

# Brief Analysis of Norovirus Data

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June 6, 2019

An in depth study on norovirus outbreaks in hospital settings, with one of three intervention strategies put in place (including control). Using resources from Gaythorpe[3][4], the SA health department[2] and Ross et al[1], a statistical model is derived to calculate the infectivity of the disease within hospitals. The study finds that each individual who is infected is expected to infect another 2 people. Or specifically, the reproduction number (the expected number of people infected by one individual) is approximately 2.2883 when there is no intervention strategy ( $T_0$ ). When the strategy  $T_1$  is put in place, This value is reduced to approximately 1.9242, corresponding to the expectation that an individual will infect just under two people over their infectious period. This is an improvement on  $T_0$ , and hence intervention will help reduce the effect of norovirus outbreaks. Intervention strategy two,  $T_2$ , reduces the value to approximately 1.5518. This is a much greater improvement on the control, and hence strategy  $T_2$  should be put in place.

These values are obtained using a statistical estimate, and obtaining the average (modal) value. The distributions for  $R_0$ ,  $\alpha_1$  and  $\alpha_2$  are shown in figure 1, where  $R_0$  is the reproduction number,  $\alpha_1$  and  $\alpha_2$  multiply with  $R_0$  to get the effective reproduction numbers under  $T_1$  and  $T_2$  respectively. The values stated above correspond to the peaks on these plots, but it is worth acknowledging that there is a reasonable probability that  $R_0$  could be between 2 and 2.6 and  $\alpha_1$  could even be greater than 1, corresponding to an *increase* in infectivity under  $T_1$ .

As a result of this analysis, more alternative intervention strategies should be investigated. In the meantime, intervention strategy  $T_2$  should be put in place as it will greatly decrease the spread of norovirus within hospital environments.

## References

- [1] Andrew J. Black and J.V. Ross. “Computation of epidemic final size distributions”. In: *Journal of Theoretical Biology* 367 (2015), pp. 159–165. ISSN: 0022-5193. DOI: <https://doi.org/10.1016/j.jtbi.2014.11.029>. URL: <http://www.sciencedirect.com/science/article/pii/S0022519314006882>.
- [2] South Australian Health Department. *Norovirus infection*. URL: <https://www.sahealth.sa.gov.au/wps/wcm/connect/public+content/sa+health+internet/health+topics/health+conditions+prevention+and+treatment/infectious+diseases/norovirus+infection>.
- [3] K. A. M Gaythorpe et al. “Norovirus transmission dynamics: a modelling review”. In: 146.2 (2018), pp. 147–158. ISSN: 0950-2688.
- [4] K.A.M. Gaythorpe, C.L. Trotter, and A.J.K. Conlan. “Modelling norovirus transmission and vaccination”. eng. In: *Vaccine* 36.37 (2018), pp. 5565–5571. ISSN: 0264-410X.

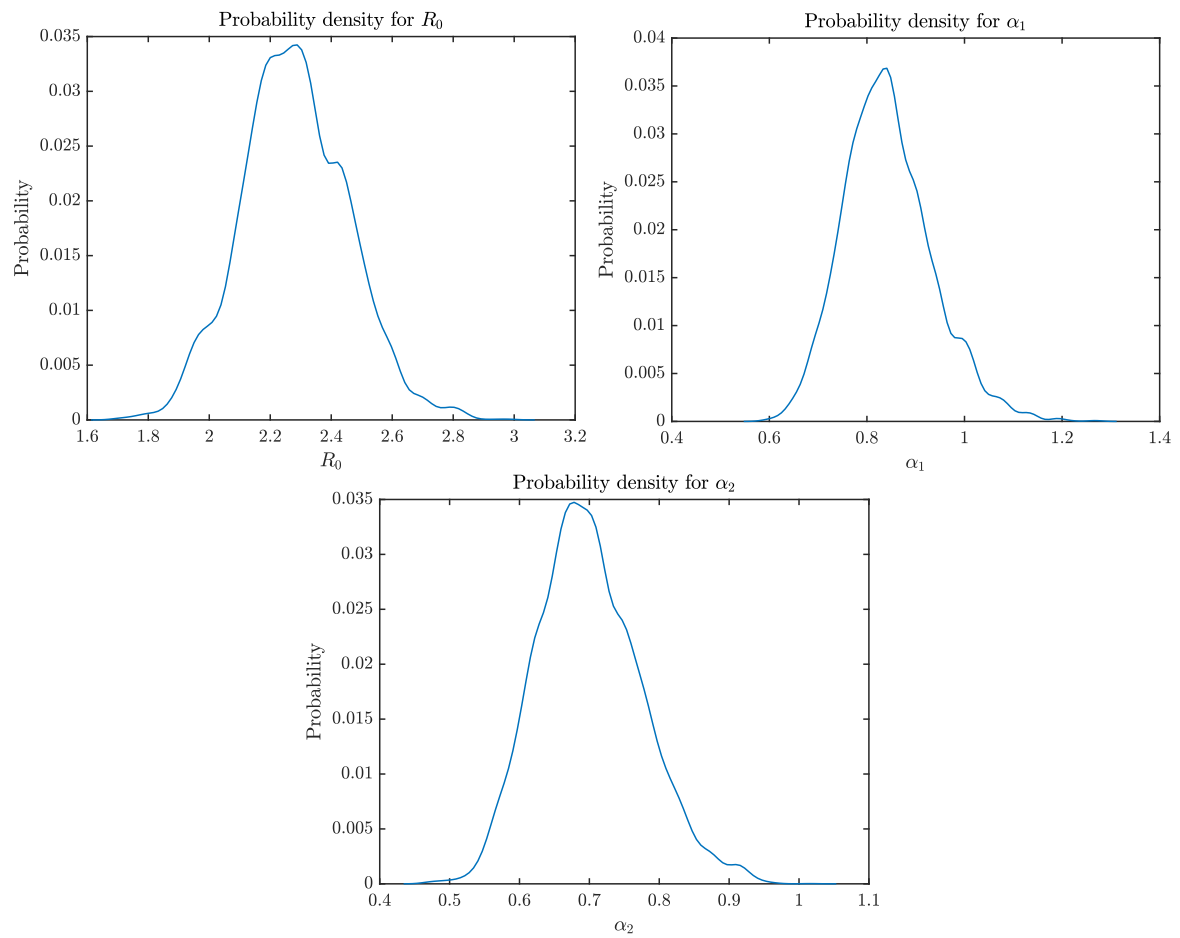


Figure 1: Probability density curves for the parameters - the horizontal axis is the parameter while the vertical is the probability