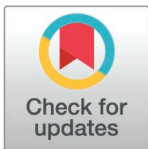


PERSPECTIVE

Why the growth of arboviral diseases necessitates a new generation of global risk maps and future projections

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Author summary

Global risk maps are an important tool for assessing the global threat of mosquito and tick-transmitted arboviral diseases. Public health officials increasingly rely on risk maps to understand the drivers of transmission, forecast spread, identify gaps in surveillance, estimate disease burden, and target and evaluate the impact of interventions. Here, we describe how current approaches to mapping arboviral diseases have become unnecessarily siloed, ignoring the strengths and weaknesses of different data types and methods. This places limits on data and model output comparability, uncertainty estimation and

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generalisation that limit the answers they can provide to some of the most pressing questions in arbovirus control. We argue for a new generation of risk mapping models that jointly infer risk from multiple data types. We outline how this can be achieved conceptually and show how this new framework creates opportunities to better integrate epidemiological understanding and uncertainty quantification. We advocate for more co-development of risk maps among modellers and end-users to better enable risk maps to inform public health decisions. Prospective validation of risk maps for specific applications can inform further targeted data collection and subsequent model refinement in an iterative manner. If the expanding use of arbovirus risk maps for control is to continue, methods must develop and adapt to changing questions, interventions and data availability.

Introduction

Global and regional risk maps of disease play an increasingly prominent role in health policy and decision making. For arboviruses, risk maps have become integral to estimating global distribution and burden [1,2], future projections [3,4], outbreak early warning systems [5,6], targeting of interventions [2,7], assessments of intervention cost effectiveness [8] and evaluation of the progress towards international goals. These needs have become increasingly acute as the global burden of dengue has ballooned to an estimated 57–390 million infections per year [1,2,9] with increasingly large outbreaks fuelled by urbanisation, travel and climate change [10]. Other *Aedes* mosquito-borne viruses (Zika, chikungunya and yellow fever), *Culex* mosquito-borne viruses (Japanese encephalitis, Rift Valley fever, West Nile fever) and tick-borne viruses (Tick-borne encephalitis, Crimean-Congo Haemorrhagic Fever) share many of the same environmental drivers and recent increases in incidence and range [11,12].

The World Health Organization Global Arbovirus Initiative (WHO GAI) [13] has identified risk mapping as a key evidence gap within the surveillance pillar, and a recent project, conducted by many of the same authors as this manuscript, has aimed to fill this gap. First, a systematic review [14] characterised the current state of the art for arbovirus risk mapping and gave key recommendations to improve current practice. Second, new global risk maps were generated for dengue, chikungunya, Zika and yellow fever that added 42,134 new contemporary data points and standardised methodology to improve comparability among arbovirus risk maps and address surveillance biases [15]. In this perspective manuscript, we aim to look further ahead and identify the key methodological leaps that need to be made to realise the range of new applications of risk maps for arbovirus control. While we focus primarily on global mapping of *Aedes*-borne arboviruses, the identified gaps and proposed solutions are also applicable to other viral diseases spread by arthropods.

Different types of data measure different types of risk

Models based on different types of data inform different types of risk which have different, but often overlapping, applications (Fig 1). The most common types of risk predicted in arbovirus risk maps are: risk of establishing local transmission if introduced, risk of ongoing transmission, risk of disease and risk of infection, each with their own area or population denominator and unit of time (Fig 1) [14]. To estimate risk in areas where arbovirus data are not available or are inadequate, risk mapping models integrate data on climate, built and natural environments, human mobility, interventions, and sociodemographics to identify correlates of arbovirus risk that are then used to make predictions and projections.

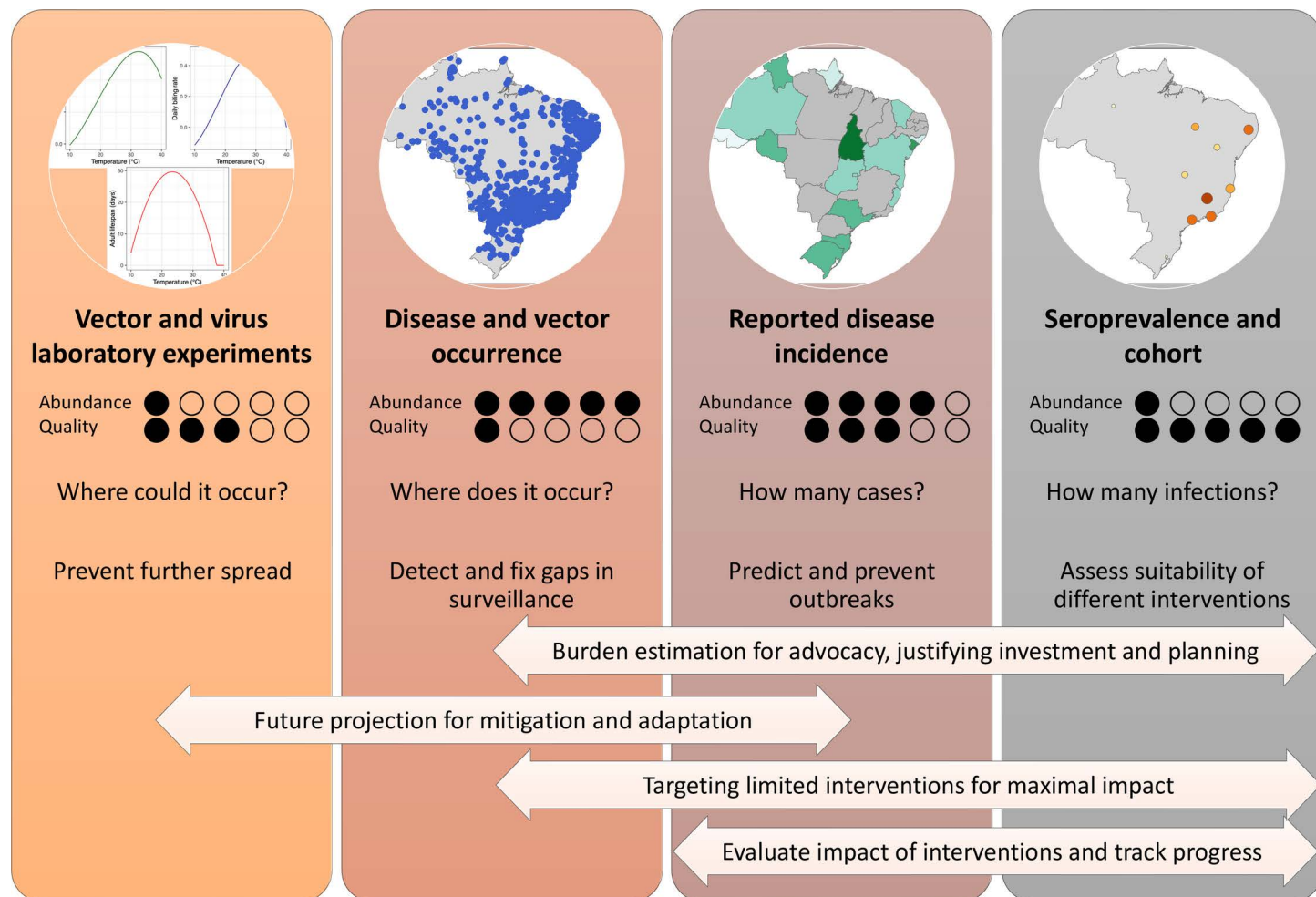


Fig 1. The main types of data currently used for arbovirus disease mapping. For each data type, the figure summarises relative abundance and quality of data (bias, representativeness and consistency among areas and over time) (as assessed by author consensus, both rated 1–5), the main questions each data type aims to answer and associated public health actions that can be undertaken with such knowledge. Use cases that can draw on multiple categories are labelled in bi-directional arrows at the bottom of the figure.

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Data from laboratory experiments on mosquitoes can be used to understand how climate variables, notably temperature, affect critical steps in arbovirus transmission [16]. Controlled laboratory conditions enable precise measurements of these effects, but experiments are performed on minority of mosquito lineages [17] and are unrepresentative of field conditions [4,18]. These physiological studies can inform which areas may be vulnerable to outbreaks [19], and predict how future climate change may influence the global limits of transmission [4,18,20].

Occurrence data [21] (presence/absence of disease in a precise location) are the most abundant form of data, and often are the only measure of risk available in data-sparse regions, making occurrence data an appropriate choice for mapping the current global distributions of arboviral diseases. Occurrence data, however, tells us little about the magnitude of risk of transmission and is affected by spatial differences in surveillance intensity. Occurrence data for vectors or reservoir species can also inform maps of disease invasion, emergence and transmission risk [22].

Case incidence data is available from many arbovirus-endemic countries and measures changing risk over time, but can be difficult to compare among countries due to differing case detection, diagnosis and reporting criteria [23]. Despite these limitations, maps based on reported incidence data give the best estimates of clinical burden [24,25] and treatment resource need, and provide the most time-sensitive and up-to-date estimates of risk, enabling the development of outbreak forecasting systems [5,6] and the evaluation of intervention impact [26]. Vector abundance data (mosquito counts over time) can also inform time-varying estimates of risk, especially in non-endemic settings with lower case counts.

Age-stratified seroprevalence data [27,28] and serological cohort studies [1], can be analysed to reconstruct a long-term history of past infection dynamics, but have coarse temporal resolution and are geographically sparse and rare in low-transmission areas. As the only types of data that measure arbovirus infections (as opposed to disease), they are the only type of data able to inform the full extent of disease burden and transmission intensity. Estimates of long-term average force of infection can also be obtained by analysing the age distribution of cases and/or severe cases provided appropriate validation with seroprevalence data [29,30].

Different approaches intentionally aim to predict different elements of transmission risk that, depending on the setting, may not correlate with one another. In many cases, choice of approach may depend on the availability of information or end-user needs. Indeed, answers to some of the biggest questions on global burden, future change and intervention impact can come from multiple separate approaches (Fig 1), at times with contrasting results that can be challenging to interpret.

Main limitations of current mapping approaches and why they matter

Because each type of data, in isolation, has sizeable gaps in space and/or time many mapping approaches aggregate data over longer time periods to give a snapshot estimate of long-term average risk. This limits a model's ability to map detailed changes in risk over time and means these approaches often cannot directly attribute such changes to variation in climate, urbanisation, travel, and intervention use, although some national and regional examples are beginning to emerge [31]. With the rapid development of new vaccines and vector control tools and a growing demand for climate change attribution studies, novel temporally dynamic maps with robust mechanistic links to causal drivers are increasingly needed.

Data comparability

Even when data are available over long time periods and broad geographic regions, they may not be comparable due to variable surveillance, diagnosis, and reporting practices, an issue that is particularly acute for arboviruses due to non-specific disease symptoms [32]. Without appropriate adjustment, this may result in risk maps representing surveillance sensitivity and specificity rather than, as intended, transmission risk. Key vulnerabilities include comparisons of incidence data among countries with different surveillance systems and seroprevalence data measured with different assays (especially in areas with Zika, or other related viruses, due to cross reactive antibodies). Global risk maps will only offer predictive advantages over local risk maps if issues with data comparability can be addressed in the modelling approach. Occurrence data models can be designed to account for the inherent spatial biases in occurrence data through different methods of background or pseudo-absence point generation, but too often random selection is used [14] (which assumes uniform surveillance) despite increasingly advanced methods that nest surveillance models in a hierarchical structure being available [29].

Prediction uncertainty

Current modelling approaches also often systematically underrepresent uncertainty, leading to overly precise risk estimates and overconfident comparisons of risk among areas. Existing frameworks are rarely capable of quantifying spatial uncertainty due to geographic gaps in data, leading to highly confident predictions in areas such as Africa despite sparse data coverage [33–35]. Choice of co-variables, their data sources, their methods of processing and extrapolation in addition to their validated accuracy are all potential areas of uncertainty that are rarely propagated. A better assessment of uncertainty informs data collection and iterative model improvement, but is also critical if such maps are to be used to make decisions on, for example, intervention targeting. Visualising uncertainty in an interpretable way on maps is challenging and current portrayals can lead to overconfident uses of the maps and, on occasion, misinterpretation of the raw data.

Generalisability

Machine learning methods have increased the complexity of the relationships we are able to fit between variables and disease risk and often appear to give superior predictive performance when evaluated via internal cross validation [14]. One consequence of this flexibility, however, is less opportunity to include prior biological, ecological and epidemiological understanding of the processes that shape the spatial distributions of these viruses. This can lead to poor generalisability with far inferior performance when evaluated against out of sample data. This is particularly acute in data sparse areas or in areas with environmental characteristics far outside the observed range, which happen to be where the largest changes in future risk are projected, for example, dengue in Africa [36]. Despite this, few models are evaluated with prospective data collection [37].

Priority areas for model development

The next generation of arbovirus risk mapping models must formally integrate different types of data to overcome the limitations discussed above and, thus, realise this new range of applications. As a collateral benefit, joint inference approaches also open opportunities for more integration of ecological and epidemiological understanding that aim to better represent the mechanisms that link risk factors to transmission. To achieve these the following priority areas will need to be addressed:

Leveraging strengths of different data types in a combined modelling framework

New models need to be formulated with a joint likelihood where transmission intensity is inferred at a high spatial and temporal resolution as a function of combined occurrence, incidence and seroprevalence data. Such an approach would take advantage of the more accurate long-term estimates of force of infection from seroprevalence data, but also characterise the high spatial and temporal heterogeneity measured through occurrence and incidence data, respectively. Currently, few areas exist globally where these three data sources overlap at scales and resolutions that would make this kind of joint estimation possible. Geospatial models will, therefore, be important for spatially projecting estimates of risk from each type of data across common areas. This geospatial model would need to be nested within the joint inference model through a hierarchical structure. Appropriately estimating and weighting uncertainty from the original data, the modifiable areal unit problem, extrapolation of the data and assessing the degree of consensus among different types of data will be key challenges, but examples from malaria risk mapping where case incidence and prevalence data are increasingly

combined show that they can be overcome [38,39]. This new modelling approach will likely not work everywhere, but discovering that data from a particular area are too sparse to characterise transmission is, in itself, an informative result.

A useful intermediate step would be a systematic comparison of risk maps derived from different approaches across different geographic and transmission strata. This analysis could assess consensus and better understand which types of risk are captured by different types of data in different settings [40]. These hypotheses can be tested in a data-driven manner through model “stacking” wherein predictions from one model are tested for inclusion as a relevant covariate in another model [41].

Longer-term, joint inference models could incorporate the growing volume of arbovirus genomic data to improve estimates of risk during emergence [42] or stratify risk by different viral lineages and the fields of phylodynamics and phylogenetics offer examples of joint models that could guide development of the models proposed here [43]. Joint inference models could also be used to combine data sets across arboviruses, leveraging their shared mosquito vectors and similar spatial and seasonal drivers, but different levels of immunity and distinct emergence histories [44]. Achieving this integration will require directly accounting for additional measurement error due to misdiagnosis and antibody cross reaction. This step would not only improve estimates for the major arboviral diseases by drawing on more data, but could also be leveraged to predict the potential spread of new emerging arboviruses with pandemic potential.

Incorporating biological, ecological and epidemiological understanding with the use of (semi) mechanistic risk functions and constraints

The next generation of arbovirus risk models should include more biologically meaningful constraints on the relationships between covariates and risk. The Ross-MacDonald equation for the reproduction number (R) of a vector borne disease can be used to explore such opportunities:

$$R = S \frac{ma^2bcp^n}{r(-\ln(p))}$$

Studying the effects of temperature mosquitoes in the laboratory has allowed parameterisation of functional relationships between temperature and daily mosquito survival rate (p), virus incubation period in the mosquito (n), human biting rate (a) and mosquito–host transmission rates (b, c) [45–47]. Humidity is also a key driver of mosquito survival (and possibly biting rate) and can be incorporated in a similar way [48]. With growing availability of species distribution models for medically important vector species, there may be new opportunities to estimate vector abundance (and thus mosquitoes per person m). Rather than using the direct estimates of occurrence probabilities that come from such models, some studies have suggested that measures of niche centrality (i.e., how closely an environments’ characteristics are to the “ideal” environment) calibrated to field estimates may more accurately estimate abundance [49].

The Ross-Macdonald equation also provides a framework for understanding how different vector species (or sub-species) jointly contribute to transmission. Incorporating covariates that summarise the different epidemiologically relevant bionomics of *Aedes aegypti* and *Aedes albopictus* may improve risk maps in emerging settings, such as Europe where only *Ae. albopictus* is present, and explain how risk changes when species-specific interventions, such as *wMel Wolbachia*, are used at scale. Genetic or phenotypic differences in key mosquito bionomics (particularly b , c , a and n), may explain broad regional differences in transmission

risk, such as comparatively low reported incidence of dengue and Zika in Africa compared with Asia and the Americas [50].

While most current mapping models focus exclusively on environmental drivers of transmission risk, human susceptibility S to infection and, to a lesser extent, duration of human infectiousness r play an increasingly important role. Dengue virus serotype, genotype and infection sequence all affect disease severity while current vaccines are inconsistently implemented and show variable effectiveness by serotype [51,52]. Incorporating this dynamic landscape of susceptibility must become a priority if models are to inform vaccination strategy and burden estimation. Some advances in this area have been made in yellow fever where demographic models and vaccination data have been integral to mapping risk [53,54]. Combining such dynamic models with a joint inference framework (Fig 2) can better inform the relationship between types of risk, disease incidence and seroprevalence. The next generation for arbovirus burden estimation and future projection models should include the mitigating effects of accumulating immunity, including how shifting future birth, death and migration rates affect population-wide immunity and susceptibility to severe disease outcomes.

Improving methods to measure, propagate and visualise uncertainty and validation of map predictions

Appropriate measures of uncertainty are essential for maps to inform public health decisions and, increasingly, target further data collection. The highest priority is to more accurately convey uncertainty related to geographic gaps in epidemiological data, particularly in Africa. This most commonly occurs because models rarely account for spatial autocorrelation in the data in their model formulation, instead relying on environmental variables alone. Accounting for spatial autocorrelation in the data, using random effects structured by proximity or mobility, provides a more robust and statistically valid test for models and are already commonplace in analyses of incidence data [55,56]. Sharing the full distribution of uncertainty in risk maps for every geographic area can empower local modellers by providing priors for variables that are not collected or difficult to estimate. Disaggregating uncertainty into its constituent parts (data, covariates, model structure, projection) will also help prioritise model refinement efforts.

When arbovirus transmission risk can be robustly theoretically and empirically linked to climatic, environmental, and socioeconomic drivers, it is important that uncertainty in estimation and extrapolation of these, often model-estimated, drivers is propagated. This is particularly acute with future projection studies where multiple climate models project multiple scenarios. More coordinated efforts are required to align projections of climate with those of demographics, urbanisation and migration [35]. For now, generating separate arbovirus risk projections for each scenario and climate model combination is a comprehensive, if computationally expensive, solution. Sharing data, predictions, and code via online repositories and platforms (e.g. Figshare, [30], Github, <https://github.com>) enables downstream analyses to better propagate scenario uncertainty (e.g. <https://dataverse.harvard.edu/dataverse/Aedesmaps>).

Even the formulation of the risk mapping model itself introduces a range of uncertain assumptions. Choice of covariates (or covariate selection procedures) and the degree of flexibility in the relationship between covariates and disease risk introduce assumptions that could be better routinely clarified using conceptual frameworks, guided by the literature and/or directed acyclic graphs. Ensembles of multiple plausible mapping model structures would bring the field in line with developments in temporal forecasting [5,57].

Communicating prediction uncertainty through maps remains an open challenge in the field of spatial epidemiology. While some innovative visualisation approaches have been proposed including pixelating more uncertain areas [58] and use of two dimensional bi-variate

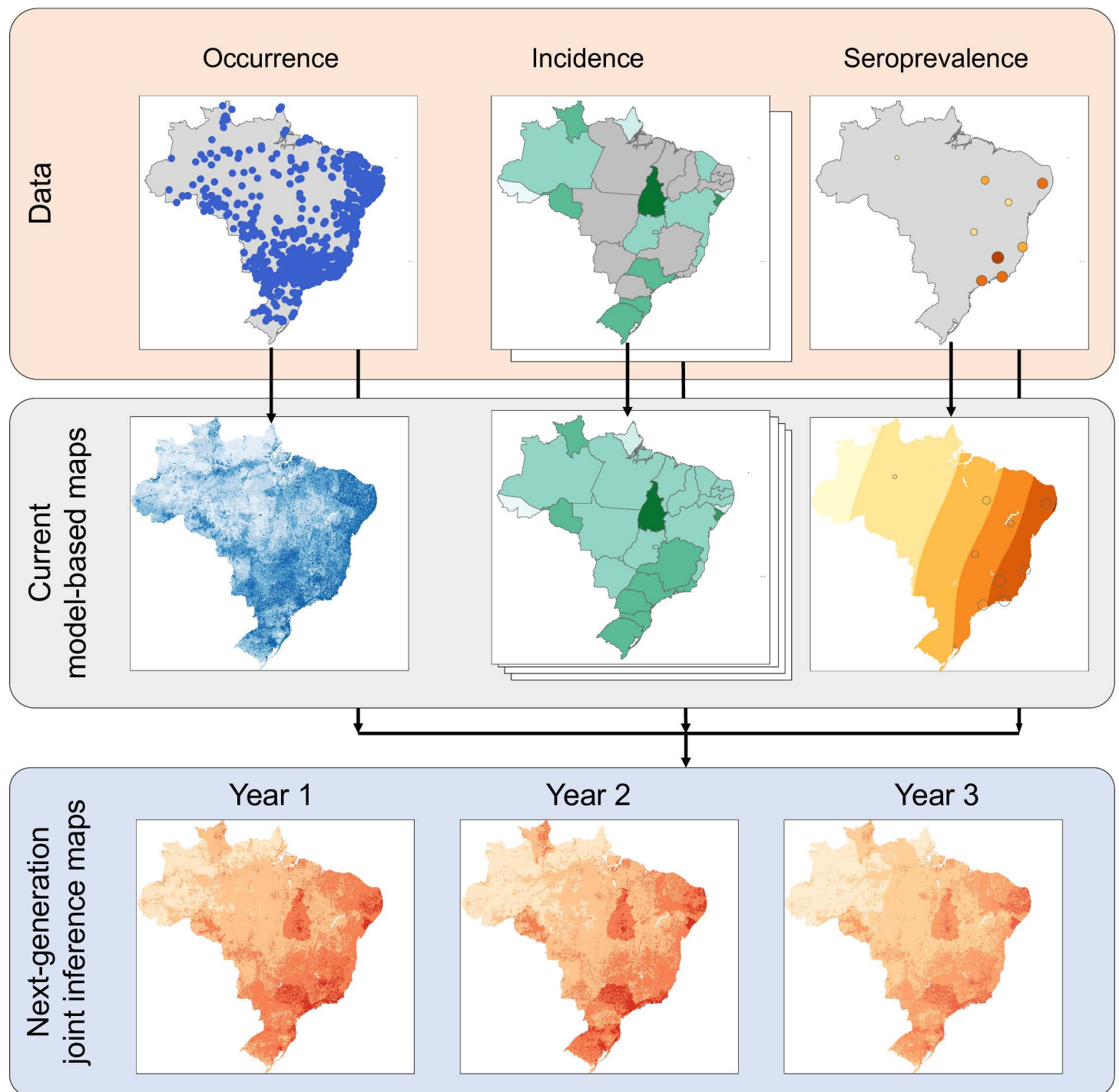


Fig 2. Conceptual overview of a joint inference mapping approach showing example occurrence, incidence and seroprevalence data for Brazil (top row), the kinds of risk maps that can be generated from each of these data sets independently using current generation methods (middle row) and the time-varying more accurate maps that could be generated from a joint-inference modelling approach (bottom row, uses a simple equal weight ensemble for illustration purposes only).

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choropleth maps [59], the best solution will depend on the specific use case of the map. Summarising probabilistic model predictions around a policy-relevant threshold (e.g. 80% certain that prevalence is above 70%) has proven an effective approach for informing mass drug administration decisions for other neglected tropical diseases [60].

Finally, validation of risk maps needs to become an iterative, multidisciplinary exercise that involves out-of-sample validation including prospective data collection. Out-of-sample validation can be accomplished by collecting or accessing new data, and gives a more accurate measure of model utility for areas without data, i.e. the areas where risk estimates are most valuable. Validation is not solely an exercise to prove the map right or wrong, but an opportunity to discuss with stakeholders across multiple levels of government the strength of evidence for arbovirus risk in different areas, strengthen surveillance and to identify key data or model gaps that could improve estimates. Interactive dashboards can facilitate this. Currently, arbovirus risk maps are validated through comparison with different measures of risk (Fig 1) [61,62] or periodically as more of the same types of data are published [63,64]. We are not aware of any published examples where a clear study design has been used for the purpose of prospective data collection to validate a disease risk map, but examples from species distribution mapping in ecology provide a framework that could be adapted for disease risk maps [65]. Further research is needed into disease-specific approaches to risk map validation. An arbovirus risk mapping project planned today should consider how structured involvement of local experts with a diverse range of expertise and potential map use cases could be used to evaluate the reliability and usefulness of risk maps.

Key data needs

The full benefits of these new models will only be realised if they are accompanied by investments in data collection, standardisation, and accessibility. High-resolution global maps should not give the illusion that further data collection is not valuable. Models can generate maps that target data collection in specific sites to fill geographic and/or environmental gaps [39]. Investment in databases to collate, standardise and make accessible arbovirus data are also important with initiatives including OpenDengue [23] (<https://opendengue.org>), ArboTracker [66] (<https://new.serotracker.com/pathogen/arbovirus/dashboard>) and the WHO Global dengue surveillance dashboard (https://worldhealthorg.shinyapps.io/dengue_global/) making progress. Similar resources for roll out of new vaccines and *Wolbachia* replacement technologies will need to be developed and lessons can be learned from yellow fever, where databases of vaccine coverage have been pivotal for understanding the distribution of the disease [67,68]. New covariates for human mobility, water and waste management infrastructure and other dimensions of the built environment at the global scale would improve estimates of risk [10]. Increasing the temporal resolution of covariates for current and historical periods is also urgently needed.

Conclusions

As arboviral diseases have emerged and re-emerged as global public health threats, a growing range of approaches to map arbovirus risk have proliferated. While these maps have been useful, we are approaching the limits of what can be achieved with current methods. Here, we call for the development of a new generation of modelling frameworks that integrate the strengths of different types of data, incorporate more epidemiological understanding and appropriately quantify uncertainty. These new joint inference mapping models could enable a significant advance in how risk maps are used by arbovirus control programmes at a time when they need to make difficult decisions about investment in novel vector control tools and vaccines.

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