# Group 16: Pandemic Flu

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## Background

Understanding the behavior of the spread of infectious diseases like flu pandemics is critical for advising policy making. For example, studying behavior of virus transmission and recovery rates allows health professional and policymakers to define how much antiviral agents should be on hand, areas and demographics to prioritize vaccination of, and other strategies intended to prevent an outbreak. Furthermore, being able to communicate the results of an infectious disease outbreak model/simulation is very important as this will facilitate adoption of containment measures.

Infectious disease epidemic models have been the subject of study since the 1980s. It was Russian scientists that first began to implement models for estimating spread patterns of influenza and other viruses (Longini et al., 1986). Reception of these models was skeptical initial, and for multiple reasons. First, the geographic areas being studied were relatively isolated, so applicability to global modeling was uncertain. Second, the algorithms for simulating flu spread were computationally expensive for the time, meaning that these models were not very practical 50 years ago.

Initially, pandemic flu was modeled using a set of ordinary differential equations (ODE), and the model assumed that we can partition the study group into multiple sub-groups: susceptible, exposed, infected, and recovered. This deterministic model is referred to as SIR or SEIR, although there are other extensions that consider additional sub-groups. With that said, recent studies have applied stochastic techniques to model pandemic flu (and other infectious diseases). While the latter models have the advantage of being potentially more flexible, they are somewhat more complicated to implement and explain. Hence, the ODE variety is still relatively common in theory and practice today.

## Completed Items

The primary focus of my work up until this point has been to familiarize myself with historic research and findings, as well as tools and data that are available to me to implement models and study pandemic flu.

So far, I have collected 22 papers from the past 49 years in which the authors have studied pandemic flu (and other infectious diseases), assessed the impact of covariates and mitigation strategies, or reviewed past pandemics to verify their extents and severity. I have reviewed these papers and used them as the foundation for a brief history of infectious disease modeling and literature review for my final report (which is still in its first draft).

Additionally, I have collected a number of R packages that have either data pertaining to epidemiology, or tools for implementing epidemiological models. Some examples include [cleanepi](#), [epiparameter](#), [epidemics](#), and many more from the Epiverse-TRACE team.

# Incomplete Items

Obviously, I still need to finish writing the final report for this project. I have already made significant progress on the literature review, but I have yet to implement any models and do any simulation. This will be my primary focus over the ensuing weeks.

So, I will begin by implementing a simple SIR model to simulate the spread of pandemic flu given current transmission and recovery rates. Time permitting, I will then add solar radiation and altitude covariates and try to identify thresholds that would reduce the reproduction ratio to reasonable levels (i.e., curtail an outbreak). And finally, also time permitting, I will implement some more sophisticated modeling techniques (e.g., stochastic metapopulation models) using data and tools available from Epiverse packages, and do a three-way comparison between the three approaches to see which one offers a good balance between accuracy and interpretability, and define any relationships between covariates and pandemic spread that can be inferred.

If additional weather data is needed, I will access that from Copernicus [ERA5](.).