More than a flying syringe: Using functional traits in vector borne disease research

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Abstract

Vectors are responsible for the transmission of many important endemic and emerging diseases. The functional traits of these animals have important consequences for pathogen transmission, but also for fitness and population dynamics of the vectors themselves. Increasing empirical evidence suggests that vector traits vary significantly at time scales relevant to transmission dynamics. Currently, an understanding of how this variation in key traits impacts transmission is hindered by a lack of empirical data as well theoretical methods for mechanistically incorporating traits into transmission models. Here, we present a framework for incorporating both intrinsic and environment-driven variation in vector traits into empirical and theoretical vector-borne disease research. This framework mechanistically captures the effect of trait variation on vector fitness, the correlation between vector traits, and how these together determine transmission dynamics. We illustrate how trait-based vector-borne disease modelling can make novel predictions, and identify key steps and challenges in the construction, empirical parameterization and validation of such models. Perhaps most importantly, this framework can also be used to prioritize data collection efforts.

Introduction

Vector borne diseases (VBDs) remain a serious threat to health and economic welfare worldwide. The alarming invasion of the mosquito-transmitted Zika virus into the Americas (Faria *et al.*, 2016) is only an episode in a long history of VBD impacts on global health. These infections are significant sources of economic and public health burdens globally. Mosquito-borne diseases alone are thought to directly impact the well-being and livelihood of at least one-third of the human population (WHO). For example, Chagas disease costs Brazil an estimated 1.3 billion USD in lost productivity each year (Lee *et al.*, 2013). VBDs also include re-emerging infections, such as dengue (San Martín *et al.*, 2010; Dick *et al.*, 2012), and new threats, such as chikungunya and Lyme disease (Lee *et al.*, 2013; Mead, 2015; CDC, 2016). The impacts of VBDs are not limited to humans. Many important and emerging diseases of plants (e.g., tomato leaf curl virus, cassava mosaic virus, and citrus greening disease (Taylor *et al.*, 2016)) and livestock (e.g., bluetongue (Wilson & Mellor, 2009)) are transmitted by vectors.

Evidence from a wealth of empirical and theoretical studies indicates that the behavior and life history of vectors are important determinants of transmission. The importance of vector abundance and life history in transmission dynamics is reflected by the fact that almost all VBD models incorporate vector biting rate, competence, adult survival, and density (Jeger *et al.*, 2004; Reiner *et al.*, 2013). These aspects of vector biology can be described as traits. A trait is any measurable feature of an individual organism. Specifically, a trait is functional when it directly (e.g., mortality rate) or indirectly (e.g., development time) determines individual fitness (McGill *et al.*, 2006; Gibert *et al.*, 2015) (henceforth we use "functional trait" and "trait" synonymously). In natural populations, trait variation between individuals, and within individuals over time is ubiquitous and has been shown to alter population and community level processes (Imura, Toquenaga, & Fujii, 2003; McGill *et al.*, 2006; Agashe, 2009; Gibert *et al.*, 2015). It is widely accepted that vector traits are also important for transmission and they are likely to vary over time and space (Smith *et al.*, 2014). Ideally, trait variation should be mechanistically incorporated (as processes) into transmission models to improve the ability of models to predict transmission through time and space.

There are two related challenges to understanding the parameter space in which trait variation could affect transmission. First, we lack data on many of these traits and how they vary for most vector species. Thus, researchers are frequently forced to infer trait values (for example, using the inverse of gonotrophic cycle lengths to infer biting rate) or use data from related species to parameterize models (Johnson et al. 2015). Second, while there are many statistical, correlative methods, we lack a theoretical framework to mechanistically incorporate trait variation into transmission models.

Trait variation can change transmission dynamics, either by changing vector abundances (dynamics) on similar time scales as pathogen transmission, or by directly changing on transmission potential itself (e.g., vector biting rate or competence). This in turn is partly due to the fact, as noted originally by May & Anderson (1979), that the majority of animal and plant disease vectors are arthropods, and therefore have significantly shorter generation times (and thus, operate at faster timescales) than their host. Furthermore, arthropods are small ectotherms, which means their abundances vary relatively directly with fluctuations in environmental variables (especially, temperature;(Dell, Pawar, & Savage, 2011; Amarasekare & Savage, 2012). Disease transmission is very much an ecological process. Until we incorporate trait variation into VBD transmission models our ability to predict transmission dynamics at longer temporal and larger spatial scales will remain limited, like any ecological model that lacks a mechanistic basis (Getz *et al.*, 2018). To incorporate trait variation robustly, the mechanistic links between biological parameters, and how their effects on vector population fitness can change population dynamics and transmission rates, need to be considered. Recent work has begun to make progress in this direction by incorporating metabolic traits into micro- and macro-parasite disease transmission (Molnár *et al.*, 2017).

Here, we propose a trait-based framework as the way forward on both empirical and theoretical fronts for making more accurate VBD transmission dynamic predictions. We begin by reviewing empirical evidence for trait variation in vectors and the degree that it has (or in some cases has not) been incorporated into previous transmission models. We then describe the trait-based framework and explain how it can be operationalized, both in terms of incorporating traits into transmission models, and data collection efforts. We provide an example of how this approach can

produce novel predictions and allows for investigation into the degree to which different traits drive transmission dynamics and underlying fitness effects. Finally, we discuss further challenges in the way of implementing a trait-based approach in VBD research.

Evidence for Trait Variation in Vectors

Variation in vector traits can be grouped into three primary types: 1) variation across the lifespan of an individual; 2) variation within a population; and 3) environmentally driven variation. These are illustrated in Fig. 1. Note that we use derivatives for quantifying over-time, with-environment and combined types of trait variation to represent the idealized scenario that the trait value function varies continuously and smoothly with respect to another variable. In reality, it may not always be possible to express these as smooth functions for to empirical or theoretical reasons.

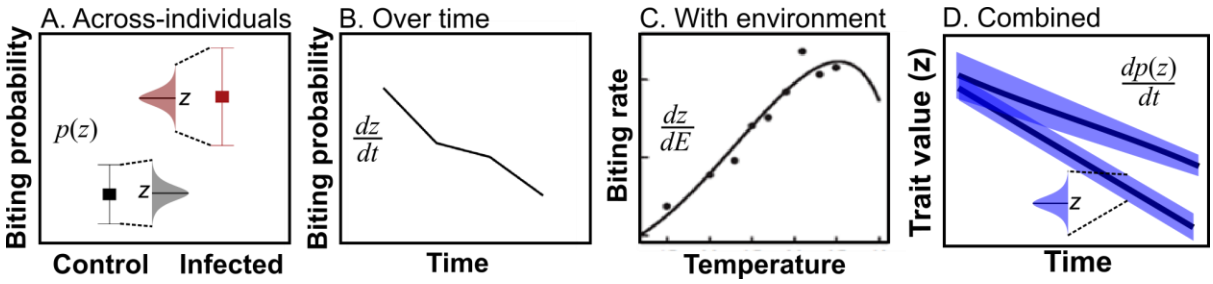


Figure 1. Types of trait variation found in all VBD systems. A: Across-individuals: for example, variation in biting probability within a population at a fixed point in time. Underlying the error bars around each mean is a quantifiable trait probability distribution *p*(*z*). In this example, variation in trait values *z* were, in part, generated by differences in infection status (Cator *et al.*, 2013). **B**: Within-individual, over time: for example, biting probability may vary over the vector's lifespan (Cator *et al.*, 2013). Such variation is quantifiable as a continuous time-dependent function *dz/dt*, where *dz* is the (differential) change in trait variation change with time (*dt*). **C:** Environment-driven: For example, biting rate varies unimodally with temperature (Mordecai *et al.*, 2013). Such variation is quantifiable as a continuous environment state-dependent function, *dz*/*dE*. **D:** Combined variation: The three types of trait variation may appear in combination. For example, across-individual trait variation may change over time. The upper line represents change in mean and variance of the trait, while the lower line represents change only in the mean.

Variation across the lifespan of an individual. For transmission to occur a vector must survive the extrinsic incubation period of the parasite, which is often long compared to vector life span. Thus, how traits vary across lifespan could impact patterns of transmission. Vector behavior and life history may vary over the lifetime of an individual, for example, due to intrinsic processes such as aging. There is evidence for age-specific vector competence (Soliman *et al.*, 1993), immune function (Hillyer *et al.*, 2005; Christensen *et al.*, 2005; Laughton, Fan, & Gerardo, 2014), flight performance (Nayar & Sauerman, 1973) and feeding behavior (Alto, Lounibos, & Juliano, 2003; Den Otter, Tchicaya, & Schutte, 2008; Bohbot *et al.*, 2013) in vectors. When multiple life stages of the vector are involved in transmission, transmission efficiency may vary with stage (Caraco *et al.*, 2002; Coletta-Filho *et al.*, 2014). All these time-dependent changes in vector traits could lead to significant variation in the number of infectious vectors and their contact rates with hosts.

Variation within a population. Variation within a population (for example due to intrinsic genetic variation) can lead to subgroups of the vector population having a disproportionate effect on the measured average individual fitness and transmission potential. There are multiple examples of this kind of within-population variation in vectors. For example, the nutritional status of vectors can alter both their vector competence and several behavioral parameters linked to VBD transmission (Takken *et al.*, 2013; Shapiro *et al.*, 2016). Body size, varies within populations (Renshaw, Service, & Birley, 1994; De Xue, Edman, & Scott, 1995; Kindlmann & Dixon, 2003) and can drive significant variation in feeding, assimilation, and respiration, and therefore development and mortality rates (Brown *et al.*, 2004; Savage, 2004; Amarasekare & Savage, 2012). Inter-individual variation in age-specific

mortality is important for transmission (Clements & Paterson, 1981; Harrington *et al.*, 2001, 2008; Styer *et al.*, 2007). Recent evidence from several different systems shows that vectors infected with a variety of pathogens exhibit altered foraging behaviors (reviewed in (Murdock, Luckhart, & Cator, 2017)). These types of variation between individuals in key traits such as biting rate, host preference, and longevity ultimately impact VBD pathogen transmission rate. This is particularly true when vector pathogen susceptibility co-varies with transmissibility (Keeling *et al.*, 2003).

Environmentally driven variation. The vast majority of vectors are small ectotherms, so their behavior and life history are sensitive to their environment. Thus, the third type of variation, due to environmental drivers, may have short- or long-term effects on vector traits of the vector (Fig. 1). The majority of data on this kind of variation, not surprisingly, comes from investigations of temperature. Many studies have measured an effect of variation in environmental temperature on vector life history (Kersting, Satar, & Uygun, 1999; Bayoh & Lindsay, 2003; Delatte *et al.*, 2009; Ciota *et al.*, 2014) and competence (Kramer, Hardy, & Presser, 1983; Murral *et al.*, 1996; Dohm, O'Guinn, & Turell, 2002; Paweska, Venter, & Mellor, 2002; Wittmann, Mellor, & Baylis, 2002). Other environmental variables, such as humidity, can also directly affect vector life history (Wittmann *et al.*, 2002; Costa *et al.*, 2010).

In addition to vector trait variation data, there are also data suggesting that these traits, and variation in them, is mechanistically linked. For example, mosquitoes infected with bird malaria parasites exhibit reduced fecundity, which in turn increases longevity (Vézilier *et al.*, 2012). These kind of classical life-history trade-offs have implications for both vector population fitness (and therefore abundance) and transmission probability. Therefore, any theoretical framework that incorporates vector traits and their variation would also account for the mechanistic relationships between these traits. Such a theoretical framework would be able to capture changes in transmission dynamics that may emerge from traits (including those not directly related to transmission), trait variation, correlations between traits, and resulting vector population dynamics. There is evidence from other areas of ecological research that this type of mechanistic incorporation of traits can yield new insights, particularly in relation to transmission (Molnár *et al.*, 2017). Work from other fields indicates that both the mean and variation of a trait's distribution can have strong effects on the dynamics of populations (Norberg *et al.*, 2001; Bolnick *et al.*, 2011; Gibert *et al.*, 2015). Further, traits and relationships between traits have been found to be metabolically linked (Charnov, 1993; Brown *et al.*, 2004; Savage, 2004) and these relationships can drive population and community-level processes (Norberg *et al.*, 2001; McGill *et al.*, 2006; Bolnick *et al.*, 2011; Gibert *et al.*, 2015; Pawar, Dell, & Savage, 2015a). For example, inter-individual variation has been used to explain population stability in insects (Agashe, 2009), persistence of host-parasitoid populations (Imura *et al.*, 2003), and community structure and ecosystem processes in herb communities (Crutsinger *et al.*, 2006).

Current approaches to incorporating traits variation into transmission dynamics

Classical compartment models

The history of including traits into models for VBDs goes back to classical compartment (SIR or SEIR) models. These models focus on the frequency of different (Susceptible, Infected, Exposed, Recovered) sub-populations of the host and vector, ignoring fluctuations in abundances of the two species' populations. For example, consider the Ross-Macdonald type model for malarial transmission by a mosquito (Fig. 2, SI Section 2), on which many current VBD models (including non-mosquito vectors) are based (MacDonald, 1957; May & Anderson, 1979; Jeger *et al.*, 2004; Smith *et al.*, 2012; Reiner *et al.*, 2013). This model focuses exclusively on the parameters (most interpretable as traits) governing transmission rate of the pathogen between susceptible and infected vector and host subpopulations, most of which are mosquito traits. It yields a relatively simple equation for basic reproduction number of the disease (R_0)—the number of new infectious cases that would arise from a single infectious case introduced into a fully susceptible host population—which quantifies its transmission potential or risk (MacDonald, 1957; Smith *et al.*, 2012) (see SI section 2 for derivation):

$$R_0 = \left(\frac{Va^2bce^{-\mu P}}{Hd\mu}\right)^{\frac{1}{2}} \qquad 1$$

Here, V is vector density, a is per-vector biting rate, b is the proportion of the bites by infective mosquitoes that produce infection in susceptible humans, c is the proportion of bites by susceptible mosquitoes on infectious humans that infect mosquitoes (thus, bc is vector competence), μ is adult vector mortality rate, P is the extrinsic incubation period of the pathogen within the vector, H is host density, and d is the rate at which infected hosts recover and acquire immunity (Fig 2).

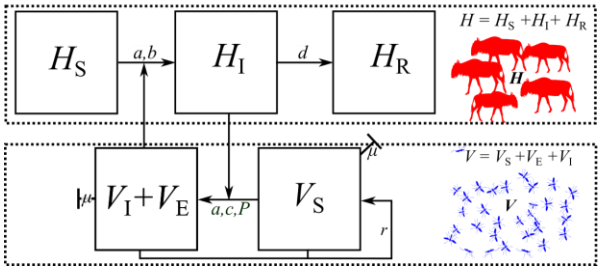


Figure 2. **Traits in classical compartment models.** As an illustration, we show here a Ross-Macdonald type model for malarial transmission by a mosquito vector. Most of the vector parameters in this model — a, b, c, P, μ — are directly measurable vector traits (a, μ), or can be derived from underlying vector and parasite traits (b, c, P). The corresponding equations and parameter definitions are shown in SI section 2.

This modelling approach omits both trait variation and vector population dynamics (that is, it effectively assumes that total vector (V) and host (H) population densities are constant) and that the vector (a, b, c, P, μ) or host (d) parameters do not vary across individuals or over time. These vector parameters are all essentially traits that are either directly-measurable properties of the vector itself (a, μ) or which can be derived from underlying traits of the vector and parasite (b, c, P). Thus, the classical models assume that vector (and host) traits do not affect total vector or host population size, and that these traits do not vary in any way (Fig. 1). Furthermore, all of the vector's biology and ecology are represented by only its adult (often female) biting rate, survival, extrinsic incubation period, competence, and abundance – all of which are assumed to be independent of each other. For example, biting rate (a) is assumed to have no effect on mortality (μ) or vector population density (V) and does not vary across individuals or over time. All individual hosts and vectors are modelled as having an identical risk of infection that remains constant over time and vectors interact exclusively with the target host. This effectively reduces the vector to a homogeneous vehicle to transmit pathogens and nothing more – a "flying syringe".

The classical compartment model with vector population dynamics

Classical compartment models have been extended to incorporate vector population dynamics, by adding vector life-stage compartments (May & Anderson, 1979; Anderson & May, 1979; Hoshi, Higa, & Chaves, 2014; Johnson *et al.*, 2018; Ng *et al.*, 2018) (Fig. 3). This introduces additional parameters for the vector's life history, all of which are directly measurable vector traits (also called demographic rates, e.g., mortality, fecundity), or parameters which can be derived from underlying traits (e.g. the transition probabilities (p_i's) in Fig. 3 can be derived from stage-specific survivorship and development time). The Anderson-May framework includes population dynamics and vector (life-history) traits, but still ignores two key features of traits. First, like in the classic compartment models, traits are still not mechanistically linked; for example, biting rate (a), mortality (μ) and fecundity (f) are considered independent parameters under this framework. Second, trait variation is not considered (Fig. 1); all vectors are assumed to have the same trait values across individuals or time (e.g., no age-related changes).

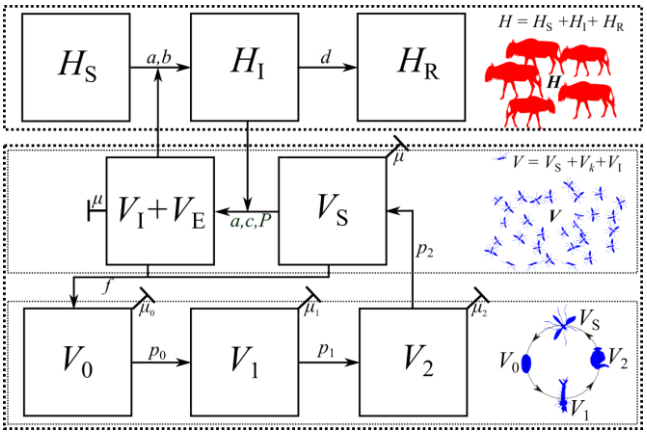


Figure 3. Traits in the classical compartment model with vector population dynamics included (Anderson-May framework). In addition to the host and vector transmission compartments, the Anderson-May framework includes the vector life-history compartments. As an illustration, we extend the classical Ross-MacDonald type models model for mosquito-borne arboviruses (Fig. 2) to include the insect's life history. This introduces additional parameters (vector life stage-specific μ's, fecundity f, and stage transition probabilities p_i's), all of which are directly measurable vector traits (the μ's, f), or which can be derived from underlying traits (the p_i's). The corresponding equations and parameter definitions are shown in SI section 2.

Other trait-focused elaborations of classical models

Subsequent studies have incorporated trait variation into the compartmental model or Anderson-May models. Reiner et al (2013) reviewed the state of modelling for mosquito-borne infections. They found that some extensions, such as parasite latency in mosquitoes, are commonplace, while others, such as heterogeneity in host – mosquito contact or variation in individual host and vector attributes, are rare (Reiner *et al.*, 2013). In studies that do include variation in a mechanistic way, the results can be dramatic. For example, Brand, Rock, & Keeling, (2016) showed that incorporating realistic variation in EIP and gonotrophic cycle length/biting rate over time (by explicitly thinking about how midge vectors interact with potential hosts) can dramatically change estimates of R0 as well as the impact of vector control for bluetongue. However, we have not found examples of studies that have systematically included both mechanistic linkages between, and variation in, traits. Instead, when links between traits and their variation are included, they may not be done so in a mechanistic fashion. For example, Brady *et al.* (2016) modelled the feedback between adult female mosquito blood feeding and egg laying and larval ecology, but did not link these traits mechanistically.

Most recently, trait variation has been incorporated directly into compartment models by "plugging in" environment driven (temporal) trait variation. That is, model parameters are defined as functions of the environmental driver(s) (Fig. 4). For example, Parham & Michael (2010) derived an equation for mean, asymptotic vector population size as a function of traits that are then allowed to be functions of environmental conditions. Mordecai et al. (2013) used the Parham & Michael (2010) approach for modelling V, but incorporated temperature driven traits variation of the underlying life history traits as well as other (transmission) traits in the Ross-MacDonald type models model more accurately. Specifically, they incorporated the temperature dependences of eggs produced by all females in the population per day, the probability that the eggs will hatch and the larva would survive to adult, and the average egg to adult development rate, and incorporated the known hump-shaped responses of these and other traits to temperature. Brand et al. (2017) took a similar approach for allowing biting/incubation parameters to depend on temperature, but model the vector population using a statistical instead of mechanistic approach.

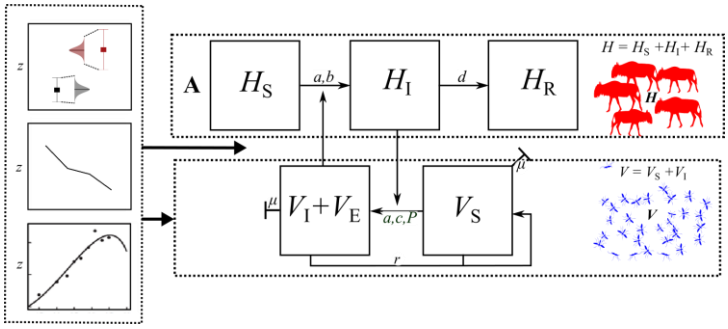


Figure 4. The plugging-in approach to incorporate trait variation into VBD dynamics. Here traits and variation in them are used to drive specific components of the classic compartment model (Fig. 2) directly. Traits are still not related to each other mechanistically, and do not drive the transmission process dynamically through changes in population abundances (e.g., as would happen in the Anderson-May model framework).

Other studies have used a similar plugging-in approach to show that variation in single traits such as age-specific mosquito mortality drives changes in the predicted sensitivity of R_0 to mosquito control (Styer *et al.*, 2007; Bellan, 2010; Novoseltsev *et al.*, 2012). Incorporating variation in single life history traits associated with infection (McElhany, Real, & Power, 1995; Koella, 2005; Lefèvre & Thomas, 2008) or nutrition (Shapiro *et al.*, 2016) have also been found to affect key VBD parameters such as biting rate. In some cases, specific components of vector ecology have been added to the Ross-MacDonald type models model and the effect of an environmental driver (Beck-Johnson *et al.*, 2013) or species interactions (Depinay *et al.*, 2004; Nakazawa, Yamanaka, & Urano, 2012) on vector immature development has affected vector abundance. All these plugging-in approaches have provided interesting insights into possible effects of trait variation, but except in cases where environmental variables (e.g., temperature) drive variation in multiple traits in a similar way (e.g., Mordecai et al 2013, 2017), do not mechanistically link traits.

A trait-based framework for VBD research

Thus, previous work has incorporated trait variation into models of vector-borne disease dynamics to varying degrees, yielding important insights into transmission dynamics. However, none of these approaches incorporate both mechanistic linkages between traits (e.g., co-variation in biting rate and survival), and trait variation (across time, space, and individuals) on population and transmission dynamics. Here, we present a general trait-based research framework that places these previous approaches in a common context, and can provide a foundation for systematically tackling the challenge of incorporating trait variation into VBD dynamics. The framework is illustrated in Fig. 5. In general, a full trait-based VBD system's specification must include (SI section 1):

1. **Transmission compartments:** For example, the SIR compartments as presented in the Ross-MacDonald type models (e.g., H_S, H_R) and may have additional host sub-compartments (H_j, where $j \geq 0$) tailored to a particular disease.
2. **Vector life history compartments:** These would include the commonly used infected susceptible vector sub populations (V_S, V_I), but additionally include the vectors' juvenile life stage subpopulations, starting at birth (V_0) and followed by immature stages (V_l, where $l \geq 0$). In adult stages, we include the potential for additional stages (V_k) leading to an infectious adults (V_I).
3. **Species interaction compartments:** These will depend on the type of interaction desired, but typically at least one consumer-resource interaction would be necessarily incorporated, as all vectors arguably experience significant mortality from predation in one or more life stages. This would require compartments for a resource species consumed by the vector (R_1) and predator species that consume the vector (C_1). In more complex systems, with multiple consumers and resources additional compartments could be added (C_n, R_m).
4. **Trait Variation**: A suite of trait (e.g., vector mortality, fecundity and biting rates) to parameter mappings that determine fitness effects, and at least a single type of trait variation, such as with an environmental factor (dz/dE; e.g., temperature) (Fig. 1, 5).

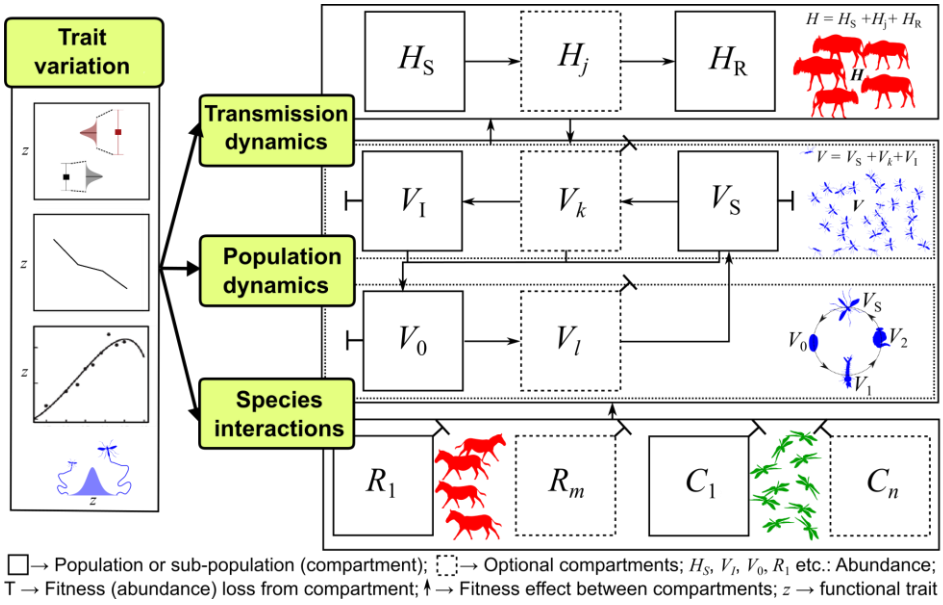


Figure 5. The trait-based framework for vector-borne disease systems. For illustration, we have used a mosquito-borne disease, but this framework can be applied to any VBD with distinct stage or age classes (further details in SI). Arrows between panels represent parameters (potentially with underlying traits) that determine population or transmission dynamics through (absolute) fitness effects. *Transmission dynamics compartments*: Number of Susceptible (S), Infected (I), and Recovered (R) hosts (H_S, H_I, H_R, respectively; additional compartments, H_j, can be added) and number of Susceptible, Infected, and Exposed (E) vectors (V_S, V_I , V_E respectively). *Vector population dynamics compartments*: number of vector individuals at egg, larval pupal and adult stages (V_0, V_1, V_2, V_S respectively; additional compartments V_k can be added); *Species interaction compartments*: Abundance of a single resource species (R_1) that is the primary energy source of the vector population (may actually be the host itself, so $R_1 = H_S$), and a single consumer species (C_1) that is the primary source of mortality for the vector population; *Trait variation*: A suite of trait to parameter mappings that determine fitness (e.g., vector mortality, fecundity and biting rates), and a single type of trait variation, such as variation with an environmental factor (dz/dE; e.g., temperature; see Fig. 3). For developing a mathematical model of such a system, the most common tool would be ordinary differential equation (ODE) systems, as illustrated in SI Section 1.

Note that in Fig. 5, we do not show explicit linkages between trait variation, consumer-resource, and life history sub-compartments because these will vary with VBD system. For example, in the case of most aphid-transmitted diseases, the resource (R) and host (H) are often the same. For other vectors, such as *Anopheles* mosquitoes, the transmission relevant hosts (H) may make up only a proportion of the resources (R) that regulate growth and reproduction (e.g. (LoGiudice *et al.*, 2003; Donnelly *et al.*, 2015)**)**.

As we have discussed above, much of the ground work for trait-based VBD research has already been laid by previous work. Our framework builds on these efforts by proposing mechanistic Trait-Parameter mappings, and incorporating trait variation (and co-variation) into these compartments, as explained below. It seeks to incorporate three key classes of functional traits:

1. *Life history traits*: These are measured in the context of life cycles (such as metabolic, mortality, and fecundity rates), without considering interactions with other organisms (e.g., host, predators or prey of the vector). If aggregated across individuals in a population, these are also called demographic rates. Variation in life history traits determines the number of susceptible vectors (V_S) by determining the total vector population's fitness. For example, variation in individual vector life-history traits, such as density-independent mortality rate (μ) and maximal fecundity (f), change population fitness and thus abundance.
2. *Interaction traits*: These determine both, interactions within the vector population (e.g., intraspecific interference or mating frequency), and between vectors and other species, including

the species which may act as resources (prey, for example). Life history and interaction traits together determine vector population abundance and realized interaction rate with potential hosts, thereby driving transmission and outbreak dynamics (Fig. 5). These interactions affect vector abundance by linking it dynamically with abundance of consumers and resources. Including interactions with both the transmission host and other species not directly involved in the transmission cycle, such as predators, is important because it allows one to mechanistically incorporate effects of species interactions occurring outside of the transmission cycle on the number of susceptible vectors available to become infected, the rate at which susceptible and infected vectors encounter hosts, and the mortality rates of vectors.

3. *Transmission traits*: These determine transmission of the pathogen between the vector and host population, and ultimately, between host subpopulations. For example, variation in biting rate and vector competence directly impact transmission rate by altering that the rates at which vectors become infected (move from V_S to V_I), and the rate at which susceptible hosts become infected (move from H_S to H_I) (Fig. 5). Certain transmission traits are also interaction traits (e.g., biting rate).

Physical traits (e.g., body size, or wing length) are also important, but only if they can be mapped onto one of these three types of traits. A key feature of a trait-based VBD framework is that model parameters need to be either interpreted as one of these classes of traits, or decomposed into one or more traits. Also, under this framework "fitness" has a more general meaning in its evolutionary connotation (see Glossary): it is the change in abundance value of any compartment (population). So, for example, mortality rate (decreases population abundance), fecundity (increases abundance), and biting rate (affects abundance thorough fecundity and mortality), are all parameters in that they exert fitness effects in the VBD system, and each can also be interpreted as a trait because it is directly measurable. In contrast, vectorial capacity is not a trait as it is a derived measure and cannot be directly measured. Thus the distinction between "trait" and "parameter" is a matter of context (see Glossary). Finally, note that a fitness effect in the transmission component (Fig. 5) changes abundances of the host's infected sub-population through changes in transmission rate (e.g., through biting rate) and reflects a change in fitness of the pathogen's (population) fitness.

A Traits-Based Framework Roadmap

How can the construction of such a framework be tackled in practise? For this, research programs may focus on as many of the following four sequential components or steps as possible. Each step requires a relationship or mapping (→) to be quantified through empirical studies coupled with mathematical modelling:

1. Trait→Parameter
2. Trait-variation→Fitness Variation
3. Fitness→Population Dynamics
4. Population Dynamics→Transmission Dynamics

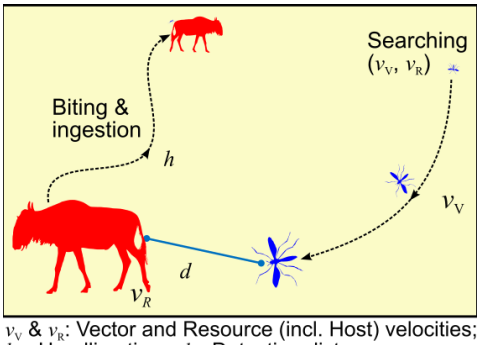
We now explain each of these steps, followed by an example.

1. *Trait→Parameter*

A key component of any trait-based framework is the mapping of trait values onto mathematical model parameters where possible (Fig. 5). This mapping entails mathematical deconstruction of parameters into mechanistic trait components. This bounds the parameter's space (its feasible range), and also reveals how different parameters are linked, and therefore interact or trade-off with one another to impact compartment fitness and ultimately, transmission dynamics. Biomechanical and metabolic approaches in ecology that link physical and performance traits are crucial for tackling this challenge (Brown *et al.*, 2004; McGill *et al.*, 2006; Amarasekare & Savage, 2012; Pawar *et al.*, 2015a). A well-known example is the scaling relationship between body size (a physical trait) and metabolic rate (a performance trait), which in turn determines individual somatic growth rate (Charnov, 1993; Brown *et al.*, 2004). Metabolic models for traits that determine encounter rate parameters between vectors and other organisms, including hosts (Fig. 1, *V*, *R*, *C*, and *H*), are now beginning to be established in ecology (Pawar, Dell, & Savage, 2012; Pawar *et al.*, 2015a; Dell, Pawar, & Savage, 2014; Gilbert *et al.*, 2014; Rizzuto, Carbone, & Pawar, 2018) and can be used in the

trait-based VBD framework. Metabolic trait models are for capturing within-host parasite dynamics are also beginning to be developed (Kirk *et al.*, 2018).

To illustrate Trait→Parameter mapping, we use recent advances in mechanistic, metabolic trait-based theory for species interactions (Pawar *et al.*, 2012, 2015a; Gibert *et al.*, 2015) to develop a mathematical model that deconstructs biting rate into its underlying functional traits and shows how it is ultimately linked to the vector's adult body size. Heterogeneity in biting behavior is considered important for determining transmission dynamics (Dye & Hasibeder, 1986; Smith *et al.*, 2014). This key transmission parameter in all VBD systems that also underpins vector fitness in the field and can be derived from body size (a physical trait) (Fig. 6, SI section 1.2)(De Leo & Dobson, 1996). Adult vector size is a key physical trait as it determines many functional traits, and also itself responds strongly and predictably to external factors such as environmental temperature and resource availability (e.g., larval nutrition).



v_V & v_R: Vector and Resource (incl. Host) velocities;
h : Handling time; d : Detection distance

Figure 6. Illustration of a Trait-Parameter mapping. We develop a mechanistic, trait-based model for biting rate (a key transmission parameter; eqn. 1) of vectors by deconstructing it into component functional traits (shown above). The model derivation is in SI section 1.2.

Consider a flying vector such as a mosquito, fly, or midge, seeking larger, warm-blooded hosts (e.g., a terrestrial mammal, which is also the energy resource for the vector). A general field encounter rate model for such vector-host interactions in two-dimensional Euclidean space (2*D*) is (Pawar *et al.*, 2012),

$$a = 2v_r d f(.) H$$

Here, a is biting rate (bites × time^{-1}) for a given host density H (individuals × area^{-1}), v_r is relative velocity between the vector and host, d is the reaction distance (minimum distance at which the vector detects and reacts to host), and $f(.)$ is the host "risk" function that determines the (biting) functional response of the vector. That is, $f(.)$ encapsulates the constraints on the vector's handling time (h) (the post-encounter phase in Fig. 2), which would be determined by its ability to land on and complete the biting action successfully. Assuming each encounter between vector and host results in one bite, we can derive biting rate as a function of body size (as physical trait) two key functional traits (vector's flight velocity and reaction distance) (details in SI section 1.2):

$$a = a_0 m_V^{p_v + 2p_d} k^{p_d} f(.) H \qquad 2$$

where a_0 is a normalization constant that also includes the effect of environmental temperature, m_V is the vector's body mass, p_v and p_d are scaling exponents for the size-dependence of vector flight velocity and reaction distance (respectively) k is the vector-host body mass-ratio (a measure of their relative size difference). In the case where hosts are relatively rare, $f(.) = 1$, but in the case where hosts are common (e.g., mosquito populations are often localized near human villages), it can be replaced with a more complex function that includes the effect of host handling time (physical limits on vector's biting & ingestion rate; Fig. 2), which itself is likely to be vector size and temperature dependent (Dell *et al.*, 2011; Pawar *et al.*, 2012). This Trait→Parameter mapping approach can be

modified to accommodate vectors with different moving or sensory modes (e.g., ticks vs. mosquitoes), and for the same host density (say, humans).

Trait-Parameter mappings can be derived for other key life-history and transmission parameters, such as vector fecundity and mortality using bio-mechanical, metabolic trait-based theory. They inevitably also establish mechanistic links between traits. For example, body size drives not just adult vector biting rate, but also its fecundity and mortality rates. Trait→Parameter mappings also generate new insights and testable hypotheses. For example, eqn 2 readily provides new insights: that smaller flying vectors will have a lower mean or maximum biting rate relative to larger ones (e.g., midges vs. mosquitoes), that biting rates will be lower for walking vectors compared to flying ones (e.g., ticks vs. mosquitoes), and explains how temperature (through the scaling constants a_0) affects biting rate (e.g., (Dell *et al.*, 2011, 2014; Mordecai *et al.*, 2013), providing a mechanistic basis for determining the effect of temperature on vector fitness as well as vectorial capacity.

Empirical studies that validate trait-fitness models for specific vectors and VBD systems are of equal importance. Ideally, such studies should measure multiple traits within individuals (for example, vector competence, fecundity, and survival) and how they relate to individual fitness. While the variation in single traits (fecundity, body size, longevity) is often measured in manipulative experiments, it is rare that the variation in traits of interest is explicitly linked to fitness (Ohm *et al.*, 2016). Indeed, traits are typically measured in isolation, which can lead to important linkages between traits being missed. For example, mosquitoes infected with bird malaria parasites exhibit reduced fecundity, which in turn increases longevity (Vézilier *et al.*, 2012). That is, infected mosquitoes reproduce at a reduced rate (decreasing V in eqn. 1) but live longer to transmit the parasite (decreasing μ in eqn 1). This trade-off, which has implications for both vector population fitness (and therefore abundance) and transmission competence, is in fact consistent with metabolic investment-longevity trait tradeoffs, and could potentially be quantified by deriving a (metabolic) trait-fitness model (Charnov, 1993).

2. *Trait-variation→Fitness*

Population-level (absolute) fitness is the distribution of fitness values across individuals. Thus a mathematical VBD model without trait variation implicitly assumes that the value of each parameter is fixed over time, and sufficiently captures the properties of its underlying distribution of traits. For example, if the parameter trait values are distributed in a Gaussian way (Fig 1, Traits panel of Fig. 5), the mean value would be a good measure of the central tendency of the trait. However, as we have discussed above, there is rapidly accumulating evidence that trait variation matters to VBD dynamics, while, at the same time, there has been very little work on quantifying the nature of this variation in parameters or traits. Therefore, the second key step in a trait-based VBD framework is to use Trait-Parameter mappings (component 1 above) to quantify how variation in functional traits generates variation in fitness. That is, after identifying key functional traits and building trait–parameter models, the effect of trait variation on the parameter, and eventually, fitness distribution in each class of compartment (Transmission, Vector population, and Interactions) needs to be quantified. Also, the same trait can affect the fitness of more than one compartment. For example, variation in biting rate or intrinsic mortality would affect both vector population fitness (e.g., $r_{\max}$) and transmission fitness (e.g., R_0). Incorporating or mapping any of the above three types of trait variation (Fig. 1) onto vector population or transmission parameter requires the re-definition of the parameters as functions (e.g., $p(z)$, dz/dt, dz/dE; Fig. 3), which are better constructed mechanistically using Trait-Parameter mappings. Below we will illustrate this using a mathematical model for incorporating environment-driven variation (dz/dE) with temperature as the driver E, into the vector population's intrinsic growth rate (a measure of population fitness) and disease transmission rate (a measure of disease fitness). This example will also illustrate the utility of a mechanistic Trait-Parameter mapping for correctly characterizing the distribution (variation) of parameters (in that case, with respect to an environmental variable: Temperature).

3. *Fitness→Population Dynamics*

The next step is to quantify how trait variation determines vector population abundance or dynamics over time through fitness effects. This requires the construction of stage-structured population dynamic models that also include species interactions (Fig. 5). There are two key challenges here. The

first is quantification of the impact of species interactions (that is, of the vector with its resources or its consumers) on its stage-structured population dynamics. This is an area of ongoing investigation not just in VBD research, but in ecology in general. Species interactions impact life history traits, especially fecundity and mortality, by shifting them from the baseline, interaction-independent values (Roux *et al.*, 2015). For example, fecundity increases with availability of the vector's resources (vector-resource or vector-host interaction), and mortality with the vector's consumers (vector-predator interaction). Tackling this first challenge will require mathematical models (and complementary empirical studies) that *tractably* include the impacts of species interactions on baseline (or idealized) life history/demographic parameters (typically measured in the laboratory), especially fecundity and mortality. One relatively simple way to make progress in this direction is to re-define the otherwise idealized life history parameter (e.g., development rate, fecundity, and mortality) functions to include losses or gains due to species interactions. This approach could circumvent the additional complexity of explicitly adding consumer-resource dynamics to vector population and transmission dynamics.

The second challenge is quantification of the impact of trait variation (Fig. 3) on the vector's stage-structured population dynamics. One approach for doing so is trait-driver theory, which provides methods inherited from quantitative genetics to study how trait variation drives abundance dynamics (Norberg *et al.*, 2001; Webb *et al.*, 2010; Enquist *et al.*, 2015). However, this theory has not yet been extended effectively to consumer-resource dynamics—a theoretical challenge that needs to be tackled not just for VBD research but for the advancement of trait-based ecology in general. This challenge may be made more difficult because most vectors have stage-structured life cycles underlying population dynamics, which may have transgenerational effects (e.g., maternal effects) or carryover effects across life stages (Lorenz & Koella, 2011). Nevertheless, initial progress can be made by simply measuring trait variation and plugging it into population dynamics models (through Trait-Parameter models) with variation to allow deviations from the standard exponential assumptions (for example see (Brand *et al.*, 2016)) to determine how sensitive abundance is to trait variation. Below, we provide an example of how trait-based fitness effects can be mapped onto vector abundance using one type of trait variation (environment-driven, specifically temperature).

4. *Population Dynamics→Transmission Dynamics*

The final step is to quantify transmission dynamics using trait-based vector population dynamics and resulting vector-host interaction rates (Fig. 1). To achieve this, two key challenges on the theoretical front need to be tackled. First, how trait variation determines the timescale of fluctuations in vector population sizes and vector-host interaction traits relative to the timescale of transmission dynamics needs to be modeled and validated. The trait-based approach, by deriving the timescales of population fluctuations mechanistically, would "naturally" determine whether and when the separation of the timescales of population and transmission dynamics, implicit in classical (compartment-type) VBD models, is valid (see example below). Second, the appropriate level of biological complexity (essentially, number of parameters or traits) needed to capture the effect of trait variation through population dynamics on transmission dynamics needs to be determined. For example, trait variation in both juveniles and adults may need to be incorporated simultaneously into transmission models (see example below; Fig. 5). In addition to vector traits that affect its population dynamics, models and data on traits that determine the ability of the vector to transmit a pathogen (e.g., P and bc in eqn. 1) and interact with the host (e.g., a in eqn. 1) will be needed. In many cases, these transmission-relevant traits will be the same as those determining fitness. For example, both, encounter rate with host and with the vector's resources (or predators) are determined by body size and velocity (Fig. 2). Indeed, the host is the primary or sole resource in many vectors (e.g., aphids) which links transmission parameters directly to the vector's fitness though biting and feeding rate.

Operationalizing the roadmap

We recognize that achieving all four of the above steps within a single VBD system is a daunting task. While the long-term goal is to develop methods for taking a fully mechanistic approach, work can begin by building on recent efforts to incorporate trait variation into VBD models (Dye & Hasibeder 1986; Depinay *et al.* 2004; Nakazawa *et al.* 2012; Beck-Johnson *et al.* 2013; Mordecai *et al.* 2013; Smith *et al.* 2014; Mordecai *et al.* 2017). In particular, progress can continue to be made by

incorporating trait variation one trait and variation type at a time, or by focusing on a single type of trait variation across multiple traits (such as the effect of temperature on transmission we describe in our example below). One could also incorporate trait variation into classical compartment (e.g., Ross-MacDonald type) models (Transmission Dynamics in Fig. 5) by modelling trait-based vector abundance and biting rate parameters. We now provide an example of how trait-based fitness effects can mapped onto vector abundance and transmission using one type of trait variation (environment-driven; temperature), and show that it can substantially change predictions about VBD transmission rate and dynamics relative to a more phenomenological approach.

An example: A trait-based model of mosquito abundance and disease transmission

As an example of the difference and kinds of insights we might hope to gain with a trait-based approach, we now show how a trait-based approach (Fig. 5) can lead to novel predictions about vector population dynamics and therefore transmission (Fig. 4). Temperature is a major source of environment-driven trait variation (Fig. 2), and affects variation in both adult and juvenile traits in vectors.

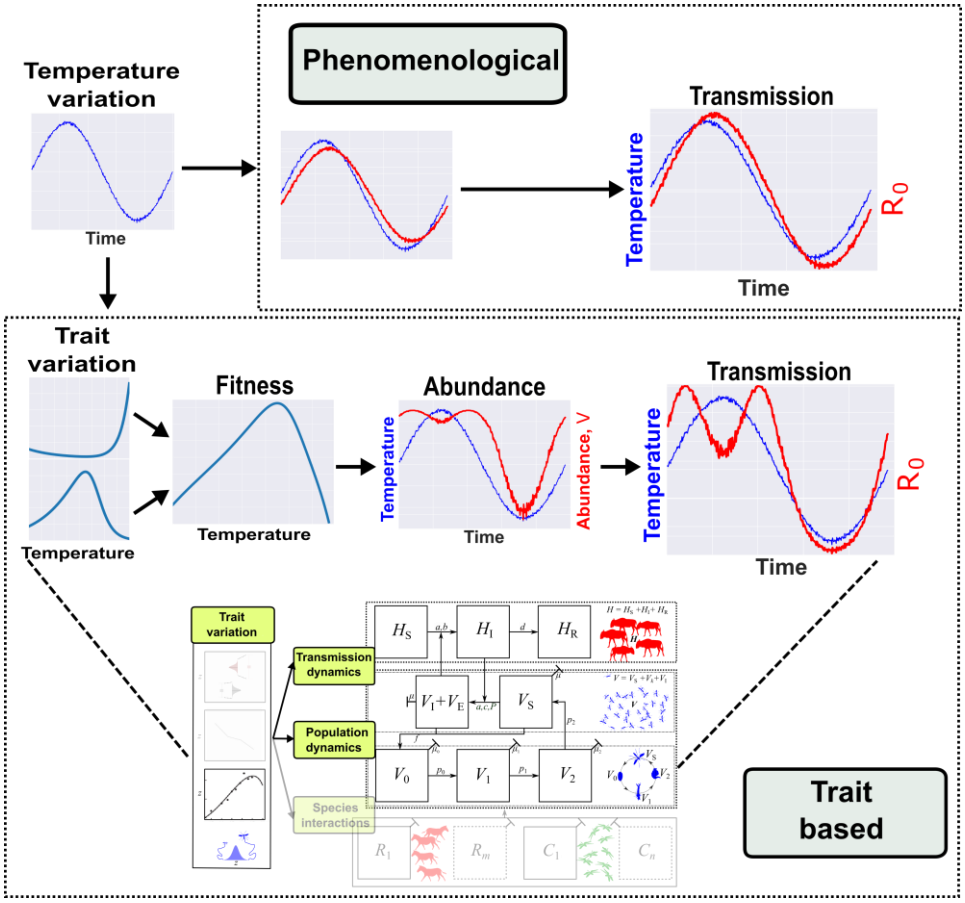


Figure 4. An example trait-based model for malarial disease transmission. We illustrate here the contrast in models and resulting dynamics produced from phenomenological vs. trait-based approaches. Both models cover a time scale of one year and seek to predict the fluctuation in transmission risk or rate (R_0) during that period. We only cover a subset of the full trait-based framework, shown in black in the lower "trait-based" box because of the lack of parameterizations available for species interaction-driven parameter s in vectors. Full details of both models can be found in SI section 3.

To incorporate trait variation into transmission, we model the effects of temperature-driven life-stage specific trait variation on vector population density, V, through the population's intrinsic growth rate, r_m. Full details of this worked example and the model are provided in SI section 3. Briefly, r_m is a function of adult peak fecundity (b_{pk}), age-related fecundity decline rate (κ), adult mortality rate (μ) and juvenile development time (α) and juvenile mortality (μ_J). Variation in each of

these traits across temperature is characterized by the thermal performance curve of each trait. By incorporating such environment-driven trait variation into a vector population abundance model we can derive the transmission dynamics over time (Fig. 4).

We contrast the trait-based approach with a phenomenological one that has been used in previous studies (Hoshi *et al.*, 2014; Johnson *et al.*, 2018; Ng *et al.*, 2018), where abundance (V) is directly associated with temperature by fitting a time-series model or where abundance is assumed, *a priori*, to follow a sinusoidal function (Bacaër & Guernaoui, 2006; Bacaër, 2007; Bacaër & Ouifki, 2007; Bacaër & Ait Dads, 2012). This results in a transmission dynamic where R_0 tracks temperature variation (Fig. 4), potentially with a time-lag. This result contrasts strongly with that from the trait-based approach that maps traits through parameter s to vector population size. Specifically, we observe key differences in predictions of both abundance dynamics and the knock-on effects on transmission: the trait-based model predicts that vector populations will emerge earlier in the year and persist later into the cooler late summer season with a dip in the warmest period of the summer. These differences in V feed through to a longer period of annual transmission with an early and late summer peak. The trait-based model predicts a longer transmission season than the phenomenological model, and reveals a decrease in transmission risk in the warmest period. The latter result in particular is surprising given the general "warmer is better" view, but is consistent with the results of Mordecai et al (2012) who used the "plugging-in approach" to incorporate variation (SI section 2.2). Interestingly, when metabolic theory was used to mechanistically model of infection of an endothermic host with an arctic nematode parasite, Molnar and colleagues observed that the continuous spring-to-fall transmission season morphed into two distinct transmission seasons as climate warmed (Molnár, 2013). The similarity in predicted transmission dynamics across these two very different systems suggests that mechanistically incorporating trait variation can reveal general constraints on VBD systems — in this case, the effect of temperature on VBD dynamics through life-history traits. Additionally, a trait-based approach enables one to determine *which* traits matter the most for determining thermal sensitivity of transmission dynamics (through trait sensitivity analyses; see next section).

The example we have developed here also illustrates a key theoretical point we raised at the start. If vector traits (eqn 1; assumption 2) change at the same or shorter timescales (here, driven by within-year temperature change) than the rate of pathogen transmission, the classical approach will fail to capture important aspects of contemporary transmission dynamics (Anderson & May, 1981; Heesterbeek & Roberts, 1995; Bacaër, 2007). One approach towards relaxing the constant vector population assumption of classical transmission models has been to build phenomenological models for time varying vector populations, for example by assuming that the vector population oscillates sinusoidally (Heesterbeek & Roberts, 1995; Bacaër, 2007). Although this approach is relatively simple, it cannot quantify or predict how variation in key vector traits or parameters (e.g., a, b, c, μ) interact to drive transmission dynamics over time. Thus a trait-based approach provides new mechanistic insights and hypotheses, and predicts non-trivial dynamics that would likely inform public health and control decisions.

The importance of trait sensitivity analyses

In addition to producing novel predictions, the trait-based approach allows investigation into the degree to which different traits drive transmission dynamics and underlying fitness effects. For example, a (local) trait sensitivity analysis of the population fitness component of the above trait-based model allows us to investigate the relative importance of juvenile versus adult traits in determining effects of temperature on abundance (and therefore transmission) (Fig. 5).

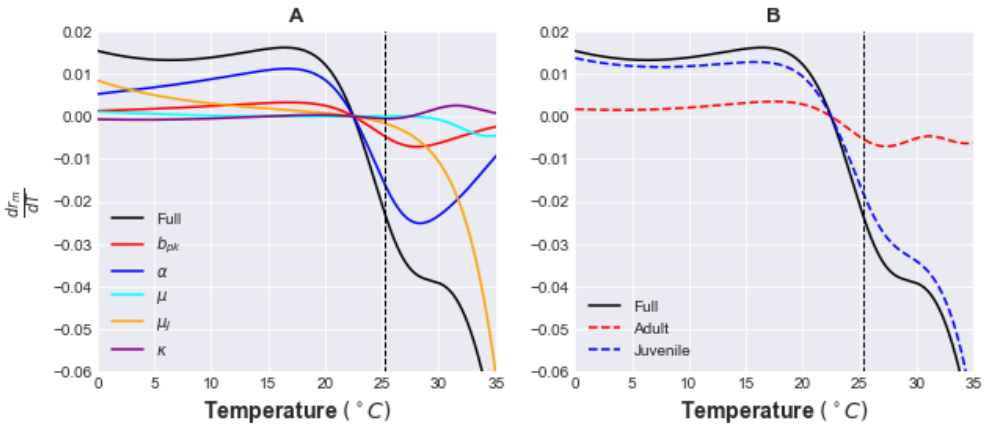


Figure 5. An example trait sensitivity analysis. Analyzing the influence of individual fitness traits on the thermal sensitivity of population fitness of mosquito vectors reveals that juvenile traits have a stronger influence than adult traits in shaping population fitness (r_m) across temperatures. The vertical dashed line marks the thermal optimum of fitness. The parameter s are: adult peak fecundity (b_{pk}), age-related fecundity decline rate (κ), adult mortality rate (z) and juvenile development time (α) and mortality (z_J). The sensitivity of r_m to the thermal dependence of each parameter can be assessed by deviation of each evaluated partial derivative with respect to each parameter (the differently colored lines) from zero. Furthermore, traits can be combined by lifestage, with development rate and juvenile mortality categorised as juvenile traits and adult mortality, fecundity, and rate of loss of fecundity as adult traits. This reveals the relative contribution of the TPC of each lifestage to the TPC of r_m, again with greater deviation from zero indicating a greater contribution. Full details of the trait sensitivity analysis are in SI Section 4.

This leads to a key insight: juvenile traits—traditionally ignored in classical VBD studies—are expected to play a major role in determining vector fitness across temperatures, and therefore abundance, and ultimately transmission. In particular, the trait sensitivity analysis adds further insight to why the trait-based approach yields very different predictions for population abundance and R_0 compared to a phenomenological approach. The thermal sensitivity of abundance (V) and the underlying population fitness (r_m) is driven by the variation of temperature-driven variation in larval stage traits. These predictions and insights provide quantitative targets for validation using field data. Sensitivity analyses of transmission measures with respect to traits also allow key traits to be identified, guiding further empirical and theoretical work on the contributions of traits to VBD system dynamics.

Key Challenges

The four components for building trait-based models that we have outlined above will each face four challenges to differing degrees; *data*: how to prioritize experiments and report data; *parameterization*: how to link model components to empirical data; *validation*: how to test the trait – fitness, trait variation – fitness, population dynamics, and transmission models; *selection*: how to pick the most parsimonious model.

Data

Experiments to quantify vector traits involve taking individual measures on small insects that are often logistically difficult to work with due to ethical (many need animal blood for reproduction and maintenance) and biosafety (many require additional containment because of their potential to transmit pathogens) concerns. As we have described above, theoretical work can help to prioritize which traits we should expect to have the greatest impact on fitness and transmission. New data collection efforts are currently underway in several disease systems, but the limited accessibility of data that have already been collected is a major issue that needs to be addressed. It is critical to get as much information as possible from these time- and labor-intensive experiments by reporting data at the most disaggregated level possible. Many studies report point estimates of trait means/demographic rates across populations, across lifespans, and over environmental gradients rather than presenting

distributions or individual values. Individual-level data are critical for accurately estimating within-population variation in trait values. Beyond individual studies, consolidating datasets with individual measurements into common formats would allow for the identification of gaps and coordinated data collection efforts to specifically target the traits and conditions that are data-poor. We have recently launched a hub for storing and accessing vector trait data (www.vectorbyte.org) and a platform for coordinating data collection efforts (www.vectorbite.org). Current data can be used to parameterize mechanistic models, including trait distributions that accurately represent uncertainty and variation within populations. This would allow us to identify which traits and types of variation in these traits are not well characterized and may play an important role in transmission.

Parameterization

Accurately quantifying the distribution of trait values within populations is a major barrier to developing and refining trait→parameter and trait variation→population fitness models. First, better identification of how individual measurements link to modeled quantities needs to be more consistently addressed. For example, many models assume a single fixed value of the extrinsic incubation period (EIP – the time it takes for an exposed vector to become infectious). However, studies may report any number of variations in EIP – such as EIP_{50} (time to 50% of vectors being infectious) of EIP_{90} (time to 90% infectious). Correctly identifying and incorporating empirical measurements from the literature to match with the meaning of the trait or parameters or transformations is necessary. Then the variation and uncertainty in the traits must be quantified. This involves the use of statistical methods for separating true biological variation from measurement error, and thereby quantifying uncertainty in estimates of trait values (e.g., the mean or variance of a trait). Using sophisticated approaches that allow quantification and propagation of uncertainty (e.g., from trait→parameter to population dynamics modelling), such as Bayesian inference, with or without prior information, will be key here (Clark, 2007; Johnson *et al.*, 2015). In addition, parameter sensitivity analyses in trait-based models (Fig. 5) are crucial, and can provide biological insights into the traits driving variation in transmission (Johnson *et al.*, 2015).

Model Validation and Selection

A fundamental goal of trait-based VBD research is to determine the conditions under which vector traits drive significant variation in realized transmission rate. This requires validation of models at each level or compartment of the framework (ideally) with data on the spatial or temporal distribution of traits/drivers as predictors. In contrast to inference or calibration of a model, validation is the process of assessing how well a parameterized model can replicate data that was not used for parameter inference/calibration (i.e., out-of-sample prediction) (Hooten & Hobbs, 2015). For example, trait→parameter models need to be validated with data on population growth rates, the subsequent population dynamics models need to be validated with data on abundance variation over space or time, and the transmission models need to be validated using disease incidence data over space and time. However, when the data available for validation are very different in nature from the data used for model fitting or model outputs do not correspond to easily measured quantities, it can be difficult to determine when a model captures sufficient detail to adequately represent reality. Efforts to develop hierarchical model validation methods for the types of dynamic, trait-based models described here are ongoing (e.g.,(Johnson, Pecquerie, & Nisbet, 2013; Johnson *et al.*, 2014). These will include Bayesian methods, which allow quantification of uncertainty and the incorporation of prior data (Clark, 2007; Hooten & Hobbs, 2015). Not only do the statistical methods for (VBD) dynamical systems need to be refined, but as they are developed it is important that these methods are made accessible for non-statisticians doing research in this area. This requires training a new generation of researchers in both the new modeling techniques (so they can develop models that include details such as behavior) as well as statistical techniques appropriate for parameterizing and validating the models as they are developed.

It is inevitable and useful that multiple models will be built to address the same question within any of the compartments of a trait-based framework (Johnson & Omland, 2004). For example, there are multiple ways to predict fitness from underlying life history traits (Amarasekare & Coutinho, 2013). Comparing the predictions from multiple models allows us to identify which models are most should

make validation data sets publically available and accessible, and standardized metrics of goodness-of-fit or similar should be reported for all models against validation sets. Second, publishing the code used to generate model outputs as a standard practice would facilitate comparing transmission models of all types—not just those incorporating trait variation. These steps would enable model comparison and multi-model ensembles to be used for future predictions.

Conclusion

This is the ideal time to undertake the development of fully trait-based approaches in VBD research. Recent public health crises have spurred government agencies to support the collection of large amounts of data on these systems. This, combined with innovations in empirical data collection and sharing, means that the necessary data for parameterizing and validating trait-based models are now becoming available. At the same time, the movement towards reproducible research has resulted in open models and computational approaches that allow more direct comparison of models and easier expansion of existing methods. Concurrently, the broader field of trait-based research is maturing across ecological systems, with both the theory and experimental methods growing apace (McGill *et al.*, 2006; Pawar, Woodward, & Dell, 2015b). This provides VBD trait-based approaches with a solid foundation. There are many other areas of ecology that are currently striving to mechanistically incorporate trait variation to understand emergent (especially community and ecosystem level) processes. Methods developed for VBDs would have utility in solving problems in these other systems, such as predicting changes in ecosystem services like primary production (Díaz *et al.*, 2007; Blanchard *et al.*, 2012). Currently, large amounts of funds are being allocated to improve our understanding VBD transmission, and data on all components of VBD systems are being collected. The gains made in this field should be used to leverage progress in others.

Building a fully trait-based approach to modeling VBD dynamics is not the "quick and easy path" (Kershner & Lucas, 1980). It is data-hungry and requires extensive efforts to building models that integrate knowledge about processes from the individual to populations and beyond. However, we argue that in comparison to phenomenological approaches (e.g., regressions or other correlative approaches) taking a more mechanistic approach, in general, provides a better way to extrapolate dynamics across time or space (Bayarri *et al.*, 2009). This kind of predictive power is becoming increasingly critical as these pathogens continue to emerge and expand their ranges in the context of a globalized and rapidly changing environment. Beyond that, incorporating traits with this bottom up approach should allow us to better understand *why* we see the patterns of transmission that we do, and potentially inform efforts at control. For instance, although we have focused on traits that directly affect vector population fitness in idealized conditions, the addition of other traits that are mediated by human intervention, such as insecticide resistance, is also possible within this framework. By explicitly modelling the fitness of a given trait and its effect on population dynamics and fitness, trait-based approaches could be used to incorporate trait evolution into transmission models. Indeed, the evolution of insecticide resistance is arguably the largest challenge to sustainable management of vector borne diseases. Thus, a trait-based approach has the potential to better understand the implication of both current (e.g., chemical pesticides) and future control measures (e.g., genetically altered vectors) that inherently alter traits while suggesting innovative and nuanced ways to apply control in a way that to anticipates changes driven by the inherent complexities of these systems.

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