

# Package ‘BaSkePro’

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**Type** Package

**Title** Bayesian Model to Archaeological Faunal Skeletal Profiles

**Version** 1.1.1

**Author**

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**Description** Tool to perform Bayesian inference of carcass processing/transport strategy and bone attrition from archaeofaunal skeletal profiles characterized by percentages of MAU (Minimum Anatomical Units). The approach is based on a generative model for skeletal profiles that replicates the two phases of formation of any faunal assemblage: initial accumulation as a function of human transport strategies and subsequent attrition. Two parameters define this model: 1) the transport preference (alpha), which can take any value between -1 (mostly axial contribution) and 1 (mostly appendicular contribution) following strategies constructed as a function of butchering efficiency of different anatomical elements and the results of ethnographic studies, and 2) degree of attrition (beta), which can vary between 0 (no attrition) and 10 (maximum attrition) and relates the survivorship of bone elements to their maximum bone density. Starting from uniform prior probability distribution functions of alpha and beta, a Monte Carlo Markov Chain sampling based on a random walk Metropolis-Hasting algorithm is adopted to derive the posterior probability distribution functions, which are then available for interpretation. During this process, the likelihood of obtaining the observed percentages of MAU given a pair of parameter values is estimated by the inverse of the Chi2 statistic, multiplied by the proportion of elements within a 1 percent of the observed value. See Ana B. Marín-Arroyo, David Ocio (2018). <doi:10.1080/08912963.2017.1336620>.

**License** GPL-3

**Encoding** UTF-8

**Depends** MASS

**NeedsCompilation** no

**Repository** CRAN

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BaSkePro

*Bayesian Model to Archaeological Faunal Skeletal Profiles*

### Description

Tool to perform Bayesian inference of carcass processing/transport strategy and bone attrition from archaeological faunal skeletal profiles characterized by percentages of MAU (Minimum Anatomical Units). The approach is based on a generative model for skeletal profiles that replicates the two phases of formation of any archaeofaunal assemblage: initial accumulation as a function of human transport strategies and subsequent attrition.

### Usage

BaSkePro(x)

### Arguments

x                    A data frame object with the MAU (Minimum Anatomical Unit) percentage of one species in this specific order: Mandible, Atlas, Axis, Cervical vertebra, Thoracic vertebra, Lumbar vertebra, Rib, Sacrum, Scapula, Humerus, Radius (or radio-ulna), Metacarpal, Pelvis, Femur, Tibia, Metatarsal.

### Details

Two parameters define this model: 1) the transport preference (alpha), which can take any value between - 1 (mostly axial contribution) and 1 (mostly appendicular contribution) following strategies constructed as a function of butchering efficiency of different anatomical elements and the results of ethnographic studies, and 2) degree of attrition (beta), which can vary between 0 (no attrition) and 10 (maximum attrition) and relates the survivorship of bone elements to their maximum bone density. Starting from uniform prior probability distribution functions of alpha and beta, a Monte Carlo Markov Chain sampling based on a random walk Metropolis-Hasting algorithm is adopted to derive the posterior probability distribution functions, which are then available for interpretation. During this process, the likelihood of obtaining the observed percentages of MAU given a pair of parameter values is estimated by the inverse of the Chi2 statistic, multiplied by the proportion of elements within a 1 percent of the observed value.

### Value

A table and histograms with posterior probability distribution functions of alpha and beta parameters (the first and fourth quartiles).

**Author(s)**

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**References**

Marín-Arroyo, A. B., & Ocio, D. (2018). Disentangling faunal skeletal profiles. A new probabilistic framework. *Historical Biology*, 30(6), 720-729. DOI:<https://doi.org/10.1080/08912963.2017.1336620>

**Examples**

```
PMAU <- as.data.frame(c(7,0,0,0,0,0,0,0,0,36,14,0,71,71,57,100))
```

```
BaSkePro (PMAU)
```

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