



Figure 2: An example network of five host species and a single parasite species, with visualizations and calculations for (A) host breadth, (B) cross-species transmission connections, and (C) a combination of both: graph density. Each node/vertex represents a host species in the community. All hosts that were present in the community were included in the analysis, even if they were not infected by the parasite in question (*e.g.*, host “E”). For host breadth (A), each host vertex was connected by a “loop” if it was infected with the parasite in question, and host breadth was calculated as the proportion of hosts that had an edge loop (E_L) out of total vertices (V). On the other hand, in (B) host vertices were connected only by potential cross-species transmission links (meaning there was geographic and temporal overlap of infection in the species, ignoring loops), and we calculated the proportion of realized direct edge connections (E_D) out of all potential links that could occur in the network. Finally in (C), we combined the two metrics—both including loops and direct edge connections for cross-species transmission—and calculated graph density as the proportion of all realized links out of all available ones.