

Environmental pathogen reservoirs and habitat heterogeneity in a metapopulation

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1 Introduction

Many wildlife diseases are caused by pathogens that can persist, and remain infectious, for long periods of time in the environment. Examples include chronic wasting disease (Miller et al (2006)), anthrax (Dragon and Rennie (1995)), plague (Eisen et al (2008)), and white nose syndrome (Lindner et al (2011)), among others. This environmental persistence creates environmental pathogen reservoirs from which hosts can become infected without direct contact with an infected individual. This additional transmission pathway can have important consequences for disease dynamics, especially in spatially structured populations (?).

Patterns and rates of host movement also play an important role in pathogen spread through a metapopulation. As shown by Hess (1996), for pathogens spread by direct contact alone, increased host movement enhances pathogen spread through a metapopulation. Further studies by Gog et al (2002) and McCallum and Dobson (2002) explore the role of additional transmission pathways by including background infection from an alternate host, while ? includes transmission from an environmental reservoir. These studies show that the effect of host movement on occupancy (and pathogen spread) depends on the relative strength of the different transmission pathways and highlight the potential for patterns of host movement and pathways of pathogen transmission to interact and influence disease dynamics.

However, the above studies assume that all patches in the metapopulation are identical, and consider movement only at the metapopulation scale. Since environmental transmission is spatially explicit (i.e. environmental reservoirs can only infect residents of the local patch), its role in disease dynamics may depend on the attributes of the specific habitat patches in which reservoirs become established. In particular, the quality of a habitat patch can affect its extinction and colonization probabilities, as well as its contribution to the colonization of other empty patches (Moilanen and Hanski (1998)). As an example, in a study of the Glanville fritillary butterfly metapopulation, Moilanen and Hanski (1998) found that increased patch quality, as measured by the density of flowering plants, decreased emigration and increased immigration. Thus, patterns of host movement, and consequently the

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role of environmental pathogen transmission, are determined at least in part by patch quality.

Many of the pathogens listed above affect spatially structured host populations (e.g. plague in prairie dog colonies), and thus understanding the consequences of environmental pathogen persistence and habitat quality for pathogen spread is critical to managing disease in these systems. In this study, we ask how pathogen longevity (how long the pathogen can persist and remain infectious in the environment), and habitat heterogeneity (the variance in the distribution of patch quality across the metapopulation) interact to influence pathogen spread through the metapopulation. Within a metapopulation, we ask what specific role low and high quality patches play in controlling pathogen spread.

We expect pathogen spread to increase with both environmental longevity and with habitat heterogeneity. Increased environmental longevity should provide greater opportunities for transmission, and thus should favor pathogen spread. The role of habitat heterogeneity is likely to be more complex, emerging from the behavior of high and low quality patches in heterogeneous metapopulations. Specifically, we expect that high quality habitat patches, which support greater host traffic than lower quality habitat, might be more likely to form pathogen reservoirs. As these reservoirs are undetectable to the host, we predict that high quality patches will continue to attract – and infect – susceptible immigrants, effectively creating an ecological trap (citations, examples?). In addition, the greater traffic through high quality patches may further facilitate pathogen spread by positioning high quality patches as metapopulation-scale superspreaders (citation). Similarly, we predict that low quality patches, which see relatively less host traffic, will be less likely to develop pathogen reservoirs and thus may serve as refuges for susceptible hosts to escape infection.

To address the above questions and evaluate our hypotheses, we build on the metapopulation framework developed by Hanski (1994) to develop and explore a theoretical stochastic patch occupancy model that incorporates pathogen transmission from environmental reservoirs and habitat heterogeneity.

2 Methods

2.1 Model Structure

To address the above questions, we developed a theoretical stochastic patch occupancy model (SPOM) in which each patch can be in one of four possible states: occupied by susceptibles (S), occupied by infecteds (I), pathogen reservoir without host population (Z), and unoccupied (by both pathogen and host) (\emptyset). State transitions are governed by host colonization, extinction, and infection rates, where a susceptible population can become infected either through direct contact with infected immigrants, or through a local pathogen reservoir.

Building on the framework developed by Hanski (1994), the rate at which patch i , with quality A_i , is colonized by individuals in state $X \in (S, I)$ is given by its connectivity:

$$C_{Xi} = A_i^{\xi_{im}} \sum_{j \neq i} \phi_j A_j^{\xi_{em}} e^{-Dd_{ij}}, \quad (1)$$

where ϕ_j is an indicator function that is 1 if patch j is in state X and is 0 otherwise; ξ_{im} and ξ_{em} control how rates of immigration and emigration, respectively, scale with patch quality; D is the inverse of mean dispersal distance; and d_{ij} is the distance between patches i and j . Essentially, C_{Xi} sums the colonization effort from all patches in state X to patch i .

The extinction rate of patch i in state X is given by:

$$E_{Xi} = \frac{e_X}{A_i^\alpha}, \quad (2)$$

where e_X is the extinction rate of a patch of unit quality in state X (here we assume that $e_I > e_S$). When an infected patch goes extinct, we assume that the infected hosts leave behind an infectious pathogen reservoir.

Susceptible populations are infected via direct contact with infected colonists at rate δC_{Ii} , where δ is the transmission probability. Environmental transmission occurs when a susceptible population occupies a reservoir patch, and occurs at rate:

$$\gamma = \gamma_0 \exp(-rt_I), \quad (3)$$

where γ_0 is the initial infection rate of the pathogen reservoir, t_I is the time since last infected occupancy, and r is the pathogen's decay rate in the environment.

Table 1 Parameters of SPOM model and their meanings.

Parameter	Interpretation	Default Value
ξ_{im}	Scaling parameter for effect of target patch quality on immigration	0.5
ξ_{em}	Scaling parameter for effect of target patch quality in emigration	0.5
D	Inverse of mean dispersal distance	5
d_{ij}	Distance between patch i and j	1 for all i, j
e_S	Extinction rate of unit quality susceptible patch	0.1
e_I	Extinction rate of unity quality infected patch	0.5
α	Strength of environmental stochasticity	1
δ	Probability of direct infection	0.5
γ_0	Initial rate of infection from reservoir patch	0.5

2.2 Model Implementation and Analysis

The model outlined above was parameterized (Table 1) according to the following assumptions. (1) High quality patches maintain higher population sizes and therefore produce more colonists than low quality patches and have lower extinction rates than low quality patches ($\xi_{im} = 0.5$, $\alpha = 1$, Hanski and Ovaskainen (2003)). (2) High quality patches attract more colonists than low quality patches ($\xi_{em} = 0.5$, Hanski and Ovaskainen (2003)). (3) Connectivity is determined entirely by quality ($d_{ij} = 1$). In addition to these assumptions, parameters were chosen so that without infection, approximately 0.75 of the metapopulation was occupied ($e_S = 0.1$, $D = 5$), and a range of epidemiological behaviors were feasible ($e_I = 0.5$, $\delta = 0.5$, $\gamma_0 = 0.5$).

With the above parameters fixed, we explored the effects of pathogen environmental persistence and habitat heterogeneity by varying pathogen longevity

(10 values from 20 to 200 time steps, with values representing the half-life of the pathogen's infectivity), and the variance of the patch quality distribution (10 values ranging from 0.02 to 0.2). For each simulation (100 replicates for each of the 100 longevity-variance combinations), qualities for 100 patches were drawn from a uniform distribution with mean 1 and given variance. In each case, an entirely susceptible population was simulated until it reached a steady state, at which point a randomly chosen occupied patch was infected. The state of the metapopulation was then tracked for 5000 time steps. To address the metapopulation-level questions above, we recorded the proportion of patches in each state at the end of each simulation and classified the simulation as host extinction, disease-free (no infected populations after 5000 time steps), endemic (both susceptible and infected populations present), or pandemic (only infected populations). In addition, to address patch-level questions, for every simulation, we recorded the quality of each patch and the proportion of time spent in each of the four states.

In the above simulations, the mean of the patch quality distribution was held constant, and thus the range was expanded symmetrically about one as the variance was increased. To further parse out the relative roles of high and low quality patches, we performed a series of simulations where we expanded the range of the quality distribution non-symmetrically to include high and low quality patches separately. For these simulations, we fixed longevity at an intermediate level (100) and ran 100 replicates for each of four patch quality distributions: low variance, (range 0.75 to 1.25); intermediate variance, high quality (range 0.75 to 1.75); intermediate variance, low quality (range 0.25 to 1.25); and high variance (range 0.25 to 1.75).

Continuous time stochastic simulations of the above model were implemented in the R language (citation) using the Gillespie algorithm (Gillespie (1977)). Code is available at <https://github.com/clint-leach/Metapop-Disease>.

3 Results

The pathogen persisted in 7087 of the 10000 simulations, spreading through the entire susceptible host population (i.e. a pandemic) in 3721 simulations. Pathogen persistence increased substantially with longevity, with intermediate longevities favoring endemic disease, and high longevities facilitating pandemic dynamics (Fig 1). The effect of longevity, however, depended on the variance of the patch quality distribution, with low variance metapopulations favoring endemic dynamics for a wider range of longevities (Fig 1a), and high variance metapopulations lowering the longevity required for pandemic dynamics (Fig 1b).

To separate the influence of high and low quality patches, we explored how susceptible and infected patch occupancy changes when high and low quality patches are included separately in the patch quality distribution. Relative to a low-variance metapopulation (patch qualities roughly between 0.75 and 1.25), shifting the distribution toward low quality patches (distribution ranging from 0.25 to 1.25) increased mean susceptible occupancy, while shifting towards high quality patches (range from 0.75 to 1.75) decreased mean susceptible occupancy, with the largest effects observed at intermediate longevities (Fig 2(a)). Conversely, a shift towards low quality patches decreased infected occupancy, while a shift towards high quality patches increased infected occupancy (Fig 2(b)).

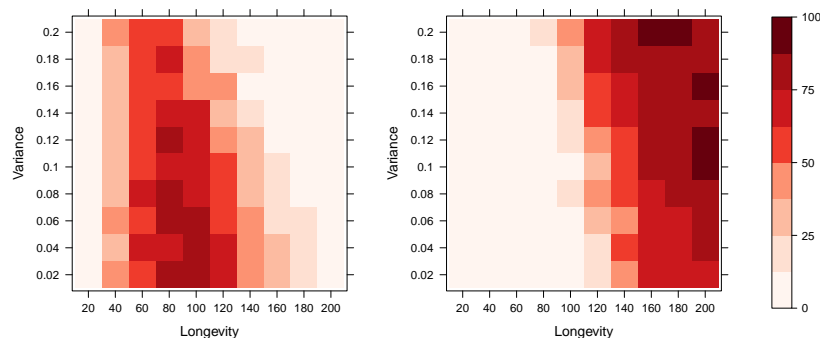


Fig. 1 Percent of simulations resulting in (a) endemic disease (both susceptibles and infecteds persist) and (b) pandemic disease (no susceptibles persist), as a function of the pathogen's environmental longevity (half-life of infectivity decay) and the variance of the patch quality distribution.

However, at high pathogen longevitys, high quality patch distributions had a net positive effect on total occupancy relative to the other patch quality distributions (Fig 2(c)). Due to their lower extinction rates, high quality patches are able to maintain stable occupancy despite widespread infection. On the other hand, at high pathogen longevitys, the positive effect of low quality distributions on susceptible occupancy is overwhelmed, and low quality patches are unable to support infected occupancy, resulting in an increase in host extinction events. Thus, the role of the patch quality distribution and the presence of high or low quality patches is generally greatest for low to intermediate pathogen longevity – once longevity is high enough, the pathogen persists and spreads easily enough that the effects of individual patches are washed out. Then the role of patch quality lies primarily in its effect on extinction rates, and whether infected hosts can persist.

To understand the mechanisms behind these effects, we further examined within patch dynamics in high variance metapopulations that produced endemic dynamics. Because of their lower extinction rate and higher recolonization rate, high quality patches support more consistent occupancy than low quality patches (Fig 3). However, as an epidemic progresses, high quality patches increasingly support infected occupants, while low quality patches support infecteds infrequently (Fig 3). In addition, while high quality patches do support susceptible occupancy, they experience a greater number of infection events (susceptible to infected transitions) than low quality patches (Fig 4). This relationship becomes weaker as longevity increases, due to the fact that as longevity increases, there are fewer susceptibles remaining in the metapopulation to become infected.

4 Discussion

The positive relationship between pathogen spread and environmental longevity demonstrated in the theoretical model above is well documented in models of empirical systems. Almgren et al (2011) find that, in plausible simulations of chronic

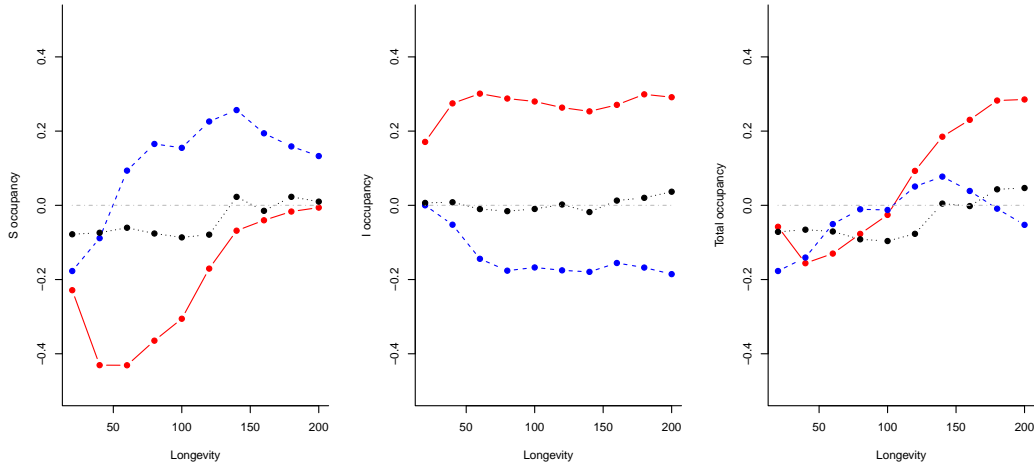


Fig. 2 The effect of the presence of high and low quality patches on (a) mean susceptible occupancy, (b) mean infected occupancy, and (c) mean total occupancy, measured relative to a low variance metapopulation. Red solid lines show high quality metapopulations, blue dashed show low quality, and black shows high variance.

wasting disease in deer, increasing prior survival in the environment increases the resulting force of infection and peak prevalence, with the importance of reservoir transmission increasing through time. Similarly, Breban et al 2009 show that environmental transmission of avian influenza virus allows it to persist in situations where direct transmission alone is insufficient. *Other examples.*

Moreover, for a given longevity, these simulations suggest that high variance metapopulations are more prone to widespread pathogen spread than low variance metapopulations. The mechanisms underlying this behavior can be understood by drawing parallels with models of pathogen spread through a contact network. In this context, our metapopulation can be viewed a network with patches as nodes connected through immigration (with the strength of the connection measured by connectivity). Many studies have shown that networks with high degree variance (where a node's degree is roughly equivalent to its total connectivity in our metapopulation model) are easily invaded by pathogens, which are then able to spread much more rapidly than in less heterogeneous networks (Pastor-Satorras and Vespignani (2001)).

In addition to allowing us to explore the effects of longevity and variance independently, this experiment also allowed us to vary the two simultaneously and explore their interaction, suggesting that the specific effect of longevity on pathogen spread is mediated by the variance of the patch quality distribution. In particular, metapopulations with high patch quality variance require lower environmental longevities to experience pandemic dynamics. In this way, the effects of environmental longevity are exacerbated by a high variance patch quality distribution, especially for intermediate longevities.

This interaction between environmental longevity and the variance of the patch quality distribution is largely attributable to the presence of high quality patches.

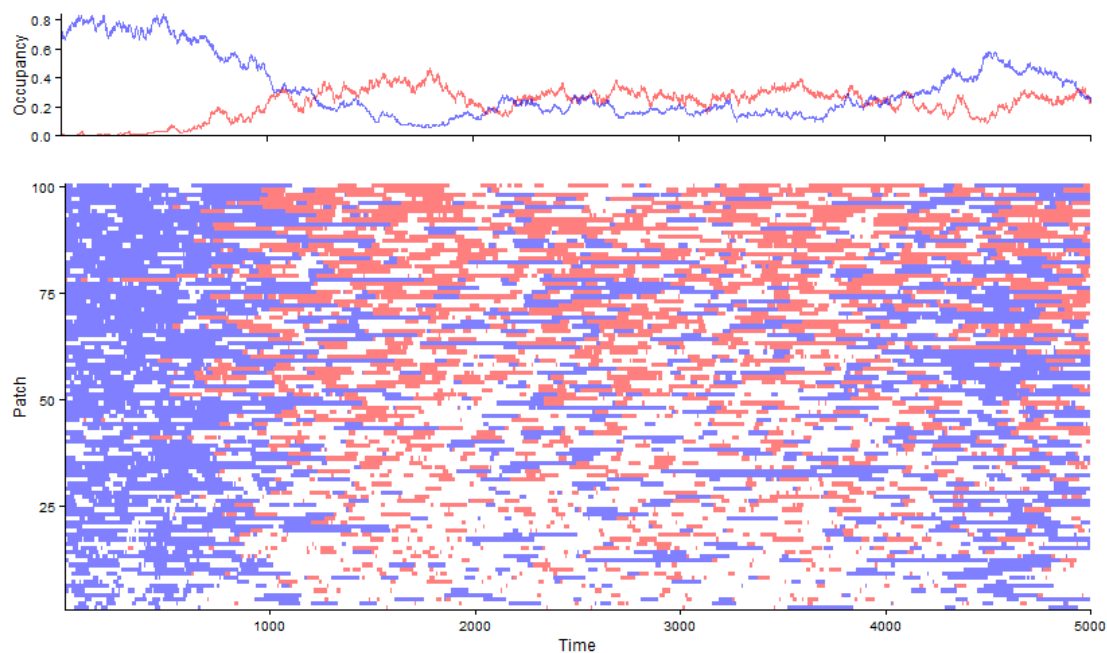


Fig. 3 Results from a single simulation with variance 0.2 and longevity 80. The top panel shows total occupancy of susceptible (blue) and infected (red) patches over time. The bottom panel shows the state – susceptible (blue), infected (red), or unoccupied (white) – of individual patches through time. Patches are stacked vertically with the lowest quality (~ 0.25) at the bottom and the highest quality (~ 1.75) at the top.

Since a patch's connectivity is determined, at least in part, by its quality, high quality patches function as highly connected hubs in the metapopulation. Specifically, high quality patches have both high in-degree (attract colonists from other patches) and a high out-degree (produce colonists that spread to other patches). These two properties have important implications for pathogen spread in the metapopulation. The high in-degree helps position high quality patches as the ecological "traps" hypothesized above, wherein susceptible hosts repeatedly colonize high quality patches and subsequently become infected (Fig 4). This infection pressure results in part from direct transmission from infected immigrants attracted to the high quality patch, reflecting results from the contact network literature that show that highly connected nodes have higher infection risk (Christley et al (2005), Keeling and Eames (2005)), but is further augmented by environmental transmission.

This trap effect, coupled with the relatively low extinction rate on high quality patches helps to create a stable platform from which the pathogen can spread through the rest of the metapopulation. Indeed, high quality patches are effectively metapopulation scale superspreaders (Lloyd-Smith et al (2005)). Once the pathogen infects high quality patches, it is able to spread to the rest of the metapopulation relatively easily. This process helps to maintain infected patches throughout the metapopulation, which in turn feed back on high quality patches to ensure a steady stream of infected colonists that maintain the trap effect. Thus,

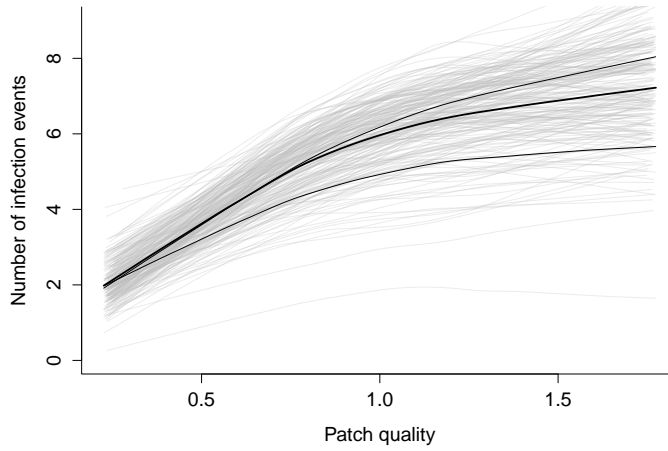


Fig. 4 The number of infection events (S to I transitions) for individual patches in endemic simulations. Light gray lines show smoothed fit for single simulations, while the thick black line shows the smoothed fit over all simulations. The thin black lines show the smoothed fits for longevities of 40 (top) and 140 (bottom).

through these two interacting mechanisms – the trap and superspreader effects – the presence of high quality patches serves to significantly increase pathogen spread.

Despite the dominating effects of high quality patches, low quality patches still play an important role in some cases by providing refuges on which susceptibles can escape infection. Even though individual low quality patches are unable to support consistent occupancy, at the metapopulation level, the presence of low quality patches increases overall susceptible occupancy, an effect that is strongest at intermediate longevities. This phenomenon represents the other side of the hub role played by high quality patches in that low quality patches are relatively weakly connected to the metapopulation and are therefore infrequently colonized by infected individuals. Moreover, the instability of low quality patches (i.e. the high extinction rate), together with the increased mortality of infected populations, means that infected populations do not persist long on low quality patches. Because low quality patches are so infrequently colonized, the environmental reservoir left behind by these infected populations generally decays before it has the opportunity to infect new susceptible colonists.

Due to their lower extinction rates, high quality patches are able to maintain stable occupancy despite widespread infection. On the other hand, at high pathogen longevities, the positive effect of low quality distributions on susceptible occupancy is overwhelmed, and low quality patches are unable to support infected occupancy, resulting in an increase in host extinction events. Thus, the role of the patch quality distribution and the presence of high or low quality patches is generally greatest for low to intermediate pathogen longevity – once longevity is high enough, the pathogen persists and spreads easily enough that the effects of

individual patches are washed out. Then the role of patch quality lies primarily in its effect on extinction rates, and whether infected hosts can persist.

In metapopulations without disease, high quality patches generally serve as sources, while low quality patches are sinks. The presence of a pathogen then considerably alters, and even inverts, these patterns. Not only do high quality patches become sinks in the presence of a pathogen with an environmental reservoir, they become ecological traps, which can be even more detrimental to the overall population (Kristan (2003)). From a management perspective, it is critical to understand this shift, as previous theoretical work suggests that management should focus on patches where conditions are most favorable (Strasser et al (2010)). Generally, this means that maintaining high quality habitat should form the focus of managers, but Strasser et al. (2010) show that stochastic disturbance (e.g. disease) can lead to cases where focusing on low quality patches is more effective in increasing population growth rate.

Habitat fragmentation and disease represent two major threats to wildlife populations. As we have seen, these two factors can interact in complex and interesting ways, especially when the pathogen is able to persist in the environment. Failing to consider these interactions and their effect on the roles played by high and low quality habitat overlooks the importance of low-quality habitat for the persistence of wildlife populations and the importance of high-quality habitat for the persistence of wildlife disease.

5 Appendix

5.1 Sensitivity Analyses

5.1.1 Lattice structure

5.1.2 Extinction scaling

5.1.3 Weak direct transmission

References

- Almberg ES, Cross PC, Johnson CJ, Heisey DM, Richards BJ (2011) Modeling routes of chronic wasting disease transmission: environmental prion persistence promotes deer population decline and extinction. *PloS one* 6(5):e19,896, DOI 10.1371/journal.pone.0019896, URL <http://dx.plos.org/10.1371/journal.pone.0019896>
- Christley RM, Pinchbeck GL, Bowers RG, Clancy D, French NP, Bennett R, Turner J (2005) Infection in social networks: using network analysis to identify high-risk individuals. *American journal of epidemiology* 162(10):1024–31, DOI 10.1093/aje/kwi308, URL <http://aje.oxfordjournals.org/cgi/content/abstract/162/10/1024>
- Dragon DC, Rennie RP (1995) The ecology of anthrax spores: tough but not invincible. *The Canadian veterinary journal La revue vétérinaire canadienne* 36(5):295–301, URL <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1686874&tool=pmcentrez&rendertype=abstract>
- Eisen RJ, Petersen JM, Higgins CL, Wong D, Levy CE, Mead PS, Schriefer ME, Griffith KS, Gage KL, Beard CB (2008) Persistence of *Yersinia pestis* in soil under natural conditions. *Emerging infectious diseases* 14(6):941–3, DOI 10.3201/eid1406.080029, URL <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=2600287&tool=pmcentrez&rendertype=abstract>
- Gillespie D (1977) Exact stochastic simulation of coupled chemical reactions. *The journal of physical chemistry* 93555(1):2340–2361, URL <http://pubs.acs.org/doi/abs/10.1021/j100540a008>
- Gog J, Woodroffe R, Swinton J (2002) Disease in endangered metapopulations: the importance of alternative hosts. *Proceedings Biological sciences / The Royal Society* 269(1492):671–6, DOI 10.1098/rspb.2001.1667, URL <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1690941&tool=pmcentrez&rendertype=abstract>
- Hanski I (1994) A Practical Model of Metapopulation Dynamics. *The Journal of Animal Ecology* 63(1):151, DOI 10.2307/5591, URL <http://www.jstor.org/stable/5591?origin=crossref>
- Hanski I, Ovaskainen O (2003) Metapopulation theory for fragmented landscapes. *Theoretical Population Biology* 64(1):119–127, DOI 10.1016/S0040-5809(03)00022-4, URL [http://dx.doi.org/10.1016/S0040-5809\(03\)00022-4](http://dx.doi.org/10.1016/S0040-5809(03)00022-4)
- Hess G (1996) Disease in metapopulation models: implications for conservation. *Ecology* 77(5):1617–1632, URL <http://www.jstor.org/stable/10.2307/2265556>
- Keeling MJ, Eames KTD (2005) Networks and epidemic models. *Journal of the Royal Society, Interface / the Royal Society* 2(4):295–307, DOI 10.1098/

- rsif.2005.0051, URL <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1578276&tool=pmcentrez&rendertype=abstract>
- Kristan I (2003) The role of habitat selection behavior in population dynamics: source-sink systems and ecological traps. *Oikos* 103(3):457–468, DOI 10.1034/j.1600-0706.2003.12192.x, URL <http://www.blackwell-synergy.com/links/doi/10.1034/j.1600-0706.2003.12192.x>
- Lindner DL, Gargas A, Lorch JM, Banik MT, Glaeser J, Kunz TH, Blehert DS (2011) DNA-based detection of the fungal pathogen *Geomyces destructans* in soils from bat hibernacula. *Mycologia* 103(2):241–6, DOI 10.3852/10-262, URL <http://www.mycologia.org/content/103/2/241.short>
- Lloyd-Smith JO, Schreiber SJ, Kopp PE, Getz WM (2005) Superspreading and the effect of individual variation on disease emergence. *Nature* 438(7066):355–9, DOI 10.1038/nature04153, URL <http://www.ncbi.nlm.nih.gov/pubmed/16292310>
- McCallum H, Dobson A (2002) Disease, habitat fragmentation and conservation. *Proceedings Biological sciences / The Royal Society* 269(1504):2041–9, DOI 10.1098/rspb.2002.2079, URL <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=1691124&tool=pmcentrez&rendertype=abstract>
- Miller MW, Hobbs NT, Tavener SJ (2006) DYNAMICS OF PRION DISEASE TRANSMISSION IN MULE DEER. *Ecological Applications* 16(6):2208–2214, DOI 10.1890/1051-0761(2006)016[2208:DOPDTI]2.0.CO;2, URL [http://www.esajournals.org/doi/abs/10.1890/1051-0761\(2006\)016\[2208:DOPDTI\]2.0.CO;2](http://www.esajournals.org/doi/abs/10.1890/1051-0761(2006)016[2208:DOPDTI]2.0.CO;2)
- Moilanen A, Hanski I (1998) Metapopulation Dynamics: Effects of Habitat Quality and Landscape Structure. *Ecology* 79(7):2503, DOI 10.2307/176839, URL <http://www.jstor.org/stable/176839?origin=crossref>
- Pastor-Satorras R, Vespignani A (2001) Epidemic dynamics and endemic states in complex networks. *Physical Review E* 63(6), DOI 10.1103/PhysRevE.63.066117, URL <http://pre.aps.org/abstract/PRE/v63/i6/e066117>
- Strasser Ca, Neubert MG, Caswell H, Hunter CM (2010) Contributions of high- and low-quality patches to a metapopulation with stochastic disturbance. *Theoretical Ecology* 5(2):167–179, DOI 10.1007/s12080-010-0106-9, URL <http://www.springerlink.com/index/10.1007/s12080-010-0106-9>