

# Package ‘BioAge’

May 25, 2020

**Type** Package

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

**Version** 0.1.0

**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: 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** flexsurv,  
htmlTable,  
survival,  
testthat,  
tidyr,  
knitr,  
rmarkdown

**VignetteBuilder** knitr

## R topics documented:

bioage_calc . . . . .	2
bioage_nhanes . . . . .	3
hd_calc . . . . .	3
hd_nhanes . . . . .	4
phenoage_calc . . . . .	5
phenoage_nhanes . . . . .	6
plot_ba . . . . .	6
plot_baa . . . . .	7

table\_health . . . . . 8

table\_ses . . . . . 9

table\_surv . . . . . 9

Index 11

---

bioage_calc	bioage_calc
-------------	-------------

---

**Description**

Calculate Klemmera-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	<i>bioage_nhanes</i>
---------------	----------------------

---

**Description**

Calculate Klemmera-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","lncrep","alp","bun"))

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

---

hd_calc	<i>hd_calc</i>
---------	----------------

---

**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	<i>hd_nhanes</i>
-----------	------------------

---

**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	<i>phenoage_calc</i>
---------------	----------------------

---

**Description**

Calculate Levine's phenotypic age

**Usage**

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

**Arguments**

<code>data</code>	The dataset for calculating phenoage
<code>age</code>	A character vector (length=1) indicating the name of the variable for chronological age
<code>time</code>	A character vector (length=1) indicating the name of the variable for survival time
<code>status</code>	A character vector (length=1) indicating the name of the variable for survival status
<code>biomarkers</code>	A character vector indicating the names of the variables for the biomarkers to use in calculating phenoage
<code>fit</code>	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", "lncrep", "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", "lncrep", "alp", "wbc"),
                        fit=train$fit)

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

---

phenoage_nhanes	<i>phenoage_nhanes</i>
-----------------	------------------------

---

### 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", "lncrep", "alp", "wbc"))

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

---

plot_ba	<i>plot_ba</i>
---------	----------------

---

### Description

Plot correlations between biological aging measures and chronological age

### Usage

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

### Arguments

data	The dataset for plotting correlations
agevar	A character vector indicating the names 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"))

f1
```

---

plot_baa	<i>plot_baa</i>
----------	-----------------

---

**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 age measures
label	A character vector indicating the labels of the biological age 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
```

---

table_health	<i>table_health</i>
--------------	---------------------

---

**Description**

Association with current health status outcomes

**Usage**

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

**Arguments**

data	The dataset for plotting corplot
agevar	A character vector indicating the names of the interested biological age measures
outcome	A character vector indicating the name of the interested current health status outcomes

**Details**

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

table2
```



---

table_ses	<i>table_ses</i>
-----------	------------------

---

**Description**

Association with socioeconomic variables

**Usage**

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

**Arguments**

- data                   The dataset for plotting corplot
- agevar                A character vector indicating the names of the interested biological age 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 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"))

table3
```

---

table_surv	<i>table_surv</i>
------------	-------------------

---

**Description**

Mortality validation for biological age measures

**Usage**

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

## Arguments

data	The dataset for plotting corplot
agevar	A character vector indicating the names of the interested biological age 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

## 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")

table1
```

# Index

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