DN, S93DN, Sabo02DN; Asilidae (2 equations): Sabo02DA, S93DB; Bombyliidae (2 equations): S93DB, Sabo02DBB; Cyclorrapha: S93DC HYM (12 equations): BN06H1, G97H, G97F, GR84H, JS00HA, R77H, S80HCF, S80HCR, S80HMF, S93HA, Sabo02H, W13H Formicidae (13 equations): BN06HF, GR84F, JS00HF, R77A, S80FCF, S80FCR, S80FMF, S93HF, S93HH, S93HI, BN06H1, G97H, G97F Apidae: Sabo02HA; Braconidae: S93HB; Halictidae: S93HH; Ichneumonidae: S93HI; Pompilidae: S93HP; Vespidae: S93HV and Sabo02HV LEP(9 equations): BN06L, G97L, JS00L, R77L, S80LCF, S80LCR, S80LMF, S93LA, W13L Noctuidae: S93LC, S93LN; Geometridae: S93LG; Microlepidoptera: S93LM; Arctiinae: S93LC.

Value

A dataframe with pollinator body size (mg) is returned for each species from selected equation/s.

References

Full reference list is available within Kendall et al. (2018) Pollinator size and its consequences: Predictive allometry for pollinating insects. In prep.

Examples

```
lengthsize(BL=c(10,5,2), Eq = c("S80DCR"))
```

lengthwidthsize	<i>Converts pollinator body length*body width to body size (dry weight (mg)).</i>
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Description

Calculates body size as dry weight (mg) from the equations described by Sample (1993) and others using body length*body width values (mm).

Usage

```
lengthwidthsize(BLW, Eq = "DIP")
```

Arguments

BLW	A vector of fly body length*body width measurments (mm).
Eq	a vector of a predictive allometry for Diptera, Hymenoptera or Lepidoptera. Options implemented are:

Value

A dataframe with body size, as dry weight (mg) is returned for each specimen from selected equation.

References

Kendall et al. (2018) Pollinator size and its consequences: Predictive allometry for pollinating insects. In prep.

Sample et al. (1993) Estimation of insect biomass by length and width. American Midland Naturalist, 234-240.

Examples

```
lengthwidthsize(BLW=c(3,5,2), Eq = c("Brachycera"))
```

pollimetry_dataset	<i>Body size and intertegular distance measurements of ~4500 pollinating insect specimens.</i>
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Description

A dataset containing the body size in dry weight (mg), intertegular distance (mm), body length (mg) and metadata for 4438 measured bee and hoverfly specimens.

Usage

```
pollimetry_dataset
```

Format

An object of class data.frame with 4438 rows and 25 columns.

tonguelength	<i>Converts ITD (cm) to tongue length for bees.</i>
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Description

Calculates tongue length (mm) from Cariveau et al. (2015) using intertegular distance (ITD) values (cm)..

Usage

```
tonguelength(IT, family, mouthpart = "all")
```

Arguments

- IT A vector of bee intertegular distance (IT) measurments in cm.
- family a vector of bee families. Only implemented 5 out of the extant 7 families: "Andrenidae", "Apidae", "Colletidae", "Halictidae", "Megachilidae".
- mouthpart The mouth part you are interested in. Options are "all", glossa", "prementum" and "tongue" (i.e. gloss + prementum)

Value

A dataframe with bee tongue length (mm) is returned for each bees species.

References

Cariveau et al. (2016) The allometry of bee tongue length an its uses in ecology and evolution.
PLoS ONE 11(3): e0151482 <doi:10.1371/journal.pone.0151482>

Examples

```
tonguelength(IT=c(10,5,2), family = c("Andrenidae", "Apidae", "Colletidae"))  
tonguelength(IT=c(10,5,2), family = c("Andrenidae", "Apidae", "Colletidae"), mouthpart = "tongue")
```

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