Package 'BioAge'

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Type Package

Title Biological Age Calculations Using Several Biomarker Algorithms

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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,
    ggplot2

Suggests flexsurv,
    htmlTable,
    survival,
    testthat,
    tidyr,
    knitr,
    rmarkdown

VignetteBuilder knitr

R topics documented:

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bioage_calc   *bioage_calc*

Description

Calculate Klemera-Doubal Method (KDM) Biological Age

Usage

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

Arguments

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

Details

Calculate KDM 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 KDM 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 HD

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 HD 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
```

---

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 chronological 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 survival 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 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","wbc"),
                         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","alp","wbc"))

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

---

plot_ba *plot_ba*

Description

Plot correlations between biological aging measures and chronological age

Usage

```
plot_ba(data, agevar, label)
```

Arguments

data   The dataset for plotting correlations

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

label   A character vector indicating the labels of the biological aging measures

Details

Plot correlations between biological aging measures and chronological age

Note

Chronological age and gender variables need to be named "age" and "gender"

Examples

```
#Calculate phenoage
f1 = plot_ba(data = data, agevar = c("bioage", "phenoage", "hd"),
             label = c("KDM\nBiological\nAge",
                       "Levine\nPhenotypic\nAge",
                       "Modified-KDM\nBiological\nAge",
                       "Modified-Levine\nPhenotypic\nAge",
                       "Mahalanobis\nDistance",
                       "Log\nMahalanobis\nDistance"))

f1
```

---

plot_baa	*plot_baa*

Description

Plot correlations between biological age advancement (BAA) and chronological age

Usage

```
plot_baa(data, agevar, label, axis_type)
```

Arguments

data	The dataset for plotting corplot
agevar	A character vector indicating the names of the interested biological aging measures
label	A character vector indicating the labels of the biological aging measures Values should be formatted for displaying along diagonal of the plot Names should be used to match variables and order is preserved
axis_type	A character vector indicating the axis type (int or float) Use variable name to define the axis type

Details

Plot correlations between BAA and chronological age

Examples

```
#Create corplot of BAA with chronologicl age
agevar = c("bioage_advance0",
           "phenoage_advance0",
           "bioage_advance",
           "phenoage_advance",
           "hd",
           "hd_log")

label = c("bioage_advance0"="KDM\nBiological\nAge",
          "phenoage_advance0"="Levine\nPhenotypic\nAge",
          "bioage_advance"="Modified-KDM\nBiological\nAge",
          "phenoage_advance"="Modified-Levine\nPhenotypic\nAge",
          "hd" = "Mahalanobis\nDistance",
          "hd_log" = "Log\nMahalanobis\nDistance")

axis_type = c("bioage_advance0"="float",
              "phenoage_advance0"="float",
              "bioage_advance"="float",
              "phenoage_advance"="flot",
              "hd"="flot",
              "hd_log"="float")

f2 = plot_baa(data, agevar, labels, axis_type)

f2
```

```
table_health                    table_health
```

Description

Association with current health status outcomes

Usage

```
table_health(data, agevar, outcome, label)
```

Arguments

data	The dataset for linear regression table
agevar	A character vector indicating the names of the interested biological aging measures
outcome	A character vector indicating the name of the interested current health status outcomes
label	A character vector indicating the labels of the biological aging measures

Details

Association with current health status outcomes, adjusting for chronological age and gender and stratified by gender, race, and age

Note

Chronological age and gender variables need to be named "age" and "gender"

Examples

```
table2 = table_health(nhanes,
                       agevar = c("bioage_advance0","phenoage_advance0",
                                  "bioage_advance","phenoage_advance",
                                  "hd","hd_log"),
                       outcome = c("health","adl","lnwalk","grip_scaled"),
                       label = c("KDM\nBiological\nAge",
                                 "Levine\nPhenotypic\nAge",
                                 "Modified-KDM\nBiological\nAge",
                                 "Modified-Levine\nPhenotypic\nAge",
                                 "Mahalanobis\nDistance",
                                 "Log\nMahalanobis\nDistance"))

table2$table
table2$n
```

---

table_ses   *table_ses*

Description

Association with socioeconomic variables

Usage

```
table_ses(data, agevar, exposure, label)
```

Arguments

data	The dataset for linear regression table
agevar	A character vector indicating the names of the interested biological aging measures
exposure	A character vector indicating the name of the interested socioeconomic variables

Details

Association with socioeconomic variables, adjusting for chronological age and gender and stratified by gender, race, and age

Note

Chronological age and gender variables need to be named "age" and "gender"

Examples

```
table3 = table_ses(nhanes,
                    agevar = c("bioage_advance0","phenoage_advance0",
                               "bioage_advance","phenoage_advance",
                               "hd","hd_log"),
                    exposure = c("edu","annual_income","poverty_ratio"),
                    label = c("KDM\nBiological\nAge",
                              "Levine\nPhenotypic\nAge",
                              "Modified-KDM\nBiological\nAge",
                              "Modified-Levine\nPhenotypic\nAge",
                              "Mahalanobis\nDistance",
                              "Log\nMahalanobis\nDistance")))

table3$table
table3$n
```

---

table_surv   *table_surv*

Description

Mortality validation for biological aging measures

Usage

```
table_surv(data, agevar, time, status, label)
```

Arguments

data	The dataset for mortality table
agevar	A character vector indicating the names of the interested biological aging measures
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 survival status
label	A character vector indicating the labels of the biological aging measures

Details

Mortality validation for biological age measures, adjusting for chronological age and gender and stratified by gender, race, and age

Note

Chronological age, gender, and race/ethnicity variables need to be named "age", "gender", and "race"

Examples

```
table1 = table_surv(nhanes,
                     agevar = c("bioage_advance0","phenoage_advance0",
                               "bioage_advance","phenoage_advance",
                               "hd","hd_log"),
                     time = "permth_exm",
                     status = "mortstat",
                     label = c("KDM\nBiological\nAge",
                               "Levine\nPhenotypic\nAge",
                               "Modified-KDM\nBiological\nAge",
                               "Modified-Levine\nPhenotypic\nAge",
                               "Mahalanobis\nDistance",
                               "Log\nMahalanobis\nDistance"))

table1
```

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