SEIR model for COVID-19

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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. (Improved to Erlang distributions in R version).

2 Parameters

All timescales are expressed in days. Day 0 of the Irish epidemic is February 28, 2020.

- L: average latent period
- C: average incubation period
- D: average infectious period
- h: multiplicative factor for reduction of effective transmission from the Asymptomatic Infected compartment, relative to Symptomatic Infected
- i: multiplicative factor for reduction of effective transmission from the Immediate Isolation compartment, relative to Symptomatic Infected
- j: multiplicative factor for reduction of effective transmission from 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
- 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 population N is assumed to be 4.9×10^6.

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: 0.01 to 0.5
- Range of i: 0.0 to 0.1
- Range of j: 0.0 to 0.1
- 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: 3.0 to $D - (C - L)$
- Range of R_0: 2.0 to 4.0, with conversion to equivalent β parameter (see Appendix)

3 Equations

Each compartment in Figure 1 has a corresponding time-dependent variable, which gives the number of individuals (from a population of $N = 4.9 \times 10^6$) that are in that compartment at time t. Starting with a single seed individual in the presymptomatic infected class ($I_p(0) = 1$, $S(0) = N - 1$, all other variables initially zero), the dynamics evolve according to the following equations:

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

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

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

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

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

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

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

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

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

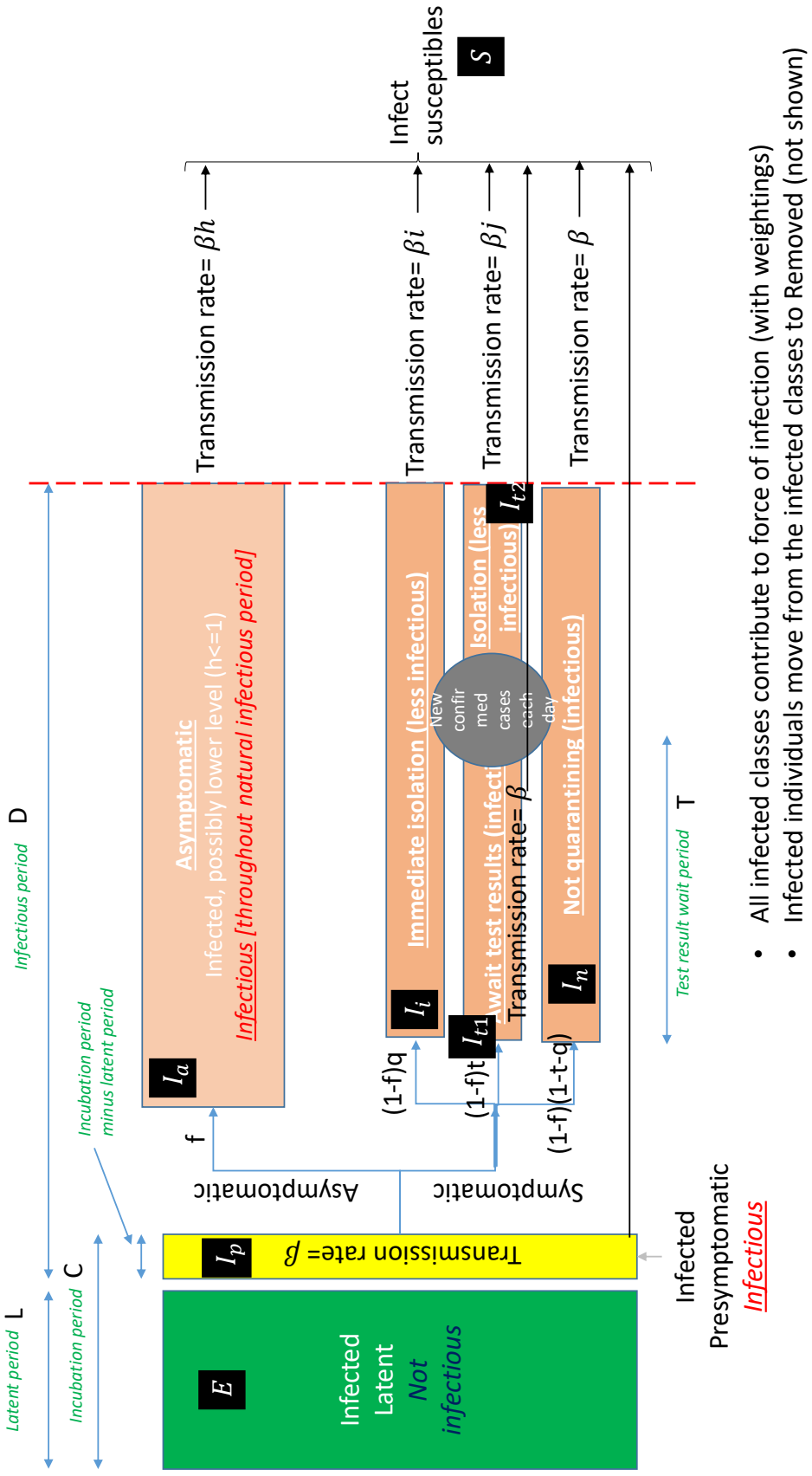

Figure 1: Model compartment structure.

In addition, we define $C_r(t)$ to be the cumulative number of new cases reported by time t, given by integrating 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 $C_r(d) - C_r(d-1)$.

4 Commentary

To calibrate the model, we choose sets of parameters from independent uniform distributions with the limits specified in the previous section. For each set of parameters, we then determine the early-time exponential growth rate from a linearization of the dynamics about the all-susceptible fixed point: the largest eigenvalue λ of the Jacobian matrix is calculated (see Appendix). If the growth rate matches the approximately 30% per day growth rate observed early in the Irish (and other European) epidemic, then the set of parameters is deemed feasible, otherwise the set is rejected. To implement this rule, we check if the value of λ is within $\pm 5\%$ of $\log(1.3) = 0.262$.

Differential equation models are not accurate when the number of cases is low, so we also apply a time offset to the model curves in order to match to the data. We do this by finding the model time when the cumulative number of cases first exceeds 200, and then we offset the model's timescale by a fixed constant to match this to the corresponding day in the epidemic.

The effects of interventions are implemented as instantaneous changes in the transmission rate β, which is assumed to be piecewise constant. Because of the linear relationship between β and the reproductive number R_0 (see Eq. (12)), these changes are usually expressed in terms of the equivalent R_0 value. In Figure 2, for example, the R_0 value is 3.85 from day 0 to day 16, then switches to $R_0 = 2.4$ for days 16 to 24 to model the closure of school and universities. On day 25 the value is changed again, to $R_0 = 1.6$ as extra restrictions were introduced, and on day 29 we change the R_0 value to 0.8 to model the lockdown. In Figure 2 we show the model's predictions for what would happen if the lockdown were ended today: these are strongly dependent on what effective reproductive number is attained post-lockdown, so several scenarios are shown (coloured curves for R_0 values ranging from 2.4 down to 0.8, as per legend).

Appendix

To calculate the basic reproductive ratio for the model we follow the approach explained in Section 2.2 of [1]. The value of R_0 is given by the spectral radius of the next generation matrix, which can be written as FV^{-1}. Defining the vector of relevant variables as $\mathbf{x} = \{E, I_p, I_a, I_i, I_{t1}, I_{t2}, I_n\}$, the

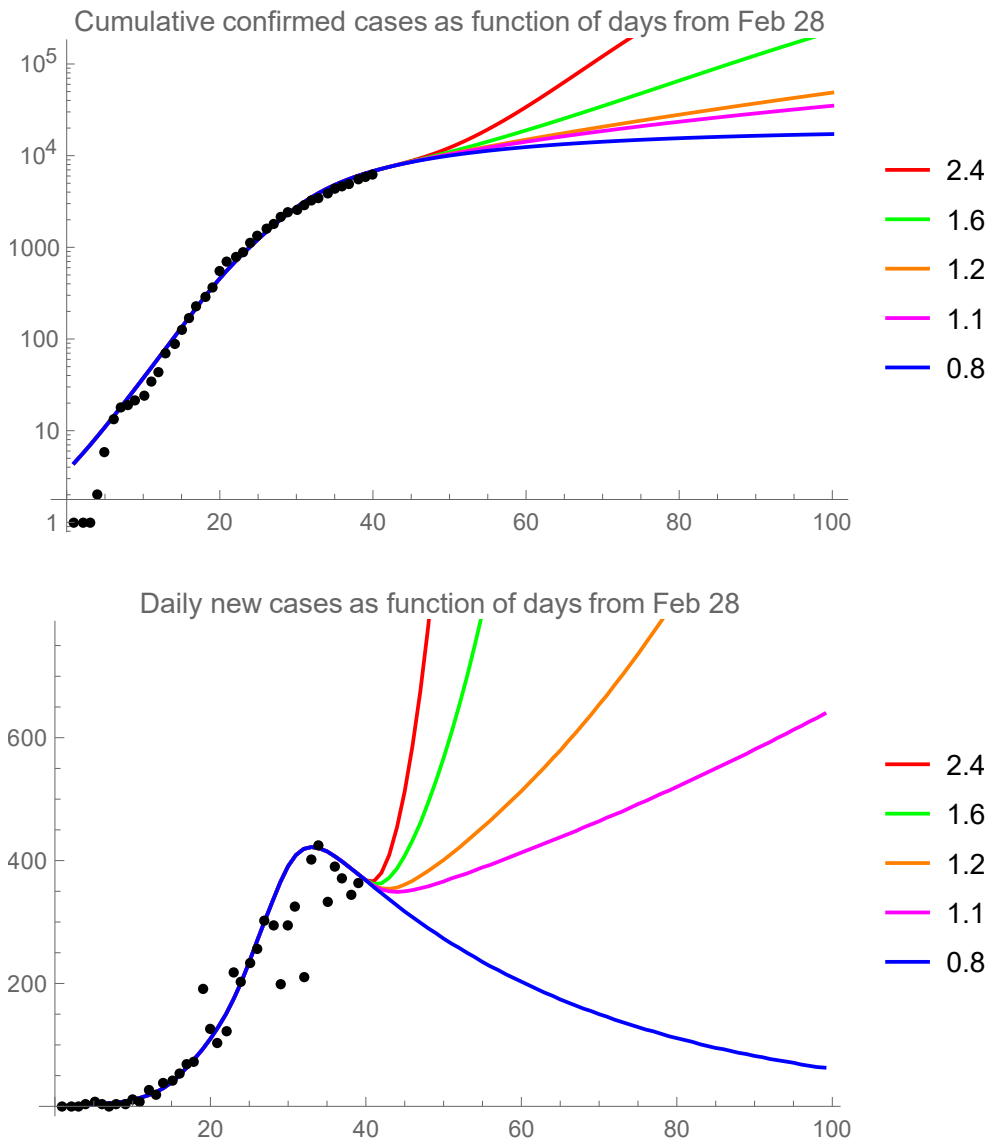

Figure 2: Example of model outputs. (a) Cumulative cases (on log scale) and (b) new daily cases (on linear scale) as functions of number of days from Feb 28, with the data as black symbols. The value of R_0 is assumed to switch at specific dates (days 16, 25 and 29) to model interventions; possible future scenarios from an immediate relaxation of lockdown are labelled in the legend by the assumed value of post-lockdown R_0. The parameter set used here is $\{L, C, D, h, i, j, f, t, q, T, \beta, R_0, \lambda\} = \{3.58, 5.79, 5.46, 0.11, 0.07, 0, 0.25, 0.55, 0.21, 3.16, 0.91, 3.85, 0.26\}$ and the offset time is 11.45.

matrix F is zero except for its first row, which is $\beta(0, 1, h, i, 1, j, 1)$. The matrix V is

$$\begin{pmatrix} \frac{1}{L} & 0 & 0 & 0 & 0 & 0 & 0 \\ -\frac{1}{L} & \frac{1}{C-L} & 0 & 0 & 0 & 0 & 0 \\ 0 & -\frac{f}{C-L} & \frac{1}{D-C+L} & 0 & 0 & 0 & 0 \\ 0 & -\frac{(1-f)q}{C-L} & 0 & \frac{1}{D-C+L} & 0 & 0 & 0 \\ 0 & -\frac{(1-f)t}{C-L} & 0 & 0 & \frac{1}{T} & 0 & 0 \\ 0 & 0 & 0 & 0 & -\frac{1}{T} & \frac{1}{D-C+L-T} & 0 \\ 0 & -\frac{(1-f)(1-q-t)}{C-L} & 0 & 0 & 0 & 0 & \frac{1}{D-C+L} \end{pmatrix} \tag{11}$$

Calculating the eigenvalues of FV^{-1} then yields the relationship

$$\begin{aligned} \frac{R_0}{\beta} &= (C-L)(-fh + (f-1)(i-1)q + f) + (f-1)(j-1)t(C-L+T) \\ &\quad + D(f(h - iq - jt + q + t - 1) + (i-1)q + (j-1)t + 1). \end{aligned} \tag{12}$$

The spectral radius of the Jacobian matrix $J = F - V$ is λ, and this defines the exponential growth rate of the epidemic in its early stages.

References

[1] Jane M Heffernan, Robert J Smith, and Lindi M Wahl. Perspectives on the basic reproductive ratio. *Journal of the Royal Society Interface*, 2(4):281–293, 2005.