

Modelling the Spread of Measles: The Effect of Vaccination-Status Clustering in Social Networks

Using agent-based epidemic modelling (MAY & JUNE) to test how social clustering of unvaccinated individuals changes measles outbreak risk in England

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Introduction

Motivations

Public health in some western countries is increasingly threatened by vaccine curable diseases. This is largely due to a decline in vaccine uptake in some areas.

For example, the WHO stated the number of measles cases in the European region had doubled to 127,350 in 2024: the highest level seen in 25 years

This means National immunisation strategy must be as effective as ever and understand new dynamics to create lifesaving policies. An underexamined precedent not accounted for in many herd immunity models is the clustering of unvaccinated individuals. This is proven to be dangerous reality most relevant to countries reaching higher vaccination coverage levels. The WHO sets a target of 95% vaccination coverage; however, some studies show this level of overall population coverage isn't enough to prevent serious outbreaks when accounting for low uptake clusters.

The overlooked variable: clustering

Unvaccinated individuals cluster together through shared socio-demographic traits (social selection) and vaccine-hesitant beliefs spreading through networks (social influence):

Novel Contributions

Prior studies approximated social networks with proxies such as shared schools, households or physical proximity. Uniquely, the MAY software used can model exact social connections between individuals in a population so clustering can be created within actual human networks of association.

Software Used

MAY

builds a synthetic English population with real person-to-person social networks

JUNE

simulates measles transmission across that network day by day

Measles and Vaccination

- Measles was chosen as the test pathogen as its highly transmissible demonstrated by its very high basic reproduction number ($R_0 \approx 12-18$, vs ≈ 2.6 for COVID-19), which should amplify any clustering effect.
- In the UK a measles vaccine was first introduced in 1968. Currently the combined MMRV Measles Mumps Rubella and varicella vaccination is offered in two doses at 12 months and 18 months
- The UK lost measles elimination status in 2019 then again in 2024 after Covid

Social Networks are illustrated in Fig 2, 3 and 4 for snippets of the Non-clustered, Cluster1 and Cluster 2 worlds respectively. This was used to verify clustering visually. The circles (nodes) are people red means unvaccinated, green means vaccinated, and the blue are those born before measles vaccines were introduced.

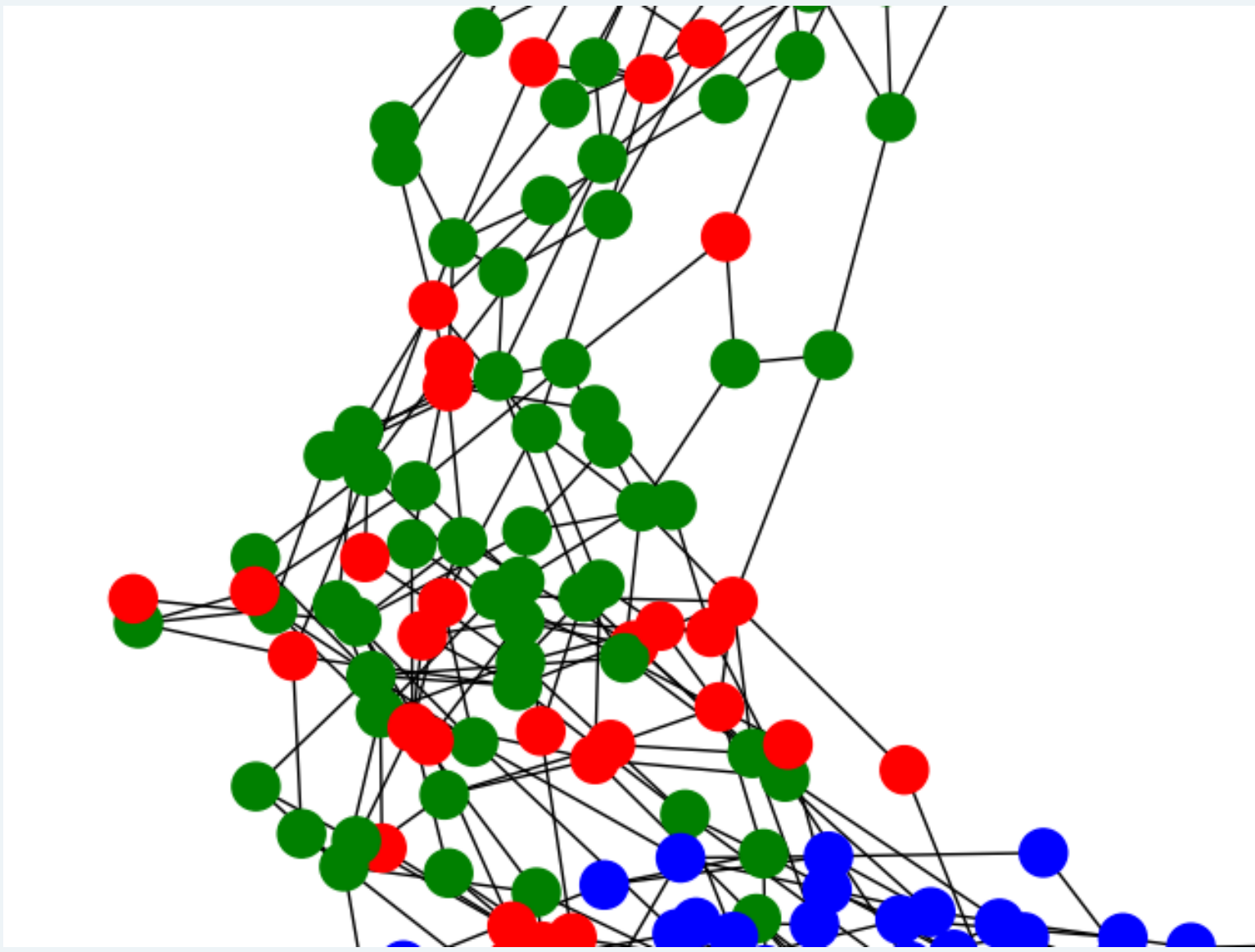


Fig 2 Snippet of social network of Un-clustered world

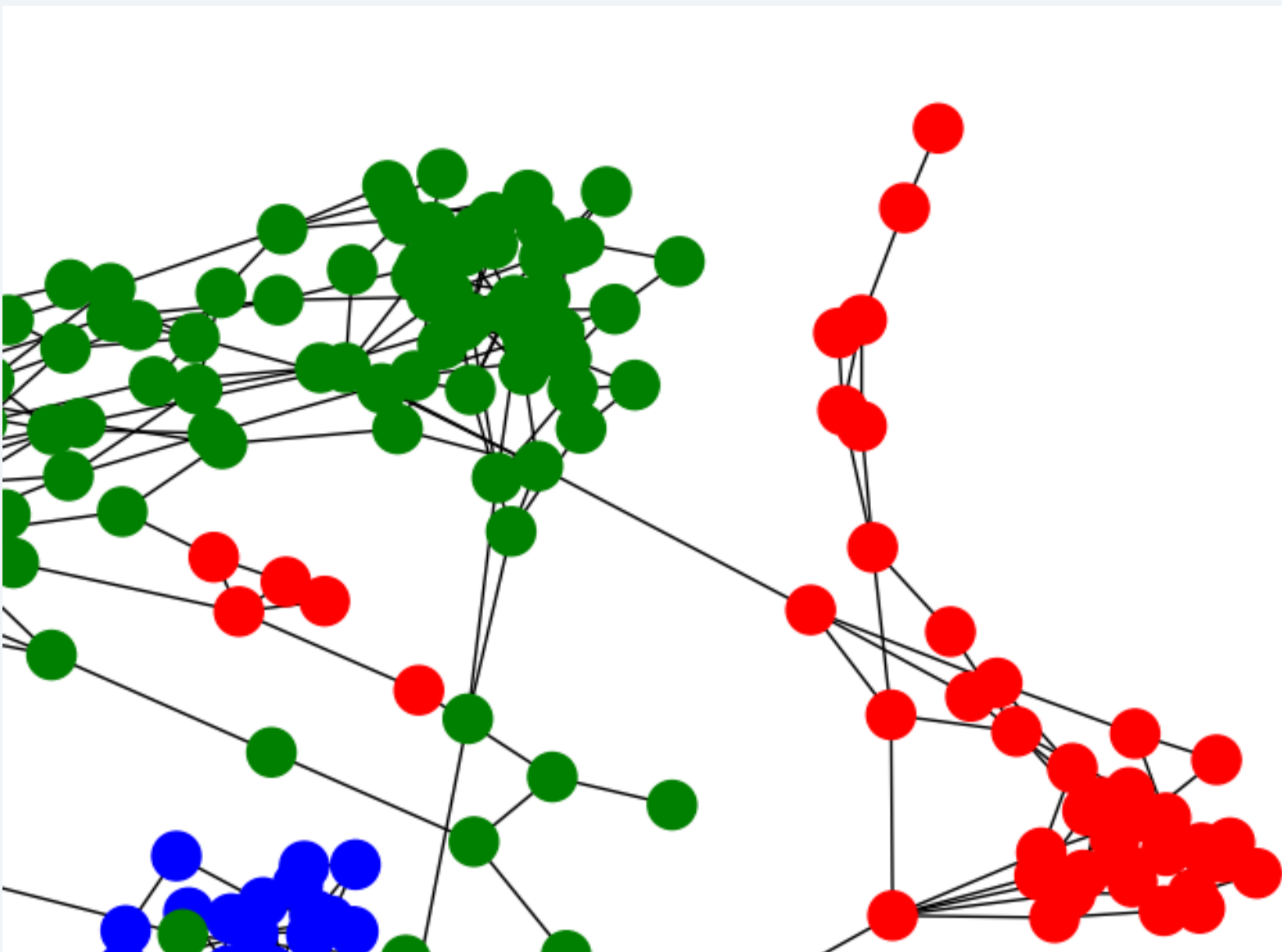


Fig 3 Snippet of social network of Cluster 1 world

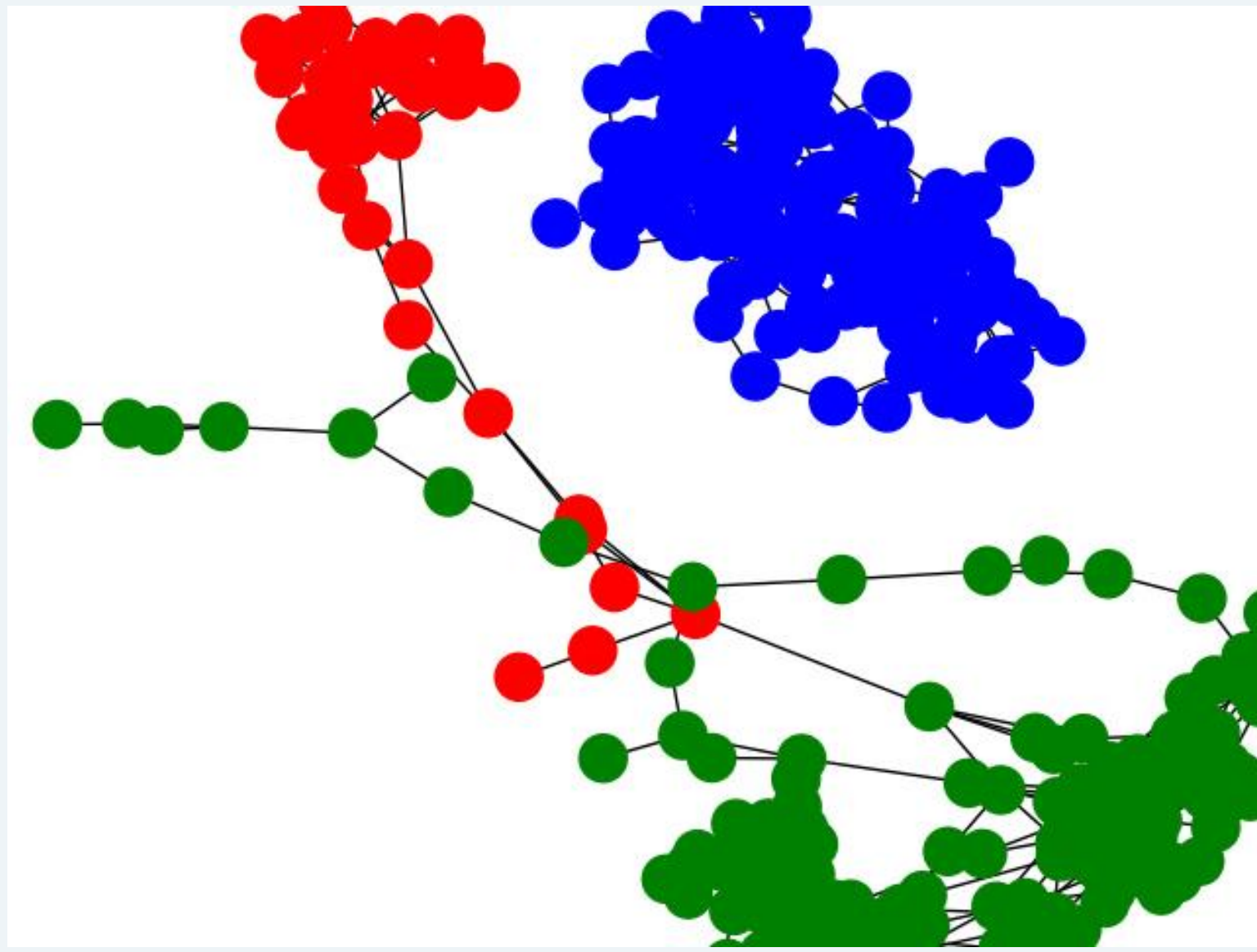


Fig 4 Snippet of social network of Cluster 3 world

Methodology

- Build the population**
MAY constructs a synthetic model of England; each agent's vaccination status is assigned probabilistically from UK COVER data by age and local authority.
- Create clustered worlds**
Two further worlds re-select an agent's social connections so they preferentially share the agent's own vaccination status (Cluster 1: 2 of ~6 connections; Cluster 2: 3 of ~6).
- Configure JUNE for measles**
Adapted from JUNE's COVID-19 template: measles clinical trajectories, 5.5× respiratory transmission scaling, MMR efficacy 96%, isolation policy.
- Simulate & compare**
Simulations were run for Wiltshire (pop. ~510,000) across all three worlds and outcomes were compared.

Table 1 — Edge-match rate by world

World	Overall	Unvax (avg)	Unvax (median)
Non-Clustered	0.75	0.29	0.33
Cluster 1	0.87	0.63	0.67
Cluster 2	0.94	0.82	0.83

An agent's ~6 social connections

- shared-venue connections — never status-constrained
- similar age & location — constrained in Cluster 1 and Cluster 2
- wider age/location — additionally constrained in Cluster 2 only

- Clustering was built by filtering the pool of possible friends by vaccination status during network generation
- Configuration verified against JUNE's simulation-event logs to confirm seeding, transmission and vaccination behaved as intended.

Results

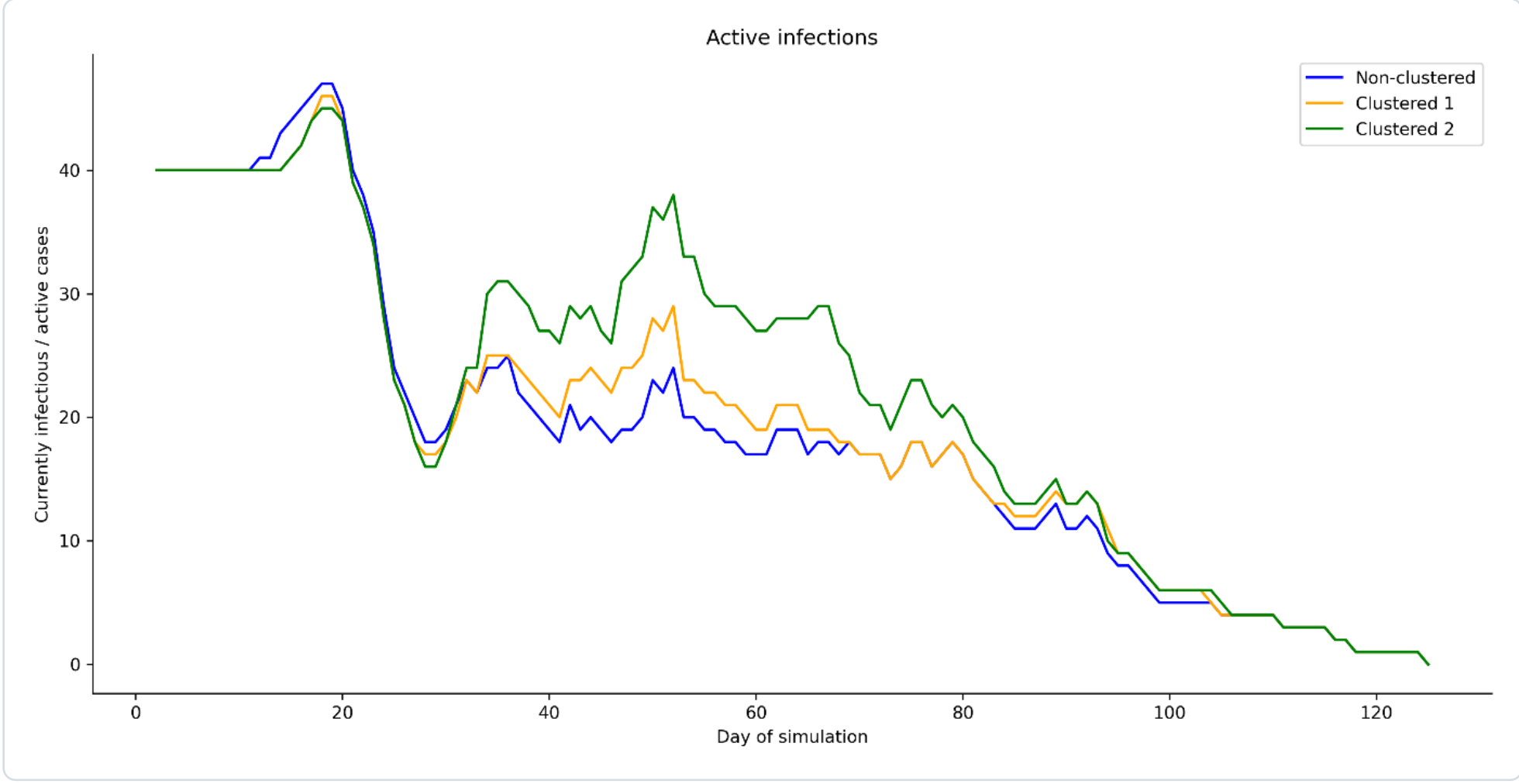


Fig. 1 — Daily active measles infections in the Wiltshire simulation, non-clustered vs. clustered worlds.

Table 2 — Simulated outcomes by world

World	Total infections	Hospitalisations	Deaths
Non-Clustered	106	20	0
Cluster 1	110	18	0
Cluster 2	124	22	0

- Fig 1 shows overall the more clustered the world the greater the outbreak as there are clearly more cases.
- Peak active infections were 44% higher in Cluster 2 than the non-clustered world (36 vs. 25 cases); total infections were 17% higher as seen in Table 2. For the 17% difference to be a result of an uncertainty on the total infections both the Non-clustered and Cluster 2 world would have to have an absolute uncertainty of 8 people which seems unrealistic meaning it is reasonable to assume this correlation is accurate.
- The relationship between the unvaccinated edge-match rate and outbreak size may be non-linear, but with only three clustering configurations this cannot be confirmed.

Day ~19 — initial peak from seeds

Nearly identical across all three worlds (~45 active cases) with any variation due to noise, the clustering effect has not appeared yet.

Day ~30 onward — outbreak in wider population

Worlds diverge sharply here — clustering amplifies onward transmission, not the initial seed.

Caveat: Wiltshire's population (~510,000) and case counts are small, so results carry substantial statistical noise — scaling to all of England is the priority next step.

Conclusion

Explicitly modelling social-network structure, rather than assuming uniform mixing, shows that clustering of unvaccinated individuals meaningfully increases measles outbreak size, even over the modest range of clustering achieved here: an unvaccinated edge-match rate rising from 0.29 to 0.82 produced a 17% increase in total infections and a 44% increase in peak active cases. This supports the view that population-level coverage targets, such as the WHO's 95% threshold, can understate real outbreak risk when unvaccinated individuals are not evenly distributed through a community, an interaction largely absent from standard herd-immunity models. As a single-county pilot with only three clustering configurations and no recorded deaths, these results are best read as a proof of concept for the MAY/JUNE clustering methodology, not a calibrated estimate of real-world risk.



Software: MAY — [idas-durham.github.io/MAY](https://github.com/idas-durham/MAY) · JUNE2 — github.com/IDAS-Durham/JUNE2 | Adapted from project report "Modelling the Spread of Disease: Considering Clustering in Vaccination Status Within Social Networks"

Key Future Work

- Scale simulations to all of England for larger, statistically robust outbreaks and rarer severe outcomes.
- Systematically vary clustering parameters to map, and test the apparent non-linearity of, the edge-match-rate/outbreak-risk relationship.
- Make clustering more realistic through further research e.g. by inserting non-vaccinated clusters to specific demographics.
- Make JUNE more accurate by calibrate transmission, campaign-uptake and isolation-compliance parameters against real observed measles outbreaks.
- Policy suggestion off the back of this research