

The role of social ecology in Chiropteran pathogen richness and zoonotic potential

Tim C. D. Lucas

A thesis submitted in partial fulfilment of the
requirements for the degree of:

*Doctor of Philosophy of
University College London – Centre for Mathematics and
Physics in the Life Sciences and Experimental Biology*

2015

Primary supervisor:

Prof. Kate E. Jones

Secondary supervisor:

Dr Hilde Herbots

*I, Tim C. D. Lucas, confirm that the work presented in this thesis is my own.
Where information has been derived from other sources, I confirm that this has
been indicated in the thesis.*

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.

Acknowledgements

Acknowledge all the things!

Contents

Contents	9
List of Figures	13
List of Tables	15
1 Introductory Material	17
1.1 General intro	18
1.2 Specific intro	18
1.2.1 Pathogen richness	18
2 Does network structure of bat populations promote viral diversity? 19	
2.1 Abstract	20
2.2 Introduction	21
2.2.1 General Intro	21
2.2.2 Specific Intro	21
2.2.3 The gap	24
2.2.4 What I did	25
2.2.5 What I found	25
2.3 Methods	26
2.3.1 Metapopulation model	26
2.3.2 Dispersal	29
2.3.3 Network structure	29
2.3.4 Parameter selection	30
2.4 Results	31
2.4.1 Invasion	31
2.4.2 Transmission	31
2.5 Discussion	33

2.5.1	Restate the gap and the main result	33
2.5.2	Link results to consequences	33
2.5.3	Discuss assumptions	34
2.6	Appendix	35
3	Does ecological and epidemiological seasonality promote viral diversity?	37
3.1	Abstract	38
3.2	Introduction	38
3.2.1	General Intro	38
3.2.2	Specific Intro	39
3.2.3	Theoretical background	39
3.2.4	Previous Studies	39
3.2.5	Rates	40
3.2.6	Choice of measure of population structure	40
3.2.7	The gap	41
3.2.8	What I did	41
3.2.9	What I found	41
3.3	Methods	41
3.3.1	Statistical analysis	44
3.4	Results	45
3.4.1	Number of Subspecies	45
3.4.2	Gene Flow	46
3.5	Discussion	49
3.6	Appendix	50
4	Does social structure affect viral diversity in wild bat populations?	51
4.1	Abstract	52
4.2	Introduction	53
4.2.1	General Intro	53
4.2.2	Specific Intro	53
4.2.3	The gap	53
4.2.4	What I did	53
4.2.5	What I found	53
4.3	Methods	54
4.3.1	Metapopulation model	54
4.3.2	Dispersal	56

4.3.3	Network structure	56
4.3.4	Parameter selection	57
4.4	Results	58
5	gREM for estimating animal density	59
5.1	Abstract	60
5.2	Introduction	60
5.3	Methods	63
5.3.1	Analytical Model	63
5.3.2	Simulation Model	67
5.4	Results	69
5.4.1	Analytical model	69
5.4.2	Simulation model	70
5.5	Discussion	72
5.5.1	Analytical model	72
5.5.2	Accuracy, Precision and Recommendations for Best Practice	74
5.5.3	Limitations	75
5.5.4	Implications for ecology and conservation	76
5.6	Data Accessibility	76
6	General Conclusions	77
	Appendices	79
A	gREM Appendix	79
A.1	Table of symbols	80
A.2	Supplementary Methods	81
A.2.1	Introduction	81
A.2.2	Gas model	81
A.2.3	Model SE1	83
A.2.4	Models NE1–3	83
A.2.5	Models SE2–4	86
A.2.6	Model NW1	88
A.2.7	Models NW2–4	89
A.2.8	Model REM	91
A.2.9	Models NW5–7	92
A.2.10	Model SW1–3	94
A.2.11	Model SW4–9	97

12 CONTENTS

A.3	Supplementary Information: Simulation model results of the gREM precision	101
A.4	Supplementary Information: Impact of parameter error	102
B	Colophon	103
	Bibliography	105

List of Figures

2.1	Schematic of the SIR model used	27
2.2	Network topologies used to compare network connectedness	29
2.3	The probability of invasion across different dispersal rates and network topologies.	32
3.1	Pruned phylogeny with dot size showing number of pathogens and colour showing family	42
3.2	Number of virus species against number of subspecies	43
3.3	Gene flow per generation (on a log scale) against viral richness with the genetic marker used shown with colour	43
3.4	Akaika variable weights for F_{ST} analysis.	44
4.1	The SIR model used.	55
5.1	Representation of sensor detection width and animal signal width . .	63
5.2	Locations where derivation of the average profile \bar{p} is the same	65
5.3	An overview of the derivation of the average profile \bar{p} for the gREM submodel SE2	66
5.4	Expressions for the average profile width	70
5.5	Simulation model results of the accuracy and precision for gREM submodels	71
5.6	Simulation model results of the accuracy and precision of four gREM submodels	72
5.7	Simulation model results of the accuracy and precision of four gREM submodels	73
A.1	The location of the focal angles $x_{i \in [1,4]}$	82
A.2	Three of the integrals in NE models	84
A.3	The second integral in SE	84

14 LIST OF FIGURES

A.4	The second and fourth profiles of NW1	88
A.5	Profile sizes when an animal approaches from behind in models NW2– 4	90
A.6	The first profile in SW models	95
A.7	Description of two profiles in SW models	98
A.1	gREM precision given a range of sensor and signal widths	101
A.2	Model sensitivity to error in parameter estimates	102

List of Tables

2.1	All symbols used.	35
3.1	Estimated variable weights and coefficients	47
3.2	Model selection results for number of subspecies analysis	47
3.3	Model selection results for gene flow analysis	48
A.1	List of symbols used to describe the gREM and simulations	80

1 Introductory Material

Some stuff about things. Some more things. Lorem ipsum dolor sit amet, consectetur adipiscing elit. Etiam lobortis facilisis sem. Nullam nec mi et neque pharetra sollicitudin. Praesent imperdiet mi nec ante. Donec ullamcorper, felis non sodales commodo, lectus velit ultrices augue, a dignissim nibh lectus placerat pede. Vivamus nunc nunc, molestie ut, ultricies vel, semper in, velit. Ut porttitor. Praesent in sapien. Lorem ipsum dolor sit amet, consectetur adipiscing elit. Duis fringilla tristique neque. Sed interdum libero ut metus. Pellentesque placerat. Nam rutrum augue a leo. Morbi sed elit sit amet ante lobortis sollicitudin. Praesent blandit blandit mauris. Praesent lectus tellus, aliquet aliquam, luctus a, egestas a, turpis. Mauris lacinia lorem sit amet ipsum. Nunc quis urna dictum turpis accumsan semper.

1.1 General intro

Total mammalian viral diversity. Known mammal viruses?

Bit about how to search for viruses? Deep pcr etc.

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.

1.2 Specific intro

1.2.1 Pathogen richness

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

2 Does network structure of bat populations promote viral diversity?

2.1 Abstract

An increasingly large fraction of emerging diseases come from wild animals and these diseases have a huge impact on human health, healthcare systems and economic development. The chance that a new zoonosis will come from any particular wild host species increases with the diversity of pathogens in that species. However, the factors that control pathogen diversity in wild populations are still unclear.

Host species traits such as population density, longevity, body size and population structure have been shown to correlate with pathogen diversity. Typically it is assumed that well-connected, unstructured populations promote the invasion of new pathogens and therefore increase pathogen diversity. However, this assumption is largely untested; in particular our mechanistic understanding of how population structure affects pathogen diversity, in the presence of inter-pathogen competition, is poor. Greater understanding is needed to clarify exactly by which mechanisms population structure affects pathogen diversity.

It is unknown whether population structure allows invading pathogens to escape from competition by stochastically creating areas of low pathogen prevalence. I hypothesise that low dispersal rates and a low number of connections in a metapopulation network will allow invading pathogens to establish more readily, thus increasing pathogen diversity. I test these hypotheses using population networks parameterised to mimic wild bat populations as bats have highly varied social structures and have recently been implicated in a number of high profile diseases such as Ebola, SARS, Hendra and Nipah.

I find that neither population connectedness nor dispersal rate affect the probability that a new pathogen will invade into a population. The assumption that factors causing high R_0 allow new pathogens to invade and therefore increase pathogen diversity is not supported. Instead we find that changes in population structure do not affect the probability of invasion of a new pathogen.

This result implies that population structure does not control pathogen diversity. Instead it seems that local dynamics, that affect the short term branching process at the very start of the epidemic control the chance of pathogen invasion. This also implies that population structure is not a useful proxy for pathogen diversity with respect to zoonotic disease surveillance, for example in bats.

2.2 Introduction

2.2.1 General Intro

The diversity of pathogens in a wild animal species strongly affects the chance that a disease from that species will infect humans. As over 50% of emerging infectious diseases have an animal source (Jones et al. 2008; Smith et al. 2014), understanding and predicting this process is a global health priority (Taylor, Latham, & Mark 2001). However, the factors that control the diversity of pathogens in a wild animal population are still unclear (Metcalf et al. 2015).

2.2.2 Specific Intro

A number of host traits have been shown to correlate with pathogen richness including body size (Kamiya et al. 2014; Arneberg 2002), population density (Nunn et al. 2003; Arneberg 2002) and range size (Bordes & Morand 2011; Kamiya et al. 2014).

However, empirical, correlative studies are often contradictory due to small sample sizes, noisy data and because empirical relationships often do not generalise across taxa (though see (Kamiya et al. 2014) for a meta-analysis). Furthermore, the correlation between many traits (e.g. (Nunn et al. 2015)) makes it hard to clearly distinguish which factors are important. Knowing the factors that correlate with pathogen richness also does not tell us how it controls richness. Mechanisms by which a trait could increase pathogen diversity include promoting the evolution of new strains within a species (Buckee et al. 2004), reduction of the rate of parasite extinction and an increased probability of pathogen invasion from other host species. These separate mechanisms have not been examined and it is difficult to see how they could be approached through comparative methods. We need explicit mechanistic models in order to tease apart these factors.

One host-species trait that has been largely understudied with respect to pathogen diversity is population structure. Population structure has been comprehensively studied with respect to single or competing epidemics in human populations, wildlife populations and technological networks. With respect to single disease epidemics it is clear that changes in population structure that increase R_0 increase the chance of a disease spreading and persisting. However, the assumption that population structures that yield high R_0 will also give high pathogen diversity (Nunn et al. 2003) is unfounded.

The processes by which a single disease spreads through a population are very well studied. One commonly taken assumption is that factors that promote high disease spread automatically promotes high diversity. However, this ignores competitive mechanisms such as cross-immunity and depletion of susceptible hosts. A number of authors have demonstrated a competitive exclusion principle where only the most optimally spreading disease will survive when infection with one pathogen prevents infection with another pathogen (Bremermann & Thieme 1989; Martcheva & Li 2013; Ackleh & Allen 2003; Ackleh & Salceanu 2014; Turner & Garnett 2002). If competitive mechanisms are strong, pathogens in populations structured such that R_0 will be high will be able to easily out-compete invading pathogens. Only if competitive mechanisms are weak will high R_0 enable the invasion of new pathogens and allow higher pathogen diversity.

Competitive affects are likely to be more or less important depending on the mechanism by which pathogen diversity is created. Competition is likely to be very strong between a newly evolved strain and the existing strain of a pathogen. In this case, there is likely to be strong cross immunity between strains. In the case of pathogens invading from other hosts species, cross immunity is likely to be less strong due to the evolutionary distance between the new and endemic pathogens. However, competition could still occur as disease induced mortality of host individuals reduces host density which promotes pathogen persistence. Finally, it is unclear how competition would affect the persistence of pathogens once they are established, though it seems that cross immunity can keep a pathogen at a low prevalence in the population (e.g. monkey pox (Rimoin et al. 2010) and monkey malaria (Cox-Singh & Singh 2008)). This would make stochastic extinction more likely.

The important affects of population structure on single disease epidemic spread and competing epidemics shows the important role structure has on disease dynamics. We can therefore expect it to have an important role in the dynamics of multidisease systems as well.

Studies of the role of population structure on pathogen diversity have been in very simple systems. These have been so simple that empirical data cannot easily be applied to them to predict pathogen diversity of real wild animal populations. There is a need for models that can be carefully and fully explored, while still capturing the complexities of the real world.

Analytical models of well mixed have widely different outcomes: infinite pathogen diversity (May & Nowak 1994; Ackleh & Salceanu 2014) or competitive exclu-

sion have both been predicted (Ackleh & Allen 2003; Bremermann & Thieme 1989; Martcheva & Li 2013; Qiu et al. 2013; Allen, Kirupaharan, & Wilson 2004). When competitive exclusion occurs, population structure has sometimes been shown to allow coexistence (Qiu et al. 2013; Allen, Kirupaharan, & Wilson 2004; Nunes, da Gama, & Gomes 2006).

Competing epidemics, or two pathogens spreading at the same time in a population, is a well studied area (Poletto et al. 2013; Poletto et al. 2015; Karrer & Newman 2011). This area is related to the study of pathogen richness in that they indicate that dynamics of multiple pathogens in a population do depend on population structure. However, the results for short term epidemic competition do not directly transfer to the study of long term disease persistence which is the relative time scale when looking at zoonotic potential of a host species.

Few studies focus on bats, despite their role in recent zoonoses. Maganga *et al.* found that distribution fragmentation predicts viral richness (Maganga et al. 2014), but (Gay et al. 2014) finds the opposite relationship. While the data set in (Gay et al. 2014) is larger, the analysis in (Maganga et al. 2014) is much more focused on fragmentation.

Genetic correlates of population structure have also been used. Turmelle *et al.* (Turmelle & Olival 2009), in a small analysis, find that high F_{st} (i.e. a structured population) correlates with high richness. However, they do not account for the widely different spatial scales found in population structure studies, nor do they deal with the differences between F_{ST} , ϕ_{ST} and other measures appropriately.

How structured a population is can be defined in many ways on many scales. The most relevant scale is that of an epidemiological population. This is the population within which a pathogen can spread in an epidemiologically relevant time period (years or decades). It is therefore closely related to a population as defined by population genetics, but with movement defined on a shorter time scale.

The epidemiological contacts within the population can be examined at the individual level (as in contact network epidemiology) or larger scales. I consider the metapopulation network the most appropriate. Ignoring the metapopulation assumes a fully mixed population which is unlikely. Trying to study the contact network relies detailed individual level detail which is not available. Metapopulation models consider a network of small subpopulations. Within subpopulations, epidemiological contacts are fully mixed and relatively fast. Between subpopulations, epidemiological contacts are dependant on an underlying network structure and relatively slow. The network underlying the metapopulation is made

up of nodes representing the subpopulations, and edges which represent movement between subpopulations. Animals, and therefore infection, can only move between two subpopulations if they are connected by an edge.

There are two factors that affect how structured a population is, given this model framework. Firstly, dispersal is the rate at which individuals move between subpopulations. Secondly, the metapopulation network structure controls population structure. The simplest measure of how structured the network is the average number of edges each node has. In the extremes, all subpopulations could be either connected to all other subpopulations or only connected to one or two other subpopulations. However, other measures that take into account second-order structure in the network are also often used.

Bats (Order Chiroptera) have, over the last decade, become a focus for disease research (Calisher et al. 2006; Hughes et al. 2007). Recently they have been implicated in a number of high profile diseases such as Ebola, SARS, Hendra and Nipah (Calisher et al. 2006; Li et al. 2005).

A number of traits have been suggested as predisposing bats towards being reservoirs of zoonotic diseases: high sympatry (Luis et al. 2013), flight (Wang, Walker, & Poon 2011) and longevity (Wang, Walker, & Poon 2011).

Bats have an unusually large variety of social structures. Colony sizes range from 10 to 1 million (Jones et al. 2009). Many bats also have interesting seasonal behaviour such as migration (Richter & Cumming 2008; Fleming et al. 2003), hibernation, birth pulses and swarming behaviours.

2.2.3 The gap

We have very abstract, simplified models that predict zero or infinite diversity depending on specifics. These cannot be easily applied to real data. They also do not easily predict quantitative or even relative diversity as they often predict either zero or infinite diversity with nothing in between.

We need models that can quantitatively or at least relatively predict diversity in a populations. This requires a middle ground of model complexity.

There are no studies that directly model bat pathogen diversity.

Specifically we use these models to test the affects of population structure on the ability of a new pathogen to invade a population. We test two aspects of structure, dispersal rate and connectedness of the metapopulation network.

2.2.4 What I did

I have run epidemiological simulations based broadly on real-world bat populations. Although still simplified, the model is complex enough that if good measurements of bat populations could be found, simulations of the real world bat population could be run.

I have studied the invasion of new pathogens as a mechanisms for increasing pathogen richness. In particular I have focussed on studying the invasion of a newly evolved pathogen that is therefore identical in epidemiological parameters to the endemic pathogen. Furthermore, this close evolutionary relationship means that cross immunity is strong.

I have studied two metrics for population structure, dispersal rate and metapopulation network topology, to test for effects of population structure on pathogen richness.

2.2.5 What I found

Here I show that given the assumptions of a metapopulation, population structure does not affect the rate of invasion of new pathogens.

2.3 Methods

2.3.1 Metapopulation model

2.3.1.1 Two pathogen SIR model

I examine a multipathogen SIR model. This is a compartment model with individuals being classed as susceptible, infected or recovered with immunity (Figure ??). Susceptible individuals are counted in class S . There are three infected classes, I_1 , I_2 and I_{12} , being individuals infected with pathogen 1, pathogen 2 or both respectively. Recovered individuals, R , are immune to both pathogens, even if they have only been infected with one. Furthermore, recovery from one pathogen moves an individual straight into the recovered class, even if the individual is infected with both pathogen. This modelling choice allows the model to be easily expanded to include more than two pathogens. The assumption of immediate recovery from all other diseases is likely to be quite accurate for very closely related pathogens as is being studied here as once an acquired immune response is activated, all infections are likely to be cleared quickly.

The coinfection rate (the rate at which an infected individual is infected with a second pathogen) is adjusted compared to the infection rate by a factor α (i.e. $\alpha = 0.5$ means coinfection happens at half the rate of infections). Birth and death rates are assumed to be equal, $b = d$ (see Table ?? for a list of symbols used). The time scale of the simulations are set by setting $b = 0.05$ per year, yielding an average host generation time of 20 years.

2.3.1.2 Metapopulation

The population is divided into a number of subpopulations. This metapopulation is modelled as a network with subpopulations being nodes and dispersal between subpopulations being indicated by edges (Figure ??). Individuals within a subpopulation interact randomly so that the subpopulation is fully mixed. Dispersal between subpopulations occurs at a rate λ . Individuals can only disperse to subpopulations connected to theirs in the network. The rate of dispersal is not affected by the number of edges a subpopulation has (the degree of the subpopulation). So the dispersal rate from a subpopulation m with degree k_m to subpopulation n is $\frac{\lambda}{k_m}$. Note this rate is independent of the degree of subpopulation n .



Figure 2.1 Schematic of the SIR model used. Individuals are in one five classes, susceptible (orange, S), infectious with pathogen 1, pathogen 2 or both (blue, I_1, I_2, I_{12}) or recovered and immune from further infection (green, R). Transitions between classes occurs only as indicated by arrows. Note that individuals in I_{12} move into R, not back to I_1 or I_2 . That is, recovery from one pathogen causes immediate recovery from the other pathogen.

2.3.1.3 Stochastic simulations

I examine this model using stochastic, continuous time simulations using the Gillespie algorithm. At each step in the simulation we calculate the rate that each possible event might occur. One event is then randomly chosen, weighted by it's rate

$$p(\text{event } i) = \frac{r_i}{\sum_i r_i} \quad (2.1)$$

where r_i is the rate that event i occurs. Finally, the length of the time step, δ , is drawn from an exponential distribution

$$\delta \sim \text{Exp} \left(\sum_i r_i \right). \quad (2.2)$$

This means that the total length of each simulation is stochastic. We define the number of events we wish to simulate instead.

We can now write down the rates of all events. I define I_p^+ to be the sum of all classes that are infectious with pathogen p , for example $I_1^+ = I_1 + I_{12}$. Assuming asexual reproduction, that all classes reproduce at the same rate and that individuals are born into the susceptible class we get

$$P(S_{nt'} = S_{nt} + 1) = b \left(S_{nt} + \sum_q I_{qnt} + R_{nt} \right) \quad (2.3)$$

where $P(S_{nt'} = S_{nt} + 1)$ is the probability that the number of susceptibles in subpopulation n will increase by 1 (a single birth) in the time interval t to t' and

$\sum_q I_{qnt}$ is the sum of all infection classes $q \in 1, 2, 12$. The rates of death, given a death rate d are given by

$$P(S_{nt'} = S_{nt} - 1) = dS_{nt}, \quad (2.4)$$

$$P(I_{qnt'} = I_{qnt} - 1) = dI_{qnt}, \quad (2.5)$$

$$P(R_{nt'} = R_{nt} - 1) = dR_{nt}. \quad (2.6)$$

Infection of a susceptible with either pathogen 1 or 2, $S \rightarrow I_p$ where $p \in \{1, 2\}$, is given by

$$P(I_{pnt'} = I_{pnt} + 1, S_{nt'} = S_{nt} - 1) = \beta S_{nt} I_{pnt}^+, \quad (2.7)$$

while coinfection, given a crossimmunity factor α , is given by

$$P(I_{12,nt'} = I_{12,nt} + 1, I_{1nt'} = I_{1nt} - 1) = \alpha \beta I_{1nt} I_{2nt}^+, \quad (2.8)$$

$$P(I_{12,nt'} = I_{12,nt} + 1, I_{2nt'} = I_{2nt} - 1) = \alpha \beta I_{2nt} I_{1nt}^+. \quad (2.9)$$

The probability of migration from colony m (with degree k_m) to colony n , given a dispersal rate λ is given by

$$P(S_{nt'} = S_{nt} + 1, S_{mt'} = S_{mt} - 1) = \frac{\lambda S_{mt}}{k_m - 1}, \quad (2.10)$$

$$P(I_{qnt'} = I_{qnt} + 1, I_{qmt'} = I_{qmt} - 1) = \frac{\lambda I_{qmt}}{k_m - 1}, \quad (2.11)$$

$$P(R_{nt'} = S_{nt} + 1, R_{mt'} = R_{mt} - 1) = \frac{\lambda R_{mt}}{k_m - 1}. \quad (2.12)$$

Finally, recovery from any infectious class occurs at a rate γ

$$P(I_{qnt'} = I_{qnt} - 1, R_{nt'} = R_{nt} + 1) = \gamma I_{qnt}. \quad (2.13)$$

In each simulation the population was seeded with 10 sets of 200 infected individuals of disease 1. These groups were seeded into randomly selected colonies with replacement. For each 200 infected individuals added, 200 susceptible individuals were removed to keep starting colony sizes constant. Disease 1 was then allowed to spread and reach equilibrium. After 3×10^5 events, 5 individuals infected with disease 2 were added to one colony. Visual inspection of preliminary simulations was used to decide on 3×10^5 as being long enough for the epidemic to reach an equilibrium state. After another 5×10^5 events the invasion of disease 2 is considered successful if any individuals are still infected with pathogen 2. Again visual inspection of preliminary simulations was used to determine whether this was long enough to be confident that an invading disease

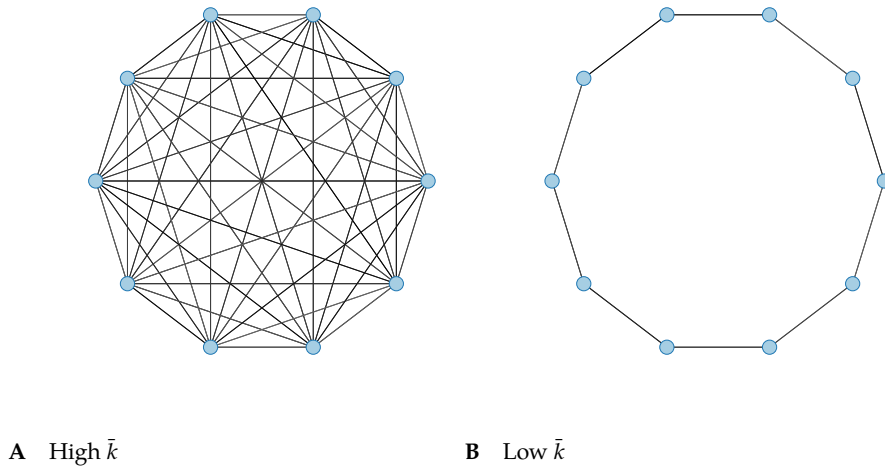


Figure 2.2 The two network topologies used to test whether network connectedness influences a viruses ability to invade. Blue circles are subpopulations of 3000 individuals. Dispersal only occurs between subpopulations connected by an edge (black line). The dispersal rate is held constant between the two topologies.

2.3.2 Dispersal

The values used for the independent variables are chosen to highlight the affects of these variables. Dispersal values are $\lambda = 0.1, 0.01$ and 0.001 dispersals per individual per year. $\lambda = 0.1$ relates to individuals moving between colonies on average twice per lifetime. Therefore exclusively juvenile dispersal would have dispersal rates similar to this. Otherwise it relates to dispersal being a rare event with animals often staying in a colony for many years. $\lambda = 0.01$ relates to 20% of individuals dispersing once in their lifetime. This value is therefore close to male-biased dispersal, with female philopatry. Finally, $\lambda = 0.001$ relates to 2% of individuals dispersing in their lifetime. This therefore relates to a population that does not habitually disperse.

2.3.3 Network structure

The network structure is synthetically created to be either fully or minimally connected (See Figure ??). 10 subpopulations was selected as a trade off between computation time and a network complicated enough that structure might have an effect. This value is artificially small compared to wildlife populations.

2.3.4 Parameter selection

The fixed parameters used are chosen to roughly reflect realistic wild bat populations. The death rate d is set as 0.05 per year giving a generation time of 20 years. The birth rate b is set to be equal to d so that the population size is stable. The recovery rate γ is set to 1 giving a average infection duration of 1 years. This is therefore a long lasting infection but not a chronic infection. It is very difficult to directly estimate infection durations in wild populations. But it seems that these infections might be long lasting ().

Cross immunity is set to 0.1 so that an individual infected with one disease is 90% less likely to be infected with another. This is a rather arbitrary value. However, the rationale of the model is that the invading species might be a newly speciated strain of the endemic species. Furthermore, the model assumes complete cross immunity after infection. Therefore cross immunity is likely to be very strong.

The population size of each subpopulation is set to 3000. This is appropriate for many bat species (Jones et al. 2009), especially the large, frugivorous *Pteropodidae* that have been particularly associated with recent zoonotic diseases.

Four values of the transmission rate β are used, 0.1, 0.2, 0.3 and 0.4. All simulations are run under all four transmission rates as this is such a fundamental parameter. Given the recovery, birth and death rates we can calculate an approximation of R_0 that ignores spatial structure. That is, this is R_0 for the local, within-subpopulation dynamics. Furthermore, it is R_0 for the first pathogen; R_0 of the invading pathogen will be lower due to competition. We can calculate that $R_0 \approx \frac{\beta b}{d(d+\gamma)}$. For our four values of $\beta = 0.1, 0.2, 0.3, 0.4$ we therefore get $R_0 \approx 13.3, 33.3, 66.6$. These values are very high in part to again find a reasonable trade off between the number of simulations and the reasonableness of the parameters. $R_0 \approx 13.3$ is similar to a highly contagious disease such as measles or pertussis.

For the simulations where an invading pathogen is added to the populations the number of invading pathogens added is set to 10. This is a trade off between getting a reasonable proportion of invasions, while still retaining the stochastic nature of invasion.

2.4 Results

2.4.1 Invasion

2.4.1.1 Dispersal

The proportion of invasions was not different across dispersal rates across 1.2×10^3 simulations run (Figure ??). This was true at all transmission levels (χ^2 test. $\beta = 0.1$: $\chi^2 = 1.98$, $df = 2$, $p = 0.37$. $\beta = 0.2$: $\chi^2 = 9.44$, $df = 2$, $p = 8.9 \times 10^{-3}$. $\beta = 0.3$: $\chi^2 = 0.29$, $df = 2$, $p = 0.87$, $\beta = 0.4$: $\chi^2 = 0.83$, $df = 2$, $p = 0.66$).

2.4.1.2 Network structure

I ran 800 simulations over 4 transmission values ($\beta = 0.1, 0.2, 0.3, 0.4$). The proportion of invasions was not different between highly connected and largely unconnected metapopulations (Figure ??). This was true at all transmission levels (χ^2 test. $\beta = 0.1$: $\chi^2 = 5.23 \times 10^{-31}$, $df = 1$, $p = 1$. $\beta = 0.2$: $\chi^2 = 0.02$, $df = 1$, $p = 0.88$. $\beta = 0.3$: $\chi^2 = 1.53$, $df = 1$, $p = 0.22$. $\beta = 0.4$: $\chi^2 = 0.26$, $df = 1$, $p = 0.61$).

2.4.2 Transmission

Inline with theory, increasing the transmission rate increased the probability of invasion (Figure ??–??). This is true for all three dispersal values (χ^2 test. $\lambda = 0.001$: $\chi^2 = 243.56$, $df = 3$, $p = 1.62 \times 10^{-52}$. $\lambda = 0.01$: $\chi^2 = 265.4$, $df = 3$, $p = 3.05 \times 10^{-57}$. $\lambda = 0.1$: $\chi^2 = 244.95$, $df = 3$, $p = 8.1 \times 10^{-53}$) and both network structures (χ^2 test. Fully connected: $\chi^2 = 267.3$, $df = 3$, $p = 1.18 \times 10^{-57}$. Minimally connected: $\chi^2 = 267.3$, $df = 3$, $p = 1.18 \times 10^{-57}$).

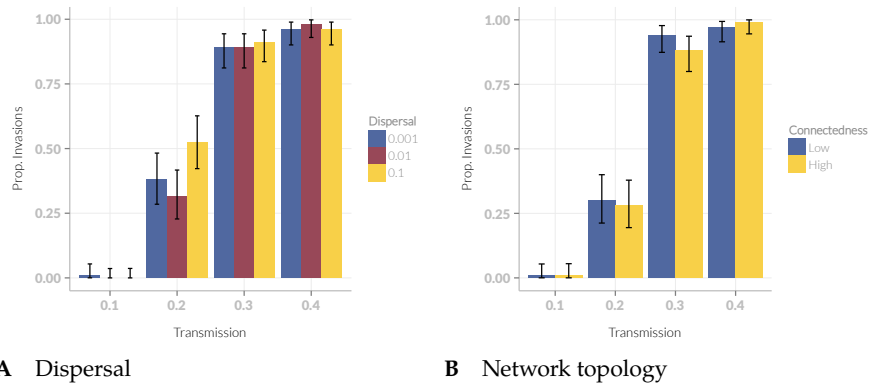


Figure 2.3 The probability of successful invasion. For three different transmission rates, the probability of invasion does not change between different a) dispersal rates or b) network structures. Error bars are 95% confidence intervals. 100 simulations were run for each treatment. Other parameters are kept constant at: $N = 10$, $b = d = 0.05$, $\gamma = 0.1$, $\alpha = 0.1$. When dispersal is varied, the population structure is fully connected. When population structure is varied, $\lambda = 0.01$.

2.5 Discussion

2.5.1 Restate the gap and the main result

Empirical studies on the role of population structure on pathogen richness are equivocal and cannot examine the specific mechanisms by which pathogen communities are created and maintained. I have used mechanistic, metapopulation models to test whether increased population structure can promote pathogen richness by facilitating invasion of new pathogens. I find that population structure does not affect the ability of a new pathogen to invade and persist in a population. Instead I find that only transmission rate affects the chance of pathogen invasion.

2.5.2 Link results to consequences

Given that we find no affect of population structure on the ability of a new pathogen to invade, this host-trait is not a useful host trait for predicting the probability that a wild species has many pathogens. This means it cannot be used as a proxy for the probability that a species carries a zoonotic pathogen.

However my simulations do highlight the importance of competition for the spread of a new pathogen. All parameters used correspong to pathogens with $R_0 > 1$. However, the competition with the endemic pathogen means that for some transmission rates the chance of epidemic spread and persistence is close to zero. This has implications for human epidemics as well — if there is strong competiton between a newly evolved strain and an endemicstrain, we ar3 unlikely to see the new strain spread, irregardless of population structure.

2.5.2.1 Population structure does not affect pathogen richness

Probably because dynamics are dominated by local processes. This goes against many predictions that increasing R_0 increases pathogen richness. Further work could examine reduced col ony sizes to test when global structure become more important. Measures of population structure should not be used to predict zoonotic potential.

2.5.2.2 Dispersal does not affect pathogen richness

Irrespective of the network topology used, at very high dispersal rates a population will be well mixed.

2.5.2.3 Network connectedness does not affect pathogen richness

This is in direct contrast to (Campos & Gordo 2006). However, the model in (Campos & Gordo 2006) is a contact network, so increasing the connectedness increases the chance of successful transmission events for the first few transmission generations. This lends support to the idea that I found no affect of connectedness due to the dominance of local dynamics.

2.5.3 Discuss assumptions

2.5.3.1 Complete cross-immunity

I have assumed that once recovered, individuals are immune to both pathogens. Furthermore, when a coinfecting individual recovers from one pathogen, it immediately recovers from the other as well. This is probably a fairly reasonable assumption given that I am modelling a newly evolved strain. However, further work could relax this assumption using a model similar to (Poletto et al. 2015) which contains additional classes for ‘infected with pathogen one, immune to pathogen two’ and ‘infected with pathogen two, immune to pathogen one’. The model here was formulated such that the study of systems with greater than two pathogens is still computationally feasible while a model such as used in (Poletto et al. 2015) contains 3^ρ classes for a system with ρ pathogen species. This quickly becomes computationally restrictive.

2.5.3.2 Identical strains

Many papers on pathogen richness have focussed on the evolution of pathogen traits and have considered a trade off between transmission rate and virulence (Nowak & May 1994; Nowak & May 1994) or infectious period (Poletto et al. 2013). However, here I am interested in host traits. Therefore we have assumed that pathogen strains are identical. It is clear however that there are a number of factors that affect pathogen richness and our focus on host population structure does not imply that pathogen traits are not important.