

Meeting 08 July 2025

July 9, 2025

In attendance: M.Ryan, R.Hickson, D.Zhang, M.Roberts, T.House, V.Isham, E.McBryde

Notes

1. Valerie noted that changing the parameters k (number of infection compartments) changes the shape of the infectious period. *Conclusions across different values of k should not be compared.* **Solution: Fix k from the outset. Matt was thinking of k as the number of days, for simplicity.**
2. Thomas asked whether renewal models might be more appropriate for answering our research question. They are more general, but might more directly relate to discussing testing on particular days.
3. Thomas is concerned that, using the compartmental models, our results will be very sensitive to the shape of the distribution of infectiousness. In particular, there might be an overwhelming shift to early testing. Renewal models might be a solution to address this.
4. It is uncertain whether endemicity can be considered in renewal models. *Thomas and Emma seem to think it can be done. Need to be careful, because generation time cannot be infinite.*
5. Mick noted that analysis of renewal models is very easy (R_0 calculations simplify), but numerics are hard. Thomas shared a paper that presents a MATLAB toolbox for numerics [1]. *Could contact Francesca if we want to use this toolbox.*

6. Thomas queried whether dynamic behaviour can be applied in renewal models. **This might involve some nice, new maths to address.**
7. In the discussion of different infectiousness curves, we discussed: renewal models, sequence of infection compartments (currently described), parallel infection compartments, and realistic age structured models [2]. *Emma noted that Michael Meehan's work suggests we only need small k for parallel or sequential compartments to represent real data dynamics.*
8. Valerie noted that, if we start exploring other models structures (i.e. parallel compartments), we will need to carefully think about how to make the models comparable. In particular, how do we ensure the testing behaviour is equivalently represented.
9. Thomas asked whether we have baked in that “behaviour is bad” in the following sense: In our model, there is no mechanism for the population to acknowledge that behaviour helps (i.e. lots of testing during one wave made the outcomes better, compared to waves without testing). *Matt confirmed this is currently in there. The behavioural model picked up from the first BaD behaviour was constructed thinking of a non-specific visual protective behaviour.*
10. Valerie asked whether there is data we can look at to investigate “positive norms” around testing. For example, school data in the UK where testing of teachers and students were mandatory.
11. Mick highlighted two interesting reads: *Vaccine Nation* by Raina MacIntyre and *The Covid Response* by Shaun Hendy.

Actions/Takeaways

Takeaway: This is an important research question that addresses some of the “so-what” of our previous paper. Interesting question of “How will dynamic behaviour effect the rollout of go-no go initiatives like RATs”.

Action : Matt to explore effects in compartmental of static behaviour vs dynamic behaviour.

Action: Matt and Roslyn to discuss behavioural assumptions to construct the behavioural dynamics. Are these appropriate for testing? Might need to discuss with Emily Brindal.

Action: Thomas and Mick to discuss renewal equations for this type of model.

Action: Valerie to think about whether certain stochasticities or stochastic models will be more appropriate to answer our research question.

References

- [1] Scarabel F, Diekmann O, Vermiglio R. Numerical bifurcation analysis of renewal equations via pseudospectral approximation. *Journal of Computational and Applied Mathematics*. 2021;397:113611.
- [2] Ferguson NM, Nokes DJ, Anderson RM. Dynamical complexity in age-structured models of the transmission of the measles virus: epidemiological implications at high levels of vaccine uptake. *Mathematical biosciences*. 1996;138(2):101-30.