

# Supplementary material to “Estimating the Attack Ratio of Dengue Epidemics under Time-varying Force of Infection using Aggregated Notification Data”

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## A remark on prior distributions and tail behaviour of the distribution of $R_t$

There are a number of approaches to deriving the distribution of  $R_t$ . Alternatively to the approach described in the main text [1], one could use the conditional distribution of  $R_t$  on  $Y_{t+1}$  and  $Y_t$  as defined in equation A7 of Nishiura et al. [2]:

$$f_R(R_t) = (Y_t R_t)^{Y_{t+1}} e^{-Y_t R_t} \quad (1)$$

Noticing the kernel of (1) is that of a gamma distribution with  $a_2 = Y_{t+1} + 1$  and  $b_2 = Y_t$ , we obtain a proper density from which to construct  $c_\alpha(R_t)$ , simply by computing the appropriate quantiles of said distribution. This density is

$$f_N(R_t|a_2, b_2) = \frac{b_2^{a_2}}{\Gamma(a_2)} R_t^{a_2-1} e^{-b_2 R_t} \quad (2)$$

In order to decide which approach to take, it may be of use analysing the tail behaviour of the derived distributions for  $R_t$ . Consider the case of using a flat *Uniform*(0, 1) prior for  $\theta_t$ . With  $a_0 = b_0 = 1$ ,  $a_1 = a_2$  and  $b_1 = b_2 + 1$ . The beta prime (inverse beta distribution) will have heavier tails compared to the conditional distribution proposed by [2], thus providing more conservative confidence/credibility intervals. To see that one needs simply take the ratio of the Beta prime and Gamma (unnormalized) densities and evaluate the limit as  $R_t$  goes to infinity:

$$\lim_{R_t \rightarrow \infty} \frac{f_P(R_t|a_1, b_1)}{f_N(R_t|a_2, b_2)} = \lim_{R_t \rightarrow \infty} \frac{e^{Y_t R_t}}{(1 + R_t)^{Y_t + Y_{t+1} + 2}} = \infty \quad (3)$$

Finally, note that we deliberately construct  $c_\alpha(R_t)$  as a equal-tailed 100 $\alpha\%$  credible set, rather than a less conservative highest posterior density (HPD) interval.

As a side note, the Bayesian approach presented in this paper will give similar results to orthodox confidence intervals [3] and [4] for  $Y_{t+1}$  and  $Y_t \gg 1$ . Under the flat uniform prior for  $\theta_t$ , the Bayesian posterior credibility interval is nearly

indistinguishable from the confidence interval proposed by Clopper & Pearson (1931) [4] for  $Y_{t+1}, Y_t > 20$ . Note also that the uniform prior ( $Beta(1, 1)$ ) for  $\theta_t$  constitutes a poor prior choice mainly because the induced distribution for  $R_t$  is only well-defined for  $b_0 > 2$ .

An advantage of the Bayesian approach is that one can devise prior distributions for  $\theta_t$  taking advantage of the intuitive parametrization and flexibility of the beta family of distributions. Prior elicitation can also be done for  $R_t$  and the hyper-parameters directly plugged into the prior for  $\theta_t$ . One can, for example, choose prior mean and variance for  $R_t$  and find  $a_0$  and  $b_0$  that satisfy those conditions. Let  $m_0$  and  $v_0$  be the prior expectation and variance for  $R_t$ . After some tedious algebra one finds

$$a_0 = \frac{m_0 v_0 + m_0^3 + m_0^2}{v_0} \quad (4)$$

$$b_0 = \frac{2v_0 + m_0^2 + m_0}{v_0} \quad (5)$$

If one wants only to specify  $m_0$  and the coefficient of variation  $c = \sqrt{v_0}/m_0$  for  $R_t$  *a priori*, some less boring algebra gives:

$$a_0 = \frac{m_0^3 c^2 + m_0^3 + m_0^2}{m_0^2 c^2} \quad (6)$$

$$b_0 = \frac{2m_0^2 c^2 + m^2 + m}{m_0^2 c^2} \quad (7)$$

This approach thus makes it possible to incorporate epidemiological knowledge about disease Biology (e.g. the magnitude of  $R_0$ ) into the computation of  $R_t$ . This may prove particularly important when disease counts are low and/or close to the detection threshold. We provide an R script to perform the above elicitation at [https://github.com/fccoelho/paperLM1/blob/master/R/elicite\\_Rt\\_prior.R](https://github.com/fccoelho/paperLM1/blob/master/R/elicite_Rt_prior.R).

## References

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