The current landscape of software tools for the climate-sensitive infectious disease modelling community

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Climate-sensitive infectious disease modelling is crucial for public health planning and is underpinned by a complex network of software tools. We identified only 37 tools that incorporated both climate inputs and epidemiological information to produce an output of disease risk in one package, were transparently described and validated, were named (for future searching and versioning), and were accessible (ie, the code was published during the past 10 years or was available on a repository, web platform, or other user interface). We noted disproportionate representation of developers based at North American and European institutions. Most tools (n=30 [81%]) focused on vector-borne diseases, and more than half (n=16 [53%]) of these tools focused on malaria. Few tools (n=4 [11%]) focused on food-borne, respiratory, or water-borne diseases. The under-representation of tools for estimating outbreaks of directly transmitted diseases represents a major knowledge gap. Just over half (n=20 [54%]) of the tools assessed were described as operationalised, with many freely available online.

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Introduction

Climate-sensitive infectious diseases (CSIDs) pose an increasing threat to public health under the combined trajectories of an increasing human population and climate change.[1–3] As urban areas expand and become increasingly dense,[4] spreading into rural and wild interfaces, the frequency of potential interactions between people, animals, disease vectors, and pathogens that drive environmentally linked diseases also increases. As climate change alters the environmental risk space along warming temperature and changing hydrological axes, we are faced with the challenge of anticipating when and where diseases will emerge, and outbreaks will occur.

Infectious disease transmission and prevalence are affected by changes in the climate at both local and global scales, calling for the use of environmental predictors when estimating disease risk.[1] Increasing global temperatures can lead to alterations in human behaviour that result in the increased transmission of pathogens and more frequent infectious disease outbreaks.[5] Climatic conditions also directly influence environmental suitability for pathogen transmission and disease vectors, affecting the spatiotemporal distribution of infectious diseases, such as malaria and its mosquito vectors.[2,6]

CSID forecasting systems that enable us to predict the effects of environmental conditions on disease responses are in great demand for public health planning and early warning systems.[1,7] These systems often rely on statistical tools and forecasting models for the estimation of infectious disease outbreaks, which, depending on the relevant goals, could refer to a range of disease activity, such as the timing, severity, or location of outbreaks. Statistical tools can support public health decision-making processes, providing valuable lead time for anticipatory action. Climate-informed tools that account for underlying environmental conditions might be more frequently used for the study of vector-borne disease systems, because there are often clear relationships between arthropod vector biology and climatic drivers, such as temperature and rainfall.[2] Yet many infectious diseases are modulated by climate conditions across spatiotemporal scales, including diseases with direct transmission pathways (eg, influenza spread via respiratory transmission), water-borne diseases (eg, cholera and giardiasis), and food-borne diseases (eg, salmonellosis).[8–10] There are a number of computational and statistical frameworks that have been applied to CSID problems. Specifically, model-based approaches offer the opportunity to identify the direction and magnitude of CSID relationships and to quantify these relationships under natural conditions (ie, not relying on experimental approaches that are unfeasible or unethical). To aid this research and promote the implementation of tools for the public health sector and other end users, software tools and packages are being created in a variety of coding languages (R, Python, Julia, etc) from a range of perspectives and specialisations,

Key messages

- We found only 37 fully developed software tools for modelling climate-sensitive infectious diseases; the majority of tools were created for vector-borne diseases
- There is a shortage of tools for respiratory, food-borne, and water-borne diseases, and there are no tools for soil-borne diseases
- More than half of the tools were described as operationalised, and many were freely available online; however, few had visually intuitive interfaces
- Most tools were developed for geographical regions where the infectious disease of interest is currently endemic; tools are needed for hotspots of disease emergence, where the risk of pathogen transmission is increasing or will increase substantially in the future
- North American and European institutions are disproportionately represented as tool creators; there is a need for greater engagement with the Global South, where many of the tools were designed to be used, both in terms of end-user involvement and representation of investigators in the co-creation of tools
- There is a gap in translating existing models and code into automated, packaged tools; providing space and resources to allow researchers, who are developing climate-sensitive infectious disease models, to work closely with software engineers will facilitate the rapid creation of new tools to serve the wider community

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Panel 1: **The ideal tool for modelling climate-sensitive infectious diseases**

An ideal tool will:

- incorporate both climate inputs and epidemiological information to produce an output as a prediction or indicator of disease risk in one package;
- be transparently described and validated;
- be named (for future searching and versioning); and,
- be accessible, where code is published, or available on a code repository, a web platform, or other user interface

Panel 2: **Information fields used to extract data from screened publications**

Publication details

- Study identifier (PubMed or DOI)
- Authors
- Institutions
- Publication date
- Foundational paper

Study information

- Country
- WHO region
- Infectious disease or vector
- Mode of transmission

Tool specifics

- Tool name
- Name acronym
- Derived model
- Name of original model
- Type of model
- Software
- Scale of study
- Input data
- Climate products
- Climate variables
- Model output

Operationalisation

- Operationalised
- Availability
- Link to tool
- Partners

reflecting the numerous disciplines that contribute to this field. These perspectives include those of professionals, such as medical and health geographers, disease ecologists, applied climate scientists, data scientists, epidemiologists, and public health or infectious disease specialist physicians.

Although climate-informed modelling systems can be useful in public health planning, there can be considerable barriers to their adoption and sustained implementation, such as gaps in local technological expertise, mismatch between model outputs and decision-making needs, and financial constraints.[7] The availability of user-friendly and accessible software tools could help to bridge important gaps in statistical knowledge and technological proficiencies. These tools make models for disease predictions that are otherwise difficult to implement more available to public health practitioners and other stakeholders, facilitating climate-informed decisions. Given the broad range of infectious diseases that are climate dependent, this Personal View aimed to identify the availability of, and need for, software tools among the CSID modelling community and model end users. We sought to identify existing, implementation-ready software tools at the intersection of climate and infectious diseases via a systematic review of the literature; to identify exemplars to describe activities within the field; and to quantitatively describe gaps in currently available modelling tools.

Approach

We conducted automated searches of the literature[11,12] for studies on CSIDs, as described in the search strategy and selection criteria. Based on our subject-matter expertise, we developed criteria to define an ideal tool for modelling CSIDs (panel 1). These criteria were used to manually screen the relevant literature returned in our searches, and to identify ideal tools for modelling CSIDs. Examples of tools meeting these criteria included named models of infectious disease systems, bespoke software programs, software packages, web applications, and code repositories. Data extraction was conducted for papers with tools meeting these criteria, and the database information fields used for extraction are presented in panel 2.

Findings

Our literature search yielded more than 30 000 unique papers (figure 1). This list was reduced by manually analysing the relevancy of search keywords and MeSH terms, resulting in 9500 publications. A relevancy score was derived by counting the number of duplicate mentions of papers appearing in the results of unique searches. Approximately 2000 of the top relevant papers were checked against a sample of papers marked as relevant and retained for manual review. Those papers that contained technical tool terms were also included. Technical tool terms consisted of keywords that might have a higher chance of finding papers that contained code or tools, such as GitHub or R packages. 2380 relevant papers from the literature search were partitioned into seven sets for screening by two independent manual reviewers to identify papers that potentially featured tools within the scope of the review. The papers with tools identified in the initial screening (n=242) were used for data extraction, during which we reviewed full publications for tools meeting the criteria, including named tools with operationalised interfaces (ie, tools that were accessible, reproducible, or validated) and a climate component.

Of these papers, 62 were identified as having potentially operationalised modelling tools. Following screening and data extraction, 48 of the papers featured a named infectious disease modelling tool that incorporated climatological or meteorological data. After accounting for studies that used the same models, we found 37 unique tools (table). Additional characteristics of these tools are provided in the appendix (p 3).

Most tools identified (n=30 [81%]) focused exclusively on vector-borne disease systems (figure 2). Of the tools dedicated to modelling vector-borne diseases (n=30), 53% (n=16) specifically focused on malaria, 13% (n=4) on dengue virus, 13% (n=4) on West Nile virus, and 7% (n=2) on Rift Valley fever. We identified five tools for vector-borne disease systems (14%) that focused on vectors more generally, rather than focusing on a discrete pathogen (eg, the AeDES model for habitat suitability of *Aedes*-borne pathogen transmission, in which *Aedes* spp mosquitoes are competent vectors for a variety of pathogens).[13] Approximately 11% (n=4) of modelling tools were applied to infectious diseases with other modes of transmission, including respiratory (n=2 [5%]), food-borne (n=1 [3%]), and water-borne (n=1 [3%]) transmission. Four (11%) of the tools identified were flexible in terms of their health focus, and surveillance data from a wide variety of user-specified infectious disease systems could be used as data inputs (eg, mapping platforms such as eRiskMapper,[26] and user-driven analytical tools, such as the EPIPOI platform).[25] One tool in this category, STEM,[44] was unique, in that although it is a flexible tool for spatiotemporal disease modelling, it was also specifically named for use with influenza and malaria in the studies we reviewed.

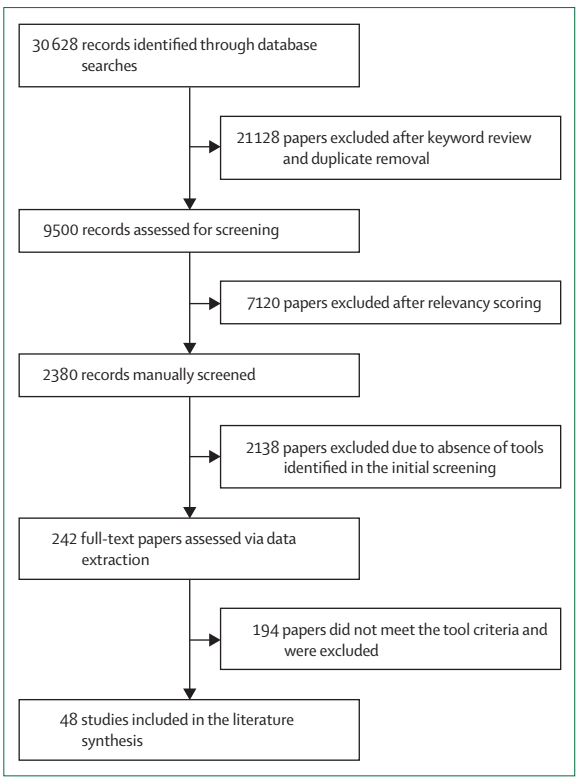

Figure 1: **Flow diagram of study selection**

Location, data scales, and data inputs

The tools found in this Personal View have been developed for use in several WHO regions, spanning Africa (44%), the Americas (15%), Europe (10%), the Western Pacific (10%), South-East Asia (6%), and the Eastern Mediterranean (2%; figure 3). Four tools (8%) did not focus on a single geographical region and could be applied globally.

The spatial scale of the 37 tools varied considerably, ranging from highly localised foci (8%), for example simulations for individual villages, to tools with a global or continental extent (16%). The majority of tools (76%) produced output at some intermediary scale (health district, country, region, etc). Scale was either dictated by the tool itself (eg, simulation models designed to replicate pathogen transmission within a single town or community), or, in many cases, the model output was dependent on user specifications, as determined by the spatial resolution of data inputs (eg, epidemiological data reported by administrative units, or the spatial resolution of gridded climate products). Many studies (29%) that used epidemiological data from health departments or surveillance networks as data inputs for models also reported their findings with the same administrative units (eg, provinces, counties, or local health reporting districts).

The climate products used as data inputs for risk predictions varied considerably, both with model type and study area. The majority (58%) of the 37 tools leveraged gridded climate products to inform models for infectious diseases or disease vectors. These climate products included remotely sensed data products (eg, NASA satellite imagery), interpolated weather station data (eg, from WorldClim, or the Global Historical Climatology Network), and modelled climate projections (eg, the Intergovernmental Panel on Climate Change global climate projections). One-third (33%) of the tools used local meteorological datasets, either from national meteorological centres or local weather stations. Temperature (85% of studies) and precipitation (68% of studies) were the most frequently used climate indicators, either as model predictors or descriptive variables. Measures of humidity were used in approximately a quarter (26%) of the studies.

Institutions and partners

102 institutions were represented in the author list of the 48 publications that included the 37 final tools in this Personal View (figure 4). More than one-third (38%) of these institutions were based in the USA or the UK.

See **Online** for appendix

For more information on **WorldClim data** see https://www.worldclim.org/

Only 24 institutions were associated with more than one paper, including universities and agencies located in Europe (n=11), the Americas (n=8), the Western Pacific (n=3), and southeast Asia (n=1). Designated corresponding authors for the 37 tools were based in the USA (32%), the UK (27%), other European countries (30%), Australia (5%), southeast Asian countries (5%), and Tanzania (3%). Nearly one-quarter (23%) of papers listed institutional partners. Partners identified by the study authors ranged from international organisations (eg, WHO, and the Pan American Health Organization), to national agencies (eg, the Centers for Disease Control and Prevention and the European Centre for Disease Prevention and Control), and regional partners, such as local health departments or academic institutions.

	Acronym	Disease system
Aedes-borne Diseases' Environmental Suitability[13]	AeDES	*Aedes* borne
albopictus (Python package)[14]	NA	*Aedes* borne
Anopheles Spatially Explicit[15]	ANOSPEX	Malaria
ArboMAP[16]		West Nile virus
Bayesian Outbreak Detection Algorithm[17]	BODA	Campylobacteriosis
Container-Inhabiting Mosquito Simulation Model and Dengue Simulation Model[18]	CIMSiM and DENSiM	Dengue virus
Disease Monitoring Dashboard[19]	DMD	West Nile virus
Dynamic Mosquito Simulation Model[20]	DyMSiM	Dengue virus and West Nile virus
European Centre for Disease Prevention and Control Vibrio Map Viewer[21]	ECDC Vibrio Map Viewer	*Vibrio* spp
Epidemic Prognosis Incorporating Disease and Environmental Monitoring for Integrated Assessment[22]	EPIDEMIA	Malaria
epidemiar (R package)[23]	NA	Malaria
EpiGraph[24]	NA	Influenza virus
Epidemiological Parameter Investigation from Population Observations Interface[25]	EPIPOI	Multiple
eRiskMapper[26]	NA	Multiple
Early Warning and Response System[27]	EWARS	Dengue virus
FleaTickRisk[28]	NA	Tick borne
Hydrology, Entomology, and Malaria Transmission Simulator[29]	HYDREMATS	Malaria
LIS-MAL[30]	NA	Malaria
Liverpool Malaria Model[31]	LMM	Malaria
Liverpool Malaria Model 2010[32]	LMM2010	Malaria
Liverpool RVF Model[33]	LRVF	Rift Valley fever
Mapping Malaria Risk in Africa[34]	MARA	Malaria
Mapping Malaria Risk in Africa Low-end Information Tool[35]	MARA LITe	Malaria
Mosquito Gene Drive Explorer 2[36]	MGDrivE 2	Mosquito borne
Modelling Framework for the Health Impact Assessment of Man-induced Atmospheric Changes[34]	MIASMA	Malaria
Mosquito-borne Viral Suitability Estimator[37]	MVSE	Mosquito borne
OpenMalaria[38]	NA	Malaria
Open Malaria Warning[39]	OMaWa	Malaria
Rapid Inquiry Facility[40]	RIF	Multiple
RVF plug-in[41]	NA	Rift Valley fever
Seasonal Climate Outlooks in Pacific Island Countries[42]	SCOPIC	Malaria
Stochastic Lattice-based Malaria model[43]	SLIM	Malaria
Spatiotemporal Epidemiological Modeler[44]	STEM	Influenza virus, malaria, and multiple other systems
Umea statistical model[34]	UMEA	Malaria
Vector-borne disease community model of the International Centre for Theoretical Physics, Trieste[45]	VECTRI	Malaria
WNV_model[46]	NA	West Nile virus
yews4denv[47]	NA	Dengue virus

NA=not applicable.

Table: **Unique tools with a climate component used for the analysis of infectious diseases**

Methodological approaches and technology

Most of the 37 tools (60%) used either mechanistic or dynamical population modelling approaches, although diverse modelling approaches were used. Other analytical methods included time-series modelling, regression methods, Bayesian modelling, decision rules, and multimodel ensembles. 40% of the studies in our final list were foundational papers, indicating the first use or description of a given tool in the literature. Many of the tools in our list (41%) were explicitly derived from existing tools, including updates to previously published models, and new models that incorporated components of existing models. Some tools provided flexible platforms for analysing or visualising infectious disease systems, as opposed to discrete models. These tools included dedicated software packages (n=9), web-based applications (n=3), and a code repository (n=1). The R programming language was used to develop or implement 30% of tools. Other programming languages or software included Python (n=4), C++ (n=3), MatLab (n=3), and FORTRAN90 (n=1).

Tools and approaches not considered

We did not consider species distribution model (SDM) frameworks as tools in this Personal View, because, with few exceptions, these frameworks are methodological approaches rather than standalone software tools. In addition, SDMs do not inherently have climate data driving their algorithms. Environmental data are supplied by the user as static inputs, and these data can include gridded climate summaries (mean temperature, mean rainfall, etc), but this input is not coded into the software. Nevertheless, papers that used SDM to model disease or vector distributions as a function of climate variables were quite prevalent in our results (18% of our initial screening list of 242 papers used these methods). MaxEnt models, often implemented in the software of the same name[48] or the R package dismo,[49] were by far the most frequently used SDM method in our results, and were used in 65% of the papers that used SDM. The prevalence of MaxEnt is probably due to the availability of an open-source software package, in addition to options for its implementation in R. Other SDM methods used in the initial screening

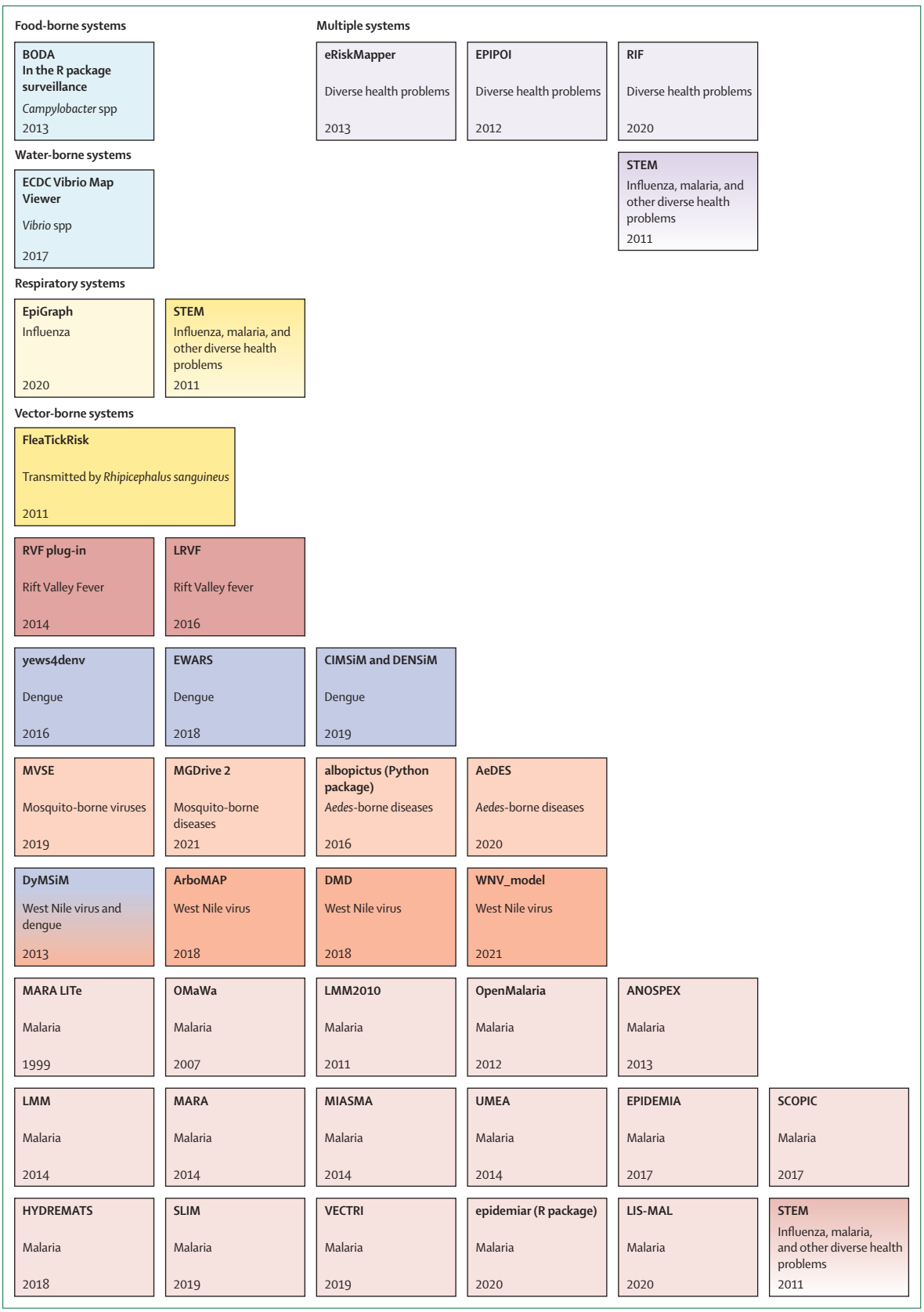

Figure 2: **The 37 climate-health tools identified**
The tools are displayed according to their disease systems and are listed chronologically within each category. Colours are indicative of the disease systems. For the vector-borne systems, yellow denotes flea-borne and tick-borne disease models, whereas the multiple shades of red differentiate between the mosquito-borne disease models. STEM (shown with a colour gradient) is a flexible tool in terms of disease systems and is therefore listed across three categories.

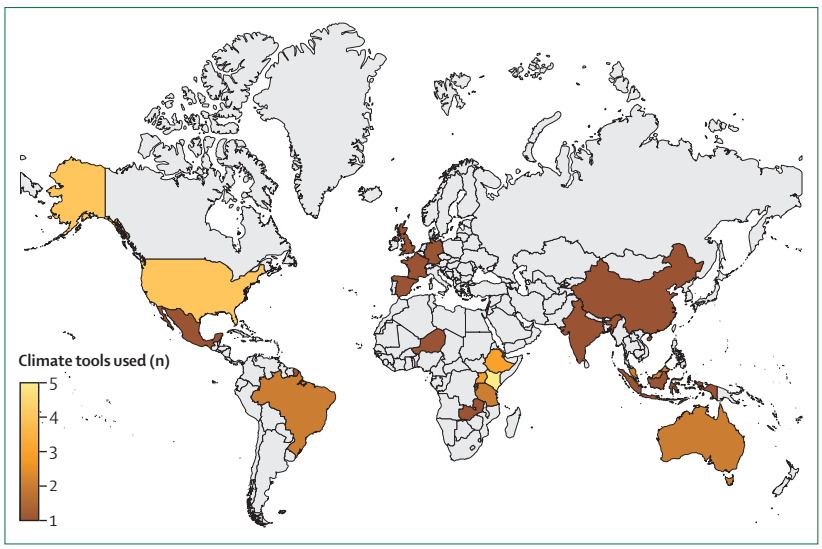

Figure 3: **Countries where climate tools have been used**

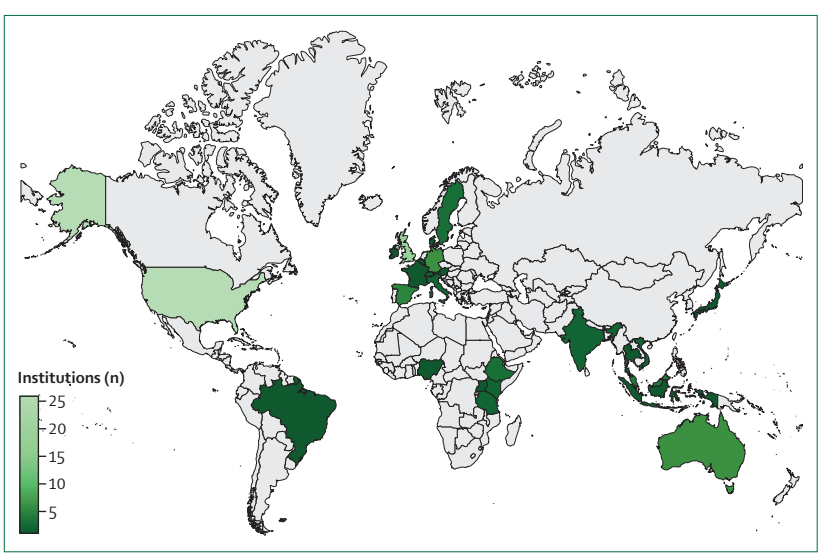

Figure 4: **Global distribution of the institutions that produced climate-health tools**

For more information on the **CRAN repository** see https://cran.r-project.org/

results included BIOMOD, boosted regression trees, classification and regression trees, GARP, and random forests.

Although much of the screened literature did not include tools developed for end users, several methods were commonly used throughout the relevant papers (ie, papers with a CSID focus that were not included in our final list of 37 tools) to assess the relationship between climatic factors and infectious disease outcomes. Regression methods were used in many studies, with terms commonly used to describe statistical analyses including logistic regression (n=78), linear regression (n=29), generalised linear model (n=27), hierarchical model (n=11), multiple linear regression (n=8), and stepwise regression (n=6). Methods used to estimate pathogen distributions and machine-learning algorithms were also frequently encountered in the search results, with studies using terms including MaxEnt (n=77), ecological niche model (n=77), species distribution model (n=41), boosted regression trees (n=15), habitat suitability model (n=9), GARP (n=5), random forests (n=5), BIOMOD (n=1), classification and regression trees (n=1), and exploratory niche factor analysis (n=1). These keywords captured some of the most implemented methods used in the relevant literature.

Operationalisation and availability

More than half (54%) of the papers in our reviewed list indicated that the featured tools were operationalised, either by presenting a tool as an accessible product (eg, a software package available for download, such as the surveillance package for R, which can be freely downloaded on the CRAN repository), or by using a tool in an implementation setting (ie, by generating results that were used to inform partners, rather than validation exercises). We note that in this context, operationalisation does not necessarily mean that available tools are actively used by the public health sector to inform decision making, as this determination was beyond the scope of this Personal View. 22 of the tools we identified (59%) were freely available in some form online, with 16% available as R packages on the CRAN repository, 16% with available source code on GitHub, and 5% available on GitLab. Additionally, 32% of tools were associated with dedicated websites (eg, a website for the tool, or page on a laboratory website for the project), which sometimes included instructions for their use and links for program downloads.

Discussion

Only 37 CSID modelling tools were identified in our Personal View, indicating that tools that met our ideal criteria (panel 1) were the exception, not the rule. The final list of tools was short, suggesting that few climate-health models move into tool development with an emphasis on end-user accessibility. Most of the tools and operationalised models identified in this Personal View focus on malaria (eg, EPIDEMIA[22] and the associated R package epidemiar).[23] This particular focus is perhaps to be expected, as vector-borne disease systems have been studied extensively in the context of climate, and malaria has been a global public health priority for decades. Nevertheless, the short supply of dedicated tools for estimating outbreaks with other modes of transmission, and other vector-borne disease transmission systems, is a major knowledge gap that could have implications for climate-informed planning and health responses. Expanding the foci of modelling tools, in terms of the diversity of both the pathogens and the health issues examined, could aid in developing resilient policies for neglected diseases, emerging infectious diseases, or a suite of climate-sensitive diseases projected to emerge in the future.

The trade-off between addressing local needs and creating generalisable tools

Most of the tools were developed for, or implemented in, geographical areas where the modelled infectious disease was endemic, principally in the Global South. Tools that are highly localised will have little, if any, transferability across geographical regions. This lack of transferability highlights a need for tools with a broader spatial focus, particularly for diseases, or disease vectors, that are expected to undergo range shifts under climate change. Although localised tools (ie, tools developed on a fine spatial scale) might limit operationalisation to specific regions, these models can have the benefit of being well validated locally, which could lead to more accurate predictions for local health authorities. Conversely, tools with very coarse resolutions (eg, global or continental model outputs) might be of little use for local stakeholders.

Global North authorship

Although local partners were likely to be included in the authorship of publications in many instances, North American and European institutions were disproportionately represented in the production of CSID tools. We recognise that categorising people and geographical regions can be a difficult issue, yet we believe it is important for highlighting crucial research gaps.[50] In this Personal View, we are choosing to use the terms Global North and Global South to describe these differences in representation. Our findings indicate a gap between the institutions involved in developing tools in the Global North and the geographical locations commonly prioritised for the study of infectious diseases in the Global South. Most papers reviewed did not explicitly name any agency or institutional partners, yet we noted that author affiliations on individual publications were quite diverse, possibly indicating the inclusion of partner organisations in the publication process. The absence of formally recognised institutional partnerships might contribute to a low rate of tool operationalisation or implementation, as the perspectives and priorities of local, southern partners that might favour the development of useful and useable tools might be subsumed by the need for academic publications in the Global North.

Incentivising non-academic contributions

Assessing the usability and actual use of tools was beyond the scope of this Personal View, but tools that were hosted on external websites (eg, GitHub), with links included in their publication, or that were available as open access software packages (eg, R packages such as surveillance[17] and epidemiar)[23] appeared to be more readily accessible. The accessibility of tools was not always apparent in the literature, because published papers often had no clear instructions on how to access the tools or information on where the tools were hosted, with some papers instructing the reader to contact the study authors for more information (eg, some applications of the VECTRI model).[51]

Limitations of the method and implications

We note that studies that did not use common keywords to describe analyses would not necessarily have been captured in the keyword analysis, emphasising the need for standardised terminology in climate-health research. This need becomes particularly evident when working across specialisations, which might have different conventions for describing methods. Very broad terms (eg, regression analysis) could be used to describe a vast array of methods. Conversely, some methods that are fundamentally similar might be described by several terms (eg, ecological niche modelling and SDM, mathematical modelling and dynamical modelling, and simulation and stochastic modelling), making categorisation of statistical methods across studies difficult at times.

Although the criteria established for this Personal View captured tools within the relevant subject area that were packaged with accessibility in mind, determining the quality of CSID modelling tools was beyond the scope of this work. Meeting our criteria does not ensure that models will perform well in practice, and the number of high-quality tools is probably fewer than 37. Large-scale spatiotemporal models that realistically incorporate both climate and epidemiological processes are difficult to parameterise, calibrate, and validate.

Although many papers found in the keyword search did not describe developed software tools, studies with well defined statistical frameworks could potentially be leveraged for the development of new tools in the future. Although we cannot comment on how easily climatic variables can be incorporated into existing models that are not currently designed to use environmental predictors, existing climate models for infectious diseases could serve as the basis for new software applications in the future. This potential underscores the need for researchers to investigate current decision-making frameworks and data infrastructures to create useful modelling tools and make them accessible to actors in the policy sector.

To illustrate this point, we have identified some examples from the literature of publications that did not meet our final criteria for named tools, yet have great potential for future tool development. Ryan and colleagues[52] used temperature-dependent models of transmission to produce projections of dengue transmission risk under different scenarios of future climate change, providing a means to model and visualise climate-mediated range shifts in pathogen transmission and risk, and to describe regional population impacts. This work has value for the development of climate-informed disease planning and response. However, although the model output is freely accessible, code and software to implement the model are not currently available.

Search strategy and selection criteria

We used an automated approach to search the literature for studies that focused on climate-sensitive infectious diseases, particularly studies with a forecasting or predictive modelling component that could be considered a usable tool in the public health sector. Using a customised Application Programming Interface, we searched PubMed on July 7, 2021, for papers published in English over the past 10 years (ie, from Jan 1, 2011, to June 30, 2021) with team-generated keyword and MeSH search term triplets combining climate, infectious disease, and technological keywords, such as statistical and modelling terms (appendix p 1; code available on GitHub).

In another example, a climate-informed dengue forecasting system was developed for Viet Nam as part of the Dengue Forecasting Model Satellite-based System project.[53] In this example, the forecasting model was explicitly developed to be used as part of an early warning system, with R code to run the model openly available on GitHub. In this case, the existing work could be developed into a discrete, named tool with little additional effort, or further developed into a standalone software package or modelling platform. Another example is a model that was developed to understand the delayed and non-linear impacts of hydrometeorological extremes on the space–time distribution of dengue outbreaks.[54] The model was adapted from a previous model developed for Barbados[55] and the model code was shared on GitHub. Although the method is being reproduced by researchers and UN agencies for Colombia, Brazil, and Peru, the model itself was not named or packaged due to human resource and technological capacity constraints.

For **available Python scripts** see https://github.com/hetco/landscape_mapping_climate_infectious_diseases

For an **expanded description of the 37 climate-health tools** see https://hetco.io/tools-for-climate-sensitive-diseases/

Conclusion

In summary, few CSID modelling endeavours met our criteria for an ideal tool. The gaps identified in our synthesis highlight important opportunities for future tool development, echoing other calls for increased science implementation efforts and intersectional stakeholder involvement in climate services for public health.[7,56] Moving forward, new projects that focus on a greater breadth of infectious diseases (ie, pathogens beyond dengue and malaria) should be prioritised and led or co-led by partners in the Global South, where climate-disease impacts are the greatest. Maintaining online repositories for tools and providing platforms to link dynamic data inputs will increase the usability of existing models. Investments in creating accessible documentation, tutorials, and training development opportunities for end users, particularly in the Global South, will help to promote the adoption of tool use by local researchers and decision makers. Additionally, there are useful models and codes associated with publications that exist on online repositories such as GitHub, but there is a gap in translating this research into automated, packaged tools. In future work, substantial resources should be dedicated to facilitating partnerships between climate–infectious disease researchers and software engineers, to increase the number of models that are developed into accessible, standalone tools.

Contributors

BAM, MCT, TC, RK, SJR, and AMS-I conceptualised this Personal View. SJ, SJR, CAL, AD, and WD curated the data. SJR, CAL, AD, WD, SJ, and SG did the formal analysis. SJR and AMS-I acquired the funding for this Personal View. SJR, CAL, AD, WD, AMS-I, RL, SJ, and SG conducted the investigation. SJR and SJ were responsible for the method. AMS-I, SJR, BAM, and TC were responsible for project administration. SJ provided the software. SJ, SJR, SG, CAL, and AMS-I conducted the data validation. CAL, SJR, SG, and SJ conducted the data visualisation. CAL, SJR, AD, WD, and AMS-I wrote the first draft. All authors contributed to the review and editing of the final draft.

Declaration of interests

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