

Epi-scanner: Scalability and Comparability for Epi-parameter Estimation

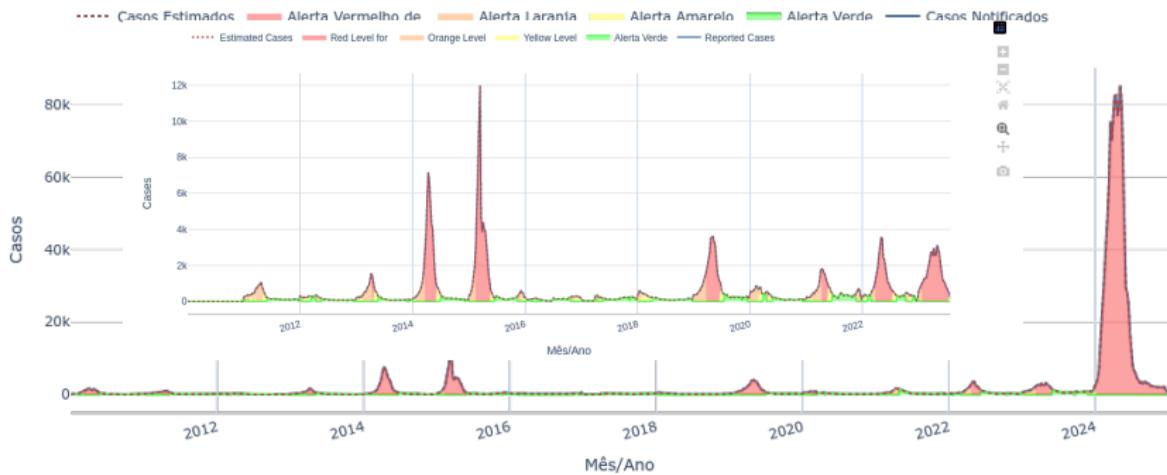
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January 27, 2025



Online Monitoring of Seasonal dengue Epidemics

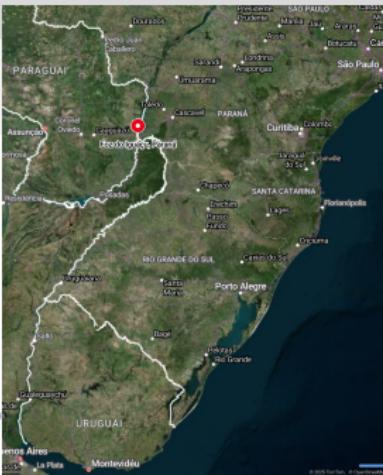
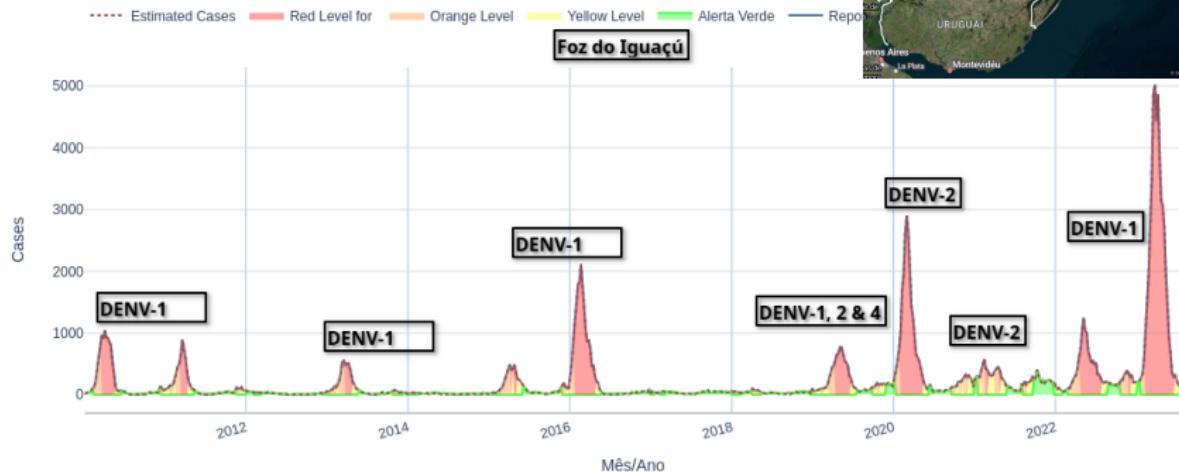
Infodengue (São Paulo city):



- Complex temporal patterns
- Timing and size are very important
- Inter-year variability
- Why are we monitoring?

Alternation of Serotypes

Dominating Serotypes:



Problem statement

MBD diseases such as dengue and chikungunya are endemic and seasonal in Brazil, sharing the same vector.

Goals:

To extract descriptors(parameters) of epidemics that can help us understand the impact of environmental and control variables on disease dynamics.

- Do it efficiently
- Do it comparably (use the same model)
- Parameters of interest: R_0 , EW of the peak,
 - R_0
 - Peak week
 - Peak size
 - Start, end, and duration of the epidemic
 - Total cases

Modeling the Epidemic curves

Simple Logistic function (Richards function) that matches cumulative incidence.

$$J(t) = L - L \left[1 + \alpha e^{b(t-t_j)} \right]^{-\frac{1}{\alpha}}$$

where $J(t)$ is the cumulative number of cases at time t , L is the total number of cases at the end of the season and t_j is the week of the peak. SIR model parameters can be obtained from this fitted function;

$$\beta = \frac{b}{\alpha}; \gamma = b \left(\frac{1}{\alpha} - 1 \right); \mathcal{R}_0 = \frac{\beta}{\gamma}$$

 arXiv > q-bio > arXiv:2407.21286

Quantitative Biology > Populations and Evolution

[Submitted on 31 Jul 2024]

Large-scale Epidemiological modeling: Scanning for Mosquito-Borne Diseases Spatio-temporal Patterns in Brazil

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Fitting the Model to Data

Let $\xi := \{L, \alpha, b, t_j\}$ be the set of parameters of the Richards function to be estimated. The model is fit to data by minimizing the following error:

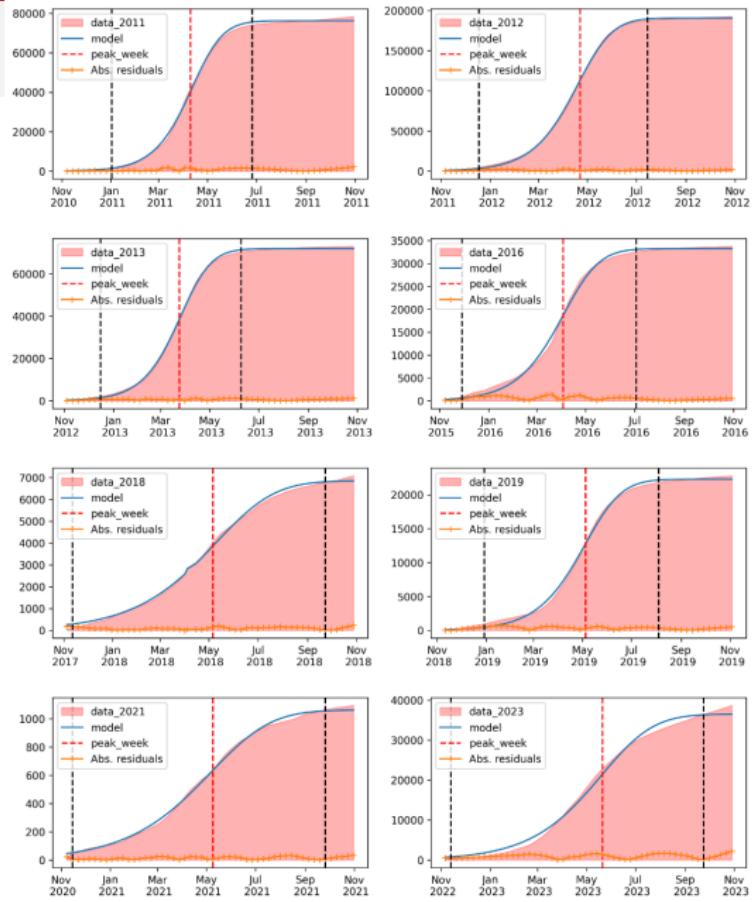
$$\operatorname{argmin}_{\xi} \sum_{t=1}^{\tau} \frac{[C(t) - J(t, \xi)]^2}{\tau}, \quad (1)$$

where $C(t)$ is the observed cumulative number of cases at week t and $\tau = 52$.

To better match the seasonality of dengue, $t = 1$ corresponds to actual EW 40.

Example fit

Rio de Janeiro



The Web tool

info.dengue.mat.br/epi-scanner

INF Real-time Epidemic Scanner
DENG Real-time epidemiology

Select disease *
Dengue

Select state *
Minas Gerais

Select city *
Belo Horizonte

Results

Abadia Dos Dourados :2 epidemic years: [2015, 2023]

Abaeté :4 epidemic years: [2013, 2015, 2019, 2023]

Abre Campo :1 epidemic years: [2016]

Almorés :5 epidemic years: [2011, 2013, 2015, 2019, 2023]

Alfenas :8 epidemic years: [2013, 2014, 2015, 2016, 2019, 2020, 2022, 2023]

Almenara :1 epidemic years: [2022]

Alpinópolis :3 epidemic years: [2016, 2019, 2023]

Alterosa :1 epidemic years: [2023]

Alto Jequitibá :1 epidemic years: [2020]

Alto Rio Doce :1 epidemic years: [2023]

Alvarenga :3 epidemic years: [2016, 2019, 2023]

Epi Report for dengue
Minas Gerais

Number of weeks of $R_t > 1$ over the last s10 years

name_muni: Belo Horizonte
transmissao: 146

Weeks
0 20 40 60 80 100 120 140

RO by City

Minas Gerais 2022

Top 10 cities

Names	Epi Weeks
Belo Horizonte	146
Uberlândia	141
Contagem	127
Uberaba	125
Patos De Minas	120
Betim	114
Unaí	107
Montes Claros	106
Santa Luzia	94
Ituiutaba	94

Top 10 ROs Year

Names	RO
Capetinga	3.29
São João Batista Do	...

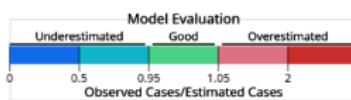
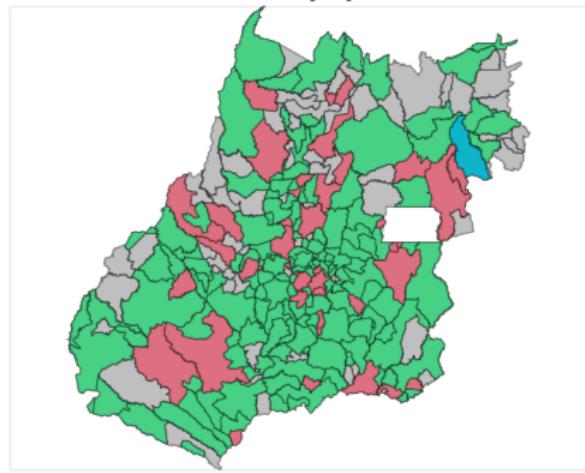
FGV EMAP

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Goodness of fit

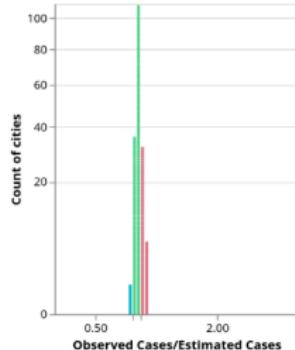
Observed Cases/Estimated Cases by city in 2022



* Cities in gray did not have an epidemic detected.

Year

2022



Range Range Counts(%)

(0.0, 0.5]	0 (0.0%)
(0.5, 0.95]	1 (0.54%)
(0.95, 1.05]	145 (78.8%)
(1.05, 2.0]	38 (20.65%)
(2.0, Inf]	0 (0.0%)

Usability

Health services base control measures on Epidemiological expectations.

Main questions:

- Are we having an epidemic next year?
- How big?
- How soon?

Requirements

- Comparable results
- FAIR (Findable, Accessible, Interoperable, Reusable)
- Up-to-date estimates

The dataset



Mosqlimate API Documentation

[Home](#) [Model Registry](#) [Datastore](#) [Tutorials](#) [Back to API](#)

[Datastore](#)

[Datastore API](#)

[Infodengue](#)

[Climate](#)

[Mosquito](#)

[EpiScanner parameters](#)

Epscanner parameters

EpiScanner Data

Here you get access to Real-time Epidemic Scanner data from the [Epi-Scanner tool](#), co-developed by the InfoDengue project. These data, described below, are based on the analyze of the expansion of dengue, zika and chikungunya in Brazil using up-to-date incidence data from Infodengue.

Usage examples

[Python3](#) [R](#) [curl](#)

`import requests`

```
episcanner_api = "https://api.mosqlimate.org/api/datastore/episcanner/"
```

```
params = {
    "disease": "dengue",
    "uf": "SP"
}
```

```
resp = requests.get(episcanner_api, params=params)
```

```
items = resp.json() # JSON data in dict format
```



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Data format

[JSON](#) [Raw Data](#) [Headers](#)

Save Copy Collapse All Expand All Filter JSON

```
▼ 0:
  disease: "dengue"
  CID10: "A98"
  year: 2024
  geocode: 5213707
  muni_name: "Montes Claros de Goiás"
  peak_week: 22.6764758408699
  beta: 0.5443679192262395
  gamma: 0.30656036899463
  R0: 1.7757282880742329
  total_cases: 784.5438190424866
  alpha: 0.43685078802032628
  sum_res: 0.5722592274021177
  ep_ini: "202351"
  ep_end: "202428"
  ep_dur: 29
```

```
▼ 1:
  disease: "dengue"
  CID10: "A98"
  year: 2024
  geocode: 52202880
  muni_name: "São Patrício"
  peak_week: 24.661602797093266
  beta: 0.5438967432832673
  gamma: 0.3844585978807575
  R0: 1.7864391037018374
  total_cases: 66.47525264807837
  alpha: 0.44022721069651227
  sum_res: 0.9493756166250191
  ep_ini: "202401"
  ep_end: "202430"
  ep_dur: 29
```

<https://api.mosqlimate.org/api/datastore/episcanner/?disease=dengue&uf=GO>

[JSON](#) [Raw Data](#) [Headers](#)

Save Copy Collapse All Expand All Filter JSON

```
▼ 0:
  disease: "chik"
  CID10: "A92.0"
  year: 2024
  geocode: 5211503
  muni_name: "Itumbiara"
  peak_week: 26.74297249882963
  beta: 0.5417300734503944
  gamma: 0.3287969789896593
  R0: 1.6476126852352613
  total_cases: 686.8337592649965
  alpha: 0.39306124008312615
  sum_res: 0.6281256738456736
  ep_ini: "202401"
  ep_end: "202433"
  ep_dur: 32
```

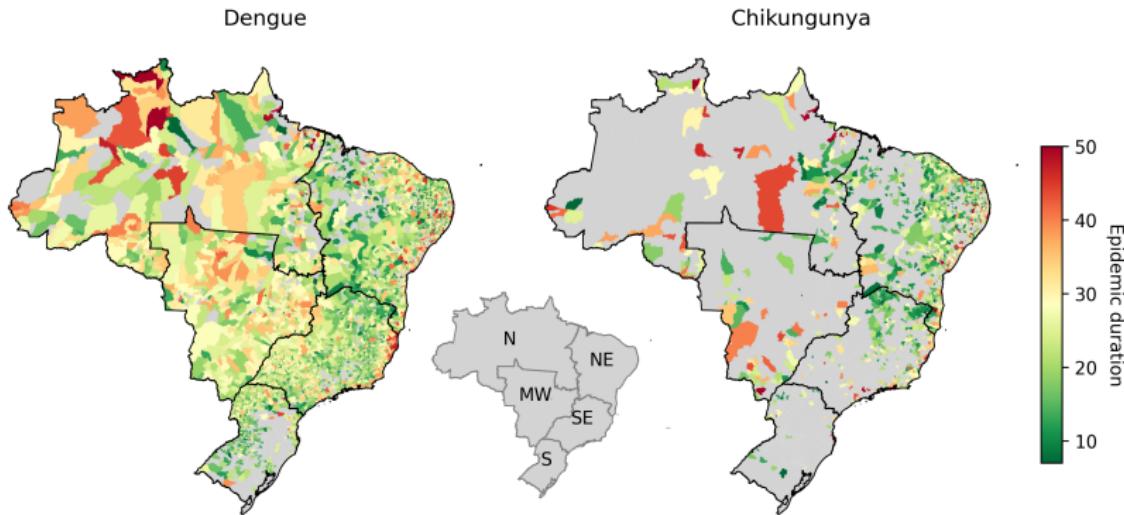
```
▼ 1:
  disease: "chik"
  CID10: "A92.0"
  year: 2024
  geocode: 5219753
  muni_name: "Santo Antônio do Descoberto"
  peak_week: 17.64547162283811
  beta: 0.45916686778227794
  gamma: 0.3110223014241406
  R0: 1.4763149317582627
  total_cases: 198.06157871172584
  alpha: 0.32263775263112776
  sum_res: 2.3352591252828563
  ep_ini: "202346"
  ep_end: "202428"
  ep_dur: 34
```

<https://api.mosqlimate.org/api/datastore/episcanner/?disease=chikungunya&uf=GO>

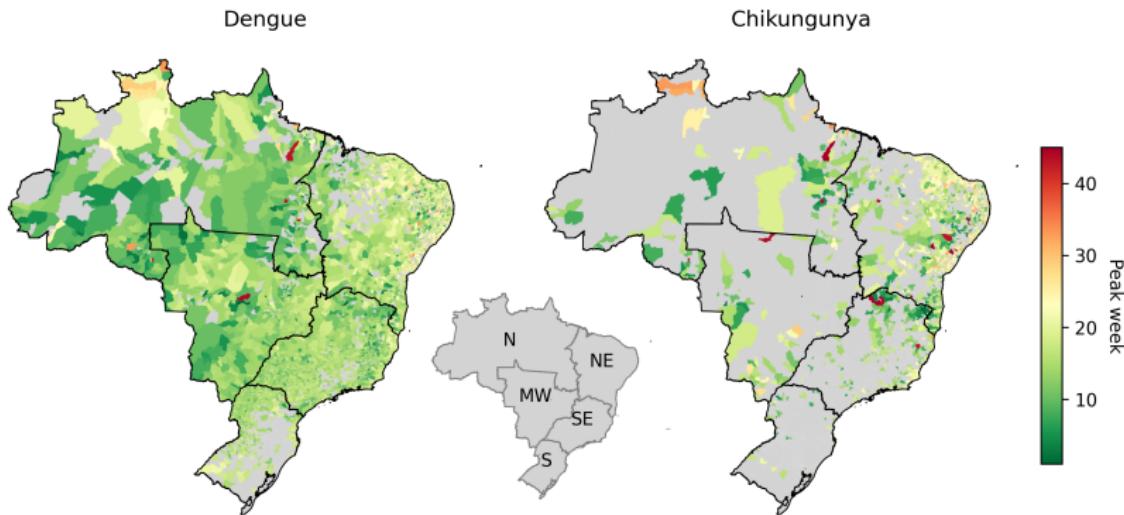


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Spatial patterns



Spatial patterns



Summary

- Episcanner is available as an opensource tool
- It can be adapted for any SIR-like epidemic curve
- Models are re-estimated every week.
- Parameters have been used successfully in forecasting models
- Main requirement for usage is consistent availability of data
- We welcome collaborators!

Acknowledgements

Episcanner has benefitted from the collective effort of the teams of Infodengue and the Mosqlimate projects.



info.dengue.mat.br



mosqlimate.org



Thank you!

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