Package 'BioAge'

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Type Package

Title Biological Age Calculations Using Several Biomarker Algorithms

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Author Dayoon Kwon

Maintainer Dayoon Kwon <dk1943@nyu.edu>

Description This package measures biological aging using data from the National Health and Nutrition Examination Survey (NHANES). The package uses published biomarker algorithms to calculate three biological age measures: Klemera-Doubal Method Biological Age, Phenotypic Age, and homeostatic dysregulation.

License GPL-3

Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

Depends R (>= 2.10)

Imports dplyr,
flexsurv

Suggests testthat,
knitr,
rmarkdown

VignetteBuilder knitr

R topics documented:

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bioage_calc	*bioage_calc*

Description

Calculate Klemera-Doubal Method Biological Age

Usage

```
bioage_calc(data, age, biomarkers, fit = NULL, s_ba2 = NULL)
```

Arguments

data	The dataset for calculating bioage
age	A character vector (length=1) indicating the name of the variable for age
biomarkers	A character vector indicating the names of the variables for the biomarkers to use in calculating bioage
fit	An S3 object for model fit. If the value is NULL, then the parameters to use for training bioage are calculated
s_ba2	A particular fit parameter. Advanced users can modify this parameter to control the variance of bioage

Details

Calculate Klemera-Doubal Method Biological Age

Value

An object of class "bioage". This object is a list with two elements (data and fit)

Examples

```
#Train KDM bioage parameters
train = bioage_calc(nhanes3,age="age",
           biomarkers=c("fev","sbp","totchol","hba1c","albumin","creat","lncrp","alp","bun"))

#Use training data to calculate KDM bioage
bioage = bioage_calc(nhanes,age="age",
              biomarkers=c("fev","sbp","totchol","hba1c","albumin","creat","lncrp","alp","bun"),
                    fit=train$fit,
                    s_ba2=train$fit$s_ba2)

#Extract bioage dataset
data = bioage$data
```

bioage_nhanes	*bioage_nhanes*

Description

Calculate Klemera-Doubal Method (KDM) Biological Age Using NHANES Dataset

Usage

```
bioage_nhanes(biomarkers)
```

Arguments

biomarkers A character vector indicating the names of the variables for the biomarkers to use in calculating bioage

Details

Calculate Klemera-Doubal Method Biological Age Using NHANES Dataset

Value

An object of class "bioage". This object is a list with two elements (data and fit)

Examples

```
#Calculate KDM bioage
bioage = bioage_nhanes(biomarkers=c("fev","sbp","totchol","hba1c","albumin","creat","lncrp","alp","bun"))

#Extract bioage dataset
data = bioage$data
```

hd_calc	*hd_calc*

Description

Calculate Homeostatic Dysregulation (HD)

Usage

```
hd_calc(data, reference, biomarkers)
```

Arguments

data	The dataset for calculating HD
reference	The reference dataset for calculating HD
biomarkers	A character vector indicating the names of the variables for the biomarkers to use in calculating HD

Details

Calculate Homeostatic Dysregulation

Value

An object of class "hd". This object is a list with two elements (data and fit)

Examples

```
#Calculate HD
hd = hd_calc(nhanes,nhanes3,
        biomarkers=c("albumin_gL","lymph","mcv","glucose_mmol","rdw","creat_umol","lncrp","alp","wbc"))

#Extract bioage dataset
data = hd$data
```

---

hd_nhanes   *hd_nhanes*

Description

Calculate Homeostatic Dysregulation (HD) Using NHANES Dataset

Usage

```
hd_nhanes(biomarkers)
```

Arguments

biomarkers   A character vector indicating the names of the variables for the biomarkers to
                    use in calculating HD

Details

Calculate Homeostatic Dysregulation Using NHANES Dataset

Value

An object of class "hd". This object is a list with two elements (data and fit)

Examples

```
#Calculate HD
hd = hd_nhanes(biomarkers=c("albumin","lymph","mcv","glucose","rdw","creat","lncrp","alp","wbc"))

#Extract HD dataset
data = hd$data
```

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phenoage_calc	*phenoage_calc*

Description

Calculate Levine's Phenotypic Age

Usage

```
phenoage_calc(data, age, time, status, biomarkers, fit = NULL)
```

Arguments

data	The dataset for calculating phenoage
age	A character vector (length=1) indicating the name of the variable for age
time	A character vector (length=1) indicating the name of the variable for survival time
status	A character vector (length=1) indicating the name of the variable for death status
biomarkers	A character vector indicating the names of the variables for the biomarkers to use in calculating phenoage
fit	An S3 object for model fit. If the value is NULL, then the parameters to use for training phenoage are calculated

Details

Calculate Levine's Phenotypic Age

Value

An object of class "phenoage". This object is a list with two elements (data and fit)

Examples

```
#Train phenoage parameters
train = phenoage_calc(nhanes3,age="age",
              biomarkers=c("albumin_gL","lymph","mcv","glucose_mmol","rdw","creat_umol","lncrp","alp","wbc

#Use training data to calculate phenoage
phenoage = phenoage_calc(nhanes,age="age",
                biomarkers=c("albumin_gL","lymph","mcv","glucose_mmol","rdw","creat_umol","lncrp","alp","w
                      fit=train$fit)

#Extract phenoage dataset
data = phenoage$data
```

---

phenoage_nhanes   *phenoage_nhanes*

Description

Calculate Levine's Phenotypic Age Using NHANES Dataset

Usage

```
phenoage_nhanes(biomarkers)
```

Arguments

biomarkers   A character vector indicating the names of the variables for the biomarkers to
                use in calculating phenoage

Details

Calculate Levine's Phenotypic Age Using NHANES Dataset

Value

An object of class "phenoage". This object is a list with two elements (data and fit)

Examples

```
#Calculate phenoage
phenoage = phenoage_nhanes(biomarkers=c("albumin_gL","lymph","mcv","glucose_mmol","rdw","creat_umol","lncrp

#Extract phenoage dataset
data = phenoage$data
```

---

plot_ba   *plot_ba*

Description

Plot Correlations Between Biological Aging Measures and Chronological Age

Usage

```
plot_ba(data, variables)
```

Arguments

data   The dataset for plotting correlations

variables   A character vector indicating the names of the biological aging measures

Details

Plot Correlations Between Biological Aging Measures and Chronological Age

Examples

```
#Calculate phenoage
f1 = plot_ba(data = data, variables = c("bioage", "phenoage", "hd"))

f1
```

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