**Forecasting Influenza-Like Illness in the United States: 2016/17 Influenza Season**

**Group Health Research Institute**

**Brief description of methodology**

Our forecasting model consists of two components. The first component forecasts the number of detected cases of laboratory-confirmed influenza in each of the 10 United States Health and Human Services (HHS) Regions. The second component estimates the percent of visits positive for influenza (ILIpercent) based on the forecasted influenza counts.

**Influenza forecasting model**

*Model development and fitting*

We use a compartmental Susceptible-Infectious-Recovered (SIR) mass action model to simulate influenza transmission within each of the 10 HHS regions. To account for the co-circulation of separate influenza virus types and subtypes [A(H1N1)pdm09, A(H3N2), and B], which may interfere with each other, we use the status-based SIR formulation of Gog and Grenfell.[[1]](#footnote-1) We use the modification to this model proposed by Minayev and Ferguson[[2]](#footnote-2) to allow for transient strain-transcending immunity following infection. Model parameters are defined from published literature wherever possible, including birth/death rates, duration of infectiousness, and duration of immunity following infection. We used region-specific weekly counts of laboratory-confirmed influenza infection for October 2014 through September 2016 (stratified by type/subtype) to estimate the remaining parameters. Parameters were estimated through a monte carlo parameter sweep. Estimated parameters include seasonally-forced R0, which are type/subtype-specific, and the proportion of infections that are detected by surveillance, which is assumed to be constant across types/subtypes within a region. We also estimated the proportion of the population susceptible to each type/subtype prior to the start of the 2014/15 influenza season.

*Forecasting influenza*

Within each region, we chose the 100 parameter sets that gave the best fit to observed influenza counts. For each parameter set we ran the SIR model from October 2014 through September 2017 and forecast the weekly observed counts of laboratory-confirmed influenza infections in each HHS region, stratified by virus type/subtype. For each of the 100 region-level forecast we summed the regional counts to estimate national counts of influenza cases identify by surveillance.

**ILIpercent conversion**

Within each HHS region, and for national-level surveillance, we used data from October 2014 through September 2016 to estimate weekly ILIpercent as a (cyclic) function of calendar time and of laboratory-confirmed influenza cases. This estimation model included separate parameters for each influenza type/subtype, allowing different types/subtypes to differentially impact ILIpercent.

For our forecasts, we use each the 100 forecasts of weekly influenza counts to estimate weekly ILIpercent, both by HHS region and nationally, using the estimated parameters for the relationship between influenza and ILIpercent. We then summarize across the 100 forecasts to predict the seasonal forecasting targets and the 1- to 4-week ahead targets.

**Updating forecasts as the season progresses**

Our forecasts are based on a long-term influenza forecasting model we have previously developed. Because of this, we do not update neither the SIR model nor the ILIpercent model on a weekly basis during the 2016/17 influenza season. However, if influenza surveillance suggests the emergence of antigenically drifted strains of A(H1N1)pdm09 or A(H3N2), we will update the model to account for increased population susceptibility to these viruses.

1. Gog and Grenfell; “Dynamics and selection of many-strain pathogens”; PNAS 2002; 99(26): 17209-14 [↑](#footnote-ref-1)
2. Minayev and Ferguson; “Improving the realism of deterministic multi-strain models: implications for modelling influenza A”; J R Soc Interface 2009; 6(35):508-18 [↑](#footnote-ref-2)