

# EPA attributable burden calculation

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## Input Data

I have already calculated following data sets. I hope I won't need to make too many adjustments to switch from the GBD exposure-response function to the one from EPA. Firstly, I have all-cause burden data by Race and Hispanic Origin measured in age-adjusted Death rates per 100,000:

```
print(total_burden)
```

##	Year	Race	Hispanic.Origin	value
## 1	2010	American Indian or Alaska Native	All Origins	6466.826
## 2	2010	Asian or Pacific Islander	All Origins	3923.177
## 3	2010	Black or African American	All Origins	9287.966
## 4	2010	White	Hispanic or Latino	5715.364
## 5	2010	White	Not Hispanic or Latino	7253.686

Secondly, I have estimated for each Ethnicity, how many persons (pop\_size) are exposed to a given level of particulate matter concentration (pm).

```
head(pm_summ)
```

##	Year	Race	Hispanic.Origin	pm	pop_size
## 1	2010	American Indian or Alaska Native	All Origins	1.53	347
## 2	2010	American Indian or Alaska Native	All Origins	1.55	12
## 3	2010	American Indian or Alaska Native	All Origins	1.58	2
## 4	2010	American Indian or Alaska Native	All Origins	1.59	26
## 5	2010	American Indian or Alaska Native	All Origins	1.80	38
## 6	2010	American Indian or Alaska Native	All Origins	1.81	21

## Calculation

Calculating  $\beta$  as in your code.

```
## 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)
```

Now the actual calculation of the population attributable fraction (paf) and the attributable burden.

```

1 paf <- pm_summ %>%
2   mutate(paf = (exp(beta * pm) - 1)) %>%
3   group_by(Year, Race, Hispanic.Origin) %>%
4   summarise(paf = weighted.mean(paf, pop_size))
5
6 attr_burden <- inner_join(total_burden, paf,
7                           by = c("Year", "Race", "Hispanic.Origin")) %>%
8   mutate(value = value * paf, paf = NULL)
9
10 print(attr_burden)

```

##	Year	Race	Hispanic.Origin	value
## 1	2010	American Indian or Alaska Native	All Origins	693.2755
## 2	2010	Asian or Pacific Islander	All Origins	522.5717
## 3	2010	Black or African American	All Origins	1339.8480
## 4	2010	White	Hispanic or Latino	741.2136
## 5	2010	White	Not Hispanic or Latino	901.0384

Line 2  $PAF = (e^{\beta \times pm} - 1)$  in the above code corresponds to line 85 in your code in [https://github.com/burke-lab/wildfire-map-public/blob/main/work/14\\_figure3.R](https://github.com/burke-lab/wildfire-map-public/blob/main/work/14_figure3.R).

## My questions

1. Does the above code correspond to how the EPA estimates are to be calculated? I am particularly uncertain, whether I understood the population scaling in line 127 in your code correctly.
2. The exposure-response function used is  $burden_{attributable} = (e^{\beta \times pm} - 1) \times burden_{allcause}$ . Can this formula be found in <https://pubmed.ncbi.nlm.nih.gov/29962895/> or deduced from somewhere?
  - Equation 1 on page 3 looks similar, but is different and would yield very different results far from 0:  $PAF = (1 - e^{-\beta \times pm})$
3.  $burden_{attributable} = (e^{\beta \times pm} - 1) \times burden_{allcause}$  is not bounded in pm. In particular, it could theoretically exceed the all-cause burden. Am I misunderstanding something?
4. Where exactly are the parametric distributions in the calculation of  $\beta$  taken from? Could you please provide the position in the EPA Documentation you are referring to?