A dynamic, ensemble learning approach to forecast dengue fever epidemic years in Brazil

Using weather and population susceptibility cycles

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- The global burden of dengue has doubled every 10 years over the last three decades.

Material and methods

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1. Signal prepossessing
2. Time-series feature extraction
3. Independent model training and prediction
4. Model selection
5. Ensemble prediction
6. Dengue cycles

Signal pre-processing

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- Windowing approach:
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- Each time interval and weather variable is summarized by 30 data points.
- Build hundreds of models on different intervals to select those with the strongest signals.

Time-series feature extraction

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1. The arithmetic means of daily temperature.
2. Mean precipitation frequency defined as the time interval between peaks of daily precipitation.

Independent model training and prediction

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Remark

Radial basis function and sigmoid kernels are used and model parameters (gamma, soft margin cost function and coefficient) using 10-fold cross-validation are tuned.

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Note

The selection of the 11 models changes from year to year as the model-building process is dynamic.

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- Use a simple majority vote of the 11 models to decide a single forecast which are produced for the last 6 years of the 17-year data-set.
- These represent the culmination of a prediction process that involves:
  7-year initial training period,
  4-year out-of-sample model calibration period,
  6-year out-of-sample ensemble prediction period.

Dengue cycles

Endemic transmission of dengue fever is typically distinguished by periodic outbreak cycles of around 3–4 years because of

1. An exhaustion of susceptible after an outbreak.
2. Short-term cross-immunity to other circulating DENV serotypes after infection.

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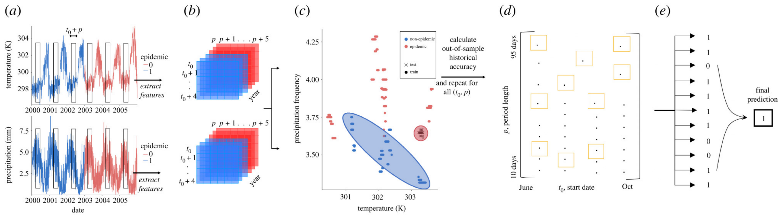
- So, implement a decision rule governed by the second- and third-order Markov transition probabilities, reflecting the transition between consecutive sequences of epidemic and non-epidemic states.
- The transition probabilities corresponding to the following 3- and 4-year cycles: 001, 110, 0001 and 1110.

Results

Figure: Ensemble forecast workflow



1. Extract features of temperature and precipitation.
2. An array of features corresponding to the mean value.
3. Train an SVM to classify next year's epidemic status.
4. Repeat for all 432 intervals and top 11 models are selected.
5. Contribute to a majority voting system.

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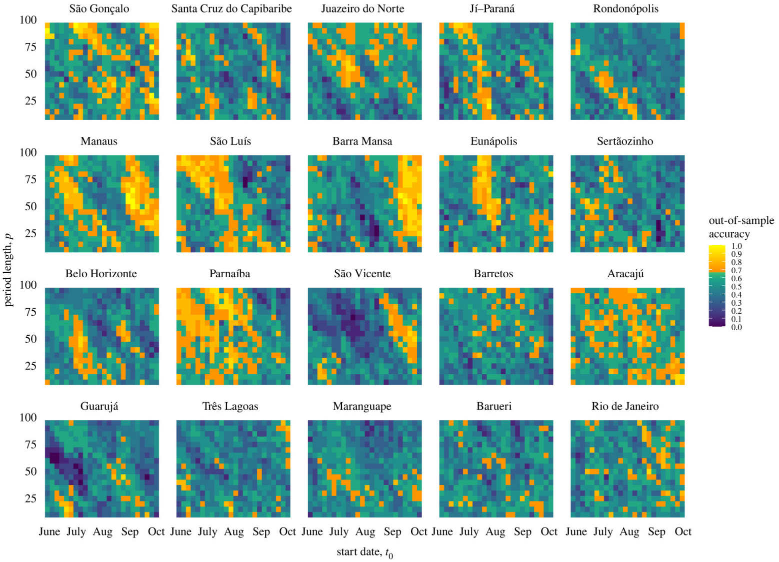
- Every year, the time intervals with high historical predictive power are automatically selected and evaluated in the upcoming year to produce out-of-sample predictions for the subsequent dengue season.
- An ensemble approach determines the system's final prediction: whether a year would be epidemic or not.

Out-of-sample forecast accuracy for 2008-2017



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  Five out of six ensemble years predict correctly for both of these two.
- Weather-based predictions are less successful due to no clear temporal trend like Rio de Janeiro.

Incorporating dengue susceptibility cycles

- Given the previously observed sequence of consecutive outbreak and non-outbreak years (dengue fever cycles), the Markov model computes the probability of the next year being an outbreak or a non-outbreak year.

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- While the weather conditions are identified to be an outbreak, there is stronger evidence that the population may have low susceptibility to infection based on multiple consecutive preceding years.

Results

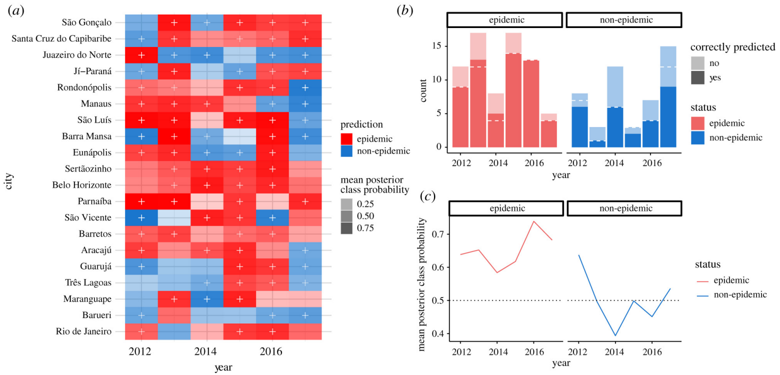

Figure: Weather-based prediction results for 120 municipality years

1. Annual out-of-sample forecasts of outbreak status.
2. Number of correctly forecasting year.
3. The mean posterior class probability across municipalities,

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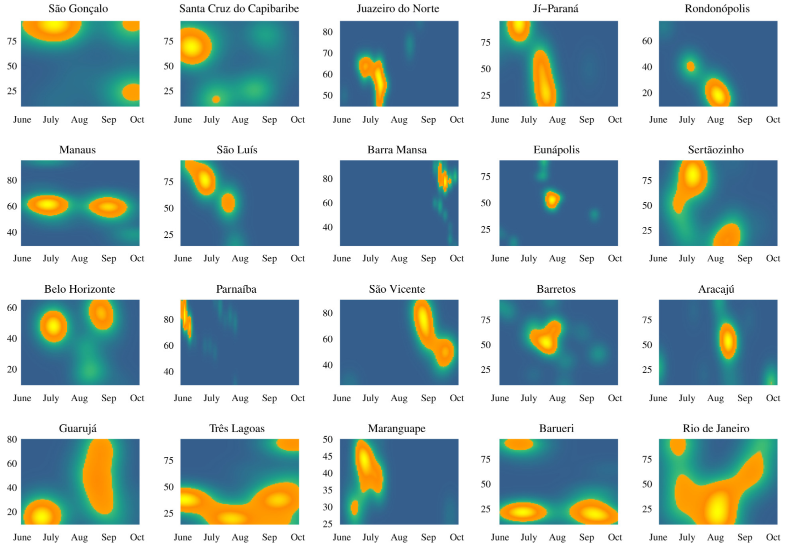
- In 2012, the most successful non-epidemic predictions are occurred with 75% accuracy.
- 80% and 85% of municipalities are correctly classified as epidemics or non-epidemics in 2015 and 2016.
- In 2014 and 2017, 45% and 35% municipalities are misclassified respectively.

Periods of the year selected into the ensemble forecast model for 2012–2017



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- But only this measure of separability is not a particularly good indicator of accuracy.

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- These models can be extended to other locations requiring no location-specific manipulation.
- Our models miss half of non-epidemics in 2014 because of the immunity provided by a large outbreak in 2013.
- Our approach achieves an overall accuracy of 75%.

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