

Description of Methods and Issues of RSV Excess Mortality Estimation

Goals

This is a summary of the methods used for influenza excess mortality estimation using mortality data; these methods were originally also proposed for use in excess mortality estimations for RSV.

Excess mortality estimation

Excess mortality estimation represents a suite methods/statistical models that may be described as *ecological* as the unit of analysis is not *individuals*, but *population group-weeks*. The population groups can be certain age groups, typically <5, 5-17, 18-49, 50-64, 65+, nationally or by HHS region.

Serfling-type model for excess mortality due to influenza

Traditionally, weekly influenza excess mortality was estimating using the following model:

$$\log \mu_k = \beta_0 + \beta_1 w_k + \beta_2 w_k^2 + \beta_3 w_k^3 + \beta_4 \sin t_k + \beta_5 \cos t_k + \beta_6 v_{A(H1)} + \beta_7 v_{A(H3)} + \beta_8 v_B \quad (1)$$

$$y_k \sim \text{Poi}(\mu_k N_k) \quad (2)$$

where $t_k = \frac{w_k 2\pi}{52.25}$, with w_k being the index week, and $v_{A(H1)pdm}, v_{A(H3)}$ and v_B are the viral surveillance indicators for influenza, typically the percent of samples tested with positive test results for influenza A(H3N2), A(H1N1)pdm09 and B, respectively, y_k is the number of deaths (e.g. respiratory and circulatory deaths, usually by age group) in week k and N_k is the population denominator. In R, this model could be implemented as follows. We look at data over six influenza seasons; the influenza indicators are actually the proportion positive multiplied by the ILI%. This type of indicator is sometimes referred to as Goldstein indicator (see Goldstein et al. (2011)):

```
filename <- 'data_National_2010_16_5ag.dat'
setwd('..') ## change to root directory
setwd('./RSVdata')
datarr <- data.frame(read.table(file = filename, header = T))
#####
### Serfling-type model, virologic indicators (Thompson et al., 2009) #####
#####
ag <- 5 ### Setting age group to 65+
agdata <- datarr[which(datarr$age==ag),]

AH1P <- agdata$AH1P
AH3 <- agdata$AH3
B <- agdata$B

mort <- agdata$rcu
pop <- agdata$pop

N <- length(mort)
time <- (1:N)/N
```

```

t <- time * N * 2* pi/52.25
#####
data <- data.frame(mort,time,t,AH1P,AH3,B,pop)
#####
Poimod <- glm(mort ~ time + time^2 + time^3 + sin(t) + cos(t) + AH1P + AH3 +
              B + offset(log(pop)), data = data,family = poisson(link = 'log'))

dataflu0 <- data.frame(mort,time,t,AH1P=AH1P*0,AH3=AH3*0,B=B*0,pop)
mortflu0 <- predict(Poimod, newdata = dataflu0, type = 'response')

EM <- sum(mort - mortflu0)
#####

```

In this case, the total number of excess deaths in people 65 and older due to influenza over six seasons is estimated at 1.50346×10^5 .

Updated models for RSV or influenza/RSV mortality

To account for a baseline mortality function that is not exactly sinusoidal, regression splines can be used. To model influenza mortality,

References

Goldstein, Edward, Sarah Cobey, Saki Takahashi, Joel C Miller, and Marc Lipsitch. 2011. "Predicting the Epidemic Sizes of Influenza A/H1N1, A/H3N2, and B: A Statistical Method." *PLoS Medicine* 8 (7). Public Library of Science: e1001051.