

To be linked from: <http://lega.uazmath.org/> & <http://brownlab.arizona.edu/>

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Globally we are faced with novel challenges due to emerging infectious diseases. Stemming an epidemic must happen with only a modicum of information. To preposition supplies and assess the success of disease control public health responders need tools to **predict the magnitude and duration** of an outbreak.

Under conditions where

- an epidemic spreads relatively quickly,
- there is a large number of susceptible individuals, and
- for a vector-borne disease, the vector is present and abundant,

we provide a simple model which **predicts the number of cases and peak growth rate** of the epidemic using Chikungunya in the Caribbean and Central America as a case study.

Technical Approach

- 1) Countries are grouped based on the number of cases and the likelihood of disease (by analogy with dengue which is transmitted by the same mosquitoes).

Table: Country Groupings by Current Cases and Vector Presence

CHIK incidence rate less than 1/100,000	Less than 20 CHIK cases			GROUP 0 (11 countries)
	More than 20 CHIK cases	DEN incidence rate less than 5/100,000		GROUP I (4 countries)
CHIK incidence rate larger than 1/100,000	More than 20 CHIK cases	DEN incidence rate less than 5/100,000		GROUP II (0 countries)
		DEN incidence rate larger than 5/100,000	1-parabola model	GROUP III (28 countries)
			2-parabola model	GROUP IV (12 countries)

- 2) Data are smoothed and interpolated to a ¼ day mesh size.
- 3) Epidemic growth rate, G , for each country is plotted as function of the number of cases, N .
- 4) The function $G=f(N)$ is approximated by an inverted parabola in the form

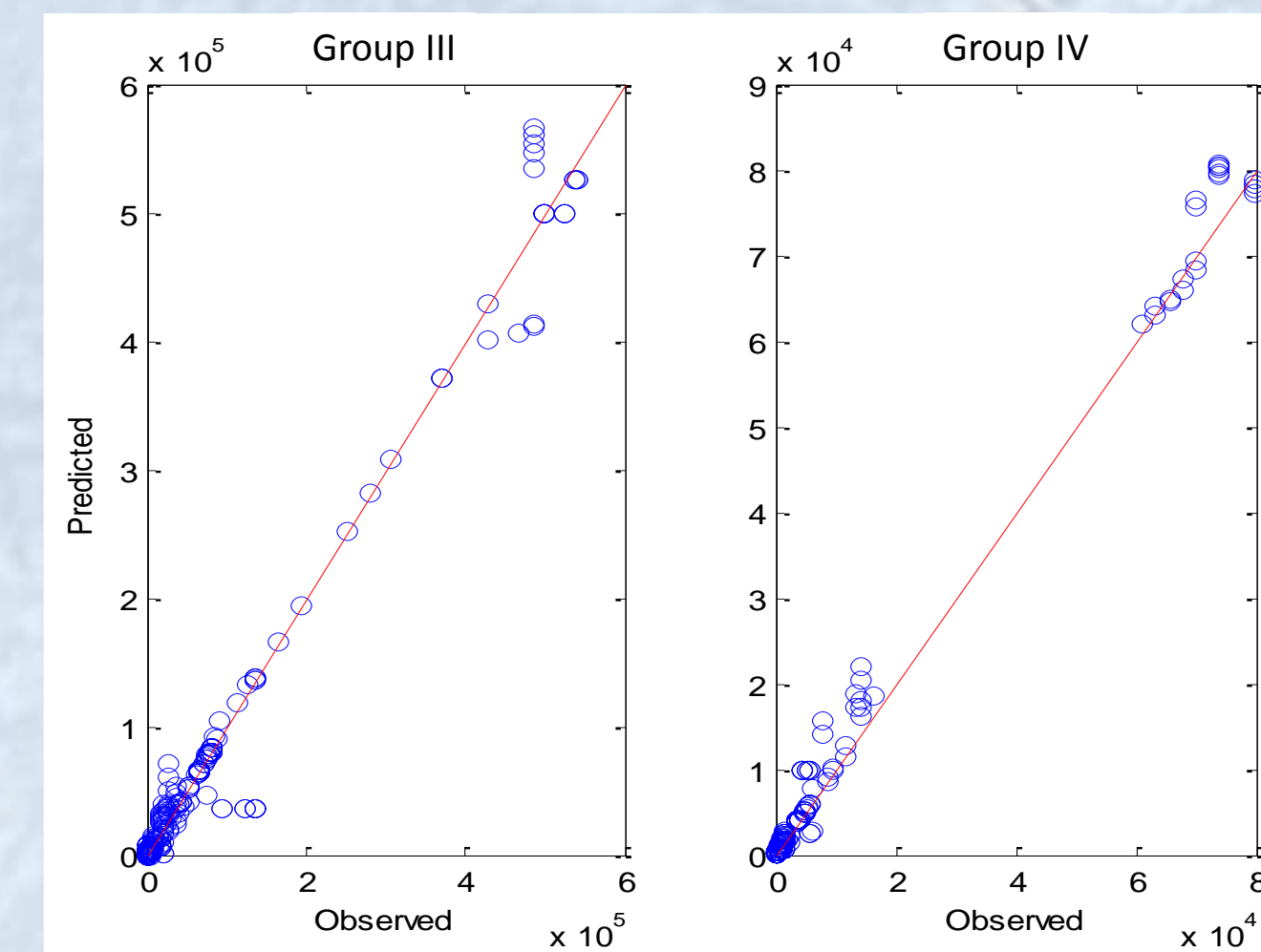
$$G_2(N) = \frac{4M}{N_0^2} N(N_0 - N),$$

and the final number of cases, N_0 , as well as the peak growth rate, M , are estimated for each country by fitting the data.

- 5) Future number of cases is estimated by integrating the differential equation $\frac{dN}{dt} = G_2(N)$ with an initial condition chosen from the smoothed, interpolated observed data (step 1).

Model Robustness

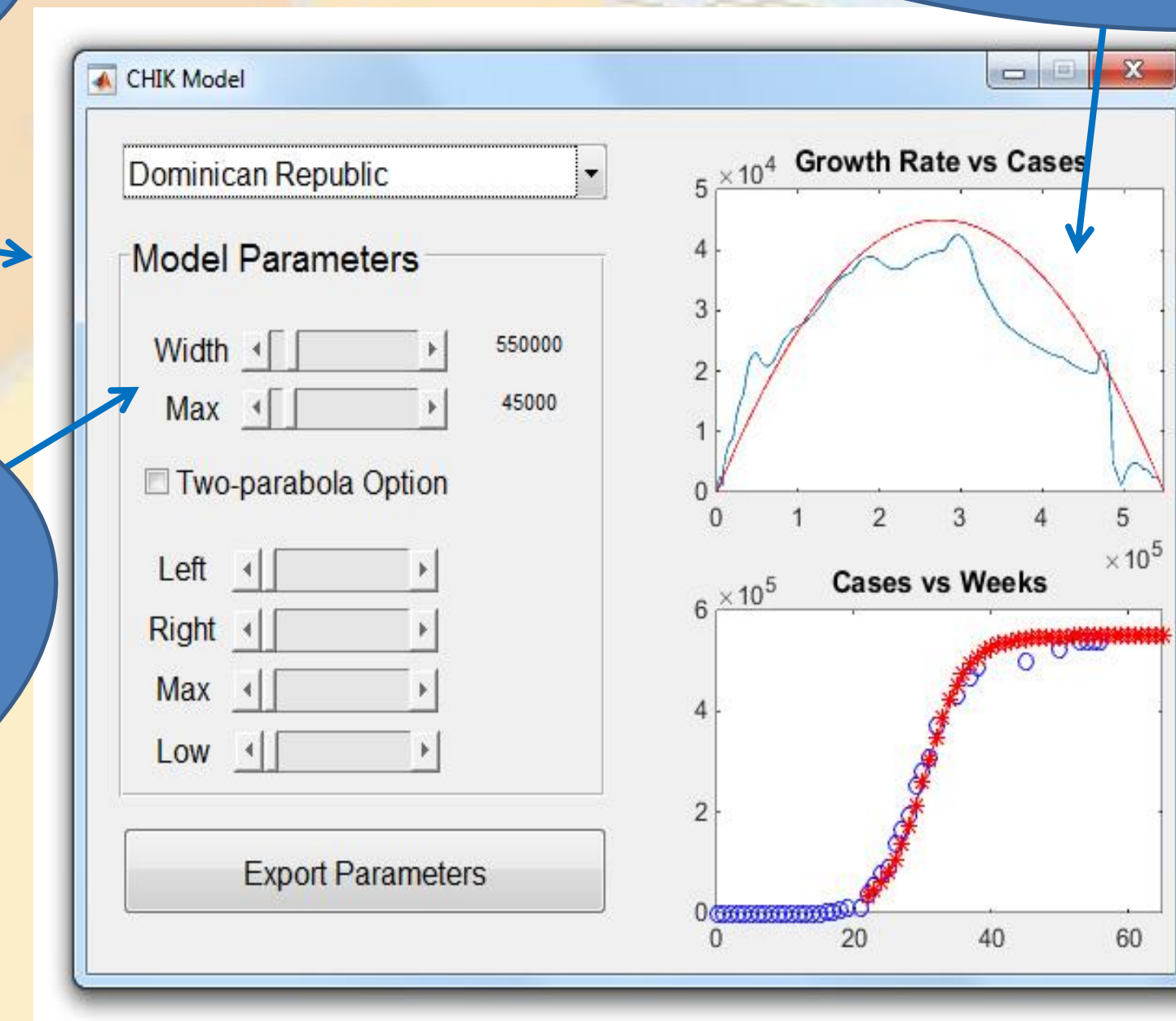
- The model is expected to have predictive value for countries in Groups III and IV.
- Due to the small number of parameters, the model is easy to use and quickly yields predictions.
- The parameters are user-estimated from the graph of G , which is obtained from observed data. Predictions become more accurate as the epidemic progresses.
- Noise in the data increases the fluctuations of G , but does not necessarily affect the choice of model parameters.



Drop-down Selection
Select country pre-loaded with observed cases of an ongoing epidemic

Visually Fit the Model
- One or two parabola option
- Sliders to fit maximum (peak growth rate) and width (final number of cases) of outbreak

Downloadable Tool



The Next Challenge

While this approach allows the user to estimate the total number of cases and peak growth rate of the epidemic, it cannot identify where, when and what the next infectious disease threat will be.

Predict Establishment

Model Input (sources)

- **Current Cases:** weekly total number of reported cases (Pan American Health Organization)
- **Proxy Data:** dengue as indicator of vector abundance and, therefore, likelihood of similar CHIK activity (PAHO)
- **Ancillary Data** (not used in final model): Economic data, Health indicators, Connectivity (various sources including: CIA, Socio-Economic Database for Latin American & Caribbean (SEDLAC), ArcGIS)