Network-Based Compartmental Modelling of Epidemic Spread and Interventions for a Multi-Ethnic Society

Keywords: complex network, epidemic modelling, compartmental model, stochastic block model, homophily

Extended Abstract

Effective epidemic management is challenging due to the dynamic nature of disease spread, making uniform public health policies impractical. This study integrates complex network models with SEIRS compartmental modelling to explore how social structure shapes COVID-19 propagation in Malaysia's multi-ethnic society. Dynamic network switching models reflect contact patterns under different government-imposed policy interventions, namely the Movement Control Order (MCO) and Conditional Movement Control Order (CMCO). Disease propagation simulations are applied separately to two baseline networks, including the Barabási–Albert (BA) model [1] and the stochastic block model (SBM) [2]. The SBM is parameterised using census data from real-world contact estimates to reflect the homophilic tendencies of Malaysia's ethnic composition.

Intervention effects, adapted from Small and Cavanagh's study [3], are simulated by rewiring the network from BA or SBM in the pre-MCO period (day 1-43), to a Watts-Strogatz lattice during the MCO (day 44-90) and finally to a BA or SBM network with a cap on mass gatherings during the CMCO (day 91-127). As shown in Table 1, the parameter values used in the SEIRS model were chosen by referring to past literature. The simulated epidemic curves are compared with real-world case data from Selangor and Kuala Lumpur.

Figure 1 contrasts epidemic simulations on the BA and SBM baseline models with 10,000 nodes each. The plot lines represent various compliance rates during the MCO, ranging from 95% to 10%. The SBM baseline model produces more spread out, wave-like infection curves that align better with observed peaks and troughs compared to the explosive nature of the BA network. Furthermore, the SBM exhibits a sharper initial surge, but showcases a stronger tapering effect during the MCO.

Figure 2 emphasises intervention effects under the SBM with 85% compliance. The control measures employed have reduced the total number of active cases by 52.80% and delayed the peak by a little over five weeks. While control measures do not completely halt disease spread, they delay the inevitable resurgence and reduce overall burden.

Between the two models tested, the SBM baseline model performs better in mirroring real-world trends by incorporating community structure. Limiting inter-group activity reduces the effectiveness of cross-ethnic transmission and slows spread. Overall, this study highlights how networks serve to enhance the explanatory and predictive capabilities of compartmental models. Evaluating past interventions using this framework can help guide the design of strategies and quantify their consequences, particularly for future pandemics.

References

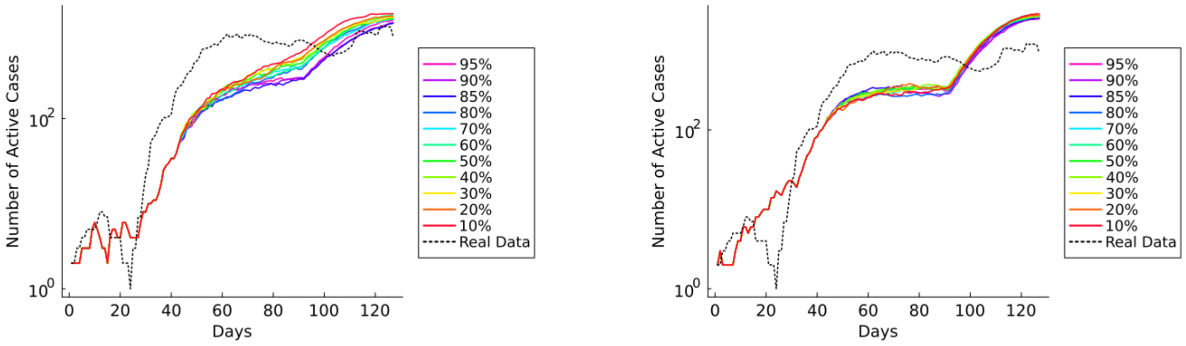
[1] Albert-László Barabási and Réka Albert. “Emergence of Scaling in Random Networks”. In: *Science* 286.5439 (1999), p. 509.

[2] Emmanuel Abbe. *Community Detection and Stochastic Block Models*. 2023. URL: `https://arxiv.org/abs/1703.10146`.

[3] Michael Small and David Cavanagh. “Modelling Strong Control Measures for Epidemic Propagation With Networks—A COVID-19 Case Study”. In: *IEEE Access* 8 (2020), pp. 109719–109731.

Table 1: **Final parameter values used in the network-based SEIRS model.** Sources and rationale for selected values are summarised for reproducibility and transparency.

Parameter	Value	Source(s)
Transmission Rate (β)	0.063	Chosen within the 0.05 to 0.07 range. Prior studies utilised $\beta = 0.052$ and $\beta = 0.0698$.
Latency Period (δ)	$\frac{1}{5}$	Consistent with the recommendations of past studies.
Recovery Rate (γ)	$\frac{1}{11}$	Recovery duration of first Selangor and Kuala Lumpur case.
Re-susceptible Rate (ξ)	0.0345	Approximately the midpoint of reinfection incidence values found in two past studies.
Initial Number of Infected Nodes	2	Based on the aggregate number of confirmed cases in Selangor and Kuala Lumpur on 4 February 2020.



(a) **BA Baseline Model** (b) **SBM Baseline Model**

Figure 1: **Comparison of epidemic curves using BA and SBM baseline models with 10,000 nodes.** The SBM produces wave-like progressions closer to that of the real-data.

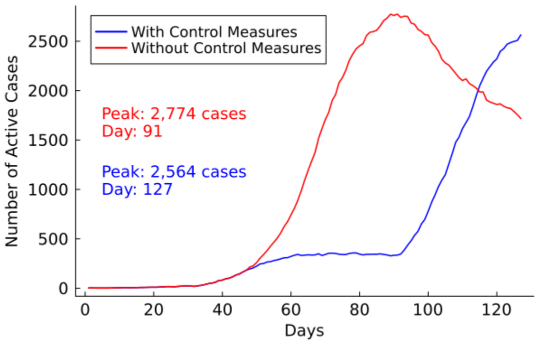


Figure 2: **Peak delay.** Simulated active cases with (85% compliance) and without (only SBM) control measures.