Estimates of the Reproduction Number for Seasonal Influenza in the European Region from 2012 to 2016

Abstract

Introduction: In the 21st century, the world is facing a wide range of public health problems related to infectious diseases. Seasonal influenza is a contagious viral infection, which affects the human respiratory system. Influenza vaccination policy plays a critical role in mitigating and controlling influenza outbreaks. Vaccination remains the most effective public health intervention to mitigate and prevent seasonal influenza. The basic reproduction number R_0 represents the transmissibility of infectious disease. Our study illustrates how seasonal influenza data from European countries can be integrated into a Bayesian framework to assess the disease's basic reproduction R_0 . This research shows that seasonal influenza R_0 varies across influenza seasons and is generally below 2. Our study illustrates a detailed picture of the transmission of seasonal influenza in European countries from 2012 to 2016.

Materials and Methods: Estimating R_0 is an essential step in understanding infectious diseases and informing public health interventions. The goal of this study is to estimate a value of R_0 for the seasonal influenza disease in the Europe region that is as reliable as possible by using sentinel incidence data of influenza-like illness (ILI). We utilized the SEIR model and the Bayesian method, Hamiltonian Monte Carlo (HMC) sampling algorithm. Mathematical modeling can be preferable when (1) there is limited data available; (2) there is a need to incorporate assumptions in complex situations, such as birth rate, death rate, under-reporting, etc; and (3) want to predict the potential impact of interventions, such as vaccination, lockdown, etc. The Bayesian approach can conduct inferences about unknown parameters in epidemiological models. In the Bayesian approach, prior knowledge about the distribution of the parameters is combined with observed data to update the prior distribution and generate a posterior distribution. The Bayesian workflow includes three stages model building, inference, and model checking/improvement. Figure 1 presents the SEIR model Bayesian prior/likelihood and calibration workflow.



Figure 1 SEIR Model / Bayesian Priors and Likelihood / Calibration Workflow

Results and Discussion: We processed 75 different fits for 15 EU member states ILI data sets from 2012 to 2016. Stan's HMC sampler provides multiple inference diagnostics by running multiple MCMC chains and monitoring mixing and divergence. Our Bayesian inference diagnostic checks provided reasonable sampling and reliable results. The chains demonstrated agreement among

themselves and exhibited rhat ≤ 1.01 . Additionally, we observed high values of ESS_bulk and ESS_tail, indicating an effective sample from the core and tail regions of the posterior distribution. Table 1 and Figure 2 present Stan basic diagnostics check results summary of Ireland 2012/13.



Figure 2 Trace Plot/ Pair Plot/ Posterior Predictive Check

The parameters R_0 , fraction and Ii estimates obtained with the Bayesian inference are also presented in Figure 3. The R_0 below 1, close to zero reflects the success of the control measures in controlling the epidemic. Overall results show that R_0 is found between 1.04 to 1.45 and incidence reporting fraction $\leq 50\%$ across five years from 2012 to 2016. The R_0 above 1 reflects the lack of control measures in controlling the epidemic in the EU states. Our results show that at the start of October, a certain number of individuals were infectious, and the outbreak is initiated by the number of individuals in their community.





Our data analysis indicates the timing of the seasonal peak occurs mainly during the winter months, November to April with the number of cases usually peaking around February in the European countries. Whereas the intensity of seasonal influenza transmission varies between countries. The R_0 may not only be used to estimate the epidemic change in regions such as EU states but also used for making appropriate changes to public health measures for managing epidemics and pandemics. This research contributes; (1) the first longitudinal study with mathematical modeling to investigate the transmission dynamics of influenza in the EU region from 2012 to 2016 and (2) presents a general model to estimate model parameters in the EU states.