Local epidemic thresholds on networks: community-specific risk from mobility-driven interactions

epidemiology, epidemic threshold, spatial networks, community risk, bifurcations

Extended Abstract

The epidemic threshold is a central concept in network epidemiology [1]. It defines the critical transmissibility above which a pathogen can establish itself, and has become a standard tool to assess epidemic risk at national and global scales [2]. It has been computed analytically on spatial networks, even assuming time changing links [3–5]. Yet, these approaches return a single global number, compressing heterogeneous communities into one risk metric. In practice, this misses crucial dimensions: the vulnerability of each community depends on when and where introductions occur, on the intensity of mobility-driven coupling, and on structural heterogeneities such as socioeconomic conditions that modulate susceptibility and transmissibility.

Existing alternatives consist in local indicators based on reproduction ratios or outbreak probabilities that however ignore spatial mixing [6]. Large metapopulation and agent-based models capture heterogeneities but at the cost of heavy parametrization, high computational burden, and possibly poor applicability in resource-constrained settings. This gap motivates the development of analytic methods that provide community-specific measures while accounting for the coupling encoded in the spatial mixing networks driven by recurrent mobility.

We present a theoretical framework that extends the notion of epidemic threshold beyond a single global value, identifying multiple critical points associated with specific spatial regions, communities and across-community structures. Through a Lyapunov-Schmidt reduction of the fixed-point equations for outbreak probabilities, we show that even a weak coupling among communities generates new critical points that, generically, leave the real axis and appear as complex conjugate pairs. The real part of these complex thresholds shifts the activation point of each community, while the imaginary part quantifies the smoothing of the activation of a particular spatial epidemic structure. Specifically, each of the various critical points in the system is linked to the activation of a community or specific combination of communities. This structures are analytically identifiable and provide principled local indicators of epidemic risk: they integrate network connectivity, mobility flows, and community heterogeneities.

The approach is analytic and data parsimonious. It requires only the parametrization of the reproduction operator [7], which can be estimated from surveillance and mobility data, and does not rely on expensive simulations. It can therefore be applied in resource-limited settings, delivering community-specific indicators that are consistent with the global organization of the system. This makes it possible to identify vulnerable communities, quantify the effect of interventions that alter connectivity, and assess how structural heterogeneities shift local activation thresholds.

Our results broaden the classical concept of epidemic threshold into a spectrum of critical points with both real and complex components. They provide a general and computationally efficient method to assess both global and local epidemic risk on networks, bridging the gap between national-scale metrics and fully individual-based models.

References

[1] Romualdo Pastor-Satorras et al. “Epidemic processes in complex networks”. In: *Reviews of Modern Physics* 87.3 (2015), pp. 925–979.

[2] Alexandre Darbon et al. “Network-based assessment of the vulnerability of Italian regions to bovine brucellosis”. In: *Preventive Veterinary Medicine* 158.March (2018), pp. 25–34. URL: `https://doi.org/10.1016/j.prevetmed.2018.07.004`.

[3] Vittoria Colizza and Alessandro Vespignani. “Invasion threshold in heterogeneous metapopulation networks”. In: *Physical Review Letters* 99.14 (2007), pp. 1–4.

[4] J. Gómez-Gardeñes, D. Soriano-Paños, and A. Arenas. “Critical regimes driven by recurrent mobility patterns of reaction–diffusion processes in networks”. en. In: *Nature Physics* 14.4 (2018). Number: 4 Publisher: Nature Publishing Group, pp. 391–395. URL: `https://www.nature.com/articles/s41567-017-0022-7`.

[5] Eugenio Valdano et al. “Epidemic graph diagrams as analytics for epidemic control in the data-rich era”. en. In: *Nature Communications* 14.1 (2023). Number: 1 Publisher: Nature Publishing Group, p. 8472. URL: `https://www.nature.com/articles/s41467-023-43856-1`.

[6] Agnese Zardini et al. “Estimating the potential risk of transmission of arboviruses in the Americas and Europe: a modelling study”. English. In: *The Lancet Planetary Health* 8.1 (2024). Publisher: Elsevier, e30–e40. URL: `https://www.thelancet.com/journals/lanplh/article/PIIS2542-5196(23)00252-8/fulltext#seccestitle80`.

[7] Piero Birello et al. “Estimates of the reproduction ratio from epidemic surveillance may be biased in spatially structured populations”. en. In: *Nature Physics* 20.7 (2024). Publisher: Nature Publishing Group, pp. 1204–1210. URL: `https://www.nature.com/articles/s41567-024-02471-7`.

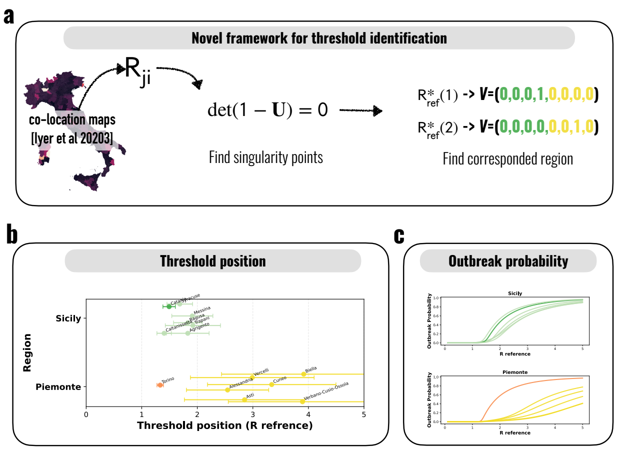

Figure 1: Case study: Italy, spread of respiratory pathogen. Spatial transmission parametrized with colocation data from Meta Data For Good. (a) Analytical framework applied to spatially structured populations. (b) Calculated thresholds for cities in Sicily (region in southern Italy) and Piedmont (northern Italy). Points correspond to the real part of the complex threshold and error bars to the imaginary part, representing threshold smearing. (c) Outbreak probability across cities. Threshold smearing is visible.