

# Package ‘PELVIS’

March 11, 2019

**Type** Package

**Title** Probabilistic Sex Estimate using Logistic Regression, Based on VISual Traits of the Human Os Coxae

**Version** 1.1.0

**Date** 2019-03-11

**Depends** R (>= 3.4.0), shiny

**Imports** MASS, DT

**Description** An R-Shiny application implementing two methods for sexing the human os coxae based on eleven trichotomic traits, following Bruzek (2002) <doi:10.1002/ajpa.10012>.

**License** GPL-3 | file LICENSE

**Encoding** UTF-8

**BugReports** <https://gitlab.com/f.santos/pelvis/issues/new>

**NeedsCompilation** no

**Author** Frédéric Santos [aut, cre] (<<https://orcid.org/0000-0003-1445-3871>>)

**Maintainer** Frédéric Santos <[frederic.santos@u-bordeaux.fr](mailto:frederic.santos@u-bordeaux.fr)>

**Repository** CRAN

**Date/Publication** 2019-03-11 07:22:38 UTC

## R topics documented:

PELVIS-package . . . . .	2
addMetavars . . . . .	2
bruzek02 . . . . .	3
indivSexing . . . . .	4
metavar . . . . .	6
refData . . . . .	7
sexingFromFile . . . . .	8
StartPELVIS . . . . .	9
tenFoldCV.glm . . . . .	10

<b>Index</b>	<b>12</b>
--------------	-----------

---

PELVIS-package	<i>Probabilistic Sex Estimate using Logistic Regression, Based on VISual Traits of the Human Os Coxae</i>
----------------	---

---

### Description

An R-Shiny application implementing two methods for sexing the human os coxae, based on eleven trichotomic traits.

### Details

Package: PELVIS  
 Type: Package  
 Version: 1.1.0  
 Date: 2019-03-11  
 License: GPL >=2

### Author(s)

Frédéric Santos, <frederic.santos@u-bordeaux.fr>

### References

Bruzek, J. (2002) A method for visual determination of sex, using the human hip bone. *American Journal of Physical Anthropology* **117**, 157–168. doi: 10.1002/ajpa.10012

Santos, F., Guyomarc'h, P., Rmoutilova, R. and Bruzek, J. (Submitted to *American Journal of Physical Anthropology*) A method of sexing the human os coxae based on logistic regressions and Bruzek's nonmetric traits

### Examples

```
if(interactive()){ StartPELVIS() }
```

---

addMetavars	<i>Internal function</i>
-------------	--------------------------

---

### Description

From a given dataset including the 11 visual traits exposed by Bruzek (2002), this function adds three corresponding main characters (PrSu, GrSN and InfP) based on the majority rule exposed in the original article.

**Usage**

```
addMetavars(dat)
```

**Arguments**

dat                    A dataframe including the 11 visual traits described by Bruzek.

**Value**

A dataframe including also the main characters derived from those visual traits.

**Note**

This is an internal function for the R-Shiny application implemented in PELVIS, documented here for testing purposes only.

**Author(s)**

Frédéric Santos, <frederic.santos@u-bordeaux.fr>

**References**

Bruzek, J. (2002) A method for visual determination of sex, using the human hip bone. *American Journal of Physical Anthropology* **117**, 157–168. doi: 10.1002/ajpa.10012

---

bruzek02	<i>Internal function for sexing the human os coxae using Bruzek's method (2002)</i>
----------	---

---

**Description**

Produces a single (and non-probabilistic) sex estimate from five characters observed on the human os coxae, following Bruzek (2002)

**Usage**

```
bruzek02(x)
```

**Arguments**

x                    A character vector of length 5, having three possible values: 'F', '0' or 'M'.

**Value**

One unique character value, 'F', 'I' or 'M', according to the majority rule exposed by Bruzek.

**Note**

This is an internal function for the R-Shiny application implemented in PELVIS, documented here for testing purposes only.

**Author(s)**

Frédéric Santos, <frederic.santos@u-bordeaux.fr>

**References**

Bruzek, J. (2002) A method for visual determination of sex, using the human hip bone. *American Journal of Physical Anthropology* **117**, 157–168. doi: 10.1002/ajpa.10012

**Examples**

```
# Here we create manually an individual:
individual <- c(PrSu="M", GrSN="F", CArc="F", InfP="0", IsPu="F")
individual
# Determination produced by Bruzek (2002): female individual.
bruzek02(individual)
```

---

indivSexing	<i>Internal function for sexing one single human os coxae using revised Bruzek's method (2018)</i>
-------------	--

---

**Description**

Produces a statistical sex estimate from eleven characters observed on the human os coxae, following Bruzek (2018), and using logistic regression models.

**Usage**

```
indivSexing(ref, newInd)
```

**Arguments**

ref	A learning dataset for logistic regression models, basically the dataset 'refData' included in PELVIS (or any other dataset with the same variables).
newInd	A new os coxae to be determined, with eleven observed traits (possibly with missing values).

**Value**

A list with the following components:

PredictedSex	One unique character value, 'F', 'I' or 'M': final sex estimate for the studied os coxae.
PostProb	Posterior probability for the individual to be a male.
BestModel	Best logistic regression model for the studied os coxae according to the BIC criterion.
VariablesUsed	Names of the variables (including part or all of the nonmissing traits for the studied os coxae) used in this best model.
cvRate	Success rate in cross-validation. Cf. Santos et al. (2018) for more details about cross-validation here.
cvIndet	Rate of individuals remaining indeterminate using the best logistic regression model.

**Note**

This is an internal function for the R-Shiny application implemented in PELVIS, documented here for testing purposes only.

**Author(s)**

Frédéric Santos, <frederic.santos@u-bordeaux.fr>

**References**

Santos, F., Guyomarc'h, P., Rmoutilova, R. and Bruzek, J. (Submitted to *American Journal of Physical Anthropology*) A method of sexing the human os coxae based on logistic regressions and Bruzek's nonmetric traits

**Examples**

```
data(refData)
# Pick the first individual of the reference dataset with its 11 traits, as an example:
individual <- refData[1, -c(1:6)]
individual
# Produce a sex estimate for this individual:
indivSexing(ref=refData, newInd=individual)
```

---

metavar	<i>Internal function used to get the five main characters described by Bruzek (2002) from the eleven visual traits observed on the human os coaxe.</i>
---------	--

---

### Description

Converts a set of three visual traits to its corresponding main character (e.g. PrSu1, PrSu2 and PrSu3 are converted to PrSu).

### Usage

```
metavar(x, seuil=2)
```

### Arguments

x	A vector of characters of length 3, having three possible values: 'f', 'i' or 'm'.
seuil	For internal purposes only.

### Value

A unique character value among three possible values: 'F', 'O' or 'M'.

### Note

This is an internal function for the R-Shiny application implemented in PELVIS, documented here for testing purposes only.

### Author(s)

Frédéric Santos, <frederic.santos@u-bordeaux.fr>

### References

Bruzek, J. (2002) A method for visual determination of sex, using the human hip bone. *American Journal of Physical Anthropology* **117**, 157–168. doi: 10.1002/ajpa.10012

### Examples

```
# Here we create a set of three values for the traits observed on the preauricular surface:
prsu <- c(PrSu1="f", PrSu2="f", PrSu3="m")
prsu
# Final determination for the main character PrSu:
metavar(prsu)
```

**Description**

This dataset includes 592 ossa coxa from five population samples. The eleven trichotomic traits are given for each os coxae (possibly with missing values for incomplete bones), along with the geographical origin and known sex of the individual. When possible, the age and stature of the individual are also given. This dataset is used as a training sample for the logistic regression models implemented in PELVIS.

**Usage**

```
data(refData)
```

**Format**

A data frame with 592 observations on the following 17 variables:

Id a factor with 592 levels (unique ID of the individual to whom the bone belongs)

Orig a factor with 5 levels (geographical origin)

Sex a factor with levels F, M (known sex)

Age a numeric vector (age of the associated individual in years)

Side a factor with levels L, R (left or right side)

Stature a numeric vector (in cm)

PrSu1 a factor with levels f, i, m

PrSu2 a factor with levels f, i, m

PrSu3 a factor with levels f, i, m

GrSN1 a factor with levels f, i, m

GrSN2 a factor with levels f, i, m

GrSN3 a factor with levels f, i, m

CArc a factor with levels F,  $\emptyset$ , M

IsPu a factor with levels F,  $\emptyset$ , M

InfP1 a factor with levels f, i, m

InfP2 a factor with levels f, i, m

InfP3 a factor with levels f, i, m

**References**

Santos, F., Guyomarc'h, P., Rmoutilova, R. and Bruzek, J. (Submitted to *American Journal of Physical Anthropology*) A method of sexing the human os coxae based on logistic regressions and Bruzek's nonmetric traits

---

sexingFromFile	<i>Internal function for sexing several single human ossa coxarum using both original and revised Bruzek's methods (2002, 2018)</i>
----------------	---

---

## Description

Produces sex estimates from each of the ossa coxarum submitted by the user through the graphical user interface of the R-Shiny application.

## Usage

```
sexingFromFile(dat, ref, updateProgressBar=NULL)
```

## Arguments

dat	A test dataset submitted by the user through the graphical user interface. The predictive factors (i.e. the eleven trichotomic traits) should have the same headers and levels as in the reference dataset 'refData' included in PELVIS. An example of valid data file can be downloaded here: <a href="http://www.pacea.u-bordeaux.fr/IMG/csv/data_test_PELVIS.csv">http://www.pacea.u-bordeaux.fr/IMG/csv/data_test_PELVIS.csv</a> (its field separator is the semicolon ";").
ref	A learning dataset for logistic regression models, basically the dataset 'refData' included in PELVIS (or any other dataset with the same variables).
updateProgressBar	Internal option for the R-Shiny application.

## Value

A complete dataframe of results displayed through the R-Shiny application.

## Note

This is an internal function for the R-Shiny application implemented in PELVIS.

## Author(s)

Frédéric Santos, <[frederic.santos@u-bordeaux.fr](mailto:frederic.santos@u-bordeaux.fr)>

## References

Santos, F., Guyomarc'h, P., Rmoutilova, R. and Bruzek, J. (Submitted to *American Journal of Physical Anthropology*) A method of sexing the human os coxae based on logistic regressions and Bruzek's nonmetric traits



**Description**

Launches a graphical user interface (GUI) allowing to use Bruzek's methods (2002, 2018) for sexing the human os coxae, based on eleven visual traits.

**Usage**

```
StartPELVIS()
```

**Details**

The R-Shiny application proposes two tabs:

- 'Data input: manual editing' can be used for both data entry and sex classification. The eleven trichotomic traits are manually edited for each os coxae through the GUI, and the corresponding sex estimates are then produced.
- 'Data input: from text file' is the classical way to get the sex estimates for a whole sample of ossa coxa correctly described in a file. PELVIS accepts .CSV or .TXT data files, but does not support .ODS or .XLS(X) files. The predictive factors (i.e. the eleven trichotomic traits) should have the same headers and levels as in the reference dataset 'refData' included in PELVIS. An example of valid data file can be downloaded here: [http://www.pacea.u-bordeaux.fr/IMG/csv/data\\_test\\_PELVIS.csv](http://www.pacea.u-bordeaux.fr/IMG/csv/data_test_PELVIS.csv) (its field separator is the semicolon ";").

In both tabs, two sex estimates are given: the visual sex estimate from Bruzek (2002), and the probabilistic sex estimate from Santos, Guyomarc'h, Rmoutilova and Bruzek (2018, submitted). Depending on the traits possibly missing on the ossa coxa submitted to the program, the logistic regression models can use various subsets of best predictors (selected by BIC). The final subset of predictors used for each os coxae is given in the table of results.

**Value**

The function returns no value by itself, but the results can be downloaded through the graphical interface. The table of results includes the following columns:

- 'Sex estimate (Bruzek 2002)': the visual sex estimate based on Bruzek's method (2002).
- 'Statistical sex estimate (2018)': a sex estimation based on a logistic regression model, following the method described in Santos, Guyomarc'h, Rmoutilova and Bruzek (2018, submitted).
- 'Prob(M)' is the probability (obtained with the logistic regression model) that the individual is a man. According to tradition in biological anthropology, we have the following decision rule: if  $\text{Prob}(M) > 0.95$  then the sex estimate is 'M'; if  $\text{Prob}(M) < 0.05$  then the sex estimate is 'F'; else the individual remains indeterminate ('I').
- 'Prob(F)', defined as  $1 - \text{Prob}(M)$ , is the probability that the individual is a woman.

- ‘Selected predictors in LR model’: for a given individual, the sex estimation proceeds as follows. First, a complete model is built using all available (i.e., nonmissing) traits for this individual. Then, a classical stepwise model selection by BIC is performed, and the subset of the most useful traits is used to produce the final sex estimate. This column gives the traits used for each individual.
- ‘10-fold CV accuracy (%)’: the rate of correct classification for the corresponding logistic regression model is estimated using a ten-fold cross-validation on the learning sample.
- ‘Indet. rate in CV (%)’: the rate of individuals remaining indeterminate in cross-validation for the corresponding logistic regression model.

### Note

The R console is not available when the GUI is active. To exit the GUI, type Echap (on MS Windows systems) or Ctrl+C (on Linux systems) in the R console.

Regardless of the size and resolution of your screen, for convenience, it is advisable to decrease the zoom level of your web browser and/or to turn on fullscreen mode.

### Author(s)

Frédéric Santos, <frederic.santos@u-bordeaux.fr>

### References

Bruzek, J. (2002) A method for visual determination of sex, using the human hip bone. *American Journal of Physical Anthropology* **117**, 157–168. doi: 10.1002/ajpa.10012

Santos, F., Guyomarc’h, P., Rmoutilova, R. and Bruzek, J. (Submitted to *American Journal of Physical Anthropology*) A method of sexing the human os coxae based on logistic regressions and Bruzek’s nonmetric traits

### Examples

```
if(interactive()){StartPELVIS()}
```

---

tenFoldCV.glm

*Internal function for evaluating the performance of logistic regression models used in Bruzek’s revised method (2018)*

---

### Description

Error rate, and rate of individuals remaining indeterminate, using 10-fold cross validation for a given logistic regression model in the context of Bruzek’s revised method.

### Usage

```
tenFoldCV.glm(dat.glm, mod, seuil=0.95)
```

**Arguments**

dat.glm	A data frame to evaluate the GLM.
mod	GLM model to be evaluated.
seuil	Threshold for sex determination, classically 0.95 following Bruzek's recommendations.

**Value**

A complete dataframe of results displayed through the R-Shiny application.

**Note**

This is an internal function for the R-Shiny application implemented in PELVIS. Please do not use this function for classical validation of GLMs outside the context of this package.

**Author(s)**

Frédéric Santos, <frederic.santos@u-bordeaux.fr>

**References**

Santos, F., Guyomarc'h, P., Rmoutilova, R. and Bruzek, J. (Submitted to *American Journal of Physical Anthropology*) A method of sexing the human os coxae based on logistic regressions and Bruzek's nonmetric traits

# Index

\*Topic **bruzek, hip bone, logistic regression, morphoscopy, os coxae, sex estimate, sex estimation**

PELVIS-package, [2](#)

\*Topic **hip bone, os coxae, ossa coxa, sex estimation**

refData, [7](#)

addMetavars, [2](#)

bruzek02, [3](#)

indivSexing, [4](#)

metavar, [6](#)

PELVIS (PELVIS-package), [2](#)

PELVIS-package, [2](#)

refData, [7](#)

sexingFromFile, [8](#)

StartPELVIS, [9](#)

tenFoldCV.glm, [10](#)