18_calc_attr_burd_alt.R

default

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```
# Author: Daniel Fridljand
# Date: 11/15/2020
# Purpose: calculate attributable burden
#
#*****************************************************************************
#*

# clear memory
rm(list = ls(all = TRUE))

# load packages, install if missing
packages <- c("dplyr", "magrittr", "data.table", "DataCombine", "testthat", "tidyverse", "tictoc", "tru

for (p in packages) {
  suppressMessages(library(p, character.only = T, warn.conflicts = FALSE, quietly = TRUE))
}
options(dplyr.summarise.inform = FALSE)
options(dplyr.join.inform = FALSE)

censDir <- "/Users/default/Desktop/paper2021/data/05_demog"
dem_agrDir <- "/Users/default/Desktop/paper2021/data/06_dem.agr"
year <- 2001
agr_by <- "nation"
source <- "nvss"

  #----read some data-----

total_burden <- fread("/Users/default/Desktop/paper2021/data/12_total_burden_parsed2/nation/nvss/total_
  filter(Gender.Code == "A" & measure1 == "Deaths" & measure2 == "age-adjusted rate" &
           source == "nvss" & attr == "overall" & Education == "666")

  total_burden <- total_burden %>%
    dplyr::group_by_at(vars(one_of("Year",  "Race", "Hispanic.Origin"))) %>%
    summarise(value = sum(value))

  #print(total_burden)
  #read pm data
  meta <- read.csv(file.path(censDir, "meta", paste0("cens_meta_", 2000, ".csv")))
  files <- list.files(file.path(dem_agrDir, agr_by, year))
  pm_summ <- lapply(files, function(file) fread(file.path(dem_agrDir, agr_by, year, file))) %>% rbindli
  pm_summ <- pm_summ %>%
    left_join(meta, by = "variable") %>%
```

```
  filter(Education == "666" & Gender.Code == "A" )

pm_summ <- pm_summ %>%
  dplyr::group_by_at(vars(one_of("Year", "Race", "Hispanic.Origin", "pm"))) %>%
  dplyr::summarise(pop_size = sum(pop_size)) %>%
  as.data.frame()

head(pm_summ)
```

```
##   Year                              Race Hispanic.Origin       pm    pop_size
## 1 2000 American Indian or Alaska Native     All Origins 1.530000   35.538714
## 2 2000 American Indian or Alaska Native     All Origins 1.610000  296.600000
## 3 2000 American Indian or Alaska Native     All Origins 1.617757 8726.603721
## 4 2000 American Indian or Alaska Native     All Origins 1.720000    2.734165
## 5 2000 American Indian or Alaska Native     All Origins 1.850000    2.049630
## 6 2000 American Indian or Alaska Native     All Origins 2.010000   10.200000
```

```
rm(meta)

## ---calculations----

# 32 https://pubmed.ncbi.nlm.nih.gov/29962895/
## get the epa beta
## using the different parametric distributions in the EPA documentation
set.seed(5)
expa <- rtruncnorm(1000, a = 0, mean = 1.42, sd = 0.89)
expc <- rtruncnorm(1000, a = 0, mean = 1.2, sd = 0.49)
expd <- triangle::rtriangle(1000, 0.1, 1.6, 0.95)
expe <- rtruncnorm(1000, a = 0, mean = 2, sd = 0.61)
expg <- rtruncnorm(1000, a = 0, mean = 1, sd = 0.19)
expi <- rtruncnorm(1000, a = 0, b = 2.273, mean = 1.25, sd = 0.53)
expj <- rweibull(1000, 2.21, 1.41)
epa <- c(expa, expc, expd, expe, expg, expi, expj)
beta <- mean(epa / 100)

pm_summ <- pm_summ %>%
  mutate(paf = (exp(beta*pm)-1)) %>%
  group_by(Year, Race, Hispanic.Origin) %>%
  summarise(paf =  weighted.mean(paf, pop_size))

attrBurden <- inner_join(total_burden, pm_summ, by = c("Year", "Race", "Hispanic.Origin")) %>%
  mutate(value = value * paf, value = NULL, paf = NULL)

print(attrBurden)
```

```
## # A tibble: 5 x 3
## # Groups:   Year, Race [4]
##    Year Race                              Hispanic.Origin
##   <int> <chr>                             <chr>
## 1  2000 American Indian or Alaska Native All Origins
## 2  2000 Asian or Pacific Islander        All Origins
## 3  2000 Black or African American        All Origins
## 4  2000 White                            Hispanic or Latino
## 5  2000 White                            Not Hispanic or Latino
```