MATTHEW J. MICHALSKA-SMITH

Dept. of Veterinary Population Medicine
1988 Fitch Ave
Saint Paul, MN 55108
E-mail: michalsm@umn.edu

February 11, 2020

Dear Dr. Åsa Langefors,

Please find enclosed the manuscript "Multi-strain disease dynamics on metapopulation networks" which we would like to have considered for publication in *Oikos* as a research article. In this work, we produce a novel mathematical framework bringing together two established areas of ecological theory: multi-strain disease dynamics and metapopulation movement networks.

Strain structure is ubiquitous among the most widespread diseases in the world today, and has been the subject of extensive epidemiological research over the past decades. Likewise, there has been extensive research on networks of interconnected populations, termed metapopulations, especially within the ecological literature. Surprisingly, however, there have been few attempts to link these two areas of research, despite a need for better understanding and control of pathogen spread in fragmented or disconnected habitats.

Utilizing an extensive simulation-based approach, we explore several small "building-block" network structures and show that there can be dramatic effects on the temporal dynamics of pathogen prevalence when migration is allowed between populations. Our analysis evinces some surprisingly simple and consistent patterns relating the dynamics of origin and destination populations. We additionally perform simulations to explore larger networks which can be thought of as composites of many smaller structures. In summary, we find that, when populations are linked, the dynamics of destination populations are significantly influenced by the dynamics of origin populations, with migration having the potential to reduce disease prevalence or even change the dynamical regime in the desitnation population. Generalizing to larger networks, we see a significant effect of network structure on total disease prevalence as well, with more heterogeneity in degree (the number of other populations a given population is connected to) leading to increased prevalence and decreased immunity in the metapopulation as a whole.

We believe that our work will instigate further research into the structures of real-world metapopulations, and, in particular the role of network structure on endemic disease dynamics. This framework will prove especially useful to researchers of systems with high migration rates, such as in the context of mobile species in fragmented landscapes or the movements of livestock between growing facilities, but we trust the generality of our theoretical approach will prove interesting across the broad readership of *Oikos*. Moreover, we hope our synthesis of metapopulation and multi-strain theoretical frameworks will help to foster further integration between members of these two fields.

Thank you for the attention dedicated to our work.

Sincerely,

Matthew J. Michalska-Smith, Kimberly VanderWaal,
Montserrat Torremorell, Cesar Corzo,
and Meggan E Craft