Importation of Variants and Border Control

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1 Summary of key results

- We are currently seeing just under a couple of vaccine escape VoC infections detected per day.
- Even if this rate continues, it would require stopping over 99% of new introductions to have a reasonable chance of stopping introduction before the 100 or so days required to produce updated vaccine.
- In the (more realistic) scenario of exponentially growing importations, success rates need to be over 99.9% successful to achieve similar results.
- Even for successfully controlled introductions, the time to extinction may mean that the UK would almost never be in a position of 'zero variants'.

2 Analysis of VoC data

Data were taken from the `VOC202012_02_linelist_20210319` file on the DSTL server. This was separated into exposure types, and the 'Traveller' stream was analysed using the methods from House (2018). These indicate introduction of new infections at a rate of approximately 1.7 per day with no evidence of exponential growth as shown in Figure 1.

The latest analysis from the ONS CIS for the B.1.1.7 variant is shown in Figure 2 and shows dynamics that are arguably consistent with a 'stochastic delay then exponential takeoff' model of strain emergence.

3 Dynamic importation and static control

We start by revisiting the simple analytic results of Scalia Tomba and Wallinga (2008). These were derived in response to simulations relating to border controls (e.g. Hollingsworth et al. (2006)). We will derive these slightly differently from the original paper, and also generalise.

First, let $X(t)$ be the cumulative number of importations at time t and let q be the probability that each introduction eventually becomes extinct (we assume these probabilities are independent). Then the probability that there has not yet been an introduction of a new variant that will lead to a large outbreak is

$$\sum_{z=0}^{\infty} \Pr(X(t)=x)q^x = G_{X(t)}(q) \ , \tag{1}$$

where G stands for a pgf – using the expression for a Poisson random variable with mean $\Lambda(t)$ (although we could generalise to a negative binomial because infections tend to be clustered as

seen in the data) we recover the main result for the time T of failure to keep the variant out from Scalia Tomba and Wallinga of

$$F_T(t) = \Pr(T \leq t) = 1 - \exp(-(1-q)\Lambda(t)) \ . \tag{2}$$

We use this equation for the choice $\Lambda(t) = 1.7t$ to produce Figure 3. As Scalia Tomba and Wallinga note, substituting

$$\Lambda(t) = \Lambda_0 \mathrm{e}^{rt} \ , \qquad t_D = \frac{\log(2)}{r} \ , \tag{3}$$

into (2), we get the following expression for the difference in median times of introduction under control of

$$\tau_q - \tau_0 = \frac{-\log(1-q)}{\log(2)} t_D \ . \tag{4}$$

Calling this delay in median time $\delta\tau$, we can derive an expression for the level of control needed to achieve this delay:

$$q(\delta\tau) = 1 - \exp\left(-\frac{\delta\tau}{t_D}\log(2)\right) \ . \tag{5}$$

Evaluating this expression for some realistic parameter values gives Figure 4.

4 Dynamic importation and onward transmission

Now we consider disease dynamics – this is done in a single-type / SIR framework for simplicity, but an equivalent multitype case is possible (Dorman et al., 2004). In this model, each particle produces a number of offspring that is an iid copy of random variable Y after a time that is $\mathrm{Exp}(\beta+\gamma)$ distributed, where

$$G_Y(s) = \sum_{y=0}^{\infty} \Pr(Y=y)s^y = \frac{1}{\beta+\gamma}\left(\beta\big(1+\frac{1}{k}(1-s)\big)^{-k}s + \gamma\right) \ . \tag{6}$$

In order to allow superspreading events (SSEs) to occur, we have chosen this offspring distribution so that the number of newly infected cases is drawn from a negative binomial distribution with mean $\frac{\beta}{\beta+\gamma}$ and dispersion parameter k (Lloyd-Smith et al., 2005). For $k=-1$ we recover standard infection dynamics, with Endo et al. (2020) estimating $k \approx 0.1$.

Using this offspring distribution, we define $q(t)$ as the probability that the lineage of a single imported case has become extinct by time t (generalising the static q above). Note that, in both cases, the mean number of secondary cases from a single infection event is given by $\frac{\beta}{\beta+\gamma} = \frac{\mathrm{d}P}{\mathrm{d}s}\big|_{s=1}$. As noted in Dorman et al. (2004) is equivalent to a birth-death chain in which the expected number of secondary cases produced over by a single individual over the course of their infection is $\frac{\beta}{\gamma} = R$.

Now let $Z(t)$ be the number of particles in a branching process model with importation of particles at rate $\lambda(t)$ with integrated intensity

$$\Lambda(t) = \int_{u=0}^{t} \lambda(u)\mathrm{d}u \tag{7}$$

We can then generalise the results of Scalia Tomba and Wallinga to obtain the probability that there is a positive number of cases time at time t,

$$\Pr(Z(t)=0) = 1 - \exp(-(1-q(t))\Lambda(t)) \tag{8}$$

Since this quantity is very close to zero for most realistic scenarios, it is most natural to investigate the behaviour of $q(t)$ through solving the Kolmogorov equations for the branching process for different values of k and reproduction number R for the new variant in the UK environment. These results are shown in Figure 5.

References

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T. D. Hollingsworth, N. M. Ferguson, and R. M. Anderson. Will travel restrictions control the international spread of pandemic influenza? *Nature Medicine*, 12(5):497–499, 2006.

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J. O. Lloyd-Smith, S. J. Schreiber, P. E. Kopp, and W. M. Getz. Superspreading and the effect of individual variation on disease emergence. *Nature*, 438(7066):355–359, 2005.

G. Scalia Tomba and J. Wallinga. A simple explanation for the low impact of border control as a countermeasure to the spread of an infectious disease. *Mathematical Biosciences*, 214(1):70–72, 2008.

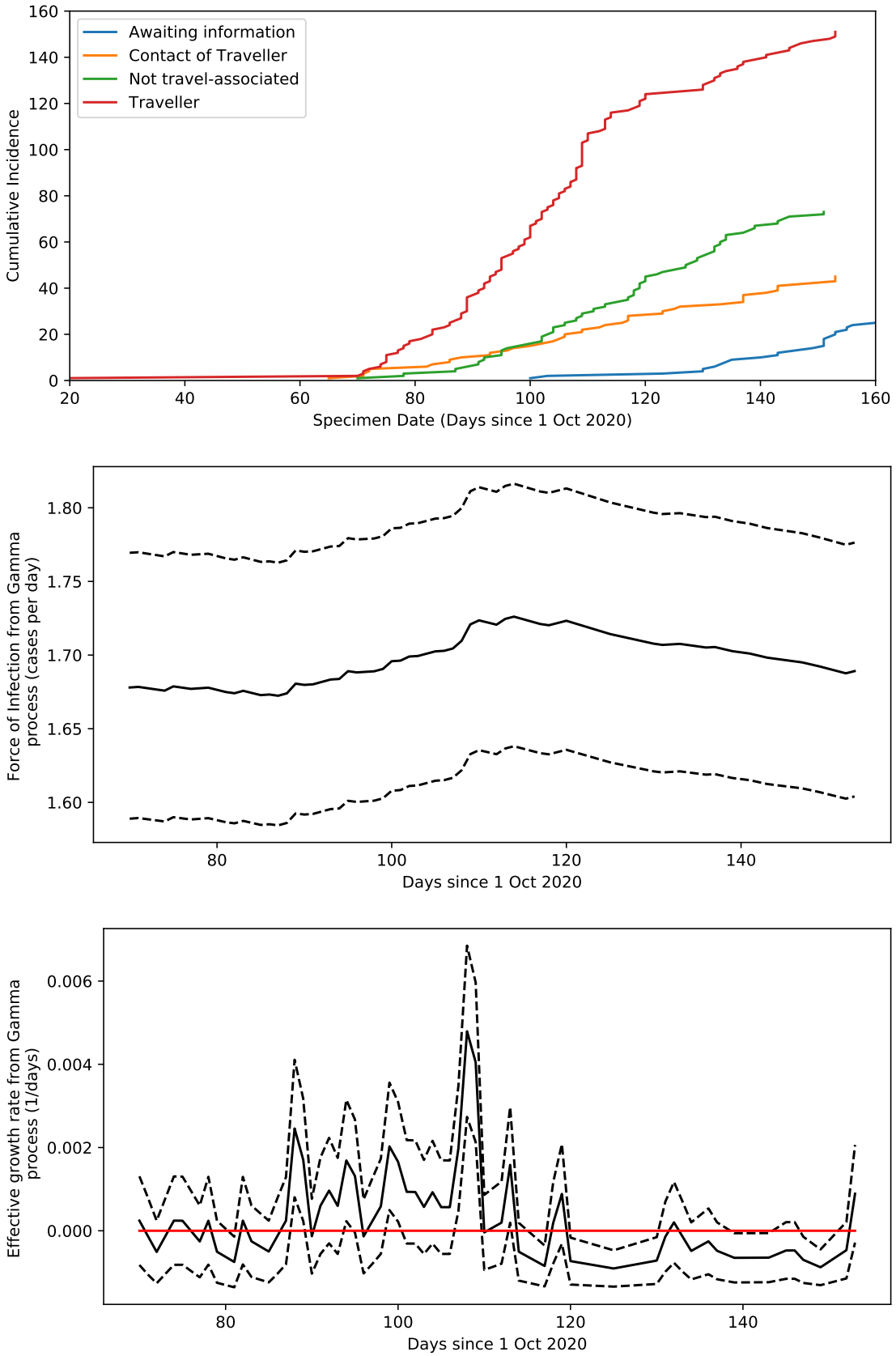
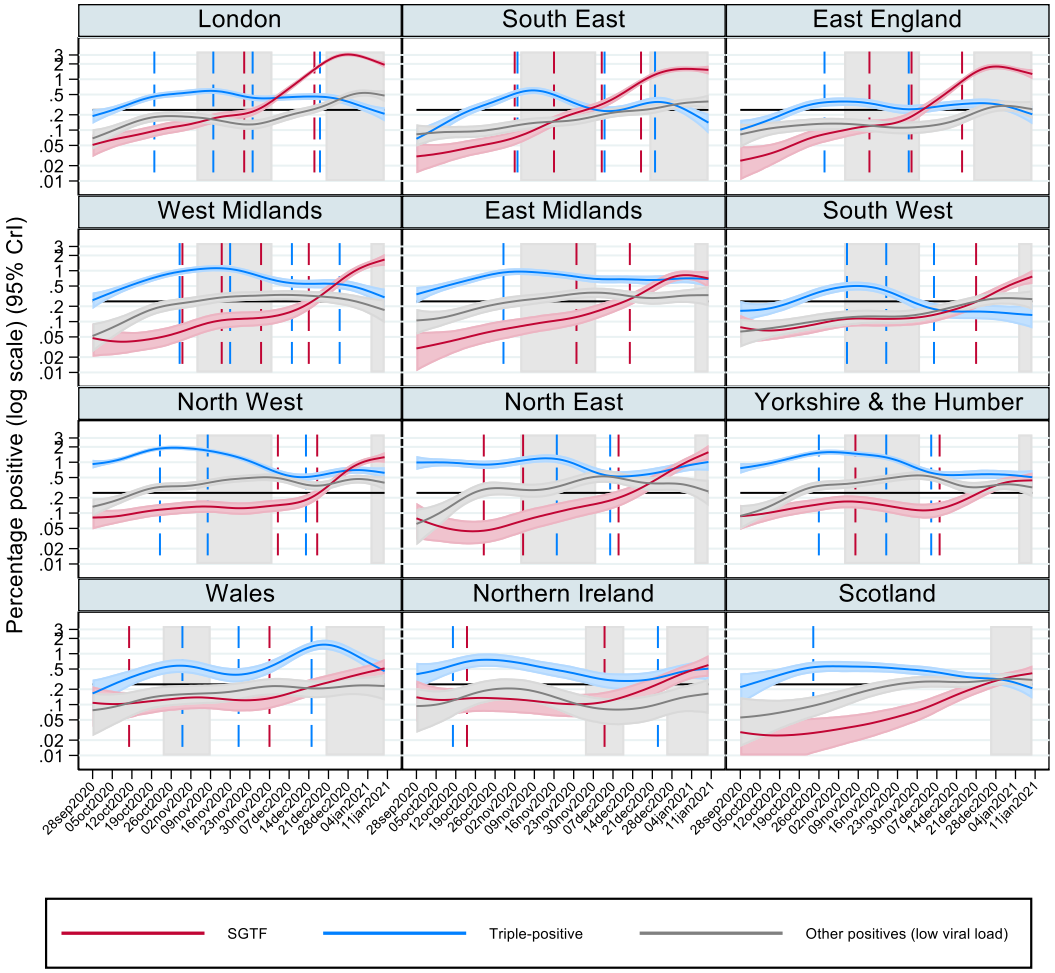


Figure 1: Analysis of data from the variant of concern.

Fig.S3 Percentage of the population positive with SGTF (ORF1ab+N positive, compatible with B.1.1.7), triple positive and other positives – log scale



Note: truncating lower 95% CrI at 0.01. Gray shading shows national restrictions/stay at home orders for the majority of the region. Black horizontal line at 0.25%. Dashed lines show changes in trend from ISR algorithm fitted from 1 September (no dashed line means no change in trend with p<0.01 (triple) or p<0.05 (SGTF) detected). See main **Figure** for probabilities on the absolute scale for SGTF and triple-positive cases.

Figure 2: **These outputs have been provided as management information for operational planning purposes. They are provisional estimates circulated before public release. This management information should not be shared widely and should only be used for operational planning purposes. This information is not to be used publicly and ahead of being released publicly by ONS.** Prevalence of wildtype and B.1.1.7 in the UK provided by the ONS CIS team, showing relatively long periods in some geographies before the establishment of exponential growth.

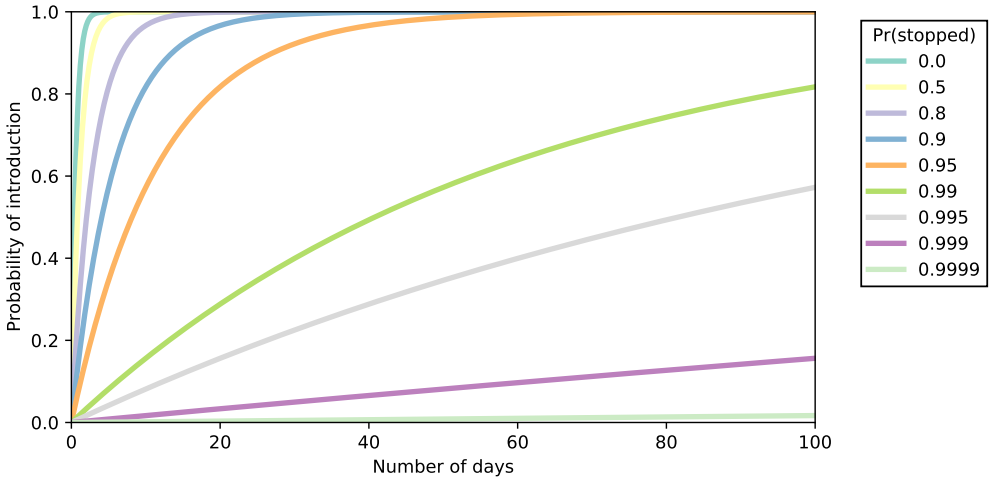


Figure 3: Constant importation rate: probability of established introduction over time for different probabilities of stopping an introduction.

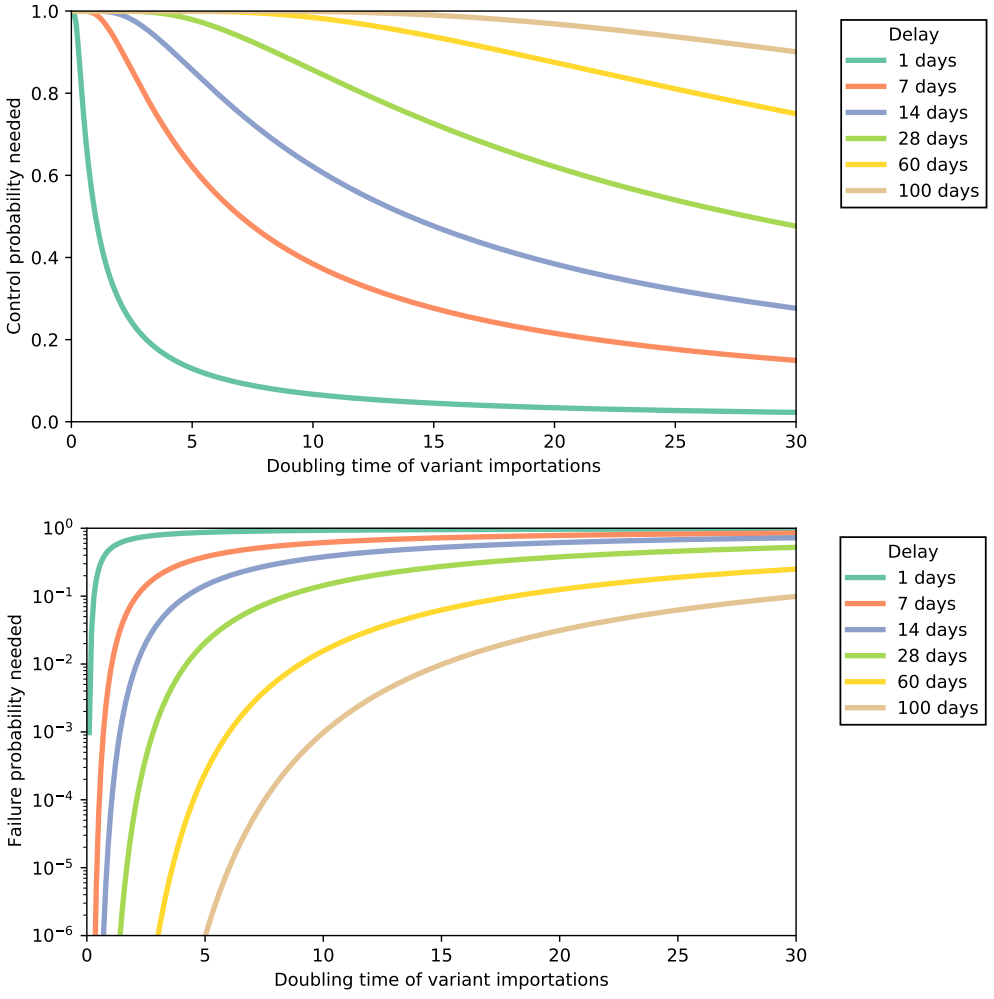


Figure 4: Exponentially growing importation rate: Levels of control needed to shift median introduction time by a desired amount.

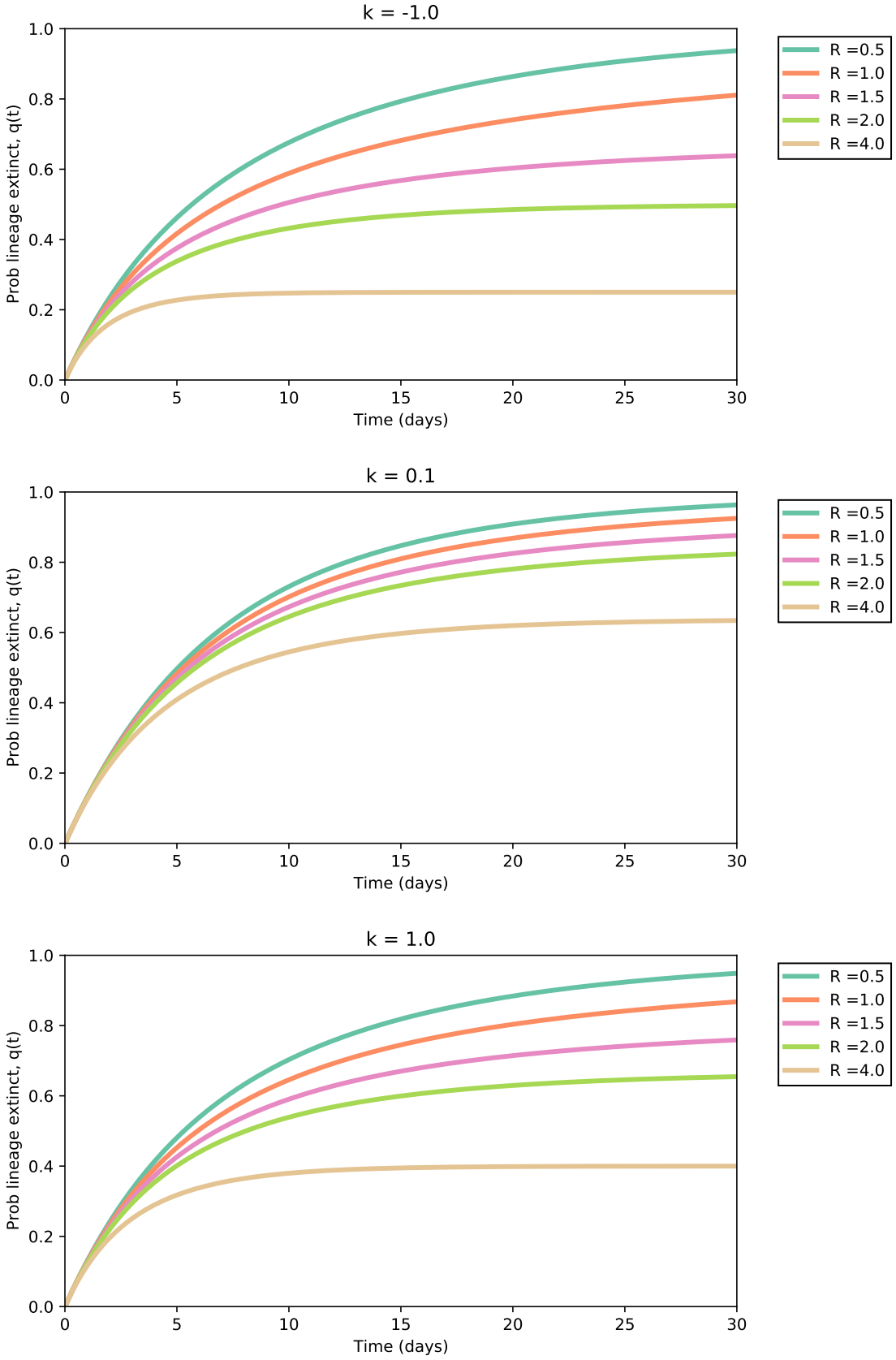


Figure 5: Extinction probabilities for single lineages over time.