predict_10yr_ascvd_risk

10-year ASCVD Risk Calculator

Description

This function implements

- the Pooled Cohort Risk equations from Goff et al, 2013.
- the updated Pooled Cohort Risk equations from Yadlowski et al, 2018

These equations predict 10-year risk of a first atherosclerotic cardiovascular disease (ASCVD) event, such as a stroke or myocardial infarction. The 2017 American College of Cardiology and American Heart Association blood pressure guideline recommends using 10-year predicted atherosclerotic cardiovascular disease risk to guide the decision to initiate or intensify antihypertensive medication. The guideline recommends using the Pooled Cohort risk prediction equations to predict 10-year atherosclerotic cardiovascular disease risk in clinical practice.

Usage

```r
predict_10yr_ascvd_risk(
  age_years,
  race,
  sex,
  smoke_current,
  chol_total_mgdl,
  chol_hdl_mgdl,
  bp_sys_mmhg,
  bp_meds,
  diabetes,
  equation_version = "Goff_2013",
  override_boundary_errors = FALSE,
  race_levels = list(black = "black", white = "white"),
  sex_levels = list(female = "female", male = "male"),
  smoke_current_levels = list(no = "no", yes = "yes"),
  bp_meds_levels = list(no = "no", yes = "yes"),
  diabetes_levels = list(no = "no", yes = "yes")
)
```

Arguments

- **age_years**: numeric vector of age values, in years.
- **race**: character vector of race values. Categories should include only 'black' or 'white'. If the race variable has additional categories other than 'black' or 'white', then group all non 'black' values into the 'white' category.
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sex character vector of sex values. Categories should include only 'male' or 'female'.

smoke_current character vector of current smoking habits. Categories should include only 'no' and 'yes'.

chol_total_mgdl total cholesterol, in mg/dL.

chol_hdl_mgdl HDL-cholesterol, in mg/dL.

bp_sys_mmhg systolic blood pressure, in mm Hg.

bp_meds character vector of blood pressure medication use habits. Categories should include only 'no' and 'yes'. For example, if currently using medication to lower blood pressure, the value should be 'yes'.

diabetes character vector of diabetes status. Categories should include only 'no' and 'yes'. For example, if diabetes is present, the value should be 'yes'.

equation_version a character value of length 1. Valid options are 'Goff_2013' and 'Yadlowsky_2018'. If 'Goff_2013' (the default option) is selected, the original Pooled Cohort risk equations are used (See Goff et al., 2013). If 'Yadlowsky_2018' is selected, the equations recommended by Yadlowsky et al., 2018 are used.

override_boundary_errors a logical vector of length 1. If FALSE (the default), then predict_10yr_ascvd_risk() will throw hard errors if you give it continuous input values that are outside the boundaries of what the Pooled Cohort risk calculator recommends. If TRUE, errors will not be thrown. Please use with caution.

race_levels a list of length 2 with names 'black' and 'white'. Values in the list should be character vectors of any length, and values in the character vectors should indicate what values in race belong to the 'black' and 'white' categories. For example, race may contain values of 'african_american', 'white', and 'hispanic'. In this case, race_levels should be list(white = c('white', 'hispanic'), black = 'african_american').

sex_levels a list of length 2 with names 'female' and 'male'. Values in the list should be character vectors of any length, and values in the character vectors should indicate what values in sex belong to the 'female' and 'male' categories (see examples).

smoke_current_levels a list of length 2 with names 'no' and 'yes'. Values in the list should be character vectors of any length, and values in the character vectors should indicate what values in smoke_current belong to the 'no' and 'yes' categories (see examples).

bp_meds_levels a list of length 2 with names 'no' and 'yes'. Values in the list should be character vectors of any length, and values in the character vectors should indicate what values in bp_meds belong to the 'no' and 'yes' categories (see examples).

diabetes_levels a list of length 2 with names 'no' and 'yes'. Values in the list should be character vectors of any length, and values in the character vectors should indicate what values in diabetes belong to the 'no' and 'yes' categories (see examples).
Details

The 2017 American College of Cardiology (ACC) / American Heart Association (AHA) blood pressure (BP) guideline recommends using 10-year predicted atherosclerotic cardiovascular disease (ASCVD) risk to guide the decision to initiate antihypertensive medication. The guideline recommends using the Pooled Cohort risk prediction equations (Goff et al, 2013) to predict 10-year ASCVD risk. The Pooled Cohort risk prediction equations have been externally validated in several studies and, in some populations, are known to overestimate 10-year ASCVD risk. In 2018, an updated set of equations were developed by Yadlowsky et al. using more contemporary data and statistical methods.

Value

a numeric vector with 10-year predicted risk values for ASCVD events.

References


Examples

```r
# example taken from Goff et al, 2013

sex = c('female', 'female', 'male', 'male')
race = c('black', 'white', 'black', 'white')
# 55 years of age
age_years = rep(55, times = 4)
# total cholesterol 213 mg/dL
chol_total_mgdl = rep(213, times = 4)
# HDL cholesterol 50 mg/dL
chol_hdl_mgdl = rep(50, times = 4)
# untreated systolic BP 120 mm Hg
bp_sys_mmhg = rep(120, times = 4)
bp_meds = rep('no', times = 4)
# nonsmoker
smoke_current = rep('no', times = 4)
# without diabetes
diabetes = rep('no', times = 4)

pcr_probs <- predict_10yr_ascvd_risk(
  sex = sex,
  race = race,
  age_years = age_years,
  chol_total_mgdl = chol_total_mgdl,
  cholhdl_mgdl = cholhdl_mgdl,
  bp_sys_mmhg = bp_sys_mmhg,
  bp_meds = bp_meds,
  smoke_current = smoke_current,
  diabetes = diabetes)
```

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chol_total_mgdl = chol_total_mgdl,
chol_hdl_mgdl = chol_hdl_mgdl,
bp_sys_mmhg = bp_sys_mmhg,
bp_meds = bp_meds,
smoke_current = smoke_current,
diabetes = diabetes
)

# note that this isn't an exact match of Table 4 in
# Goff et al supplement - this is because the table's
# coefficients are rounded to a lower decimal count than
# the coefficients used in predict_10yr_ascvd_risk()
round(100 * pcr_probs, 1)

# using a data frame with more granular categories and names

some_data <- data.frame(
    gender = c('woman', 'woman', 'man', 'male'),
race_3cats = c('AA', 'white', 'AA', 'other'),
    # 55 years of age
age_years = rep(55, times = 4),
    # total cholesterol 213 mg/dL
chol_total_mgdl = rep(213, times = 4),
    # HDL cholesterol 50 mg/dL
chol_hdl_mgdl = rep(50, times = 4),
    # untreated systolic BP 120 mm Hg
bp_sys_mmhg = rep(120, times = 4),
    # nonsmoker
smoke_current = c("no", "former", "no", "never"),
    # without diabetes
diabetes = rep('No', times = 4),
stringsAsFactors = FALSE
)

pcr_probs <- with(
    some_data,
    predict_10yr_ascvd_risk(
        sex = gender,
        sex_levels = list(female = 'woman', male = c('man', 'male')),
race = race_3cats,
age_years = age_years,
chol_total_mgdl = chol_total_mgdl,
chol_hdl_mgdl = chol_hdl_mgdl,
bp_sys_mmhg = bp_sys_mmhg,
bp_meds = bp_meds,
smoke_current = smoke_current,
diabetes = diabetes,
race_levels = list(black = 'AA', white = c('white', 'other')),
smoke_current_levels = list(no = c('no', 'former', 'never'), yes = 'Yes'),
bp_meds_levels = list(no = 'no', yes = 'Yes'),
diabetes_levels = list(no = 'No', yes = 'Yes')
)
)
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