

¹ climepi: A Python package for modeling climate suitability for vector-borne diseases

³ William S. Hart  ¹ and Robin N. Thompson  ¹

⁴ 1 Mathematical Institute, University of Oxford, Oxford, OX2 6GG, UK

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Software

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⁵ Summary

⁶ climepi (clim-epi) is a Python package for combining climate projections with models of climate ⁷ suitability for vector-borne disease (VBD). Utilizing the [xarray](#) library (Hoyer & Hamman, 2017) ⁸ for handling labeled multi-dimensional arrays, climepi provides methods for: accessing climate ⁹ projection data from a range of sources; defining, parameterizing, and running models of ¹⁰ climate suitability for VBD; and assessing the impacts of different sources of climate uncertainty ¹¹ (uncertainty in emissions scenarios, structural uncertainty across climate models, and natural ¹² climate fluctuations that occur alongside anthropogenic climate change). The package also ¹³ provides a front-end application that can be used to explore impacts of climate change and ¹⁴ its uncertainties using example climate datasets and climate-VBD suitability models (a [web](#) ¹⁵ [interface](#) is available).

Statement of need

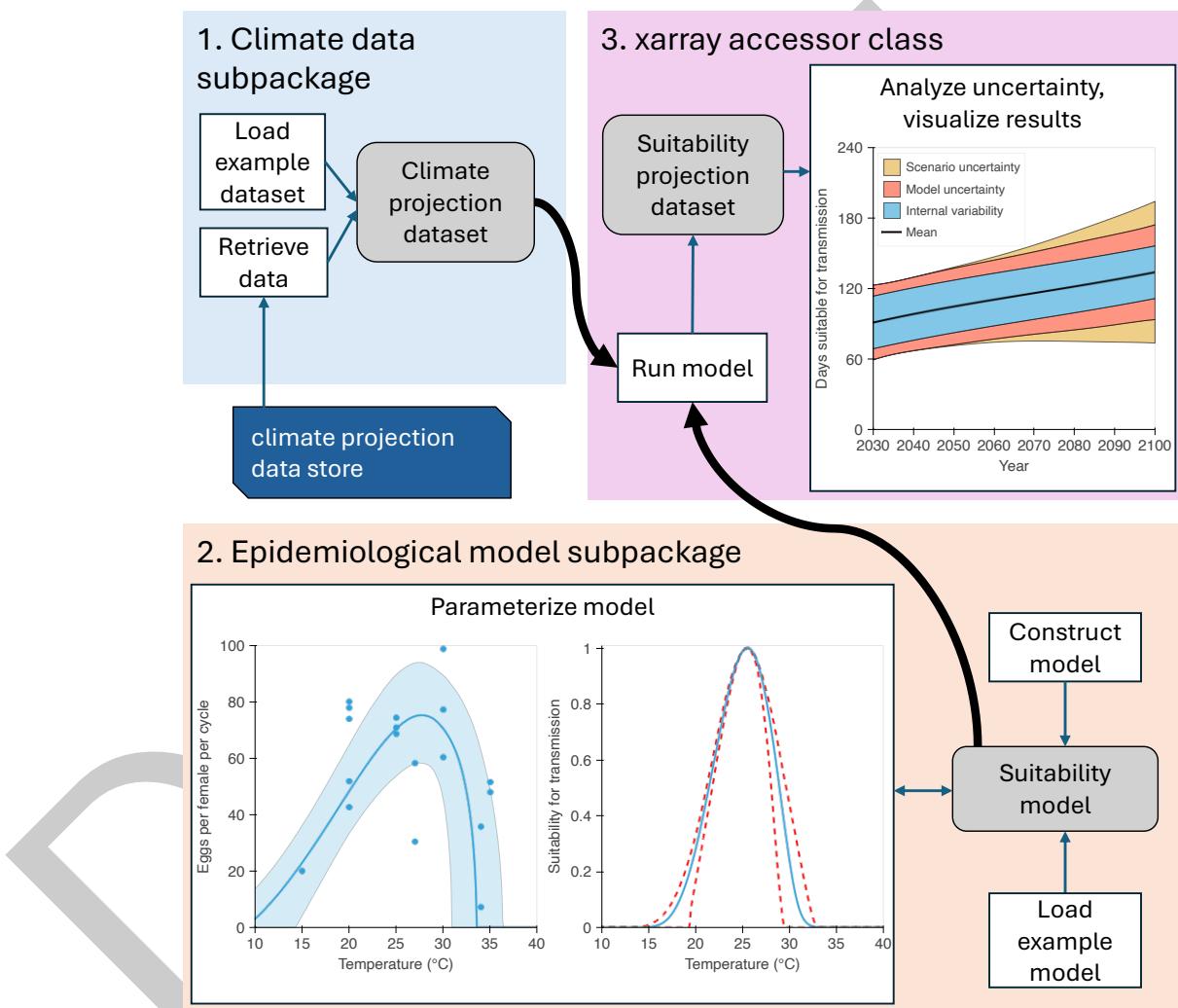
¹⁹ Climate change is altering the dynamics of a range of infectious diseases, particularly VBDs ²⁰ such as malaria and dengue (Ryan et al., 2019). Quantitative estimates of future VBD risks ²¹ are important for targeting vector and pathogen surveillance resources, and for planning public ²² health interventions. However, a recent review paper highlighted that few operational software ²³ tools exist for assessing climate-sensitive disease risks (Ryan et al., 2023). climepi contributes ²⁴ to addressing this gap by providing a flexible and extensible Python package, as well as a ²⁵ user-friendly front-end application, which can be used by climate-health researchers and other ²⁶ users (such as public health professionals) to assess future climate suitability for VBD and ²⁷ uncertainty therein.

²⁶ State of the field

²⁷ The review article by Ryan and colleagues (Ryan et al., 2023) identified 30 fully developed ²⁸ software tools for climate-sensitive VBD modeling. However, most of these tools are ²⁹ implementations of specific models for particular vector-pathogen systems. We are not aware ³⁰ of existing software providing a general framework for parameterizing mechanistic models ³¹ of climate suitability for VBD and combining them with climate data or projections, with ³² previous studies relying on custom code written in R (Mordecai et al., 2017; Taylor et al., ³³ 2019; Villena et al., 2022) and MATLAB (Kaye et al., 2024). Consequently, we have opted ³⁴ to build this extensible and open source software framework, in which different climate ³⁵ data and epidemiological models describing climate suitability for VBD can be incorporated ³⁶ straightforwardly.

37 Software design

38 climepi represents climate datasets and epidemiological model outputs as xarray Dataset
 39 objects, enabling seamless integration of climepi with the range of tools for analyzing gridded
 40 datasets provided by xarray and its wider [ecosystem](#). In particular, climepi supports xarray's
 41 [integration with Dash](#), enabling lazy evaluation and parallel computation on larger-than-memory
 42 datasets. climepi is designed with a modular structure, comprising three main components
 43 corresponding to different stages of a typical climate-VBD suitability modeling workflow
 44 (Figure 1):



45 1. Climate data (climdata) subpackage: enables users to access climate projection data
 46 from different sources through a single interface. Rather than providing comprehensive

47 access options for a large number of datasets, the focus is on facilitating straightforward
48 access to data sources and climate variables (temperature and precipitation) that are
49 particularly useful for analyzing the impacts of different types of climate uncertainty on
50 future climate-VBD suitability. Supported data sources include the [Inter-Sectoral Impact
Model Intercomparison Project \(ISIMIP\)](#) ([Lange & Büchner, 2021](#)), which provides
51 downscaled and bias-adjusted data from multiple [Coupled Model Intercomparison Project
Phase 6 \(CMIP6\)](#) ([Eyring et al., 2016](#)) climate models and emissions scenarios, and the
52 [Community Earth System Model version 2 Large Ensemble \(LENS2\)](#) ([Rodgers et al.,
2021](#)), which provides 100 ensemble members for analyzing internal (natural) climate
53 variability.

54 2. Epidemiological model (`epimod`) subpackage: provides classes and methods for models
55 of climate suitability for VBD, in which a suitability metric (e.g., the basic reproduction
56 number, R_0) is defined as a function of temperature and/or precipitation. Methods are
57 also provided for parameterizing mechanistic suitability models by fitting the temperature
58 dependence of model parameters describing vector and pathogen traits to laboratory
59 data ([Mordecai et al., 2017](#)). A selection of climate-VBD suitability models from the
60 literature are also available as built-in examples ([Kaye et al., 2024](#); [Mordecai et al., 2017](#);
61 [Parham & Michael, 2010](#); [Ryan et al., 2019](#); [Taylor et al., 2019](#); [Villena et al., 2022](#);
62 [Yang et al., 2009](#)).

63 3. Accessor class for `xarray` datasets (`xarray.Dataset.climepi`): provides methods for
64 combining climate data with epidemiological models and for assessing and visualizing
65 the importance of different climate uncertainty sources ([Hart et al., 2025](#); [Hawkins &
66 Sutton, 2009](#)), as well as other supporting functions.
67

68 In addition, `climepi` includes a further subpackage (`app`) that can be used to run the front-end
69 application locally.
70

72 Research impact statement

73 In a recent study, we used `climepi` to assess the relative contributions of climate scenario
74 uncertainty and climate model uncertainty, as well as internal climate variability, to uncertainty
75 in future climate suitability for dengue virus transmission in a range of locations that do not
76 currently experience substantial outbreaks ([Hart et al., 2025](#)). The `climepi` documentation
77 includes a detailed usage example demonstrating how results from that study can be reproduced.

78 Further example pages show how `climepi` can be used to recreate results from two other studies
79 (that did not originally use `climepi`) ([Kaye et al., 2024](#); [Mordecai et al., 2017](#)): specifically,
80 these examples involve parameterizing the temperature-dependent dengue virus transmission
81 suitability model developed by Mordecai et al. (2017) and recreating the analysis of the
82 impact of internal climate variability on climate suitability for *Aedes aegypti* (a vector of VBDs
83 including dengue and yellow fever) by Kaye et al. (2024). These detailed examples illustrate
84 the wide applicability of `climepi` for conducting climate-VBD suitability modeling workflows.

85 AI usage disclosure

86 Generative AI tools (ChatGPT and GitHub Copilot) were used to suggest and autocomplete
87 short segments of code and documentation, to assist with code review and to provide grammar
88 and style recommendations in the manuscript. All AI-assisted outputs were reviewed, edited
89 and validated by the authors, who made all of the core design decisions.

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