

# 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 . . . . .       | 2 |
| kdm_calc . . . . .        | 3 |
| kdm_nhanes . . . . .      | 4 |
| phenoage_calc . . . . .   | 5 |
| phenoage_nhanes . . . . . | 6 |
| plot_ba . . . . .         | 6 |

plot\_baa . . . . . 7

table\_health . . . . . 8

table\_ses . . . . . 9

table\_surv . . . . . 10

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|         |         |
|---------|---------|
| 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(NHANES4, NHANES3,
             biomarkers=c("albumin_gl", "lymph", "mcv", "glucose_mmol", "rdw", "creat_umol", "lncrep", "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
```

---

`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", "lncrep", "alp", "bun"))

#Use training data to calculate KDM Biological Age
kdm = kdm_calc(NHANES4,
  biomarkers = c("fev", "sbp", "totchol", "hba1c", "albumin", "creat", "lncrep", "alp", "bun"),
  fit = train$fit,
  s_ba2 = train$fit$s_ba2)

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

---

kdm\_nhanes

---

*kdm\_nhanes*


---

**Description**

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

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

---

|               |                      |
|---------------|----------------------|
| phenoage_calc | <i>phenoage_calc</i> |
|---------------|----------------------|

---

**Description**

Calculate Levine's Phenotypic Age

**Usage**

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

**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 |
| orig       | TRUE to compute the original Levine's Phenotypic Age  |

**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(NHANES4,
                        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> |
|-----------------|------------------------|

---

**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("kdm", "phenoage", "hd"),
             label = c("Modified-KDM\nBiological\nAge",
                       "Modified-Levine\nPhenotypic\nAge",
                       "Mahalanobis\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("kdm_advance0",
           "phenoage_advance0",
           "kdm_advance",
           "phenoage_advance",
           "hd",
           "hd_log")

label = c("kdm_advance0"="KDM\nBiological\nAge",
          "phenoage_advance0"="Levine\nPhenotypic\nAge",
          "kdm_advance"="Modified-KDM\nBiological\nAge",
          "phenoage_advance"="Modified-Levine\nPhenotypic\nAge",
          "hd" = "Mahalanobis\nDistance",
          "hd_log" = "Log\nMahalanobis\nDistance")

axis_type = c("kdm_advance0"="float",
              "phenoage_advance0"="float",
              "kdm_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, 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(data,
  agevar = c("kdm_advance0", "phenoage_advance0",
    "kdm_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 | <i>table_ses</i> |
|-----------|------------------|

---

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(data,
  agevar = c("kdm_advance0", "phenoage_advance0",
    "kdm_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 | <i>table_surv</i> |
|------------|-------------------|

---

**Description**

Mortality validation for biological aging measures

**Usage**

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

**Arguments**

|        |   |
|--------|---|
| data   | The dataset for mortality table   |
| 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           |

**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(data,
  agevar = c("kdm_advance0", "phenoage_advance0",
    "kdm_advance", "phenoage_advance",
    "hd", "hd_log"),
  label = c("KDM\nBiological\nAge",
    "Levine\nPhenotypic\nAge",
    "Modified-KDM\nBiological\nAge",
    "Modified-Levine\nPhenotypic\nAge",
    "Mahalanobis\nDistance",
    "Log\nMahalanobis\nDistance"))

table1
```