




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

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## Software

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## Summary

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

## Statement of need

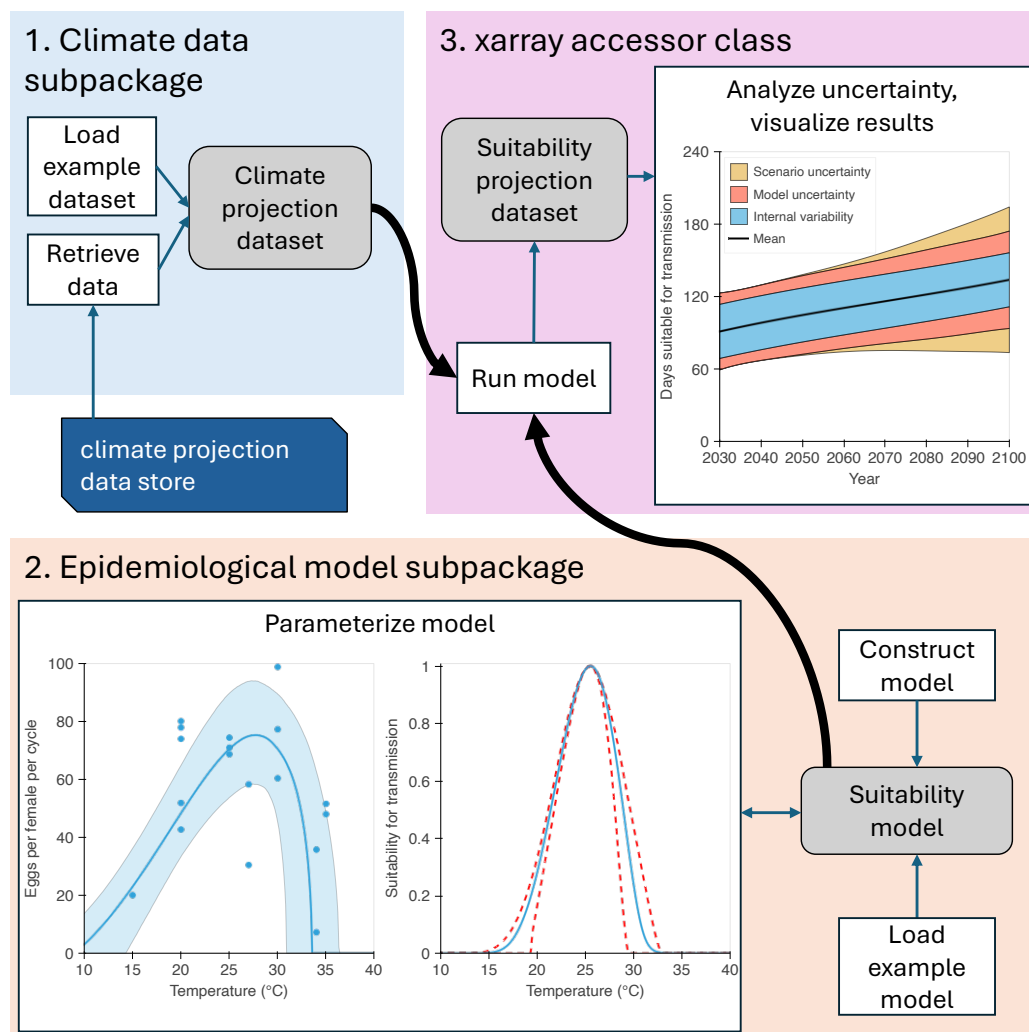
Climate change is altering the dynamics of a range of infectious diseases, particularly VBDs such as malaria and dengue ([Ryan et al., 2019](#)). Quantitative estimates of future VBD risks are important for targeting vector and pathogen surveillance resources, and for planning public health interventions.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

## State of the field

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

## Software design

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



**Figure 1:** Schematic illustrating typical workflows using climepi. (1) The `climdata` subpackage can be used to access climate data from an external source, or to load a pre-defined example climate dataset. (2) The `epimod` subpackage can be used to define a mechanistic model describing climate suitability for VBD, infer temperature response curves of trait parameters using laboratory data (left plot), and determine the overall temperature dependence of the suitability metric (right plot). Pre-defined epidemiological models from the literature are also available as built-in examples. (3) The `climepi` accessor for xarray datasets can be used to combine a climate dataset with an epidemiological model of climate suitability for VBD to obtain suitability projections, to assess the contributions of different sources of climate uncertainty, and to visualize results. See the package [documentation](#) for detailed usage examples.

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

access options for a large number of datasets, the focus is on facilitating straightforward access to data sources and climate variables (temperature and precipitation) that are particularly useful for analyzing the impacts of different types of climate uncertainty on future climate-VBD suitability. Supported data sources include the [Inter-Sectoral Impact Model Intercomparison Project \(ISIMIP\)](#) ([Lange & Büchner, 2021](#)), which provides 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 [Community Earth System Model version 2 Large Ensemble \(LENS2\)](#) ([Rodgers et al., 2021](#)), which provides 100 ensemble members for analyzing internal (natural) climate variability.

2. Epidemiological model (`epimod`) subpackage: provides classes and methods for models of climate suitability for VBD, in which a suitability metric (e.g., the basic reproduction number,  $R_0$ ) is defined as a function of temperature and/or precipitation. Methods are also provided for parameterizing mechanistic suitability models by fitting the temperature dependence of model parameters describing vector and pathogen traits to laboratory data ([Mordecai et al., 2017](#)). A selection of climate-VBD suitability models from the literature are also available as built-in examples ([Kaye et al., 2024](#); [Mordecai et al., 2017](#); [Parham & Michael, 2010](#); [Ryan et al., 2019](#); [Taylor et al., 2019](#); [Villena et al., 2022](#); [Yang et al., 2009](#)).
3. Accessor class for xarray datasets (`xarray.Dataset.climepi`): provides methods for combining climate data with epidemiological models and for assessing and visualizing the importance of different climate uncertainty sources ([Hart et al., 2025](#); [Hawkins & Sutton, 2009](#)), as well as other supporting functions.

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

## Research impact statement

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

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

## AI usage disclosure

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

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