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Contact heterogeneity in network reconstruction: evaluating synthetic graph generators for rabies transmission modeling

Inhalt

Canine rabies remains endemic across much of Africa and Asia, causing approximately 59,000 human deaths annually. Network-based models can capture the heterogeneous contact patterns driving rabies transmission, but generating synthetic networks that faithfully reproduce empirical contact structures and downstream transmission dynamics is non-trivial. We compared five network generators (Erdős-Rényi model (ERM), stochastic block model (SBM), degree-corrected stochastic block model (DCSBM), spatially explicit network construction algorithm (SENCA), and Newman clustered random-graph generator (NCRG)) against an empirical free-roaming dog contact network from N'Djamena, Chad, as well as four additional dog-proximity datasets. We evaluated each generator's reproduction of six topological summary measures and of outbreak dynamics under SEIR (Susceptible-Exposed-Infectious-Recovered) and SIS (Susceptible-Infectious-Susceptible) simulations. The DCSBM most consistently reproduced empirical topology across all networks. Under SEIR dynamics with a short infectious period, as in rabies, the DCSBM also most closely matched empirical case patterns, underscoring the joint importance of degree and community structure in shaping outbreak patterns. Under SIS dynamics with longer infectious periods, generator-specific differences in outbreak dynamics attenuated, suggesting that capturing network heterogeneity matters more for fast-burning pathogens like rabies than for slower-spreading ones.

Keywords

canine rabies; generative models; contact network reconstruction; free-roaming dogs; disease transmission modeling

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Yes, I am a Junior Scientist.

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Strong preference for talk, happy with a poster.

Eingereicht von **DERKX, Inez** <inez.derkx@swisstph.ch> am **Montag, 22. Juni 2026**