Impact

Josh Horsley and Richard Broome 2020-09-21

This vignette demonstrates impact assessment with various lag choices

Reduce PM_{2.5} by 1 $\mu g/m^3$

For this example we will use the HRAPIE mean relative risk estiamte RR = 1.06 per 10 $\mu g/m^3$ of PM_{2.5}.

No cessation lag

Functions in this package use demographic data in a standardised format stored in demog_data. For this example we will use the included single_year_data to create demog_data.

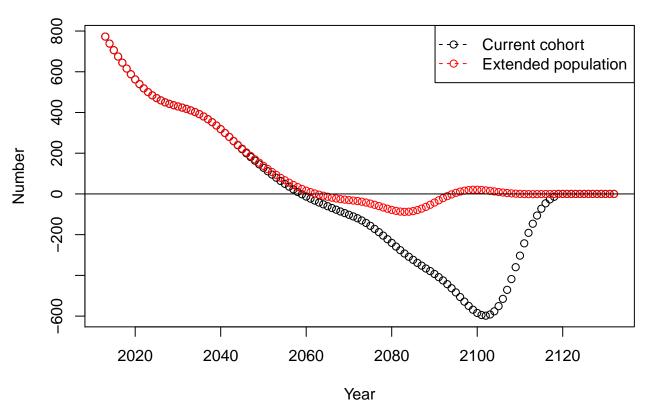
```
head(single_year_data)
        measure sex age time value
#> 1 Population Males 0 2005 132477
#> 2 Population Males 0 2006 136681
#> 3 Population Males 0 2007 145930
#> 4 Population Males 0 2008 149299
#> 5 Population Males 0 2009 151627
#> 6 Population Males 0 2010 152773
population <- subset(single_year_data,</pre>
                      time == 2011 & sex == "Persons" & measure == "Population")
population <- population[, c("age", "value")]</pre>
population$age <- as.numeric(gsub(" .+", "", population$age))</pre>
colnames(population)[2] <- "population"</pre>
deaths <- subset(single_year_data,</pre>
                 time == 2011 & sex == "Persons"& measure == "Deaths")
deaths <- deaths[, "value"]</pre>
demog_data <- data.frame(population, deaths = deaths)</pre>
```

Calculate the impact assuming there is no lag between exposure reduction and health outcomes

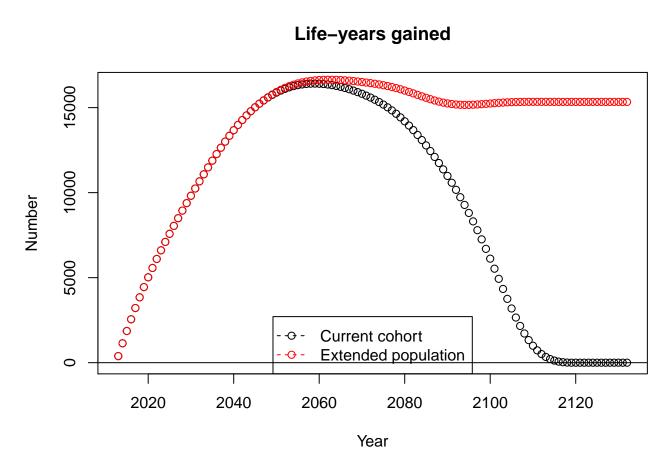
```
no_lag <- impact(demog_data)
no_lag <- data.frame(lapply(no_lag, colSums))</pre>
```

Compare deaths avoided

Deaths avoided



Comapre life-years gained



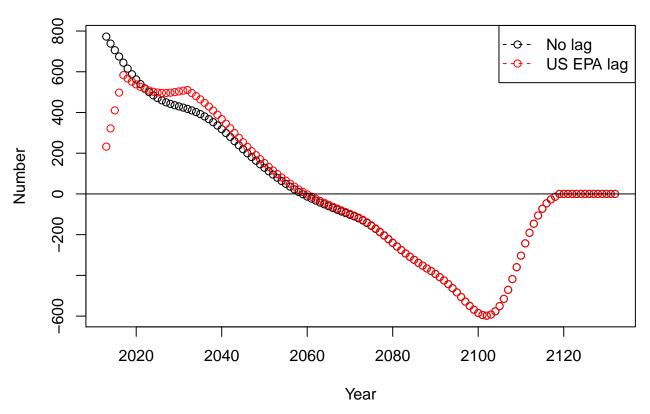
Calculate the impact assuming the US EPA lag between exposure reduction and health outcomes

```
lag <- cumsum(c(0.3, rep(0.5/4, 4), rep(0.2/15, 15)))
epa_lag <- impact(demog_data, lag_structure = lag)</pre>
epa_lag <- data.frame(lapply(epa_lag, colSums))</pre>
```

Plot a comparison of no lag and US EPA lag (Current cohort)

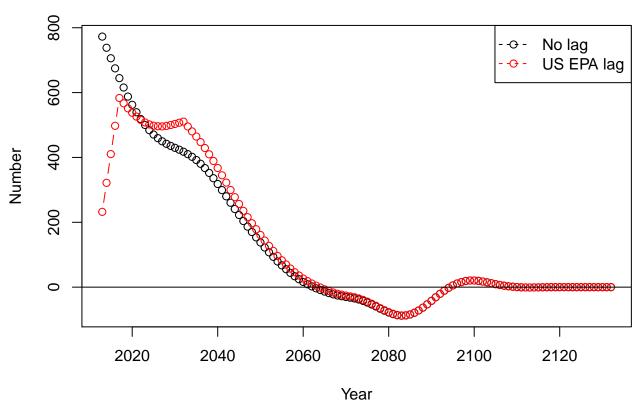
```
plot(rownames(no_lag), no_lag$deaths_current,
     xlab = "Year", ylab = "Number",
     main = "Deaths avoided (current cohort)", type = "b")
points(rownames(epa_lag), epa_lag$deaths_current, col = "red", type = "b")
abline(h = 0)
legend("topright", c("No lag", "US EPA lag"),
       col=c("black", "red"), pch = 21, lty=2)
```

Deaths avoided (current cohort)



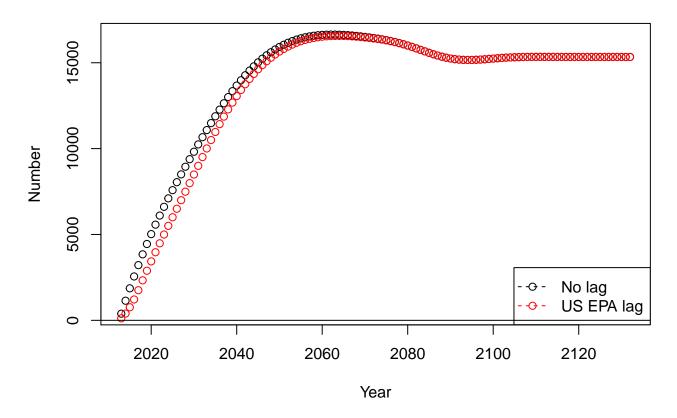
Plot a comparison of no lag and US EPA lag (Extended cohort)

Deaths avoided



Compare total life-years gained

Life-years gained



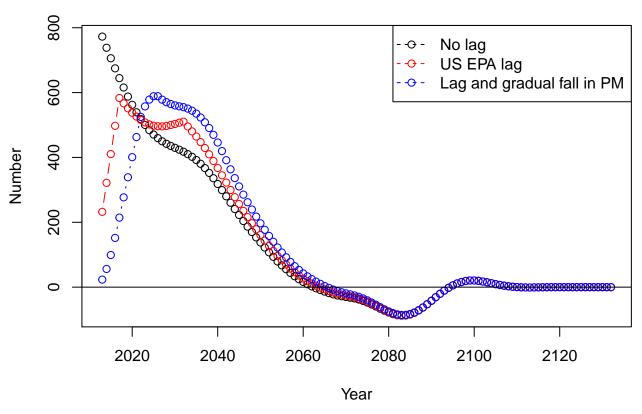
Assuming PM_{2.5} takes 10 years to fall by 1 $\mu g/m^3$ and US EPA cessation lag

Calculate results

```
pm <- seq(0.1, 1, 0.1)
slow_pm <- impact(demog_data, delta_pm = pm, lag_structure = lag)
slow_pm <- data.frame(lapply(slow_pm, colSums))</pre>
```

Compare deaths avoided

Deaths avoided



Compare life years gained

Life-years gained

