Climate factors related to the dengue incidence in Costa Rica and future projections under scenario SSP5-8.5.

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*This manuscript has been submitted to: Science in One Health

Abstract

This article has three objectives: 1) modeling the climate-dengue relationship at the smallest administrative division (districts) using high-resolution data; 2) use of an objective algorithm for the selection of predictors that results in parsimonious models, cross-validated to prevent overfitting; and 3) using estimates from CMIP6 climate models to provide mid-century (2035-2065) potential dengue incidence projections under a pessimistic scenario (SSP5-8.5) with seasonal windows actionable by region in Costa Rica to guide preparedness decisions. Results show that temperature and precipitation data are significantly related to dengue

incidence. Projections of dengue cases for mid-century show increments of up to 42 more cases in some districts compared to the historical scenario. It should be remembered that ultimately dengue variations and change are related to climatic and non-climatic factors and the results presented here represent a future potential increase of the dissemination of the disease, based on the projected climate change of the most pessimistic scenario.

Introduction

The limited success of international efforts to reduce global warming at levels established in the Paris Agreement, and the increasing frequency and strength of climate impacts, highlight the urgent need for adaptation, particularly in developing countries as in the region of Central America [1]. Mention that there is a high level of confidence that Central America will face a risk of severe health effects due to increasing epidemics, particularly vector-borne diseases such as dengue, under a warming climate change scenario by the end of the 21st century [2]. Unfortunately, current levels of adaptation initiatives are not enough to counteract the observed impacts and projected risks from climate change in Latin America and the Caribbean [1]. Climate change effects on health across Central America are diverse and are related to different hydroclimatological drivers. Temperature increases, increased pluvial and riverine floods, and decreased water quality, for example, are also likely to drive higher incidences of vector-borne diseases such as malaria, dengue, zika, and chikungunya, and the unprecedented spread of these diseases to places located at higher elevations [3]. However there is still a clear need to improve data availability and to increase the number of studies on projections of changes in the climate, risks, impacts, vulnerability, and adaptation from the region to inform decision-makers and practitioners.

Dengue is considered a climate-sensitive disease, with fluctuations in temperature, humidity, and rainfall influencing the mosquito vector's biological processes, behavior, reproductive capacity, virus transmission potential, and interactions with human populations [4-7]. Several climate variables were considered by Barboza et al. [7] for fitting General Additive Models and Random Forest models to predict dengue case counts in Costa Rica. Among these variables, these authors used as covariates daily precipitation data, an index representing El Niño-Southern Oscillation (ENSO), Normalized Vegetation Index (NDVI) data, daytime land-surface temperature data, and the Tropical Northern Atlantic (TNA) Index [7]. Although the fitted models showed good skill at predicting the relative risk of dengue for the first three months of 2021 using a training period from 2000-2020, in terms of projected data from models there is an extra layer of complexity when using these covariates in climate projections. Although ENSO indices, TNA index and NDVI can be derived with the addition of an extra link in the chain of uncertainty from climate models coupled with vegetation models, they will need to be downscaled using dynamical models, increasing also the complexity of the procedure. It should be remembered that high spatial resolutions of the covariates are needed in regions of complex topography with small districts such as Costa Rica. To circumvent this problem, we used high-resolution (1km x 1km) precipitation and temperature projections that are readily available [8]. Precipitation and temperature are first order variables from the downscaled climate model output that, as it will see later, are proven to be related to dengue incidence in previous studies.

Although this is improving, GCMs are known to produce climate estimates that have horizontal spatial resolutions on the order of around 50-250 km, which is clearly too coarse to capture the local-scale climate variations of Costa Rica. Costa Rica is a country located in Central America, characterized by being a relatively narrow stretch of land between two oceans and with changes in topography within a few hundred kilometers. These two aspects contribute to a myriad of microclimates. Added to that, the data for dengue counts that we used in our study are available at the district level (the smallest Costa Rican administrative division), and some of them are very small (on the order of a few square kilometers). For this reason, a process known as downscaling needs to be applied to the GCM coarse scale to bring it to a finer scale (a few kilometers' resolution). There are three types of downscaling: statistical (ESD), dynamical (RCM), and hybrid (just a combination of the other two) [9]. Each method has its respective advantages and disadvantages. RCMs are more computationally demanding, which limits the number of simulations that can be processed, but they are based on the physical and dynamical principles of the climate system, allowing for the generation of a broader range of climate variables. In contrast, ESDs are empirical methods that require fewer computational resources, as they handle a smaller set of meteorological variables. However, they allow for a larger number of simulations, enabling the evaluation of a greater variety of models and greenhouse gas concentration scenarios.

The data from 8 GCMs and 3 concentration scenarios (optimistic, medium and pessimistic) were downscaled using ESD resulting in climate change projections of precipitation (P), maximum and minimum temperature (Tmax and Tmin, respectively) at 1 km spatial resolution, and at monthly time-scales for the 1979-2099 period over Central America and Dominican Republic [9]. These data will be used in the second part of the analysis to determine potential future changes using climate data with linear models calibrated with the observed data. It should be remembered here that the projections represent a climate potential for the development of dengue, but the actual incidence is driven by a convergence of factors, climate and non-climate, including global trade and travel, rapid urbanization, population growth, serotypes, vector control, population behavior and climate change/variability, that collectively shape its epidemiological landscape [10]. This statement is part of a review article that explores the influence of climate, particularly temperature, on the capacity of vectors to initiate and maintain outbreaks, as well as how climatic variations impact the transmission dynamics of dengue [10]. Other research has strengthened this understanding by documenting how each driver influences dengue dynamics: international travel and commerce facilitate the introduction of both infected individuals and *Aedes* vectors into novel regions, while urban expansion creates dense human–vector interfaces and breeding sites [11]. Importantly, climatic variables, particularly temperature and precipitation, play a critical role in determining the geographic range, population dynamics, and vector competence of *Aedes aegypti* and *Aedes albopictus*. For example, rising mean temperatures and altered rainfall patterns have accelerated larval development, increased adult mosquito survival, and enabled range expansions into temperate regions like Southern Europe and parts of Iran and Colombia [12-14]. Concurrently, global average temperatures have risen approximately 0.8 °C over the past century (~ 0.15–0.20 °C per decade), and projections indicate that weather variability will intensify in a spatially heterogeneous manner under continued warming scenarios [15] [16]. These climatic shifts are projected to expand the seasonal and geographic window of dengue transmission, potentially adding 6–7 million additional cases annually in Latin America by mid-century under a ~ 3.7 °C warming scenario, an estimate reduced but not eliminated by limiting warming to 1.5 °C [15]. Such trends have already been observed during recent outbreaks in Latin America and Europe, where elevated temperatures, extreme rainfall events (*e.g.*, during El Niño years), and increased urban vulnerability combined to fuel record dengue epidemics [17][18]. Climate change is increasingly recognized as a critical driver of dengue transmission in Latin America, where the disease already poses a significant public health burden. Evidence indicates a nonlinear relationship between temperature and dengue incidence, with transmission rising sharply at lower temperatures, peaking near 27.8°C, and declining at higher temperatures. Historical warming has contributed to an estimated 18% increase in dengue cases in the region. In comparison, projections suggest further increases of 40% to 57% by mid-century, with some localities experiencing up to 200% growth in incidence under high-emissions scenarios. Importantly, lower-emissions pathways could substantially reduce these impacts, underscoring the need to integrate climate mitigation and adaptation strategies into regional public health planning [19].

In summary, a synthesis of literature from 2015 to 2025 confirms that anthropogenic environmental change, demographic dynamics, and climate variability synergistically enhance *Aedes*-borne disease risk, underscoring the urgent need for integrated surveillance, urban planning, climate mitigation-adaptation, and vector control strategies to curb the future burden of dengue. The relevance of this work is three-fold: 1) modeling the climate-dengue relationship at the smallest administrative division (districts) using high-resolution data; 2) use of an objective algorithm for the selection of predictors that results in parsimonious models, cross-validated to prevent overfitting; and 3) using estimates from CMIP6 climate models to provide mid-century (2035-2065) potential dengue incidence projections under a pessimistic scenario (SSP5-8.5) with seasonal windows actionable by region in Costa Rica to guide preparedness decisions.

Data

- *Dengue counts:* Dengue counts consisting mostly of clinical reports were obtained from public health centers in Costa Rica from 2011-2023. The data counts of reported cases were aggregated at monthly totals and for each district.
- *"Observed" climate data:* A gridded blend of satellite and meteorological station precipitation (P) data from the Climate Hazards and Infrared Precipitation (P) with stations [20] was used to represent "observations" from 1981 to 2023. These data have a spatial resolution of approximately 5 x 5 km horizontal. This data set is called CHIRPs. Similarly, maximum and minimum temperatures (Tx and Tn, respectively) data were obtained from a corresponding dataset for temperature [21] for the period 1983−2023. This data set is called CHIRTs Average temperature (Tavg) was computed from the mean of Tx and Tn. Both CHIRPs and CHIRTs datasets have shown good agreement with station data in several locations across Central America and the Caribbean region [22-27]. A table with comparison statistics can be found in the Supplementary Material #2 of [26]. The daily precipitation data were used to create 4 monthly indexes: 1) mean monthly precipitation, 2) number of rainy days (number of days of the month when P>=0.1 mm), 3) number of days of the month that are greater than the 90th percentile of the 1983-2023 precipitation during the respective month, and 4) similar to 3, but for the

number of days below the 20th percentile. The Tx, Tn, and Tavg data were averaged to monthly means (Table 2).

- Model climate data: daily data for the same precipitation and temperature variables as for the CHIR data from GCMs at 1 x 1 km spatial resolution for Costa Rica were obtained from [9]. The daily model data were used to produce the same monthly indices as for the CHIR data. The source of the data is simulations from 8 GCMs (Table 1) from the Climate Model Intercomparison Project version 6 (CMIP6) that represent the most recent available version of this type of simulations. The data were downscaled for each model individually, and the ensemble was produced by averaging the results of all different model outputs. The data contains daily simulations from 1985-2065 of P, Tx, and Tn. Average temperature was computed from the average of Tx and Tn in the same manner as with the CHIRT data.
- *Climate regions of Costa Rica:* A geographical layer of the delimitation of Costa Rica's climate regions was obtained from the National Meteorological Institute of Costa Rica [28] [29].
- *Administrative boundaries:* The delimitations of municipalities (local governments) and districts (the administrative units that conform to a municipality) in Costa Rica were obtained from the Geographical National Institute of Costa Rica [30]. The population data from the 2022 census was obtained from INEC [31].

Methods

The seasonal cycles of the dengue counts by climate region were calculated to compare them with the precipitation and temperature seasonal cycles and to provide a general assessment of the possible relation of the seasonal cycles of the availability of water (providing water for the proliferation of vectors) and temperature (for the optimum temperature preferred by the vectors).

For each district and month, the climate indices of Table 2 were related to the dengue counts. The covariates included lagged versions of the indices for -2, -1, and 0 month lags. Since the number of covariates in the linear equations could be large (3 lags x 7 indices = 21 covariates), there is a possibility of overfitting the models. For this reason, an objective procedure/algorithm was used to select the possible retained predictors in the equations. The algorithm is based on [32] and aims to generate cross-validated, parsimonious models. The procedure consists of the following:

1. Given a set of potential covariates of the models (X_1, X_2, X_3, … X_n) where *n* is the total number of indices with their lags (*n* = 21) for *each* district, and Y is the predictand variable (in this case, the average counts of dengue cases for *that district*).
2. Calculate the r_n partial correlations of the potential predictors with the predictand variable Y.
3. Start with models of only one predictor (e.g., forward) and consider only for those variables where the partial correlation is statistically significant.

4. Starting with the predictor with the highest absolute r_n, evaluate the Cross-Validation Standard Error (CVSE) by deleting one month and using the rest of the data to predict it. Then, the second month is removed, the prediction is stored, and the process repeats. At the end of the series of predictions, the methodology is compared to Y, and the error is computed according to the following formula:

$$CVSE = \sqrt{\frac{\sum_{i}^{m}\left(Y_i - \hat{y}_{(i)}\right)^2}{(n-p)}} \quad \text{(Eq. 1)}$$

Where Y_i is the value of the predictand (dengue counts) at month i; $\hat{y}_{(i)}$ is the fitted response of the ith month with the ith observation removed, *m* is the number of months in the dataset, and p is the number of regression coefficients.
5. When the CVSE of all cases with possible 1-variable predictors was calculated, the model with the minimum CVSE was stored temporarily as the potential solution.
6. Then, the model of the predictor selected as the best for a 1-variable combination will be added one variable at a time (in order of partial correlation) to produce possible models with 2-variables.
7. Which 2-variables will be selected is determined using the following subprocedure (see also [32]).
   a. The retention of variables in the models depends on two tests: a t-test and a *sign test*.
   b. Perform a Principal Component Analysis (PCA) on the two candidate variables, resulting in two principal components (PC1 and PC2).
   c. Perform a linear regression of PC1 with Y.
   d. If the coefficient of the regression equation passes a statistically significant t-test, then check for the sign test as described next.
   e. If the sign of the regression coefficients of Y with PC1 expressed *in terms of the original variables* (by multiplying the regression coefficients of the PCA regression by the eigenvectors of the PCA) are of the same sign as the sign of the partial correlations of the two variables respectively, then the sign test is passed and PC1 is retained and the the model with the two variables are accepted as a possible model.
   f. Next, test PC2 in the regression (as they should be introduced in order).
   g. If PC2 does not pass the t-test, then only retain PC1, and the procedure is finished.
   h. If the introduction of PC2 also passes the sign test, then PC2 is also retained.
   i. *In the case of introducing more than two variables later on, then continue with PC3:* If PC2 passes the t-test, but not the sign test, temporarily retain PC2 and add PC3. If they pass the t-test and the sign test, retain PC3; if not, only retain PC1.
   j. A new subset of variables is then tested, and the procedure returns to point b.
8. The subset of all possible combinations of 2 variables are tested, and if the CVSE for combinations of 2 variables is larger than for the CVSE for 1-variable, then the model accepted consists of only 1-variable and the procedure stops.

9. Then the combinations of 3-variables are tested and so on, until the combination with the most parsimonious model with the lowest CVSE is found.
10. The combinations of variables tested can be very large and prohibitively expensive to test all possible combinations. We tested at most 5,000,000 combinations for each district, and the variables that enter the subsets tested were introduced in order of their decreasing partial correlation strength.
11. The procedure satisfies the requirement of parsimonious models and that the predictor variables represent the nature of the proper relationship with the predictand variable and are conceptually acceptable [32][33], and thus reduce the probability of overfitting.

Once the parsimonious quasi-optimal models were fitted, the same covariates from the GCM data were used in the resulting models to generate estimations of dengue for the mid-century. The maps of the difference between the future (2030-2065) minus historical (1985-2015) were then produced.

Results

The climate regions of Costa Rica can be found in Fig. 1, and the seasonal cycles of the average monthly sums of the counts of dengue cases of all districts in each climate region can be found in Fig. 2. In general, dengue cases peak in July-August in most of the climatic regions; those conditions are associated with precipitation decrease during the mid-summer drought [34] in the Pacific Slope and maximum peaks in the Caribbean Slope [35]. Although in some of the regions the dengue peaks do not correspond to one of the maximum precipitation peaks of the rainy season, it should be taken into consideration the possible 1-3 months lags between the climate-dengue response and that the May or June peak in precipitation may be also playing a role [35]; similar hypothesis can be drawn for the temperature variable. In summary, it seems that wet and hot conditions may be associated with higher dengue incidence. A description of the temperature and precipitation main annual cycles in Central America can be found in [36]. Conversely, the dengue minimums in these regions might generally be associated with lower temperatures and a reduction in precipitation. These types of generalizations will help us in verifying the sign of the regression equations in the linear models that are going to be fitted in the following sections.

In Table 3, the 6-highest number of times (corresponding to the number of districts) in which each climate variable appears in the fitted models for models calibrated for each month of the year and for the annual case. As can be seen, the covariates representing temperature variations dominate the top-6 predictors found in feasible regression models, except for August, September, and October (generally part of the second second and largest peak of the wet season), where precipitation indexes dominate. Note also that in some of the models, the climate variables (precipitation and temperatures) are lagged, in many cases by two months, suggesting that the climate information in previous months provides the required conditions for dengue outbreaks in some later months. However, it is noticeable to see that some of the climate variables occurring at lag zero also influence the dengue counts in that same month. We hypothesize that perhaps there could be really smaller lagged time scale processes like weeks, which cannot be captured in monthly data, related to the development of the illness in cases finally appearing in health centers.

In Figures 5 and 6, the adjusted R-square (Adj. R^2) and the CVSE for the fitted models relating climate to dengue are shown, respectively. It is noticeable that the Pacific slope districts have better skill. Interestingly, it is the Pacific slope where the majority of future changes occur (Figures 7 and 8) during part of the dry season (November, December and January). In particular, the North Pacific Region within the Pacific slope is a season with high seasonal dengue counts, while other districts of the slope usually present low seasonal incidence (Fig. 2). In the case of the Caribbean slope, the highest future increases in dengue cases were found in April, May and June, months that represent a transitional period between lowest seasonal dengue incidence and peak in August and September.

Discussion and conclusions

Future changes in dengue counts suggest *potential* increases on the order of 45 more cases than historical (1985-2015) during mid-century (2035-2065) in some of the districts, for the most pessimistic (SSP5-8.5 concentration scenario). While that represents a potential, in the sense that the climate conditions are favorable for developing dengue, there are also other non-climatic factors required for the development of outbreaks, including the presence of infected patients in the first place that propagate the disease, serotypes, travel, population behavior, rapid urbanization, population growth, serotypes, vector control, and others. Also, the use of a pessimistic climate scenario represents, in a certain way, the most critical set of conditions for the development of possible cases. Nevertheless, considering the influence of temperature, as an important controlling factor in the modeling of dengue cases, the use of a most pessimistic scenario and for the mid-century horizon estimates, the changes found are on the same order of magnitude projected in other studies [19] [37].

One should also mention a limitation of linear models, such as the ones used in this article in the case of simulating the temperature-dengue relationship. Recent studies consistently show that temperature is a key, but nonlinear, driver of dengue counts. A global meta-analysis found the temperature–dengue relationship peaks near ~24 °C and weakens at cooler and hotter means, with effects further shaped by rainfall and socioeconomic context, implying that warming can strengthen transmission primarily where climates sit near that optimum (and where variability is high) [38]. Complementing this, a 2023 systematic review (54 studies in the meta-analysis) estimated that each 1 °C increase in high temperatures raises dengue risk by ~13%, with larger effects in tropical monsoon and humid subtropical zones [37]. The temperature conditions mentioned in these two studies are met in many districts of Costa Rica, and justify the sharp increases in dengue counts projected for the future.

Without excluding the influence of temperature, precipitation is a dominant factor during July, August, September, and October, months of high precipitation in both slopes of Costa Rica. Recent work finds that precipitation influences dengue in context-dependent, lagged, and often nonlinear ways. A 2022 systematic review and meta-analysis reported that monthly precipitation shows the strongest pooled correlation with dengue among common climate variables, typically peaking at 1–3-month lags (e.g., $r \approx 0.38$), consistent with rainfall creating breeding sites for *Aedes* mosquitoes [39]. The same authors highlight a dual role: in the Philippines and Puerto Rico, rainfall increased dengue where dry-season length varies greatly (more intermittent rains and containers), but decreased dengue where dry seasons are more regular, likely due to "flushing" of larval habitats during heavy, sustained rains. Consistent with [39], in our case, dengue outbreaks lags precipitation variables found at 0, -1, and -2 months, with -2 months being frequently observed. It is interesting to note the relationships at lag 0 with precipitation and temperature variables, it is hypothesized here that small lags may be related at least partially to dengue processes occurring at a submonthly scale, which can not be resolved by the monthly resolution of the data.

Communities can reduce climate change–amplified dengue risk by adopting integrated vector management that prioritizes environmental control (routine removal of container habitats, reliable solid-waste services, and secure, covered household water storage) alongside targeted larval source management (e.g., Bacillus thuringiensis israelensis or pyriproxyfen where appropriate) and adult control guided by entomological surveillance and insecticide-resistance monitoring. Climate-informed early-warning systems that couple seasonal forecasts with local case and vector data should trigger pre-emptive, neighborhood-level actions before high-risk heat–rainfall windows. Urban adaptation, expanded piped water, covered tanks, improved drainage and stormwater management to prevent standing water, and housing measures such as window/door screens, exposure while conferring co-benefits for other climate hazards. Sustained, equity-focused community engagement (schools, workplaces, faith groups), clear risk communication, and provision of low-cost protective materials (lids, screens, repellents) strengthen adherence. Finally, coordinated governance that aligns municipal sanitation, public health, and climate services, with routine monitoring and evaluation, underpins durable, climate-resilient dengue prevention.

Acknowledgements

The author(s) declare that financial support was received for the research and/or publication of this article. This study was funded by the National Institutes of Health Fogarty International Center (grant number D43TW011403) for the project entitled "International Training Program in Environmental Health over the Lifespan" (Claudio L and van Wendel de Joode B, PIs), a grant awarded to the Icahn School of Medicine at Mount Sinai and Universidad Nacional, Costa Rica (SIA 0019-23 EcoSalud). Additional support was provided by Vicerrectoría de Investigación, Universidad de Costa Rica grant: Influencia del cambio climático en la incidencia de enfermedades tropicales infecciosas: El caso de Cuajiniquil, La Cruz, Guanacaste, Costa Rica (EcoSalud, C4226). HH and EA wish to also acknowledge the UCR projects C5067, C2103, C3991 (UCREA), A4906 (PESCTMA), C3195 and B0-810. EA, and HH were partially supported by a grant awarded by the International Development Research Centre (IDRC), Ottawa, Canada, and the Central American University Council (CSUCA-SICA) to the Red Centroamericana de Ciencias sobre Cambio Climático (RC4) project (CR-66, C4468, SIA

0054-23, the opinions expressed here do not necessarily represent those of IDRC, CSUCA, or the Board of Governors).

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Table 1. General Circulation Models (GCMs) used in this study

Model	**Native resolution**
ACCESS	1.875° x 1.25°
AWI	0.9375° x 0.9375°
CAMS	1.25° x 1.12149°
EC-EARTH3	0.703125° x 0.703125°
EC-EART3-veg	0.703125° x 0.703125°
MPI	0.9375° x 0.9350616°
GFDL	0.703125° x 0.703125°
UKESM1	1.875° x 1.25

Table 2. Variables used as covariates. All covariates were tested at 0, -1, -2 month lags with respect to dengue counts.

Variable	Description	Units	Sign of the relationship with dengue counts
Pmon	Monthly mean precipitation from daily data	mm	-
daysP	Number of rainy days from daily data	days	+
P20	Number of days of the month with precipitation lower than the 20th percentile precipitation for each month over all years (2011-2023)	days	+
P80	Number of days of the month with precipitation higher than the 80th percentile precipitation for each month over all years (2011-2023)	days	-
Tmax	Monthly mean maximum temperature	ºC	+
Tmin	Monthly mean minimum temperature	ºC	+
Tprom	Monthly mean average temperature (Tprom=(Tmax+Tmin)/2)	ºC	+

Table 3. The 6-highest number of times (corresponding to districts) each climate variable appears in the fitted models for all districts for models calibrated for each month of the year and for the annual case. The variables names are average temperature (Tavg), minimum temperature (Tmin), maximum temperature (Tmax), number of days of the month when precipitation greater than 0.1 mm, monthly mean precipitation (Pmon) and number of days of the month when the precipitation is greater than the 80th historical percentile (P80). Each variable was analized at three month lags: 0, -1 and -2 (denoted as l0, l-1 and l-2 respectively).

Jan	Var.	Tavg_l-2	Tmin_l-1	Tmax_l-2	daysP_l0	Tmin_l-2	Tmax_l-1
	times app.	57	53	51	50	49	48
Feb	Var.	Tmin_l-1	Tavg_l-1	Tmax_l0	Tmin_l0	daysP_l-2	Pmon_l-2
	times app.	62	59	56	50	50	50
Mar	Var.	Tmin_l-2	Tavg_l0	Tavg_l-1	Tmin_l0	Tmax_l-1	Tmax_l0
	times app.	42	40	39	38	38	33
Apr	Var.	Tmin_l-2	Tmax_l0	daysP_l0	Tmax_l-2	Tavg_l0	Pmon_l0
	times app.	40	38	37	37	36	34
May	Var.	Tmin_l-1	daysP_l-2	Tmax_l-1	Tmin_l0	Tmax_l0	Tmin_l-2
	times app.	31	29	28	24	21	21
Jun	Var.	Tmax_l0	Tmin_l0	daysP_l-2	Tavg_l0	Pmon_l-2	P80_l-2
	times app.	58	49	49	40	34	34
Jul	Var.	daysP_l-2	Tmin_l0	Pmon_l-2	P80_l-2	Tavg_l0	P80_l0
	times app.	95	64	60	60	39	38
Aug	Var.	Pmon_l-1	daysP_l-1	P80_l-1	P80_l-2	Pmon_l-2	daysP_l-2

	times app.	79	77	60	42	38	32
Sep	Var.	daysP_I0	P80_I0	Pmon_I0	P80_I-1	daysP_I-1	Tmax_I-2
	times app.	48	42	39	37	34	34
Oct	Var.	daysP_I0	P80_I-2	Tmax_I-1	daysP_I-2	P80_I-1	Pmon_I-2
	times app.	44	44	42	40	38	35
Nov	Var.	Tmax_I-2	Tmax_I0	daysP_I-2	Tmin_I-2	daysP_I0	Tavg_I-2
	times app.	87	73	68	68	67	61
Dec	Var.	Tmax_I-1	daysP_I-1	Tavg_I-1	Pmon_I-2	daysP_I-2	P80_I-1
	times app.	75	60	50	47	40	37
Ann	Var.	Tmax_I-1	daysP_I0	Tmax_I0	Tmin_I-1	daysP_I-2	Tmin_I-2
	times app.	20	19	17	17	12	12

Fig. 1 Climate regions (larger named divisions) and administrative districts divisions (smaller unnamed divisions) of Costa Rica according to the National Meteorological Institute of Costa Rica and the National Geographical National Institute of Costa Rica respectively.

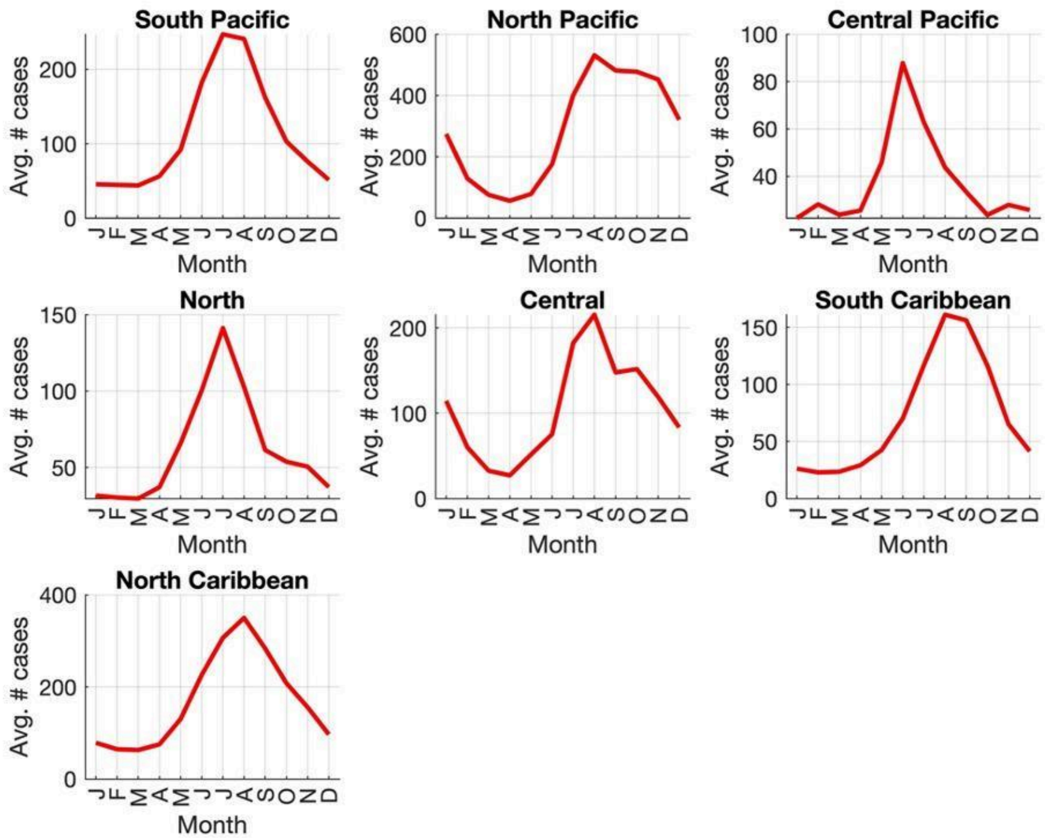

Fig. 2. Seasonal cycle (2011-2023) of the average number of dengue cases reported in the sum of the cases reported in all districts of each climate region.

Table 1.

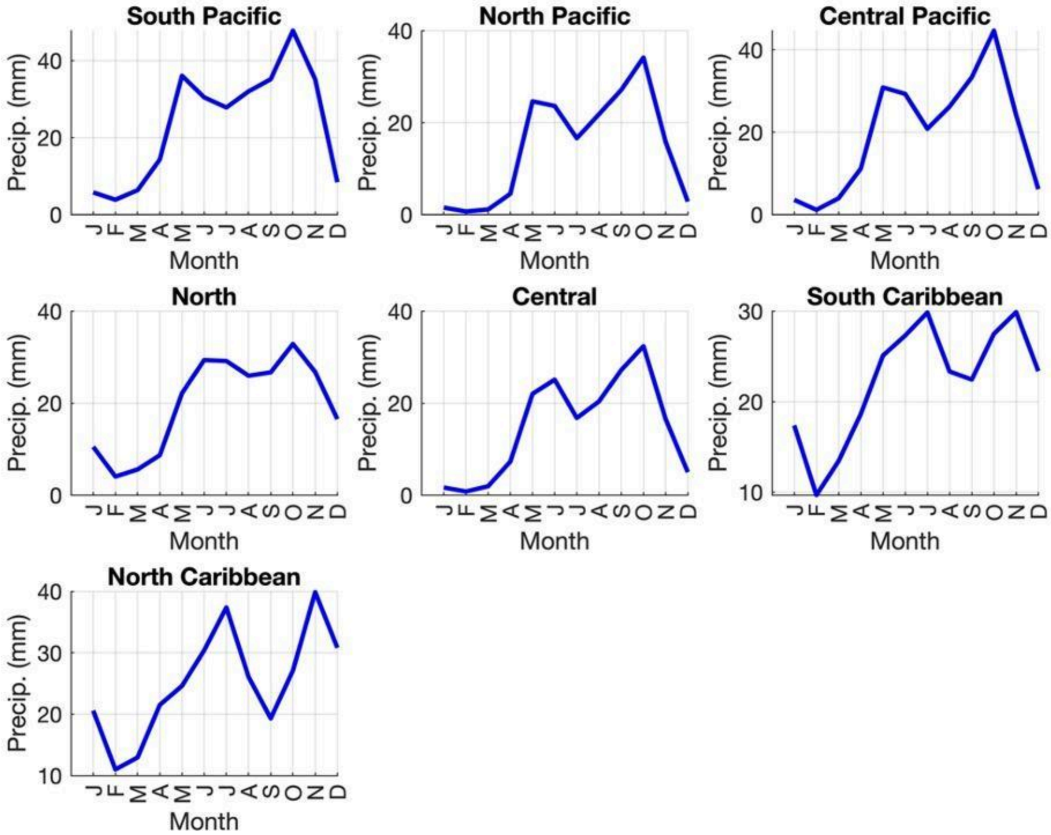

Fig. 3. Same as Fig. 2, but for precipitation averages.

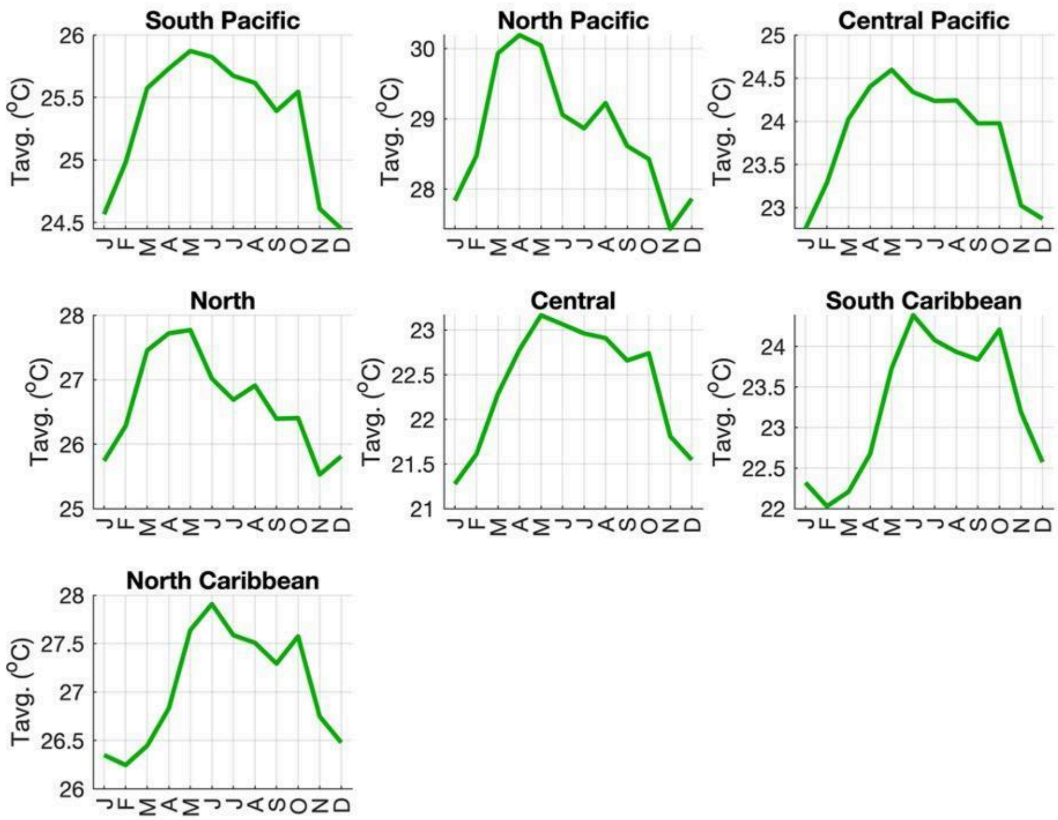

Fig. 4. Same as Fig. 2, but for average temperature.

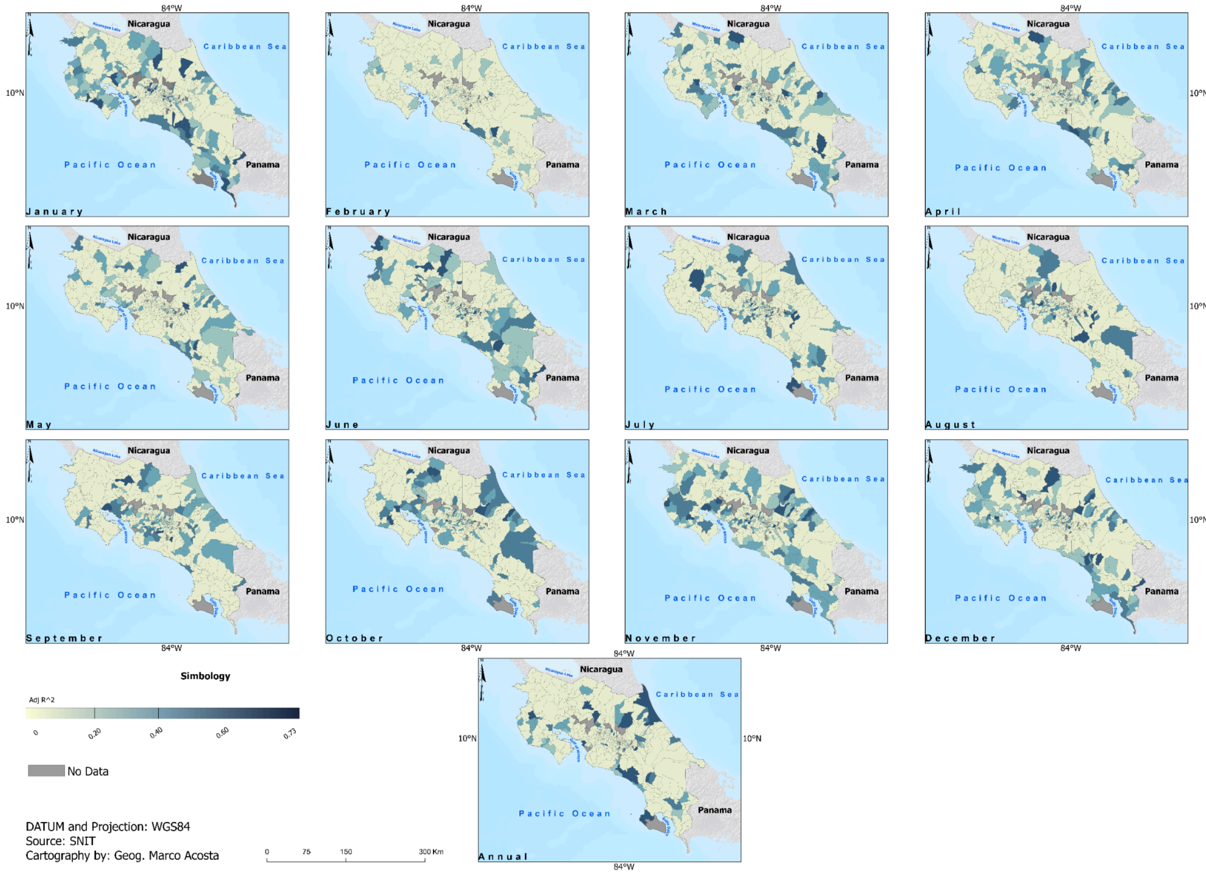

Fig. 5. Adjusted R square of fitting linear models relating climate variables and dengue counts (2011-2023) for different months and annual.

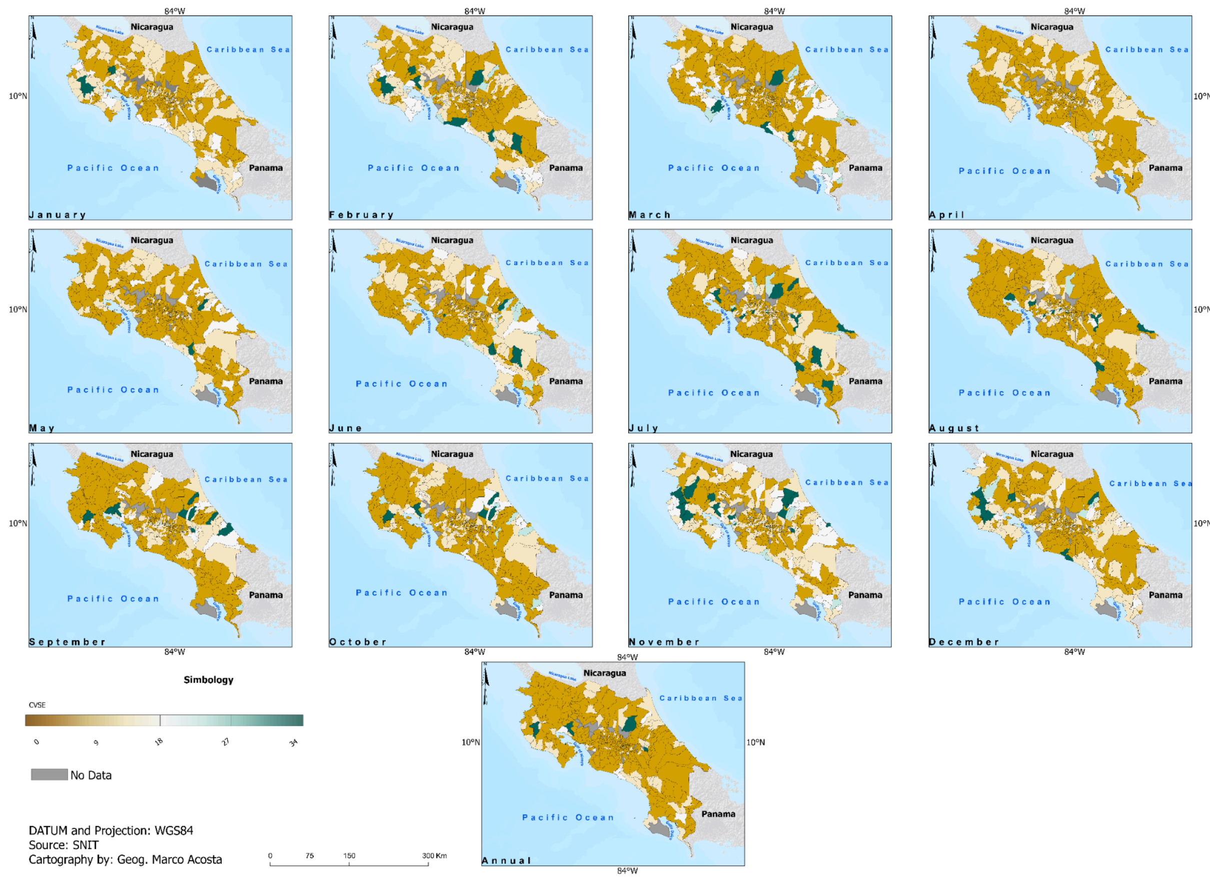

Fig. 6. Same as Fig.5, except for the variable Cross Validation Standard Error (CVSE).

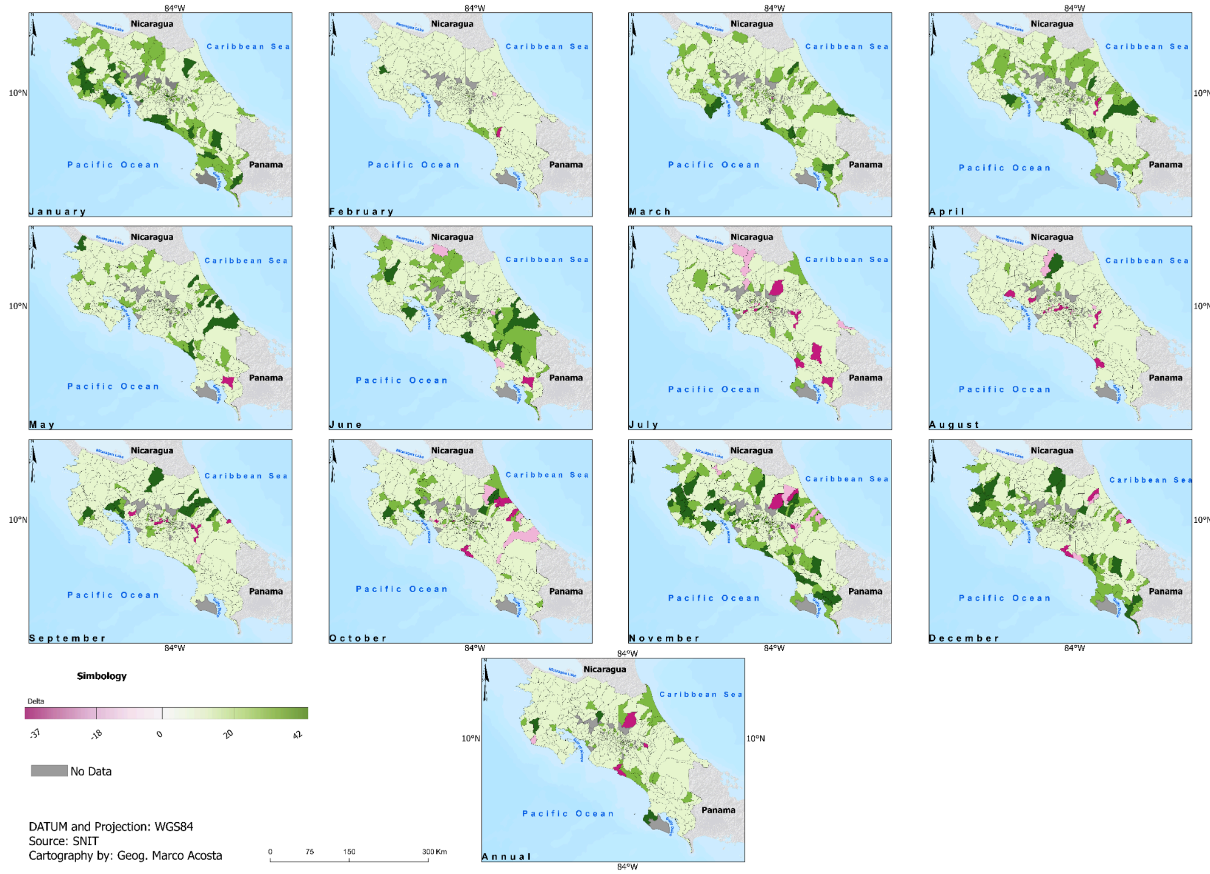

Fig. 7. Future (2035-2065) minus historical scenario (1985-2015) in dengue counts.

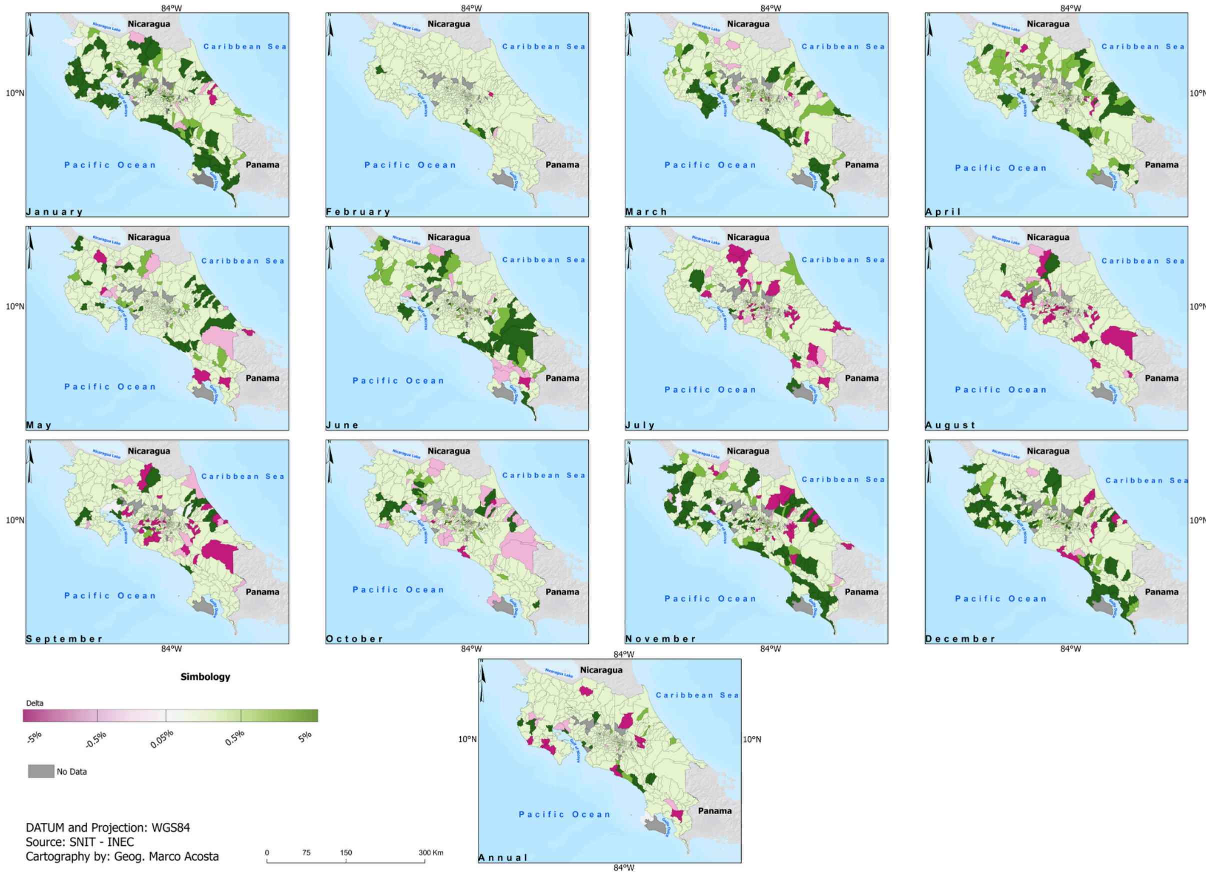

Fig. 8 Same as 7, but for change divided by the 2022 population of each district (%).