Was Boris Right?

Modelling the Effect of Lockdowns on the Spread of the UK COVID-19 Outbreak

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Introduction

- COVID-19 is an infectious disease caused by the SARS-CoV2 virus, that is transmitted via contact, airborne droplets and fomites[1].
- The first identified cases in the UK were reported in late January 2020[2].
- COVID-19 was declared a pandemic by the WHO on 11th March 2020[3].
- In March 2020, prior to the vaccine rollout, the UK Government imposed national lockdown measures to curb the spread of COVID-19[4].
- Despite these measures, by the 12th August 2020 there were 313,798 cases and 46,706 deaths from COVID-19 in the UK[2].
- Infection with the virus primarily causes respiratory illness ranging from mild disease to severe disease and death[1]. This put a major strain on the UK's healthcare service.

The objective of this study is to investigate the relationship between the timing of lockdown measures and their overall effectiveness in controlling an outbreak.

Aims

The aim of this study is to use an agent-based model to:

- **Assess the impact of lockdown measures** by simulating the "stay at home" and physical distancing restrictions that were used in the UK through parameters that govern the number of individuals in the population who are moving and their magnitude of movement.
- **Assess the impact of intervention timing** by simulating the introduction of lockdown measures at varying stages of an outbreak as defined by the initial number of individuals infected.
- **Investigate the interaction between lockdown measures and intervention timing** to evaluate how these factors combine to influence the number of people infected.

Methodology

- The data for this study were generated using a stochastic agent-based model in NetLogo (version 7.0.0)[5]. Each time step (tick) involved sequential checks for infection, mortality, recovery, and movement for every individual in the population (Figure 1).

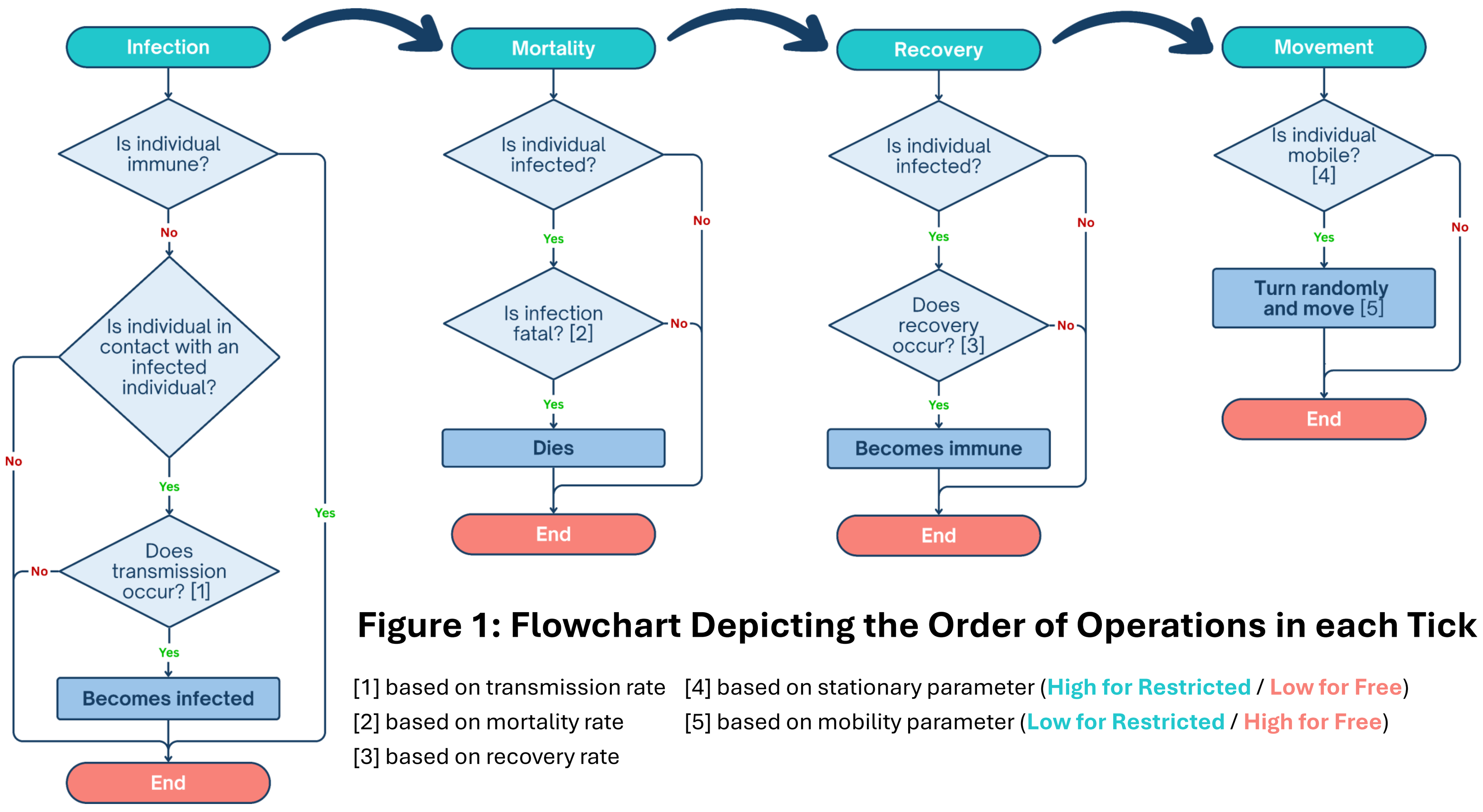

Figure 1: Flowchart Depicting the Order of Operations in each Tick

[1] based on transmission rate
[2] based on mortality rate
[3] based on recovery rate
[4] based on stationary parameter (High for Restricted / Low for Free)
[5] based on mobility parameter (Low for Restricted / High for Free)

- Experimental parameters combined two movement regimes (free and restricted) with 10 initial infection levels (ranging from 5 to 50). The total population size was set to 671, representing a 1:100,000 scale relative to the UK population of 67.1 million[6].
- Ten independent simulation runs were executed for every combination of movement regime and initial infection level. Each of the 200 runs continued for a duration of 50 ticks or until there were either no more infected individuals or no more susceptible individuals.
- The infection peak was defined as the highest point of the infection trajectory over time (Figure 2). These peak values were analysed using a GLM (Figure 3). Model selection was confirmed via AIC comparison and residual diagnostics plots, which ensured the assumptions of normality and homoscedasticity were satisfied.
- All analyses were performed using R (version 4.4.1)[7].

Results

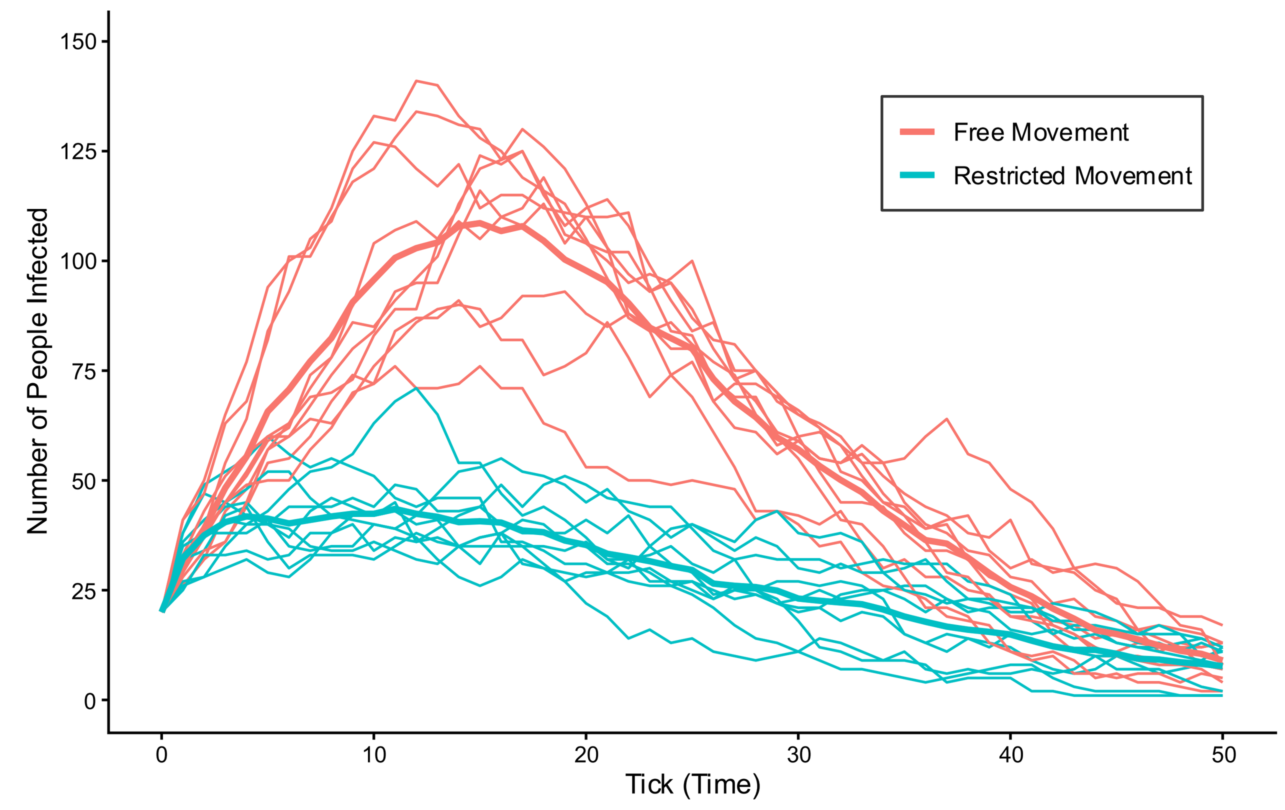

Figure 2: Representative Simulation of Infection Spread

The plot shows the number of infected individuals over time for 10 runs each of movement regime (free in red vs. restricted in blue), starting with 20 initial infections (i.e. 3% of the population). Bold lines indicate the means across runs. The highest point of each individual curve represents the infection peak. These were the data used in the subsequent GLM analysis (Figure 3).

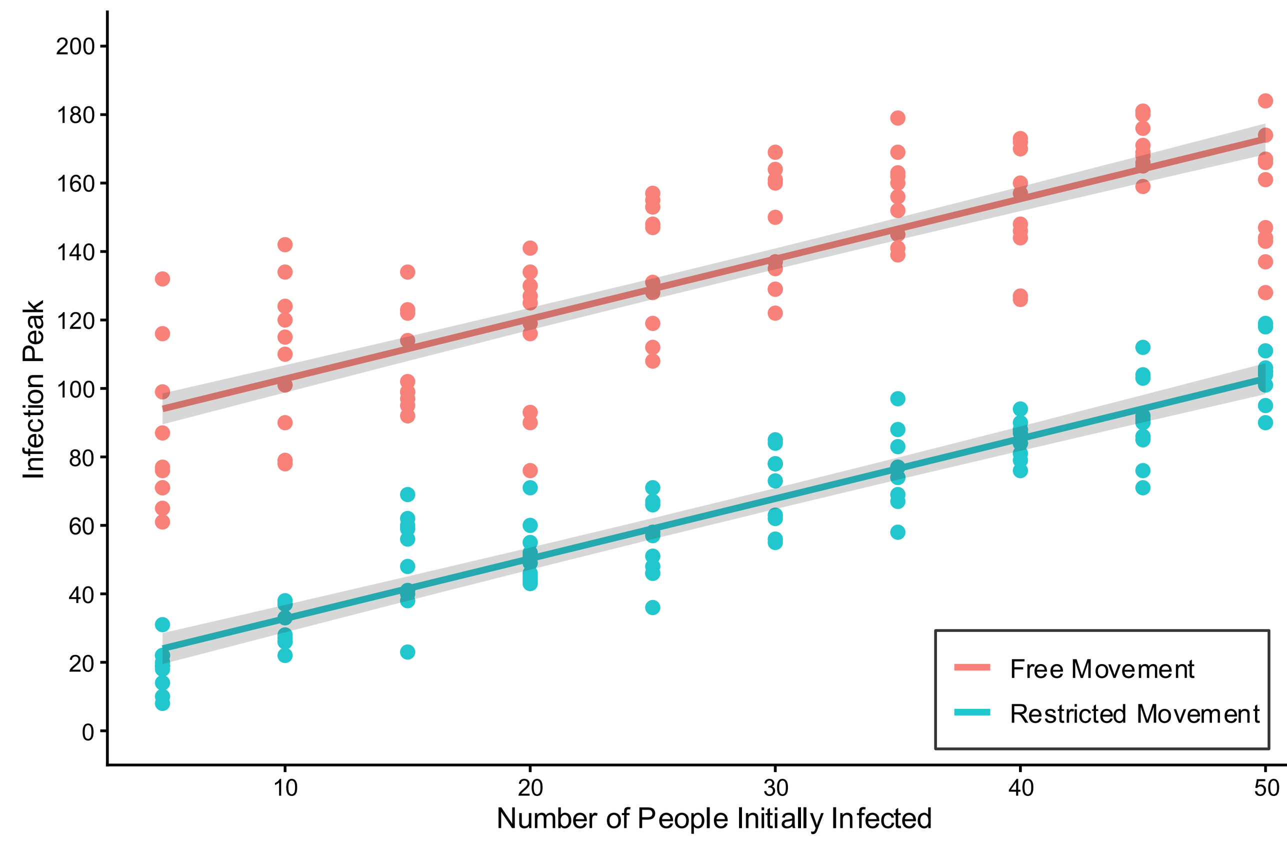

Figure 3: Restricted Movement Significantly Reduces Infection Peak Regardless of Initial Infection Level

The data points represent the maximum number of infections recorded for each of the 10 initial infection levels under the two movement regimes. The overlaid regression lines are derived from an additive Gaussian GLM, simplified by removing the **non-significant interaction effect** ($p = 0.678$). While count data are often modelled using a Poisson distribution, diagnostic checks and AIC comparison revealed that the Gaussian GLM provided a superior fit (AIC = 1665 vs. 2057). Shaded regions denote 95% confidence intervals.

Discussion

- **Impact of Movement Regime:** Restricted movement reduces the infection peak by approx. 70 individuals compared to free movement, regardless of the initial infection level ($p < 0.001$). This supports the retrospective evidence that COVID-19 lockdowns were effective at reducing transmission regardless of existing community prevalence[8].
- **Impact of Initial Infection Level:** For every additional person initially infected, the peak infection increases by approx. 1.8 individuals ($p < 0.001$). This illustrates that intervention timing is critical for maximising the suppressive efficacy of movement restrictions.

Limitations: While this study demonstrates that lockdowns are a powerful tool for suppressing infection peaks, it has many limitations. The initial infection levels used here provide a controlled baseline for comparison, yet they do not capture the unpredictable ways a virus can spread through a real population. Similarly, the binary movement regimes (free vs. restricted) overlook the nuances of human behaviour and varying compliance, even under strict lockdown conditions. Crucially, the study also does not take into account the significant social and economic costs of a lockdown.

Was Boris Right? Our findings suggest that while the decision to implement a lockdown was fundamentally effective at reducing transmission, its success was highly sensitive to the initial infection level. This aligns with recent findings from the UK COVID-19 public enquiry (2025), which concluded that locking down just one week earlier (March 16th instead of March 23rd) could have reduced first-wave deaths by nearly half (approx. 23,000 lives)[9]. From a purely public health perspective, Boris was right to use lockdown measures - but was wrong on the timing.

Acknowledgements

Thanks to Dr. Richard Bingham, Dr. James Stockdale, workshop demonstrators, the University of York Biology department, and my teammates for their guidance and contributions to this poster.

References and Supporting Material

Please follow this QR code to find the references list, the NetLogo model code and parameters, the raw data file, the RStudio project and the figures as SVG files.

A digital version of this poster is also on this site.

If you are unable to scan the QR code, you can follow the URL below:

https://student-y3945249.github.io/BABS3/