Package: IDmeasurer (via r-universe)

August 22, 2024

Type Package

Title Assessment of Individual Identity in Animal Signals

Version 1.0.0

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Description Provides tools for assessment and quantification of individual identity information in animal signals. This package accompanies a research article by Linhart et al. (2019) <doi:10.1101/546143>: ``Measuring individual identity information in animal signals: Overview and performance of available identity metrics''.

Depends R (>= 2.10)

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Encoding UTF-8

LazyData true

Imports MASS, infotheo, lme4

RoxygenNote 6.1.1

Suggests knitr, rmarkdown

VignetteBuilder knitr

NeedsCompilation no

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Repository CRAN

Date/Publication 2019-05-09 15:10:10 UTC

Contents

`ANmodulation` *Little owl,* Athene noctua *- frequency modulation*

Description

- **Species:** Little owl, *Athene noctua*
- **Number of individuals:** 33
- **Number of calls per individual:** 10
- **Number of acoustic variables:** 11
- **Individual identity:** HS=3.48
- **Reference:** Linhart, P., & Salek, M. (2017). The assessment of biases in the acoustic discrimination of individuals. PLOS ONE, 12(5), e0177206. doi:10.1371/journal.pone.0177206

Calls of little owls were collected in Czech Republic and Hungary. Territorial calls of each male were recorded for three minutes after a short playback provocation (1 min) inside their territories from up to 50 m distance from the individuals. The recordings were made during comparable, favourable meteorological conditions (without strong wind or precipitation), from sunset until midnight between March and April of 2013 and 2014. This period covered the mating season. The period and the time of the day for recording were selected with regard to the peak in vocal activity of little owls both within a day and within a season. The original dataset included 54 males with more than 20 calls each (20-41 calls per individual, mean, SD = 26.9, 6.0) with good recording quality.The number of individuals and calls per individual was reduced to match parameters of the other datasets.

Eleven variables were measured to describe the modulation of the fundamental frequency within the call (shape of the call on spectrogram) and the duration of the call. Fundamental frequency was measured at ten measuring points spread equidistantly throughout the call duration. Variables were extracted in SASLab Pro by Avisoft.

Usage

```
ANmodulation
```

Format

A data frame with 330 rows and 12 variables:

id factor, identity code of an individual emitting the call

f1, f3, f5, f7, f9, f11, f13, f15, f17, f19 fundamental frequency at the specific measuring point, in Hertz

dur numeric, duration of the call, in seconds

Source

Linhart, P., & Salek, M. (2017). The assessment of biases in the acoustic discrimination of individuals. PLOS ONE, 12(5), e0177206. doi:10.1371/journal.pone.0177206

`ANspec` *Little owl,* Athene noctua - *spectrum properties*

Description

- **Species:** Little owl, *Athene noctua*
- **Number of individuals:** 33
- **Number of calls per individual:** 10
- **Number of acoustic variables:** 7
- **Individual identity:** HS=4.68
- **Reference:** Linhart, P., & Salek, M. (2017). The assessment of biases in the acoustic discrimination of individuals. PLOS ONE, 12(5), e0177206. doi:10.1371/journal.pone.0177206

Calls of little owls were collected in Czech Republic and Hungary. Territorial calls of each male were recorded for three minutes after a short playback provocation (1 min) inside their territories from up to 50 m distance from the individuals. The recordings were made during comparable, favourable meteorological conditions (without strong wind or precipitation), from sunset until midnight between March and April of 2013 and 2014. This period covered the mating season. The period and the time of the day for recording were selected with regard to the peak in vocal activity of little owls both within a day and within a season. The original dataset included 54 males with more than 20 calls each (20-41 calls per individual, mean, SD = 26.9, 6.0) with good recording quality.The number of individuals and calls per individual was reduced to match parameters of the other datasets.

Variables were selected to measure basic parameters of call spectrum like the peak frequency, distribution of frequency amplitudes within spectrum, and range of the frequencies (minimum and maximum). Additionally, the duration of the call was measured. Variables were extracted in SASLab Pro by Avisoft.

Usage

```
ANspec
```

Format

A data frame with 330 rows and 8 variables:

id factor, identity code of an individual emitting the call

dur duration of the call, in seconds

df frequency of maximum amplitude within the spectrum - peak frequency, in Hertz

minf, maxf minimum and maximum fequency at -25dB relative to the call peak amplitude, in Hertz

q25, q50, q75 frequencies at the three quartiles of amplitude distribution; frequencies below which lie 25, 50 and 75 percent of the energy of the call, respectively, in Hertz

Source

Linhart, P., & Salek, M. (2017). The assessment of biases in the acoustic discrimination of individuals. PLOS ONE, 12(5), e0177206. doi:10.1371/journal.pone.0177206

`calcDistT` *Calculate total distance in given dataset*

Description

This function calculates centroid of all samples in a given dataset and sums distances between the centroid and each sample. Euclidean distances are used.

Usage

```
calcDistT(df)
```

Arguments

`df`	A data frame with the first column indicating individual identity.

Value

Numeric. Total distance.

See Also

Other calcHM support function: `calcDistW`, `calcMeanVec`

Examples

```
calcDistT(ANmodulation)
```

`calcDistW` *Calculate average within individual distance*

Description

This function calculates centroid for each individual and sums distances of samples from centroid for that particular individual. When the within individual sum of distances is known for each individual, it calculates their mean. Euclidean distances are used.

Usage

```
calcDistW(df)
```

Arguments

`df`	A data frame with the first column indicating individual identity.

Value

Numeric. Average within individual distance in dataset.

See Also

Other calcHM support function: `calcDistT`, `calcMeanVec`

Examples

```
calcDistW(ANmodulation)
```

`calcDS` *Calculates discrimination score (DS)*

Description

This function will take the specified data frame and will perform linear discrimination analysis with leave-one-out crossvalidation and equal priors for each individual (e.g., all priors will be set to 1/10 in case that the dataset contains 10 individuals). Variables are not modified in any way; scaling, centering, transformation of variables, or principal component analysis, etc., if required, need to be done on dataset before calling this function.

Reference: e.g. Hafner, G. W., Hamilton, C. L., Steiner, W. W., Thompson, T. J., & Winn, H. E. (1979). Signature information in the song of the humpback whale. Journal of the Acoustical Society of America, 66, 1-6. doi:10.1121/1.383072

Usage

```
calcDS(df)
```

Arguments

`df`	A data frame with the first column noting individual identity of the sample.

Value

Proportion of samples correctly classified by LDA in `df`.

See Also

Other individual identity metrics: `calcF`, `calcHM`, `calcHSngroups`, `calcHSnpergroup`, `calcHSntot`, `calcHSvarcomp`, `calcHS`, `calcMI`, `calcPICbetweenmeans`, `calcPICbetweentot`, `calcPIC`

Examples

```
calcDS(ANmodulation)
```

`calcF` *Calculate F-values for individual identity traits*

Description

This function calculates ANOVA F-values (type I sum of squares) for all identity traits in dataset along with its significance. Each trait is used as dependent and identity code as independent variable.

Reference: e.g., Miller, D. B. (1978). Species-typical and individually distinctive acoustic features of crow calls of red jungle fowl. Zeitschrift Fur Tierpsychologie-Journal of Comparative Ethology, 47, 182–193.

Usage

```
calcF(df)
```

Arguments

`df`	A data frame with the first column indicating individual identity.

Value

A data frame with 11 rows and 3 columns (trait, f-value, and p-value).

See Also

Other individual identity metrics: `calcDS`, `calcHM`, `calcHSngroups`, `calcHSnpergroup`, `calcHSntot`, `calcHSvarcomp`, `calcHS`, `calcMI`, `calcPICbetweenmeans`, `calcPICbetweentot`, `calcPIC`

Examples

```
calcF(ANmodulation)
```

`calcHM` *Calculate information capacity (HM)*

Description

This function calculates information capacity of a signal.

Reference: Searby, A., & Jouventin, P. (2004). How to measure information carried by a modulated vocal signature? Journal of the Acoustical Society of America, 116, 3192-3198. doi:10.1121/1.1775271

Usage

```
calcHM(df)
```

Arguments

`df`	A data frame with the first column indicating individual identity.

Value

Numeric value. Individual identity information capacity HM (in bits) in dataset.

See Also

Other individual identity metrics: `calcDS`, `calcF`, `calcHSngroups`, `calcHSnpergroup`, `calcHSntot`, `calcHSvarcomp`, `calcHS`, `calcMI`, `calcPICbetweenmeans`, `calcPICbetweentot`, `calcPIC`

Examples

```
calcHM(ANmodulation)
```

`calcHS` *Calculate Beecher's information statistic (HS, variant = HSnpergroup)*

Description

This function calculates Beecher's information statistic (HS) for all variables within the dataset.

Reference: Beecher, M. D. (1989). Signaling Systems for Individual Recognition - an Information-Theory Approach. Animal Behaviour, 38, 248-261. doi:10.1016/S0003-3472(89)80087-9.

`calcHS` (equivalent to `calcHSnpergroup`) is the correct variant of the function calculating Beechers information statistic. The other variants use total sample size (`calcHSntot`) or number of individuals in dataset (`calcHSngroups`) instead of number of samples per individual to calculate HS. `calcHSvarcomp` calculates HS from variance components of mixed models. HS values calculated by `calcHSvarcomp` were found to be twice as large compared to HS calculated by standard approach.

Please note, `sumHS = TRUE` should be used in datasets where individuality traits are uncorrelated. If traits are correlated, Principal component analysis (PCA) should be applied and HS should be calculated on uncorrelated principal componenets instead of original trait variables.

Usage

```
calcHS(df, sumHS = TRUE)
```

Arguments

`df`	A data frame with the first column indicating individual identity.
`sumHS`	`sumHS = TRUE` (default) will sum partial HS values of each trait variable; `sumHS = FALSE` provides partial HS values separately for each individuality trait in a dataset.

Value

For `sumHS = TRUE`: Numeric vector of two elements indicating indicating: 1) HS summed over variables that significantly differ between individuals (in one-way Anova with individual as independent and a specific signal trait as dependent variable; or 2) HS summed over all variables in dataset.

For `sumHS = FALSE`: Data frame with thre columns and number of rows equal to number of variables in dataset. First column includes names of traits considered for individuality. Second column includes significance test for each trait (from one-way ANOVA with individual identity as independent factor and trait as dependent variable). Third column includes values of HS for each variable trait.

See Also

Other individual identity metrics: `calcDS`, `calcF`, `calcHM`, `calcHSngroups`, `calcHSnpergroup`, `calcHSntot`, `calcHSvarcomp`, `calcMI`, `calcPICbetweenmeans`, `calcPICbetweentot`, `calcPIC`

Examples

```
calcHS(ANmodulation)
temp <- calcPCA(ANmodulation)
calcHS(temp)
```

`calcHSngroups` *Calculate Beecher's information statistic (HS, variant = HSngroups)*

Description

This function calculates Beecher's information statistic (HS) for all variables within the dataset.

Reference: from Beecher, M. D. (1989). Signaling Systems for Individual Recognition - an Information-Theory Approach. Animal Behaviour, 38, 248-261. doi:10.1016/S0003-3472(89)80087-9.

`calcHS` (equivalent to `calcHSnpergroup`) is the correct variant of the function calculating Beechers information statistic. The other variants use total sample size (`calcHSntot`) or number of individuals in dataset (`calcHSngroups`) instead of number of samples per individual to calculate HS. `calcHSvarcomp` calculates HS from variance components of mixed models. HS values calculated by `calcHSvarcomp` were found to be twice as large compared to HS calculated by standard approach.

Please note, `sumHS = TRUE` should be used in datasets where individuality traits are uncorrelated. If traits are correlated, Principal component analysis (PCA) should be applied and HS should be calculated on uncorrelated principal componenets instead of original trait variables.

Usage

```
calcHSngroups(df, sumHS = T)
```

Arguments

`df`	A data frame with the first column indicating individual identity.
`sumHS`	`sumHS = TRUE` (default) will sum partial HS values of each trait variable; `sumHS = FALSE` provides partial HS values separately for each individuality trait in a dataset.

Value

For `sumHS = TRUE`: Numeric vector of two elements indicating indicating: 1) HS summed over variables that significantly differ between individuals (in one-way Anova with individual as independent and a specific signal trait as dependent variable; or 2) HS summed over all variables in dataset.

For `sumHS = FALSE`: Data frame with thre columns and number of rows equal to number of variables in dataset. First column includes names of traits considered for individuality. Second column includes significance test for each trait (from one-way ANOVA with individual identity as independent factor and trait as dependent variable). Third column includes values of HS for each variable trait.

See Also

Other individual identity metrics: `calcDS`, `calcF`, `calcHM`, `calcHSnpergroup`, `calcHSntot`, `calcHSvarcomp`, `calcHS`, `calcMI`, `calcPICbetweenmeans`, `calcPICbetweentot`, `calcPIC`

Examples

```
calcHSngroups(ANmodulation)
temp <- calcPCA(ANmodulation)
calcHSngroups(temp)
```

`calcHSnpergroup` *Calculate Beecher's information statistic (HS, variant = HSnpergroup)*

Description

This function calculates Beecher's information statistic (HS) for all variables within the dataset.

Reference: from Beecher, M. D. (1989). Signaling Systems for Individual Recognition - an Information-Theory Approach. Animal Behaviour, 38, 248-261. doi:10.1016/S0003-3472(89)80087-9.

`calcHS` (equivalent to `calcHSnpergroup`) is the correct variant of the function calculating Beechers information statistic. The other variants use total sample size (`calcHSntot`) or number of individuals in dataset (`calcHSngroups`) instead of number of samples per individual to calculate HS. `calcHSvarcomp` calculates HS from variance components of mixed models. HS values calculated by `calcHSvarcomp` were found to be twice as large compared to HS calculated by standard approach.

Please note, `sumHS = TRUE` should be used in datasets where individuality traits are uncorrelated. If traits are correlated, Principal component analysis (PCA) should be applied and HS should be calculated on uncorrelated principal componenets instead of original trait variables.

Usage

```
calcHSnpergroup(df, sumHS = TRUE)
```

Arguments

`df`	A data frame with the first column indicating individual identity.
`sumHS`	`sumHS = TRUE` (default) will sum partial HS values of each trait variable; `sumHS = FALSE` provides partial HS values separately for each individuality trait in a dataset.

Value

For `sumHS = TRUE`: Numeric vector of two elements indicating indicating: 1) HS summed over variables that significantly differ between individuals (in one-way Anova with individual as independent and a specific signal trait as dependent variable; or 2) HS summed over all variables in dataset.

For `sumHS = FALSE`: Data frame with thre columns and number of rows equal to number of variables in dataset. First column includes names of traits considered for individuality. Second column includes significance test for each trait (from one-way ANOVA with individual identity as independent factor and trait as dependent variable). Third column includes values of HS for each variable trait.

See Also

`calcPIC`, `calcHS`

Other individual identity metrics: `calcDS`, `calcF`, `calcHM`, `calcHSngroups`, `calcHSntot`, `calcHSvarcomp`, `calcHS`, `calcMI`, `calcPICbetweenmeans`, `calcPICbetweentot`, `calcPIC`

Examples

```
calcHSnpergroup(ANmodulation)
temp <- calcPCA(ANmodulation)
calcHSnpergroup(temp)
```

`calcHSntot` *Calculate Beecher's information statistic (HS, variant = HSntot)*

Description

This function calculates Beecher's information statistic (HS) for all variables within the dataset.

Reference: from Beecher, M. D. (1989). Signaling Systems for Individual Recognition - an Information-Theory Approach. Animal Behaviour, 38, 248-261. doi:10.1016/S0003-3472(89)80087-9.

`calcHS` (equivalent to `calcHSnpergroup`) is the correct variant of the function calculating Beechers information statistic. The other variants use total sample size (`calcHSntot`) or number of individuals in dataset (`calcHSngroups`) instead of number of samples per individual to calculate HS. `calcHSvarcomp` calculates HS from variance components of mixed models. HS values calculated by `calcHSvarcomp` were found to be twice as large compared to HS calculated by standard approach.

Please note, `sumHS = TRUE` should be used in datasets where individuality traits are uncorrelated. If traits are correlated, Principal component analysis (PCA) should be applied and HS should be calculated on uncorrelated principal componenets instead of original trait variables.

Usage

```
calcHSntot(df, sumHS = T)
```

Arguments

`df`	A data frame with the first column indicating individual identity.
`sumHS`	`sumHS = TRUE` (default) will sum partial HS values of each trait variable; `sumHS = FALSE` provides partial HS values separately for each individuality trait in a dataset.

Value

For `sumHS = TRUE`: Numeric vector of two elements indicating indicating: 1) HS summed over variables that significantly differ between individuals (in one-way Anova with individual as independent and a specific signal trait as dependent variable; or 2) HS summed over all variables in dataset.

For `sumHS = FALSE`: Data frame with thre columns and number of rows equal to number of variables in dataset. First column includes names of traits considered for individuality. Second column includes significance test for each trait (from one-way ANOVA with individual identity as independent factor and trait as dependent variable). Third column includes values of HS for each variable trait.

See Also

`calcPIC`, `calcHS`

Other individual identity metrics: `calcDS`, `calcF`, `calcHM`, `calcHSngroups`, `calcHSnpergroup`, `calcHSvarcomp`, `calcHS`, `calcMI`, `calcPICbetweenmeans`, `calcPICbetweentot`, `calcPIC`

Examples

```
calcHSntot(ANmodulation)
temp <- calcPCA(ANmodulation)
calcHSntot(temp)
```

`calcHSvarcomp` *Calculate Beecher's information statistic (HS, variant = HSvarcomp)*

Description

This function calculates Beecher's information statistic (HS) for all variables within the dataset.

Reference: from Beecher, M. D. (1989). Signaling Systems for Individual Recognition - an Information-Theory Approach. Animal Behaviour, 38, 248-261. doi:10.1016/S0003-3472(89)80087-9.

`calcHS` (equivalent to `calcHSnpergroup`) is the correct variant of the function calculating Beechers information statistic. The other variants use total sample size (`calcHSntot`) or number of individuals in dataset (`calcHSngroups`) instead of number of samples per individual to calculate HS. `calcHSvarcomp` calculates HS from variance components of mixed models. HS values calculated by `calcHSvarcomp` were found to be twice as large compared to HS calculated by standard approach.

Please note, `sumHS = TRUE` should be used in datasets where individuality traits are uncorrelated. If traits are correlated, Principal component analysis (PCA) should be applied and HS should be calculated on uncorrelated principal componenets instead of original trait variables.

Usage

```
calcHSvarcomp(df, sumHS = T)
```

Arguments

`df`	A data frame with the first column indicating individual identity.
`sumHS`	`sumHS = TRUE` (default) will sum partial HS values of each trait variable; `sumHS = FALSE` provides partial HS values separately for each individuality trait in a dataset.

Value

For `sumHS = TRUE`: Numeric vector of two elements indicating indicating: 1) HS summed over variables that significantly differ between individuals (in one-way Anova with individual as independent and a specific signal trait as dependent variable; or 2) HS summed over all variables in dataset.

For `sumHS = FALSE`: Data frame with thre columns and number of rows equal to number of variables in dataset. First column includes names of traits considered for individuality. Second column includes significance test for each trait (from one-way ANOVA with individual identity as independent factor and trait as dependent variable). Third column includes values of HS for each variable trait.

See Also

`calcPIC`, `calcHS`

Other individual identity metrics: `calcDS`, `calcF`, `calcHM`, `calcHSngroups`, `calcHSnpergroup`, `calcHSntot`, `calcHS`, `calcMI`, `calcPICbetweenmeans`, `calcPICbetweentot`, `calcPIC`

Examples

```
calcHSvarcomp(ANmodulation)
temp <- calcPCA(ANmodulation)
calcHSvarcomp(temp)
```

`calcMeanVec` *Calculate the centroid of the individual identity traits*

Description

This function calculates centroid of the individual identity traits. Euclidean distances are used.

Usage

```
calcMeanVec(df)
```

Arguments

`df`	A data frame with the individual identity traits without identity codes (NA will be produced for the column with identity code).

Value

Numeric vector with the centroid values for each trait.

See Also

Other calcHM support function: `calcDistT`, `calcDistW`

Examples

```
#incorrect use (with identity codes, NA will be produced):
calcMeanVec(ANmodulation)

#correct use (with identity codes removed)
calcMeanVec(ANmodulation[-1])
```

`calcMI` *Calculate Mutual information (MI)*

Description

This function calculates Mutual information of actual and predicted individual identities in the dataset. It uses Linear discrimination analysis (MASS::lda) to predict individual identity. Settings for LDA are identical to those used in `calcDS` function, i.e., LDA uses leave-one-out cross-validation and priors are equal for each individual in dataset.

Reference: Mathevon, N., Koralek, A., Weldele, M., Glickman, S. E., & Theunissen, F. E. (2010). What the hyena's laugh tells: Sex, age, dominance and individual signature in the giggling call of Crocuta crocuta. BMC Ecology, 10, 9-Article No.: 9. doi:10.1186/1472-6785-10-9

Usage

```
calcMI(df)
```

Arguments

`df`	A data frame with the first column indicating individual identity.

Value

Numeric value of mutual information (in bits).

See Also

`calcPIC`, `calcHS`

Other individual identity metrics: `calcDS`, `calcF`, `calcHM`, `calcHSngroups`, `calcHSnpergroup`, `calcHSntot`, `calcHSvarcomp`, `calcHS`, `calcPICbetweenmeans`, `calcPICbetweentot`, `calcPIC`

Examples

```
calcMI(ANmodulation)
```

`calcPCA` *Convert raw trait variables into principal components*

Description

This function subjects the trait variables from the original dataset to the Principal component analysis (PCA, `stats:prcomp`) and calculates principal componenets scores for each sample. All variables are centered by subtracting the variable mean from a particular value and scaled to the unit variance by dividing the value by the standard deviation of a trait (`stats::prcomp` parameters `center = T`, `scale = T`). Some functions like, for example, `calcHS` require uncorrelated input variables to calculate individual identity information properly.

Usage

```
calcPCA(df)
```

Arguments

`df`	A data frame with the first column indicating individual identity.

Value

df A data frame with the same attributes like the `df`, but the original individuality traits are replaced by principal components.

Examples

```
summary(ANmodulation)
temp <- calcPIC(ANmodulation)
summary(temp)
```

`calcPIC` *Calculates potential of identity coding (PIC, variant=PICbetweentot)*

Description

This function calculates Potential of individual coding for all variables within the dataset.

Reference: Robisson, P. (1992). Roles of pitch and duration in the discrimination of the mate's call in the King penguin Aptenodytes patagonicus. Bioacoustics, 4, 25-36.

Usage

```
calcPIC(df)
```

Arguments

`df`	A data frame with the first column indicating individual identity.

Value

Numeric vector with PIC values for each variable in `df`.

See Also

Other individual identity metrics: `calcDS`, `calcF`, `calcHM`, `calcHSngroups`, `calcHSnpergroup`, `calcHSntot`, `calcHSvarcomp`, `calcHS`, `calcMI`, `calcPICbetweenmeans`, `calcPICbetweentot`

Examples

```
calcPIC(ANmodulation)
```

`calcPICbetweenmeans` *Calculates potential of identity coding (PIC, variant=PICbetweenmeans)*

Description

This function calculates Potential of individual coding for all variables within the dataset.

Reference: Robisson, P. (1992). Roles of pitch and duration in the discrimination of the mate's call in the King penguin Aptenodytes patagonicus. Bioacoustics, 4, 25-36.

Usage

```
calcPICbetweenmeans(df)
```

Arguments

`df`	A data frame with the first column indicating individual identity.

Value

Numeric vector with PIC values for each variable in `df`.

See Also

Other individual identity metrics: `calcDS`, `calcF`, `calcHM`, `calcHSngroups`, `calcHSnpergroup`, `calcHSntot`, `calcHSvarcomp`, `calcHS`, `calcMI`, `calcPICbetweentot`, `calcPIC`

Examples

```
calcPICbetweenmeans(ANmodulation)
```

`calcPICbetweentot` *Calculates potential of identity coding (PIC, variant=PICbetweentot)*

Description

This function calculates Potential of individual coding for all variables within the dataset.

Reference: Robisson, P. (1992). Roles of pitch and duration in the discrimination of the mate's call in the King penguin Aptenodytes patagonicus. Bioacoustics, 4, 25-36.

Usage

```
calcPICbetweentot(df)
```

Arguments

`df`	A data frame with the first column indicating individual identity.

Value

Numeric vector with PIC values for each variable in `df`.

See Also

Other individual identity metrics: `calcDS`, `calcF`, `calcHM`, `calcHSngroups`, `calcHSnpergroup`, `calcHSntot`, `calcHSvarcomp`, `calcHS`, `calcMI`, `calcPICbetweenmeans`, `calcPIC`

Examples

```
calcPICbetweentot(ANmodulation)
```

`CCformants` *Corncrake,* Crex crex *- formants*

Description

- **Species:** Corncrake, *Crex crex*
- **Number of individuals:** 33
- **Number of calls per individual:** 10
- **Number of acoustic variables:** 4
- **Individual identity:** HS=10.51
- **Reference:** Budka, M., & Osiejuk, T. S. (2013). Formant Frequencies are Acoustic Cues to Caller Discrimination and are a Weak Indicator of the Body Size of Corncrake Males. Ethology, 119, 960-969. doi:10.1111/eth.12141

Corncrake calls were recorded at three sites in Poland and one in the Czech Republic Recordings were made during the corncrake breeding season, from 8 to 30 July, in 2011 and in 2012. Males were recorded when calling spontaneously, in favourable conditions, at night (from 22.00 to 03.30, local time) from a distance of ca. 5-10 m. The original dataset comprised 104 males with 10 calls measured from each male.

Formants (second to fifth) were measured within the first syllable of the call. Formants were extracted by PRAAT.

Usage

```
CCformants
```

Format

A data frame with 330 rows and 5 variables:

id factor, identity code of an individual emitting the call

s1f2, s1f3, s1f4, s1f5 formants 2 to 5, respectively, measured within the first syllable of the call, in Hertz

Source

Budka, M., & Osiejuk, T. S. (2013). Formant Frequencies are Acoustic Cues to Caller Discrimination and are a Weak Indicator of the Body Size of Corncrake Males. Ethology, 119, 960-969. doi:10.1111/eth.12141

`CCspec` *Corncrake,* Crex crex *- spectrum properties*

Description

- **Species:** Corncrake, *Crex crex*
- **Number of individuals:** 33
- **Number of calls per individual:** 10
- **Number of acoustic variables:** 7
- **Individual identity:** HS=5.68
- **Reference:** Budka, M., & Osiejuk, T. S. (2013). Formant Frequencies are Acoustic Cues to Caller Discrimination and are a Weak Indicator of the Body Size of Corncrake Males. Ethology, 119, 960-969. doi:10.1111/eth.12141

Corncrake calls were recorded at three sites in Poland and one in the Czech Republic Recordings were made during the corncrake breeding season, from 8 to 30 July, in 2011 and in 2012. Males were recorded when calling spontaneously, in favourable conditions, at night (from 22.00 to 03.30, local time) from a distance of ca. 5-10 m. The original dataset comprised 104 males with 10 calls measured from each male.

Seven variables were selected to measure duration of the first syllable of the call and its basic spectral parameters of each first syllable of the call like the peak frequency, distribution of frequency amplitudes within spectrum, and range of the frequencies (minimum and maximum). Additionally, the duration of the call was measured. Variables were extracted in SASLab Pro by Avisoft.

Usage

```
CCspec
```

Format

A data frame with 330 rows and 8 variables:

id factor, identity code of an individual emitting the call

dur duration of the call, in seconds

df frequency of maximum amplitude within the spectrum - peak frequency, in Hertz

minf, maxf minimum and maximum fequency at -25dB relative to the call peak amplitude, in Hertz

q25, q50, q75 frequencies at the three quartiles of amplitude distribution; frequencies below which lie 25, 50 and 75 percent of the energy of the call, respectively, in Hertz

Source

Budka, M., & Osiejuk, T. S. (2013). Formant Frequencies are Acoustic Cues to Caller Discrimination and are a Weak Indicator of the Body Size of Corncrake Males. Ethology, 119, 960-969. doi:10.1111/eth.12141

`convertDStoHS` *Convert DS to HS*

Description

This function converts DS to HS. Because the model used to convert values is derived from `stats::loess model`, it cannot make predictions outside the range of the values used to construct the model. The model was tailored to the sampling frequently used by studies on individuality:
- number of individuals should be between 5 and 40 individuals
- number of observations per individual should be between 5 - 20
- DS value should be between 0 - 1

Consider increasing your sampling if number of individuals and/or number of observations are lower than 5. If number of individuals and observations exceeds the function limits, it might be acceptable to use the largest possible values allowed by the model to get the estimate - biases get smaller with larger sampling, so, if your sampling exceeds function limits a little bit, the estimate should be still quite precise.

Usage

```
convertDStoHS(nindivs, nobs, DS, se = FALSE)
```

Arguments

`nindivs`	Number of individuals. Must be within 5-40 individuals.
`nobs`	Number of observations per individual. Must be within 5-20 observations.
`DS`	DS value to be converted into HS. Must be within 0-1.
`se`	should standard errors be computed (takes more time)?

Value

If `se = FALSE`, Numeric value. DS for a specified number of individuals and number of observations per individual.
If `se = TRUE`, a list containing components fit, se, residual.scale, df. See `predict.loess` for more details.

See Also

Other metric conversion: `convertHStoDS`

Examples

```
convertDStoHS(nindivs=10, nobs=10, DS=0.7)
```

`convertHStoDS` *Convert HS to DS*

Description

This function converts HS to DS. Because the model used to convert values is derived from `stats::loess model` model, it cannot make predictions outside the range of the values used to construct the model.
Our model was tailored to the values frequently used by studies on individuality:
- number of individuals should be between 5 and 40 individuals
- number of observations per individual should be between 5 - 20
- HS value should be between 0 - 12.9

Consider increasing your sampling if number of individuals and number of observations are lower than 5. If number of individuals and observations exceeds the function limits, it might be possible to use the largest possible values allowed by the model to get the estimate - biases get smaller with large sampling, so, if your sampling exceeds function limits a little bit, the estimate should be still quite precise.

Usage

```
convertHStoDS(nindivs, nobs, HS, se = FALSE)
```

Arguments

`nindivs`	Number of individuals. Must be within 5-40 individuals.
`nobs`	Number of observations per individual. Must be within 5-20 observations.
`HS`	HS value to be converted into DS. Must be within 0-12.9 bits.
`se`	should standard errors be computed (takes more time)?

Value

If `se = FALSE`, Numeric value. DS for a specified number of individuals and number of observations per individual.
If `se = TRUE`, a list containing components fit, se, residual.scale, df. See `predict.loess` for more details.

See Also

Other metric conversion: `convertDStoHS`

Examples

```
convertHStoDS(nindivs=10, nobs=10, HS=5)
```

`GenerateMultivariate` *Generate dataset with multiple individual identity traits*

Description

This functions generates a dataset with desired parameters (number of individuals and number of observations per individual, number of variables and covariance between variables, individuality). Unlike for the function `GenerateUnivariate`, trait means are not customizable and are always set to 0.

Usage

```
GenerateMultivariate(nindivs, nobs, nvars, covar, individuality)
```

Arguments

`nindivs`	Indicates how many individuals should be in dataset
`nobs`	Indicates how many observations per individual should be in dataset
`nvars`	Indicates how many trait variables should be in dataset.
`covar`	Indicates covariance between variables in dataset. covar=0 for uncorrelated variables; covar=1 for fully correlated variables
`individuality`	Indicates the ratio of between to within individual variation in each trait variable.

Value

Data frame with the identity codes in the first column and trait variables in subsequent columns. Number of rows and columns depends on the parameters used to generate dataset.

See Also

Other Operations with datasets: `GenerateUnivariate`

Examples

```
id1 <- GenerateMultivariate(nindivs=10, nobs=10, nvars=2, covar=0, individuality=1)
```

`GenerateUnivariate` *Generate dataset with a single individual identity trait*

Description

This functions generates a dataset with desired parameters (number of individuals and number of observations per individual, mean of the parameter, individuality).

Usage

```
GenerateUnivariate(nindivs, nobs, betweenM, individuality)
```

Arguments

`nindivs`	Indicates how many individuals should be in dataset
`nobs`	Indicates how many observations per individual should be in dataset
`betweenM`	Indicates the mean value of the trait.
`individuality`	Indicates the ratio of between to within individual variation.

Value

Data frame with two columns. Identity codes are in the first column and the trait values are in the second column.

See Also

Other Operations with datasets: `GenerateMultivariate`

Examples

```
GenerateUnivariate(nindivs=10, nobs=10, betweenM=1000, individuality=2)
```

`IDmeasurer` *IDmeasurer: A package for calculation of individual identity metrics in animal signals.*

Description

The `IDmeasurer` package provides functions for calculation of univariate and multivariate individual identity metrics, functions generating dataset for simulation of individual identity in signals, and functions for conversions between the metrics

IDmeasurer functions

- `calcF`
- `calcPIC`
- `calcHS`
- `calcDS`
- `calcMI`
- `calcHM`
- `GenerateUnivariate`
- `GenerateMultivariate`
- `convertHStoDS`
- `convertDStoHS`

Please, use `vignette('idmeasurer-workflow-examples')` to learn more about the functions.

`LAhighweewoo` *Yellow-breasted boubou,* Laniarius atroflavus - *spectrum properties*

Description

- **Species:** Yellow-breasted boubou, *Laniarius atroflavus*
- **Number of individuals:** 33
- **Number of calls per individual:** 10
- **Number of acoustic variables:** 6
- **Individual identity:** HS=3.83
- **Reference:** Osiejuk, unpublished data

Male Yellow-breasted boubous were recorded in Bamenda region in Cameroon. Birds were recorded between 06.00 to 10.00 in the morning in 2016, typically, from the distance of 10 - 20 meters. The calls were recorded after short provocation with playback. Repertoire of males at the field site included three distinct call types and only the most common call typed labeled as “High wee woo” was used for this study. The original dataset comprised 33 individuals and 10 calls per individual.

Variables were selected to measure basic spectral parameters of each “high weewoo” call like the peak frequency, distribution of frequency amplitudes within spectrum, and range of the frequencies (minimum and maximum). Additionally, the duration of the call was measured. Variables were extracted in Raven Pro 1.5 by the Cornell Bioacoustic Research Program.

Usage

```
LAhighweewoo
```

Format

A data frame with 330 rows and 7 variables:

id factor, identity code of an individual emitting the call

dur duration of the call, in seconds

df frequency of maximum amplitude within the spectrum - peak frequency, in Hertz

minf, maxf minimum and maximum fequency at -25dB relative to the call peak amplitude, in Hertz

q25, q75 frequencies at the two quartiles of amplitude distribution; frequencies below which lie 25 and 75 percent of the energy of the call, respectively, in Hertz

Source

Osiejuk, unpublished data

`SSgrunts` *Domestic pig,* Sus scrofa domestica - *piglet grunts*

Description

- **Species:** Domestic pig, *Sus scrofa domestica*
- **Number of individuals:** 33
- **Number of calls per individual:** 10
- **Number of acoustic variables:** 10
- **Individual identity:** HS=3.18
- **Reference:** Syrova, M., Policht, R., Linhart, P., & Spinka, M. (2017). Ontogeny of individual and litter identity signaling in grunts of piglets. The Journal of the Acoustical Society of America, 142(5), 3116-3121. doi:10.1121/1.5010330

Piglet grunts were recorded in 2014 and 2015 at the research farm of Institute of Animal Science in Prague. To elicit the calls piglets were separated from the litter and sow and were recorded in social isolation in age of 25-30 days after birth from the distance of 1m. Piglets were recorded opportunistically during the day. The original dataset comprised 97 piglets coming from 13 different litters and 10 calls per individual piglet.

Variables were selected to be the most informative regarding the individual identity by the reference study. Variables were extracted using the LMA 2008 software for analysis of animal sounds by Kurt Hammerschmidt.

Usage

```
SSgrunts
```

Format

A data frame with 330 rows and 8 variables:

id factor, identity code of an individual emitting the call

fp1amean mean amplitude of the 1st frequency peak, relative amplitude

q1mean mean frequency of the 1st DFreqA; equivalent to q25 in ANspec, CCspec, and LAhighweewoo, in Hertz

csmean mean correlation coefficient of successive time segments

tonalF0 estimation of segments with detectable fundamental frequency, in percents

q3mean mean frequency of the 3nd DFreqA; equivalent to q75 in ANspec, CCspec, and LAhighweewoo, in Hertz

noise percentage of noise time segments, in percents

ranmean mean frequency range, in Hertz

q2mean mean frequency of the 2nd DFreqA; equivalent to q50 in ANspec, CCspec, and LAhighweewoo, in Hertz

df2pr percentage of time segments where 2nd DomFreqB detected, in percents

q2min min frequency of the 2nd DFreqA, in Hertz

Source

Syrova, M., Policht, R., Linhart, P., & Spinka, M. (2017). Ontogeny of individual and litter identity signaling in grunts of piglets. The Journal of the Acoustical Society of America, 142(5), 3116-3121. doi:10.1121/1.5010330

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