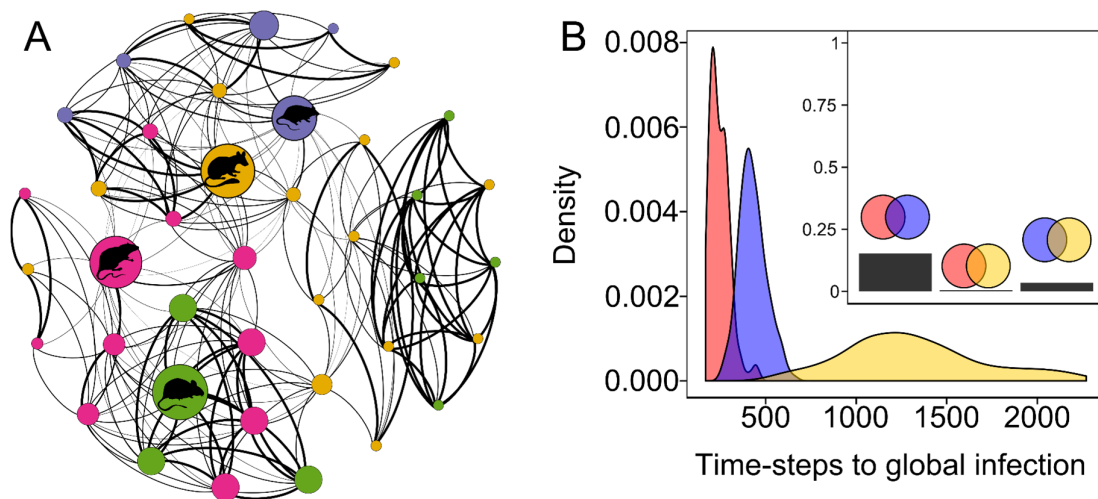


# Potential parasite transmission in multi-host networks based on parasite sharing

PILOSOF S, MORAND S, KRASNOV, BR, NUNN, CL

Epidemiological networks are commonly used to explore dynamics of parasite transmission among individuals in a population of a given host species. However, many parasites infect multiple host species, and thus multi-host networks may offer a better framework for investigating parasite dynamics. We investigated the factors that influence parasite sharing – and thus potential transmission pathways – among rodent hosts in Southeast Asia. We focused on differences between networks of a single host species and networks that involve multiple host species. In host-parasite networks, modularity (the extent to which the network is divided into subgroups of rodents that interact with similar parasites) was higher in the multi-species than in the single-species networks. This suggests that phylogeny affects patterns of parasite sharing, which was confirmed in analyses showing that it predicted affiliation of individuals to modules. We then constructed “potential transmission networks” based on the host-parasite networks, in which edges depict the similarity between a pair of individuals in the parasites they share. Simulations revealed that parasite dynamics differed between multi- and single-species networks. We conclude that multi-host networks based on parasite sharing can provide new insights into the potential for transmission among hosts in an ecological community. In addition, the factors that determine the nature of parasite sharing (i.e. structure of the host-parasite network) may impact transmission patterns.



**(A) An example for a multihost network. (B) Density plot depicting the distribution of time to global infection (TGI) for transmission-potential networks (TPNs).** TPNs were of equal size and connectance under three conditions: single-species (red), multi-species with infection probability ( $\vartheta_m$ ) varying among species (yellow) and multi-species with fixed  $\vartheta_m$  (blue), as a control to eliminate effect of multiple species. The panel describes a comparison of a single-species network to a multi-species network. Skewness to the left indicates a faster infection and curve height is indicative of the probability that global infection occurs at a certain pace. Insets shows the similarity (overlap) between two curves (depicted by the colored circle above the bar) calculated as the integral of the area common to both curves.