THESIS INTRODUCTION

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1. ABSTRACT

ABSTRACT. Pathogens make up a huge proportion of global diversity and their role in disease strongly affects human disease, economics and development as well as having an important ecological role. However, the factors that control the number of pathogen species are poorly understood.

The patterns of contacts between individuals — in both human and animal populations — are nonrandom and depend on the density of individuals. Population structure and density have important epidemiological consequences, but their role in the control of pathogen richness is unknown.

It is still unknown whether population structure and density controls pathogen richness in bats. Furthermore, the specific mechanisms by which structure might influence pathogen richness have not been studied.

In this thesis I have studied how population structure and density control pathogen richness using bats as a case study. I have used epidemiological simulations and comparative analyses of data from wild bat populations to show that population structure does not have a strong affect on pathogen richness. Using further simulations I have shown that the interaction between population density and population structure is an important consideration. Finally, I have created a model for estimating bat densities — previously an incredibly challenging task — using acoustic data. Together, these studies clarify the relative roles of population density and structure and facilitate further study of population density in bats as a driver of pathogen richness.

While theory previously predicted that population structure should increase pathogen richness, the expectation in the ecological literature was that population structure would decrease pathogen richness. My studies support neither of these views, instead suggesting that population structure does not have a strong affect in either direction.

2. INTRODUCTION

Some stuff about things. Some more things.

The diversity of pathogens is huge and largely unknown. Recent large studies have found tens (**anthony2013strategy**) or even hundreds of virus species in a single host species (**anthony2015non**). This suggests the number of mammalian viruses globally is of the order of hundreds of thousands of virus species (**anthony2013strategy**) while only three thousand species in total are currently described (**ICTV**).

Number of known zoonotic viruses/pathogens. Number of known from mammals. Examples of mortality rates and examples of scale of outbreaks.

Some outbreaks caused by bats. Number of known bat viruses, known bat zoonoses.

Bats are second largest order of mammals. Long lived, social and fly.

It is still not clear whether bats harbour more virus species that other well studies mammallian orders (**luis2013comparison**; **olival2015bats**).

However the factors that control pathogen richness are still unclear. Whether bats are unusual in their pathogen richness and zoonotic potential is still unclear (**luis2013comparison**; **olival2015bats**). And if they unusual, the specific factors that drive this are also not well understood (**luis2013comparison**; **wang2011mass**; **o2014bat**; **dobson2005links**)

3. Specific intro

3.1. **Pathogen richness.** Define. Simple count of pathogens across whole species. Ignores heterogeneity in prevalence, across space and time.

4. Thesis overview