

Approximating Influenza Dynamics

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Abstract

Mathematical epidemiology is the application of mathematics to modeling the spread of infectious diseases. The most fundamental epidemiology compartment model is the SI (susceptible-infectious) model which breaks a population into two health states—those susceptible to being infected and those who are infectious. Using weekly data published by the Center for Disease Control (CDC), an SI compartment model $I(t)$ was created in an attempt to predict the dynamics of seasonal type A influenza in the United States, a disease usually approached with an SIR (susceptible-infectious-recovered) compartment model. A derivative of the SI function was found $I'(t)$ in order to produce a curve identical to that of an SIR infection curve. The parameter values for $I'(t)$ were found using computational techniques and the CDC 2014-2015 data, which resulted in a theoretical SIR function $I'(t)$ that very accurately estimates the annual infection curve for type A influenza for the years 2012 through 2015. This finding suggests there may be possible applications for an SI compartment model in estimating the dynamics of more complex infectious diseases.

Introduction

- Mathematical Epidemiology:** The study of infectious diseases and how they spread throughout a population.
- Compartment Models in Epidemiology:** A mathematical framework for describing and modeling the spread of a disease. These compartment models are usually done through a system of differential equations.
- Different Kinds of Models:** SI (susceptible-infectious), SIS (susceptible-infectious-susceptible), SIR (susceptible-infectious-recovered), and SEIR (susceptible-exposed-infectious-recovered) [1].
- Selecting the Right Model:** Depending on the disease in focus, there is generally one compartment model that most accurately approximates the dynamics of the disease. More complex diseases = more complex of a compartment model.

References

- [1] Nakul Chitnis. Introduction to Mathematical Epidemiology: Deterministic Compartmental Models. *Swiss Tropical and Public Health Institute*, pages 1–2, 2011.
- [2] G. Chowell, M.A. Miller, and C. Viboud. Seasonal Influenza in the United States, France, and Australia: Transmission and Prospects for Control. *Epidemiology and Infection*, 136(6), June 2007.
- [3] Centers for Disease Control. How Flu Spreads, September 2013.
- [4] Nakul Chitnis. Introduction to Mathematical Epidemiology: The Basic Reproductive Number. *Swiss Tropical and Public Health Institute*, page 1, 2011.
- [5] CDC. National and Regional Level Outpatient Illness and Viral Surveillance, February 2016.

Endemic Model

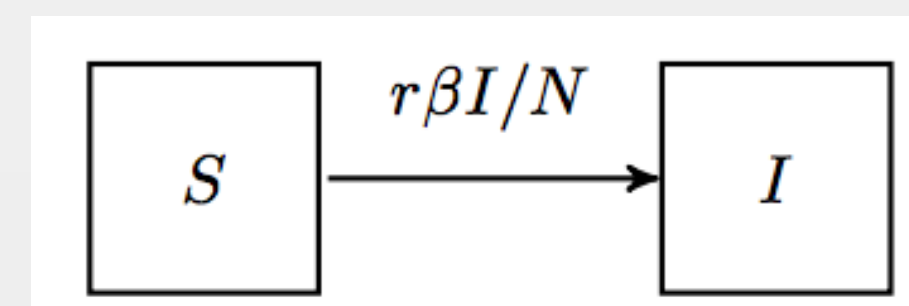


Figure 1: Susceptible-Infectious model.

The SI model divides the total population N into two health states: susceptible S and infectious I . The rate at which susceptible individuals become infected is the number of contacts per unit of time r , multiplied by the probability a contact will become infected by the disease β [1]. The fractional population that is infected is: I/N [1]. This model assumes infectious hosts stay infected for the rest of their lives and no deaths occur during the influenza season.

$$\frac{dS}{dt} = -r\beta(N - I)\frac{I}{N} \quad (1a)$$

$$\frac{dI}{dt} = r\beta S\frac{I}{N} \quad (1b)$$

$$\frac{dI}{dt} = r\beta(N - I)\frac{I}{N}. \quad (2)$$

$$I(t) = \frac{I_0 N}{(N - I)e^{-r\beta t} + I_0} \quad (3)$$

Data

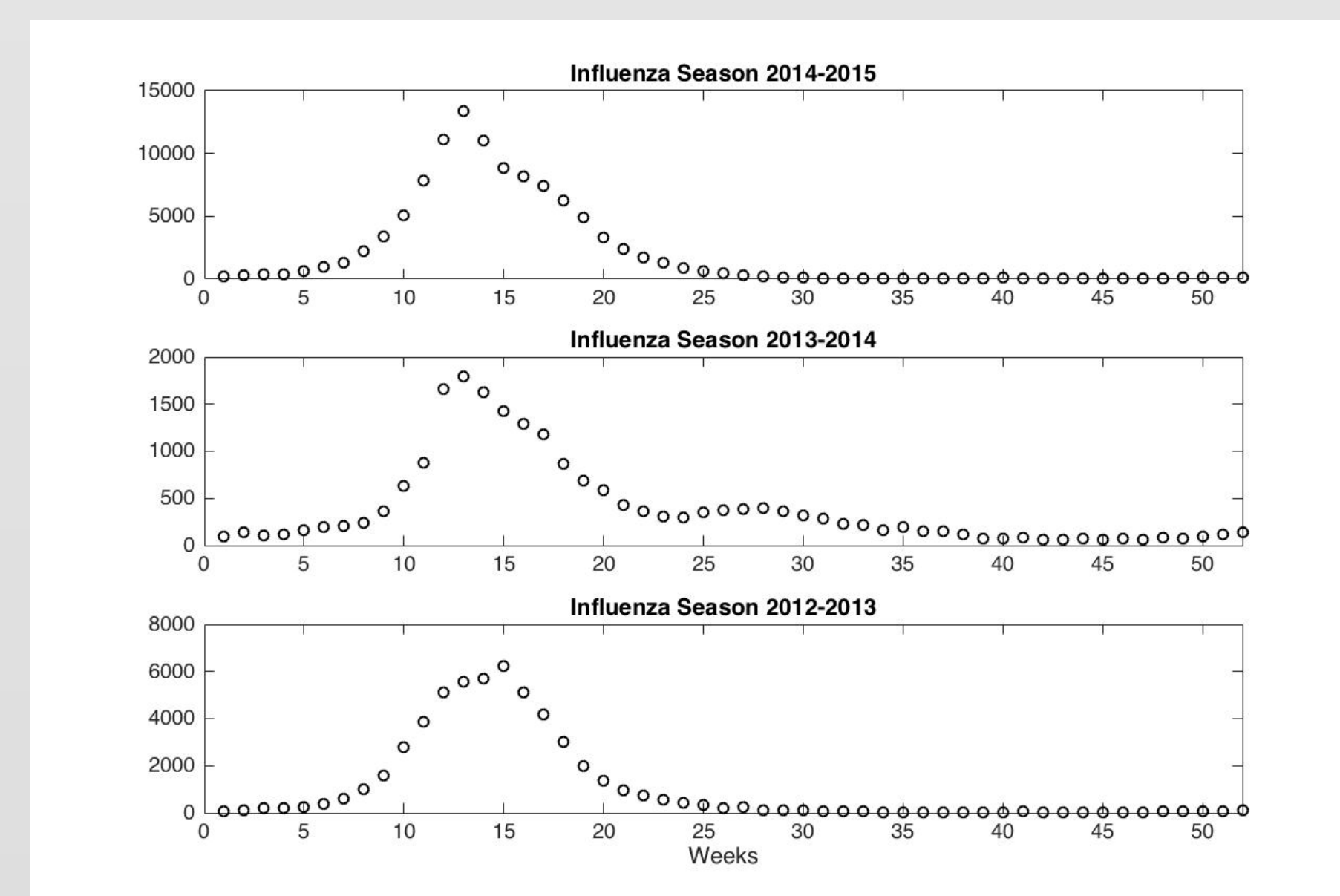


Figure 2: A number of infections vs. time plot for each influenza season through the years 2012-2015. Top graph: Influenza season 2014-2015. Middle graph: Influenza season 2013-2014. Bottom graph: Influenza season 2012-2013. Note: All data only includes infections from type A virus strains.

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Determining Parameters

We found that the values for r and β were approximately 1.5912 and 0.2749 respectively. More accurately, the coefficient value of t in equation (3) should be approximately 0.4374.

```
% Integrate SIR function for 2015 Influenza.
x_data = 1:52;
si15 = integrate(curve_fits{3}, x_data, 0);

% Fit theoretical SIR to CDC SIR.
[xData, yData] = prepareCurveData( x_data, si15 );

% Set up fittype and options.
ft2 = fittype( '(106500*197)/(((106500-197)*exp(-r*b*t)+197));',
    'independent', 't', 'dependent', 'I' );
opts = fitoptions( 'Method', 'NonlinearLeastSquares' );
opts.Display = 'Off';
opts.StartPoint = [6 0.4];

% Fit model to data.
[si15_approx, si15_approx_gof] = fit( xData, yData, ft2, opts );

% Display coefficient values.
r = si15_approx.r;
b = si15_approx.b;
```

Results

$$I'(t) = \frac{dI}{dt} = \frac{NI_0(N - I_0)r\beta e^{-r\beta t}}{((N - I_0)e^{-r\beta t} + I_0)^2}. \quad (4)$$

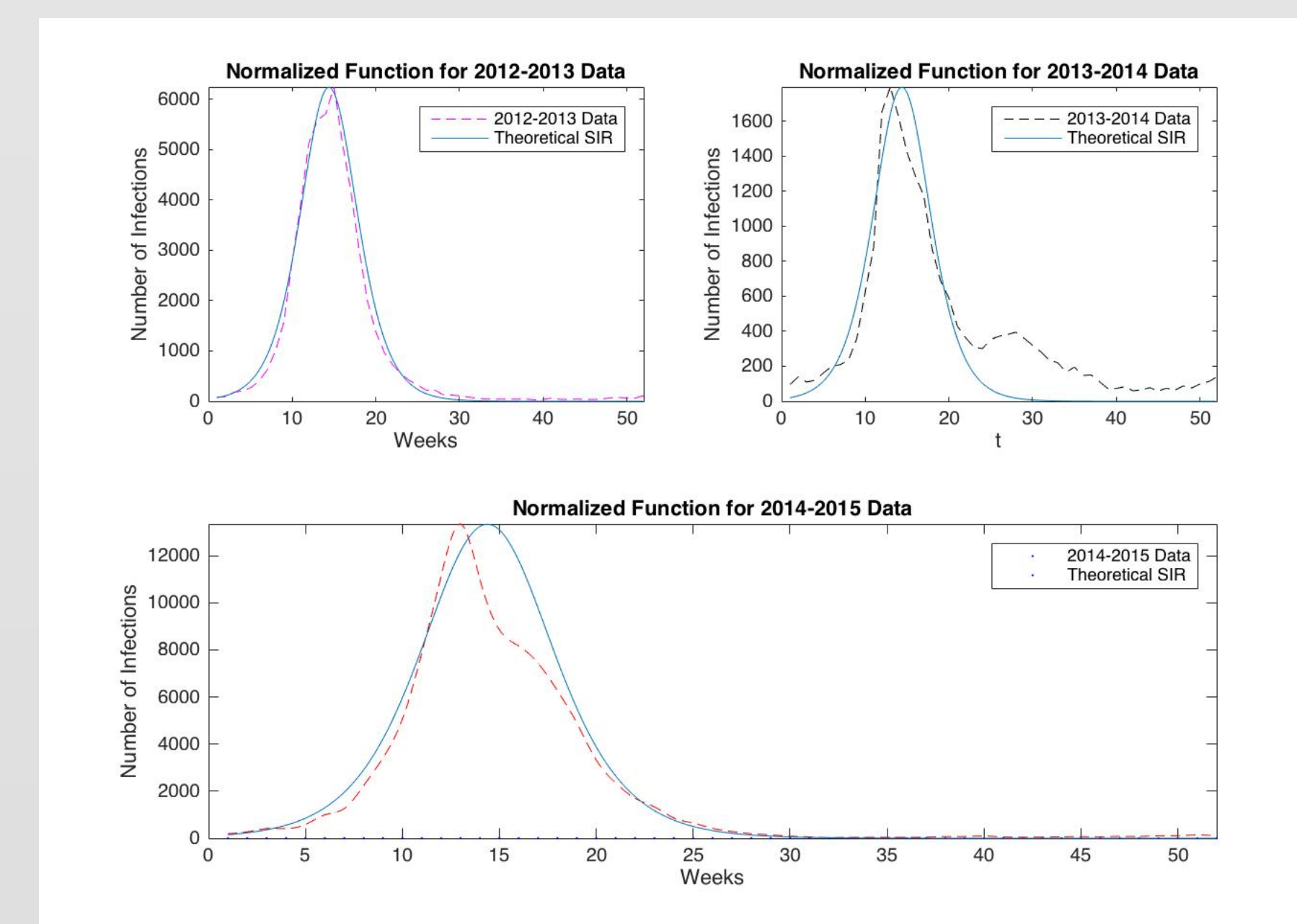


Figure 3: Top left corner: a normalized theoretical SI function plotted against the CDC data curve for the 2012-2013 influenza season. Top right corner: normalized theoretical SI function plotted against the CDC data curve for the 2013-2014 influenza season. Lower half: a normalized theoretical SI function plotted against the CDC data curve for the 2014-2015 influenza season.

Conclusions and Future Research

- Our findings suggest** there exists more applications of an SI model than simply modeling a disease with only a susceptible and infectious group.
- Equation (4) is a very good approximation** of the CDC infection curves from the past three years of seasonal type A influenza data. This statement is shown by the results in figure 3.
- As the United States enters the 2015-2016 influenza season**, we predict our theoretical SIR model should offer a reliable estimation for the number of type A influenza infections given the initial amount of infected people at time zero I_0 and the total population size N .
- A note regarding the "reproduction number" of influenza:**
 - Our team attempted to find the parameter values for r and β by using what is known as the "reproduction number." The reproduction number R_0 of a disease is the total number of secondary cases a single infectious host will produce [4].
 - Mathematically, $R_0 = (r\beta)(T)$ where T is the length of time a host remains infected. Using the CDC's estimate of eight days for T [3], and influenza's average reproduction number of 1.28 [2], we solved for the product of r and β .
 - This did not produce a reliable and accurate result, and the error can be attributed to the reproduction number not having been adjusted for an SI model. Further evaluation should be performed to determine how the parameter values can adjusted in order to fit the compartment model being used.
- Further research should be performed** to revise the model as influenza continuously evolves over time. In addition, the limitations of an SI model are not quite clear from our findings in regards to approximating diseases with multiple health states and should be further studied.