ABSTRACT

Predicting an infectious disease can help reduce its impact by advising public health interventions and personal preventive measures. Novel data streams, such as Internet and social media data, have recently been reported to benefit infectious disease prediction. However, few efforts have quantitatively assessed the predictive benefit of novel data streams in comparison to more traditional data sources, especially at fine spatiotemporal resolutions. As a case study of dengue in Brazil, we have combined multiple traditional and non-traditional, heterogeneous data streams (satellite imagery, Internet, weather, and clinical surveillance data) across its 27 states on a weekly basis over seven years. For each state, we nowcast dengue based on several time series models, which vary in complexity and inclusion of exogenous data (seasonal autoregressive integrated moving average, vector autoregression, seasonal trend decomposition based on locally estimated scatterplot smoothing, and their variants). The top-performing model varies by state, motivating our consideration of ensemble approaches to automatically combine these models for better outcomes at the state level. For a trimmed mean ensemble approach, 25 states achieve Pearson correlation coefficients (between fitted and observed values in the 2015-16 testing window) exceeding 80%; meanwhile, the median value over the 27 states is 91.75%, and the maximum is 96.44%. Associated 95% prediction intervals reach approximately 96% empirical coverage or more for half the states. Model comparisons suggest that predictions often improve with the addition of exogenous data, although similar performance can be attained by including only one exogenous data stream (either weather data or the novel satellite data) rather than combining all of them. Among the Brazilian states, the model performance is spatially autocorrelated and associated with measures involving education, employment, and population. Our results demonstrate that Brazil can be nowcasted at the state level with high accuracy and confidence, inform the utility of each individual data stream, and reveal potential geographic contributors to predictive performance. Our work can be extended to other spatial levels of Brazil, vector-borne diseases, and countries, so that the spread of infectious disease can be more effectively curbed.

Introduction

In the past 15 years, dengue hemorrhagic fever and classic dengue have increased in many Latin American countries, including Brazil\(^1,2\). In addition to higher morbidity and mortality of dengue, the transmission pattern has changed from long intervals to annual outbreaks in multiple locations and persistent co-circulation of several serotypes\(^1-4\). Understanding and accurately predicting dengue can improve mitigation efforts as well as inform modeling approaches for newly emergent mosquito-borne diseases. With over one million cases some years, Brazil as a country suffers among the highest numbers of dengue epidemics in the world\(^5\). Despite its substantial global burden, dengue has received less attention than some other diseases (e.g., the flu).
within the modeling community. We aim to address this gap by combining disparate data streams to nowcast dengue in Brazil at the state level.

Advances in computing, remote sensing, and modeling have enabled the creation and analysis of big data for public health applications. In particular, novel approaches have been developed that combine non-traditional, heterogeneous data streams with clinical surveillance data. For example, several epidemiological studies have assessed the impact of climatic factors, Internet, and remote sensing data for monitoring and forecasting disease. To address challenges associated with novel data streams for disease surveillance, Althouse et al. have promoted a three-step system in a recent survey: “(1) Quantitatively define the surveillance objective(s); (2) build the surveillance systems and model(s) by adding data (existing and novel) in until there is no additional improvement in model performance to achieve stated objectives, assessed by (3) performing rigorous validation and testing.” For (2), few studies have studied the relative contribution of each data stream when predicting disease; additionally, “performance can be over-stated” when comparing models with novel data streams to “trivial instances of traditional models.” Meanwhile, a number of studies have failed to satisfy (3), raising concerns about “over-fitting” and inflated predictive performance.

Our main contributions are as follows. 1) We combine traditional and nontraditional data sources (including remote sensing, Internet, climatological, and clinical surveillance data), which together have rarely been used for disease modeling and never for dengue modeling in Brazil. 2) For each of the 27 states in Brazil, weekly dengue is nowcasted over a six to seven year period; few disease modeling studies involving disparate data streams have attempted to model an entire country simultaneously at the state level. 3) For this task, we consider a selection of statistical models for time series: nontrivial baselines containing only past dengue case counts (seasonal autoregressive integrated moving average (SARIMA) and seasonal trend decomposition based on LOESS), variants of SARIMA that contain transformed and dimension-reduced variables from the diverse data streams, and a multivariate vector autoregressive model including transformed and dimension-reduced data. To automatically combine nowcasts, ensemble methods are also explored. 4) We compare cross-validated model performance for 2015-16 along several metrics (root mean square error (RMSE), relative RMSE, Pearson correlation, mean absolute error (MAE), and relative MAE); cross-validation mirrors practical nowcasting by training with data that would be available at that time. 5) We refit our models for subsets of data to quantitatively assess the benefit of each individual data stream versus their combination. Overall, we produce an accurate nowcasting system at the state level of Brazil and establish a spatiotemporal framework that does not assume one model for the entire nation. Beyond dengue in Brazil, we followed the standards outlined by Althouse et al. by empirically demonstrating how nowcasting is affected by model, space, and inclusion of certain data streams.

Dengue & mosquito-borne disease modeling
Recently, mathematical, statistical, climate-driven, and computational models have been used to understand, simulate, and predict infectious diseases, particularly vector-borne diseases. In our study, we consider models of dengue from statistics and machine learning, so we briefly summarize trends among similar works. Often, dengue has been modeled with traditional distributions for count data from statistics. For example, Quasi-Poisson and negative binomial distributions have been applied because they account for over-dispersion in count data. In other cases, dengue has been modeled as a continuous quantitative variable or a categorical risk level (e.g., high risk vs. low risk). Many studies have utilized methods not adapted to time series data (e.g., linear regression), while others have explicitly accounted for temporal dependency through time series models (e.g., autoregressive). Traditional models from statistics have been explored (e.g., linear regression, generalized linear models, and SARIMA), while methods from statistical and machine learning have also been deployed in recent years (e.g., tree-based methods, support vector machines, rule-based learning, and least absolute shrinkage and selection operator (LASSO) regression). For prediction, various performance metrics have been reported, including correlation-based measures (e.g., coefficient of determination $R^2$ and correlation coefficient $R$) and error estimates (e.g., root mean square error (RMSE) and relative RMSE, root mean squared percentage error, mean absolute percentage error (MAPE), and mean absolute error (MAE) and relative MAE). For classification, performance metrics include classification accuracy, sensitivity, specificity, and area under the curve. Lowe et al. have highlighted several issues in dengue prediction studies, including a lack of proper validation; indeed, Althouse et al. have confirmed that only 41% of selected papers on novel data streams contained any form of validation. Cross-validation or out-of-sample testing are essential for estimating true predictive performance and, hence, establishing the utility of a model.

Internet data streams for disease applications
A number of studies have analyzed the potential use of Internet data streams, such as Twitter, Google, and Wikipedia, to inform disease surveillance, since people use the Internet to search and share health-related information. For example, before visiting a doctor’s office, people experiencing fevers, headaches, and other symptoms might search “dengue symptoms” on Google, and tracing these searches could provide an early warning of an outbreak. Comprehensive surveys have been written, but here we highlight some studies focusing on dengue, particularly those in Brazil or using similar methods.
Althouse et al. analyzed Google search terms and dengue incidence data from Singapore and Bangkok and concluded that Google search terms helped predict dengue with high accuracy (out-of-sample $R^2$ up to 0.948). Chan et al. used Google search query volume for dengue-related queries in Brazil, among other countries; for the national level of Brazil, they reported an extremely high correlation coefficient of $R = 0.99$ in a holdout set. Gomide et al. identified a strong correlation of 0.9578 between tweets from Twitter and dengue incidence data in Singapore and Bangkok, although there was no cross-validation or out-of-sample validation. Generous et al. used Wikipedia access logs and clinical surveillance data to monitor and forecast dengue in Brazil and Thailand; while they reported an $R^2$ value of 0.85 for the nation of Brazil, their work included no cross-validation or out-of-sample validation. De Almeida et al. nowcasted and forecasted dengue in Brazil at the national and city level using weekly forecasts within 3-64 weeks; at the national level, they reported adjusted $R^2$ ranging from 0.94 (for nowcasting) to 0.87 (for forecasting up to 8 weeks in advance). Guo et al. have nowcasted and forecasted dengue within cities of a province of China based on Baidu search queries, as well as climate-related variables; support vector regression achieved a correlation coefficient of up to 0.999 in a 12 week forecast window. Yang et al. predicted dengue at the national level of Brazil, among other countries; they reported $R = 0.971$ in the recursive prediction window and demonstrated that inclusion of Google data improved model performance. Finally, Infodengue continually combines Twitter data with climate and case count data to nowcast dengue in 788 cities across Brazil and reports the information online (https://info.dengue.mat.br). In addition to the lack of validation in several studies and focus on the national level in most studies, few consider the contribution of Internet data to dengue prediction when past dengue count is already included in the model. In some countries, dengue clinical case data is limited, so surveillance efforts based only on Internet data are valuable. However, in Brazil, we assume good availability of clinical case data (up to a two week lag in reporting), so we believe the utility of Internet data should be judged against models already containing case data. With the exception of two studies, none of the selected studies on dengue in Brazil compare the performance of models containing Internet data to models already containing lagged case data. Similarly to Hii et al., we develop models under the fundamental time series assumption that past behavior is the greatest influence of future behavior. All our models contain past dengue cases and are quantitatively compared to models separately adding each exogenous data stream (out of Google Health Trends, satellite, and climatological/weather) then combining all data streams.

**Satellite imagery for disease applications**

Traditional epidemiology can benefit from collection and analysis of satellite imagery, since environmental factors influencing health can be identified remotely. Due to the difficulty of obtaining mosquito count data across time and space, satellite data have been used as proxies of mosquito habitat suitability and mosquito density, especially in studies of dengue, malaria, West Nile virus, and Rift Valley Fever. For example, mosquitoes primarily subsist on vegetation, so the normalized difference vegetation index (NDVI), a satellite-derived measure of live green vegetation, can signal good mosquito habitats and high mosquito counts. We summarize several studies of dengue that are similar in scope to ours and note that dengue surveillance studies involving satellite data are limited (compared to studies exploiting weather and Internet data streams). Laureano et al. have measured sea surface temperature (SST), temperature, precipitation, and humidity variables, which account for 42% of variation in dengue cases in a Mexican state. For an area of Costa Rica, Troyo et al. have collected low, medium, and high resolution satellite imagery and explored potential relationships between NDVI, urban structural variables, and dengue cases. Buczak et al. have included measures of temperature, rainfall, altitude, NDVI, EVI, southern oscillation index, and sea surface temperature anomaly (SSTA), as well as demographic and political stability data to forecast dengue (as binary risk) for six districts in Peru; one classifier could detect outbreaks with 58.3% accuracy and non-outbreaks with 96.1% accuracy. A commonality of the selected studies is the small considered geographic scale: one state, one area, and six districts in a province. In contrast, we have collected every Landsat and Sentinel image over Brazil across seven years, derived weekly local-level indicators of vegetation, water, cloud cover, and burned areas, and then aggregated by over 5000 municipalities. Our data covers the approximate 3.3 million square miles of Brazil, the fifth largest country in the world by area. Hence, the satellite data alone are over 13 terabytes, and the processed indices include over 32 million entries over the seven-year period across over four satellites for Brazil. Additionally, with the exception of Buczak et al., the discussed studies only explore potential relationships among satellite data and dengue, rather than reporting validated predictive results. We compare cross-validated nowcasting results for various statistical models and empirically assess the contribution of each data stream to prediction.

**Weather data streams for disease applications**

“Health and climate have been linked since antiquity,” and infectious disease modeling has investigated this connection in countless studies. For dengue modeling in particular, no exogenous variables have been explored as extensively as weather, due to the effects temperature, precipitation, and related variables have on mosquito habitat and life cycles. For example, three of the four mosquito life stages occur in stagnant water, so relatively high precipitation can often correspond to a large presence and count of mosquitoes. There are several studies of dengue prediction using weather variables, and the interested reader...
may refer to Viana et al. for a systematic review and to the World Health Organization for recent guidelines. Here, we describe a selection of studies aligning most closely with our goals. Hii et al. included mean temperature and rainfall, as well as past dengue cases, in a model to predict dengue in Singapore; they reported training $R^2$ of 0.84, as well as good ability to classify outbreaks in the testing set. Lowe et al. forecasted dengue in Brazil based on temperature and precipitation data, plus population density, altitude, and past dengue relative risk, in a spatiotemporal hierarchical Bayesian model; three-month-ahead forecasts for June, 2014 achieved a hit rate of 57%. As previously mentioned, Buczak et al. combined temperature and weather variables with demographic, political, and other environmental variables to forecast dengue in Peru using rule-based learning. Shi et al. forecasted dengue in Singapore based on temperature and humidity, in addition to past dengue case counts and demographic information, and reported mean absolute percentage error (MAPE) ranging from 17% (for one week forecasts) to 24% (for three month forecasts). As referenced previously, Guo et al. combined weather data (mean temperature, relative humidity and rainfall) with Internet data to nowcast and forecast dengue in the Chinese province Guangdong.

While traditional dengue surveillance and these selected studies indicate the importance of weather variables, few studies have quantified the combined contribution of weather data with novel data streams. In our study, we integrate the novel Google Health Trends and satellite data streams with the weather data (summary statistics of temperature, relative humidity, and daily temperature range) to nowcast dengue for all 27 states of Brazil. We quantify the contribution of each individual data stream by refitting our statistical models with subsets of the data and comparing the cross-validated performance across model and data subset. However, unlike Buczak et al., we do not use time series relating to political stability and demographics, since only 2010 yearly census data are available for Brazil.

**Results**

**Model Comparison**

Literature review and an exploratory analysis (Figures 8, 9, 10, 11, and 12) reveal spatial and temporal variation in each of the variables from diverse data streams (out of dengue clinical case count, Google Health Trends, satellite, and weather data). Such spatiotemporal heterogeneity through 2010-16 in Brazil has motivated consideration of several time series models, varying in complexity and inclusion of certain variables: seasonal autoregressive integrated moving average (SARIMA), SARIMAX with variables transformed through principal component analysis (PCA), SARIMAX with variables transformed through partial least squares (PLS), multiplicative and additive seasonal trend decomposition based on LOESS (STL), and vector autoregression (VAR) with variables transformed through PCA. We believe SARIMA, SARIMAX, STL, and VAR represent a reasonable selection of well-established time series models from statistics: SARIMA and STL contain only past dengue cases, while SARIMAX and VAR additionally contain the exogenous data streams, so we can fairly test the contribution of integrated Internet, satellite, and weather data for dengue nowcasting. For each state, each of these models is fit in the training weeks (2010-14) and recursively nowcasted for the testing weeks (2015-16). Our approach mirrors practical nowcasting, by accounting for the potential two week lag in dengue case reporting and utilizing an expanding training window. For real-time implementation, we need an automated method to generate good nowcasts for each state. To address this need, we explore ensemble approaches that combine the nowcasts: the first approach computes the trimmed mean, while the second approach calculates a weighted mean, where weights are chosen to be proportional to least absolute error in the training set.

The relative mean absolute error (RMAE) of these methods (the six individual models plus two ensembles) is compared in Figures 1 and 2, while numeric summaries for several performance metrics are presented in Table 1. Each metric is computed within the testing set. Figure 1 demonstrates that the “best” model often varies by state, reinforcing the spatial heterogeneity of Brazil and the importance of separately modeling each state. Generally, the ensembles outperform the individual models, while the individual models SARIMA and SARIMAX (with PCA or PLS) outperform STL (additive or multiplicative) and VAR. For the RMAE performance metric, the ensembles yield optimum results in 15 states, while the individual models reach minimum error in 12 states. Of the individual models, SARIMAX (with PCA or PLS) attains minimum RMAE in seven states, while SARIMA, STL, and VAR are optimal for RMAE in only five states. Altogether, the models containing only past dengue count as a regressor reach minimal RMAE in only four states of the 27. These results indicate that the inclusion of exogenous data streams often improves dengue prediction, compared to when only past dengue counts are included in the model. The ensembles are shown to be helpful for improving average performance, e.g., the mean, median, and standard deviation of RMAE over the states are lowest for the ensembles. Similarly, the ensembles prevent bad nowcasts from occurring in a state, e.g., the maximum RMAE is lower for the ensembles than the individual models. In no cases have the ensembles produced the worst nowcasts; i.e., for each state and performance metric (out of MAE, RMAE, R, RMSE, and RRMSE), the highest error (or lowest R) are suffered by the individual models. For the trimmed mean ensemble method, Pearson correlations (between observed and predicted values in testing) are high, ranging from 0.733 to 0.964 with a median value of 0.918. We conclude that dengue can be accurately nowcasted for each state of Brazil, dengue prediction generally benefits from the inclusion of exogenous data streams, and nowcast performance can be improved by automatically combining models for each state through ensemble approaches.
Figure 1. Heatmap of relative mean absolute error (RMAE) by model and state. Among six statistical models of dengue and two ensembles to combine the models, we compare testing RMAE from recursive nowcasts in each Brazilian state. For a fixed state, the displayed RMAE is standardized among the methods: dark purple corresponds to higher standardized RMAE (worse methods), while dark green colors indicate lower standardized RMAE (better methods).

Nowcast Results for Trimmed Mean Ensemble Approach

Additional visualizations and performance metrics are provided for the trimmed mean ensemble approach, because of its relevance to practical nowcasting and generally good performance. As displayed in Figure 3, the observed and nowcasted dengue counts for the testing weeks (2015-16) are very close for the selected states (results for all states are included as supplementary materials). In many cases, the observed dengue count is captured within the 95% prediction interval; empirical coverage for each state ranges from 81% to 100%, and the median and mean empirical coverage are approximately 96.3% and 95.3%, respectively. Our strong results show that dengue within a state can be nowcasted with high accuracy and confidence.

For improved application to public health decision-making, we assign the nowcasted dengue counts to risk categories. The National Dengue Control Programme of the Brazilian Ministry of Health defines low risk as less than 100, medium risk as between 100 and 300, and high risk as greater than 300 cases per 100,000 people in a year\(^71\). According to this definition, we convert the observed and nowcasted dengue case counts for each Brazilian state in 2015 to low, medium, or high risk (we do not consider 2016 here, since the dengue case counts are unavailable for the full year). Figure 4 compares the observed versus predicted dengue risk and shows that all states’ risk levels are correctly classified, further validating the performance of our approach.

Figure 5 demonstrates that RMAE varies across the states; e.g., the states RS, SC, MA, RN, PB, PE, and SE have suffered the highest error, while the states AC, AM, RR, PA, and MS have achieved the lowest error. While the spatial autocorrelation of RMAE among adjacent states is relatively low (Moran’s\(^72\) \(I = 0.21\)), it is statistically significant with a \(p\)-value of 0.03 (from a Monte Carlo test assuming randomly distributed RMAE across Brazilian states). Regression analyses in Figure 6 reveal relationships among the states’ RMAE, features of the dengue case count time series, and census variables relating to education, employment, health, and population. For each potential explanatory variable, we consider both its unlogged and natural logged form and report the strongest correlation of the two. For qualities of time series that could impact prediction, we examine sum of observations and define a measure of volatility. The sum and the volatility are respectively expressed as

\[
\sum_{i=1}^{n} y_i \quad \text{and} \quad \frac{\sum_{i=1}^{n} |y_i - y_{i-1}|}{n \sum_{i=1}^{n} y_i},
\]

where \(y_i\) is the observed dengue case count for a state and \(n = 342\) is the number of observations from 2010 to 2016. RMAE is most strongly correlated with the volatility \((R = 0.794)\), followed by the logged sum of case counts \((R = -0.788)\). State error tends to increase as volatility of the case counts increases, which could be due to noise obscuring the underlying signal.
1) SARIMA 2) SARIMAX − PCA 3) SARIMAX − PLS 4) STL − add. 5) STL − mult. 6) VAR − PCA 7) Ensemble − mean 8) Ensemble − w. mean

Figure 2. Side-by-side boxplots of relative mean absolute error (RMAE) by model. Over the 27 Brazilian states, we compare the testing RMAE among six individual models of dengue and two ensemble methods that combine the individual models.

Meanwhile, high error generally corresponds with low sums of case counts, suggesting that some states might suffer from small sample size issues. However, population size is not a strong predictor of volatility, sum of case counts, or RMAE ($R = -0.35$). The census variables explaining the most variation in state RMAE are logged percentage of adults who are self-employed, logged unemployment rate among the population aged 15 to 17 years, logged rate of school attendance among the population aged 25-29 years, logged survival probability up to age 40, and logged urban population size. Many census variables have nonobvious regression effects on RMAE. For example, we would generally expect a high unemployment rate in a state to contribute to higher error, due to potentially worse health infrastructure and access. In contrast, a high unemployment rate among minors might have the opposite effect, since unemployed minors might enjoy greater educational and wealth privileges that positively correlate with health infrastructure and access. Indeed, this latter interpretation is suggested by the negative correlation between RMAE and unemployment rate among 15-17-year-olds. Evidently, employment, education, health, urban population size, and qualities of the dengue case time series itself might affect nowcast performance in complex ways.

Assessing Utility of Individual Data Streams

We empirically assess the benefit of each individual data stream to dengue nowcasting in Brazil, by refitting several statistical models with three subsets of data: 1) past case counts and Google Health Trends variables, 2) past case counts and satellite variables, and 3) past case counts and weather variables. The resulting error from each subset and model can help quantify the utility of each exogenous data stream (out of Google, weather, and satellite), when past dengue case counts are already included in the model. We consider SARIMAX with PCA, SARIMAX with PLS, and VAR with PCA (i.e., all the models able to incorporate such data) and nowcast dengue following the same protocol as above, where the only distinction is which data streams are included.

Figure 7 displays the RMAE for each considered model paired with individual data stream, as well as previous results from combining data streams. For the SARIMAX models (with PCA or PLS), the distribution of RMAE is very close for all data streams. For the VAR model, the satellite and weather data streams yield performance similar to the combination of data streams, while the Google data suffer visibly higher RMAE and two severe outliers.

Next, we compare the models using individual data streams (SARIMAX and VAR) to models using no exogenous data (STL and SARIMA) and models combining the exogenous data (SARIMAX, VAR, and the ensembles). For 13 out of 27 states, minimum RMAE is attained when combining the exogenous data streams; for 9 of these 13 states, the “best” model
Figure 3. Observed vs. nowcasted dengue by Brazilian state from trimmed mean ensemble approach. Time series of dengue are displayed for a selection of Brazilian states. The vertical dashed line marks the boundary between training and testing weeks. The black time series corresponds to observed dengue in the training weeks (years 2010-14). The blue and red lines correspond to predicted and observed dengue, respectively, within the testing weeks (years 2015-16), while the gray shadings are the associated 95% prediction intervals.
We have integrated various traditional and novel data streams, including clinical case, weather, Google Health Trends, and satellite data. The model attaining minimum RMAE varies across the states, which has supported our decision to model at the state level versus other models confirm that the exogenous data sources (out of Google, weather, and satellite) offer additional information beyond past dengue case count. However, we have found that similar nowcast performance can be attained by using only one of the data sources (especially satellite or weather) in a model, rather than combining all three. This finding reflects the general yet practical, real-time nowcasting render our ensemble approach particularly promising. Performance comparison of the baselines containing only past dengue cases (SARIMA, multiplicative STL, and additive STL), two extensions of SARIMA using past dengue cases and transformed, dimension-reduced exogenous data (SARIMAX with PCA and SARIMAX with PLS), and a multivariate model of past dengue cases and transformed, dimension-reduced exogenous data (SARIMAX - PLS), and a multivariate model of past dengue cases and transformed, dimension-reduced exogenous data (V AR with PCA). The model attaining minimum RMAE varies across the states, which has supported our decision to model at the state level and motivated methods to automatically generate good nowcasts for each state. For the latter, we have explored ensemble approaches from statistical and machine learning. For each state, we have fit six individual time series models: several good baselines containing only past dengue cases (SARIMA, multiplicative STL, and additive STL), two extensions of SARIMA using past dengue cases and transformed, dimension-reduced exogenous data (SARIMAX with PCA and SARIMAX with PLS), and a multivariate model of past dengue cases and transformed, dimension-reduced exogenous data (V AR with PCA). The model attaining minimum RMAE varies across the states, which has supported our decision to model at the state level and motivated methods to automatically generate good nowcasts for each state. For the latter, we have explored ensemble approaches from statistical and machine learning, including a trimmed and weighted mean of the individual model nowcasts. The median Pearson correlation coefficient (between observed and nowcasted values) over the states for the trimmed mean ensemble is 0.918. Meanwhile, the corresponding 95% prediction intervals reached approximately a mean empirical coverage of 95% over the states. The low error of point estimates, the excellent coverage of prediction intervals, and the application to practical, real-time nowcasting render our ensemble approach particularly promising. Performance comparison of the baselines versus other models confirm that the exogenous data sources (out of Google, weather, and satellite) offer additional information beyond past dengue case count. However, we have found that similar nowcast performance can be attained by using only one of the data sources (especially satellite or weather) in a model, rather than combining all three. This finding reflects the general yet counterintuitive fact that more data does not guarantee more accuracy. Regardless, our integration of these big, heterogenous data has generated very accurate nowcasts, which reach up to a 97% Pearson correlation with observed dengue count in testing and enable 100% classification accuracy of state risk level in 2015.

Through definition of several well-established performance metrics (RMSE, RRMSE, Pearson correlation coefficient R, MAE, and RMAE), empirical comparison of nontrivial models containing various subsets of data streams, and rigorous cross-validation that simulates practical nowcasting of dengue in Brazil, we believe we have met the standards outlined by Althouse et al. for integrating novel data streams into disease surveillance systems. We have established a flexible spatiotemporal framework for predicting dengue in Brazil that does not impose the assumption of a uniform model across space. Few studies have combined four or more data sources to predict disease across an entire nation at the state level or finer, and our work demonstrates that such modeling efforts are capable of obtaining strong predictive results. Further improvements are possible.
Figure 4. Observed vs. nowcasted dengue risk in Brazilian states for the trimmed mean ensemble approach.

Observed dengue risk and nowcasted dengue risk are displayed for the 2015 testing year in Brazil. In each state, low risk, medium risk, and high risk are respectively defined from the Brazilian Ministry of Health as under 100, between 100 and 300, and more than 300 cases per 100,000 people per year. All 27 states are correctly classified.

particularly through dimension reduction techniques tailored to time series data, direct multi-step forecasting, and the addition of more diverse models in the ensemble. Our next steps will involve extending our nowcasting system to forecasting at increased lead times and performing systematic comparison by model, lead time, and inclusion of certain data streams. Additionally, our methodology will be applied to the remaining spatial levels of Brazil, e.g., mesoregion, microregion, and municipality, to investigate how performance is affected by spatial granularity. Finally, methodology and results can be generalized to similar countries and mosquito-borne viruses.

Methods

In the Data section, we describe our data’s source, its aggregation, and its exploratory analysis. The data exhibit strong seasonality, autocorrelation, spatial heterogeneity, and high-dimensionality, motivating our predictive modeling approach. In the Predictive Modeling Approach section, we discuss cross-validation, dimension reduction, and our spatiotemporal modeling framework. In the Individual Predictive Models section, we explain the considered time series models of dengue in Brazil. Finally, the Combining Predictive Models section details ensemble methods to automatically generate good nowcasts for each state.

Data

Over the seven year period from January 3, 2010 to July 17, 2016, we use as data streams multispectral satellite imagery, climatological data, and Google Health Trends to describe and predict clinical surveillance data of dengue count in Brazil. All data streams have been aggregated to the state level and weekly time unit for modeling, which results in up to 115 time series variables over 342 weeks for each state. When aggregating, we consider several summary statistics (minimum, mean, maximum, and standard deviation), as a compromise between retaining valuable statistical information and limiting the data’s dimension.

Satellite Imagery

For each municipality from 2010 to 2016, we have collected data via the Descartes Labs platform from four satellites (Sentinel-2 and Landsats 5, 7, 8) that imaged the full municipality each day. Various indices related to mosquito habitat (e.g., normalized burn ratio) are computed at the 10-30 meter resolution. To aggregate the daily values to weekly values, we compute over the seven days of each week several summary statistics: minimum, mean, and maximum. Next, these weekly variables, collected from the municipality level, are aggregated to the state level. For each state, summary statistics (minimum, mean, maximum,
Figure 5. Relative mean absolute error (RMAE) over the Brazilian states from the trimmed mean ensemble approach. Among the 27 Brazilian states, we compare the testing RMAE, where map breaks are chosen as quartiles. There is a low but statistically significant spatial autocorrelation in the states’ error.

and standard deviation) of each weekly satellite variable are computed over the municipalities. This results in a total of 52 satellite variables per state, summarized in Table 2. For example, for the state of Minas Gerais (MG), the minimum, mean, maximum, and standard deviation of the mean NDVI variable are calculated over its 853 municipalities.

For each state, the variables resulting from the mean summary statistic (over municipality) are plotted in Figure 8. The satellite variables tend to reach more extreme values during the years 2010 to 2013, as compared to 2014-6; e.g., in Roraima (RR), the variables Minimum Green NDWI, Minimum NBR, Minimum NDVI, Minimum SWIR, and Mean Green NDWI reach lower values in 2010-13 (than in 2014-16), while the remaining variables achieve higher values in 2010-13 (than in 2014-16). Meanwhile, differences can be observed in the satellite variables between states. For example, the Mean NBR variable has exhibited approximately no changes over time (zero variance) in all shown states, except for RR, RJ, SC, and DF. Additionally, the Minimum SWIR NDWI variable reaches lower values in RR and PA than the other shown states. Such spatiotemporal distinctions between states’ satellite variables may correspond to spatiotemporal differences in mosquito habitat, motivating our decision to model each state’s dengue count with these satellite time series variables.

Climatological Data
We have collected data from weather stations via the “Global Surface Summary of the Day” (GSOD) dataset from the National Oceanic and Atmospheric Administration (NOAA). There are 613 weather stations across Brazil that provide daily climatological data. We select a subset of measures associated with dengue, including summary statistics of temperature and humidity. Since there are 5564 municipalities in Brazil (as of 2010), many localities are not covered by these stations. To address this limitation, we have used kriging methods to interpolate the values across the entire nation. After kriging, we calculate an additional weather variable, daily range in temperature. To aggregate the daily data to the weekly unit, we compute summary statistics (minimum, mean, and maximum) of each value over the seven days. Similar to the satellite variables, the weekly weather variables are then aggregated to the state level by computing summary statistics (minimum, mean, maximum, and standard deviation) over the municipalities. This results in a total of 40 weather variables for each state.

For each state, the weather variables corresponding to the mean summary statistic (over the municipalities) are plotted from 2010-16 in Figure 9. As expected, these variables are strongly periodic, peaking at approximately the same time each year. However, there are notable differences between states in terms of volatility and the amplitude of seasonality. For example, the
Figure 6. Correlating relative mean absolute error (RMAE) with variables across the Brazilian states. We use census variables and features of the dengue case count time series (volatility and logged sum of case counts) to predict state RMAE through simple linear regression models. For each explanatory variable, the corresponding fitted line, observed points, and Pearson correlation coefficient $R$ are displayed.
Figure 7. Quantifying the contribution of individual data streams vs. combination of data streams. Relative mean absolute error (RMAE) across the states is compared for models containing subsets of data streams, e.g., the boxplots marked with “Google” correspond to models fit using the Google Health trends data and past case counts, while boxplots marked with “All” correspond to models fit using all exogenous data streams (Google, weather, and satellite) and past case counts.
| Category       | Source                  | Variables                                                                 |
|---------------|-------------------------|---------------------------------------------------------------------------|
| Satellite     | Descartes Labs          | Normalized Difference Vegetation Index (NDVI)                             |
|               |                         | - Minimum, mean, and maximum (over 7 days)                                |
|               |                         | - Minimum, mean, maximum, and standard deviation (over municipalities)     |
|               |                         | Green Normalized Difference Water Index (NDWI)                            |
|               |                         | - Minimum, mean, and maximum (over 7 days)                                |
|               |                         | - Minimum, mean, maximum, and standard deviation (over municipalities)     |
|               |                         | SWIR Normalized Difference Water Index (NDWI)                             |
|               |                         | - Minimum, mean, and maximum (over 7 days)                                |
|               |                         | - Minimum, mean, maximum, and standard deviation (over municipalities)     |
|               |                         | SWIR Normalized Burn Ratio (NBR)                                          |
|               |                         | - Minimum, mean, and maximum (over 7 days)                                |
|               |                         | - Minimum, mean, maximum, and standard deviation (over municipalities)     |
|               |                         | SWIR Proportion of Cloudy Pixels                                          |
|               |                         | - Minimum, mean, and maximum (over 7 days)                                |
|               |                         | - Minimum, mean, maximum, and standard deviation (over municipalities)     |
| Weather       | NOAA GSOD73             | Temperature                                                                |
|               |                         | - Minimum, mean, and maximum (over 7 days)                                |
|               |                         | - Minimum, mean, maximum, and standard deviation (over municipalities)     |
|               |                         | Relative humidity                                                          |
|               |                         | - Minimum, mean, and maximum (over 7 days)                                |
|               |                         | - Minimum, mean, maximum, and standard deviation (over municipalities)     |
|               |                         | Daily Range in Temperature                                                 |
|               |                         | - Minimum, mean, and maximum (over 7 days)                                |
|               |                         | - Minimum, mean, maximum, and standard deviation (over municipalities)     |
| Google        | Google Trends74         | “aedes”                                                                    |
|               |                         | “aedes aegypti”, “aedes egípcio”, “aegypti”, “egípcio”                    |
|               |                         | “dengue”                                                                  |
|               |                         | “dengue virus”, “dengue é vírus”, “dengue fever”, “dengue hemorrhagic fever”, “dengue sintomas”, “DENV”, “DHF” |
|               |                         | “mosquito”                                                                 |
|               |                         | “mosquito dengue”, “mosquitoes”, “novo vírus da dengue”, “sintomas da dengue, vírus da dengue” |
| Clinical Dengue Cases | Brazilian Ministry of Health71 | Count of confirmed dengue cases |

Table 2. Summary of data streams for modeling dengue in each Brazilian state.

states RJ, SP, SC, RS, and DF are the most volatile here, and PA is the least. DF tends to exhibit a higher seasonal amplitude in its variables (reflecting more extreme seasonal changes in weather), while states like RR have lower seasonal amplitudes. Such spatial differences reinforce the importance of modeling at the state, rather than the national level. Meanwhile, the prominent seasonality of these variables inspire consideration of time series methods that can handle such data, e.g., seasonal differencing or seasonal trend decomposition based on LOESS (STL).

**Google Search Trends**

We have collected weekly data from Google Health Trends, since Google is the most widely used search engine and has a 97% market share in Brazil75. Google provides de-identified, normalized, region-specific trends in search activity via the Google Trends website74. At the country and state levels of Brazil from January 2011 to June 2017, we have obtained data for 19 dengue-related keywords (listed in Table 2), including Portuguese and English terms for “dengue”, “mosquito,” and “aedes aegypti,” the primary vector of dengue1.

In Figure 10, the values of the Google variables are shown for a selection of states over the years 2010-16 (DF has Google data unavailable prior to 2014). For most displayed variables, there are seasonal spikes approximately coinciding with dengue season. However, the variables differ substantially across space and time. For many states, the variables are more volatile in 2010-11 than in 2012-16, and SE features gaps in 2010-11. The state RR exhibits very high noise in its Google variables, compared to the more periodic seasonal patterns formed in the other states. Among most states (PA, BA, RJ, SC, RS, and DF),
Figure 8. Satellite variables in each Brazilian state. For a selection of Brazilian states, satellite variables are plotted from 2010 to 2016. (Variables with approximately zero variance in all states are omitted.) Plots for the remaining 18 states are included as supplementary materials.

a prominent global maximum is attained in 2016, while SP peaks in 2015 (but also attains a very high local maximum in 2016), and SE peaks in 2010-11. Perhaps most notably, the most common Google search keywords differ substantially by state. Searches for “dengue fever” are the most common in PA, BA, and SC; searches for “dengue”, “sintomas da dengue”, “mosquito”, and “dengue hemorrhagic fever” are dominant in RJ, SP, RS, and DF; and searches for “DHF” are popular in RR and SE. Among the considered exogenous data streams (out of Google, satellite, and weather), the Google variables feature the greatest distinctions temporally and spatially.

Dengue Case Data
The Brazilian Ministry of Health for Dengue provided the epidemiological dengue data from January 3, 2010 to July 17, 2016. This dataset contains newly diagnosed cases per epidemiological week for each of the 5564 municipalities. In Brazil, dengue case investigation forms include information on basic demographic data, dates of symptom onset and sample collection, case classification (dengue fever, DHF, DSS, or discarded case), and outcome. Individual data are locally entered into Brazil’s National Reportable Disease Information System (SINAN) and subsequently transmitted to state and national levels. These data are considered “gold standard” for mosquito-borne disease reporting, covering both time and space in Brazil. However, like most disease surveillance data, they are subject to underreporting; SINAN contains only about half the cases reported to the National Unified Health System (SUS).

The dengue cases are summarized spatially and temporally in Figures 11 and 12, respectively. Figure 11 maps the total
Figure 9. Weather variables in each Brazilian state. For a selection of Brazilian states, weather variables are plotted from 2010 to 2016. (Variables with approximately zero variance in all states are omitted.) Plots for the remaining 18 states are included as supplementary materials.

number of dengue cases per person for each state, where population estimates are obtained from the 2010 Brazilian state census data. Among the states, cases range from approximately 0.0923% to 13.2% of the population, with states in the Center-West (DF, GO, MS, MT) and Southeast (ES, MG, RJ, SP) regions experiencing the greatest burden. In Figure 12, the number of dengue cases from 2010 to 2015 is displayed for each epidemic week in a state. As expected, these curves generally exhibit symmetric epidemic curves in the June-October months (“dengue season”), peaks around April, decreases until December, and small increases starting April. Surprisingly, this pattern is less pronounced for some states: RR and DF experience peaks as late as September-October, while PA and SE have approximately bimodal structures. There are several potential explanations for these results: 1) some states’ dengue transmission may deviate from the classic dengue epidemic curve, e.g., due to presence of new serotypes or tourism effects; 2) some states’ clinical case data contain reporting biases, e.g., misreporting of chikungunya or Zika cases as dengue; or 3) small states experience greater sampling variation. Regardless, this spatial variation in dengue cases encourages a model-fitting and nowcasting process specific to each state.

Predictive Modeling Approach
Literature review (Introduction) and exploratory analysis (Methods - Data) have suggested the importance of diverse data streams for accurately modeling dengue. Each of the variables in our dataset (out of Google, weather, satellite, and clinical dengue case count) generally feature distinctions across states and time. Meanwhile, obtaining specialized forecasts for each state in Brazil might benefit public health decision-making; by understanding the risks specific to each area, specialists can
Figure 10. Google variables in each Brazilian state. For a selection of Brazilian states, Google Health Trends variables are plotted from 2010 to 2016. (Variables with approximately zero variance in all states are omitted.) Plots for the remaining 18 states are included as supplementary materials.

more effectively tailor resources and policy. Hence, we develop the following spatiotemporal modeling framework: dengue is separately modeled for each of the 27 states and assumed to be affected only by neighboring states. For example, the state of Rio de Janeiro (RJ) can be modeled using satellite, weather, and Google data defined for the state, as well as dengue case counts for the states SP, MG, and ES; forecasts are subsequently generated specific to RJ. Unlike most past work on dengue modeling, we do not assume there is one “best” model across all states and instead allow each state to potentially be modeled differently than others. While spatial interactions between states may be more complex, we believe our framework to be a good balance between model simplicity, nowcast accuracy, and practical application to public health. All predictive modeling is implemented in the statistical programming environment R, and task parallelism (fitting and nowcasting across the 27 states) is performed through the R packages snow and parallel.

Cross-Validation
Due to limited availability of Brazilian case count data, we estimate the predictive performance of our methods within the dataset. Such estimation is prone to optimistic results from model “over-fitting”, i.e. fitting the model to the specific dataset rather than to the underlying data-generating phenomenon. Cross-validation (CV) is essential to provide less biased estimates of model error (or accuracy), so we implement CV through independent training and testing weeks. There are 342 weeks of dengue data total: we assign weeks 1 through 261 to be for training, and weeks 262 through 342 for testing. This approximate 76 : 24 training:testing split of weeks is chosen to ensure at least one full year for testing, while having sufficient training data.
Figure 11. Number of dengue clinical cases per person in each Brazilian state. For each state, the number of dengue clinical cases (from January, 2010 to July, 2016) per person is displayed. Map breaks are chosen as quartiles (five full seasons) to account for high variation in dengue count between years. We choose as metrics the root mean square error (RMSE), relative RMSE (RRMS), Pearson correlation, mean absolute error (MAE), and relative MAE (RMAE), defined here as

\[
\text{RMSE} = \sqrt{\frac{1}{n} \sum_{t=1}^{n} (y_t - \hat{y}_t)^2},
\]

\[
\text{RRMS} = \sqrt{\frac{1}{n} \sum_{t=1}^{n} (y_t - \hat{y}_t)^2} = \frac{\text{RMSE}}{\sqrt{\sum_{t=1}^{n} y_t}},
\]

\[
R = \frac{\sum_{t=1}^{n} (y_t - \bar{y})(\hat{y}_t - \bar{\hat{y}})}{\sqrt{\sum_{t=1}^{n} (y_t - \bar{y})^2} \sqrt{\sum_{t=1}^{n} (\hat{y}_t - \bar{\hat{y}})^2}},
\]

\[
\text{MAE} = \frac{\sum_{t=1}^{n} |y_t - \hat{y}_t|}{n}, \quad \text{and}
\]

\[
\text{RMAE} = \frac{\text{MAE}}{\sum_{t=1}^{n} y_t},
\]

where \(y_t, \hat{y}_t, \bar{y}_t\), and \(\bar{\hat{y}}_t\) are, respectively, observed dengue, predicted dengue, sample mean dengue, and sample mean predicted dengue within a state for week \(t\) out of \(n\) total weeks. The predictive performance must be assessed from the testing set, so we set the summation indices to \(t = 262, \ldots, 342\) when calculating these metrics. RMSE and MAE are some of the most common performance metrics for quantitative data and can be used to compare model performance, but they are not unitless measures and hence cannot be compared across states. RRMS, \(R\), and RMAE are unitless alternatives that can be used to compare performance across states.

To simulate real-time dengue prediction in Brazil, we obtain nowcasts for the testing weeks in each state using only data we would expect to be available at that time. In practice, we expect that health agencies can provide dengue case reports within two weeks of incidence. Hence, for every testing week, we update our training dengue case count variables from as recent as two weeks prior and produce 2-step-ahead forecasts (which are thus nowcasts corresponding to current time \(t\)). More precisely, for week \(t\) in the testing set (where \(t\) is an integer above 4), we train a model using all 261 training weeks plus the prior testing
Figure 12. Mean dengue cases over epidemic weeks in each Brazilian state. For a selection of Brazilian states, the number of dengue cases per epidemic week (computed over all weeks from 2010 to 2015) is displayed in gray from June to May. The black lines correspond to the mean number of dengue cases per epidemic week during the same period. The year 2016 is omitted due to unavailable data for the full year. The remaining 18 Brazilian states’ case counts are plotted in the supplementary materials section.
weeks, 262, 263, . . . , 262 + t − 4. When neighboring dengue case counts are included as predictors in a model for a state, the two week lag time is addressed by forecasting the values for the two weeks through a simple SARIMA model. Meanwhile, the weather, satellite, and Google variables can be updated in real-time, so we allow dengue to be forecasted at time \( t \) with values of these variables for as recent as time \( t \).

**Dimension Reduction of Exogenous Variables**

Several of our models presented in the next section include the satellite, climate, Google Health Trends variables, and dengue case counts from neighboring states. Unless otherwise noted, we refer to these variables as exogenous variables and denote them as \( \{z_1\}, \{z_2\}, \ldots, \{z_m\} \), while the true dengue count for the modeled state is considered the endogenous variable and denoted as \( \{y_t\} \). Here, we discuss our motivations and methods for reducing their dimension.

There are up to \( m = 115 \) exogenous variables per state, and including all or most of those variables in our models could violate model assumptions and decrease nowcast accuracy. The models in the next section require the exogenous variables to be uncorrelated, which is an assumption frequently violated; for example, four summary statistics (minimum, mean, maximum, and standard deviation) of the maximum temperature are represented as variables and expected to have high correlations among themselves. Additionally, including too many predictors can contribute to over-fitting, resulting in severe reductions of testing accuracy. To address such issues, we apply techniques of dimension reduction, expressing information from the full set of variables in a smaller, more concise subset.

First, we omit any variables with zero-variance in the training or testing set. Then we consider principal component analysis (PCA) and partial least squares (PLS), two well-established methods from statistics that transform and reduce the dimension of the exogenous variables through singular value decomposition (SVD). PCA and its variants have been applied to time series analysis\(^\text{81}\). Briefly, PCA is an orthogonal linear transformation that maximizes the covariance of the predictors in the lowest dimension possible (through the top “principal components”). PCA is considered an unsupervised method, because it does not incorporate information about the response variable. PLS can be viewed as a supervised modification of PCA, transforming the variables such that they are strongly correlated with the response, uncorrelated among themselves, and maximize covariance. The relationship between these methods is discussed in\(^\text{82}\), among other works. Our approach for incorporating principal components and partial least squares scores into a model is specific to the model, so we refer further explanation to the next section.

**Individual Predictive Models**

We discuss the individual models considered for nowcasting dengue in Brazil. For a fixed state, all models are separately fit for that state, using the expanding training weeks as previously defined. Subsequently for that state, recursive nowcasts (2-step ahead forecasts) are obtained for the testing weeks.

We consider six different time series models, chosen because they are well-understood in statistics, explicitly account for temporal dependency, and range in complexity and inclusion of variables. These models, as well as two methods for combining them (detailed in a later section), are summarized in Table 3. SARIMA (1) and the STL models (4, 5) contain only past dengue case counts, while SARIMAX (2, 3) and VAR (6) additionally contain the exogenous variables from heterogenous data streams (Google Health trends, weather, satellite, and neighboring state case counts). Hence, models (1, 4, 5) can represent nontrivial baselines that can be compared against the models combining novel and traditional data streams (2, 3, 6). For each model, we produce both point estimates and the standard 95% prediction intervals based on asymptotic normality of errors. We note that the dengue response is not constrained to be a count, which would limit choice of time series models and availability of statistical software. In some rare cases, dengue forecasts are slightly below 0, which we simply convert to 0.

**Seasonal Autoregressive Integrated Moving Average Model**

SARIMA is one of the most popular models in time series analysis. The model can be denoted by ARIMA\((p,d,q) \times (P,D,Q)\), where \( p,d,q \) are respectively the autoregressive, difference, and moving average components of orders \( P,D,Q \), and \( p,d,q \) are the seasonal autoregressive, difference, and moving average components. Define \( B \) to be the backshift operator, i.e., \( B y_t = y_{t-1} \). We can define order \( k \) of \( B \) as \( B^k y_t = y_{t-k} \), where \( k \) is a nonnegative integer. Similarly, define \( \Delta \) as the difference operator, i.e., \( \Delta^k = (1-B)^k \) for any nonnegative integer \( k \). The model can be expressed as

\[
\Phi_p(B^S) \phi(B) \Delta^D \delta' y_t = \delta + \Theta_Q(B^S) \theta(B) w_t,
\]

where \( \delta \) is an intercept, \( w_t \) is white noise, \( \phi(B) \) and \( \theta(B) \) are respectively autoregressive and moving average components of orders \( p \) and \( q \) (i.e., \( \phi(B) = 1 - \phi_1 B - \phi_2 B^2 - \ldots - \phi_p B^p \) and \( \theta(B) = 1 + \theta_1 B + \theta_2 B^2 + \ldots + \theta_q B^q \)), \( S \) is the seasonal order, \( \Phi_p(B^S) \) and \( \Theta_Q(B^S) \) are seasonal autoregressive and moving average components with orders \( P \) and \( Q \), and \( \Delta^D = (1-B)^D \) are the ordinary and seasonal difference components\(^\text{83}\). In practice, a major challenge of forecasting through SARIMA is choosing appropriate orders, which can drastically affect predictive performance. Additionally, a fundamental assumption of SARIMA is that the time series \( \{y_t\} \) is stationary.
where whether they include exogenous variables or no exogenous variables. The exogenous variables include Google, weather, and satellite data (from as recent as the current week), as well as neighboring state case counts (from as recent as two weeks prior). All individual models additionally contain past dengue count for the state (from as recent as two weeks prior). We also list ensemble methods, which aggregate nowcasts from the individual models. "Exogenous" variables are technically considered endogenous in a VAR model, which is multivariate.

Any nonstationarity is addressed by first performing the Box-Cox transformation $f_\lambda : \{y_t\} \to \mathbb{R}$ defined by

$$f_\lambda (y_t) = \begin{cases} \frac{y_t^\lambda - 1}{\lambda}, & \text{if } \lambda \neq 0 \\ \log(y_t), & \text{if } \lambda = 0, \end{cases}$$

where the parameter $\lambda$ is estimated from the time series $\{y_t\}$. Next, the difference orders $d$ and $D$ are constrained to be less than 3 and 2, respectively, and chosen through unit root tests. The remaining orders $p, q, P$, and $Q$ are identified through model selection. To reduce the number of possible combinations and the potential for overspecified models, we consider only the orders $p = 0, 1, \ldots, 5$, $q = 0, 1, \ldots, 5$, $P = 0, 1, 2$, and $Q = 0, 1, 2$. For each combination of these orders, we fit a model and assess the fit through some chosen criterion. We choose a popular criterion from statistics, Akaike’s Information Criterion (AIC), defined in general as

$$\text{AIC} = -2\log(L) + 2K,$$

where $L$ is the maximized likelihood of the model fitted to the data and $K$ is the number of parameters in the model. For SARIMA specifically, $K = p + q + P + Q + \delta$, where $\delta = 1$ if the intercept $\delta \neq 0$ and 0 otherwise. (We tested another well-established criterion, the Bayesian Information Criterion (BIC), but it often produced models that were too sparse.) Here, we determine the “best” model for a state to be the one whose orders yield the lowest AIC. This modeling process is implemented through the R package forecast.

**SARIMAX**

For methods (2) and (3), we incorporate the exogenous variables from diverse data streams by generalizing the SARIMA model from (1). The exogenous variables are transformed through PCA or PLS, where $k$ is an integer satisfying $k \leq m$. Then the model for (2) or (3) can be denoted by SARIMAX($p, d, q, (P, D, Q, \delta)$), defined as

$$y_t = \beta_1 s_{1t} + \ldots + \beta_k s_{kt} + u_t,$$

where $\beta_j$ for $j = 1, \ldots, k$ is a coefficient, and the error $u_t$ is modeled as SARIMA($p, d, q, (P, D, Q, \delta)$, i.e.,

$$\Phi_p(B^\delta)\phi(B)\Delta_p^d\Delta^d u_t = \delta + \Theta_Q(B^\delta)\theta(B)w_t,$$

with all notation as in Equation 3.

A similar model selection process is followed for PCA and PLS. We retain a dimension of five to encourage model parsimony and reduce risk of over-fitting. For each of the $2^5 = 32$ nonempty subsets of transformed variables, we fit a SARIMAX model (with model orders simultaneously identified following the same AIC-minimizing process as above). The final model is chosen as the subset of variables and combination of model orders with minimum AIC. The distinction is that for PLS, we reduce the dimension to five by choosing the top partial least squares scores. For PCA, we choose the five principal components most strongly correlated with dengue case count. Since PCA is unsupervised, without the correlation condition, it is possible that the top “principal components” could be unrelated to dengue forecasting.

### Table 3. Summary of models to nowcast dengue in each Brazilian state.

We list the individual models of dengue and whether they include exogenous variables or no exogenous variables. The exogenous variables include Google, weather, and satellite data (from as recent as the current week), as well as neighboring state case counts (from as recent as two weeks prior). All individual models additionally contain past dengue count for the state (from as recent as two weeks prior). We also list ensemble methods, which aggregate nowcasts from the individual models. 11 “Exogenous” variables are technically considered endogenous in a VAR model, which is multivariate.

| Type | Model | Description |
|------|-------|-------------|
| **Individual Models** | (1) Seasonal autoregressive integrated moving average (SARIMA) | no exogenous variables |
| | (2) SARIMAX with principal component analysis (PCA) | exogenous variables |
| | (3) SARIMAX with partial least squares (PLS) | exogenous variables |
| | (4) Additive seasonal trend decomposition based on LOESS (STL) | no exogenous variables |
| | (5) Multiplicative STL | no exogenous variables |
| | (6) Vector autoregression with PCA-transformed data | “exogenous” variables |
| **Combining Models** | (7) Trimmed mean ensemble | robustly computes mean of predictions |
| | (8) Weighted mean ensemble | computes weighted mean of predictions |

$\Phi_p(B^\delta)$ represents the autoregressive polynomial, $\phi(B)$ the autoregressive polynomial in $B$, $\Delta_p^d$ is the $d$th order difference, $\Delta^d$ is the $d$th order difference, $\Theta_Q(B^\delta)$ represents the moving average polynomial, $\theta(B)$ the moving average polynomial in $B$, $w_t$ is the error term, and $\delta$ is the intercept.
Seasonal Trend Decomposition Based on LOESS (STL)

Seasonal trend decomposition based on LOESS (STL) is a nonparametric, univariate decomposition of a time series into three components: seasonal, trend, and remainder. STL is among the most popular time series decomposition methods, and its advantages over others include its fast computation, flexibility in extent of trend or seasonality smoothing, robustness to outliers, and greater specificity of the seasonal component’s period. We have considered both additive and multiplicative forms of the model, i.e.,

\[
y_t = T_t + S_t + R_t
\]

and

\[
y_t = T_t S_t R_t,
\]

respectively, where \(T_t, S_t,\) and \(R_t\) are the trend, seasonal, and remainder components at time \(t\). The components \(T_t\) and \(S_t\) are estimated through successive passes of a nested (inner and outer) loop algorithm, which applies several smoothers (LOESS and moving average) and robustness weights to flexibly and robustly fit the data. There are six main parameters that must be specified: the periodicity \((D)\) of the time series, the number of inner and outer loops \((i, o,\) respectively), and the span of the LOESS window for seasonal component estimation, trend component estimation, and the low-pass filter \((n_i, n_o, n_t,\) respectively). We specify the seasonal periodicity as \(D = 52\), to reflect the yearly pattern followed by weekly dengue count. The respective parameters \(i\) and \(o\) are chosen as 1 and 15, the recommended values for robust fitting of STL. The low-pass filter span \(n_t\) is specified as 53, the minimum odd integer greater than or equal to \(D\), as suggested in. We have specified the remaining parameters as \(n_i = 155\) and \(t_i = 25\), by comparing model fit within the training set for a range of odd values.

The seasonal component \(S_t\) is forecasted through an exponential state smoothing model, which visually produces forecasts repeating a similar periodic pattern. The deseasonalized time series \((Y_t - S_t)\) for an additive model and \(Y_t/S_t\) for multiplicative) is forecasted through SARIMA, following the same process outlined in the SARIMA section. Finally, the forecasted series is reconstructed by summing or multiplying the predicted components, similarly as in Equations 8 and 9. The SARIMAX fitting and forecasting is implemented through the R package `forecast`.

Vector Autoregression (VAR)

For each time step \(t\), the SARIMAX model in Equation 6 includes the exogenous variables only at \(t\). However, these variables may relate to the dengue count \(\{y_t\}\) at lagged times. To accommodate such lags, we consider the vector autoregression model (VAR).

VAR is a popular, flexible, and powerful method for modeling and forecasting multiple time series. In contrast to the previously presented models, VAR is multivariate, modeling multiple response variables simultaneously as a response vector. While our priority is forecasting dengue (not other variables), a multivariate model can help capture complex temporal dynamics between variables and improve the accuracy of dengue forecasts.

Let \(y_t = (y_{t1}, y_{t2}, \ldots, y_{tm})^T\) denote a \(k \times 1\) response vector at time \(t\), where \(y_{ti}\) is the dengue count for a state and for each \(i = 2, \ldots, k\), \(y_{ti} = z_{ti}\) is one of the \(m\) “exogenous” variables. For clarity, we continue referring to these variables as “exogenous”, even though they are considered endogenous in a multivariate model such as VAR.) A VAR(\(p\)) model can be specified as

\[
y_t = A_1 y_{t-1} + \ldots + A_p y_{t-p} + w_t,
\]

where \(A_i\) for \(i = 1, \ldots, p\) are \(k \times k\) coefficient matrices and \(w_t\) is a white noise vector.

With some algebra, each entry of the response vector \(y_t\) can be expanded from Equation 10, e.g., dengue count can be expressed as

\[
y_{t1} = y_{t1} = A_{11} y_{t-1,1} + \ldots + A_{1k} y_{t-1,k} + A_{21} y_{t-2,1} + \ldots + A_{2k} y_{t-2,k} + \ldots + A_{p1} y_{t-p,1} + \ldots + A_{pk} y_{t-p,k} + w_{t1},
\]

where \(A_{iMN}\) is the entry in row \(M\) and column \(N\) in the coefficient matrix \(A_i\), for \(i = 1, \ldots, p\). This equation for dengue will be used to obtain forecasts in the testing weeks. Similarly to the models from previous sections, a challenge of VAR in practice is selecting appropriate variables and the autoregressive order \(p\). To reduce model complexity and risk of over-fitting, we limit the maximum order to be \(p = 8\).

We apply PCA to the set of “exogenous” variables. (PLS is not applied here, as its supervised algorithm would fail to identify relationships between lagged variables.) Similarly as in SARIMAX with PCA, we seek the principal components that might help predict dengue. We calculate the cross-correlation function between dengue count and each principal component for lags up to 8 (lags beyond 8 need not be considered, since we have constrained the autoregressive order \(p\) to be less than or
equal to 8); the principal components are ranked by strength of cross-correlation when leading dengue and the top five are selected. To identify an appropriate autoregressive order $p$ for the VAR($p$) model, we proceed with model selection on this reduced feature set. We fit a model in training for all combinations of the five principal components and autoregressive orders $p = 1, 2, \ldots, 8$. The “best” model is selected as the one that minimizes the AIC\(^{84}\), chosen for similar reasons as for SARIMA and defined in Equation 5 with $K = p(k + 1) + 2$ (where $k$ is the length of the response vector). This model is subsequently used to forecast within the testing weeks. The VAR fitting and forecasting is implemented through the \texttt{vars} package in R\(^{92}\).

### Combining Predictive Models

As demonstrated in the Results section, the “best” statistical model of dengue (achieving minimum testing error) differs across states. However, high temporal variation in dengue count indicates that a state’s “best” method in the testing weeks (2015-16) might not be the best in the future. For real-time, practical nowcasting, we consider ensemble methods to automatically generate robust predictions for each state. Ensembles are statistical learning models that combine individual models, with the goal of capturing the strengths of each individual in a diverse set\(^{93,94}\). Theoretically and empirically, ensembles have often outperformed individual models for general prediction tasks\(^{93}\), as well as time series prediction\(^{95}\). Common approaches involve perturbing the data (e.g., through bagging), altering the individual models (e.g., by adding regularization terms), or aggregating the outputs from individual models (e.g., by computing the mean)\(^{95}\). Due to the good performance of our individual models in training, we expect simple, common aggregation methods to perform well and consider a trimmed and weighted mean.

A trimmed mean robustly measures center by removing extreme observations from a sample before computing its mean\(^{95}\). We specify the trimmed mean to remove the most extreme 20% of observations, which here corresponds to omitting the minimum and maximum nowcasts. For each state and week $t = 262, \ldots, 342$ in testing, the trimmed mean ensemble nowcast is computed as the mean of the trimmed sample \{\hat{y}^{(2)}_{t}, \hat{y}^{(3)}_{t}, \ldots, \hat{y}^{(5)}_{t}\}, which has omitted the minimum and maximum nowcasts $\hat{y}^{(1)}_{t}$ and $\hat{y}^{(6)}_{t}$. To produce 95% prediction intervals, we use a conservative approach: the bounds are selected as the minimum and maximum of the 95% prediction interval bounds (previously computed through the standard asymptotic normality procedures) associated with the nowcasts in the trimmed sample \{\hat{y}^{(2)}_{t}, \hat{y}^{(3)}_{t}, \ldots, \hat{y}^{(5)}_{t}\}.

Weighted means are another common approach in aggregation-based ensembles, where the weights are often chosen based on individual model performance in the training or validation set\(^{95}\). For the purposes of selecting weights, we divide our main training set into a smaller training set (weeks $t = 1, 2, \ldots, 157$) and a validation set (weeks $t = 158, 159, \ldots, 261$). On the validation set, we refit each individual model by mirroring the previously discussed cross-validation approach. The weights for a state are selected as the proportion of times an individual model’s prediction has minimized the $l_1$ norm (between observed and predicted dengue) in the validation set. For example, suppose that $\hat{y} = \hat{y}^{\text{VAR}}$ minimizes $|\hat{y} - y|$ only for the three weeks $t = 158, 159, 162$; then the weight for VAR would be $\frac{3}{261-157+1}$. For each state, using its weights computed from the validation set, the weighted mean is calculated for each nowcast in the testing weeks. The 95% prediction intervals are computed similarly as above.

### Acknowledgements

We acknowledge Descartes Labs for remote sensing data and the Ministry of Health of Brazil for reported case counts data. Research presented in this article was supported by the Laboratory Directed Research and Development program of Los Alamos National Laboratory 20190581ECR, and 20180740ER. The content is solely the responsibility of the authors and does not necessarily represent the official views of the sponsors. SDV was supported in part by NIH/NIGMS grant R01-GM130668-02. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript. Los Alamos National Laboratory is operated by Triad National Security, LLC, for the National Nuclear Security Administration of U.S. Department of Energy (Contract No. 89233218CNA000001).

### Author contributions statement

KK wrote the manuscript, designed and implemented the statistical part of the study, analyzed the results, and prepared figures, KM cleaned and fused data and assisted with figures, AS did kriging for the data, JC helped plan the manuscript, fused data, and analyzed results, GF and AZ acquired and processed the remote sensing data and weather data and co-conceived the project, NP pulled GHT data, did data fusion, and assisted with computational methods, DO helped design the statistical methodology, NG provided case surveillance data and co-conceived the project, SDV co-conceived the project and led the team, CM co-conceived and coordinated the study, team, and methods. All authors reviewed the final manuscript.

### References

1. WHO report on global surveillance of epidemic-prone infectious diseases (2015). URL http://www.who.int/csr/resources/publications/surveillance/WHO_CDS_CSR_ISR_2000_1/en/.
2. Cafferata, M. L. et al. Dengue epidemiology and burden of disease in Latin America and the Caribbean: a systematic review of the literature and meta-analysis. *Value health regional issues* 2, 347–356 (2013).

3. Wilder-Smith, A., Yoksan, S., Earnest, A., Subramaniam, R. & Paton, N. I. Serological evidence for the co-circulation of multiple dengue virus serotypes in Singapore. *Epidemiol. & Infect.* 133, 667–671 (2005).

4. De Simone, T. et al. Dengue virus surveillance: the co-circulation of DENV-1, DENV-2 and DENV-3 in the State of Rio de Janeiro, Brazil. *Transactions Royal Soc. Trop. Medicine Hyg.* 98, 553–562 (2004).

5. Guo, C. et al. Global epidemiology of dengue outbreaks in 1990 - 2015: a systematic review and meta-analysis. *Front. cellular infection microbiology* 7, 317 (2017).

6. Dolley, S. Big data’s role in precision public health. *Front. public health* 6, 68 (2018).

7. Salathe, M. et al. Digital epidemiology. *PLoS computational biology* 8, e1002616 (2012).

8. Brownstein, J. S., Freifeld, C. C. & Madoff, L. C. Digital disease detection — harnessing the Web for public health surveillance. *New Engl. J. Medicine* 360, 2153–2157 (2009).

9. Wu, P.-C., Guo, H.-R., Lung, S.-C., Lin, C.-Y. & Su, H.-J. Weather as an effective predictor for occurrence of dengue fever in Taiwan. *Acta tropica* 103, 50–57 (2007).

10. Lu, L. et al. Time series analysis of dengue fever and weather in Guangzhou, China. *BMC Public Heal.* 9, 395 (2009).

11. Johansson, M. A., Cummings, D. A. & Glass, G. E. Multiyear climate variability and dengue—El Nino southern oscillation, weather, and dengue incidence in Puerto Rico, Mexico, and Thailand: a longitudinal data analysis. *PLoS medicine* 6, e1000168 (2009).

12. Colón-González, F. J., Fezzi, C., Lake, I. R. & Hunter, P. R. The effects of weather and climate change on dengue. *PLoS neglected tropical diseases* 7, e2503 (2013).

13. Rosa-Freitas, M. G., Schreiber, K. V., Tsouris, P., Weimann, E. T. d. S. & Luitgards-Moura, J. F. Associations between dengue and combinations of weather factors in a city in the Brazilian Amazon. *Revista Panam. de Salud Pública* 20, 256–267 (2006).

14. Hii, Y. L. et al. Optimal lead time for dengue forecast. *PLoS neglected tropical diseases* 6, e1848 (2012).

15. Hii, Y. L., Zhu, H., Ng, N., Ng, L. C. & Rocklöv, J. Forecast of dengue incidence using temperature and rainfall. *PLoS neglected tropical diseases* 6, e1908 (2012).

16. Lowe, R. et al. Evaluating probabilistic dengue risk forecasts from a prototype early warning system for Brazil. *Elife* 5, e11285 (2016).

17. Lowe, R. et al. Dengue outlook for the World Cup in Brazil: an early warning model framework driven by real-time seasonal climate forecasts. *The Lancet infectious diseases* 14, 619–626 (2014).

18. Shi, Y. et al. Three-month real-time dengue forecast models: an early warning system for outbreak alerts and policy decision support in Singapore. *Environ. health perspectives* 124, 1369–1375 (2015).

19. Buczak, A. L., Koshtute, P. T., Babin, S. M., Feighner, B. H. & Lewis, S. H. A data-driven epidemiological prediction method for dengue outbreaks using local and remote sensing data. *BMC medical informatics decision making* 12, 124 (2012).

20. de Wet, N. et al. Use of a computer model to identify potential hotspots for dengue fever in New Zealand. *New Zealand Med. J.* 114, 420 (2001).

21. Viana, D. V. & Ignotti, E. The occurrence of dengue and weather changes in Brazil: a systematic review. *Revista Brasileira de Epidemiol.* 16, 240–256 (2013).

22. Campbell, L. P. et al. Climate change influences on global distributions of dengue and chikungunya virus vectors. *Phil. Trans. R. Soc. B* 370, 20140135 (2015).

23. Gharbi, M. et al. Time series analysis of dengue incidence in Guadeloupe, French West Indies: forecasting models using climate variables as predictors. *BMC infectious diseases* 11, 166 (2011).

24. Pollett, S., Althouse, B. M., Forshey, B., Rutherford, G. W. & Jarman, R. G. Internet-based biosurveillance methods for vector-borne diseases: Are they novel public health tools or just novelties? *PLOS Neglected Trop. Dis.* 11 (2017). URL http://journals.plos.org/plosntds/article?id=10.1371/journal.pntd.0005871. DOI 10.1371/journal.pntd.0005871.

25. Yang, S. et al. Advances in using Internet searches to track dengue. *PLoS computational biology* 13, e1005607 (2017).
26. Chan, E. H., Sahai, V., Conrad, C. & Brownstein, J. S. Using web search query data to monitor dengue epidemics: a new model for neglected tropical disease surveillance. *PLoS neglected tropical diseases* **5**, e1206 (2011).

27. Milinovich, G. J. *et al.* Using internet search queries for infectious disease surveillance: screening diseases for suitability. *BMC infectious diseases* **14**, 690 (2014).

28. Althouse, B. M., Ng, Y. Y. & Cummings, D. A. Prediction of dengue incidence using search query surveillance. *PLoS neglected tropical diseases* **5**, e1206 (2011).

29. Gluskin, R. T., Johansson, M. A., Santillana, M. & Brownstein, J. S. Evaluation of Internet-based dengue query data: Google Dengue Trends. *PLoS neglected tropical diseases* **8**, e2713 (2014).

30. Priedhorsky, R. *et al.* Measuring global disease with Wikipedia: Success, failure, and a research agenda. In *Proceedings of the 2017 ACM Conference on Computer Supported Cooperative Work and Social Computing*, 1812–1834 (ACM, 2017).

31. Althouse, B. M. *et al.* Enhancing disease surveillance with novel data streams: challenges and opportunities. *EPJ Data Sci.* **4**, 17 (2015).

32. Gomide, J. *et al.* Dengue surveillance based on a computational model of spatio-temporal locality of Twitter. In *Proceedings of the 3rd international web science conference*, 3 (ACM, 2011).

33. de Almeida Marques-Toledo, C. *et al.* Dengue prediction by the web: tweets are a useful tool for estimating and forecasting dengue at country and city level. *PLoS neglected tropical diseases* **11**, e0005729 (2017).

34. Guo, P. *et al.* Developing a dengue forecast model using machine learning: a case study in China. *PLoS neglected tropical diseases* **11**, e0005973 (2017).

35. Kalluri, S., Gilruth, P., Rogers, D. & Szczur, M. Surveillance of arthropod vector-borne infectious diseases using remote sensing techniques: a review. *PLoS pathogens* **3**, e116 (2007).

36. McFeeters, S. Using the normalized difference water index (NDWI) within a geographic information system to detect swimming pools for mosquito abatement: A practical approach. *Remote. Sens.* **5**, 3544–3561 (2013).

37. Louis, V. R. *et al.* Modeling tools for dengue risk mapping - a systematic review. *Int. journal health geographics* **13**, 50 (2014).

38. Nakhapsakorn, K. & Tripathi, N. K. An information value based analysis of physical and climatic factors affecting dengue fever and dengue haemorrhagic fever incidence. *Int. J. Heal. Geogr.* **4**, 13 (2005).

39. Machault, V. *et al.* Mapping entomological dengue risk levels in Martinique using high-resolution remote-sensing environmental data. *ISPRS Int. J. Geo-Information* **3**, 1352–1371 (2014).

40. Laureano-Rosario, A. E., Garcia-Rejon, J. E., Gomez-Carro, S., Farfan-Ale, J. A. & Muller-Karger, F. E. Modelling dengue fever risk in the State of Yucatan, Mexico using regional-scale satellite-derived sea surface temperature. *Acta tropica* **172**, 50–57 (2017).

41. Troyo, A., Fuller, D. O., Calderón-Arguedas, O., Solano, M. E. & Beier, J. C. Urban structure and dengue incidence in Puntarenas, Costa Rica. *Singapore journal tropical geography* **30**, 265–282 (2009).

42. Chang, A. Y. *et al.* Combining Google Earth and GIS mapping technologies in a dengue surveillance system for developing countries. *Int. journal health geographics* **8**, 49 (2009).

43. Hay, S., Snow, R. & Rogers, D. From predicting mosquito habitat to malaria seasons using remotely sensed data: practice, problems and perspectives. *Parasitol. Today* **14**, 306–313 (1998).

44. Brown, H., Diuk-Wasser, M., Andreadis, T. & Fish, D. Remotely-sensed vegetation indices identify mosquito clusters of West Nile virus vectors in an urban landscape in the northeastern United States. *Vector-Borne Zoonotic Dis.* **8**, 197–206 (2008).

45. Allen, T. R. & Wong, D. W. Exploring GIS, spatial statistics and remote sensing for risk assessment of vector-borne diseases: a West Nile virus example. *Int. J. Risk Assess. Manag.* **6**, 253–275 (2006).

46. Young, S. G., Tullis, J. A. & Cothren, J. A remote sensing and GIS-assisted landscape epidemiology approach to West Nile virus. *Appl. Geogr.* **45**, 241–249 (2013).

47. Lacaux, J., Tourre, Y., Vignolles, C., Ndione, J. & Lafaye, M. Classification of ponds from high-spatial resolution remote sensing: Application to Rift Valley Fever epidemics in Senegal. *Remote. Sens. Environ.* **106**, 66–74 (2007).

48. McGough, S. F., Brownstein, J. S., Hawkins, J. B. & Santillana, M. Forecasting Zika incidence in the 2016 Latin America outbreak combining traditional disease surveillance with search, social media, and news report data. *PLoS neglected tropical diseases* **11**, e0005295 (2017).
49. Santillana, M. et al. Combining search, social media, and traditional data sources to improve influenza surveillance. *PLoS computational biology* **11**, e1004513 (2015).

50. Majumder, M. S. et al. Utilizing nontraditional data sources for near real-time estimation of transmission dynamics during the 2015-2016 Colombian Zika virus disease outbreak. *JMIR public health surveillance* **2** (2016).

51. Generous, N., Fairchild, G., Deshpande, A., Del Valle, S. Y. & Priedhorsky, R. Global disease monitoring and forecasting with Wikipedia. *PLoS computational biology* **10**, e1003892 (2014).

52. Andraud, M., Hens, N., Marais, C. & Beutels, P. Dynamic epidemiological models for dengue transmission: a systematic review of structural approaches. *PloS one* **7**, e40985 (2012).

53. Lowe, R. et al. The development of an early warning system for climate-sensitive disease risk with a focus on dengue epidemics in Southeast Brazil. *Stat. medicine* **32**, 864–883 (2013).

54. Tegnér, J. N. et al. Computational disease modeling - fact or fiction? *BMC systems biology* **3**, 56 (2009).

55. Johansson, M. A., Reich, N. G., Hota, A., Brownstein, J. S. & Santillana, M. Evaluating the performance of infectious disease forecasts: A comparison of climate-driven and seasonal dengue forecasts for Mexico. *Sci. reports* **6**, 33707 (2016).

56. Promprou, S., Jaroensutasinee, M. & Jaroensutasinee, K. Forecasting Dengue Haemorrhagic Fever cases in Southern Thailand using ARIMA models. *Dengue Bull.* (2006).

57. Luz, P. M., Mendes, B. V., Codeço, C. T., Struchiner, C. J. & Galvani, A. P. Time series analysis of dengue incidence in Rio de Janeiro, Brazil. *The Am. journal tropical medicine hygiene* **79**, 933–939 (2008).

58. Eastin, M. D., Delmelle, E., Casas, I., Wexler, J. & Self, C. Intra-and interseasonal autoregressive prediction of dengue outbreaks using local weather and regional climate for a tropical environment in Colombia. *The Am. journal tropical medicine hygiene* **91**, 598–610 (2014).

59. Silawan, T. et al. Temporal patterns and forecast of dengue infection in Northeastern Thailand. *Southeast Asian J. Trop. Medicine Public Heal.* **39**, 90 (2008).

60. Rahmawati, D. & Huang, Y.-P. Using C-support vector classification to forecast dengue fever epidemics in Taiwan. In *2016 International Conference on System Science and Engineering (ICSSE)*, 1–4 (IEEE, 2016).

61. Codeço, C. et al. InfoDengue: a nowcasting system for the surveillance of dengue fever transmission. *BioRxiv* 046193 (2016).

62. Codeço, C. et al. Infodengue: A nowcasting system for the surveillance of arboviruses in Brazil. *Revue d’Épidémiologie et de Santé Publique* **66**, S386 (2018).

63. Bowerman, B. & Oconnel, R. *FORECASTING AND TIME SERIES, AN APPLIED APPROACH* (Pacific Grove, 1993).

64. Hay, S. An overview of remote sensing and geodesy for epidemiology and public health application. *Adv. parasitology* **47**, 1–35 (2000).

65. Rogers, D. F. *Remote sensing and geographical information systems in epidemiology*, vol. 47 (Elsevier, 2000).

66. Council, N. R. et al. *Under the weather: climate, ecosystems, and infectious disease* (National Academies Press, 2001).

67. Yang, H., Macoris, M. d. L. d. G., Galvani, K., Andrighetti, M. & Wanderley, D. Assessing the effects of temperature on the population of Aedes aegypti, the vector of dengue. *Épidemiol. & Infect.* **137**, 1188–1202 (2009).

68. Watts, D. M., Burke, D. S., Harrison, B. A., Whitmire, R. E. & Nisalak, A. Effect of temperature on the vector efficiency of Aedes aegypti for dengue 2 virus. *The Am. journal tropical medicine hygiene* **36**, 143–152 (1987).

69. Hopp, M. J. & Foley, J. A. Global-scale relationships between climate and the dengue fever vector, Aedes aegypti. *Clim. change* **48**, 441–463 (2001).

70. Organization, W. H. et al. Using climate to predict infectious disease epidemics. In *Communicable Diseases Surveillance and Response, Protection of the Human Environment, Roll Back Malaria* (World Health Organization, 2005).

71. Ministério da Saúde. Informe Epidemiológico da Dengue Janeiro a Junho de 2008 (2008).

72. Moran, P. A. Notes on continuous stochastic phenomena. *Biom.* **37**, 17–23 (1950).

73. Oceanic, N. & Administration, A. Global Surface Summary of the Day (2019).

74. Google Trends Help Center. URL https://support.google.com/trends/?hl=en.

75. Search Engine Market Share Brazil. URL http://gs.statcounter.com/search-engine-market-share/all/brazil.
76. Siqueira Jr, J. B., Martelli, C. M. T., Coelho, G. E., da Rocha Simplicio, A. C. & Hatch, D. L. Dengue and dengue hemorrhagic fever, Brazil, 1981 - 2002. Emerg. infectious diseases 11, 48 (2005).
77. Coelho, G. E., Leal, P. L., de Paula Cerroni, M., Simplicio, A. C. R. & Siqueira Jr, J. B. Sensitivity of the Dengue surveillance system in Brazil for detecting hospitalized cases. PLoS neglected tropical diseases 10, e0004705 (2016).
78. R: A Language and Environment for Statistical Computing (Version 3.5.2).
79. Tierney, L., Rossini, A. J., Li, N. & Sevcikova, H. snow: Simple Network of Workstations (2018). URL https://CRAN.R-project.org/package=snow. R package version 0.4-3.
80. R Core Team. R: A Language and Environment for Statistical Computing. R Foundation for Statistical Computing, Vienna, Austria (2018). URL https://www.R-project.org/.
81. Shang, H. L. A survey of functional principal component analysis. AStA Adv. Stat. Analysis 98, 121–142 (2014).
82. Dunn Iii, W., Scott, D. & Glen, W. Principal components analysis and partial least squares regression. Tetrahedron Comput. Methodol. 2, 349–376 (1989).
83. Shumway, R. H. & Stoffer, D. S. Time series analysis and its applications: with R examples (Springer, 2017).
84. Akaike, H. Information theory and an extension of the maximum likelihood principle. In Selected papers of hirotugu akaike, 199–213 (Springer, 1998).
85. Hyndman, R. J., Khandakar, Y. et al. Automatic time series for forecasting: the forecast package for R. 6/07 (Monash University, Department of Econometrics and Business Statistics . . . , 2007).
86. Schwarz, G. et al. Estimating the dimension of a model. The annals statistics 6, 461–464 (1978).
87. Hyndman, R. J. et al. Package ‘forecast’. Online] https://cran.r-project.org/web/packages/forecast/forecast.pdf (2019).
88. Cleveland, R. B., Cleveland, W. S., McRae, J. E. & Terpenning, I. STL: A seasonal-trend decomposition. J. official statistics 6, 3–73 (1990).
89. Cleveland, W. S. Robust locally weighted regression and smoothing scatterplots. J. Am. statistical association 74, 829–836 (1979).
90. Hyndman, R., Koehler, A. B., Ord, J. K. & Snyder, R. D. Forecasting with exponential smoothing: the state space approach (Springer Science & Business Media, 2008).
91. Lütkepohl, H. New introduction to multiple time series analysis (Springer Science & Business Media, 2005).
92. Pfaff, B. et al. VAR, SVAR and SVEC models: Implementation within R package vars. J. Stat. Softw. 27, 1–32 (2008).
93. Dietterich, T. G. Ensemble methods in machine learning. In International workshop on multiple classifier systems, 1–15 (Springer, 2000).
94. Hastie, T., Tibshirani, R., Friedman, J. & Franklin, J. The elements of statistical learning: data mining, inference and prediction. The Math. Intell. 27, 83–85 (2005).
95. Allende, H. & Valle, C. Ensemble methods for time series forecasting. In Claudio Moraga: A Passion for Multi-Valued Logic and Soft Computing, 217–232 (Springer, 2017).

Supplementary Material

Figures
Figure 13. Satellite variables in each Brazilian state (2).
Figure 14. Satellite variables in each Brazilian state (3).
Figure 15. Weather variables in each Brazilian state (2).
Figure 16. Weather variables in each Brazilian state (3).
Figure 17. Google variables in each Brazilian state (2).
Figure 18. Google variables in each Brazilian state (3).
Figure 19. Mean dengue cases over epidemic weeks in each Brazilian state (2).
Figure 20. Mean dengue cases over epidemic weeks in each Brazilian state (3).
Figure 21. Observed vs. nowcasted dengue by Brazilian state from trimmed mean ensemble approach (2).
Figure 22. Observed vs. nowcasted dengue by Brazilian state from trimmed mean ensemble approach (3).