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Three-Month Real-Time Dengue Forecast Models: An Early Warning System for Outbreak Alerts and Policy Decision Support in Singapore

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Abstract

Background: With a tropical rainforest climate, rapid urbanization, changing demography and ecology, Singapore experiences endemic dengue, with the last large outbreak in 2013 culminating in 22170 cases. In the absence of a vaccine on the market, vector control is the key approach for prevention.

Objectives: We sought to forecast the evolution of dengue epidemics in Singapore to provide early warning of outbreaks and to facilitate public health response to moderate an impending outbreak.

Methods: We developed a set of statistical models using least absolute shrinkage and selection operator (LASSO) methods to forecast the weekly incidence of dengue notifications over a three-month time horizon. This forecasting tool makes use of a variety of data streams, updatable weekly, including recent case data, meteorological data, vector surveillance data, and population-based national statistics. The forecasting methodology was compared to alternative approaches that have been proposed to model dengue case data (seasonal autoregressive integrated moving average and step-down linear regression) by fielding them on the 2013 dengue epidemic, the largest on record in Singapore.

Results: Operationally useful forecasts were obtained at a three month lag using the LASSO-derived-models. Based on mean average percentage error, the LASSO approach provided more accurate forecasts than the previously-published methods we assessed. We demonstrate its utility in Singapore's dengue control program by providing a forecast of the 2013 outbreak for advance preparation of outbreak response.

Conclusions: Statistical models built using machine learning methods such as LASSO have the potential to markedly improve forecasting techniques for recurrent infectious disease outbreaks such as dengue.

Introduction

Dengue is an acute infectious disease common to tropical and sub-tropical areas. The dengue viruses are transmitted by *Aedes* mosquitoes, mainly *Aedes aegypti* and *Aedes albopictus* (Rosen et al. 1983). Globally, the World Health Organization has estimated that there are 50–100 million dengue infections per year (Rigau-Pérez et al. 1998), although more recent estimates have elevated this to 390 million of which ~96 million are symptomatic (Bhatt et al. 2013). Dengue infection in humans is mostly self-limiting—although antiviral drugs are under development (Lim et al. 2013; Rathore et al. 2011)—but may require hospital admission, and more severe manifestations of dengue may lead to death (Murphy and Whitehead 2011). Case fatality rates of dengue fever and severe dengue vary from 0–5% to 3–5% (Halstead 1999).

The city-state of Singapore, which lies approximately 130km north of the equator, has a tropical rainforest climate in the Köppen–Geiger climate classification system (Peel et al. 2007) with no distinctive seasons. The climate, combined with Singapore’s highly urbanized environment, favors the presence of *Aedes* mosquitoes and transmission of dengue virus (Thu et al. 1998), thus making Singapore highly vulnerable to dengue outbreaks. All four serotypes are endemic to Singapore with frequent introduction and circulation of different genotypes of the virus (Lee et al. 2010, 2012). With an annual notified incidence in the range of 20–330 per 100,000 people, the economic impact of dengue in Singapore from 2000 to 2010 was estimated to be US\$0.85–1.15 billion, or approximately US\$200 per capita per year (Carrasco et al. 2011). Since 2003, over 100 dengue related deaths have been reported (MOH 2012).

Antiviral drugs and vaccines have yet to reach the market (Douglas et al. 2013) and initial results from trials have been discouraging (Halstead 2012; Mahalingam et al. 2013; Sabchareon et al. 2012). In the absence of an effective vaccine against dengue, suppressing the mosquito vector

population remains the key thrust of Singapore's dengue control program (Lee et al. 2013). From 2000 to 2009, the country spent over US\$85 million per annum (Carrasco et al. 2011) on this endeavour. The National Environment Agency (NEA) has, since 2006, introduced virological surveillance for early warning of outbreak (Lee et al. 2010) and a novel mosquito breeding index which estimates the spatial distribution of *Ae. aegypti*, the main dengue vector in Singapore. Previous predictive capability relies on a qualitative understanding based on temperature, circulating serotype, vector data from the field and estimated immunity level of the human population. If automated, statistical models hold the promise of being able to provide real-time quantitative forecasts of the appearance and evolution of a dengue outbreak, which may be used to efficiently guide the deployment of vector control operations.

Any statistical approach to forecast dengue would need to meet certain criteria to be practical: (i) it uses only data that are available at the time the forecast is made; (ii) it is capable of forecasting weeks or months into the future to give a lead time for preparing a public health response (for instance, hiring of new control staff); (iii) its predictive performance is validated and demonstrated in data that were not used in its construction, to prevent over-fitting and ascertain confidence levels; and lastly, (iv) it is able to process new data rapidly. Population dynamic modeling of dengue exploits epidemiological or entomological knowledge and is valuable for modelling what-if scenarios, such as the effect of introducing changes to the host or mosquito populations (such as introducing vaccination into the pediatric vaccination schedule (Coudeville and Garnett 2012) or of releasing genetically modified sterile mosquitoes or those infected by *Wolbachia* (Hughes and Britton 2013)), and may be useful for predicting longer term changes to epidemic dynamics caused by changing levels of herd immunity or the age structure of a population (Cummings et al. 2009; Egger et al. 2008). A limitation of population dynamic

models is that they are difficult to integrate with real-time data streams, such as meteorological or incidence data. Although success has been achieved for epidemiologically simpler diseases such as influenza (Baguelin et al. 2010; Ong et al. 2010), the complexity caused by having several serotypes potentially circulating simultaneously and by the influence of the environment on the vector makes these models a relatively unattractive choice for short-term forecasts of dengue. In contrast, correlative statistical approaches—which describe the phenomenon but not the underlying process—are well suited to integration with multiple live data streams, and may have good predictive accuracy if future conditions do not stray too far from the conditions used to parameterize them.

Other researchers have sought to develop statistical time series models to predict dengue in Singapore. Earnest et al (2012) compared one-week-ahead dengue forecasts based on two popular modeling methods—the Autoregressive Integrated Moving Average (ARIMA) and the Knorr-Held two component (K-H) model—and showed that the K-H model was slightly more accurate. Hii et al (2012a, 2012b) developed a forecasting model using Poisson multivariate regression to predict the number of cases over a 4-month interval, demonstrating that past temperature and rainfall data are good predictors of future dengue incidence. Another study (Althouse et al. 2011) predicted 1-week and 1-month dengue incidence in Singapore and Bangkok, respectively, based on internet search engine queries that might signal the early stages of an outbreak. The authors compared three statistical approaches based on these data—a step-down linear regression, generalized boosted regression, and negative binomial regression—and concluded that the step-down linear model was superior. While these previous models meet many of the criteria above, it is noteworthy that none has been validated against data not used in

their construction, and none was developed explicitly for operational use, suggesting that their predictive performance and usefulness to operations were not tested.

In this paper, we describe a new approach to forecast dengue that is used by Singapore's NEA in planning vector control and public communication. The model specifically optimizes predictive accuracy over a 3-month time horizon, with model complexity selected, and predictive performance evaluated, using out of sample forecasting. We show that this approach, which uses the least absolute shrinkage and selection operator (LASSO) to fit large regression models, has better predictive performance than other modeling approaches.

Materials and Methods

Statistical analyses

LASSO: The Least Absolute Shrinkage and Selection Operator (LASSO) is a technique proposed in the 1990s (Tibshirani 1994) that has inspired much interest in the statistical methodology community on 'small n large p' problems (Tibshirani 1994). This framework extends standard regression and related models such as logistic regression by simultaneously selecting which parameters to include in the model and what their values should be. Rather than optimizing the (log) likelihood $L(y|\beta, x)$ for dependent variable y , independent variables x and coefficients β , as in standard regression, LASSO optimizes the sum of the log-likelihood and a penalty term controlled by an additional parameter λ , which controls model complexity. In particular, the optimal coefficients are the β s that maximise

$$L(y|\beta, x) - \lambda \sum_k |\beta_k|.$$

The penalty term λ controls model complexity: for a specific value of the penalty parameter, the optimal fit will have some (or many) coefficients set to 0, i.e. some covariates are not used in the model. The penalty term is usually selected by cross-validation, in which (i) the data are partitioned into several training and test sets, (ii) for each training set, a series of values of λ are considered, (iii) for each λ , the best values of β are found and then used to predict the test data so that the out-of-sample performance can be measured. The value of λ that maximised the average out-of-sample performance is then used to select the final model. This implicitly means that the model complexity is selected to optimize predictive accuracy for a given set of independent variables. We used the glmnet algorithm (Friedman et al. 2010) implemented in the R statistical language (R Core Team 2014) to fit the models.

Our approach was to develop a tailored submodel unique to each forecast window from 1 week to 12 weeks in the future. For each submodel, the outcome variable is the weekly number of cases (natural log transformed, with 1 added to avoid logging 0), and a large set of potential input variables were considered (details may be found in the data section). The formulation for each submodel is a multivariable linear regression. LASSO was used to select a (potentially different) set of predictors for each forecast window along with the values of their coefficients, with ten-fold cross validation used to determine optimal model complexity, before the forecasts were ‘stitched together’ graphically to create the impression of a single predictive routine.

Covariates were considered at lags of up to 20 weeks, based on a previous study by Hii et al (2012a, 2012b), but in contrast to their approach we allowed the effect of a single factor (such as temperature) to have multiple lags in influencing future dengue cases. The framework used in developing the models is presented in Figure 1.

Other approaches

We applied two of the statistical methods used by Earnest et al (2012) and Althouse et al (2011) to compare with the LASSO approach described above.

In the SARIMA algorithm, models are composed of non-seasonal factors (p, d, q) and seasonal factors (P, D, Q), where d and D define the order (i.e. number of weeks in the past) of nonseasonal and seasonal differencing in the time series (between successive values, used to reduce the effects of non-stationarity of the time series), p and P the autoregressive (AR) terms, q and Q the moving average terms, respectively. SARIMA models can vary from very simple—for instance, a non-seasonal AR1 model, where the dependent variable is regressed upon itself ($y_t = \beta_0 + \beta_1 y_{t-1} + \epsilon_t$)—to very complex, where the dependent variable depends on several past weeks, on moving averages of past weeks' data, and on recurrent seasonal factors, in this case 52 weeks ago. The values of (p, d, q, P, D, Q) with the lowest Akaike information criterion (AIC) during model training are selected for the optimal model. (A definitive introduction is provided by (Chatfield 2013).)

In the step-down linear regression (LR) model, we developed a submodel for each forecast window as in the LASSO approach, starting with a model containing all predictors (at multiple lags) and progressively eliminating variables one at a time according to AIC score, until no further improvement was possible without removing two or more terms simultaneously.

Model Comparison

Models were compared using the mean absolute percentage error (MAPE), as proposed by Armstrong (1985) and modified and re-proposed by Flores (1986), for each forecast window. If D_{t+w} is the actual number of dengue cases w weeks after time t when the prediction is made, and

D_{t+w}^m is the number of cases forecasted by model m , the MAPE for that model and forecast window is

$$MAPE(m, w) = \frac{100\%}{|\mathcal{V}|} \sum_{t \in \mathcal{V}} \left(\frac{|D_{t+w} - D_{t+w}^m|}{D_{t+w}} \right)$$

where \mathcal{V} is the validation set. We used data from 2001 to 2010 as training data to parameterize the models and from 2011 to 2012 to validate the models, with the validated models being applied in 2013 to evaluate their performance. The same training and validation datasets were used for all three models.

Predictions are accompanied by 95% intervals using point estimates from the models with overlaid error using the estimated standard deviation of residuals from the fitted model, and calculated the coverage of these intervals, i.e. the proportion of time points in which the eventual data point fell within the prediction interval, to compare whether the actual coverage of the three approaches was at or above the nominal coverage.

Data

Weekly covariates were used in order to match the frequency of reported dengue data made available by Singapore's Ministry of Health, with finer resolution data coarsened to this level, and coarser data assumed to be homogeneous over each reporting interval. The time horizon used for all variables unless otherwise denoted was January 2001 to December 2012. The variables used and their sources are:

Case data: The weekly number of cases (natural log transformed, +1) is provided by the Ministry of Health, Singapore, and can be obtained from their Weekly Infectious Diseases Bulletin (Ministry of Health, Singapore).

Population data: Mid-year population sizes for residents and foreign non-residents were obtained for each year from the Singapore Department of Statistics (Department of Statistics Singapore), natural log transformed, and applied to all weeks within the corresponding calendar year.. These were applied to all weeks within that calendar year.

Meteorological data: Weekly mean temperature (T) in degrees Celsius, maximum hourly temperature and number of hours of high temperature ($> 27.8^{\circ}\text{C}$) each week, and weekly relative humidity (RH) were obtained from the Meteorological Services Singapore. Absolute humidity for any week (H_A) was calculated from the weekly mean temperature (T) and relative humidity (H_R) using standard formulae (Xu et al. 2014).

Vector surveillance data: The weekly breeding percentage (BP) is an in-house index developed by NEA, which provides an estimate of the proportion of *Ae. aegypti*, the primary vector of dengue in Singapore, compared to all *Aedes* spp. As part of vector control operations, potential breeding sites are sought, samples are taken when breeding is found, and the species is determined in our laboratory. Because this is part of routine vector control and not solely for surveillance, efforts are not temporally or spatially regular, and tend to favour outbreak periods and areas with transmission. This has the effect of biasing estimates upwards for both (i) total incidence of breeding sites and (ii) *Ae. aegypti* breeding. To overcome the biases in data collection, we use the proportion of identified *Ae. aegypti* breeding out of all identified breeding sites to quantify the amount of ‘relevant’ breeding. The justification for this assumption is two-fold: (1) another *Aedes* species, *Ae. albopictus*, is so widespread that the amount of *Ae. albopictus* breeding found is a good proxy for total effort in identifying breeding sites, and (2) that *Ae. aegypti* is the primary vector for dengue in Singapore, being more efficient at transmission, being more often found to be infected, and being necessary for sustained

transmission in any neighborhood. The breeding percentage for week t , BP_t , was calculated from the weekly number of *Aedes* mosquito breeding sites recorded during ground inspections carried out by NEA using the following formula:

$$BP_t = \frac{N_{aegypti}(t)}{N_{total}(t)}$$

where $N_{aegypti}(t)$ and $N_{total}(t)$ are the number of breeding sites containing only *Ae. aegypti* or containing either *Ae. aegypti* or *Ae. albopictus*, respectively, in week t . This index has been found to have a high correlation with dengue cases (unpublished data) and to be negatively correlated in space with Chikungunya cases, for which *Ae. albopictus* is the more competent vector (Ng et al. 2009).

Trend and seasonality data: Besides the climatic factors, dengue is also affected by other factors such as changes to vector control and circulating serotypes. To address the impact of such non-climatic factors on disease dynamics, we decompose dengue incidence into terms for trend and for annual seasonality.

To account for changes, both gradual and abrupt, we extracted trends and seasonality from the weekly time series by using the Breaks For Additive Seasonal and Trend (BFAST) algorithm (Verbesselt et al. 2010). Specifically, BFAST decomposes time series into seasonality and trend components through iterative estimation of time series parameters and the detection of break points, delimiting time windows in which different seasonal and trend patterns apply. Within each time window, the effect of seasonality is assumed to be sinusoidal, but the characteristics of the sinusoidal functions vary across time windows. Similarly, trend is defined to be piecewise linear between breakpoints. The inferred seasonal and trend terms are extracted from BFAST and allowed to be used as covariates in the LASSO model.

Results

Data are presented in Figure 2. There is little overall variation in weather seasonality in Singapore over this time period (2001 to 2010), with slightly hotter temperatures (around 1–2°C higher) registered in the middle of the year, along with slightly higher absolute humidity. Relative humidity does not display any notable patterns, while the breeding percentage (i.e. the relative amount of *Ae. aegypti*) varies without any clear pattern. In contrast, dengue fluctuates between low level endemic and larger epidemic states.

In cross-validation, 12 sets of optimal model complexity parameters were selected for the 12 forecast windows. These included covariates whose effect was lagged from 1 to 20 weeks, and counting each lag separately in a total of 226 data streams, including seasonality and trend. We present the 12-week forecasts, including 95% prediction intervals, at various time points over the period 2001–2012 in Figure 3 for the LASSO and two other methods (step-down linear regression and SARIMA) (Dynamic 12-week forecasts for each model are presented in Supplemental Material, Video Files S1, S2, and S3). The LASSO and step-down approaches yield forecasts that can more accurately presage short-term incidence than the SARIMA model. The start and end of several epidemics are accurately forecasted by both LASSO and step-down approaches, although the peak of the large 2005 outbreak is not well described by the LASSO model.

The relative forecast accuracy is assessed more formally by dividing the dataset into training (2001–2010) and validation sets (2011–2012), and comparing the Mean Absolute Percentage Error (*MAPE*) of the best guess of the forecast and the coverage of the forecast interval. The results (Figure 4) support the use of LASSO to construct the forecasts: the LASSO approach yields more accurate forecast time periods for all except the first two-week window, in which the

performance of LASSO and step-down approaches are approximately equal. It is notable how slowly the *MAPE* degrades over time under the LASSO approach, with a rise from 17% error (95%CI 16—19%) forecasting one week to 24% error (95%CI 22—26%) forecasting three months into the future. In contrast, both the step-down and SARIMA approaches had a MAPE of 29% at three months ahead (95%CI 26—32% [SARIMA], 27—32% [step-down]). In addition, while the LASSO and SARIMA predictions were conservative, in the sense that the actual coverage of prediction intervals exceeded the target of 95%, the step down approach led to forecasts that under-stated uncertainty, with a coverage that sometimes fell below the nominal level of 95% (Figure 4).

Interpretation of climatic and other factors is made difficult because the strength of their association varies between forecast windows and they operate over different time lags, however recent dengue incidence (the autoregressive component) over a lag window of 1–5 weeks generally increased the forecast number of dengue cases, higher average weekly temperatures had a mostly dampening influence on forecast dengue cases, consistent with some findings in the literature (Morin et al. 2013), while the breeding percentage, reflecting the preponderance of *Ae. aegypti*, was mostly positively correlated with forecast dengue incidence. Dengue incidence over the next 4–5 weeks is positively associated with high levels of absolute humidity over the last month, and negatively associated with high humidity 15–20 weeks ago.

The forecasts at various time points in Singapore's record breaking 2013 epidemic, in which 22170 cases were reported, are presented in Figure 5. Early in the epidemic (Figure 5a), the model forecast was of a mild rise, which was exceeded by the actual epidemic. By February (Figure 5b), the forecast was an almost perfect match to the data. At the end of April (Figure 5c), the forecast was of a decline, but the range of possible scenarios (the 95% interval for the

forecast) included the subsequently observed peak at ~800 cases per week. The end of the epidemic, starting in July, was also successfully forecast. Overall, the model predicted a slightly more rapid end to, and smaller size of, the epidemic than occurred.

Discussion

Penalized regression, of which LASSO is the most prominent methodology, is an idea that dates back to the 1990s (Tibshirani 2011), and which has over the last decade led to substantial theoretical and methodological advances in “small n large p” problems in which the number of observations is smaller than the number of potential predictors. By optimizing a combination of model goodness of fit (via the likelihood) and model complexity (via a penalty that grows with the size of the parameters in the model), and using cross-validation to identify the optimal penalty term, penalized regression can simultaneously handle both model building and parameter estimation, avoids over-fitting, and improves out-of-sample predictive accuracy (Hoerl and Kennard 1970; Zhao et al. 2006). By shrinking regression coefficients of less importance to or towards zero, and thereby retaining only the most important predictors, LASSO is able to obtain good interpretability and stability (Zhao et al. 2006).

Despite being a well-established methodology that is frequently used in bioinformatics and other big-data applications (González-Recio et al. 2009; Shi et al. 2007; Wu et al. 2009), there are few applications of LASSO in epidemiology (for instance, Walter and Tiemeier 2009) or neglected tropical diseases. In this paper, we have demonstrated the use of LASSO in forecasting an endemic and high-burden disease—dengue—in Singapore which, by virtue of its location near the equator and concomitant lack of seasonality, leads to unpredictable outbreaks above the usual endemic level. The methodology has several advantages over traditional approaches: (i) model selection is rapid (approximately 2 minutes), automatic and objective, in contrast to more

laborious and sometimes subjective approaches such as the Hosmer-Lemeshow (2000) purposeful approach to model building or common approaches such as forward selection using p -values (Grechanovsky and Pinsker 1995); (ii) tautologically, by selecting the model complexity using cross validation to optimize predictive performance, predictive performance of the routine is optimized, and so the task of making better and more accurate forecasts is reduced to that of finding potentially informative covariates; (iii) LASSO allows large numbers of possible predictors to be considered without prejudicing the accuracy of the routine, as non-predictive variables obtain zero coefficients for optimal values of the penalty term and thereby drop-out of the final model; (iv) By using distinct models for 1-week forecasts, 2-week forecasts, and so on, the variables used and the values of their associated coefficients can be tailored to the specific requirements of forecasting at different lengths into the future. While recent dengue cases (over the last 4 weeks) are important in forecasting for 1–12 weeks, average temperature is not useful in short-term forecasts (1–3 weeks) though it is for longer forecasts (4–12 weeks), highlighting the need for separate submodels for different forecast windows. Having distinct submodels also obviates the need to forecast future values of the predictors, as would be the case if a single model for one-week ahead were used and then iterated to obtain longer term forecasts. This approach led to high accuracy for both immediate (next week, MAPE 17%) and longer term (3 months, MAPE 24%) predictions. Although the forecast accuracy degrades as the forecast window is extended (see Figures 4), this degradation is surprisingly slight and we were able to predict the large outbreaks of both 2013 and 2014 over 10 weeks in advance, giving advance warning to allow operations to be rolled out. We restricted the forecast window to 12 weeks to avoid the higher level of inaccuracy that accompanies longer term projection and because short

(several weeks) and medium term (several month) projections are the most useful for local planning purposes.

There are, however, some limitations to this approach, the most major of which is that, although very good predictive accuracy can be achieved, the collection of 12 models built using LASSO methods are not amenable to interpretation as they are constructed for their predictive accuracy, not to explain the etiology of outbreaks. In particular, attempts to explain to stakeholders why the model forecast a large epidemic in 2013 were hindered by the numerous covariates acting at different lags. Interpretation is increasingly difficult at longer forecast windows. For example, around 60 predictors out of the complete set of more than 200 were selected for the 12-week-ahead sub-model. Among these 60 variables, often the same covariate at different lags was selected, and frequently with differently signed coefficients at those different lags. The complexity needed for good forecasts reflects the multitude of factors operating on the vector and virus-vector interactions. One plausible way to reduce the apparent complexity would be to combine our approach with a mechanistic model of drivers of the mosquito life cycle, for instance via the Focks model (1995), with output from the mechanistic model replacing some or all of the environmental drivers in the statistical model. The variables we used include meteorological data, case data, vector surveillance data and human population data. Other relevant indicators of risk, particularly on circulating serotypes, genotypes, and evidence on herd immunity via occasional sero-epidemiological surveys, may subsequently be incorporated. However, because comprehensive analysis of genotype and serotype of dengue cases in Singapore started around 2006, and testing protocols have evolved since, we need to explore the best way to incorporate these sources of information.

The forecasting tool described in this paper has become an integral part of Singapore's dengue control program. The final model is embedded in a "real-time" schedule, with data (at present) being updated weekly and predictions sent out to our operational partners (examples of the forecasts used in the 2013 outbreak are shown in Figure 5), including the Ministry of Health and the Environmental Public Health Operations Department of NEA. During the 2013 epidemic, our forecasts helped guide hospital bed management and public health interventions, including pre-emptive source reduction measures, recruitment of ground staff, and education campaigns. In late March 2013, our models forecasted an earlier than usual increase in dengue cases in June 2013, which could potentially peak at 800 cases/week. Specifically, the forecast predicted a peak in case count of 863 during the 26th week of 2013, which is very close to the observed number of cases, which peaked at 842 cases/week during the 25th week. On top of resource planning, this also facilitated early risk communication to the public, and the advanced launch of Dengue Campaign in April, two months ahead of its traditional June launch.

Future work will automate the data handling process so that predictions can be generated and posted online without the routine being rerun manually; such automation will also allow the forecast to be made daily and hence to be genuinely 'real time'. Extending the forecasts beyond 12 weeks may be challenging as some of the key drivers, such as local weather conditions, may have a short term but strong effect on dengue that requires integrating the predictive model with weather forecasting models, where longer term forecasts may not be readily available.

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Figure Legends

Figure 1: Model framework. Raw data from 2001 to 2010 including dengue cases, breeding percentage, temperature, humidity and population statistics are collated from Ministry of Health, National Environment Agency, and Department of Statistics Singapore before being transformed and divided into sets each containing predictors and a single output (dengue incidence at a future time point). In the third step, the LASSO method is employed to train and select the optimal models for future dengue forecast. In total 12 models are generated, one per forecast week. In the final step, the 12 models are aggregated together to make predictions over a 12-week window.

Figure 2: Model input from 2001 to 2012. (a) dengue incidence, (b) breeding percentage (BP), defined as the proportion of *Ae. aegypti*, the primary vector of dengue in Singapore, compared to all *Aedes* spp (c) temperature, (d) relative humidity and (e) absolute humidity from 2001 to 2012. Data sources are described in the text.

Figure 3: Comparison of dengue forecast from 2001 to 2012. Dengue forecast using (a) LASSO, (b) step-down linear regression and (c) SARIMA. For the LASSO, step-down linear regression and SARIMA methods, we selected all the data (2001 to 2012) except the year being forecast to develop the model (to approximate the out of sample predictive performance in the other results). In each plot, red lines represent model-based point estimates and the pink contours represent corresponding 95% prediction intervals. Each segment of predicted data (i.e., each pink and red region) represents the estimates from one 12-week forecast made at a previous point in time. Forecasts at other times are suppressed to simplify the figure, but are presented in Supplemental Material, Video Files S1, S2, and S3.

Figure 4: Comparison of model performance among SARIMA, Step-Down linear regression and LASSO using Mean Absolute Percentage Error (MAPE %) and coverage of nominal 95% intervals. (a) MAPE comparison among LASSO, step-down linear regression and SARIMA over 1 to 12 weeks forecast windows. MAPE with 95% confidence intervals for LASSO, step-down linear regression and SARIMA are represented with vertical bars, filled orange polygons and filled blue polygons, respectively. The MAPE degrades slower over time under the LASSO approach, with a rise from 17% error forecasting one week to 24% error forecasting three months, although the LASSO approach yields comparable accuracy as step-down linear regression and SARIMA for the first two weeks. (b) Coverage of LASSO, step-down LR and SARIMA. For each forecast window period, the percentage coverage is calculated using the number of observations which fall within the 95% interval derived by overlaying the estimated error distribution on top of the forecast. The dashed line represents the nominal coverage of 95%.

Figure 5: Illustration of model forecast in 2013 at weeks 1 (a), 8 (b), 16 (c) and 24 (d) using the LASSO method. In each panel, the x-axis represents time (2012/2013) and the y-axis the weekly number of dengue cases. The black lines indicate observed cases, the black dots indicate predicted (forecast) cases, and the pink contours indicate 95% intervals for the forecasts.

Figure 1.

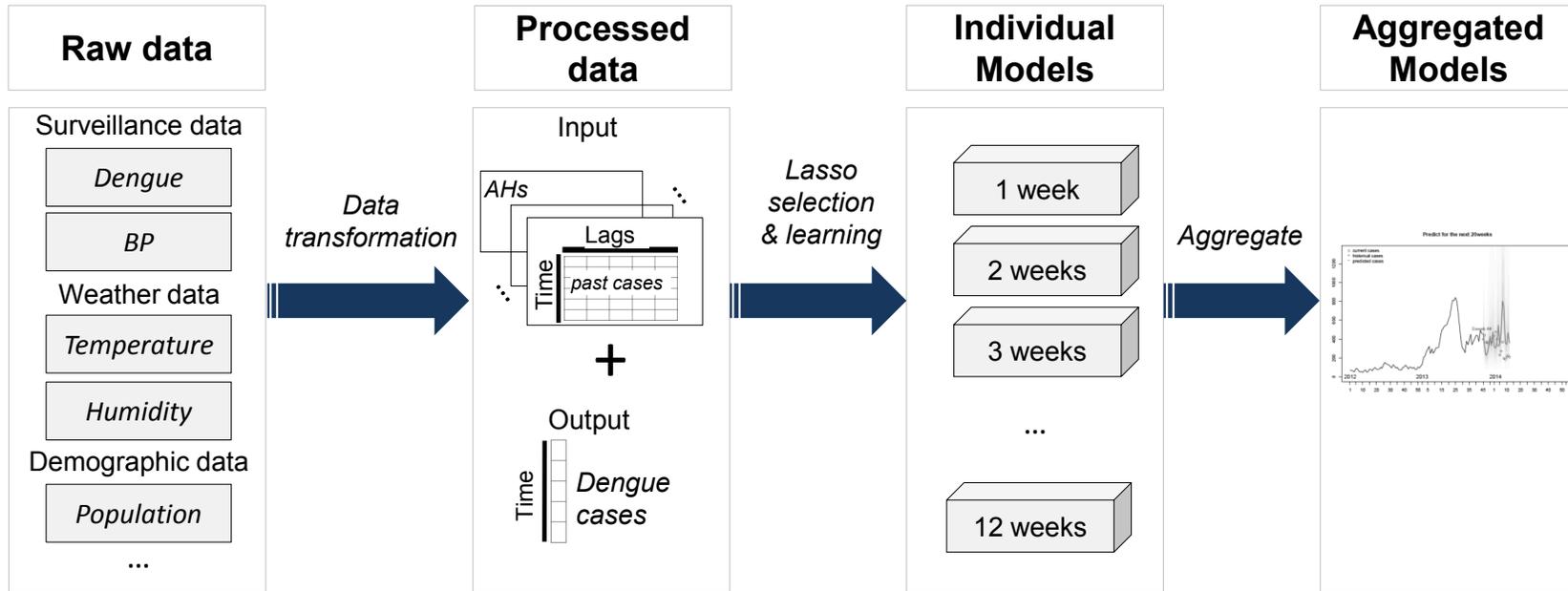


Figure 2.

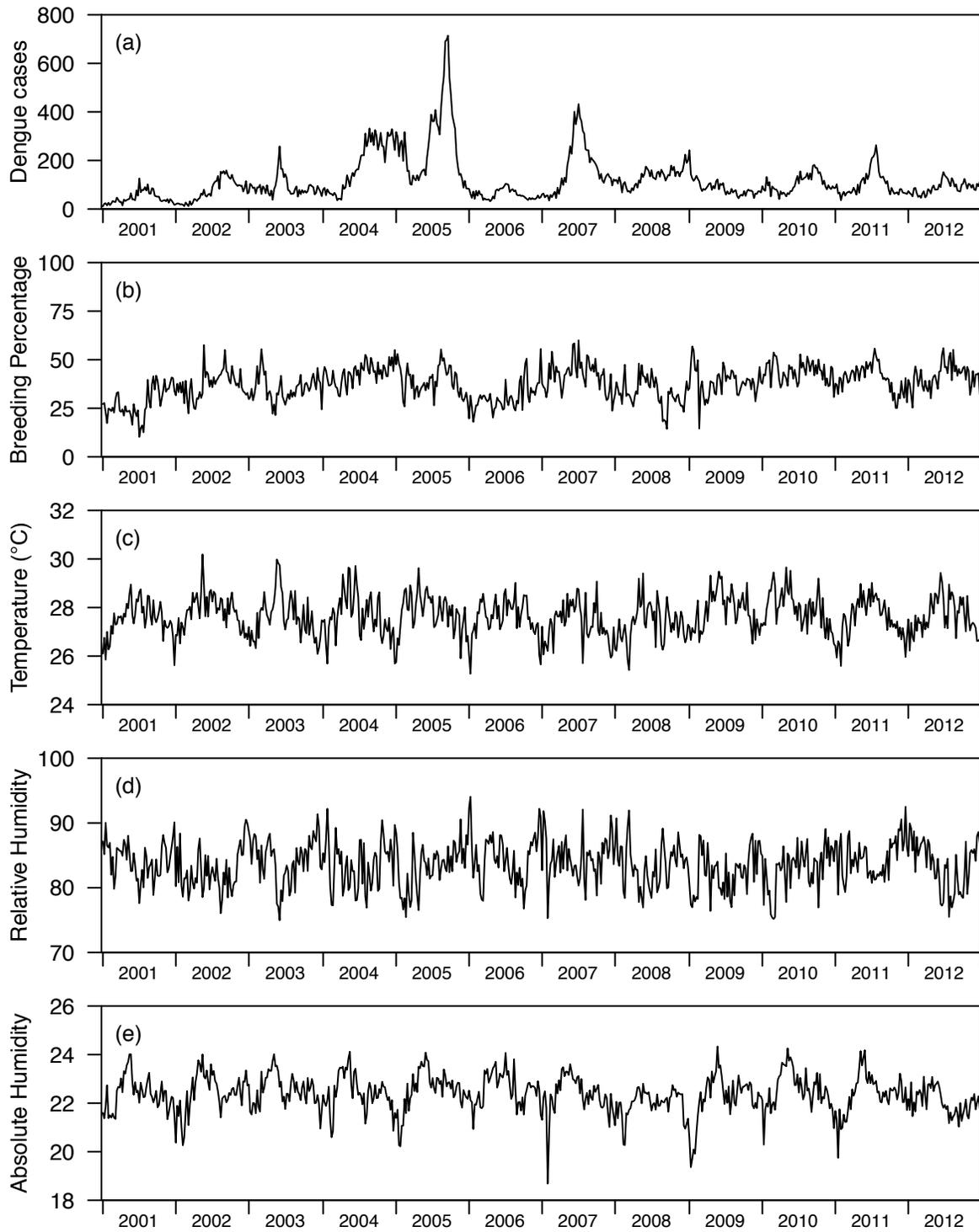


Figure 3.

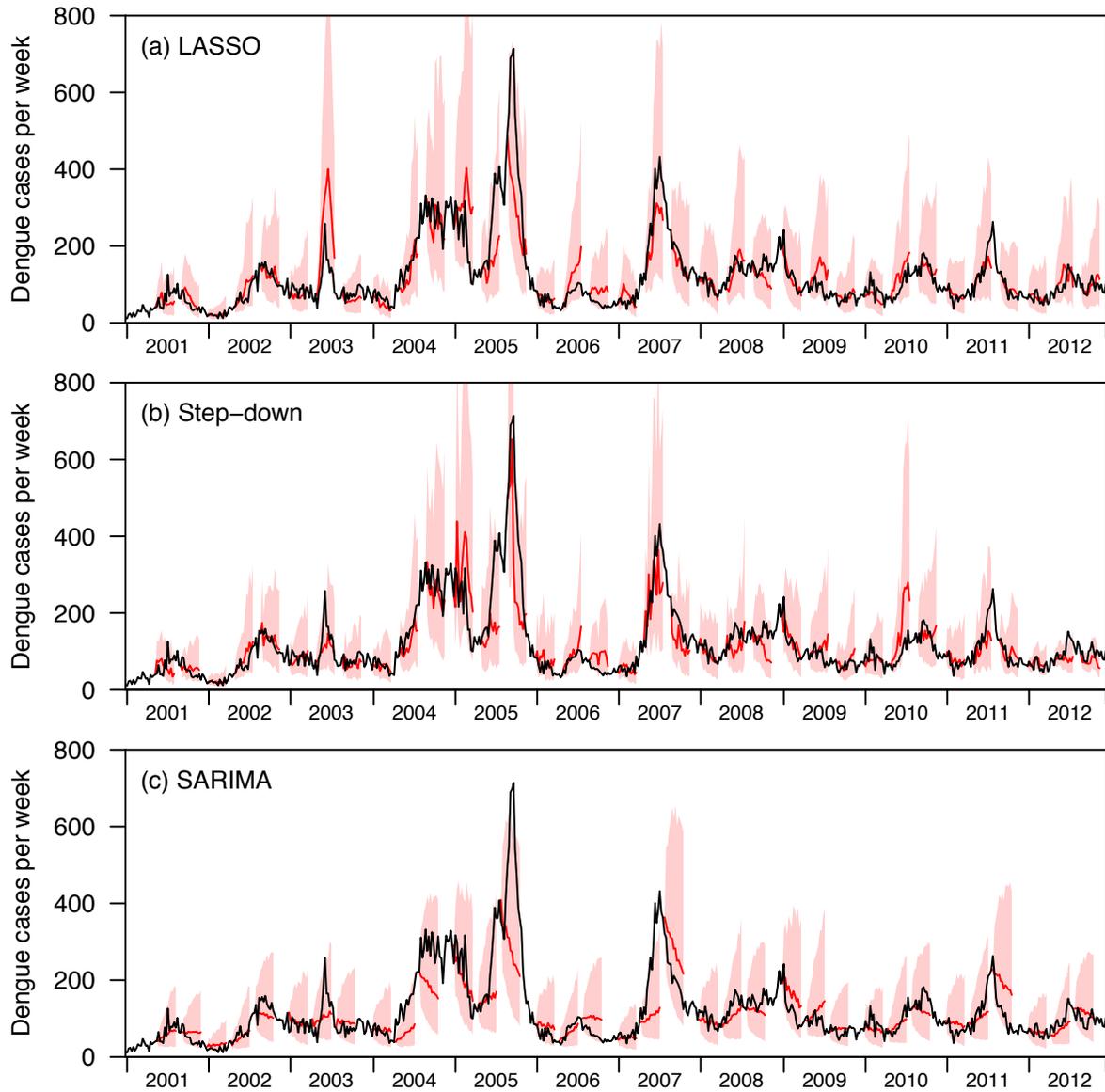


Figure 4.

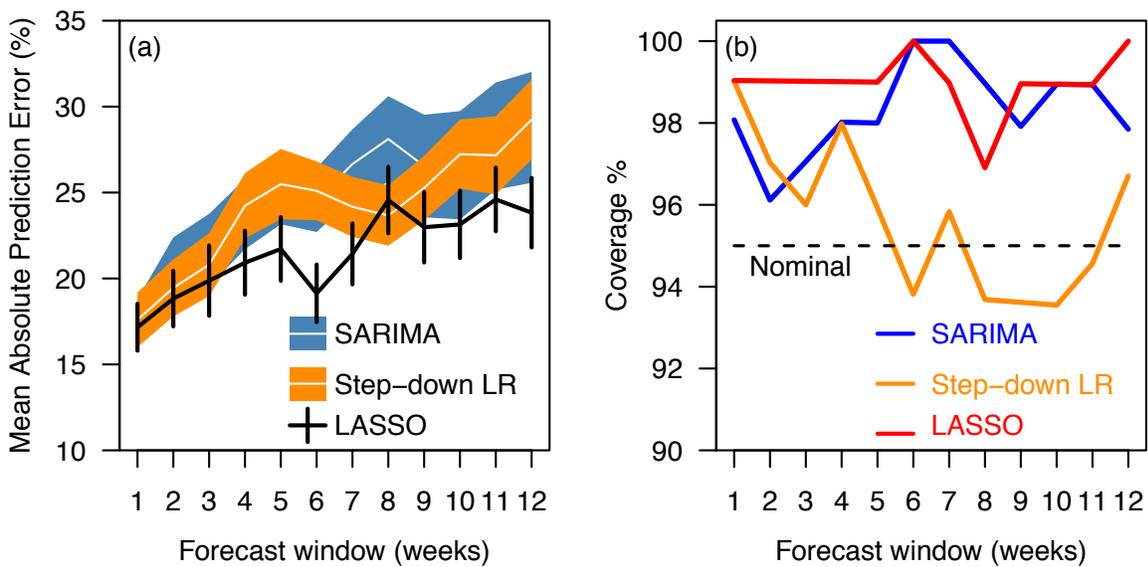


Figure 5.

