Data-Driven Modeling of Reproduction Numbers, the Most Critical Epidemic Index, of Climate-influenced Vector-Borne Diseases

Effective management for preventing and controlling of vector-borne infectious diseases depends on accurate estimates of the basic reproduction number (R0) and the effective reproduction number (Rt), which measure disease outbreaks and transmission trends. However, existing maximum likelihood-based methods often fail to capture the complexities of climate-influenced indirect transmission via vectors, potentially limiting their accuracy in complex epidemiological settings. In this study, we first develop a random forest-based method with climate predictors to map weekly dengue fever case data from Nepal to daily case data. We then create a data-driven modeling framework to accurately estimate R0 and Rt for climate-influenced vector-borne diseases. By leveraging the imputed daily case data, our framework provides improved estimates of reproduction numbers of climate-influenced dengue fever in Nepal. This approach allows us to better capture the dynamic interactions between vectors and humans that affect climate-influenced disease outbreaks and transmission patterns.

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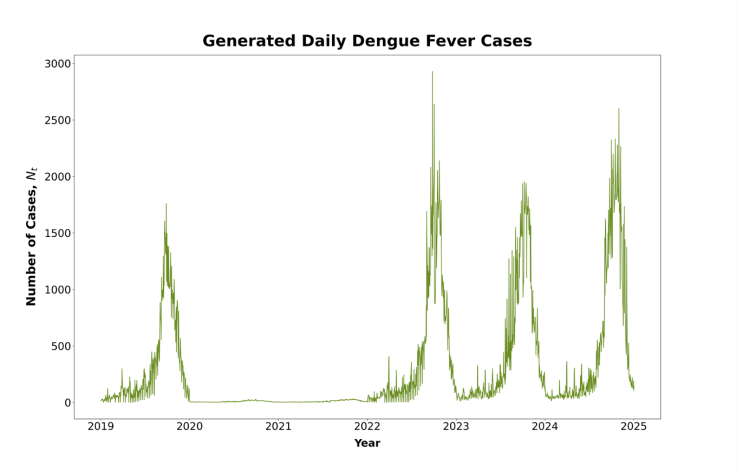
This research is supported by the SDSU University Graduate Fellowship, the Simons Foundation grant (MPS-TSM-00008139), the National Science Foundation grants (2527286 & 2324008), and the Computational Science Research Center (CSRC) at San Diego State University

Weekly dengue fever cases

Random forest regression

Daily climate data

Generated daily dengue fever cases, N_t

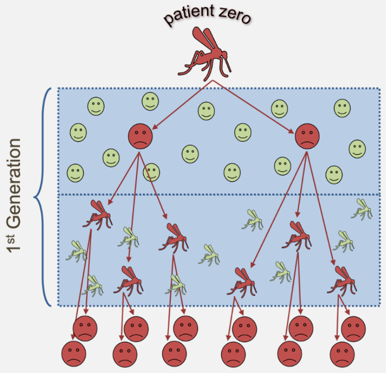


Maximize:

$$\mathbb{L}\left(R^{VH}, R^{HV}\right) = \prod_{t=1}^{t_{final}} \frac{e^{-\lambda_t}\lambda_t^{N_t}}{N_t}, \quad \lambda_t = \sum_{s=1}^{t}\left(R^{VH} w_s^V \sum_{k=1}^{t-s}\left(R^{HV} N_{t-s-k} w_k^H\right)\right)$$

Using in R^{VH}, R^{HV} estimates → $R = \sqrt{R^{VH}R^{HV}}$

Reproduction numbers, R_t



Example: $R_0 = \sqrt{R^{VH}R^{HV}} = \sqrt{2 * 3} = 2.44.$