Comparing Dengue Transmission Network Complexity Between High-Density and Low-Density Districts in Malaysia

Keywords: Dengue; Network Epidemiology; Spatiotemporal Networks; Exponential Random Graph Model (ERGM); Health System Complexity

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Extended Abstract

Motivation. Dengue transmission is a complex epidemiological process driven by interactions between the dengue virus, *Aedes* mosquitoes, human hosts, and the environment [1]. It is shaped particularly through mosquito breeding and biting opportunities, human exposure, the built environment, sociodemographic heterogeneity, and vector control. In practice, hotspot maps identify concentrations of cases but do not explicitly capture space–time relationships between cases, limiting insight into why local clusters form. Network epidemiology complements conventional mapping by representing cases as nodes and transmission opportunities as edges, enabling quantification of fragmented clusters linked to nodal factors, which is highly relevant to Health System Complexity [2,3].

This study asks: **RQ1:** How can dengue transmission networks in Petaling and Sepang be constructed using the spatiotemporal relationship between cases?
RQ2: How do these district-level networks differ in structure and centralisation?
RQ3: Which nodal attributes, nodal homophily, and structural factors influence edge formation in these networks?
Petaling and Sepang were selected as contrasting high-density and low-density districts to examine differences in dengue network complexity and implications for targeted vector control.

Approach and Methodology. We analysed laboratory-confirmed dengue cases in Petaling and Sepang districts, Selangor from January–December 2023. District-level networks were constructed by linking case pairs within ≤200 m and ≤14 days, thresholds frequently adopted in dengue spatiotemporal analyses and grounded in established knowledge of *Aedes* flight range and dengue incubation intervals [4]. We compared network structure and centralisation using Social Network Analysis (SNA), then fitted district-specific ERGMs with occupation, citizenship, housing-type homophily, and gwdegree (decay = 0.25) to explain edge formation. The conceptual framework is shown in Figure 1. Generative AI was used solely for language editing, with all analyses, modelling, and interpretations conducted and verified by the authors.

Results.
RQ1: Using the spatiotemporal linkage rule (≤200 m, ≤14 days), 12,978/19,549 cases (66.4%) in Petaling and 846/2,325 cases (36.4%) in Sepang formed district-level transmission networks.

RQ2: The networks differed markedly. Petaling was much larger but highly sparse and fragmented (12,978 nodes; 21,424 edges; density 0.00025; 2,957 components; degree centralisation 0.0023), whereas Sepang was smaller but denser and more centralised (846 nodes; 742 edges; density 0.00208; 307 components; degree centralisation 0.0157).

RQ3: ERGM showed different edge-formation mechanisms. In Petaling, edges were driven mainly by nodal and homophily effects (student OR 1.07, 95% CI 1.05–1.10; high-rise homophily OR 6.66; low-rise OR 4.34; non-citizen homophily OR 3.96) with minimal structural dependence (gwdegree OR 0.98, 95% CI 0.91–1.06). In Sepang, structural dependence was strong (gwdegree OR 13.67, 95% CI 9.06–20.62) alongside pronounced housing homophily (high-rise OR 11.26, 95% CI 8.76–14.47; low-rise OR 3.17, 95% CI 2.43–4.14), while the student effect was not significant (OR 1.10, 95% CI 0.93–1.31).

Conclusions and Outlook. Petaling exhibits a large, sparse, fragmented dengue network dominated by nodal and homophily effects, whereas Sepang shows a smaller, denser network with stronger structural reinforcement. These findings suggest that network structure and transmission dynamics differ markedly between a high-density and a low-density district, highlighting the need for district-specific approaches to dengue control. By the conference, we will complete robustness testing across both districts using alternative spatiotemporal thresholds.

Ethics Statement. Approved by Medical Research and Ethics Committee (MREC), Ministry of Health Malaysia (NMRR ID-24-01515-I8B) and The National University of Malaysia Research Ethics Committee (FF-2024-296). Data were handled confidentially.

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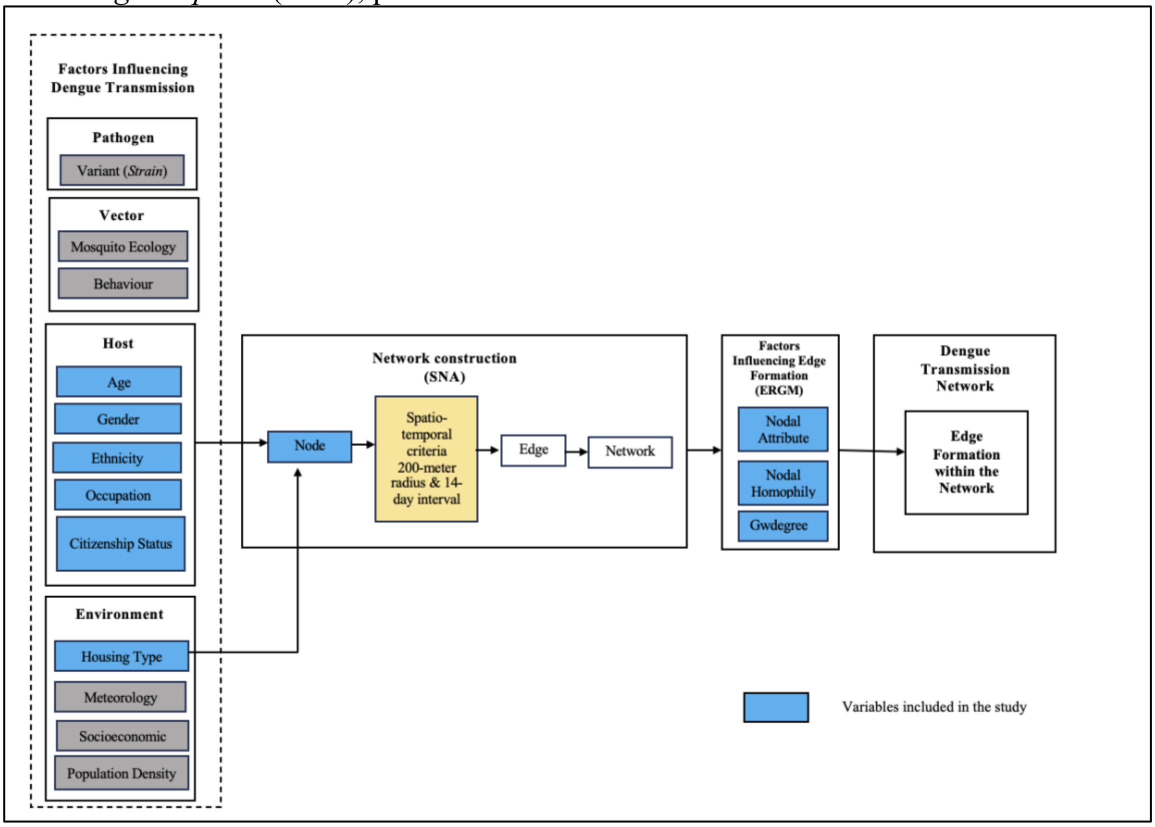

Figure 1. **Conceptual framework of the spatiotemporal SNA–ERGM workflow**. Cases are nodes; edges connect pairs within ≤200 m and ≤14 days to form district networks (SNA). ERGM tests nodal attributes, homophily, and gwdegree effects on edge formation. Blue boxes denote analysed independent variables. Edge formation within the network is the dependent variable.