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## SUMMARY

### INTRODUCTION

- Susceptible - Exposed - Infectious - Recovered (SEIR) models are commonly used to model how infectious diseases such as measles propagate through a population.
- Using historical data to parameterise and validate an SEIR model, this study aims to accurately simulate the outbreak of measles in a paediatric population in an isolated town, to subsequently assess the impact that varied levels of vaccination coverage have on disease propagation.

### METHODS

- Using the Hagelloch dataset, a well-studied historic dataset detailing a measles outbreak in an unvaccinated paediatric population in Hagelloch, Germany, varying stochastic SEIR models were tested for goodness-of-fit, with the best model differentiating infection risk by school group (preschool, primary, secondary).
- The model then applied a risk reduction relative to the MMR vaccine efficacy to varying proportions of the cohort to simulate disease propagation with this altered cohort.
- Infection rates, both total and disaggregated by vaccinated/non-vaccinated, were recorded as well as the amplitude of the peak infections and trajectory of the major breakout.

### FINDINGS

- In the original case with no vaccinations, the entire cohort were infected by roughly five weeks after the initial case.
- With increasing vaccination coverage, greater proportions of the cohort avoided infection entirely, with 17% of the cohort avoiding infection at 25% coverage, and 36% avoiding infection at 50% coverage.
- By 90% coverage, around half of the unvaccinated cohort avoided infection, indicating mild indirect protection.
- With no coverage, peak simultaneous infections hit 50% of the population, with 35% and 22% for the 25% and 50% coverage respectively.
- By 90% there was no notable peak infection point, with simultaneous infections never greater than 2%.

### DISCUSSION

- The outputs of the model indicate that whilst herd immunity is possible, it requires significantly high rates of coverage, estimated to be greater than 90%.
- Conversely, lower coverage rates increase infection risk to the vaccinated cohort, leading to heightened infection rates in this population.

## BACKGROUND

- Infectious disease modelling is a key tool for understanding epidemic dynamics and evaluating potential intervention strategies. While modern outbreaks have emphasised its importance, historical datasets provide uniquely detailed insights that allow transmission mechanisms to be explored in a controlled setting.
- The **1861 measles outbreak in Hagelloch, Germany**, is one of the most comprehensively documented epidemics, with individual-level data capturing symptom onset, household composition, and classroom membership for 188 children<sup>1</sup>. This level of detail enables the investigation of how social structure influences disease spread.
- Stochastic **SEIR (Susceptible - Exposed - Infectious - Recovered)** models are commonly used to represent epidemic propagation. However, models assuming homogeneous mixing may fail to capture key transmission pathways, particularly those driven by repeated close contacts within schools and households. Previous work has shown that incorporating these structures substantially improves model fit and better reflects observed transmission patterns.
- Building on this foundation, structured SEIR models can be extended to explore how interventions, such as vaccination, influence epidemic outcomes within realistically modelled populations.

## AIMS

- This study aims to utilise the SEIR framework to **simulate a measles outbreak in an isolated population** based on the Hagelloch dataset.
- Using this model, the study **evaluates the impact that differing proportions of vaccination coverage** have on disease propagation.

## METHODS

### Model Structure

- A stochastic SEIR model was used to simulate disease transmission within the closed population. Individuals transition sequentially through health states (S → E → I → R) using discrete daily time steps.
- To reflect real-world transmission vectors, the **model accounted for infection risk relative to school membership** (preschool, primary school, secondary school). This allows higher transmission between individuals within the same class compared to those in different groups, capturing key social mixing behaviour observed in the Hagelloch dataset.
- The model was initialised with a single infectious individual, with the remaining population assumed susceptible. In each model cycle, the susceptible individuals had a probability of infection relative to the number of present infectious individuals both within their class or not.

### Transmission Modelling

- Transmission was modelled using the concept of an escape probability, defined as the probability that a susceptible individual avoids infection from an infectious individual on a given day.
- The probability of infection increases with the number of infectious individuals present (both from within the same class and externally), and the number of new exposures each day was modelled probabilistically using a binomial process. This stochastic framework allows for variability in epidemic trajectories across simulations.

**Table 1. Total infections observed in the simulated cohorts**

Coverage	Peak simultaneous infections % of total cohort (95% CI)	Total unvaccinated infections % of sub-cohort (95% CI)	Total vaccinated infections % of sub-cohort (95% CI)	Total infections % of total cohort (95% CI)
VC 0%	50% (40%, 61%)	100% (99.5%;100%)	NA	100% (99.5%;100%)
VC 25%	35% (28%, 43%)	99.9% (99.3%;100%)	33.9% (14.6%;54.2%)	82.8% (77.4%;88.2%)
VC 50%	22% (18%, 27%)	99.5% (97.8%;100%)	28.4% (13.8%;43.6%)	63.6% (55.4%;71.5%)
VC 90%	2% (0.5%, 5%)	51.2% (0%;100%)	6.6% (0%;24.1%)	10.2% (0%;30.3%)

## Vaccination Scenarios

- Vaccination was incorporated as a reduction in infection risk for vaccinated individuals. Specifically, vaccination was modelled as a proportional decrease in susceptibility, applied as a hazard, such that **vaccinated individuals have a reduced probability of infection by 97%**<sup>2</sup> when in contact with an infectious individual.
- A range of vaccination coverage levels (0%, 25%, 50%, and 90%) was simulated by varying the proportion of vaccinated individuals within the population. For each scenario, multiple stochastic simulations were performed to evaluate the resulting epidemic dynamics.

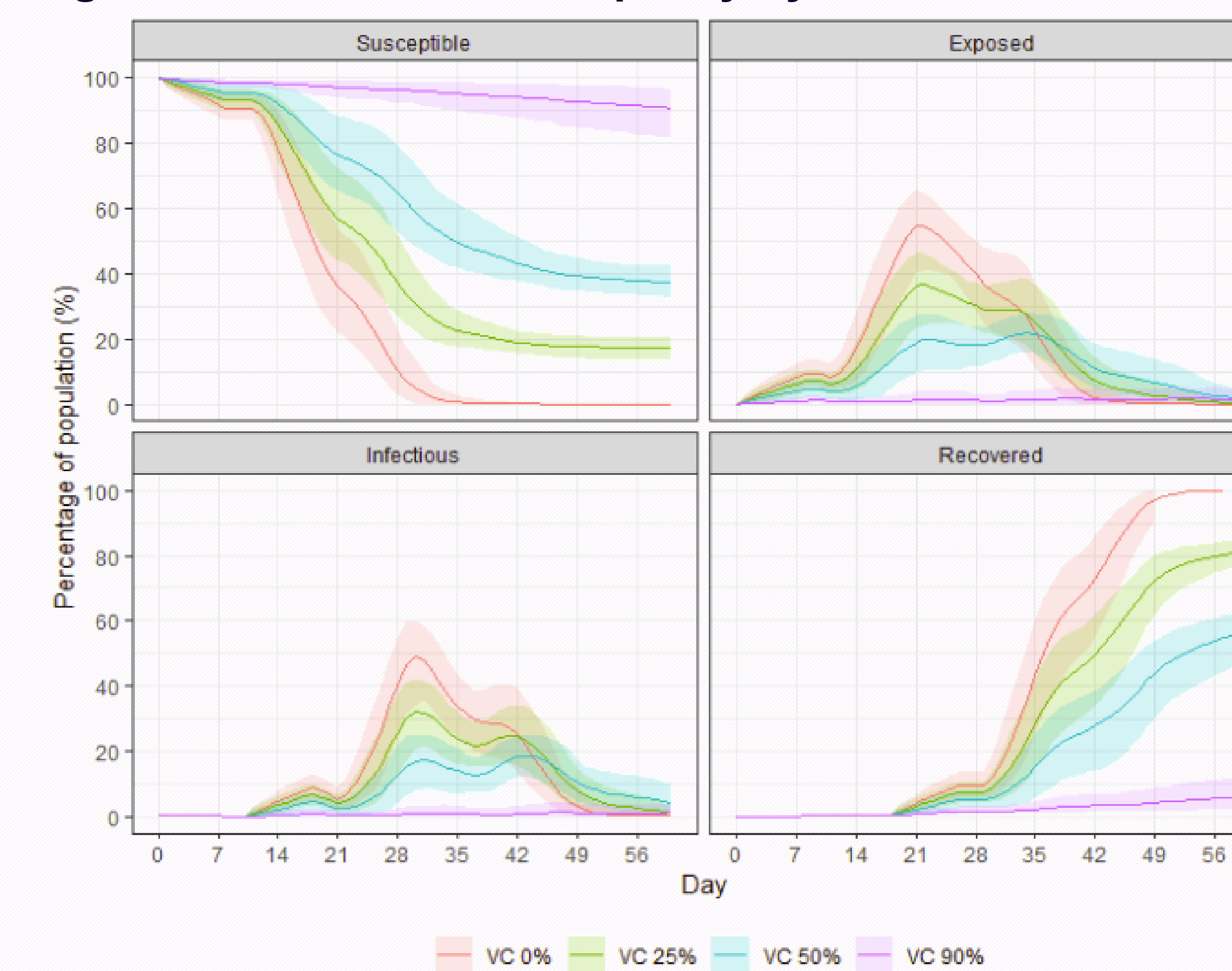
## Simulation Approach

- The model was initialised with a single infectious individual, with the remaining population assumed susceptible. Simulations were run iteratively until no exposed or infectious individuals remained.
- For each vaccination scenario, 1000 simulations were conducted to generate average epidemic trajectories and corresponding uncertainty intervals, allowing comparison of outbreak size and progression across coverage levels.

## RESULTS

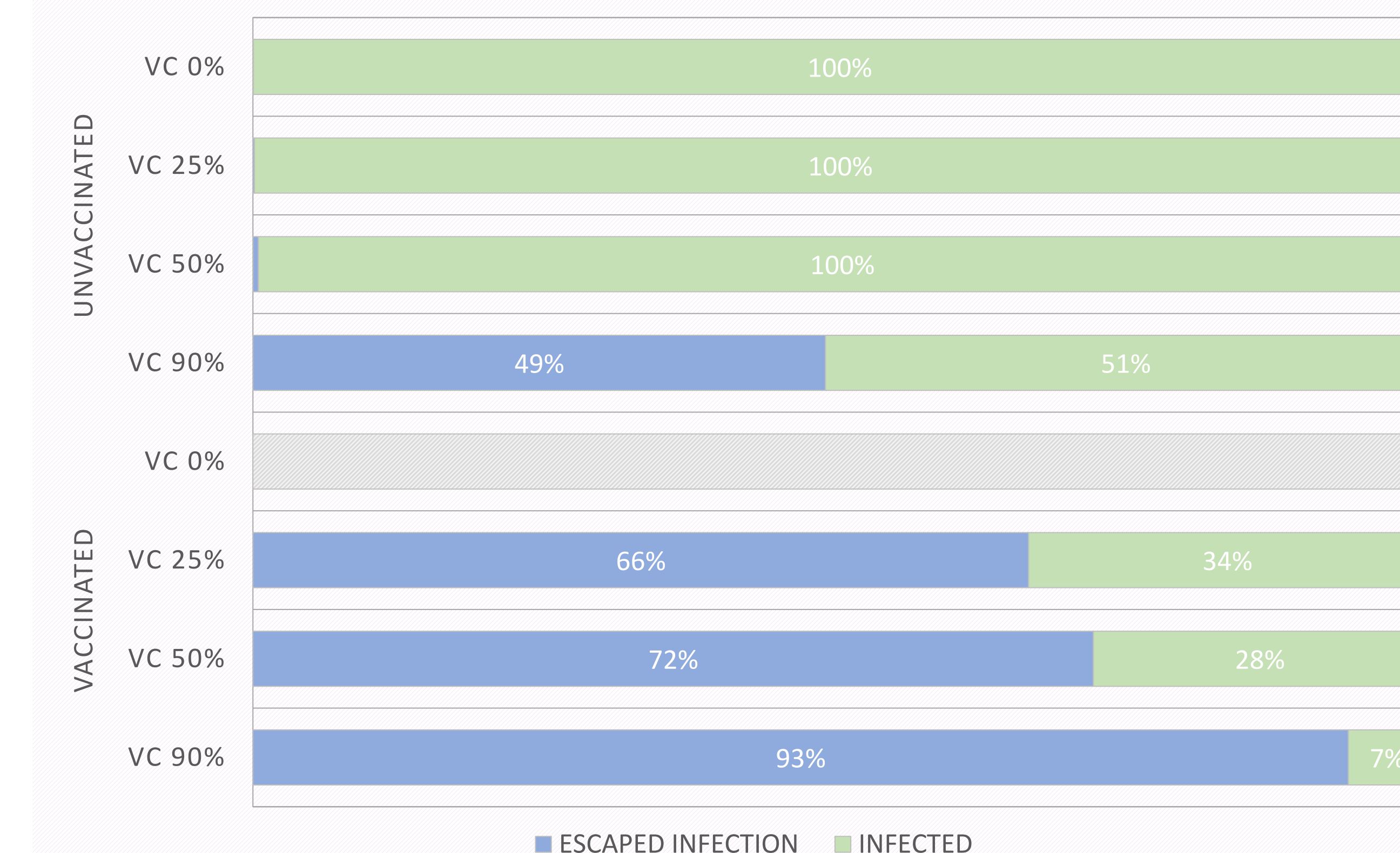
- Simulation of the stochastic SEIR model demonstrated a substantial reduction in outbreak magnitude with increasing vaccination coverage (Figure 1). In the absence of vaccination (VC 0%), the outbreak propagated rapidly through the cohort, with the population entirely infected by the end of the simulation period.
- Increasing vaccination coverage progressively attenuated epidemic propagation, resulting in smaller exposed and infectious peaks, preservation of the susceptible population, and fewer cumulative infections overall.

**Figure 1. Health-state occupancy by vaccination coverage**



- The effect of vaccination on peak outbreak intensity was clear (Table 1). Peak simultaneous infectiousness declined from 50% (95% CI: 40%, 61%) of the cohort at VC 0% to 35% (28%, 43%) at VC 25%, and further to 22% (18%, 27%) at VC 50%. At VC 90%, limited transmissions were observed, with peak infections reduced to 2% (0.5%, 5%) of the full cohort.

**Figure 2. Percentage of vaccinated and unvaccinated sub-cohorts infected by the end of the simulated outbreak, by vaccination coverage**



- When stratified by vaccination status (Figure 2), unvaccinated individuals remained at high risk of infection at lower vaccination coverages, with approximately all unvaccinated individuals infected at VC 25% and VC 50%.
- However, at VC 90%, infections within the unvaccinated subgroup fell substantially to 51% (0%, 100%), suggesting the emergence of indirect protection through reduced community transmission.
- Vaccinated individuals consistently experienced lower infection rates than their unvaccinated counterparts across all vaccination scenarios, with only 6.6% (0%, 24.1%) infected at VC 90%. Where the unvaccinated cohort rose dramatically with reduced coverage, with 33.9% (14.6%;54.2%) infected at VC 25%.
- Collectively, these findings suggest that increasing vaccination coverage not only reduces total infections, but also suppresses peak transmission intensity and generates indirect protection for unvaccinated individuals through reduced epidemic propagation.

## CONCLUSIONS

- **Increasing vaccination coverage substantially reduced outbreak magnitude and transmission intensity** within the simulated cohort. Higher coverage levels were associated with lower peak infectious occupancy, fewer cumulative infections, and greater probability of entirely escaping infection. The reduction in transmission appeared strongly non-linear, with the greatest effect observed at 90% vaccination coverage, where only limited onward propagation occurred.
- **Stratified analysis of vaccinated and unvaccinated sub-cohorts demonstrated both direct and indirect protective effects of vaccination.** Vaccinated individuals consistently experienced lower infection rates, whilst infections amongst unvaccinated individuals remained high at lower coverage levels. However, at 90% coverage, infection rates in the unvaccinated subgroup were substantially reduced, suggesting suppression of transmission within the wider population.
- Overall, the analysis demonstrates that the stochastic SEIR framework was capable of reproducing key epidemic dynamics whilst evaluating the impact of vaccination coverage on disease propagation. The findings highlight the importance of incorporating realistic transmission structure within infectious disease models and demonstrate the flexibility of the framework for assessing intervention strategies.

## References

1. Surveillance package for R. Hagelloch dataset - 1861 Measles Epidemic in Hagelloch. [rdrr.io. \[Online\] 2025. \[Cited: 7 September 2025.\] https://rdrr.io/cran/surveillance/man/hagelloch.html.](https://rdrr.io/cran/surveillance/man/hagelloch.html)
2. <https://www.idsociety.org/ID-topics/infectious-disease/measles/know-the-facts>