# Niche partitioning and differential transmission of infectious agents

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The transmission potential of an infection, usually measured *via* the basic reproduction ratio $R_0$, is determined by three main factors: (i) duration of latent and infective periods (ii) probability of interaction (relevant to the transmission pathway) between an infective and a susceptible and (iii) probability of transmission when such interaction occurs. While (i) and (ii) can be determined experimentally and through behavioural observations, (iii) is difficult to establish by direct means and is typically estimated *via* mathematical modelling and observable data, e.g. infection prevalence. A common assumption in such procedures is that the transmissibility of infection is constant across physiologically similar hosts and minor variations of the infective agent. This assumption is not always true. For example, the results in [1] revealed that despite physiological similarities between hosts the transmissibility of the *Bartonella* bacterium differed markedly. In this study we investigate how different variants of the same infectious agent may have differential transmissibility, and therefore variable transmission potential, due to niche partitioning within the host.

In the field of medical infectious disease research there are numerous of examples of pathogens that display tissue tropism, analogous to the ecological concept of niche partitioning. These include HIV, a viral agent that is transmitted horizontally (either sexually or through blood) and *Trypanosoma cruzi*, the vector-borne agent for Chagas disease which may be transmitted horizontally (eg. through blood transfusions) or congenitally, with the vertically transmitted pathogen persisting after child birth. Here we consider infectious diseases of animals for which there is some evidence of tissue tropism, and devise a preliminary mathematical model to investigate the downstream effects of niche partitioning on pathogen transmission.

## References

[1] H Brettschneider, R Anguelov, CT Chimimba, A Bastos, A mathematical epidemiological model of gram-negative Bartonella bacteria: does differential ectoparasite load fully explain the differences in infection prevalence of Rattus rattus and Rattus norvegicus?, Journal of Biological Dynamics Vol. 6(2) (2012), 763-781