Package: EMMLi (via r-universe)

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Type Package

Title A Maximum Likelihood Approach to the Analysis of Modularity

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Description Fit models of modularity to morphological landmarks. Perform model selection on results. Fit models with a single within-module correlation or with separate within-module correlations fitted to each module.

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Imports stats, utils

Suggests testthat

LazyData true

URL `https://github.com/timcdlucas/EMMLi`

RoxygenNote 5.0.1

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

RemoteUrl https://github.com/timcdlucas/emmli

RemoteRef HEAD

RemoteSha e85d77e36aac83f506b451e6083d108e8dd63f81

Contents

`EMMLi` *Evaluating modularity with maximum likelihood*

Description

Calculates the AICc values, model likelihoods, and posterior probabilities of different models of modularity, as described in Goswami and Finarelli (2016).

Usage

```
EMMLi(corr, N_sample, mod, saveAs = NULL, abs = TRUE, pprob = 0.05)
```

Arguments

`corr`	Lower triangle or full correlation matrix. n x n square matrix for n landmarks.
`N_sample`	The number of specimens
`mod`	A data frame defining the models. The first column should contain the landmark names. Subsequent columns should define which landmarks are contained within each module with integers, factors or characters. If a landmark should be ignored for a specific model (i.e., it is unintegrated in any module), the element should be NA.
`saveAs`	A character string defining the filename and path for where to save output. If NULL, the output is not saved to file
`abs`	Logical denoting whether absolute values should be used. Default is TRUE, as in Goswami and Finarelli (2016)
`pprob`	posterior probability cutoff for reporting of models. Default is 0.05, as suggested in Goswami and Finarelli (2016)

Details

The publication describing this analysis is A. Goswami and J. Finarelli (2016) EMMLi: A maximum likelihood approach to the analysis of modularity. Evolution `http://onlinelibrary.wiley.com/doi/10.1111/evo.12956/abstract`.

Value

A list containing two elements. The first (results) gives the AIC results for each model. The second (rho) gives the within and between module correlations. Optionally, the output is saved to the file defined by the saveAs argument with only models with a posterior probability > 0.01 being saved.

Examples

```
set.seed(1)

# Chose a filename and directory for output
dir <- tempdir()
```

```
file <- paste0(dir, 'EMMLiTest.csv')

# Examine a correlation matrix and model dataframe
dim(macacaCorrel)
head(macacaModels)

# run EMMLi
output <- EMMLi(macacaCorrel, 20, macacaModels, file)

unlink(file)

# run EMMLi without writing output
output <- EMMLi(macacaCorrel, 20, macacaModels)

# Raw data example to illustrate pitfalls
corrPath <- system.file("extdata", "M1lmcorrel.csv", package = "EMMLi")
corr <- read.csv(corrPath, header = FALSE)

modelPath <- system.file("extdata", "macaca_landmarklist.csv", package = "EMMLi")
mod <- read.csv(modelPath, header = TRUE, row.names = 1)

# First column should be character or factor. Subsequent columns integer
sapply(mod, class)

out <- EMMLi(corr, 42, mod)
```

`macacaCorrel` *Correlation matrix for 61 landmarks from Japanese macaque (*Macaca fuscata*) craniums.*

Description

3D coordinates for 61 landmarks on the crania of 42 juvenile Japanese macaque (*Macaca fuscata*) from the Primate Research Institute at Inuyama, Japan, was aligned and scaled with Generalized Procrustes superimposition. The vector congruence coefficient correlation was then calculated for each pair of landmarks

Usage

`macacaCorrel`

Format

A 61 x 61 matrix

Details

#'@seealso `macacaModels`

Source

Goswami, A. and P. D. Polly. 2010. Methods for studying morphological integration and modularity. Pp. 213-243 in J. Alroy, and E. G. Hunt, eds. Quantitative Methods in Paleobiology. Paleontological Society Special Publications.

`macacaModels` *Models of (*Macaca fuscata*) cranial modularity.*

Description

Seven models of cranial landmark modularity. These models group the 61 landmarks in `macacaCorrel` into modules. See Goswami and Finarelli (2016) for more details.

Usage

```
macacaModels
```

Format

A data frame with 61 rows (one for each landmark) and 8 coluumns.

- X.1Landmark names (character or factor)
- Other columnsModel specification. Integers determine which module each landmark is in. NAs indicate that a landmark is not in any module.

Source

A. Goswami and J. Finarelli (2016) EMMLi: A maximum likelihood approach to the analysis of modularity. Evolution `http://onlinelibrary.wiley.com/doi/10.1111/evo.12956/abstract`.

See Also

`macacaCorrel`

Index