

Nested Networks in Health: Linking Microbiomes and Interspecies Contact to Address Cross-Scale Complexity

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Extended Abstract

Complexity is often viewed as a barrier to problem solving, yet it also provides opportunities for innovation. Ecosystems and human health are interdependent complex systems¹. Infectious diseases exemplify this complexity, posing risks to human, domestic and wild animal lives, with each acting as reservoirs of infection that influence the others' health¹. These diseases represent nested complex systems^{2,3}, spanning intra-host processes (e.g. immunity, microbiome diversity and dynamics) and multi-host dynamics across species^{4,5}. Classic infectious disease examples include zoonoses such as Ebola virus⁶ and *Campylobacter*⁷ and environmentally transmitted parasites such as *Cryptosporidium*⁸. Despite advances in 'whole system' thinking^{9,10}, interventions are rarely designed using frameworks that explicitly connect processes across scales or that integrate empirical experimental evidence.

Here we highlight new opportunities for network science to address long-standing gaps, conducted under existing ethical approvals, with the aim of generating benefits for local communities, animal health, and conservation. If we could link microbial interaction networks within host microbiomes to contact networks among people, domestic animals, and wildlife, we could begin to ask whether patterns of centrality or modularity in social and ecological systems align with microbial diversity, coinfection risk, or the spread of antimicrobial resistance genes. If we could embed microbiomes within larger host and interspecies networks, we might identify whether leverage points at one scale cascade predictably across others. Such questions are rarely posed, partly due to their complexity, yet answering them would allow us to identify emergent properties, evaluate intervention targets, and design monitoring strategies that reflect the realities of complex socio-ecological systems.

The edge of Bwindi Impenetrable Forest National Park, Uganda, illustrates the potential. In this landscape, people, livestock, and wildlife live in close proximity¹¹, creating overlapping networks of contact and shared microbial exposure (Figure 1). Our existing multi-year collaboration has already revealed interlinked human-animal contact networks and shared microbes such as *Acinetobacter baumannii* bacteria in people and gorillas, suggesting that nested networks can capture meaningful biological connections. If we could scale such approaches, integrating among-species contact data, network analyses¹¹, and microbiome datasets¹², we could test whether intervention strategies (e.g. handwashing, livestock management) shift both microbial and social network structures in predictable ways. By posing these kinds of questions, we aim to stimulate cross-disciplinary discussion on how network science can move beyond single-layer or single-scale analyses. Linking microbiomes to interspecies contact networks provides a provocative example of how network approaches might be applied in domains where they have rarely been considered, offering both methodological challenges and opportunities for transformative insight.

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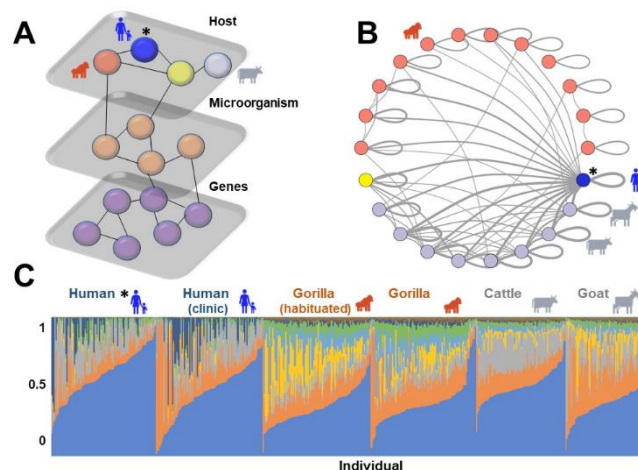


Figure 1. Linking Host Contact Networks and Microbiomes Across Species at the Human–Wildlife Interface in Buhoma, Uganda. A) multi-layered host-infection-gene networks. B) Reported human and animal contact networks (people, blue; wildlife, red; peri-domestic rodents, yellow; domestic species, grey) C) Faecal microbiomes (~600). Bars show the proportion of 12 different bacterial phyla (e.g. Firmicutes, blue; Proteobacteria, orange), highlighting species differences and similarities. Left-right: people; unwell hospital patients (clinic); human-habituated gorillas; unhabituated gorillas; local cattle and goats. *shows the network position, contacts and microbiomes of the 100 surveyed people for metadata. Coloured icons show the hosts for which microbiome data are currently available in C.