Package 'Jcvrisk'

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Type Package

Title Risk Calculator for Cardiovascular Disease in Japan

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Description A calculation tool to obtain the 10-
year risk of cardiovascular disease from various risk models (Hisayama, Suita, EPOCH Japan).

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Contents

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epoch_chd	*10-year risk of death from CHD from the EPOCH Japan study participants*

Description

epoch_chd() calculates the absolute 10-year risk of death from coronary heart disease (CHD).

Mandatory variables: "age", "sex", "urineprotein", "sbp", "t2dm", "tc", "hdl", "smoking" These variables must be applied with the above spelling.

The details of this prediction model should be referred to the original article. "Estimation of 10-Year Risk of Death from Coronary Heart Disease, Stroke, and Cardiovascular Disease in a Pooled Analysis of Japanese Cohorts: EPOCH-JAPAN"

DOI:10.5551/jat.58958

PMID:33041313

PMCID:PMC8326173

Usage

```
epoch_chd(data)
```

Arguments

data	A data frame containing the variables to estimate risk.

Value

Based on the mandatory variables, a risk probability will be calculated for each line. The primary cautions are as follows,

1."Data frame must contain the following columns.":

If you contact this warning message, the data frame did not contain required variables. Please check the data frame contain the mandatory variables in the designated spelling.

2."Data frame contains NA values in required columns.":

epoch_chd() returns the NA if the required variables were missing, or NAs were generated in the calculation process.

3."Some individuals are aged 80 or older. results may not be accurate.":

4."Some individuals are aged 40 or younger. results may not be accurate.":

Examples

```
data <- data.frame(
  age = c(39, 85, 70),
  sex = c(1, 2, 2),
  sbp = c(120, 130, 135),
  t2dm = c(NA, 1, 1),
```

```
    tc = c(180, 110, 185),
    hdl = c(55, 45, 58),
    urineprotein = c(1, 1, 0),
    smoking = c(0, 1, 0)
)

# age          :age(continuous)
# sex          :sex(category: 1 = male, 2 = female)
# sbp          :systolic blood pressure(continuous)
# t2dm         :diabetes mellitus(category: 0 = non-prevalent DM, 1 = prevalent DM)
# tc           :total cholesterol(continuous)
# hdl          :high-density lipoprotein cholesterol(continuous)
# urineprotein :proteinuria(category: 0 = negative, 1 = positive)
# smoking      :smoking status(category: 0 = never/past smoker, 1 = current smoker)

epoch_chd(data)
```

---

epoch_cvd	*10-year risk of death from CVD from the EPOCH Japan study participants*

Description

epoch_cvd() calculates the absolute 10-year risk of death from cardiovascular disease (CVD).

Mandatory variables: "age", "sex", "urineprotein", "sbp", "t2dm", "smoking". These variables must be applied with the above spelling.

The details of this prediction model should be referred to the original article. "Estimation of 10-Year Risk of Death from Coronary Heart Disease, Stroke, and Cardiovascular Disease in a Pooled Analysis of Japanese Cohorts: EPOCH-JAPAN"

DOI:10.5551/jat.58958

PMID:33041313

PMCID:PMC8326173

Usage

```
epoch_cvd(data)
```

Arguments

data   A data frame containing the variables to estimate risk.

Value

Based on the mandatory variables, a risk probability will be calculated for each line. The primary cautions are as follows,

1."Data frame must contain the following columns.":

If you contact this warning message, the data frame did not contain required variables. Please check the data frame contain the mandatory variables in the designated spelling.

2."Data frame contains NA values in required columns.":

epoch_cvd() returns the NA if the required variables were missing, or NAs were generated in the calculation process.

3."Some individuals are aged 80 or older. results may not be accurate.":

4."Some individuals are aged 40 or younger. results may not be accurate.":

Examples

```
data <- data.frame(
  age = c(39, 85, 70),
  sex = c(1, 2, 1),
  sbp = c(120, 130, 140),
  t2dm = c(NA, 1, 0),
  urineprotein = c(1, 1, 0),
  smoking = c(0, 1, 1)
)

# age          :age(continuous)
# sex          :sex(category: 1 = male, 2 = female)
# sbp          :systolic blood pressure(continuous)
# t2dm         :diabetes mellitus(category: 0 = non-prevalent DM, 1 = prevalent DM)
# urineprotein :proteinuria(category: 0 = negative, 1 = positive)
# smoking      :smoking status(category: 0 = never/past smoker, 1 = current smoker)


epoch_cvd(data)
```

---

epoch_stroke	*10-year risk of death from stroke from the EPOCH Japan study participants*

Description

epoch_stroke() calculates the absolute 10-year risk of death from stroke.

Mandatory variables: "age", "urineprotein", "sbp", "t2dm", "smoking" These variables must be applied with the above spelling.

The details of this prediction model should be referred to the original article. "Estimation of 10-Year Risk of Death from Coronary Heart Disease, Stroke, and Cardiovascular Disease in a Pooled Analysis of Japanese Cohorts: EPOCH-JAPAN"

DOI:10.5551/jat.58958

PMID:33041313

PMCID:PMC8326173

Usage

```
epoch_stroke(data)
```

Arguments

data   A data frame containing the variables to estimate risk.

Value

Based on the mandatory variables, a risk probability will be calculated for each line. The primary cautions are as follows,

1."Data frame must contain the following columns.":

If you contact this warning message, the data frame did not contain required variables. Please check the data frame contain the mandatory variables in the designated spelling.

2."Data frame contains NA values in required columns.":

epoch_stroke() returns the NA if the required variables were missing, or NAs were generated in the calculation process.

3."Some individuals are aged 80 or older. results may not be accurate.":

4."Some individuals are aged 40 or younger. results may not be accurate.":

Examples

```
data <- data.frame(
  age = c(39, 85, 70),
  sbp = c(120, 130, 140),
  t2dm = c(NA, 1, 0),
  urineprotein = c(1, 1, 0),
  smoking = c(0, 1, 1)
)

# age          :age(continuous)
# sbp          :systolic blood pressure(continuous)
# t2dm         :diabetes mellitus(category: 0 = non-prevalent DM, 1 = prevalent DM)
# urineprotein :proteinuria(category: 0 = negative, 1 = positive)
# smoking      :smoking status(category: 0 = never/past smoker, 1 = current smoker)


epoch_stroke(data)
```

---

hisayama   *10-year risk calculation for ASCVD based on the Hisayama study*

Description

hisayama() calculates the 10-year probability of developing the first atherosclerotic cardiovascular disease (ASCVD) event. Mandatory variables: "age", "sex", "sbp", "t2dm", "hdl", "ldl", "urineprotein", "smoking", "exercise". These variables must be applied with the above spelling.

The details of this prediction model should be referred to the original article. "Development and Validation of a Risk Prediction Model for Atherosclerotic Cardiovascular Disease in Japanese Adults: The Hisayama Study"

DOI:10.5551/jat.61960

PMCID:PMC8894117

PMID:33487620

Usage

```
hisayama(data)
```

Arguments

data   A data frame containing the variables to estimate risk.

Value

Based on the mandatory variables, a risk probability will be calculated for each line. The primary cautions are as follows,

1."Data frame must contain the following columns.":

If you contact this warning message, the data frame did not contain required variables. Please check the data frame contain the mandatory variables in the designated spelling.

2."Data frame contains NA values in required columns.":

hisayama() returns the NA if the required variables were missing, or NAs were generated in the calculation process.

3."Some individuals are aged 80 or older. results may not be accurate.":

4."Some individuals are aged 40 or younger. results may not be accurate.":

This risk prediction model was developed based on the Hisayama study participants(older than 40 and younger than 80). In the calculation process, when the participants' age is outside of the range, the result is returned as follows.

1. Younger than 30: same value for 30-40.

2. Older than 80: same value for 75-79.

Examples

```
data <- data.frame(
  age = c(45, 55, 90),
  sex = c(1, 2, 1),
  sbp = c(120, 130, 145),
  t2dm = c(0, 1, 0),
  hdl = c(55, 45, 35),
```

```
  ldl = c(110, 130, 160),
  urineprotein = c(NA, 1, 0),
  smoking = c(0, 1, 0),
  exercise = c(1, 0, 1)
)

# age        :age(continuous)
# sex        :sex(category:1 = male,2 = female)
# sbp        :systolic blood pressure(continuous)
# t2dm       :diabetes mellitus(category:0 = non-prevalent DM,1 = prevalent DM)
# hdl        :high-density lipoprotein cholesterol(continuous)
# ldl        :low-density lipoprotein cholesterol(continuous)
# urineprotein:proteinuria(category:0 = negative,1 = positive)
# smoking    :smoking status(category:0 = never/past smoker,1 = current smoker)
# exercise   :weekly exercise(category:0 = less than 3 times,1 = 3 times or more)


hisayama(data)
```

---

suita	*10-year risk calculation for CVD events based on the Suita study without electrocardiogram model*

Description

suita() calculates the 10-year probability of developing the first incidence of cardiovascular disease(CVD) (stroke or coronary heart disease) without electrocardiogram (ECG).

Mandatory variables: "age", "sex", "sbp", "dbp", "t2dm", "tc", "hdl", "ldl", "urineprotein", "smoking". These variables must be applied with the above spelling.

The details of this prediction model should be referred to the original article.

"Development of Cardiovascular Disease Risk Prediction Model Using the Suita Study, a Population-Based Prospective Cohort Study in Japan"

DOI:10.5551/jat.48843

PMID:32023562

PMCID:PMC7803836

Usage

```
suita(data)
```

Arguments

data   A data frame containing the variables to estimate risk.

Value

Based on the mandatory variables, a risk probability will be calculated for each line. The primary cautions are as follows,

1."Data frame must contain the following columns.":

If you contact this warning message, the data frame did not contain required variables. Please check the data frame contain the mandatory variables in the designated spelling.

2."Data frame contains NA values in required columns.":

suita() returns the NA if the required variables were missing, or NAs were generated in the calculation process.

3."Some individuals are aged 80 or older. results may not be accurate.":

4."Some individuals are aged 30 or younger. results may not be accurate.":

This risk prediction model was developed based on the Suita study participants(older than 30 and younger than 80). In the calculation process, when the participants' age is outside of the range, the result is returned as follows.

1. Younger than 30: same value for 30-40.

2. Older than 80: same value for 75-79.

Examples

```
data <- data.frame(
  age = c(45, 55, 90),
  sex = c(1, 2, 1),
  sbp = c(120, 130, 145),
  dbp = c(80, 90, 110),
  t2dm = c(0, 1, 0),
  tc = c(180, 160, 210),
  hdl = c(55, 45, 35),
  ldl = c(110, 100, 160),
  urineprotein = c(1, 1, 0),
  smoking = c(0, 1, 0)
)

# age          :age(continuous)
# sex          :sex(category: 1 = male, 2 = female)
# sbp          :systolic blood pressure(continuous)
# dbp          :diastolic blood pressure(continuous)
# t2dm         :diabetes mellitus(category: 0 = non-prevalent DM, 1 = prevalent DM)
# tc           :total cholesterol(continuous)
# hdl          :high-density lipoprotein cholesterol(continuous)
# ldl          :low-density lipoprotein cholesterol(continuous)
# urineprotein :proteinuria(category: 0 = negative, 1 = positive)
# smoking      :smoking status(category: 0 = never/past smoker, 1 = current smoker)

suita(data)
```

---

suita_ecg	*10-year risk calculation for CVD events based on the Suita study with electrocardiogram model*

Description

suita_ecg() calculates the 10-year probability of developing the first ASCVD event. Mandatory variables: "age", "sex", "sbp", "dbp", "t2dm", "tc", "hdl", "ldl", "urineprotein", "smoking", "af", "lvh". These variables must be applied with the above spelling.

The details of this prediction model should be referred to the original article. "Development of Cardiovascular Disease Risk Prediction Model Using the Suita Study, a Population-Based Prospective Cohort Study in Japan"

DOI:10.5551/jat.48843

PMID:32023562

PMID:PMC7803836

Usage

```
suita_ecg(data)
```

Arguments

data   A data frame containing the variables to estimate risk.

Value

Based on the mandatory variables, a risk probability will be calculated for each line. The primary cautions are as follows,

1."Data frame must contain the following columns.":

If you contact this warning message, the data frame did not contain required variables. Please check the data frame contain the mandatory variables in the designated spelling.

2."Data frame contains NA values in required columns.":

suita_ecg() returns the NA if the required variables were missing, or NAs were generated in the calculation process.

3."Some individuals are aged 80 or older. results may not be accurate.":

4."Some individuals are aged 30 or younger. results may not be accurate.":

This risk prediction model was developed based on the Suita study participants(older than 30 and younger than 80).In the calculation process, when the participants' age is outside of the range, the result is returned as follows.

1. Younger than 30: same value for 30-40.

2. Older than 80: same value for 75-79.

Examples

```
data <- data.frame(
  age = c(45, 55, 90),
  sex = c(1, 2, 1),
  sbp = c(120, 130, 145),
  dbp = c(80, 90, 110),
  t2dm = c(0, 1, 0),
  tc = c(180, 160, 210),
  hdl = c(55, 45, 35),
  ldl = c(110, 100, 160),
  urineprotein = c(1, 1, 0),
  smoking = c(0, 1, 0),
  af = c(1, 0, 1),
  lvh = c(1, 0, 1)
)

# age          :age(continuous)
# sex          :sex(category: 1 = male, 2 = female)
# sbp          :systolic blood pressure(continuous)
# dbp          :diastolic blood pressure(continuous)
# t2dm         :diabetes mellitus(category: 0 = non-prevalent DM, 1 = prevalent DM)
# tc           :total cholesterol(continuous)
# hdl          :high-density lipoprotein cholesterol(continuous)
# ldl          :low-density lipoprotein cholesterol(continuous)
# urineprotein :proteinuria(category: 0 = negative, 1 = positive)
# smoking      :smoking status(category: 0 = never/past smoker, 1 = current smoker)
# af           :atrial fibrillation(category: 0 = negative, 1 = positive)
# lvh          :left ventricular hypertrophy(category: 0 = negative, 1 = positive)

suita_ecg(data)
```

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