

# Package ‘BioAge’

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**Type** Package

**Title** Biological Age Calculations Using Several Biomarker Algorithms

**Version** 0.1.0

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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: Klemmera-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** broom,  
flexsurv,  
htmlTable,  
survival,  
testthat,  
tidyr,  
knitr,  
rmarkdown

**VignetteBuilder** knitr

## R topics documented:

hd_calc . . . . .	2
hd_nhanes . . . . .	3
kdm_calc . . . . .	3
kdm_nhanes . . . . .	4
phenoage_calc . . . . .	5
phenoage_nhanes . . . . .	6
plot_ba . . . . .	7

plot\_baa . . . . .

table\_health . . . . .

table\_ses . . . . .

table\_surv . . . . .

Index

7

8

9

10

12

hd_calc	hd_calc
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Description

Calculate homeostatic dysregulation (HD)

Usage

hd\_calc(data, reference, biomarkers)

Arguments

- data

reference

biomarkers
- The dataset for calculating HD

The reference dataset for calculating HD

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
```

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`kdm_calc`*kdm\_calc*

---

**Description**

Calculate Klemera-Doubal Method (KDM) Biological Age

**Usage**

```
kdm_calc(data, biomarkers, fit = NULL, s_ba2 = NULL)
```

**Arguments**

data	The dataset for calculating KDM Biological Age
biomarkers	A character vector indicating the names of the variables for the biomarkers to use in calculating KDM Biological Age
fit	An S3 object for model fit. If the value is NULL, then the parameters to use for training KDM Biological Age are calculated
s_ba2	A particular fit parameter. Advanced users can modify this parameter to control the variance of kdm

**Details**

Calculate KDM Biological Age

**Value**

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

**Examples**

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

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

#Extract kdm dataset
data = kdm$data
```

---

kdm\_nhanes

---

*kdm\_nhanes*


---

**Description**

Calculate Klemra-Doubal Method (KDM) Biological Age using NHANES dataset

**Usage**

```
kdm_nhanes(biomarkers)
```

**Arguments**

biomarkers	A character vector indicating the names of the variables for the biomarkers to use in calculating KDM Biological Age
------------	--

**Details**

Calculate KDM Biological Age using NHANES dataset

**Value**

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

**Examples**

```
#Calculate KDM Biological Age
kdm = kdm_nhanes(biomarkers=c("fev", "sbp", "totchol", "hba1c", "albumin", "creat", "lncrp", "alp", "bun"))

#Extract kdm dataset
data = kdm$data
```

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phenoage_calc	<i>phenoage_calc</i>
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**Description**

Calculate Levine's Phenotypic Age

**Usage**

```
phenoage_calc(data, biomarkers, fit = NULL)
```

**Arguments**

data	The dataset for calculating phenoage
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,
                      biomarkers=c("albumin_gL", "lymph", "mcv", "glucose_mmol",
                                    "rdw", "creat_umol", "lncrp", "alp", "wbc"))

#Use training data to calculate phenoage
phenoage = phenoage_calc(nhanes,
                        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	<i>phenoage_nhanes</i>
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---

**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 chronological 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"="float",
              "hd"="float",
              "hd_log"="float")

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

f2
```

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table_health	<i>table_health</i>
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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
```

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table_ses	<i>table_ses</i>
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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
```

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table_surv	<i>table_surv</i>
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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
```

# Index

hd\_calc, [2](#)  
hd\_nhanes, [3](#)  
  
kdm\_calc, [3](#)  
kdm\_nhanes, [4](#)  
  
phenoage\_calc, [5](#)  
phenoage\_nhanes, [6](#)  
plot\_ba, [7](#)  
plot\_baa, [7](#)  
  
table\_health, [8](#)  
table\_ses, [9](#)  
table\_surv, [10](#)