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Unravelling Transmission in Epidemiological Models and its Role in the Disease-Diversity Relationship.

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Abstract

There are a multitude of pathways a pathogen can invade and spread through a host population. The assumptions of the transmission model used to capture disease propagation determines our prediction of outbreak potential, the pathogen's net reproductive success (R_0). This review offers a n i nsight i nto t he a ssumptions a nd motivation behind common transmission mechanisms, and introduces a general framework with which we unify them, where contact rate, the most important parameter in disease dynamics, determines the transmission model. This general transmission model framework helps bridge the gap between mathematical disease modelling and the much debated disease-diversity relationship, by expanding common disease models to multiple host systems, and in considering the role of host diversity in disease transmission. By describing the mechanisms of transmission as a stepwise process, we provide a guide for modelling pathogens in multi-host systems, elaborate how these transmission mechanisms can affect h ost c ommunities, a nd h ow h ost c ommunities a ffect th e pa thogen's success. We further expand on these models and introduce an approach for including host species' evolutionary history into transmission dynamics, contributing to the debate on the effect of biodiversity and community composition on disease outbreak potential.

Keywords: Epidemiological Models; Transmission; Biodiversity; Dilution Effect

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1 Introduction

Worldwide, many natural populations are declining rapidly due to anthropogenic influences (IPBES, 2020), resulting in a shift in the abundance of humans and livestock relative to wildlife species (Bar-On et al., 2018). Simultaneously, we are seeing an increase in disease outbreaks originating from wildlife (Daszak et al., 2000; Jones et al., 2008; Smith et al., 2014). Demographic changes have led to increasing contact between humans and livestock with wildlife, providing new opportunities for disease spillover (Graham et al., 2008). Most emerging pathogens in humans are directly transmitted viruses or bacteria that have crossed the species barrier, perhaps multiple times, likely facilitated by changes to the environment made by humans (Dobson and Foufopoulos, 2001; Smith et al., 2014). To understand how recent biodiversity losses and the increasing abundance of humans and domesticated species have reshaped the disease landscape, we need to consider the role of multi-species communities in the maintenance and onward transmission of diseases (Keesing et al., 2010) and the establishment of pathogens in novel hosts.

In disease models, transmission describes the process by which an infected individual transmits a pathogen to an uninfected individual, and is a critical step in disease outbreak and spillover (Park et al., 2018). When interspecific transmission is sufficiently high, a pathogen may invade the novel host population (Daszak et al., 2000; Fenton and Pedersen, 2005; Wolfe et al., 2007). An example of disease spillover is shown in Figure 1. A key strategy for preventing spillover is to reduce transmission from the reservoir (a population of a single species that can maintain the disease) to a susceptible, novel target population (Haydon et al., 2002). Understanding the process of transmission within and between species is thus an essential step for mitigating the risk of future disease emergence events.

Transmission is a complex, stepwise process (see Box 1 and Figure 1); however, underlying assumptions are opaque, often hidden within a single composite parameter. Additionally to this complexity, transmission is known to have a trade-off with the pathogen-induced mortality, known as *virulence* (Box 2), which are both often measured in pathogen load (See Box 1 and 2). In the susceptible-infected-recovered (SIR) compartmental model (Kermack and McKendrick, 1927; Anderson and May, 1982), the focal model for this paper, the transmission process is frequently simplified as being *density-dependent*, *density-independent* or some intermediate between these two extremes. However, transmission is determined not only by the inherent behaviour of the pathogen, but also by that of the host or vector, as most pathogens rely on their host for reproduction (Rohani et al., 2003; Han et al., 2015). Properties of the host population that affect disease transmission include contact rates, population density, and individual birth and death rates, whereas other disease parameters, such as recovery and transmission rates are considered pathogen dependent parameters (Han et al., 2020). In addition, transmission is unlikely a homogeneous process, but integrates across many heterogeneities at different stages of transmission, including host contact rates and susceptibility (McCallum et al., 2017; Smith et al., 2009). Nonetheless, in many epidemiological models, transmission is represented as a simple, singular constant.

The choice of transmission model affects the projected disease dynamics, and thus the potential management de-

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cisions that follow. It is critical, therefore, to choose the model that best represents the pathogen life-history and host population behaviour. Here, we synthesize assumptions underlying common transmission models, and how they affect the dynamics of the simple compartmental (SIR) model of infectious disease spread. Specifically, we explore the effect of host contact rate and structure on disease transmission and show they are the most important determinant of transmission dynamics. While limited in epidemiological complexity, focusing on this subset of models allows us to examine details of the transmission process relevant for inter-specific disease transmission, spillover and the much debated *disease-diversity relationship* (Halliday and Rohr, 2019).

Box 1: The Biology of Transmission

Transmission is the transfer of infectious particles, or propagules, from an infected (donor) host, to a naive, receiving host. Transmission potential is then dependent on a threshold propagule load within the donor host (Wilber et al., 2016; Blaser et al., 2014). As pathogen propagule particles often have to travel through space between leaving the donor host and establishing in the recipient host, the environment and the time a particle is *free-roaming* can play a role in transmission success (Tien and Earn, 2010). McCallum et al. (2017) deconstructed transmission into five discrete stages:

- Stage 1: Dynamics of propagules within donor host.
- Stage 2: Production of pathogen-infective stages in donor host.
- Stage 3: Pathogen survival and growth in the environment (including the environment of an intermediate host).
- Stage 4: Dose acquired by recipient host at exposure.
- Stage 5: Pathogen load in the recipient host.

Between these stages of transmission, heterogeneities can arise and threshold-like behaviours may emerge. Conventional, linear frameworks of transmission may overlook such heterogeneity, such as *super-spreaders* resulting from high infection loads (McCallum et al., 2017). For example, nematode crowding within hosts causes an increased immune response, and saturates the relationship between transmission Stages 1 and 2, such that at high pathogen levels the production of the dispersal pathogen (nematode) life-stage plateaus (McCallum et al., 2017). Age of infection, host immunosuppressive capabilities and pathogen competition (in case of co-infection) can also have an effect on the production of pathogen dispersal stages (Stage 2). One well studied example is Malaria, where physiological traits affect the susceptibility of individuals: people with sickle cell anaemia are more resistant to the disease (Elguero et al., 2015). In diseases such as cholera, high pathogen loads cause diarrhoea and vomiting and therefore increased shedding of infectious particles.

For Stage 3, the environment determines the subsequent received load, but the donor/recipients host behaviour is of importance too, determining the exposure to the shed pathogen. Some dispersal stages can linger outside hosts longer than others. For example, the decay rate of *Mycobacteria*, causing tuberculosis, is dependent on the temperature of the medium and likely also to light-exposure, therefore differs among seasons (Fine et al., 2011). However, some pathogens (e.g. HIV) are never exposed to the environment, and are directly transmitted, these pathogens skip Stage 3.

The load the recipient host acquires depends on its exposure (Stage 4), which is impacted by multiple factors including: the relative density of the donor and recipient hosts, the survival rate of the free-living pathogen stage, and, for trophically transmitted pathogens, the Holling type II function response.

The final load that establishes in the recipient host (Stage 5) depends on the quality of the received particle, the host immune response (which may depend on its genotype), and the presence of other pathogens (co-infection). These stages can differ between each pathogen, complicating their simplification into standard models. Figure 1 shows these transmission stages in the spillover of the bacterium bovine Tuberculosis (bTB) from the reservoir host (African buffalo, *Syncerus caffer*), to a novel host (elephant, *Loxodonta africana*) (Miller et al., 2021). This example emphasises the complex dynamics underlying transmission.

A key challenge in modeling transmission, and the focus of this manuscript, is capturing the inherent nature of host

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density and contact rates. Contacts cannot indefinitely increase with population density, as is assumed in some models (Smith et al., 2009). Contact structure and animal behaviour can have a large impact on disease dynamics, as shown in bovine Tuberculosis (bTB, cause by *mycobacterium bovis*) models for African buffalo (*Syncerus caffer*) by Cross et al. (2004, 2007), where allowing for social groupings broke down standard SIR disease dynamics. Another illustrative case study is provided by the European badger, also a reservoir for bTB, where culling intended to reduce number of infected individuals instead resulted in an increased contact rate (as aggregation increased in lower-density groups), and thus increased disease prevalence (Vicente et al., 2007). The epidemiological contact process, and the emergent relationship between host density and contact rate, can be modeled both explicitly, in the form of density-dependent or density-independent compartmental models, and implicitly, for example, as a network or individual-based model. Here, we focus on the representation of transmission in the SIR compartmental model. We provide a step-by-step guide to decomposing transmission, and introduce a novel contact rate-function that allows us to unify existing models. We examine how the biology of transmission and the mathematical assumptions in our models inform our understanding of the disease-diversity relationship. Finally, we present a novel approach for including host species' identities (evolutionary history) into our framework, adding to our understanding of host community structure and biodiversity on disease outbreak potential.

Box 2: The transmission-virulence trade-off

Pathogen load can also be used as a proxy for *virulence*, the pathogen-induced host mortality. A higher pathogen load also translates to a higher rate of transmission (Box 1 - stage 2), as there are more dispersal propagules (McCallum, 2016; Wilber et al., 2016). For successful transmission, a sufficient number of propagules needs to be produced within the donor host, survive the intermediate stages, and establish in the recipient host. When virulence is high, transmission may be reduced due to the negative effect of high pathogen load on host behaviour, for example, high fevers in influenza immobilizes patients, reducing pathogen spread (Dieckmann et al., 2005), and a pathogen that kills its host quickly reduces its window of opportunity for infection. This is known as the *transmission - virulence trade-off* (Cressler et al., 2016). However, pathogen load is not always a good predictor of transmission success. For example, HIV has highest transmission potential at intermediate viral loads (McKay et al., 2020), and the trade-off between transmission and virulence has increasingly been questioned.

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2 Decomposing the transmission function, $F(S, I)$

In the classic SIR model, the transmission rate describes the rate of new infections per unit of time. It is often modeled as a single constant, but can represent a composite of many different underlying processes. These dynamics are described by the *transmission function*, $F(S, I)$, encompassing S and I individuals and the rate of transmission, β, which has been described in numerous formulations (see Table 1). The transmission term can also be described as the product of the force of infection and the density of susceptible individuals (de Jong et al., 1995). The transmission function is represented in the SIR model in the derivative for S and I as:

$$\frac{dS}{dt} = -F(S, I) \tag{1a}$$

$$\frac{dI}{dt} = F(S, I) - \Gamma I \tag{1b}$$

Where t is time and Γ the removal rate (recovery and mortality rates, combined). S and I are the number of susceptible and infected individuals, respectively. Throughout this paper the host population size is defined as $N = S + I + R$, unless specified otherwise. Assuming infection is a probability, the rate of infection can be described as (Begon et al., 2002):

$$F(S, I) = \beta S \frac{I}{N} \tag{2}$$

where β determines the speed with which a susceptible individual (S) is infected by an infected individual (I). Encountering an infected individual is a probability event, $\frac{I}{N}$. There are several equally valid models, this one being the most common in ecology.

Here we decompose the various commonly used transmission functions, $F(S, I)$, of compartmental SIR models (Table 1). We begin with the different relationships between susceptible and infected individuals for homogeneously and heterogeneously mixing populations (not including explicit contact networks), and finish with explaining how the contact rate between hosts determines the density or frequency-dependent nature of transmission, together with the probability of successful transmission. We provide a schematic illustrating our framework in Figure 2, starting with standard homogeneity where we decompose β (left column) and then give some examples of heterogeneity (right column). Table 2 summarizes the parameters that are used here and in the equations throughout this review.

In the above transmission model, the criterion for a disease outbreak is directly determined by the transmission rate, β. The basic reproductive rate, R_0, describes the number of secondary infections arising from a single infected host in a fully susceptible host population. This quantity is also known as the *lifetime reproductive success* or *fitness* of the pathogen. We provide the definition and derivation of R_0 in an SIR model with density-dependent transmission in Box 3. Emergence of disease, or pathogen persistence in a community, will occur when $R_0 > 1$. If $R_0 < 1$, the pathogen will be lost from the host community, whereas an R_0 equal to 1 represents an endemic disease. When the

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transmission rate (β) increases, so will the R_0, β thus determines the endemic size and intrinsic rate of increase of the pathogen.

2.1 Homogeneity

In the simplest case, we can assume a homogeneous population in which all individuals are equally susceptible and interact with equal probability (Figure 2, left column). There are various different options for modelling the interaction between susceptible and infected individuals, and a pathogen's transmission rate, β (McCallum et al., 2001; Begon et al., 2002; Hoch et al., 2008). However, all formulations of transmission depend on the contact rate (here defined as κ), representing the average number of contacts per host per unit time, and the probability of infection given contact, c. It is usual, therefore, to derive transmission rate in terms of these two parameters, as we summarize in this review. Here we introduce a novel general contact rate function from which we will show we can derive most transmission rate functions commonly used in the literature (Table 1).

Decomposing transmission rate, β

As the rate of transmission is determined by the number of contacts an individual has per time unit (κ) and the probability with which a contact leads to infection (c), transmission (β) in a homogeneous population is then simply a function of the contact rate and probability of successful transmission. We can formalize this as $\beta = -\kappa \cdot \ln(1-c)$ (see Keeling and Rohani (2011) Box 2.1 for a formal derivation). When the probability of infection given contact, c, is small this equation can be simplified into the more intuitive form of the product of the contact rate (κ) and the proportion of those contacts resulting in infection (c), $\beta = \kappa \cdot c$, as we shown in Appendix Eqn (2) (McCallum et al., 2001, 2017). This gives us a new definition of the transmission function:

$$F(S,I) = \beta S \frac{I}{N} = \kappa c S \frac{I}{N} \tag{3}$$

Importantly, using this simplified formulation of β, and the duration of infection (τ), we can empirically determine the R_0 of a disease as $R_0 = \kappa \cdot c \cdot \tau$ (Anderson et al., 1992).

General contact rate

Pathogens can be transmitted in various ways, such as directly via host-host contact or via intermediate vectors. Some directly transmitted diseases are limited in their transmission, and contacts between infected and susceptible individuals may be independent of population size. The contact rate thus determines whether infection dynamics are density-dependent (DD) or frequency-dependent (FD). We present a generalized version of this contact rate function that can be adapted to capture the spread of disease in a population assuming different contact structures (Table 1):

$$\kappa(N) = \frac{\xi}{\omega} N^q \tag{4}$$

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Here, ξ is a parameter that represents the number of contacts per unit time, its dimensions depending on the type of transmission model. Whether the transmission rate is density-dependent (DD), as in directly transmitted diseases, frequency-dependent (FD), as in sexually transmitted diseases, or some intermediate between these (Smith et al., 2009), is determined by parameter q: Setting $q = 1$ returns DD dynamics, and setting $q = 0$ returns FD dynamics. If transmission is density independent, ξ represents solely the number of contacts and is the same across populations of different sizes. When transmission depends on density, ξ represents the fraction of population $(\frac{1}{N})$ contacted. This causes the dimensions of β to differ between density-dependent and independent models (Table 1). Transmission is also influenced by the area in which the individuals interact, which may be characterized by Michaelis-Menten-like dynamics, which are captured by the parameter ω. Because interaction behaviour can differ between the classes of individuals, S, I and R, we can additionally allow for heterogeneity in contact rate among these classes, and the transmission function can be extended such that classes can have different density limiting effects via the corresponding parameters ω_S, ω_I and ω_R.

2.1.1 Frequency-Dependence

When the transmission of a pathogen is independent of the number of contacts an infected individual has with susceptible individuals, but is, for example, limited by the number of possible interactions per time unit, we model the pathogen as Frequency-Dependent (FD). Common examples of FD transmission include sexually transmitted diseases for which transmission relies on the limited number of contacts or 'transmission events' between sexual partners. Here, the *proportion* of the population each infected host interacts with per unit time, ξ, is constant regardless of the total host population size, N. Therefore, the contact rate (κ) is constant per time unit, creating a transmission rate independent of host population density: $\beta_F = \kappa \cdot c = \xi \cdot c$, which returns the familiar FD transmission function shown in row 1 of Table 1. In this simple model, infections rise with the probability $\left(\frac{I}{N}\right)$, the *density* of infected hosts. Note that here ξ represents the *proportion* of the population contacted, therefore making κ independent on N (Table 1). Vectored diseases, such as Lyme's disease, can also be approximated assuming FD dynamics, with transmission dependent on contact with an intermediate host. Here, the vector determines the speed of transmission, which may be limited by, for example, the number of meals the vector has per time unit. The FD transmission dynamic is shown in Figure 4A and the equation and its derivation are provided in panel 3 of Figure 3 and Appendix Eqn (4).

If populations remain near their carrying capacity, a particularly useful approximation of FD transmission can be obtained by using the carrying capacity (K), instead of population size (N) (Row 5, Table 1). We can replace $NwithK$ in any population for which it is assumed the host population is at equilibrium, no demography is included in the SIR model, as for example in the host-parasite model by Gubbins et al. (2000), where in the absence of disease, the hosts where at carrying capacity. This reduces mathematical complexity by removing the dependence of the dynamics on a ratio of the state variables, S and I. We detail this dynamic, which we refer to as Carrying Capacity Dependent transmission, in Figure 4D. Note that the dimensions of β are the same as in FD (Row 5 Table 1), as replacing N with K brought us back to the dynamics (order) of FD transmission.

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2.1.2 Density-dependence

When the density of the population determines the spread of disease, the transmission of the pathogen is considered Density Dependent (DD). This is most appropriate when encounters between individuals are assumed to be brief (Begon et al., 2002; Smith et al., 2009). Density Dependent transmission is often referred to as *(pseudo-) mass action*. Here, the resulting number of interactions per host scales linearly with population density (N), and pathogen spread is determined by the *proportion* of the population each individual comes into contact with per unit time and unit area, ξ.

In density dependent dynamics, the contact rate, κ is dependent of the population size, such that the rate of contacts increases with increasing density of hosts, in contrast to in FD, making β a density dependent rate. We can modify Eqn 4 to include the effect of population density, N, such that $\kappa(N) = \frac{\xi N}{A}$. This definition for κ is shown in Appendix Eqn (5) and Figure 3. The transmission function $F(S, I)$ now shows the number of contact events increasing linearly with the density of hosts (Anderson and May, 1982; Antonovics, 2017). This brings us to Equations 2 and 3 in Table 1. This derivation can be found in Appendix Eqn 6 Frequently, area is simply considered a constant (giving our third equation in Table 1), as it is assumed that with constant area, an increase in number of individuals causes an increase in density (Kermack and McKendrick, 1927). See Appendix Eqn (7).

In Eqn (1b), all terms have to be in the same units, and thus they are of the same *order*: the influx term ($F(S, I)$) must be of the same dimension as the outflux term (ΓI), in units of ind^{-1}, the magnitude of change per individual, N. In FD, $\beta = \beta_F$ is simply of *order* 1 and has the dimension t^{-1}, so is independent of N (Table 1 row 1). To satisfy these dimensions in DD, $\beta = \beta_D$ has to be of *order* $\frac{1}{N}$, meaning β_D requires the dimension of ind^{-1}, as shown in Table 1 rows 2 and 3. Therefore, β_D is an order of magnitude higher than β_F, which must be taken into account when one parameterizes a model. These values cannot be interchanged.
The DD transmission model (Figure 4B) can fit well to directly transmitted diseases, such as the common cold or influenza, and it is used for modeling wildlife diseases, including rabies virus in dogs and tuberculosis in possums (White et al., 2017; Rhodes et al., 1998; Barlow, 1991). The DD models are summarized in Panel 1 of Figure 3 and the derivations are described in the SI.

Comparison between DD and FD transmission

Models assuming FD and DD vary importantly in their disease dynamics. For example, increasing city size decreased mean transmission, β, of measles during an outbreak in England (Bjørnstad et al., 2002), suggesting the per-capita transmission declined with increasing population size ($\hat{\beta} = \frac{1}{SI}\frac{dI}{dt}$) (Ferrari et al., 2011), as predicted by FD dynamics ($\hat{\beta}_{FD} = \frac{\beta}{N}$). Because $\hat{\beta}$ for DD transmission is independent of population size ($\hat{\beta}_{DD} = \beta$), we would not have predicted declining transmission under DD dynamics. Critically, under assumptions of FD, R_0 remains constant across varying N, but under assumptions of DD, R_0 increases with N (Ferrari et al., 2011), as a consequence DD

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models predict a critical population density as an invasion threshold, which is not the case for FD (see Box 3). The assumptions of DD and FD dynamics are often violated when empirical data are examined, for example, as with phocine distemper virus in seals, for which $\hat{\beta}$ was inversely related to population size (idiosyncratic to FD). Phocine distemper is assumed to be a directly transmitted virus, but was better modelled as FD (Swinton et al., 1999). This shows the difficulty of choosing the right model for any one system.

2.1.3 Intermediate DD-FD

It is rare to find a system that is truly FD or DD, and host contact behaviour (when homogeneous mixing is assumed) is often somewhere on the DD-FD continuum (Anderson et al., 1992; Smith et al., 2009; Ferrari et al., 2011). For example, it is unlikely that contact rates either increase indefinitely with N, as is assumed under DD, or is completely density independent, as assumed in FD (McCallum et al., 2001). Our general contact rate function, Equation (4), can be adapted to capture intermediate DD-FD transmission (see Appendix (8)) by defining $0 < q < 1$. The parameter q can be interpreted as the relative importance of a single added host within a population to the average contact rate. Equations are shown in panel 2 of Figure 3 and the derivation for $F(S, I)$ is in Appendix Eqn (9). By allowing q to vary, it is possible to capture seasonal dynamics, for example, cowpox in voles shifting towards FD dynamics in late summer and more DD dynamics in late winter Smith et al. (2009), and variation with life stages, as in the phocine distemper virus outbreak in the Dutch Wadden Sea, where infection dynamics of less social juveniles and adult seals are better explained by FD, and subadults by DD. (Klepac et al., 2009). This transmission function is of order $\frac{1}{N^q}$, which gives us units for $\beta = \beta_q$ of $\text{ind}^{-q}t^{-1}$ (See Table 1). Thus, at values of $0< q <0.5$, β_q has FD units (t^{-1}), and at values $0.5< q <1$, β_q has units as in DD ($\text{ind}^{-1}t^{-1}$). These intermediate FD-DD dynamics are displayed in Figure 4C.

2.1.4 Asymptotic transmission

Some diseases are more likely to spread asymptotically, such that at low host densities contacts are directly proportional to host density i.e. (DD), but a maximum rate of contact is obtained at high host densities (e.g. due to spatial or social distribution) (Diekmann and Kretzschmar, 1991; McCallum et al., 2001). Including an additional term for the saturation of contacts at high population sizes, we can model these dynamics by allowing transmission to vary between DD and FD depending on the total population size (Antonovics, 2017). The equation for this contact function can be found in Appendix Eqn (10). Here there is a shift from DD to FD with increasing N (see Appendix for definition of asymptotic contact rate). The transmission function $F(S, I)$ is shown in Table 1, row 6. Note that this transmission rate is identical to that for frequency dependent transmission, β_F as they have similar dimensions (and thus $F(S, I)$ is again of order N). We can therefore identify the critical level after which contacts start to saturate as $X = N^*$ (with $1 < X < \infty$), the half saturation constant in Michealis-Menten kinetics. The lower X, the higher the affinity of individual contacts and the quicker saturation of contacts is reached. Figure 4E shows the asymptotic transmission dynamics and the equations and derivations can be found in Appendix Eqn (11) and abbreviated in panel 4 of Figure 3.

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2.2 Heterogeneity

The models described above assume individuals are homogeneous in their susceptibility, and that epidemiologically relevant contacts between hosts occur at random, known as the assumption of *random mixing*. However, this is not always the case, for example, a host's behaviour can change the probability of encountering an infected individual and the geographic distribution and movement of hosts plays a significant role in modifying host contact rates (Pope et al., 2007; Vicente et al., 2007). This heterogeneity can affect the overall disease spread (Ferrari et al., 2011). We can compose the transmission function, $F(S, I)$, in various ways to portray this heterogeneous mixing, as shown in Figure 2 (right column).

Behavioural heterogeneity

There are various approaches that allow us to include heterogeneity in behaviour of S and I, including network or individual-based models (Ferrari et al., 2011). Here, we review some simplified and commonly adopted formulations for our compartmental SIR model from Eqns (1).

2.2.1 Power-law transmission

Encounters between individuals S and I are not necessarily linear. In animals, idiosyncratic behaviour or behaviour caused by infections can result in non-linear contact patterns. In plant-parasite interactions, the production of free-living stages such as spores or other microparasites may cause accelerating infection responses in plant communities that also depart from the linear assumptions of homogeneous mixing and mass-action dynamics of the common SIR model (Gubbins et al., 2000). The Power-law transmission function aims to encapsulate the accelerating and decelerating responses that may be found in empirical systems by introducing *heterogeneity parameters* m and n. This transmission function simulates heterogeneous interactions between S and I individuals with accelerating and decelerating disease spread by raising S and I to the powers m and n, respectively (Hochberg, 1991), as shown in Table 1, Row 7. These heterogeneity parameters determine how the densities S and I affect the *per capita* transmission efficiency of the pathogen, such as the susceptibility (by m) or the infectivity (by n) of an individual (Hochberg, 1991; Novozhilov, 2008), and thus determine the speed of infection. When both parameters are unity, the model describes simple DD (with constant area).

There are many possible response types, as theoretically $-\infty < m, n < \infty$. Here we consider some biologically relevant ones. Assuming $n = 1$, when $m > 1$, $F(S, I)$ accelerates, and new infections arise exponentially with linearly increasing number of susceptible individuals. When $n = 1$ and $m < 1$, rate of new infections decelerates. Figure 4F shows the power law transmission dynamics with varying n. We could find no real world examples of exponents $0< m <1$, but it would represent a case when increasing S decreases the rate of transmission (Novozhilov, 2008). Greer et al. (2008) found that the *Ambystoma tigrinum* virus in its host was best described with a Power-law function with $m = 1$ and $n = 0.255$, suggesting that infection scales positively but non-linearly with I. When $m <$ 0, S is inversely related to $F(S, I)$, and when $n <0$, I is inversely related to $F(S, I)$. An example of the latter is

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seen in *Bacillus thuringiensis* infections of *Plodia interpunctella* moths, here, transmission requires cannibalism of infected individuals, and thus transmission increases with S, and decrease with I (Knell et al., 1996). In addition to capturing accelerating and decelerating behaviours, the power-law function can also represent scenarios where the infection risk is constant, and independent of the density of infected individuals, as is the case where there is constant re-inoculation of the disease from another host, for example, rabies from a bat reservoir host (Greer et al., 2008; Mollentze et al., 2020). This could be modelled as $n = 0$. By sampling from distributions of m and n, the power-law function can also approximate heterogeneity in transmission rate among S and I individuals (White et al., 2017).

Spatial heterogeneity

The assumption in SIR models of spatially homogeneous populations is also an obvious oversimplification of real population dynamics, especially for species exhibiting territoriality, sociality and other complex group or individual behaviours (Cross et al., 2004; Viana et al., 2014; White et al., 2017). Contact networks provide a useful approach to model more realistic population behaviour (Craft, 2015), but can rapidly become analytically intractable. Here we illustrate how spatial heterogeneity in contacts can be included into our compartmental SIR models, making a few simplifying assumptions, and holding transmission rate, β, constant.

2.2.2 Refuge effect

The refuge model attempts to include spatial aggregation of hosts, with the transmission function incorporating host clustering (Barlow, 1991). Possums in New Zealand provide an example of aggregated spatial prevalence for TB, due to variation in carrying capacity across habitat patches (Barlow, 1991; May and Anderson, 1984). In this model, the population consists of patches with and without disease, and p is the proportion of the total area that is occupied by diseased individuals and represents how aggregated the disease is in space. The more the disease is aggregated (the smaller p), the lower the probability that an infectious individual will encounter a susceptible individual. This dynamic is shown in Row 8 of Table 1. Assuming $N = S+I$, so in this case a simple Appendix model excluding the R compartment, the number of susceptible individuals is $S = Np - I$. If $p = 1$, the diseased patch equals the total area, there is no aggregation of the disease, and the transmission function simplifies to $F(S, I) = \beta_D I(N - I) = \beta_D SI$, DD dynamics. With greater aggregation, transmission $F(S, I)$ decreases, as individuals are now less homogeneously distributed. For $I = pN$, which is the maximum density of individuals in the diseased patch, $F(S, I) = 0$. Figure 5A shows this transmission dynamic for three different values of p.

2.2.3 Negative binomial

The negative binomial model builds upon the Refuge effect (Barlow, 1991) and was also fit to model TB in possums, but with varying carrying capacities (different resource availability) per patch, and therefore allowed for increased contact rates by concentrating hosts (Civitello et al., 2018). Transmission now includes a heterogeneous mixing term, θ (ind^{-1} t^{-1}), which can take any value $0 < \theta < \infty$ (Barlow, 2000). This model assumes that the probability of infection is higher when a susceptible individual has an infected neighbor, and so infections are clustered in space.

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Small θ corresponds to highly aggregated infections. As θ decreases ($\theta \to 0$), $F(S, I)$ decreases as the mean number of infected individuals encountered per susceptible individual is reduced. As θ increases ($\theta \to \infty$), aggregation is reduced, and $F(S, I)$ again simplifies to DD transmission. This transmission function can be found in Row 9 of Table 1 and is shown in Figure 5B.

2.3 Summary of transmission functions

The contact rate between hosts determines the shape of transmission dynamics. There are multiple approaches for describing the spread of a pathogen through a host population, the most common distinction is between DD and FD dynamics, but there are numerous variations, reflecting differences in the biology of the pathogen and the behaviour of the host. For example, wildlife diseases are almost always modeled assuming DD dynamics, regardless of the pathogen, as host behaviour, including local heterogeneities, is more likely to approximate mass-action dynamics at larger scales (White et al., 2017). In contrast, local dynamics in human interactions commonly depart from assumptions of DD (people frequently form small contact networks), and might thus be better modelled using FD dynamics or, more realistically, with asymptotic transmission. However, many empirical studies have shown evidence of both FD and DD dynamics in the same system, with DD dynamics more often observed at low population densities, and FD dynamics more common at higher densities (Antonovics, 2017; Roberts and Heesterbeek, 2018). Unsurprisingly, more complex dynamics are also found in many disease systems. Within a host population, not all individuals are the same, and they may vary in susceptibility and infectivity, as captured by the concept of *superspreaders*, which dramatically influences outbreak potential and disease dynamics (Lloyd-Smith et al., 2005). Similar concepts can be extended to *super-movers*, *super-recipients*, *super-shedders*, and *super-susceptibles* (Streicker et al., 2013; Craft, 2015; White et al., 2017). Additionally, hosts likely do not have a homogeneous contact structure, as these may be modified through networks or variation in population density. For example, in feline retrovirus, infrequent encounters at low host densities make contact rates close to constant (FD), at intermediate densities contact rate becomes proportional to density (DD), while at high densities there is a further increase in contact rate due to overlapping territories (Fromont et al., 1998). These and other well known case studies, as in the above example of culling of badgers, illustrate how contact structure can be important for modeling wildlife diseases (Vicente et al., 2007; Pope et al., 2007; McCallum, 2016; White et al., 2017). However, contacts in complex networks tend to homogenize over time (Cross et al., 2004). Therefore over longer timescales, heterogeneity can average out, providing an opportunity to simplify otherwise complex models.

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Box 3: Derivation of pathogen net reproductive success, R_0

To calculate R_0, we want to know when the pathogen can grow in the population, i.e. $\frac{dI}{dt} > 0$, from Eqn 1:

$$F_F(S, I) > \Gamma I \tag{a}$$

For frequency dependent transmission, we get:

$$\frac{\beta S I}{N} > \Gamma I \tag{b}$$

Then, dividing by I and rearranging we return:

$$\begin{aligned} \frac{S}{N} &> \frac{\Gamma}{\beta} \\ \frac{\beta}{\Gamma} X &> 1 \quad \text{where } X = \frac{S}{N} \end{aligned} \tag{c}$$

When $S \sim N$, fraction $X = 1$, so assuming a fully susceptible population (which is the assumption in the definition of R_0),the disease will spread when $\frac{\beta}{\Gamma}$ is greater than unity:

$$R_0 = \frac{\beta}{\Gamma} \tag{d}$$

For density dependent transmission, the definition of R_0 is the same (Eqn (d)), but has a different implementation. We again derive it from setting $\frac{dI}{dt} > 0$:

$$F_D(S, I) > 0 \tag{e}$$

Substituting the DD definition of F(S,I), we get:

$$\beta S I > \Gamma I \tag{f}$$

As R_0 is by definition the number of secondary individuals that arise from a *single* infected individual in a *fully* susceptible population, we plug in $I = 1$. Solving this for S, we obtain:

$$S^* > \frac{\Gamma}{\beta} \tag{g}$$

By definition, for a disease to spread in a population, the product of the number of susceptibles (S) causing secondary infections (R_0) must be greater than unity ($R_0 S > 1$), and thus $R_0 > \frac{1}{S}$. Therefore, in DD transmission, we define S^* as a critical threshold host density for invasion of the pathogen, which does not exist in FD.

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3 Transmission in multi-host systems

Pathogens that infect only a single host are rare, and it is common for pathogens to infect a number of different host species (Woolhouse et al., 2001), which can significantly alter disease dynamics. Thus, host community structure can both affect and be affected by pathogen dynamics. In multi-host systems, transmission is determined by multiple shedding hosts, each of which can contribute differently to disease prevalence, depending on their inter- and intraspecific ecological interactions (Haydon et al., 2002; Streicker et al., 2013; Fenton et al., 2015). This complicates models and how we estimate transmission, which may be asymmetric among hosts, with some hosts acting as pathogen reservoirs, and pathogens may express different life-history syndromes in different hosts (Haydon et al., 2002; Gandon, 2004). In this section, we describe how multi-host, single-pathogen systems may be influenced by host diversity, and how transmission can be defined in such systems.

3.1 Host community dynamics

The dynamics of multi-host diseases can vary greatly with the species composition of the host community. One important relationship in wildlife disease dynamics is that between disease prevalence and host community diversity. The disease-diversity relationship is a well-known and highly-disputed concept in disease ecology.

3.1.1 Host community effects on pathogen prevalence

The *dilution effect* suggests higher diversity of hosts reduces the probability of a pathogen infecting a new host, either directly, by reducing encounters, and therefore transmission between hosts or indirectly, by changing total host abundance (Keesing et al., 2006, 2010) (Table 3). A modelled example of encounter reduction (also known as *frequency-dependent dilution*) is provided in FD systems by Rudolf and Antonovics (2005), here a host is rescued from pathogen mediated-extinction (*apparent mutualism*) by a second host that is infected by the same disease. In this model, the secondary host is assumed less competent, and therefore functions as a buffer, reducing further disease spread by replacing contacts (and therefore transmission events) with the original host, effectively reducing frequency of contacts between competent hosts. Lyme disease is a frequently cited example of the dilution effect where diversity of vertebrates hosts decreases the risk of spillover to humans. The bacterial pathogen (*Borrelia burgdorferi*) is vectored by the black legged tick (*Ixodes scapularis*), and uses the white footed mouse (*Peromyscus leucopus*) as a primary host; however, prevalence of *B. burgdorferi* decreases when a secondary, less competent host, the eastern chipmunk (*Tamias striatus*), increases in density (Keesing et al., 2006). Several other systems have also provided evidence for a dilution effect, for example, bovine TB in sub-Saharan Africa, which may be reduced at higher mammal density (Huang et al., 2013, 2014).

In contrast to the dilution effect, the *amplification* effect suggests that higher host diversity increases disease prevalence either *directly*, elevating contact rates by increasing total host density (Rudolf and Antonovics, 2005) or by the addition of a highly competent, super-spreader host (a phenomenon parallel to *the selection effect* in biodiversity science (Loreau and Hector, 2001)), or *indirectly* by changing host densities through competition (Holt and Bonsall,

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2017) (see Table 3). For example, higher amphibian diversity is thought to have increased Chytrid disease (caused by *Batrachochytrium dendrobatidis*) prevalence in some species of frogs, as highly competent (amplifying) hosts are more abundant in species-rich habitats (Ostfeld and Keesing, 2012). The amplification effect may also arise in vectored diseases (often modelled as FD due to density-independent contacts) if increased diversity supports more competent host species (Ostfeld and Keesing, 2000).

In FD, amplification depends on host *identity* and, by extension, host competence. Under strict assumptions of DD, amplification will always occur, as contacts increase with host density, and contacts are always additive and never substitutive (Dobson, 2004; Rudolf and Antonovics, 2005). Increasing the number of hosts simply increases encounter rates between S and I individuals, and will therefore always amplify the disease, regardless of the competence of the hosts. In contrast, the direct effect of diversity in FD transmission, assuming a constant number of contacts per time unit and varying competence, are mixed. The addition of a less competent host will always have a diluting effect, whereas the addition of a highly competent host may have an amplifying effect. In Table 3 we summarise how transmission type can cause dilution or amplification. Predicting the *indirect effects* of diversity is more challenging. Changes in prevalence will reflect changes in the relative abundance of hosts and their relative disease competence, and thus how communities are altered by the introduction of novel host species (Ostfeld and Keesing, 2000). Community evenness is a particularly important dimension in multi-host systems, as the relative dominance of the most competent host will largely determine disease dynamics (Ostfeld and Keesing, 2000; Sintayehu et al., 2017). For example, dilution can occur indirectly in Lyme's disease when the alternative host reduces the density of the main reservoir through competition (Ogden and Tsao, 2009). In all cases, it is assumed that the pathogen is a generalist and that hosts differ in competence, except for direct amplification in DD systems, which assumes contacts are additive and there is no limit to contacts per time unit. However, these latter assumptions may be unrealistic for many empirical systems (Ostfeld et al., 2008) and, as we discuss above, host contacts likely saturate over higher density (Antonovics, 2017). Thus, at a certain density, disease dynamics may switch from DD to FD dynamics, and so we might predict dilution effects to be generally more common at higher densities.

3.1.2 Pathogen effects on host community

While we expect a pathogen's persistence to reflect host abundance, host abundance might also be influenced by the pathogen. For example, pathogen sharing among hosts can result in *apparent competition* (Holt and Pickering, 1985). A reservoir host can indirectly suppress the density of a spillover host by acting as a source of infection, and if the reservoir host has a better adapted immune system to the pathogen, it can reduce the density of the spillover host via pathogen induced mortality. One example of apparent competition is spillover of the vector-transmitted Barley Yellow Dwarf virus (genus *Luteovirus*) from wild oats (*Avena fatua*), which reduced the abundance of the spillover host species, *Setaria*, allowing the wild oat to maintain ecological dominance (Power and Mitchell, 2004). Although disease dynamics may appear similar, and feedback into dilution or amplification effects, apparent competition describes the effect of pathogen prevalence on hosts, whereas, dilution and amplification describe the effects of

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host diversity on pathogen prevalence. Apparent competition is typically only a property of DD systems, but may be possible in FD systems if the pathogen is not directly diluted by a less susceptible, spillover host(s).

Apparent mutualism can occur in FD systems when hosts have equal competence. In this case, the introduction of a novel host can reduce the disease prevalence in the original host community members by replacing contacts. There is no 'competition' as all hosts are equally affected by the pathogen (Holt and Bonsall, 2017), and all hosts benefit from the addition of additional hosts. Apparent mutualism differs from dilution, as dilution assumes difference in host competence, while apparent mutualism assumes hosts are identical in their competence.

In summary, under assumptions of FD dynamics, increasing host diversity can result in apparent mutualism when hosts are equal in their competence, and dilution can occur when hosts have unequal competence. Under assumptions of DD dynamics, increasing diversity results in amplification, irrespective of differences in host competence, assuming each host adds to overall disease transmission. However, apparent competition is possible if hosts vary in competence and one host experiences lower pathogen related mortality, for example, through having a superior immune system.

3.2 Interspecific transmission

Changing host community structure changes intraspecific and interspecific contact rates, and thus disease dynamics. The interspecific transmission rate determines the effect of species richness on the outbreak potential, R_0. Disease competence determines a host's role as amplifier or diluter, as we have seen, the persistence of a disease in multiple hosts is determined by the interspecific and intraspecific transmission dynamics (section 3.1.1). For example, jackals (*Canis adustus*) need to be frequently reinoculated by rabies virus from domestic dogs to support an infection in the population (Rhodes et al., 1998; Keesing et al., 2006) as their intraspecific transmission is too low to sustain endemic prevalence, and thus jackals more likely a diluter than an amplifier of rabies. There are many approximations for interspecific transmission, focusing on the ecology of hosts or the co-evolution of pathogens and hosts, for example by using matching-allele and gene-for-gene models (Poullain and Nuismer, 2012). In this section we consider some approaches that we think may be most promising for addressing questions on the disease-diversity relationship. We also touch upon some methods of empiricalal quantifications of transmission paramters in Box 4.

Interspecific transmission can be modeled in a WAIFW-matrix (Who Acquired Infection From Who), an n by n - matrix showing the transmission between species in an n-species system, where intraspecific transmission can be found on the diagonal, and interspecific transmission on the off-diagonals (Dobson and Foufopoulos, 2001; Diekmann et al., 2010). In this matrix, transmission can be defined as $\beta_{i,j}$, where i is the receiving host and j the donating host (j infects i). This matrix can be used to calculate the community R_0, which determines the overall disease prevalence in the systems, and the contributions of each individual host (Diekmann et al., 2010). One way to estimate the interspecific transmission rate is to take the average of the intraspecific transmission rates, using a scaling parameter to account for differences in transmission potential between species i and j (Dobson, 2004). This

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scaling parameter can determine the magnitude of diluting and amplifying behaviour of each species in the system. A similar approach can also be applied to contact rates, κ, as defined in $\beta = \kappa \cdot c$, if one wants to define c separately for individual host species, rather than the community average (Anguelov et al., 2014). However, there can be asymmetrical transmission between hosts, for example Blancou and Aubert (1997) suggest that for a fox with rabies to infect another species, such as a dog or cat, requires a million times more virus particles than would be necessary to infect another fox (Ostfeld et al., 2008). Such asymmetries may be overlooked when using the average of the intraspecific transmission rates.

3.3 Quantifying contacts

Heterogeneity in contacts can drastically change the initial spread and final outbreak of a disease (Eames and Keeling, 2003). Craft (2015) argued that network models are required to accurately model wildlife populations. In wildlife diseases, for instance, identifying super-spreaders and their role in the network can be critical for intervention management. As example, in a simulation study of wild chimpanzees, Rushmore et al. (2014) show that vaccinating the most connected individuals reduces the vaccination threshold by 35% compared to random vaccination. New advances in biomonitoring methods can help in the construction of contact network models, capturing the complexity in interactions that many animals show, including territoriality, sociality, and individual variation in movements (Viana et al., 2014; White et al., 2017). These networks can also be useful if we wish to describe transmission between inter-connected populations. While we do not review this complexity here, we expand on some of these exciting methods in the supplementary material. However, obtaining the data to construct robust network models is research intensive, and simplifying assumptions of homogeneity are frequently adopted. As social networks homogenize over time (Cross et al., 2004), such simplifying assumptions might not be unrealistic. Nonetheless, new methods, such as use of camera-trapping of animals at aggregation sites, can be adopted to estimate intraspecific and interspecific contact rates (Barasona et al., 2017) and usefully inform SIR models.

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Box 4: Empirical approximations of intra-species transmission

Estimating β directly: Because it is challenging to quantify transmission rates directly, often approximations are used. For instance, viral particles activate effector T-cells, and so data on infection load can be approximated by measuring T-cells from serological samples of animal hosts (Blaser et al., 2014; Almocera and Hernandez-Vargas, 2019). Individual infection status can be determined for viral pathogens by (q)PCR, and viral pathogen load can be used to derive transmission rates (Streicker et al., 2010; Blaser et al., 2014; Almocera and Hernandez-Vargas, 2019; McCallum et al., 2017). Similarly for macroparasites, egg (dispersal stage) counts can be used to infer transmission rates (McCallum et al., 2017). Genome sequencing is a promising technique for estimating transmission rates for bacterial pathogens, as was illustrated for *Mycobacterium bovis*, and can also reveal spatial patterns of transmission (Biek et al., 2012). For viruses, we can adopt phylodynamic approaches to infer transmission rates from birth-death models (MacPherson et al., 2020). Basic host demography parameters, such as δ (host natural mortality) and r (host birth rate) are easily available, and can be allometrically scaled with host body size, we can similarly scale β (De Leo and Dobson, 1996). For vector transmitted diseases, surveys of vectors associated with hosts can give an approximation of the rate of spread of the disease, and may provide insights into interspecific transmission (Lu et al., 2010).

Estimating the probability of successful transmission, c: Even when the contact structure of the population is known, for example, through biological monitoring, it is still challenging to define the infectivity of a contact - the probability of successful transmission after contact (Craft, 2015; White et al., 2017). One approach used in wildlife disease dynamics is to quantify the Secondary Attack Rate (SAR), which is the ratio of the number of exposed hosts that developed the disease to the number of exposed hosts that did not (Childs et al., 2007). To accurately calculate the SAR, a clear distinction must be made between primary and secondary cases. For sexually transmitted diseases, which follow FD dynamics, the probability of becoming infected after contact can be calculated using the binomial distribution (Childs et al., 2007). The maximum likelihood of this probability following a single contact is identical to the SAR. While estimating c remains a challenge, compounded by the fact that most disease models summarize the process of transmission into a single parameter, it is important to capture accurately. These methods are described in further detail in the supplementary material.

4 Future challenges and conclusion

Defining the shape of the transmission function between species is challenging, and seemingly small differences can have dramatic effects on predictions from multi-species models (Dobson, 2004). Given current rate of biodiversity and habitat degradation worldwide, there is an urgent need for studies on the importance of how reduced diversity and environmental carrying capacity of wild species may influence the transmission rates of their pathogens, and how this might cascade to possible spillover events. Habitat fragmentation and a decrease in the carrying capacity of an ecosystem can both affect transmission dynamics (Childs et al., 2007; Lafferty and Holt, 2003), and at the interface

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between natural and converted landscape we can find increased interspecific transmission (Wolfe et al., 2005; Faust et al., 2018; Goldberg et al., 2008).

As most hosts and pathogens exist within multi-host systems, we need to better understand how transmission affects disease outbreaks in such systems. The next-generation matrix (Diekmann et al., 2010), described in section 3.2, which allows us to calculate the community R_0 and each host's relative contribution, is one promising framework for modelling the dynamics of multi-host pathogens and disease maintenance in the reservoir. However, the complexity in quantifying transmission, with asymmetries in interspecific rates and among potential hosts following spillover events (Wolfe et al., 2007; Auld et al., 2017), can make the application of such models fraught. Additional challenges include accounting for spatial heterogeneity and contact structure, although over longer timescales transmission dynamics may appear more homogeneous (Cross et al., 2004). However, as pathogen sharing is affected by the overlapping geographical ranges of hosts (Davies and Pedersen, 2008), investigating the effect of local versus global dynamics remains important.

It is also becoming increasingly clear that the evolutionary relationship between species plays a role in disease transmission, with strong evidence of phylogenetic signal in the likelihood of pathogen sharing among hosts (Davies and Pedersen, 2008; Farrell et al., 2019; Streicker et al., 2019; Olival et al., 2017). It is likely, for example, that similarity in the immune defenses of closely related species due to the evolutionary conservation of the cellular, immunological, or metabolic traits, favours virus exchange between them (Kuiken et al., 2006; Streicker et al., 2010). Similar phylogenetic signature in pest and pathogen sharing is observed in plants (Gilbert and Webb, 2007; Gilbert et al., 2012; Parker et al., 2015; Ssebuliba and Davies, 2021), and phylogeny is also suggested to be a strong predictor of pathogen impact, with declining severity of the effect of the disease with increasing evolutionary distance between hosts (Gilbert et al., 2015; Gougherty and Davies, 2021). It would be relatively straightforward to include this information in our models. For instance, following Parker et al. (2015), we can define the probability of successful transmission, c, to be dependent on the evolutionary relationship between hosts. Assuming that intra-species probability of successful transmission $c_i = \lambda_i$, we can simply define the probability of successful transmission of a pathogen from the recipient species, i, to the donor species j, c_{ij}, as:

$$c_{ij} = \lambda_j \cdot \frac{1}{1 + \psi PPd_{ij}} \tag{5}$$

where ψ is a scaling constant and PPd the Pairwise Phylogenetic Distance between the two hosts, such that at low PPd (closely related species), $c \approx 1$. That way, at low PPd, c converges to λ_j, the probability of successful transmission of the donating host. While the phylogenetic diversity (PD) of hosts - the sum of the evolutionary branch lengths connecting species - (Faith, 1992) can provide a useful predictor of disease prevalence (Rolland et al., 2012; Huang et al., 2013, 2014), the phylogenetic distance separating species may be a more useful metric for scaling the probability of interspecific transmission, and in predicting novel host shifts (Poullain and Nuismer, 2012).

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Spillover events are the driver of zoonotic epidemics, including that which precipitated the COVID-19 pandemic, and pathogen transmission rate is our best predictors of future host shifts and disease emergence (Poullain and Nuismer, 2012). In this paper we decomposed transmission into its separate parameters, and show how these are involved in the outbreak process. We defined a general contact rate that can encompass most common variations of the transmission function, and describe how contact rate underlies each.

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Tables

Nr.	$F(S,I)$	**Description**	**units** β_x	**Source**
		Homogeneous population		
1	$\frac{\beta_F SI}{N}$	Frequency-Dependence (FD)	t^{-1}	Anderson et al. (1992)
2	$\frac{\beta_A SI}{A}$	Density-Dependence (DD)	$ind^{-1}\ m^2\ t^{-1}$	Anderson and May (1982)
3	$\beta_D SI$	DD with constant area	$ind^{-1}\ t^{-1}$	Anderson et al. (1992)
4	$\beta_q SIN^{(q-1)}$	Intermediate	$ind^{-q}\ t^{-1}$	Smith et al. (2009)
5	$\frac{\beta_F SI}{K}$	Carrying capacity dependence	t^{-1}	This manuscript
6	$\beta_F \frac{SI}{N+X}$	Asymptotic transmission	t^{-1}	Diekmann and Kretzschmar (1991)
		Behavioural heterogeneity		
7	$\beta_{PL} S^m I^n$	Power law	$ind^{1-m-n}\ t^{-1}$	Hochberg (1991); Novozhilov (2008)
		Spatial heterogeneity		
8	$\beta_D I(N - \frac{I}{p})$	Refuge effect	$ind^{-1}\ t^{-1}$	Barlow (1991)
9	$\theta S \cdot \ln(1 + \frac{\beta_D I}{\theta})$	Negative binomial	$ind^{-1}\ t^{-1}$	Barlow (2000); Greer et al. (2008)

Table 1: Alternative compositions of the variables S and I and the transmission rate, β, in the transmission function,$F(S,I)$, in traditional SIR models. Note that for each model β assumes different values, depending on the units. See Table 2 for parameter definitions.

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Parameter	Description	Unit
β_x	Transmission rate	See Table 1
κ	Contact rate (individuals contacted per unit time)	t^{-1}
c	Probability of successful transmission	-
ξ	Number of contacts	Depending on the model
A	Area	m^2
q	Contribution of an added individual to average κ	-
X	Critical population size (half saturation time)	ind^{-1}
m	Contribution of an S individual	-
n	Contribution of an I individual	-
ω	Biotic/Abiotic factor	-
p	Aggregation	-
θ	Heterogeneous mixing term	ind^{-1} t^{-1}

Table 2: Parameters used in the transmission functions described in Section 2 and Table 1 and their corresponding units. The dimensions of parameter β depend on the transmission function and are described in Table 1.

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Mechanism:	**Dilution**	**Amplification**
FD	Direct: Encounter reduction	Indirect
DD	Indirect	Direct: Additive encounters or Selection effect

Table 3: Dilution and amplification occurring through various mechanisms. Varying host competence is assumed in all combinations, except in amplification for DD (bottom right cell), where varying host competence is not required.

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Figure legends

Figure 1

Spillover event of bovine Tuberculosis (bTB) from its reservoir, the African buffalo (*Syncarus caffer*), to a spillover host, the African bush elephant (*Loxodonta africana*). Graphs in figure show an approximation of the stages of transmission as described by McCallum et al. (2017). Both direct and indirect (environmental) transmission modes are shown, typical for transmission of the bTB pathogen. In orange the progression of the *mycobacterium* is shown, in the lungs of both hosts, as well as in their dispersal propagules. The figure gives an empirical example of the complexity of a pathogen's transmission cycle. Figure credit: Sylvia Herediaz, UBC Zoology.

Figure 2

Graphical representation of the decomposition of the transmission function, $F(S, I)$, in traditional SIR compartmental disease models. β is the transmission parameter, κ the contact rate and c the probability of successful transmission. On the left, we decompose the transmission parameter for homogeneously distributed host populations. On the right we show heterogeneously distributed host population, of which the dynamics are more complex and the transmission function is not as easily decomposed.

Figure 3

Flow chart showing how the contact rate function, $\kappa(N)$, determines the density- or frequency-dependent nature of the transmission function, $F(S, I)$, which in turn determines the dimensions of the transmission coefficient β_x. The first 3 panels show a spectrum from fully DD to FD, determined by parameter q. The right panel shows a transmission function that can vary from DD to FD with population size N.

Figure 4

Transmission function, F(S,I), in homogeneous populations with S constant at 100 individuals. A: FD transmission. B: DD transmission C: Intermediate transmission. With $q = 0.7$ in light blue, $q = 0.9$ in dark blue, and $q = 1$ in black. D:Carrying capacity with $K = 100$. E: Asymptotic transmission with ω_0=1 in red, ω_0=10 in purple, and ω_0=100 in blue. F: Power law transmission, with $n = 0.2$ in black, $n = 0.5$ in dark green, and $n = 0.8$ in light green. Note, differing scales on y-axis.

Figure 5

Transmission function, F(S,I), in spatially heterogeneous populations, with $S = 100$. A: Refuge effect. Red: $q = 1$, orange: $q = 0.8$, blue: $q = 0.7$. Solid line indicates the range of biologically relevant transmission. B: Negative binomial. Gray: $k = 1$, orange: $k = 1.5$, red: $k = 3$. Note, differing scales on y-axis.

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5 Figures

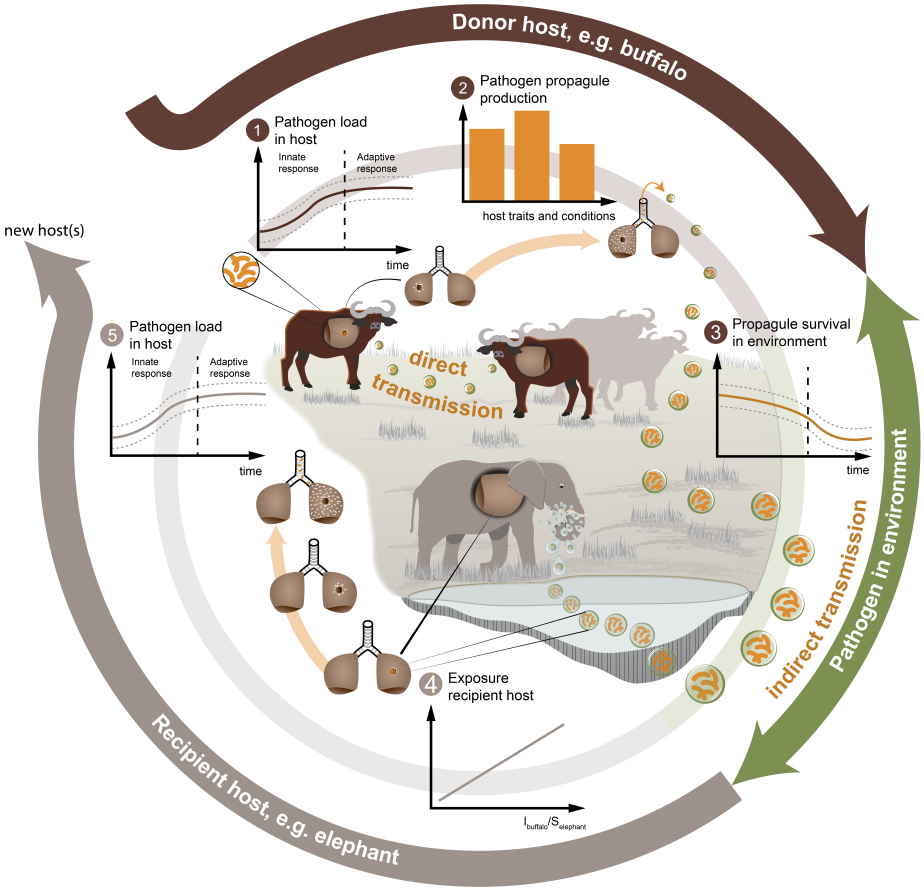

Figure 1

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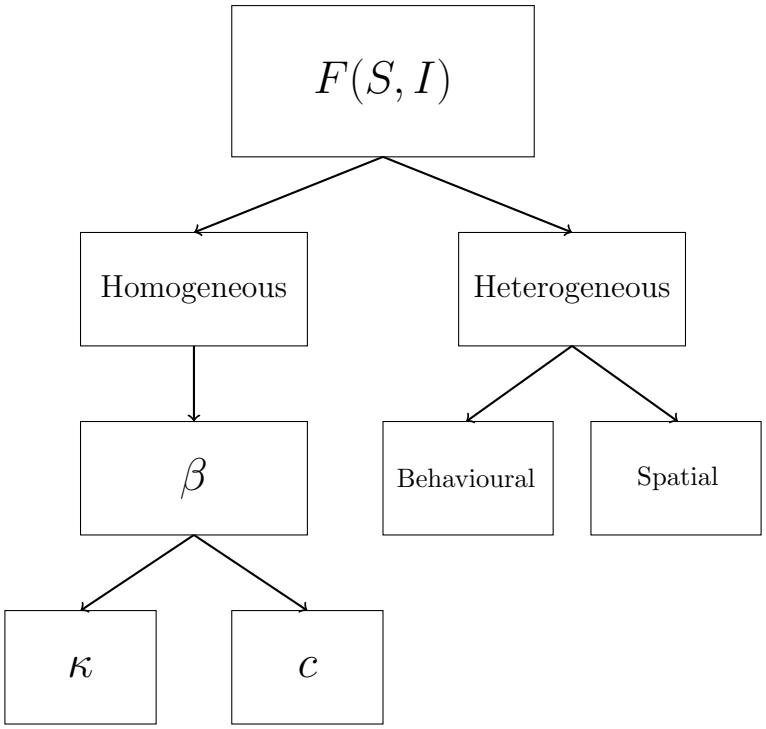

Figure 2

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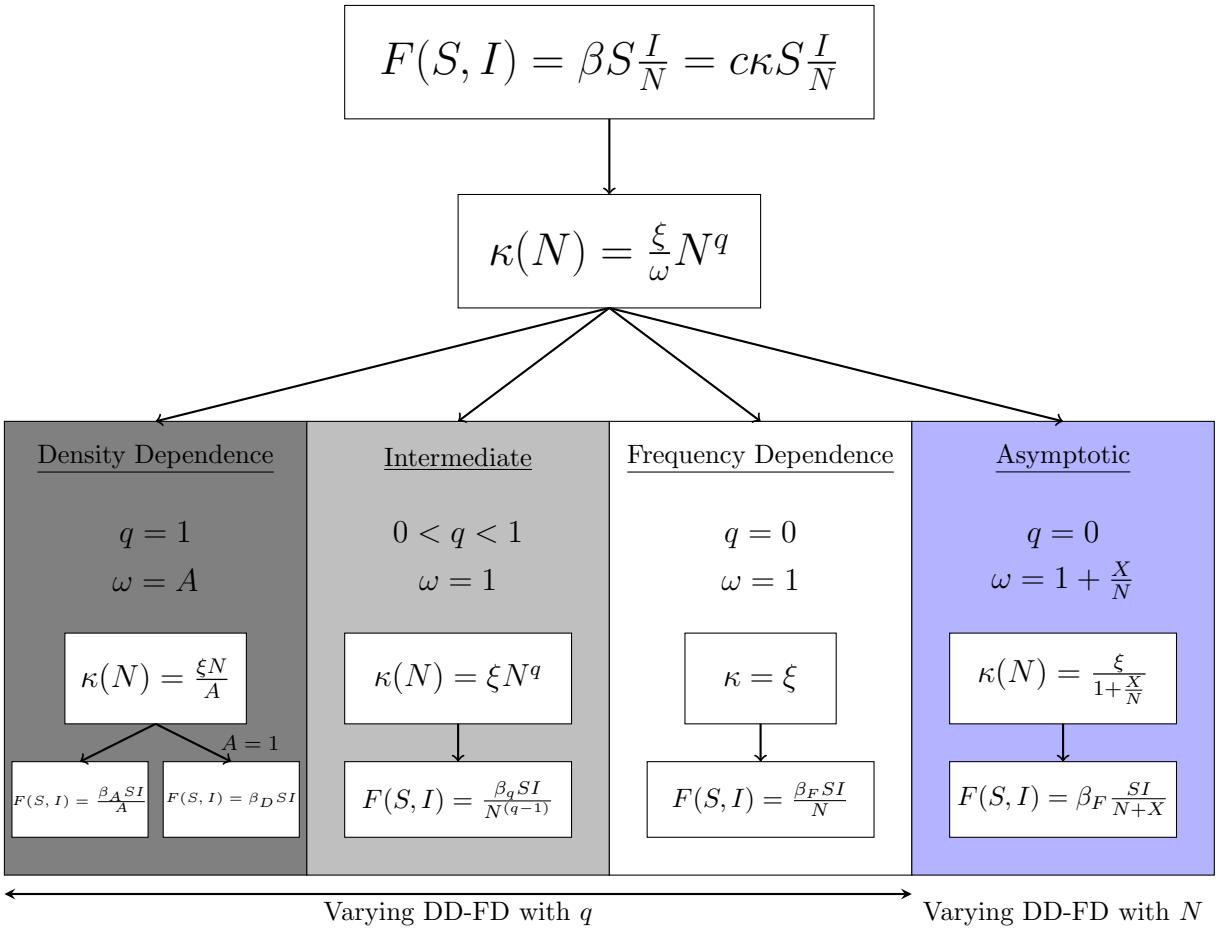

Figure 3

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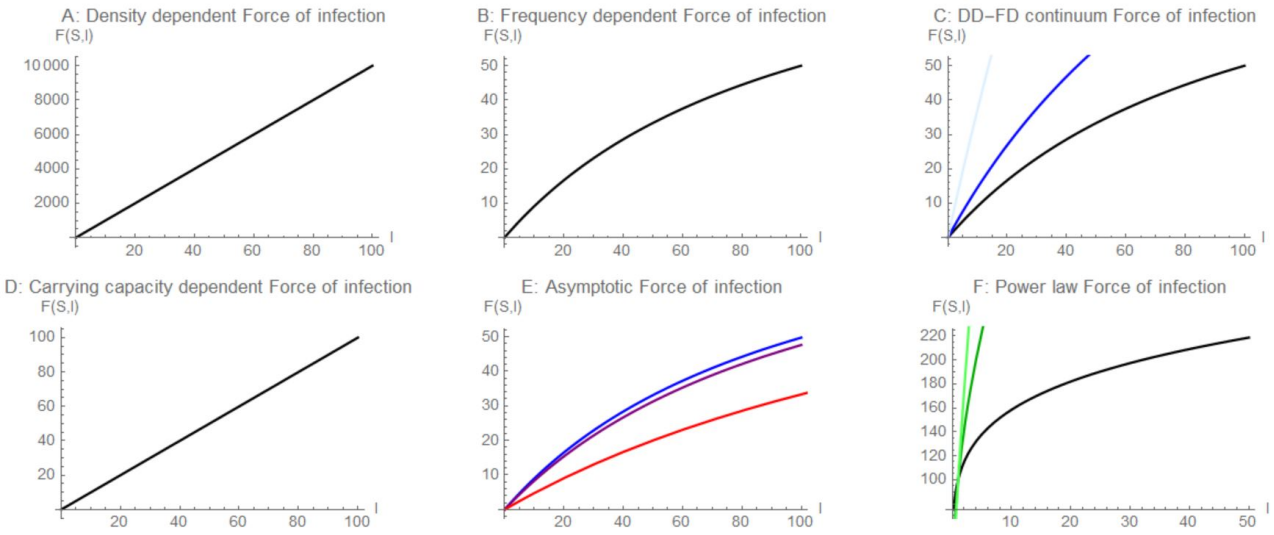

Figure 4

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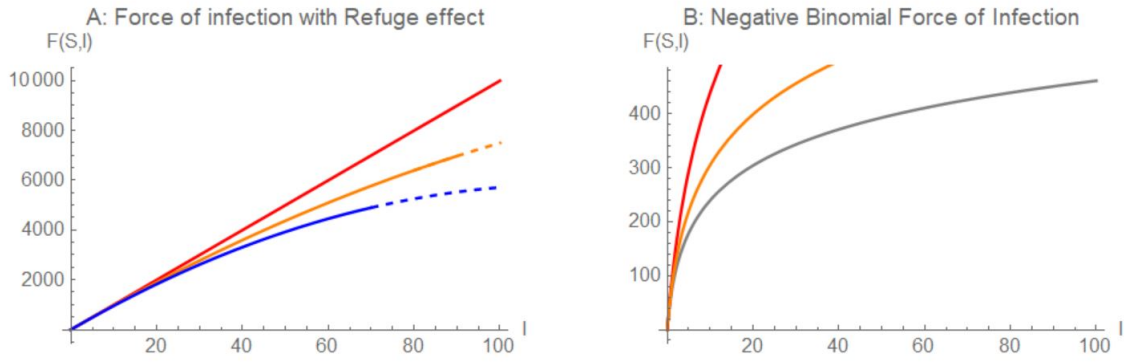

Figure 5