Cohort model to solve for the duration of infectiousness distribution

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1 Cohort model

Consider an SIR model with non-linear recovery:

$$S' = \mu S - \beta SI \tag{1}$$
$$I' = \beta SI - \gamma I \mathcal{K}(I) \tag{2}$$

Note that equation (2) can be rewritten as a per-capita rate of prevalence change

$$\frac{I(t)'}{I(t)} = \beta S(t) - \gamma \mathcal{K}(I(t)) \tag{3}$$

where the time dependence $(t > 0)$ has been explicitly made.

In order to find the expression of the duration of infectiousness distribution, we consider the cohort of individuals who acquired the disease at exactly time $\alpha > 0$. Let's label the size of this cohort (as a proportion of the whole population) c_α. This cohort is depleted at the same per-capita rate as the one given in equation (3). Hence, if $c_\alpha(\tau)$ is the size of this cohort τ units of time after disease acquisition, we have:

$$\frac{c_\alpha(\tau)'}{c_\alpha(\tau)} = -\gamma \mathcal{K}(I(\alpha + \tau)) \tag{4}$$

The initial condition for c_α is theoretically arbitrary, and if we choose $c_\alpha(0) = 1$, we can interpret $c_\alpha(\tau)$ as the probability of still being infectious τ units of time after having acquired the disease at time α, in other words, the duration of infectiousness distribution.

Let's express (4) with the original time variable $t = \alpha + \tau$:

$$\frac{c_\alpha(t - \alpha)'}{c_\alpha(t - \alpha)} = -\gamma \mathcal{K}(I(t)) \tag{5}$$

and for convenience, let's introduce p as

$$p_\alpha(t) = c_\alpha(t - \alpha)$$

The function $1 - p_\alpha$ is the cumulative distribution of duration of infectiousness conditional on disease acquisition at time α. It can be determined numerically by solving the following system:

$$S' = \mu S - \beta SI \tag{6}$$
$$I' = \beta SI - \gamma I \mathcal{K}(I) \tag{7}$$
$$p'_\alpha = -\gamma p_\alpha \mathcal{K}(I) \tag{8}$$

with the initial conditions $I(0) = i_0$, $S(0) = 1 - i_0$ and $p_\alpha(\alpha) = 1$. Note that p_α is not epidemiologically defined for $t < \alpha$, but it is nonetheless possible to arbitrary set $p_\alpha(t) = 1$ for $t \leq \alpha$. Moreover, the density of the infectiousness duration is given by the derivative $-p'_\alpha$.

2 Numerical solutions

The right-hand side of equation (8) is always negative, hence the distribution p_α is always

decreasing. In particular, it cannot have a "bumped" shape (with a maximum at a positive time), that may be desirable in a epidemiological context.

Figure 1 show the resulting distribution p_α for several α when solving numerically the ODEs. The simulations were run using:

- $R_0 = 2.0$
- $\gamma = 1/4$
- $\mathcal{K}(I) = (a + bI)^c$

The top panel is effectively a SIR model and we can verify that the distribution p_α is indeed an invariable exponential distribution (top centre panel, straight line on the log-scale) with a constant mean at $1/\gamma = 4$ days (top right panel).

Considering the second, third and fourth rows that depict $\mathcal{K}(I) = I^c$ with $c = 0.5, 1, 2$ respectively, the centre panel confirms the convergence towards an exponential distribution (straight line on the log-scale) at equilibrium. Moreover, when using $\mathcal{K}(I) = I^c$ with $c > 0$, the per-capita recovery rate is dramatically reduced (equation (3)), increasing the length of the recovery: this is illustrated in the right panels, where the mean is very large as c increases.
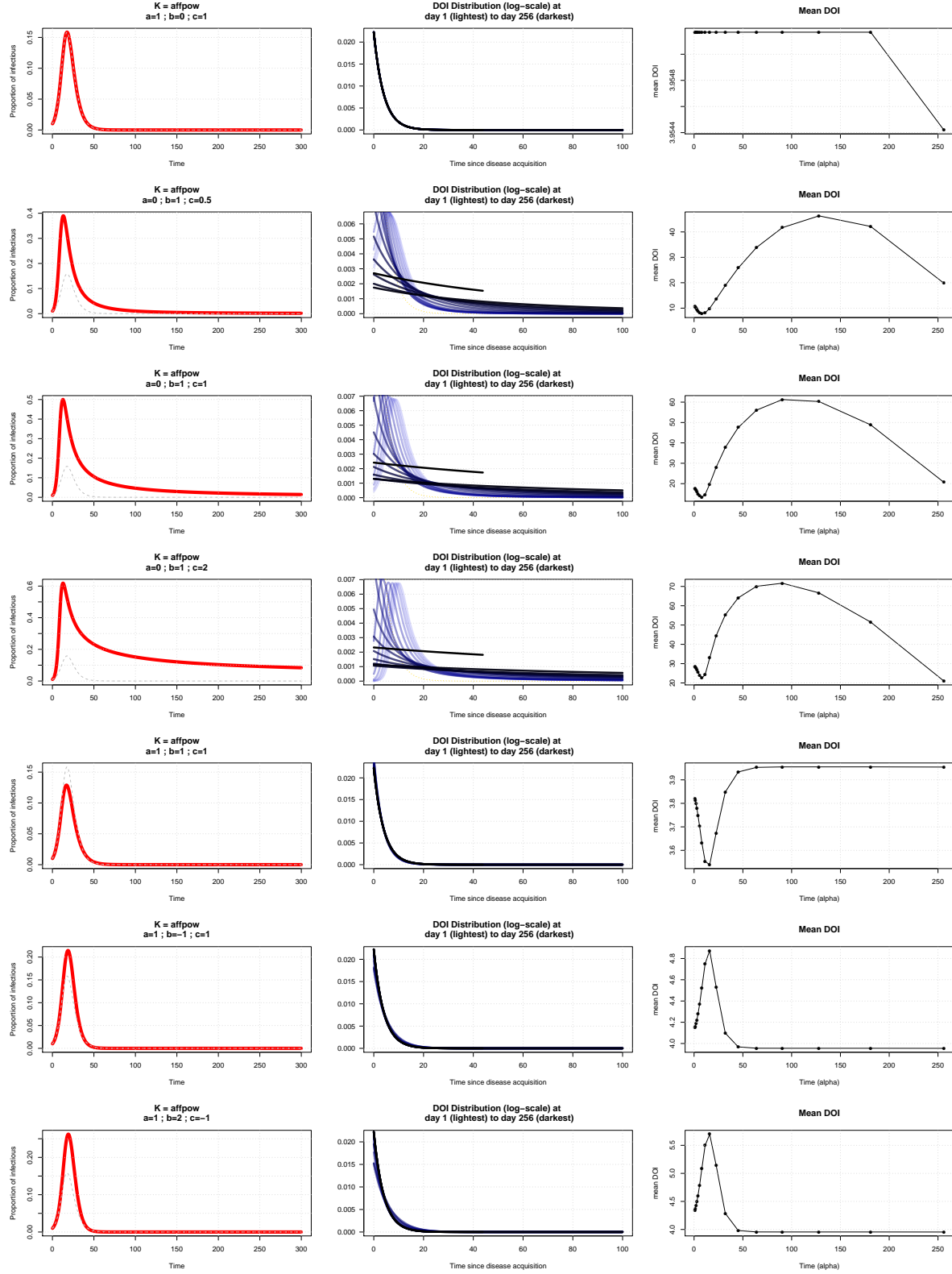
Figure 1: Left panels: time series of the proportion of infectious individuals (dashed line is to compare with the benchmark SIR model). Centre panels: distribution p_α (on the log-scale) for various values of α. Right panels: mean of p_α (for the same given value of α, each point is the mean of the distribution represented in the centre panel). See main text.

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