

Host Ecology, Environmental Change, and Infectious Disease Transmission Dynamics: A Multidisciplinary Modelling Perspective

Moshood Ayinde[1*], Habeeb Damilola Yusuf[2], Kazeem Abdulrazaq[3]

[1]Trinity Health, IA, USA.
[2]Owen Graduate School of Management, Vanderbilt University, Nashville, Tennessee, USA.
[3]Department of Public Health Sciences, New Mexico State University, Las Cruces, New Mexico, USA.
*Corresponding Author Email: moshoodayinde35@gmail.com

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Abstract

Models of infectious disease transmission inherited a structure from Ross and Macdonald that assumes homogeneous biting, well-mixed host populations, age-independent vector mortality and a single vector species. Every substantial advance in the field since has consisted of relaxing one of those assumptions, and the relaxations have not been independent: host heterogeneity, spatial structure, thermal dependence and human mobility interact, so that a model correcting one assumption while retaining the others can be worse calibrated than the original. This review examines what host ecology and environmental change have contributed to transmission modelling, and what the resulting models can and cannot support. It argues four positions. First, host competence is properly treated as a continuous, condition-dependent organismal trait rather than a species-level constant, and when it is, transmission in multi-host systems is found to be dominated by a small number of highly competent and preferentially fed-upon species — making community-mean quantities close to uninformative. Second, the biodiversity–disease relationship is not a general law in either direction; the current synthesis makes the direction a testable prediction from host traits and community assembly rules, and the largest available meta-analysis finds biodiversity loss, pollution, climate change and introduced species associated with increased disease while urbanisation is associated with decreased disease and natural biodiversity gradients are comparatively unimportant. Third, thermal-performance modelling has changed the sign of projected warming effects in warm regions by establishing that transmission optima are unimodal and substantially lower than earlier models assumed, with temperate mosquito-borne virus transmission peaking between 23°C and 26°C and malaria near 25°C. Fourth, model credibility now rests on forecast evaluation rather than on fit, and the honest results of open forecasting challenges — in which many submitted models did not clearly outperform historical baselines — should temper claims about predictive capability. The review concludes with a research agenda emphasising mechanism-specific hypotheses, proper scoring of probabilistic forecasts, explicit treatment of surveillance bias and detection probability, and coupling of ecological models to behavioural, economic and equity components rather than adjustment for them as confounders.

Keywords: *Transmission dynamics; Host competence; Reservoir ecology; Dilution effect; Thermal biology; Species distribution models; Forecast evaluation; One Health; Land-use change*

INTRODUCTION

Infectious disease transmission modelling occupies an unusual epistemic position. It is quantitative and mathematically explicit, which invites confidence; it is calibrated to surveillance data of highly variable quality, which should temper it; and it is used to inform decisions with substantial consequences, which raises the cost of being wrong in ways that the field's internal validation practices do not always reflect.

The canonical structure is the Ross–Macdonald model, in which the mosquito-borne basic reproduction number is quadratic in the human-biting rate and exponentially sensitive to the product of the extrinsic incubation period and adult vector mortality — which is why small changes in vector longevity dominate model output (Smith *et al.*, 2012). Smith

et al. (2012) trace how this structure, assembled from Ross's 1911 mosquito model and Macdonald's 1950s synthesis, embedded four assumptions: homogeneous biting, age-independent mosquito mortality, well-mixed host populations, and a single vector species. Reiner *et al.* (2013) systematically reviewed four decades of mosquito-borne transmission models from 1970 to 2010 and found that the overwhelming majority remained direct descendants of that form, with comparatively few incorporating heterogeneous biting, spatial structure or immunity.

Two bodies of work have done most to change this. The first is host ecology, which established that the "*host*" in these models is not a single well-mixed compartment but a community of species differing by orders of magnitude in their capacity to infect vectors, and differing again in how often vectors feed on them. The second is environmental change research, which established that the parameters treated as constants in classical models — biting rate, vector survival, extrinsic incubation period, vector distribution — are functions of temperature, land cover and hydrology, and are therefore non-stationary over the timescales on which models are now used for projection.

This review synthesises both. The following three sections treat the conceptual foundations, host competence and reservoir ecology, and the biodiversity–disease relationship, respectively. The subsequent two sections treat environmental change drivers and the thermal biology of transmission. Thereafter, the three sections treat modelling methodology: approaches and trade-offs, data integration and its limits, and validation and uncertainty. Multidisciplinary integration and worked example systems, and modelling of interventions are discussed thereafter, followed by a research agenda.

CONCEPTUAL FOUNDATIONS

Fig. 1 summarises the conceptual progression discussed in this section and, more broadly, in this review: the classical Ross–Macdonald framework has been successively relaxed through host heterogeneity, spatial structure and mobility, and thermal and environmental dependence, producing modern transmission models that are mechanism-specific, data-integrated and forecast-evaluated.

Reproduction Numbers and Vectorial Capacity

Garrett-Jones (1964) defined vectorial capacity as the daily rate of potentially infective contacts delivered by a vector population, giving field entomology a transmission-relevant summary statistic that does not require human infection data. This remains the conceptual bridge between entomological measurement and epidemiological inference, and its structure — quadratic in biting rate, exponential in the product of extrinsic incubation period and mortality — is why entomological programmes that measure only abundance discard most of the information that matters.

For structured populations, the basic reproduction number is properly obtained as the spectral radius of the next-generation matrix (Diekmann *et al.*, 1990), with Diekmann *et al.* (2010) supplying the practical recipe for partitioning new-infection and transition terms in compartmental models. This is the standard route to a reproduction number in multi-host, multi-vector systems, and it matters for the argument of this review because it makes explicit that the reproduction number of a multi-host system is not an average of per-host reproduction numbers. A system in which one host species has high competence and low abundance, and another has low competence and high abundance is not equivalent to a single-host system with intermediate parameters.

Smith and McKenzie (2004) give the companion statics-and-dynamics treatment, deriving the sporozoite rate and entomological inoculation rate from mosquito survivorship and the extrinsic incubation period rather than assuming them, and general force-of-infection formulations with their frequency- and density-dependent variants are set out by Grassly and Fraser (2008) and Keeling and Rohani (2008).

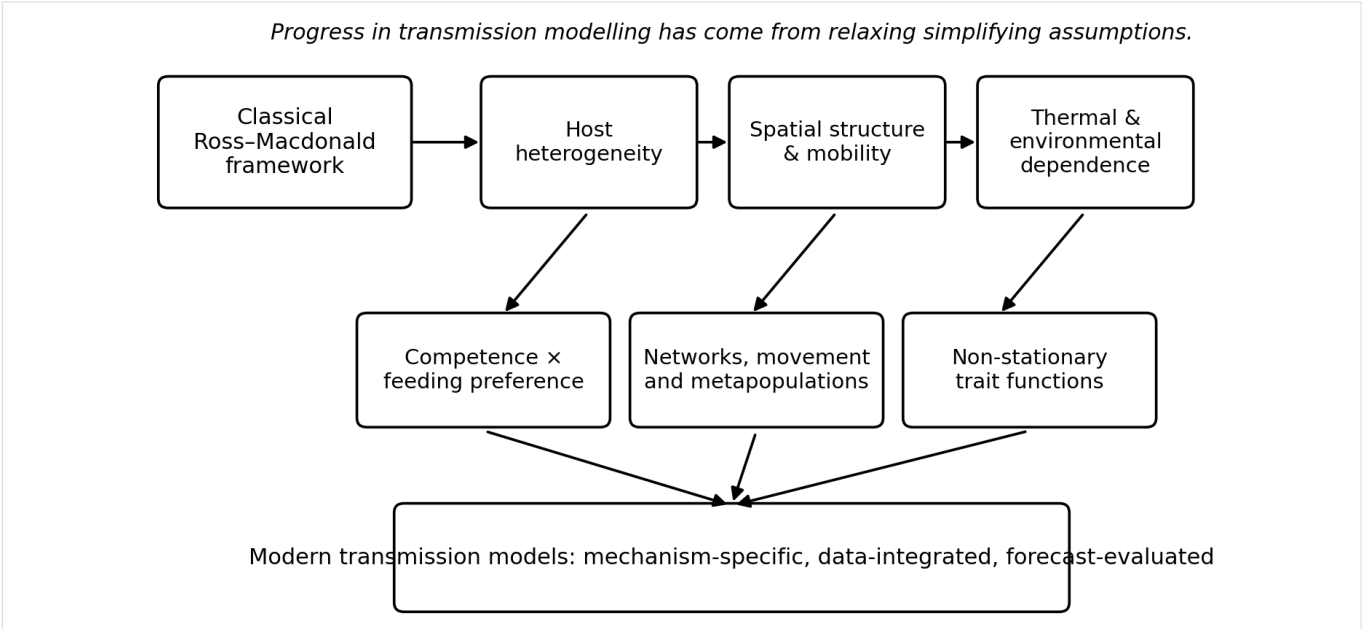


Fig. 1: Evolution of transmission modelling through progressive relaxation of classical simplifying assumptions.

What The Classical Framework Assumes Away

It is worth stating plainly what the four Ross–Macdonald assumptions cost. Homogeneous biting assumes that all hosts are equally accessible to vectors, which is empirically false by an order of magnitude or more in every system where it has been measured. Well-mixed host populations assume that transmission is not spatially structured, which fails at the scale at which vectors actually operate — typically hundreds of metres. Age-independent vector mortality assumes that a mosquito's probability of dying today is independent of its age, which is convenient because it makes survival exponential and therefore analytically tractable, and which is contradicted by senescence data. And the single-vector assumption discards the fact that most transmission systems involve multiple vector species with different host preferences, seasonal phenologies and thermal optima.

HOST COMPETENCE AND RESERVOIR ECOLOGY

The Reservoir as A Population Assemblage

Haydon *et al.* (2002) formalised the reservoir as a population or assemblage epidemiologically connected to a target population, which shifted the empirical question from "which species carries the pathogen?" to "*which set of populations sustains transmission and maintains connection to the target?*" This reframing has substantial modelling consequences. A reservoir defined as an assemblage cannot be represented by a single compartment; it requires either explicit multi-species structure or a defensible aggregation, and the choice between them is a modelling decision that should be justified rather than made by default.

Martin *et al.* (2016) took the next step, reframing host competence as an organismal trait with immunological mechanisms — pathogen load, shedding duration, infectiousness to vectors — and arguing that it should be modelled as a continuous, condition-dependent and often season-dependent quantity rather than a species-level constant. This matters because competence measured in experimental infection of healthy captive animals may not represent competence in wild animals under nutritional or thermal stress, and because within-species variation in competence can be comparable to between-species variation.

Avian Competence and West Nile Virus

The West Nile virus system provides the most complete quantification available. Komar *et al.* (2003) experimentally infected 25 bird species from 17 families with the New York 1999 strain and ranked them by a reservoir competence index combining viraemia magnitude, duration and infectiousness; passerines and charadriiforms were most competent, with peak viraemias in blue jays, common grackles, house finches and American crows sufficient to infect a high proportion of feeding Culex, and corvid infection frequently fatal.

Kilpatrick *et al.* (2006a) then showed that this competence variation, combined with vector feeding preference, means host heterogeneity rather than mean host density dominates transmission, with a small number of highly fed-upon and highly competent species carrying most of the amplification. Kilpatrick *et al.* (2006b) documented the mid-season shift in Culex pipiens blood meals away from American robins toward humans, coincident with robin dispersal and with the onset of human cases, establishing feeding-behaviour phenology as a direct driver of spillover timing. Hamer *et al.* (2009) quantified the pattern in Chicago, finding that approximately 80% of *Cx. pipiens* blood meals were avian and that American robins were fed upon far out of proportion to their abundance. Simpson *et al.* (2012) formalised host-feeding preference in a multi-host model and showed that preference, not competence alone, determines each species' amplification fraction.

The modelling lesson is specific and transferable: in a multi-host system, the product of competence and feeding preference determines contribution to the reproduction number, and either factor alone is insufficient. Models parameterised from competence data without feeding data — which describes a large fraction of the published multi-host literature — are therefore mis-specified in a direction that cannot be signed a priori.

Reservoir Hierarchies in Tick-Borne Systems

Mather *et al.* (1989) established *Peromyscus leucopus* as the most competent rodent reservoir for *Borrelia burgdorferi* by comparing the proportion of xenodiagnostic larval ticks infected across sympatric rodent species. LoGiudice *et al.* (2003) extended this into a community model, showing that white-footed mice infect the large majority of larvae feeding on them whereas opossums, squirrels and most other vertebrates infect only a small fraction, so that community composition rather than tick abundance alone sets nymphal infection prevalence.

The tick-borne case differs from the mosquito-borne case in a way that matters for modelling. Because ticks feed once per life stage and remain attached for days, the relevant quantity is the distribution of larval meals across host species rather than a continuous biting rate, and the transmission process is stage-structured with generation times of a year or more. Models that treat tick-borne and mosquito-borne systems with the same compartmental structure therefore misrepresent the temporal dynamics of at least one of them.

BIODIVERSITY–DISEASE RELATIONSHIPS

The Dilution Position and Its Critiques

Ostfeld and Keesing (2000) introduced the Lyme disease case for dilution: adding less-competent hosts to a community reduces the proportion of tick meals taken on competent P. leucopus, lowering nymphal infection prevalence. Keesing *et al.* (2010) and Ostfeld and Keesing (2012) generalised this into a mechanism set — encounter reduction, transmission reduction, susceptible-host regulation, infected-host mortality, recovery augmentation — and argued that because species lost first from disassembling communities tend to be the less competent ones, biodiversity loss should systematically amplify risk. Civitello *et al.* (2015) reported broad meta-analytic support for dilution across effect sizes spanning plant and animal, human and wildlife parasites.

The critiques are substantive. Salkeld *et al.* (2013) meta-analysed biodiversity–zoonotic-risk associations and

concluded the relationship is idiosyncratic, with heterogeneous and frequently weak effect sizes sensitive to study design and scale. Halsey (2019) argued that the debate had become substantially semantic and that progress requires specifying mechanism, spatial scale and disease endpoint before testing.

The Current Synthesis

Rohr *et al.* (2020) proposed the common ground that now organises the field: dilution is expected when pathogens are generalist and community assembly or disassembly is non-random with respect to competence; amplification is expected when added species are competent or when diversity covaries with vector abundance. This converts the direction of the effect from a general law into a testable prediction derivable from host traits — which is both more useful and more demanding, because it requires trait data that are frequently unavailable.

The largest available synthesis is Mahon *et al.* (2024), which analysed 2,938 observations across 1,497 host–parasite combinations and found that biodiversity loss, chemical pollution, climate change and introduced species were each associated with increases in disease endpoints, urbanisation with decreases, and natural biodiversity gradients, deforestation and forest fragmentation comparatively unimportant or idiosyncratic, with context-dependence common throughout. The pattern is worth stating carefully: biodiversity loss increasing disease and natural biodiversity gradients not predicting disease are compatible findings, because loss is a non-random process with respect to host competence while a gradient need not be. This is precisely the distinction Rohr *et al.* (2020) predicted would matter.

Gibb *et al.* (2025) argue the field should now move past dilution-versus-amplification toward a people-and-nature framing that treats land use, host community change and human exposure as jointly determined rather than as a driver and a response. Pfenning-Butterworth *et al.* (2024) make the parallel case that climate change, biodiversity loss and infectious disease are coupled rather than additive drivers, which has the specific modelling implication that their effects cannot be estimated as separate main effects and summed.

Competence–Abundance Relationships and Community Assembly

The mechanism underlying non-random community disassembly has been identified. Joseph *et al.* (2013) tested whether life history mediates the competence–persistence relationship and showed that species with fast life histories — which tend to persist in disturbed, disassembled communities — are frequently the more competent hosts. This supplies a mechanistic basis for negative diversity–risk relationships without requiring dilution as an axiom, and it makes life-history data a usable proxy where competence data are absent.

Anthropogenic modification operates through additional channels. Becker *et al.* (2015) meta-analysed anthropogenic resource provisioning and found that supplemental food and human-subsidised aggregation altered wildlife–pathogen dynamics in both directions, with increased prevalence common where provisioning raised host density and contact rates. Murray *et al.* (2019) meta-analysed wildlife health across urbanisation gradients and found higher prevalence for several parasite and pathogen groups in urban populations even where body condition indices sometimes improved — a dissociation that matters directly for models using body condition or abundance as competence proxies. Gibb *et al.* (2020) provide the global-scale version: in human-dominated land uses, species known to host human-shared pathogens constitute a greater share of both local richness and total abundance than in nearby undisturbed sites, concentrated in rodents, bats and passerines. Han *et al.* (2015) approached the same problem predictively, using boosted regression trees on rodent life-history traits to identify likely undiscovered zoonotic reservoirs.

ENVIRONMENTAL CHANGE DRIVERS

Land Use and Land Cover

Gibb *et al.* (2020) demonstrated that agricultural and urban land use produces a systematic compositional shift toward zoonotic reservoir hosts, operating through community reassembly rather than through host richness. Faust *et al.* (2018) modelled spillover across a land-conversion gradient and found a hump-shaped relationship, with spillover peaking at intermediate conversion where wildlife habitat and human contact are both substantial — implying that risk-minimising land-use configurations are not simply "*more forest*". Rulli *et al.* (2025) provide the current cross-disciplinary review spanning hydrology, land-system science and epidemiology.

For specific systems, MacDonald and Mordecai (2019) used Amazon panel data to estimate a bidirectional relationship in which forest loss increased malaria incidence while high malaria burden in turn reduced subsequent forest clearing — a feedback that biases any unidirectional causal model, and a reminder that disease burden is an economic variable as well as an outcome. Olivero *et al.* (2017) found Ebola virus disease outbreaks spatially and temporally associated with recent loss of closed forest, concentrating in fragmented forest-edge landscapes. Rohr *et al.* (2019) link emerging human infectious disease to global food production, distinguishing agricultural expansion, intensification, irrigation and aquaculture as pathways with distinct modelling requirements, and Hassell *et al.* (2017) describe the urbanising wildlife–livestock–human interface and the contact-structure changes it produces. For fragmentation specifically, Allan *et al.* (2003) showed that the smallest forest fragments carried the highest densities of Borrelia-infected nymphs, and Diuk-Wasser *et al.* (2021) review how land-use change and fragmentation restructure tick-borne disease eco-epidemiology across scales.

Environmental measurement at the resolution these processes require is itself a methodological problem. Geostatistical characterisation of agricultural soils demonstrates how spatially explicit sampling and interpolation can resolve land-use and soil-property gradients at scales relevant to vector and host habitat suitability (Kianguebene-Koussingounina *et al.*, 2023), and digital-twin approaches to environmental compliance monitoring illustrate how continuously updated

representations of a physical system can be maintained and queried rather than periodically resurveyed (Ike *et al.*, 2025). Both are directly applicable to the covariate layers that land-use disease models depend on, and both are better developed in their originating literatures than in disease ecology.

Climate Variability and Inter-Annual Dynamics

Climate change is usually modelled as a trend, but a substantial fraction of the disease-relevant signal is variability. Cazelles *et al.* (2005) used wavelet analysis to show a non-stationary El Niño–Southern Oscillation–dengue coupling in Thailand, with epidemic synchrony locking to El Niño only in some epochs — a direct argument against fixed-coefficient climate–disease regressions. Hart *et al.* (2025) show that interannual climate variability, not mean change alone, drives the outbreak-preparedness burden, and Kaye *et al.* (2024) quantify natural climate variability's effect on the global *Aedes aegypti* distribution. Trebski *et al.* (2025) find that climate sensitivity is widely but unevenly distributed across zoonotic diseases, which argues against generic climate-sensitivity assumptions in multi-pathogen risk assessments.

For Rift Valley fever, the variability signal is strong enough to support operational forecasting. Linthicum *et al.* (1999) forecast Kenyan epizootics from Pacific and Indian Ocean sea-surface temperature anomalies plus vegetation index data at two to five months' lead, and Anyamba *et al.* (2009) issued and validated a prospective outbreak prediction on the same basis.

THERMAL BIOLOGY OF TRANSMISSION

The most consequential methodological development in this literature is trait-based thermal modelling. Mordecai *et al.* (2013) fitted unimodal thermal response curves to each Ross–Macdonald component trait — biting rate, vector competence, extrinsic incubation rate, adult survival, development — and showed that the resulting optimum for Plasmodium falciparum transmission is near 25°C, roughly 6°C below the approximately 31°C assumed in earlier models, with transmission collapsing above about 28°C. Because the correction moved the optimum below the current temperature of many endemic regions, it reversed the sign of projected warming effects in those regions — a rare instance of a methodological improvement changing a policy-relevant conclusion in direction rather than magnitude.

Mordecai *et al.* (2017) applied the same Bayesian trait-based framework to Aedes-borne Zika, dengue and chikungunya transmission, and Mordecai *et al.* (2019) synthesised the thermal biology of mosquito-borne disease across systems, reporting transmission optima clustered in the approximately 23–29°C range with sharp declines on either side. Shocket *et al.* (2020) extended the approach to West Nile virus and five other temperate mosquito-borne viruses and found transmission peaks between 23°C and 26°C — cooler than for tropical Aedes viruses, and the reason temperate West Nile virus risk can decrease under extreme summer heat. Huber *et al.* (2018) showed that seasonal temperature variation, not mean temperature alone, influences climate suitability, because a unimodal response function integrated over a varying temperature distribution does not equal the response at the mean.

Projections built on these foundations are correspondingly more credible. Colón-González *et al.* (2021) ran a multi-model, multi-scenario inter-comparison and projected transmission suitability lengthening by approximately 1.6 additional months for malaria in tropical highlands and 4.0 additional months for dengue in lowlands, with population at risk rising by up to 4.7 billion by 2070 relative to a 1970–1999 baseline under the highest emissions and population pathway. Ryan *et al.* (2019) mapped thermal-suitability-based expansion and redistribution of Aedes-borne virus risk. Childs *et al.* (2025) provide the most rigorous attribution to date, estimating from 21 countries that dengue incidence responds non-linearly to temperature with peak incidence at 27.8°C (95% CI 26.9–29.4), attributing approximately 18% (95% CI 11–27%) of 1995–2014 dengue incidence to anthropogenic warming already realised, and projecting mid-century increases of 49% (16–136%) under SSP1-2.6 and 76% (27–239%) under SSP3-7.0.

Erazo *et al.* (2024) performed the corresponding counterfactual attribution for West Nile virus in Europe, training ecological niche models on 1901–2019 conditions and comparing factual against detrended-climate counterfactual simulations; the suitable area expanded markedly under observed climate but remained largely static without the climate trend, with population at risk driven jointly by climate and population-density change. IPCC (2022) supplies the assessed attribution and vector-borne disease risk statements, and Romanello *et al.* (2024) the annual indicator-based tracking.

Ticks again behave differently. Ogden and Lindsay (2016) argue that tick-borne systems respond to climate through development and diapause rates rather than through the short-generation dynamics governing mosquitoes, so that warming projections must be built on stage-structured models; Ogden *et al.* (2005) provide such a model for *Ixodes scapularis* range and seasonality; Levi *et al.* (2015) document advanced blacklegged tick phenology under warming; and Randolph and Rogers (2000) show that tick-borne encephalitis virus's requirement for synchronous larval–nymphal co-feeding makes its transmission cycle fragile and potentially disrupted, rather than simply expanded, by warming. Kilpatrick and Randolph (2012) provide the integrative treatment of drivers, dynamics and control across vector-borne zoonoses, and Carlson *et al.* (2022) model the cross-species viral transmission consequences of climate-driven range shifts.

MODELLING APPROACHES AND THEIR TRADE-OFFS

Compartmental and Trait-Driven Formulations

Temperature-dependent susceptible–exposed–infectious formulations for both vector and host plug the thermal response curves presented in Thermal Biology of Transmission section directly into compartmental equations, and this is how the suitability projections and attribution studies above are generated (Colón-González *et al.*, 2021; Erazo *et al.*, 2024; Ryan *et al.*, 2019). Keeling and Rohani

(2008) remain the reference for the underlying structures and their stochastic analogues. The trade-off is transparency against realism: compartmental models are analytically interpretable and their sensitivity structure is legible, and they cannot represent the spatial and individual heterogeneity that Host Competence and Reservoir Ecology and Biodiversity–Disease Relationships establish as dominant.

Agent-Based and Individual-Based Models

Eubank *et al.* (2004) demonstrated that synthetic-population, activity-based urban contact networks produce outbreak dynamics and intervention responses that mean-field models cannot reproduce. Magori *et al.* (2009) built a stochastic, spatially explicit, container-level Aedes aegypti model designed specifically to evaluate population replacement and suppression strategies — the archetype for individual-based vector intervention modelling, and the appropriate structure when the intervention operates on individual mosquitoes or individual containers rather than on population means.

Multi-agent coordination modelling in adjacent fields has developed relevant machinery. Frameworks for swarm intelligence in autonomous mobile agent fleets address exactly the problem of representing many interacting units with local information and emergent collective behaviour (Akanbi *et al.*, 2025), integrated path-planning and allocation models formalise movement and resource-use decisions under spatial constraint (Akanbi and Sunday, 2024), and systematic review of this literature documents the design choices and their consequences (Akanbi and Sunday, 2025). The formal correspondence with agent-based epidemiological models is close, and the cross-disciplinary transfer has been largely one-directional and incomplete.

Metapopulation, Network and Mobility Models

Balcan *et al.* (2009) coupled global air-traffic and commuting layers in a multiscale metapopulation framework, showing that short-range commuting alters local epidemic timing while long-range travel sets global invasion order. Wesolowski *et al.* (2012) used the movements of approximately 15 million mobile-phone subscribers in Kenya to map malaria parasite importation routes and source–sink structure. Tizzoni *et al.* (2014) then tested mobility proxies against mobile-phone ground truth and found that epidemic invasion predictions are robust to proxy choice at coarse spatial scales but not at fine ones — an unusually useful negative result, because it specifies where cheap proxies suffice and where they do not. Kraemer *et al.* (2020) quantified the effect of mobility and travel restrictions on COVID-19 spread using the same data class. Perkins *et al.* (2013) formalised how heterogeneous biting and human movement interact to determine the spatial scale at which mosquito-borne transmission should be modelled at all — which is logically prior to choosing a model structure and is rarely addressed explicitly.

Species Distribution and Niche Models

Phillips *et al.* (2006) introduced maximum entropy modelling for presence-only data, and Elith *et al.* (2011) supplied the statistical interpretation — MaxEnt as a Poisson point-process or log-linear model — which matters because it clarifies what "suitability" is and is not, and therefore how it may legitimately be calibrated against incidence. Kraemer *et al.* (2015) produced the first global compiled occurrence database and boosted-regression-tree maps for *Aedes aegypti* and *Ae. albopictus*, and Kraemer *et al.* (2019) extended these to past and future spread. Bhatt *et al.* (2013) and Messina *et al.* (2019) applied the same class of ensemble machinery to global dengue burden and population at risk, and Messina *et al.* (2015) to Crimean-Congo haemorrhagic fever.

The standing weakness of this model class is that presence-only occurrence data conflate the distribution of the organism with the distribution of sampling effort. Data Integration and Its Limits section returns to this.

Machine Learning and Bayesian Spatiotemporal Inference

Farooq *et al.* (2022) applied machine learning with eco-climatic drivers to predict West Nile virus outbreaks in Europe, and Han *et al.* (2015) used trait-based boosted regression trees for reservoir prioritisation. For inference, Rue *et al.* (2009) introduced integrated nested Laplace approximation for latent Gaussian models and Lindgren *et al.* (2011) the stochastic partial differential equation link between Gaussian fields and Gaussian Markov random fields, together making continuous-space spatiotemporal Bayesian models computationally routine — the machinery behind Lowe *et al.* (2018, 2021). Joint species distribution modelling (Ovaskainen *et al.*, 2017; Warton *et al.*, 2015) offers the natural route to modelling whole host communities and residual co-occurrence rather than species one at a time, which is what Host Competence and Reservoir Ecology and Biodiversity–Disease Relationships imply is required.

Machine learning applied to risk prediction in other domains supplies a relevant cautionary literature. Applications of machine learning to underwriting and risk classification demonstrate both the predictive gains available from flexible models and the interpretability and fairness problems they introduce when the resulting scores drive consequential decisions (Oluwo *et al.*, 2024), and analytics-driven decision frameworks show how model outputs are actually consumed by decision-makers, which is frequently not as probability distributions (Oluwo *et al.*, 2025). Data-driven methods applied to poorly characterised measurement systems produce confident and wrong outputs (Adaramola *et al.*, 2020), and this is the principal risk in applying machine learning to surveillance data whose generating process includes substantial and spatially structured detection bias. Reliability engineering and failure analysis frameworks offer a discipline that transmission modelling largely lacks: systematic enumeration of the ways a complex system can fail, and explicit analysis of which failure modes the monitoring architecture would detect (Gideon *et al.*, 2019).

DATA INTEGRATION AND ITS LIMITS

Fig. 2 organises the data-integration problem treated in this section. It shows that a credible transmission-risk forecast integrates host competence and community structure, vector traits and feeding, climate/land use/hydrology, human mobility/behaviour/equity, detection probability/surveillance

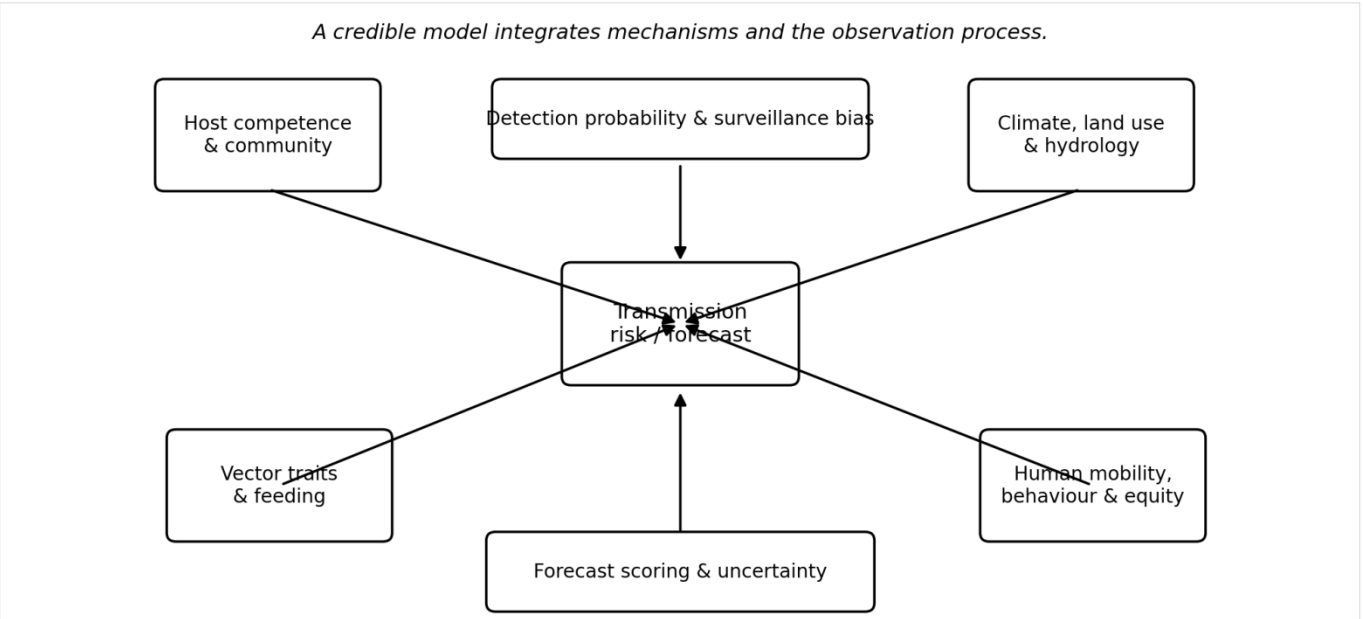


Fig. 2: Integrated determinants of transmission-risk modelling and forecast credibility.

bias, and forecast scoring/uncertainty; the observation process is modelled as a component of the system rather than treated as a nuisance after fitting.

Under-Ascertainment and Reporting Delay

Bhatt *et al.* (2013) estimated 390 million dengue infections annually, of which approximately 96 million are apparent — roughly three times the then-official global figure — which establishes under-ascertainment as a first-order rather than second-order modelling problem. A model fitted to reported cases without an ascertainment model is estimating a transformation of the transmission process, and the transformation is neither constant in space nor stationary in time.

Reporting delay is the tractable part. Höhle and an der Heiden (2014) give a Bayesian hierarchical nowcast for occurred-but-not-yet-reported cases, developed on the German STEC O104:H4 outbreak, which is now the standard template for delay-adjusted real-time incidence. Adoption in vector-borne disease modelling remains patchy, with the consequence that recent weeks of surveillance data are routinely interpreted as declining incidence when they represent incomplete reporting.

Detection Probability and Occupancy

MacKenzie *et al.* (2002) provide the estimator for site occupancy when detection is imperfect, which is the statistically correct treatment for vector presence–absence and tick drag-sampling data. In practice, non-detection is routinely treated as absence in niche models built on raw occurrence, which biases estimated environmental envelopes toward the conditions under which sampling is easiest. Given that the resulting maps are the exposure layer for a large fraction of published risk modelling, this is not a minor methodological quibble.

Earth Observation and Covariate Layers

Parselia *et al.* (2019) scope the use of satellite Earth observation in malaria, dengue and West Nile virus models, cataloguing normalised difference vegetation index, land surface temperature, precipitation and surface-water products and the resolution and latency trade-offs each imposes. Linthicum *et al.* (1999) and Anyamba *et al.* (2009) remain the operational demonstrations. The recurring difficulty is scale mismatch: satellite products are available at resolutions that do not correspond to the scales at which vectors respond, and aggregation to administrative units — the scale at which case data exist — discards the heterogeneity that determines transmission.

Citizen Science and Open Data Infrastructure

Nieto *et al.* (2018) used a nationwide crowdsourced tick-submission programme to characterise tick-bite exposure and to document ticks in counties with no prior records, illustrating both the spatial reach and the sampling-effort bias of citizen-science vector data. Heberling *et al.* (2021) quantify how aggregated biodiversity data enable global synthesis while documenting its taxonomic and geographic gaps, and Amos *et al.* (2022) describe the integrated pathogen, vector and host bioinformatics resource infrastructure. Gibb *et al.* (2021) diagnose the reconciliation problem directly: proliferating, overlapping, inconsistently curated viral-ecology datasets whose combination can manufacture apparent signal — a warning that applies with particular force to meta-analyses assembled from heterogeneous secondary sources.

VALIDATION, FORECAST SCORING AND UNCERTAINTY

Proper Scoring Rules

Gneiting and Raftery (2007) give the decision-theoretic foundation: a scoring rule is proper if it is optimised by the forecaster's true predictive distribution, which rules out point-accuracy metrics for probabilistic forecasts and

motivates the logarithmic score and the continuous ranked probability score. Bracher *et al.* (2021) derive the weighted interval score as a quantile-based approximation to CRPS computable from the interval-format submissions that forecast hubs actually collect, with a decomposition into dispersion, over-prediction and under-prediction penalties. The availability of a proper score computable from interval forecasts removes the last practical excuse for evaluating epidemiological forecasts by point accuracy.

What Open Forecasting Challenges Actually Found

Johansson *et al.* (2019) report the dengue forecasting challenge across Puerto Rico and Peru, in which multiple independent teams predicted peak week, peak incidence and season totals from a common dataset; predictive skill varied substantially by target and season, and multi-model ensembles were competitive with or better than the best individual models. Holcomb *et al.* (2023) report the analogous open West Nile virus neuroinvasive disease challenge, and the result deserves to be stated without softening: the majority of submitted models did not clearly outperform simple historical baselines. Ray *et al.* (2023) find, for COVID-19, that simple untrained ensemble combinations are difficult to beat robustly, and Funk *et al.* (2019) provide the real-time Ebola case study in which calibration degrades sharply beyond short horizons.

Taken together these results define the honest state of predictive capability: short-horizon nowcasting is achievable, seasonal-scale epidemic forecasting has modest and target-dependent skill, ensembles are robustly better than model selection, and claims of substantial predictive skill for vector-borne disease incidence should be treated as requiring out-of-sample demonstration rather than assumed.

Structural Uncertainty and Equifinality

Beven and Freer (2001) articulate equifinality — many distinct parameterisations and structures fitting the calibration data equally well — and a framework for propagating it, a framing that transfers directly to transmission models with weakly identified vector parameters. Colón-González *et al.* (2021) is the worked demonstration that inter-model spread can exceed inter-scenario spread, which means that in some projection exercises the choice of model matters more than the choice of emissions pathway. Shea *et al.* (2020) argue for deliberate multi-model decision analysis rather than post hoc model selection; Metcalf and Lessler (2017) survey the structural-uncertainty limits of emerging-disease modelling; and Cross *et al.* (2019) treat the specific identifiability problem of estimating spillover from data that cannot separate exposure, susceptibility and detection.

MULTIDISCIPLINARY INTEGRATION

Coupling Frameworks

Zinsstag *et al.* (2011) trace the movement from "*one medicine*" to "*One Health*" and systemic approaches, making the case for models whose objective functions include animal and human health jointly rather than treating livestock as a covariate. Whitmee *et al.* (2015) set out the planetary-health framing requiring ecological, epidemiological, economic and equity components in a single analysis. Both imply a model class that is rare in practice: coupled models in which the ecological and economic components exchange state rather than one supplying parameters to the other.

Behavioural Feedbacks

Ferguson (2007) put the problem on the agenda: models omitting adaptive human behaviour will mis-time and mis-size epidemics. Funk *et al.* (2010) model awareness spreading on the same network as the pathogen and show that local behavioural response can suppress endemic prevalence in ways that mean-field awareness terms do not capture. Verelst *et al.* (2016) systematically reviewed behavioural-change transmission models and found most to be theoretical, with few calibrated to empirical behavioural data — which remains the key gap. Behavioural feedback is particularly consequential in vector-borne systems because the principal protective behaviours (bed net use, container management, repellent use, outdoor activity timing) are individually chosen and respond to perceived risk.

Socioeconomic Vulnerability, Participation and Decision Support

Lowe *et al.* (2021) show the practical route: a Bayesian spatiotemporal model for Brazil in which drought and extreme-rainfall hazards interact with urbanisation and water-supply covariates, so that dengue risk is estimated as a function of socio-environmental vulnerability rather than climate alone. Tusting *et al.* (2013) meta-analysed socioeconomic development as a malaria intervention and support treating income and housing as causal covariates rather than confounders to be adjusted away — a methodological point with substantial consequences, because adjusting for housing quality removes from the estimate precisely the mechanism through which development reduces transmission. Redding *et al.* (2019) combine environmental and socioeconomic drivers in a single Ebola emergence-and-epidemic-potential model.

Voinov and Bousquet (2010) provide the reference treatment of participatory modelling with stakeholders — problem framing, model co-construction, and the legitimacy such processes confer — and Shea *et al.* (2020) close the loop by embedding multiple models in a formal management-decision structure. Organisational readiness is the under-modelled determinant of whether any of this reaches practice: comparative analysis of management capability for integrating generative artificial intelligence into healthcare operations across high-income and low- and middle-income settings documents how far institutional absorptive capacity, not technical availability, governs adoption (Ayinde *et al.*, 2025). Models built without regard to the decision process they are meant to inform are frequently not used, and the reasons are organisational rather than analytical.

Multi-layered risk architectures developed for public–private infrastructure partnerships offer a formal structure for the allocation and propagation of risk across institutional boundaries (Ike *et al.*, 2024) — a framework relevant to One Health modelling, where the sectors bearing the cost of

prevention and the sectors receiving its benefit are frequently different. And the workforce question that underlies multidisciplinary modelling capability is addressed in the technical and vocational education literature: strategic directions for future-proofing technical skills in Global South economies (Joseph *et al.*, 2025a), comparative evidence on workforce readiness across national systems (Joseph *et al.*, 2025b), and the role of government policy in shaping training outcomes (Joseph *et al.*, 2025c). Multidisciplinary modelling requires people trained across ecology, statistics, computation and epidemiology, and no standard curriculum produces them.

WORKED EXAMPLE SYSTEMS

- *West Nile virus, North America.* The competence–preference–phenology chain established by Komar *et al.* (2003), Kilpatrick *et al.* (2006a, 2006b), Hamer *et al.* (2009) and Simpson *et al.* (2012) is the best-documented multi-host amplification system available. Paull *et al.* (2017) add the climate dimension, showing that drought — interacting with accumulated host immunity — is a strong determinant of epidemic intensity, so that projected epidemic size depends on drought frequency as much as on mean warming. Holcomb *et al.* (2023) supply the sobering forecasting-performance counterpart.
- *West Nile virus, Europe.* Erazo *et al.* (2024) provide the counterfactual climate attribution, Farooq *et al.* (2022) a machine-learning early-warning system on eco-climatic drivers, and Costa *et al.* (2024) the temperature boundary conditions delimiting where circulation is possible at all.
- *Dengue, Brazil and Southeast Asia.* Lowe *et al.* (2021) is the Brazilian hazard-plus-urbanisation spatiotemporal model and Lowe *et al.* (2018) the Barbados nonlinear-lagged climate model using distributed lag nonlinear terms within a Bayesian hierarchical framework. Van Panhuis *et al.* (2015) demonstrated region-wide synchrony and travelling waves of dengue across eight Southeast Asian countries, with waves radiating outward from Bangkok — evidence for hierarchical spatial coupling that single-country models structurally cannot represent. Childs *et al.* (2025) supply the attribution and projection layer.
- *Lyme disease.* LoGiudice *et al.* (2003), Mather *et al.* (1989), Allan *et al.* (2003), Ogden *et al.* (2005), Levi *et al.* (2015) and Diuk-Wasser *et al.* (2021) together cover reservoir competence, fragmentation, stage-structured tick population modelling, phenological shift and land-use eco-epidemiology — arguably the most complete integration of host ecology and transmission modelling for any system.
- *Rift Valley fever and ENSO.* Linthicum *et al.* (1999) and Anyamba *et al.* (2009) provide the forecasting record, and Cecilia *et al.* (2022) systematically review mechanistic transmission models, cataloguing how vector, livestock and vertical-transmission structures differ across published models and where they diverge in prediction.
- *Schistosomiasis and trophic intervention.* Sokolow *et al.* (2015) showed that restoring a native river prawn, a predator of the snail intermediate host, reduced snail density and human Schistosoma haematobium reinfection at a Senegalese site — an ecology-based intervention validated in the field. Hoover *et al.* (2019) then coupled the ecological model to an economic one, modelling prawn aquaculture as a joint poverty-alleviation and schistosomiasis-control intervention. This is the clearest existing example of the coupled ecological–economic model class that the Multidisciplinary Integration: Coupling frameworks section argues for.
- *Avian influenza in wild and domestic birds and mammals.* The Global Consortium for H5N8 and Related Influenza Viruses (2016) established the role of migratory wild birds in intercontinental spread through combined phylogenetic and migration analysis; Verhagen *et al.* (2021) set the research and surveillance agenda at the wild–domestic interface in Europe; and Nguyen *et al.* (2025) reconstruct the emergence and interstate spread of H5N1 in United States dairy cattle — a livestock-movement and cross-species transmission problem rather than a wild-bird one, and a demonstration that the appropriate model structure can change within a single pathogen's history.
- *Tick-borne encephalitis and Crimean-Congo haemorrhagic fever.* Randolph and Rogers (2000) for the fragility of co-feeding transmission cycles under climate change, and Messina *et al.* (2015) for the global distribution of Crimean-Congo haemorrhagic fever and the tick–host–environment covariates defining it.

INTERVENTIONS EVALUATED IN MODELS

- *Wolbachia.* Hoffmann *et al.* (2011) demonstrated stable field establishment of *wMel* in *Aedes aegypti*. Ferguson *et al.* (2015) translated measured virus-blocking into transmission terms, estimating the achievable reduction in the reproduction number from paired human-viraemia and mosquito-infection experiments — the model that underwrote scale-up decisions. Utarini *et al.* (2021) then reported the cluster-randomised trial in Yogyakarta: 77.1% protective efficacy against virologically confirmed dengue (95% CI 65.3–84.9) and an 86.2% reduction in dengue hospitalisation. Brady *et al.* (2020) modelled national scale-up in Indonesia and found it cost-effective under plausible deployment costs; Turner *et al.* (2023) provide the Vietnam economic evaluation. This sequence — mechanism, model, trial, economic evaluation, scale-up model — is the template that intervention modelling should aim to follow and rarely does.
- *Vaccination.* The RTS,S Clinical Trials Partnership (2015) reported final phase 3 results for RTS,S/AS01, with efficacy against clinical malaria over approximately four years of about 36% in children aged 5–17 months with a booster and lower efficacy in young infants — the efficacy and waning profile that malaria models must reproduce. Datoo *et al.* (2024) reported phase 3 results for R21/Matrix-M with roughly 75% efficacy at seasonal sites and about 68% at standard sites over 12 months, changing supply and cost assumptions in deployment models. For dengue, Biswal *et al.* (2019) reported overall

efficacy of about 80% against virologically confirmed dengue at 12 months for TAK-003, and Tricou *et al.* (2024) reported 4.5-year cumulative efficacy of approximately 61% against virologically confirmed dengue and 84% against hospitalised dengue, with serostatus- and serotype-dependent variation that is the central complication for dengue vaccination models.

- *Vector control and resistance dynamics.* Bhatt *et al.* (2015) estimated the *P. falciparum* burden averted in Africa between 2000 and 2015 and attributed the majority of the effect to insecticide-treated nets, providing the empirical anchor for intervention-coverage models. Ranson and Lissenden (2016) document the spread and mechanisms of pyrethroid resistance in African Anopheles, and South and Hastings (2018) give the model-based comparison of insecticide mixtures against sequences, showing that mixtures generally delay resistance relative to sequential deployment across a range of fitness and cross-resistance assumptions — a result sensitive to the assumed resistance-cost structure, and therefore a good illustration of where structural uncertainty is decision-relevant.
- *Host-targeted interventions.* Kilpatrick *et al.* (2014) related deer density reduction to tick abundance and human Lyme disease incidence in a residential community, the key empirical test of host-reduction strategies. Dolan *et al.* (2004) evaluated rodent-targeted acaricide bait boxes against immature *I. scapularis* on Borrelia-reservoir rodents in Connecticut. Both are the logical intervention implied by the host-competence literature, and the modest and variable effect sizes reported illustrate how much easier it is to identify the key host in a model than to reduce its contribution in the field.

A RESEARCH AGENDA

- *State mechanism, scale and endpoint before testing biodiversity–disease hypotheses.* Halsey (2019) and Rohr *et al.* (2020) have specified what a productive version of this literature looks like, and Mahon *et al.* (2024) demonstrates the value of distinguishing biodiversity loss from biodiversity gradient. The remaining work is largely a matter of discipline in study design.
- *Parameterise multi-host models with feeding data, not competence data alone.* The product of competence and feeding preference is what determines contribution to transmission (Simpson *et al.*, 2012), and blood-meal analysis is now inexpensive enough that its absence from multi-host model parameterisation is a choice rather than a constraint.
- *Model detection explicitly.* Occupancy and ascertainment models exist (Höhle and an der Heiden, 2014; MacKenzie *et al.*, 2002) and are not routinely used. Niche models built on presence-only occurrence without a detection component estimate sampling effort as much as distribution.
- *Score forecasts properly and publish the scores.* Given the Holcomb *et al.* (2023) finding that many West Nile virus models did not outperform historical baselines, proper scoring against a naive baseline should be a publication requirement for predictive claims, not an optional robustness check.
- *Build coupled rather than nested ecological–economic models.* Hoover *et al.* (2019) and Lowe *et al.* (2021) demonstrate what this looks like. The prevailing practice of using economic variables as covariates in an epidemiological model, or epidemiological outputs as inputs to a separate economic model, cannot represent the feedbacks that MacDonald and Mordecai (2019) show to be present.
- *Report inter-model spread alongside inter-scenario spread.* Where model choice contributes more variance than scenario choice (Colón-González *et al.*, 2021), presenting scenario ranges without model ranges misstates the uncertainty in a systematically reassuring direction.

CONCLUSION

The classical transmission modelling framework was built on four simplifying assumptions, and the productive history of the field is the history of relaxing them. Host ecology has relaxed the assumption of a well-mixed, homogeneous host population and replaced it with something considerably more demanding: a community of species whose contributions to transmission are the product of competence and vector feeding preference, in which a small minority of species typically dominate and community means are close to uninformative. Environmental change research has relaxed the assumption of constant parameters and replaced it with unimodal thermal response functions, land-cover-dependent community composition, and non-stationary climate couplings — with the consequence, in the malaria case, of reversing the projected sign of warming effects across substantial parts of the endemic range.

These are real advances, and they have been accompanied by an honest accounting of predictive limits that the field deserves credit for. Open forecasting challenges found modest and target-dependent skill, with many submitted models failing to beat historical baselines. Multi-model inter-comparisons found inter-model spread sometimes exceeding inter-scenario spread. Mobility-proxy validation found predictions robust at coarse scales and not at fine ones. Each of these results narrows the claims that can responsibly be made, and each is more useful than a confident projection.

What remains most under-developed is integration in the strong sense. Ecological, epidemiological, behavioural and economic components are usually coupled sequentially, with one supplying parameters to the next, rather than exchanging state. Detection and ascertainment are usually treated as nuisances rather than as modelled processes, despite under-ascertainment being demonstrably first-order. And the workforce capable of building genuinely multidisciplinary models — competent simultaneously in community ecology, spatial statistics, computational implementation and epidemiology — is produced by no standard training pathway and assembled ad hoc in individual research groups. The next substantive gains in this field are as likely to come from

addressing those three deficits as from further methodological refinement of any single component.

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Conflict of Interest

The authors declare that there is no conflict of interest regarding the publication of this manuscript. In addition, the ethical issues, including plagiarism, informed consent, misconduct, data fabrication and/ or falsification, double publication and/or submission, and redundancy, have been completely observed by the authors.

Life Science Reporting

No life science threat was practised in this research.

REFERENCES

1) Adaramola, T.S., Fadero, S. and Gideon, E.N. (2020) 'Machine learning and data-driven methods for industrial automation and process control', *International Journal of Engineering and Modern Technology*, 6(3), pp. 103–128. https://doi.org/10.56201/ijemt.vol.6.no3.2020.pg103.128
2) Akanbi, O. and Sunday, E.A. (2024) 'An integrated path-planning and slotting optimization model for AMR-enabled high-density warehousing', *International Journal of Advanced Multidisciplinary Research and Studies*, 4(6), pp. 3226–3243. https://doi.org/10.62225/2583049X.2024.4.6.6181
3) Akanbi, O. and Sunday, E.A. (2025) 'A systematic review of AI-driven autonomous mobile robots (AMR) in scalable micro-fulfillment centers', *International Journal of Advanced Multidisciplinary Research and Studies*, 5(6), pp. 2363–2379. https://doi.org/10.62225/2583049X.2025.5.6.6182
4) Akanbi, O., Ganiu, O.S. and Sunday, E.A. (2025) 'A multi-agent AI framework for swarm intelligence in autonomous mobile robot (AMR) fleet coordination', *International Journal of Scientific Research in Humanities and Social Sciences*, 2(1), pp. 81–109.
5) Allan, B.F., Keesing, F. and Ostfeld, R.S. (2003) 'Effect of forest fragmentation on Lyme disease risk', *Conservation Biology*, 17(1), pp. 267–272. https://doi.org/10.1046/j.1523-1739.2003.01260.x
6) Amos, B., Aurrecoechea, C., Barba, M., *et al.* (2022) 'VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center', *Nucleic Acids Research*, 50(D1), pp. D898–D911. https://doi.org/10.1093/nar/gkab929
7) Anyamba, A., Chretien, J.-P., Small, J., *et al.* (2009) 'Prediction of a Rift Valley fever outbreak', *Proceedings of the National Academy of Sciences*, 106(3), pp. 955–959. https://doi.org/10.1073/pnas.0806490106
8) Ayinde, M., Ojukwu, P.U. and Ohunyon, G. (2025) 'Organizational readiness for generative AI integration in healthcare operations: comparative management capabilities between the U.S. and low- and middle-income countries', *International Journal of Advanced Multidisciplinary Research and Studies*, 5(6), pp. 2207–2222.
9) Balcan, D., Colizza, V., Goncalves, B., *et al.* (2009) 'Multiscale mobility networks and the spatial spreading of infectious diseases', *Proceedings of the National Academy of Sciences*, 106(51), pp. 21484–21489. https://doi.org/10.1073/pnas.0906910106
10) Becker, D.J., Streicker, D.G. and Altizer, S. (2015) 'Linking anthropogenic resources to wildlife–pathogen dynamics: a review and meta-analysis', *Ecology Letters*, 18(5), pp. 483–495. https://doi.org/10.1111/ele.12428
11) Beven, K. and Freer, J. (2001) 'Equifinality, data assimilation, and uncertainty estimation in mechanistic modelling of complex environmental systems using the GLUE methodology', *Journal of Hydrology*, 249(1–4), pp. 11–29. https://doi.org/10.1016/S0022-1694(01)00421-8
12) Bhatt, S., Gething, P.W., Brady, O.J., *et al.* (2013) 'The global distribution and burden of dengue', *Nature*, 496(7446), pp. 504–507. https://doi.org/10.1038/nature12060
13) Bhatt, S., Weiss, D.J., Cameron, E., *et al.* (2015) 'The effect of malaria control on Plasmodium falciparum in Africa between 2000 and 2015', *Nature*, 526(7572), pp. 207–211. https://doi.org/10.1038/nature15535
14) Biswal, S., Reynales, H., Saez-Llorens, X., *et al.* (2019) 'Efficacy of a tetravalent dengue vaccine in healthy children and adolescents', *New England Journal of Medicine*, 381(21), pp. 2009–2019. https://doi.org/10.1056/NEJMoa1903869
15) Bracher, J., Ray, E.L., Gneiting, T., *et al.* (2021) 'Evaluating epidemic forecasts in an interval format', *PLOS Computational Biology*, 17(2), e1008618. https://doi.org/10.1371/journal.pcbi.1008618
16) Brady, O.J., Kharisma, D.D., Wilastonogoro, N.N., *et al.* (2020) 'The cost-effectiveness of controlling dengue in Indonesia using wMel Wolbachia released at scale: a modelling study', *BMC Medicine*, 18(1), 186. https://doi.org/10.1186/s12916-020-01638-2
17) Carlson, C.J., Albery, G.F., Merow, C., *et al.* (2022) 'Climate change increases cross-species viral transmission risk', *Nature*, 607(7919), pp. 555–562. https://doi.org/10.1038/s41586-022-04788-w
18) Cazelles, B., Chavez, M., McMichael, A.J., *et al.* (2005) 'Nonstationary influence of El Niño on the synchronous dengue epidemics in Thailand', *PLoS Medicine*, 2(4), e106. https://doi.org/10.1371/journal.pmed.0020106
19) Cecilia, H., Drouin, A., Metras, R., *et al.* (2022) 'Mechanistic models of Rift Valley fever virus transmission: a systematic review', *PLOS Neglected Tropical Diseases*, 16(11), e0010339. https://doi.org/10.1371/journal.pntd.0010339
20) Childs, M.L., Lyberger, K., Harris, M.J., *et al.* (2025) 'Climate warming is expanding dengue burden in the Americas and Asia', *Proceedings of the National Academy of Sciences*, 122(37), e2512350122. https://doi.org/10.1073/pnas.2512350122
21) Civitello, D.J., Cohen, J., Fatima, H., *et al.* (2015) 'Biodiversity inhibits parasites: broad evidence for the dilution effect', *Proceedings of the National Academy of Sciences*, 112(28), pp. 8667–8671. https://doi.org/10.1073/pnas.1506279112
22) Colón-González, F.J., Sewe, M.O., Tompkins, A.M., *et al.* (2021) 'Projecting the risk of mosquito-borne diseases in a warmer and more populated world: a multi-model, multi-scenario intercomparison modelling study', *The Lancet Planetary Health*, 5(7), e404–e414. https://doi.org/10.1016/S2542-5196(21)00132-7
23) Costa, E.de-F., Streng, K., Santos, M.Ade-S., *et al.* (2024) 'The effect of temperature on the boundary conditions of West Nile virus circulation in Europe', *PLOS Neglected Tropical Diseases*, 18(5), e0012162. https://doi.org/10.1371/journal.pntd.0012162
24) Cross, P.C., Prosser, D.J., Ramey, A.M., *et al.* (2019) 'Confronting models with data: the challenges of estimating disease spillover', *Philosophical Transactions of the Royal Society B: Biological Sciences*, 374(1782), 20180435. https://doi.org/10.1098/rstb.2018.0435
25) Datoo, M.S., Dicko, A., Tinto, H., *et al.* (2024) 'Safety and efficacy of malaria vaccine candidate R21/Matrix-M in African children: a multicentre, double-blind, randomised, phase 3 trial', *The Lancet*, 403(10426), pp. 533–544. https://doi.org/10.1016/S0140-6736(23)02511-4
26) Diekmann, O., Heesterbeek, J.A.P. and Metz, J.A.J. (1990) 'On the definition and the computation of the basic reproduction ratio R0 in models for infectious diseases in heterogeneous populations', *Journal of Mathematical Biology*, 28(4), pp. 365–382. https://doi.org/10.1007/BF00178324
27) Diekmann, O., Heesterbeek, J.A.P. and Roberts, M.G. (2010) 'The construction of next-generation matrices for compartmental epidemic models', *Journal of the Royal Society Interface*, 7(47), pp. 873–885. https://doi.org/10.1098/rsif.2009.0386
28) Diuk-Wasser, M.A., VanAcker, M.C. and Fernandez, M.P. (2021) 'Impact of land use changes and habitat fragmentation on the eco-epidemiology of tick-borne diseases', *Journal of Medical Entomology*, 58(4), pp. 1546–1564. https://doi.org/10.1093/jme/tjaa209
29) Dolan, M.C., Maupin, G.O., Schneider, B.S., *et al.* (2004) 'Control of immature Ixodes scapularis (Acari: Ixodidae) on rodent reservoirs of Borrelia burgdorferi in a residential community of southeastern Connecticut', *Journal of Medical Entomology*, 41(6), pp. 1043–1054. https://doi.org/10.1603/0022-2585-41.6.1043
30) Elith, J., Phillips, S.J., Hastie, T., *et al.* (2011) 'A statistical explanation of MaxEnt for ecologists', *Diversity and Distributions*, 17(1), pp. 43–57. https://doi.org/10.1111/j.1472-4642.2010.00725.x
31) Erazo, D., Grant, L., Ghisbain, G., *et al.* (2024) 'Contribution of climate change to the spatial expansion of West Nile virus in Europe',

Nature Communications, 15(1), 1196. https://doi.org/10.1038/s41467-024-45290-3

32) Eubank, S., Guclu, H., Kumar, V.S.A., *et al.* (2004) 'Modelling disease outbreaks in realistic urban social networks', *Nature*, 429(6988), pp. 180–184. https://doi.org/10.1038/nature02541

33) Farooq, Z., Rocklöv, J., Wallin, J., *et al.* (2022) 'Artificial intelligence to predict West Nile virus outbreaks with eco-climatic drivers', *The Lancet Regional Health – Europe*, 17, 100370. https://doi.org/10.1016/j.lanepe.2022.100370

34) Faust, C.L., McCallum, H.I., Bloomfield, L.S.P., *et al.* (2018) 'Pathogen spillover during land conversion', *Ecology Letters*, 21(4), pp. 471–483. https://doi.org/10.1111/ele.12904

35) Ferguson, N.M. (2007) 'Capturing human behaviour', *Nature*, 446(7137), p. 733. https://doi.org/10.1038/446733a

36) Ferguson, N.M., Kien, D.T.H., Clapham, H., *et al.* (2015) 'Modeling the impact on virus transmission of Wolbachia-mediated blocking of dengue virus infection of Aedes aegypti', *Science Translational Medicine*, 7(279), 279ra37. https://doi.org/10.1126/scitranslmed.3010370

37) Funk, S., Camacho, A., Kucharski, A.J., *et al.* (2019) 'Assessing the performance of real-time epidemic forecasts: a case study of Ebola in the Western Area region of Sierra Leone, 2014–15', *PLOS Computational Biology*, 15(2), e1006785. https://doi.org/10.1371/journal.pcbi.1006785

38) Funk, S., Gilad, E. and Jansen, V.A.A. (2010) 'Endemic disease, awareness, and local behavioural response', *Journal of Theoretical Biology*, 264(2), pp. 501–509. https://doi.org/10.1016/j.jtbi.2010.02.032

39) Garrett-Jones, C. (1964) 'Prognosis for interruption of malaria transmission through assessment of the mosquito's vectorial capacity', *Nature*, 204(4964), pp. 1173–1175. https://doi.org/10.1038/2041173a0

40) Gibb, R., Albery, G.F., Becker, D.J., *et al.* (2021) 'Data proliferation, reconciliation, and synthesis in viral ecology', *BioScience*, 71(11), pp. 1148–1156. https://doi.org/10.1093/biosci/biab080

41) Gibb, R., Redding, D.W., Chin, K.Q., *et al.* (2020) 'Zoonotic host diversity increases in human-dominated ecosystems', *Nature*, 584(7821), pp. 398–402. https://doi.org/10.1038/s41586-020-2562-8

42) Gibb, R., Redding, D.W., Friant, S., *et al.* (2025) 'Towards a "people and nature" paradigm for biodiversity and infectious disease', *Philosophical Transactions of the Royal Society B: Biological Sciences*, 380(1917), 20230259. https://doi.org/10.1098/rstb.2023.0259

43) Gideon, E.N., Adaramola, T.S. and Fadero, S. (2019) 'Reliability engineering and failure analysis in complex engineering systems', *IRE Journals*, 2(11), pp. 703–727. https://doi.org/10.64388/IREV2111-1722490

44) Global Consortium for H5N8 and Related Influenza Viruses (2016) 'Role for migratory wild birds in the global spread of avian influenza H5N8', *Science*, 354(6309), pp. 213–217. https://doi.org/10.1126/science.aaf8852

45) Gneiting, T. and Raftery, A.E. (2007) 'Strictly proper scoring rules, prediction, and estimation', *Journal of the American Statistical Association*, 102(477), pp. 359–378. https://doi.org/10.1198/016214506000001437

46) Grassly, N.C. and Fraser, C. (2008) 'Mathematical models of infectious disease transmission', *Nature Reviews Microbiology*, 6(6), pp. 477–487. https://doi.org/10.1038/nrmicro1845

47) Halsey, S. (2019) 'Defuse the dilution effect debate', *Nature Ecology & Evolution*, 3(2), pp. 145–146. https://doi.org/10.1038/s41559-018-0764-3

48) Hamer, G.L., Kitron, U.D., Goldberg, T.L., *et al.* (2009) 'Host selection by Culex pipiens mosquitoes and West Nile virus amplification', *American Journal of Tropical Medicine and Hygiene*, 80(2), pp. 268–278. https://doi.org/10.4269/ajtmh.2009.80.268

49) Han, B.A., Schmidt, J.P., Bowden, S.E., *et al.* (2015) 'Rodent reservoirs of future zoonotic diseases', *Proceedings of the National Academy of Sciences*, 112(22), pp. 7039–7044. https://doi.org/10.1073/pnas.1501598112

50) Hart, W.S., Hurrell, J.W., Kaye, A.R., *et al.* (2025) 'Climate variability amplifies the need for vector-borne disease outbreak preparedness', *Proceedings of the National Academy of Sciences*, 122(34), e2507311122. https://doi.org/10.1073/pnas.2507311122

51) Hassell, J.M., Begon, M., Ward, M.J., *et al.* (2017) 'Urbanization and disease emergence: dynamics at the wildlife–livestock–human interface', *Trends in Ecology & Evolution*, 32(1), pp. 55–67. https://doi.org/10.1016/j.tree.2016.09.012

52) Haydon, D.T., Cleaveland, S., Taylor, L.H., *et al.* (2002) 'Identifying reservoirs of infection: a conceptual and practical challenge', *Emerging Infectious Diseases*, 8(12), pp. 1468–1473. https://doi.org/10.3201/eid0812.010317

53) Heberling, J.M., Miller, J.T., Noesgaard, D., *et al.* (2021) 'Data integration enables global biodiversity synthesis', *Proceedings of the National Academy of Sciences*, 118(6), e2018093118. https://doi.org/10.1073/pnas.2018093118

54) Hoffmann, A.A., Montgomery, B.L., Popovici, J., *et al.* (2011) 'Successful establishment of Wolbachia in Aedes populations to suppress dengue transmission', *Nature*, 476(7361), pp. 454–457. https://doi.org/10.1038/nature10356

55) Höhle, M. and an der Heiden, M. (2014) 'Bayesian nowcasting during the STEC O104:H4 outbreak in Germany, 2011', *Biometrics*, 70(4), pp. 993–1002. https://doi.org/10.1111/biom.12194

56) Holcomb, K.M., Mathis, S., Staples, J.E., *et al.* (2023) 'Evaluation of an open forecasting challenge to assess skill of West Nile virus neuroinvasive disease prediction', *Parasites & Vectors*, 16(1), 11. https://doi.org/10.1186/s13071-022-05630-y

57) Hoover, C.M., Sokolow, S.H., Kemp, J., *et al.* (2019) 'Modelled effects of prawn aquaculture on poverty alleviation and schistosomiasis control', *Nature Sustainability*, 2(7), pp. 611–620. https://doi.org/10.1038/s41893-019-0301-7

58) Huber, J.H., Childs, M.L., Caldwell, J.M., *et al.* (2018) 'Seasonal temperature variation influences climate suitability for dengue, chikungunya, and Zika transmission', *PLOS Neglected Tropical Diseases*, 12(5), e0006451. https://doi.org/10.1371/journal.pntd.0006451

59) Ike, P.N., Aifuwa, S.E., Nnabueze, S.B., *et al.* (2024) 'Quantitative risk architecture for public–private partnerships: a multi-layered model for allocating public and private risk', *International Journal of Advanced Multidisciplinary Research and Studies*, 4(6), pp. 2669–2682. https://doi.org/10.62225/2583049X.2024.4.6.5021

60) Ike, P.N., Okojie, J.S., Nnabueze, S.B., *et al.* (2025) 'Digital twin-driven environmental compliance models for sustainable procurement in oil, gas, and utilities', *International Journal of Advanced Multidisciplinary Research and Studies*, 5(5), pp. 562–576.

61) IPCC (2022) *Climate change 2022: impacts, adaptation and vulnerability*. Contribution of Working Group II to the Sixth Assessment Report of the Intergovernmental Panel on Climate Change. Cambridge University Press. https://doi.org/10.1017/9781009325844

62) Johansson, M.A., Apfeldorf, K.M., Dobson, S., *et al.* (2019) 'An open challenge to advance probabilistic forecasting for dengue epidemics', *Proceedings of the National Academy of Sciences*, 116(48), pp. 24268–24274. https://doi.org/10.1073/pnas.1909865116

63) Joseph, M.B., Mihaljevic, J.R., Orlofske, S.A., *et al.* (2013) 'Does life history mediate changing disease risk when communities disassemble?', *Ecology Letters*, 16(11), pp. 1405–1412. https://doi.org/10.1111/ele.12180

64) Joseph, O.B., Ijiga, O.M., Olateji, M., *et al.* (2025b) 'Comparative perspectives on TVET: lessons from the United States and developing economies for workforce readiness and economic inclusion', *International Journal of Advanced Multidisciplinary Research and Studies*, 5(2), pp. 2493–2506.

65) Joseph, O.B., Olateji, M., Ijiga, O.M., *et al.* (2025a) 'Future-proofing skills in the Global South: strategic directions for transforming technical and vocational education and training (TVET)', *International Journal of Advanced Multidisciplinary Research and Studies*, 5(2), pp. 2478–2492. https://doi.org/10.62225/2583049X.2025.5.2.4730

66) Joseph, O.B., Olateji, M., Okoli, I., *et al.* (2025c) 'Policy, power, and performance: the role of government in shaping successful TVET outcomes — a cross-national study', *International Journal of Advanced Multidisciplinary Research and Studies*, 5(2), pp. 2507–2521. https://doi.org/10.62225/2583049X.2025.5.2.4732

67) Kaye, A.R., Obolski, U., Sun, L., *et al.* (2024) 'The impact of natural climate variability on the global distribution of Aedes aegypti: a mathematical modelling study', *The Lancet Planetary Health*, 8(12), e1079–e1087. https://doi.org/10.1016/S2542-5196(24)00238-9

68) Keeling, M.J. and Rohani, P. (2008) *Modeling infectious diseases in humans and animals*. 1st ed. Princeton, NJ: Princeton University Press. https://doi.org/10.1515/9781400841035

69) Keesing, F., Belden, L.K., Daszak, P., *et al.* (2010) 'Impacts of biodiversity on the emergence and transmission of infectious diseases', Nature, 468(7324), pp. 647–652. https://doi.org/10.1038/nature09575

70) Kianguebene-Koussingounina, C.E., Olajide-Kayode, J.O., Oyediran, I.A., *et al.* (2023) 'Geostatistical assessment of soils in Ibadan, Southwest Nigeria: focus on agricultural lands', *Environmental and Sustainability Indicators*, 19, 100287. https://doi.org/10.1016/j.indc.2023.100287

71) Kilpatrick, A.M. and Randolph, S.E. (2012) 'Drivers, dynamics, and control of emerging vector-borne zoonotic diseases', *The Lancet*, 380(9857), pp. 1946–1955. https://doi.org/10.1016/S0140-6736(12)61151-9

72) Kilpatrick, A.M., Daszak, P., Jones, M.J., *et al.* (2006a) 'Host heterogeneity dominates West Nile virus transmission', *Proceedings of the Royal Society B: Biological Sciences*, 273(1599), pp. 2327–2333. https://doi.org/10.1098/rspb.2006.3575

73) Kilpatrick, A.M., Kramer, L.D., Jones, M.J., *et al.* (2006b) 'West Nile virus epidemics in North America are driven by shifts in mosquito feeding behavior', *PLoS Biology*, 4(4), e82. https://doi.org/10.1371/journal.pbio.0040082

74) Kilpatrick, H.J., LaBonte, A.M. and Stafford, K.C. (2014) 'The relationship between deer density, tick abundance, and human cases of Lyme disease in a residential community', *Journal of Medical Entomology*, 51(4), pp. 777–784. https://doi.org/10.1603/ME13232

75) Komar, N., Langevin, S., Hinten, S., *et al.* (2003) 'Experimental infection of North American birds with the New York 1999 strain of West Nile virus', *Emerging Infectious Diseases*, 9(3), pp. 311–322. https://doi.org/10.3201/eid0903.020628

76) Kraemer, M.U.G., Reiner, R.C., Brady, O.J., *et al.* (2019) 'Past and future spread of the arbovirus vectors Aedes aegypti and Aedes albopictus', Nature Microbiology, 4(5), pp. 854–863. https://doi.org/10.1038/s41564-019-0376-y

77) Kraemer, M.U.G., Sinka, M.E., Duda, K.A., *et al.* (2015) 'The global distribution of the arbovirus vectors *Aedes aegypti* and *Ae. albopictus*', *eLife*, 4, e08347. https://doi.org/10.7554/eLife.08347

78) Kraemer, M.U.G., Yang, C.-H., Gutierrez, B., *et al.* (2020) 'The effect of human mobility and control measures on the COVID-19 epidemic in China', *Science*, 368(6490), pp. 493–497. https://doi.org/10.1126/science.abb4218

79) Levi, T., Keesing, F., Oggenfuss, K. *et al.* (2015) 'Accelerated phenology of blacklegged ticks under climate warming', *Philosophical Transactions of the Royal Society B: Biological Sciences*, 370(1665), 20130556. https://doi.org/10.1098/rstb.2013.0556

80) Lindgren, F., Rue, H. and Lindström, J. (2011) 'An explicit link between Gaussian fields and Gaussian Markov random fields: the stochastic partial differential equation approach', *Journal of the Royal Statistical Society: Series B*, 73(4), pp. 423–498. https://doi.org/10.1111/j.1467-9868.2011.00777.x

81) Linthicum**,** K.J., Anyamba, A., Tucker, C.J., *et al.* (1999) 'Climate and satellite indicators to forecast Rift Valley fever epidemics in Kenya', *Science*, 285(5426), pp. 397–400. https://doi.org/10.1126/science.285.5426.397

82) LoGiudice, K., Ostfeld, R.S., Schmidt, K.A. *et al.* (2003) 'The ecology of infectious disease: effects of host diversity and community composition on Lyme disease risk', *Proceedings of the National Academy of Sciences*, 100(2), pp. 567–571. https://doi.org/10.1073/pnas.0233733100

83) Lowe, R., Gasparrini, A., Van Meerbeeck, C.J., *et al.* (2018) 'Nonlinear and delayed impacts of climate on dengue risk in Barbados: a modelling study', *PLoS Medicine*, 15(7), e1002613. https://doi.org/10.1371/journal.pmed.1002613

84) Lowe, R., Lee, S.A., O'Reilly, K.M., *et al.* (2021) 'Combined effects of hydrometeorological hazards and urbanisation on dengue risk in Brazil: a spatiotemporal modelling study', *The Lancet Planetary Health*, 5(4), e209–e219. https://doi.org/10.1016/S2542-5196(20)30292-8

85) MacDonald, A.J. and Mordecai, E.A. (2019) 'Amazon deforestation drives malaria transmission, and malaria burden reduces forest clearing', *Proceedings of the National Academy of Sciences*, 116(44), pp. 22212–22218. https://doi.org/10.1073/pnas.1905315116

86) MacKenzie, D.I., Nichols, J.D., Lachman, G.B., *et al.* (2002) 'Estimating site occupancy rates when detection probabilities are less than one', *Ecology*, 83(8), pp. 2248–2255. https://doi.org/10.1890/0012-9658(2002)083[2248:ESORWD]2.0.CO;2

87) Magori, K., Legros, M., Puente, M.E., *et al.* (2009) 'Skeeter Buster: a stochastic, spatially explicit modeling tool for studying Aedes aegypti population replacement and population suppression strategies', *PLOS Neglected Tropical Diseases*, 3(9), e508. https://doi.org/10.1371/journal.pntd.0000508

88) Mahon, M.B., Sack, A., Aleuy, O.A., *et al.* (2024) 'A meta-analysis of the biodiversity–disease relationship', Nature**,** 629**(**8014**),** pp. 1073–1079. https://doi.org/10.1038/s41586-024-07380-6

89) Martin, L.B., Burgan, S.C., Adelman, J.S. *et al.* (2016) 'Host competence: an organismal trait to integrate immunology and epidemiology', *Integrative and Comparative Biology*, 56(6), pp. 1225–1237. https://doi.org/10.1093/icb/icw064

90) Mather, T.N., Wilson, M.L., Moore, S.I., *et al.* (1989) 'Comparing the relative potential of rodents as reservoirs of the Lyme disease spirochete (*Borrelia burgdorferi*)', *American Journal of Epidemiology*, 130(1), pp. 143–150. https://doi.org/10.1093/oxfordjournals.aje.a115306

91) Messina, J.P., Brady, O.J., Golding, N., *et al.* (2019) 'The current and future global distribution and population at risk of dengue', *Nature Microbiology*, 4(9), pp. 1508–1515. https://doi.org/10.1038/s41564-019-0476-8

92) Messina, J.P., Pigott, D.M., Golding, N., *et al.* (2015) 'The global distribution of Crimean-Congo hemorrhagic fever', *Transactions of the Royal Society of Tropical Medicine and Hygiene*, 109(8), pp. 503–513. https://doi.org/10.1093/trstmh/trv050

93) Metcalf, C.J.E. and Lessler, J. (2017) 'Opportunities and challenges in modeling emerging infectious diseases', *Science*, 357(6347), pp. 149–152. https://doi.org/10.1126/science.aam8335

94) Mordecai, E.A., Caldwell, J.M., Grossman, M.K., *et al.* (2019) 'Thermal biology of mosquito-borne disease', *Ecology Letters*, 22(10), pp. 1690–1708. https://doi.org/10.1111/ele.13335

95) Mordecai, E.A., Cohen, J.M., Evans, M.V., *et al.* (2017) 'Detecting the impact of temperature on transmission of Zika, dengue, and chikungunya using mechanistic models', *PLOS Neglected Tropical Diseases*, 11(4), e0005568. https://doi.org/10.1371/journal.pntd.0005568

96) Mordecai, E.A., Paaijmans, K.P., Johnson, L.R., *et al.* (2013) 'Optimal temperature for malaria transmission is dramatically lower than previously predicted', *Ecology Letters*, 16(1), pp. 22–30. https://doi.org/10.1111/ele.12015

97) Murray, M.H., Sanchez, C.A., Becker, D.J., *et al.* (2019) 'City sicker? A meta-analysis of wildlife health and urbanization', *Frontiers in Ecology and the Environment*, 17(10), pp. 575–583. https://doi.org/10.1002/fee.2126

98) Nguyen, T.-Q., Hutter, C.R., Markin, A., *et al.* (2025) 'Emergence and interstate spread of highly pathogenic avian influenza A(H5N1) in dairy cattle in the United States', *Science*, 388(6745), eadq0900. https://doi.org/10.1126/science.adq0900

99) Nieto, N.C., Porter, W.T., Wachara, J.C., *et al.* (2018) 'Using citizen science to describe the prevalence and distribution of tick bite and exposure to tick-borne diseases in the United States', *PLOS ONE*, 13(7), e0199644. https://doi.org/10.1371/journal.pone.0199644

100) Ogden, N.H. and Lindsay, L.R. (2016) 'Effects of climate and climate change on vectors and vector-borne diseases: ticks are different', *Trends in Parasitology*, 32(8), pp. 646–656. https://doi.org/10.1016/j.pt.2016.04.015

101) Ogden, N.H., Bigras-Poulin, M., O'Callaghan, C.J., *et al.* (2005) 'A dynamic population model to investigate effects of climate on geographic range and seasonality of the tick Ixodes scapularis', *International Journal for Parasitology*, 35(4), pp. 375–389. https://doi.org/10.1016/j.ijpara.2004.12.013

102) Olivero, J., Fa, J.E., Real, R., *et al.* (2017) 'Recent loss of closed forests is associated with Ebola virus disease outbreaks', *Scientific Reports*, 7(1), 14291. https://doi.org/10.1038/s41598-017-14727-9

103) Oluwo, K., Bola-Sadipe, D. and Aliliele, C. (2025) 'Conceptual framework for data analytics driven financial decision making in banking sector organizations', *Shodhshauryam, International Scientific Refereed Research Journal*, 8(5), pp. 259–302. https://doi.org/10.32628/SHISRRJ258529

104) Oluwo, K., Dada, T. and Isiekwu, C.P. (2024) 'Transforming insurance underwriting with machine learning: a review and application cases', *International Journal of Advanced Multidisciplinary Research and Studies*, 4(6), pp. 3008–3019. https://doi.org/10.62225/2583049x.2024.4.6.5876

105) Ostfeld, R.S. and Keesing, F. (2000) 'Biodiversity and disease risk: the case of Lyme disease', *Conservation Biology*, 14(3), pp. 722–728. https://doi.org/10.1046/j.1523-1739.2000.99014.x

106) Ostfeld, R.S. and Keesing, F. (2012) 'Effects of host diversity on infectious disease', *Annual Review of Ecology, Evolution, and Systematics*, 43(1), pp. 157–182. https://doi.org/10.1146/annurev-ecolsys-102710-145022

107) Ovaskainen, O., Tikhonov, G., Norberg, A., *et al.* (2017) 'How to make more out of community data? A conceptual framework and its implementation as models and software', *Ecology Letters*, 20(5), pp. 561–576. https://doi.org/10.1111/ele.12757

108) Parselia, E., Kontoes, C., Tsouni, A., *et al.* (2019) 'Satellite Earth observation data in epidemiological modeling of malaria, dengue and West Nile virus: a scoping review', *Remote Sensing*, 11(16), 1862. https://doi.org/10.3390/rs11161862

109) Paull, S.H., Horton, D.E., Ashfaq, M., *et al.* (2017) 'Drought and immunity determine the intensity of West Nile virus epidemics and climate change impacts', *Proceedings of the Royal Society B: Biological Sciences*, 284(1848), 20162078. https://doi.org/10.1098/rspb.2016.2078

110) Perkins, T.A., Scott, T.W., Le Menach, A., *et al.* (2013) 'Heterogeneity, mixing, and the spatial scales of mosquito-borne pathogen transmission', *PLOS Computational Biology*, 9(12), e1003327. https://doi.org/10.1371/journal.pcbi.1003327

111) Pfenning-Butterworth, A., Buckley, L.B., Drake, J.M., *et al.* (2024) 'Interconnecting global threats: climate change, biodiversity loss, and infectious diseases', *The Lancet Planetary Health*, 8(4), e270–e283. https://doi.org/10.1016/S2542-5196(24)00021-4

112) Phillips, S.J., Anderson, R.P. and Schapire, R.E. (2006) 'Maximum entropy modeling of species geographic distributions', Ecological Modelling, 190(3–4), pp. 231–259. https://doi.org/10.1016/j.ecolmodel.2005.03.026

113) Randolph, S.E. and Rogers, D.J. (2000) 'Fragile transmission cycles of tick-borne encephalitis virus may be disrupted by predicted climate change', *Proceedings of the Royal Society B: Biological Sciences*, 267(1454), pp. 1741–1744. https://doi.org/10.1098/rspb.2000.1204

114) Ranson, H. and Lissenden, N. (2016) 'Insecticide resistance in African Anopheles mosquitoes: a worsening situation that needs urgent action to maintain malaria control', *Trends in Parasitology*, 32(3), pp. 187–196. https://doi.org/10.1016/j.pt.2015.11.010

115) Ray, E.L., Brooks, L.C., Bien, J., *et al.* (2023) 'Comparing trained and untrained probabilistic ensemble forecasts of COVID-19 cases and deaths in the United States', *International Journal of Forecasting*, 39(3), pp. 1366–1383. https://doi.org/10.1016/j.ijforecast.2022.06.005

116) Redding, D.W., Atkinson, P.M., Cunningham, A.A., *et al.* (2019) 'Impacts of environmental and socio-economic factors on emergence and epidemic potential of Ebola in Africa', *Nature Communications*, 10(1), 4531. https://doi.org/10.1038/s41467-019-12499-6

117) Reiner, R.C., Perkins, T.A., Barker, C.M., *et al.* (2013) 'A systematic review of mathematical models of mosquito-borne pathogen transmission: 1970–2010', *Journal of the Royal Society Interface*, 10(81), 20120921. https://doi.org/10.1098/rsif.2012.0921

118) Rohr, J.R., Barrett, C.B., Civitello, D.J., *et al.* (2019) 'Emerging human infectious diseases and the links to global food production', *Nature Sustainability*, 2(6), pp. 445–456. https://doi.org/10.1038/s41893-019-0293-3

119) Rohr, J.R., Civitello, D.J., Halliday, F.W., *et al.* (2020) 'Towards common ground in the biodiversity–disease debate', *Nature Ecology & Evolution*, 4(1), pp. 24–33. https://doi.org/10.1038/s41559-019-1060-6

120) Romanello, M., Walawender, M., Hsu, S.-C., *et al.* (2024) 'The 2024 report of the Lancet Countdown on health and climate change: facing record-breaking threats from delayed action', *The Lancet*, 404(10465), pp. 1847–1896. https://doi.org/10.1016/S0140-6736(24)01822-1

121) RTS,S Clinical Trials Partnership (2015) 'Efficacy and safety of RTS,S/AS01 malaria vaccine with or without a booster dose in infants and children in Africa: final results of a phase 3, individually randomised, controlled trial', *The Lancet*, 386(9988), pp. 31–45. https://doi.org/10.1016/S0140-6736(15)60721-8

122) Rue, H., Martino, S. and Chopin, N. (2009) 'Approximate Bayesian inference for latent Gaussian models by using integrated nested Laplace approximations', *Journal of the Royal Statistical Society: Series B*, 71(2), pp. 319–392. https://doi.org/10.1111/j.1467-9868.2008.00700.x

123) Rulli, M.C., D'Odorico, P., Galli, N., *et al.* (2025) 'Land use change and infectious disease emergence', *Reviews of Geophysics*, 63(2), e2022RG000785. https://doi.org/10.1029/2022RG000785

124) Ryan, S.J., Carlson, C.J., Mordecai, E.A., *et al.* (2019) 'Global expansion and redistribution of Aedes-borne virus transmission risk with climate change', *PLOS Neglected Tropical Diseases*, 13(3), e0007213. https://doi.org/10.1371/journal.pntd.0007213

125) Salkeld, D.J., Padgett, K.A. and Jones, J.H. (2013) 'A meta-analysis suggesting that the relationship between biodiversity and risk of zoonotic pathogen transmission is idiosyncratic', *Ecology Letters*, 16(5), pp. 679–686. https://doi.org/10.1111/ele.12101

126) Shea, K., Runge, M.C., Pannell, D., *et al.* (2020) 'Harnessing multiple models for outbreak management', *Science*, 368(6491), pp. 577–579. https://doi.org/10.1126/science.abb9934

127) Shocket, M.S., Verwillow, A.B., Numazu, M.G., *et al.* (2020) 'Transmission of West Nile and five other temperate mosquito-borne viruses peaks at temperatures between 23°C and 26°C', *eLife*, 9, e58511. https://doi.org/10.7554/eLife.58511

128) Simpson, J.E., Hurtado, P.J., Medlock, J., *et al.* (2012) 'Vector host-feeding preferences drive transmission of multi-host pathogens: West Nile virus as a model system', *Proceedings of the Royal Society B: Biological Sciences*, 279(1730), pp. 925–933. https://doi.org/10.1098/rspb.2011.1282

129) Smith, D.L. and McKenzie, F.E. (2004) 'Statics and dynamics of malaria infection in Anopheles mosquitoes', *Malaria Journal*, 3(1), 13. https://doi.org/10.1186/1475-2875-3-13

130) Smith, D.L., Battle, K.E., Hay, S.I., *et al.* (2012) 'Ross, Macdonald, and a theory for the dynamics and control of mosquito-transmitted pathogens', *PLoS Pathogens*, 8(4), e1002588. https://doi.org/10.1371/journal.ppat.1002588

131) Sokolow, S.H., Huttinger, E., Jouanard, N., *et al.* (2015) 'Reduced transmission of human schistosomiasis after restoration of a native river prawn that preys on the snail intermediate host', *Proceedings of the National Academy of Sciences*, 112(31), pp. 9650–9655. https://doi.org/10.1073/pnas.1502651112

132) South, A. and Hastings, I.M. (2018) 'Insecticide resistance evolution with mixtures and sequences: a model-based explanation', *Malaria Journal*, 17(1), 80. https://doi.org/10.1186/s12936-018-2203-y

133) Tizzoni, M., Bajardi, P., Decuyper, A., *et al.* (2014) 'On the use of human mobility proxies for modeling epidemics', *PLOS Computational Biology*, 10(7), e1003716. https://doi.org/10.1371/journal.pcbi.1003716

134) Trebski, A., Gourlay, L., Gibb, R., *et al.* (2025) 'Climate sensitivity is widely but unevenly spread across zoonotic diseases', *Proceedings of the National Academy of Sciences*, 122(50), e2422851122. https://doi.org/10.1073/pnas.2422851122

135) Tricou, V., Yu, D., Reynales, H., *et al.* (2024) 'Long-term efficacy and safety of a tetravalent dengue vaccine (TAK-003): 4–5-year results from a phase 3, randomised, double-blind, placebo-controlled trial', *The Lancet Global Health*, 12(2), pp. e257–e270. https://doi.org/10.1016/S2214-109X(23)00522-3

136) Turner, H.C., Quyen, D.L., Dias, R., *et al.* (2023) 'An economic evaluation of Wolbachia deployments for dengue control in Vietnam', *PLOS Neglected Tropical Diseases*, 17(5), e0011356. https://doi.org/10.1371/journal.pntd.0011356

137) Tusting, L.S., Willey, B., Lucas, H., *et al.* (2013) 'Socioeconomic development as an intervention against malaria: a systematic review and meta-analysis', *The Lancet*, 382(9896), pp. 963–972. https://doi.org/10.1016/S0140-6736(13)60851-X

138) Utarini, A., Indriani, C., Ahmad, R.A., *et al.* (2021) 'Efficacy of Wolbachia-infected mosquito deployments for the control of dengue', *New England Journal of Medicine*, 384(23), pp. 2177–2186. https://doi.org/10.1056/NEJMoa2030243

139) van Panhuis, W.G., Choisy, M., Xiong, X., *et al.* (2015) 'Region-wide synchrony and traveling waves of dengue across eight countries in Southeast Asia', *Proceedings of the National Academy of Sciences*, 112(42), pp. 13069–13074. https://doi.org/10.1073/pnas.1501375112

140) Verelst, F., Willem, L. and Beutels, P. (2016) 'Behavioural change models for infectious disease transmission: a systematic review (2010–2015)', *Journal of the Royal Society Interface*, 13(125), 20160820. https://doi.org/10.1098/rsif.2016.0820

141) Verhagen, J.H., Fouchier, R.A.M. and Lewis, N. (2021) 'Highly pathogenic avian influenza viruses at the wild–domestic bird interface in Europe: future directions for research and surveillance', *Viruses*, 13(2), 212. https://doi.org/10.3390/v13020212

142) Voinov, A. and Bousquet, F. (2010) 'Modelling with stakeholders', *Environmental Modelling & Software*, 25(11), pp. 1268–1281. https://doi.org/10.1016/j.envsoft.2010.03.007
143) Warton, D.I., Blanchet, F.G., O'Hara, R.B., *et al.* (2015) 'So many variables: joint modeling in community ecology', *Trends in Ecology & Evolution*, 30(12), pp. 766–779. https://doi.org/10.1016/j.tree.2015.09.007
144) Wesolowski, A., Eagle, N., Tatem, A.J., *et al.* (2012) 'Quantifying the impact of human mobility on malaria', *Science*, 338(6104), pp. 267–270. https://doi.org/10.1126/science.1223467
145) Whitmee, S., Haines, A., Beyer, C., *et al.* (2015) 'Safeguarding human health in the Anthropocene epoch: report of The Rockefeller Foundation–Lancet Commission on planetary health', *The Lancet*, 386(10007), pp. 1973–2028. https://doi.org/10.1016/S0140-6736(15)60901-1
146) Zinsstag, J., Schelling, E., Waltner-Toews, D., *et al.* (2011) 'From "one medicine" to "one health" and systemic approaches to health and well-being', *Preventive Veterinary Medicine*, 101(3–4), pp. 148–156. https://doi.org/10.1016/j.prevetmed.2010.07.003