Extended SEIR model

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Abstract

An extended SEIR model is defined and calibrated to the Irish data. The parameter f, which is the fraction of infections that remain asymptomatic is shown to be crucial in determining the likely future scenarios.

1 Assumptions

- Fully-mixed, homogeneous population (no spatial aspect or contact networks).
- SEIR model, based on differential equations (no stochastic inputs).
- See Figure 1 for model structure and notation.
- Exponential distributions for residence times in all compartments.

2 Parameters

- L: average latent period (days)
- C: average incubation period (days)
- D: average infectious period (days)
- h: multiplicative factor for reduction of infectiousness in the Asymptomatic Infected compartment, relative to Symptomatic Infected
- i: multiplicative factor for reduction of infectiousness in the Immediate Isolation compartment, relative to Symptomatic Infected
- j: multiplicative factor for reduction of infectiousness in the Post-test isolation compartment, relative to Symptomatic Infected
- f: fraction of infected who are Asymptomatic
- t: fraction of symptomatic cases that are tested
- q: fraction of symptomatic cases that are quarantined until recovery
- T: average wait for test results (days)
- β: Transmission rate that enters the force of infection.

The parameter β is not input directly; instead the relation between basic reproductive number R_0 and β is derived for this model (see Appendix) and an input R_0 value is converted to the equivalent β value.

The parameters used in runs are the results of random searches of parameter space, with the following upper and lower bounds for (independent) uniform distributions:

- Range of L: 3.3 to 3.9.
- Range of C: L to 6.0 (lower limit ensures $C - L$ is nonnegative).
- Range of D: $C - L$ to 15 (lower limit ensures $D - (C - L)$ is nonnegative).
- Range of h: 0.1 to 1.0
- Range of i: 0.0 to 0.2
- Range of j: 0.0 to 0.2
- Range of f: 0.0 to 1.0
- Range of t: 0.5 to 1.0
- Range of q: 0.0 to $1 - t$ (upper limit ensures $1 - q - t$ is nonnegative)
- Range of T: 1.0 to $D - (C - L)$
- Range of R_0: 2.0 to 4.0, with conversion to equivalent β parameter

3 Commentary

The fraction of infections that are asymptomatic (or, more properly, "undocumented") is a hugely sensitive parameter for the model. In Figures 2 and 3 we demonstrate this sensitivity by showing three scenarios: $f = 0.25$ (top), $f = 0.50$ (middle) and $f = 0.75$ (bottom). Figure 2 shows the daily new cases as a function of day (measured from Feb 28th). The multiple curves in each scenario correspond to different feasible sets of parameters, with the value of f fixed. The variability between the three scenarios is much greater than the variation amongst the curves in any one scenario, indicating that the parameter f strongly controls the dynamics, with all other parameters playing a subsidiary role.

Figure 3 shows cumulative cases (on log scale) and new daily cases for the same three scenarios ($f = 0.25$ (top), $f = 0.50$ (middle) and $f = 0.75$ (bottom)). The blue curves are predictions for the unmitigated cases, while the red curves are determined by fitting a social-distancing reduction factor on the transmission rate from March 13th onwards. The level of mitigation is fitted to match the observed data over the last week.

In Figure 4 we compare the predictions across the three scenarios. While they differ in their long-term predictions, all agree on the short-term predictions (as we would expect, as they are essentially exponential growth curves fitted to recent data).

The sensitivity to the fraction f of undocumented infections makes long-term prediction essentially impossible (unless f can be determined by other means). However, the short-to-medium term predictions are consistent across the scenarios with various f values. We caution that these predictions are essentially extrapolations of the recent exponential growth rate, and further interventions will likely change this growth rate further.

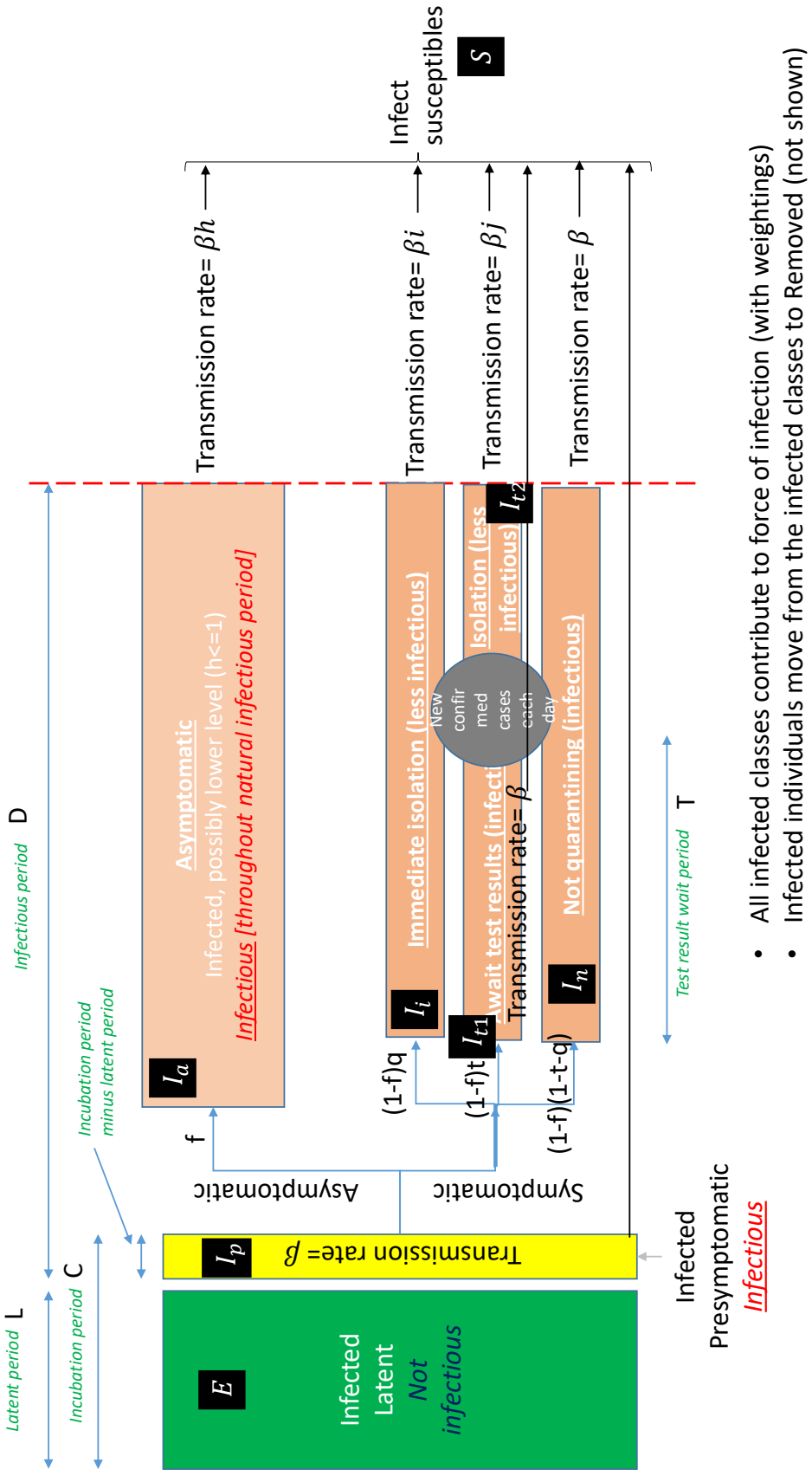

Figure 1: Model compartment structure.

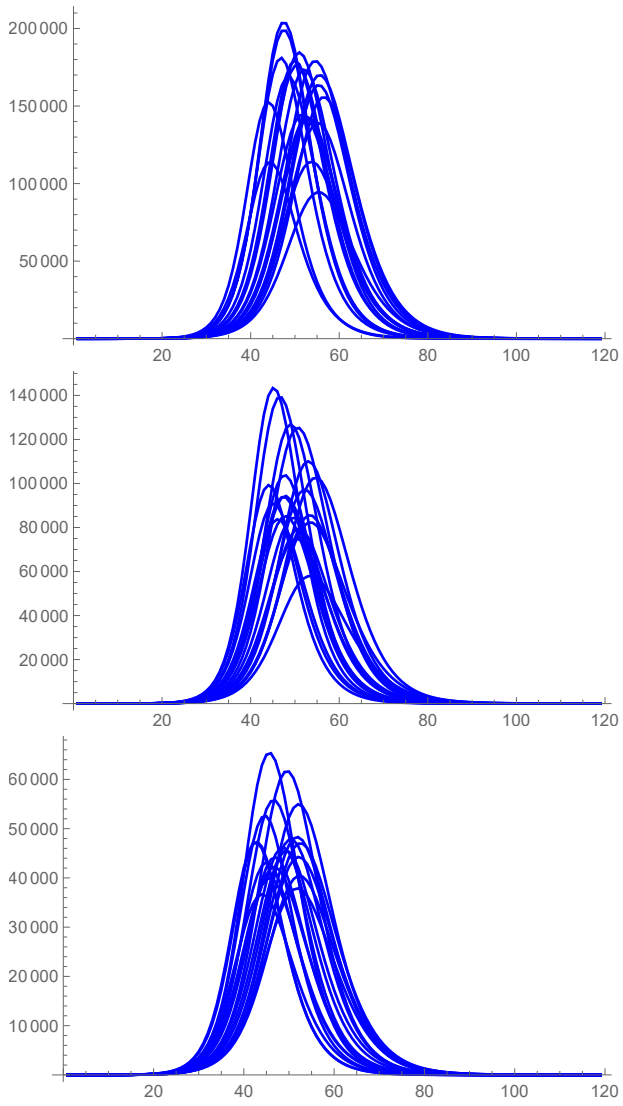

Figure 2: Scenario analysis (new daily cases as a function of days from Feb 28th) using multiple trajectories for calibrated, unmitigated cases with (a) $f = 0.25$, (b) $f = 0.50$, (c) $f = 0.75$. Note the different scales on vertical axes. The mean peak height in each case is (a) $158,000$, (b) $98,000$, (c) $47,000$. The mean time to peak shows very little variation with f: (a) 51 days (20 April), (b) 49 days (18 April), (c) 48 days (17 April).

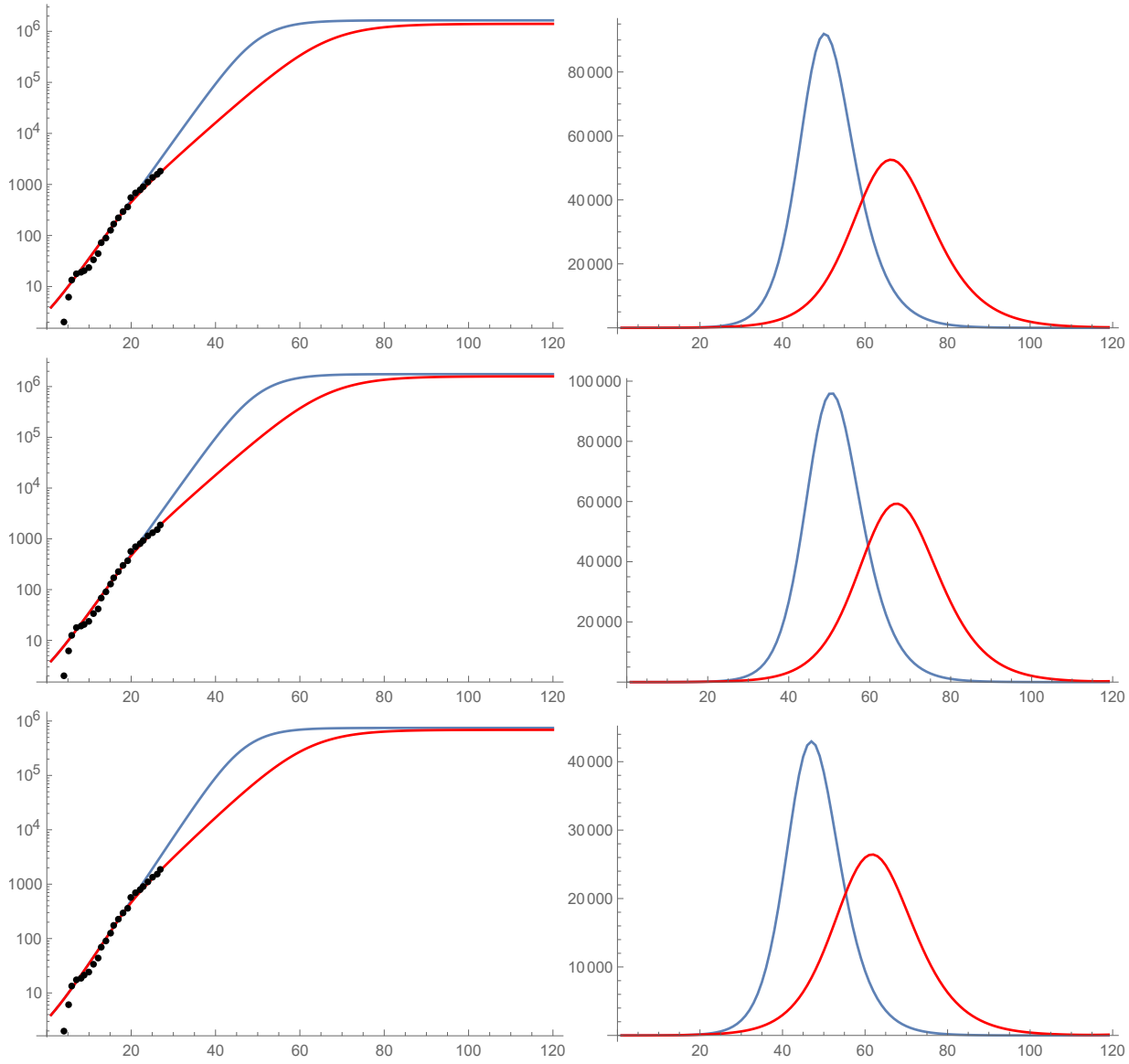

Figure 3: Left panels: cumulative reported cases, wth Irish data (black symbols), unmitigated (blue) and mitigated (red); note the logarithmic scale. Right panels: daily new cases for unmitigated (blue) and mitigated cases (red); note that difference in (linear) scales in the three scenarios. From top to bottom the scenarios are typical cases for (a) $f = 0.25$, (b) $f = 0.50$, (c) $f = 0.75$.

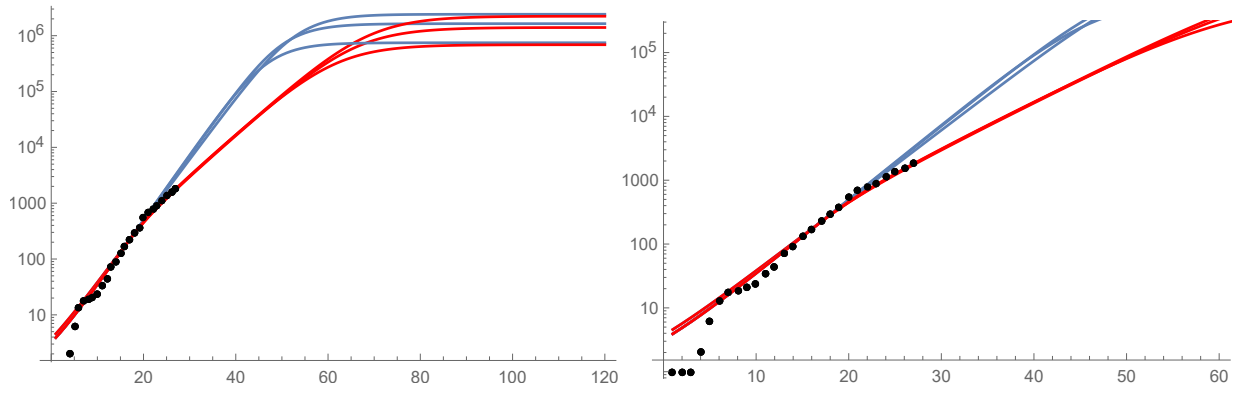

Figure 4: Left panel shows all three scenarios from Fig. 3 (cumulative cases). The right panel is a zoom of days 0 to 60 to show the agreement across scenarios for short-to-medium term predictions.

4 Equations

Each compartment in Figure 1 has a corresponding time-dependent variable, which gives the number of individuals (from a population of $N = 4.8 \times 10^6$) that are in that compartment at time t. Starting with a single seed individual in the presymptomatic infected class ($I_p(0) = 1$), the variables evolve according to the following equations:

$$\frac{dS}{dt} = -\beta S \left(I_p + hI_a + iI_i + I_{t1} + jI_{t2} + I_n\right)/N \tag{1}$$

$$\frac{dE}{dt} = \beta S \left(I_p + hI_a + iI_i + I_{t1} + jI_{t2} + I_n\right)/N - \frac{1}{L}E \tag{2}$$

$$\frac{dI_p}{dt} = \frac{1}{L}E - \frac{1}{C-L}I_p \tag{3}$$

$$\frac{dI_a}{dt} = \frac{f}{C-L}I_p - \frac{1}{D-C+L}I_a \tag{4}$$

$$\frac{dI_i}{dt} = \frac{(1-f)q}{C-L}I_p - \frac{1}{D-C+L}I_i \tag{5}$$

$$\frac{dI_{t1}}{dt} = \frac{(1-f)t}{C-L}I_p - \frac{1}{T}I_{t1} \tag{6}$$

$$\frac{dI_{t2}}{dt} = \frac{1}{T}I_{t1} - \frac{1}{D-C+L-T}I_{t2} \tag{7}$$

$$\frac{dI_n}{dt} = \frac{(1-f)(1-q-t)}{C-L}I_p - \frac{1}{D-C+L}I_n \tag{8}$$

$$\frac{dR}{dt} = \frac{1}{D-C+L}I_a + \frac{1}{D-C+L}I_i + \frac{1}{D-C+L-T}I_{t2} + \frac{1}{D-C+L}I_n. \tag{9}$$

In addition, we define $C_r(t)$ to be the cumulative number of new cases reported by time t, given by the flux out of the I_{t1} (waiting-for-test) compartment:

$$\frac{dC_r}{dt} = \frac{1}{T}I_{t1} \tag{10}$$

and we also report the number of new daily cases on day d, defined by $C_r(d) - C_r(d-1)$.

Appendix

THe relationship between R_0 and the transmission rate β is given by

$$\frac{R_0}{\beta} = (C-L)(f(-h)+(f-1)(i-1)q+f)+(f-1)(j-1)t(C-L+T) \\ + C(f(h-iq-jt+q+t-1)+(i-1)q+(j-1)t+1). \tag{11}$$