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Research article

The transmission of chikungunya virus

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Abstract: The global resurgence of chikungunya virus (CHIKV) in 2025, with significant outbreaks reported in the Americas, islands in the Indian Ocean, Asia, and Western Pacific region, has raised new public health concerns. Brazil remains one of the most heavily affected countries, with more than 180,000 reported cases. This global situation makes understanding early signals and cross-regional transmission patterns increasingly important. Chikungunya and dengue are spread by the same vectors: Aedes mosquitoes. Hence, comparative analysis of transmission of chikungunya virus (CHIKV) and dengue virus (DENV) can be productive. Our comparative analysis found that both the 2013 CHIKV outbreak and the monthly proportion of DENV serotype 2 in Singapore were ahead of those in Brazil, thus playing the role of a herald wave (early warning). This study further investigated the epidemic dynamics of CHIKV in comparison with DENV, focusing on Brazil from 2017 to 2025. Using national surveillance data, we analyzed spatiotemporal heterogeneity, demographic distributions, and infection attack rates for both arboviruses. We found that chikungunya exhibited greater regional heterogeneity and lower temporal synchrony than dengue, likely due to differences in the basic reproduction number (R0) and population immunity. Case burdens were highest among working-age adults, while infants and the elderly experienced more severe outcomes. The higher case numbers reflect the larger population size in this age group rather than higher individual infection risk. To reconstruct long-term epidemic trajectories at the regional level, we developed a modified SEIR5S compartmental model. We estimated the time-varying basic reproductive number for dengue and chikungunya, and showed that they shared a common component and also had distinct components.

Keywords: global spread; chikungunya; dengue; cocirculation; mathematical model

1. Introduction

Chikungunya is a mosquito-borne disease caused by the chikungunya virus (CHIKV), primarily transmitted to humans by infected *Aedes*. Large outbreaks have been reported across the Americas, Asia, and Africa, with occasional smaller outbreaks in Europe [1]. According to the WHO [1], the virus was first identified in Tanzania in 1952 and later reported in other parts of Africa and Asia [2]. Urban outbreaks were first recorded in Thailand in 1967 and in India in the 1970s [3]. Since 2004, the frequency and geographic extent of outbreaks have expanded significantly, partly due to viral adaptations that enhance transmission by *Aedes albopictus* [1]. As a matter of fact, chikungunya has spread to more countries/regions worldwide. The virus was first reported in the Americas (St. Martin Island) in 2013 and, within a year, had affected more than one million people across the region [4]. Currently, an estimation of around 5.6 billion people in 119 countries is at risk due to the spread of Aedes mosquitoes (*Aedes aegypti* and *Aedes albopictus*) [5, 6].

These species, which also transmit dengue and Zika viruses [1,7], can acquire CHIKV from infected humans. The virus takes 2–8 days to incubate in the mosquito [8]. Non-human primates also serve as natural reservoirs of the chikungunya virus [8].

To prevent a recurrence of the 2004–2005 global chikungunya epidemic, the World Health Organization (WHO) issued an urgent call for action on July 22, 2025 [5, 9]. The ongoing chikungunya outbreak, which began in early 2025, has once again centered on Indian Ocean islands such as La Réunion, Mayotte, and Mauritius. According to the Pacific Community [10], approximately one-third of the total La Reunion's population has already been infected, with 54,410 reported cases, 2860 emergency room visits, 578 hospital admissions, and 28 fatalities. These numbers correspond to a reporting ratio of 18% and an infection fatality ratio of less than 0.01%. The virus has also spread in Southeast Asia, affecting countries such as India, Sri Lanka, and Bangladesh [6]. Recent infections have been identified in France and Italy among patients without any travel links to the Indian Ocean islands. Diagnosis may be hindered in Europe where physicians have limited experience with chikungunya [5, 11].

In China, no major outbreaks have occurred since the COVID-19 pandemic [12]. However, resurgence began with the first imported cases identified in Foshan, Guangdong Province, on July 8, 2025. More than 8000 cases had been reported in Guangdong alone by August 15, 2025 [13]. Imported cases have also been reported in the Hong Kong Special Administrative Region (HKSAR) and the Macao Special Administrative Region (MSAR). HKSAR confirmed its first imported, laboratory-diagnosed case since 2019 [14]; while Macao reported eight cases as of August 4, 2025, including two locally transmitted cases [15].

To better understand the current global resurgence of chikungunya virus, we conducted an analysis of international trends, with a particular focus on Brazil—the country with the highest reported case burden to date. Given the epidemiological similarities between chikungunya and dengue, we adopted a comparative framework to assess transmission dynamics and infection attack rates. We also compiled age-stratified spatial data to examine risk patterns across demographic and geographic

groups. Based on these observations, we developed mechanistic transmission models to better understand the temporal dynamics of the 2025 chikungunya trend in Brazil. For additional comparison, we included HKSAR and Singapore in our analysis.

In Brazil, dengue, chikungunya, and Zika diseases co-circulated. Between 2017 and 2025 (week 29 of 2025), the numbers of confirmed cases were 14,401,079 (dengue), 1,890,401 (chikungunya), and 236,030 (Zika), with a ratio of approximately 61 : 8 : 1. Given the relatively low prevalence of Zika, this study focused on the comparison of dengue and chikungunya.

Table 1 shows a comparison of virological and clinical characteristics of the three mosquito-borne infections.

Table 1. Comparison of dengue (DENV), chikungunya (CHIKV), and Zika virus disease (ZIKV) based on virological and clinical characteristics.

Items	DENV	CHIKV	ZIKV
Family/genus	Flaviviridae/Flavivirus	Togaviridae/Alphavirus	Flaviviridae/Flavivirus
Type/subtype	Four serotypes	One serotype; four lineages with different virulence and cross-protection	One serotype; two lineages
Life-long immunity	None; reinfection with different serotypes	Largely true	Assumed life-long
Antibody-dependent enhancement (ADE)	Yes	–	–
Infection fatality ratio	2–5% for severe dengue with proper care; up to 20% if untreated (WHO)	about 0.05% in general; 2.8% in children; 1.6% in elderly	Children with congenital Zika syndrome are 11.3 to 14.3 times more likely to die than those without the syndrome
Mosquito vector	*Aedes aegypti* and *Aedes albopictus*		
GBS (Guillain-Barré syndrome) risk	Low or rare	Odds ratios 8.3 [16]	One for each 4000 ZIKV infections in French Polynesia [17]; odds ratio 8.04 among ZIKV acute infection [18]
Sexual transmission	–	–	Documented in humans
Vertical transmission	True for mosquito; rare in humans	15.5–50% among humans [19]; documented for mosquito	25–47% in humans [20]; documented for mosquito
Neurological complications/Microcephaly	–	Documented in [21]	Approximate 20-fold increase in numbers of microcephaly cases during Zika virus outbreak [22]
Cross-reactivity	–	–	Maternal immunity to DENV may enhance fetal infection with Zika, worsen the microcephaly phenotype in mouse model [23]. Pre-existing immunity to other flaviviruses (DENV) can offer some cross-protective immunity against ZIKV [24].
Invasion time in Brazil	1846	September 2014	April 2015

1.1. Current global hotspots (2025)

In Africa, chikungunya circulates in a forest-dwelling (enzootic) cycle between non-human primates (e.g., monkeys) and arboreal *Aedes* mosquitoes, occasionally infecting humans [25, 26]. The

current hotspots worldwide include the Indian Ocean islands (Réunion with more than 51,000 cases in 2025, Mayotte, and Mauritius), which are experiencing severe outbreaks, with spread to Madagascar, Kenya, and Somalia [5]); the Americas (Brazil remains a hotspot with 141,436 cases, with ongoing transmission in Argentina, Bolivia, and Peru); and Asia (India, Sri Lanka, Pakistan, and Bangladesh report recurrent outbreaks, with additional active transmission in Guangdong Province, China, Singapore, and the Philippines).

1.2. Symptoms, complications, and control strategies

According to [2], in symptomatic patients, chikungunya disease onset is typically 4–8 days (range 2–12 days) after the bite of an infected mosquito. The illness often starts suddenly with high fever accompanied by severe joint pain. As pointed out by Dr. Diana Rojas Alvarez, the WHO's lead expert on arboviruses, the symptoms of chikungunya are mostly acute. Despite very high fever and severe joint pain, patients may also face swelling, muscle pain, skin rash, and severe fatigue, headache, and nausea. The similarity of symptoms with dengue may result in misdiagnosis of chikungunya cases.

The joint pain for chikungunya patients usually lasts for a few days, but up to 40% of the people who are infected with chikungunya experience long-term disabilities that can last for a few months or even years. Most patients recover fully from the infection; however, occasional cases may experience eye, heart, and neurological complications. Infants, elderly, and patients with comorbidities with underlying medical conditions may develop symptoms that require hospitalization. The case fatality rate was less than 0.1% [7]. Recovery generally confers long-lasting immunity [2, 9]. Chikungunya virus may be detected directly in blood samples collected during the first week of illness and the antibody levels (specifically IgM antibodies) can still be detected for about 2 months.

The demographic features of human infection with the chikungunya virus vary by age, gender, occupation, and geographic location. Below is a detailed breakdown based on the latest data.

- **Adults (20–60 years)**: Most symptomatic cases occur in this group due to higher exposure to mosquito bites (e.g., outdoor work or travel) [27].
- **Infants and Neonates**: High risk of severe outcomes, including encephalitis, hemorrhagic complications, and neuro developmental delays (up to 50% of infected newborns) [1].
- **Elderly (>65 years)**: More likely to develop chronic arthritis, myocarditis, and neurological complications, with higher mortality rates (approximately 1 in 1000) [5]. No significant bias in infection rates, but chronic joint pain is more frequently reported in women, possibly due to autoimmune factors [28].
- **Pregnant women**: Risk of vertical transmission (15–50%) if infected near delivery, leading to severe neonatal disease (e.g., sepsis, intracranial hemorrhage) [29].
- **Outdoor workers**: Based on [30], outdoor workers (e.g., farmers, construction laborers) are at higher risk due to prolonged mosquito exposure.
- **Urban slum dwellers**: Poor water storage and high *Aedes* mosquito density increase outbreaks (e.g., São Paulo, Brazil).
- **Low-income regions**: Underdiagnosis is common due to limited healthcare access, masking true infection rates (e.g., Africa's seroprevalence up to 63% in Rwanda).

Currently, there are no virus-specific antiviral therapies. Clinical management is limited to

supportive care, using antipyretic and analgesic drugs such as paracetamol to alleviate fever or joint pain [1]. Preventive measures include repellents, protective clothing, and eliminating mosquito breeding sites [11]. Two chikungunya vaccines have received national approvals (one vaccine has been approved in the United States (USA), European Union (EU), United Kingdom (UK), Canada, and Brazil; another in the USA, EU, and UK, but global recommendations await further efficacy data.

1.3. Basic reproduction number R_0

From empirical outbreak data spanning 2000–2019 including regions such as Africa, Asia, Europe, and the Americas, the weighted mean basic reproduction number (R_0) of chikungunya virus based on outbreak size was 3.4 (95% CI 2.4–4.2) and varied for 2 primary chikungunya mosquito vectors: 4.1 (95% CI 1.5–6.6) for *Aedes aegypti* and 2.8 (95% CI 1.8–3.8) for *Ae. albopictus* [31]. The higher R_0 for *Ae. aegypti* may be due to its preference in biting humans, while *Ae. albopictus* feeds on other animals as well, which potentially reduced its human transmission efficiency.

As indicated in [32], there are obviously variations of the basic reproduction number of chikungunya virus with tropical regions of mean $R_0 = 3.44$; subtropical regions of mean $R_0 = 10.29$ (though with high variability); and temperate regions of mean $R_0 = 2.03$. This variation may be attributed to the higher temperatures and humidity in tropical zones, which enhance mosquito activity and viral replication, thereby facilitating virus transmission.

The basic reproduction number R_0 also shows variations in regional outbreaks. For example, the La Réunion outbreak (2006) had an R_0 ranged from 0.89 to 4.1, with *Ae. albopictus* as the dominant vector [31]; the Colombia outbreak (2014–2016) had R_0 estimates varied from 1 to 9, with most municipalities reporting an R_0 between 1 and 2 [33]; and the Rio de Janeiro outbreak (2015–20) had an R_0 estimated at 1.2–1.6, with seasonal peaks in transmission linked to mosquito activity [34].

The following key factors may influence the basic reproduction number: Temperature: positively correlated with higher R_0 due to faster mosquito development and viral replication [34, 35]. Urbanization: larger urban areas may see lower R_0 due to reduced mosquito-human contact density [34]. Vector competence: *Ae. aegypti* is generally more efficient than *Ae. albopictus* in transmitting chikungunya [31]. In summary, R_0 is not static and varies with viral evolution, vector ecology, climate, immunity, and human interventions. Long-term trends may show an increase of R_0 in temperate regions due to climate change expanding *Aedes* habitats [32]. Real-time monitoring of the instantaneous reproduction number R_t (as has been done in Rio de Janeiro) can help keep track of the disease severity in the population [34].

After large outbreaks, infected individuals acquire immunity, thereby lowering the effective reproduction number ($R_{\text{effective}}$). However, due to the immunity waning over time as well as an influx of susceptible population (e.g., births), resurgence can occur in the future [36]. Resurgence may also be driven by the emergence of new viral strains due to mutation. For example, in Brazil, recurrent outbreaks (e.g., Ceará in 2016, 2017, and 2022) were driven by the emergence of new viral lineages and the invasion into a naïve populations.

1.4. Population susceptibility and outbreak recurrence

The susceptibility of an initial population to the chikungunya virus depends on several factors, including prior exposure, immunity, vector presence, and environmental conditions. In

immunologically naïve populations, the susceptibility is high. For instance, the 2013–2014 Caribbean outbreak spread rapidly due to the lack of pre-existing immunity in the Americas [29, 37]. In such populations, attack rates could exceed 50% during outbreaks, as seen in La Réunion (2005–2006) and the Caribbean [29]. In endemic regions (e.g., parts of Africa and Asia), lower susceptibility is observed due to prior exposure and herd immunity. Seroprevalence in endemic areas like India and Brazil ranges from 7.8% to 14.6% in children aged 10 years, reflecting partial immunity [38]. This justifies our choice of 80% initial susceptibility in 2017 in Brazil. In epidemic regions like Europe and the Americas during initial outbreaks, population susceptibility approaches 100% [29, 37].

Factors influencing susceptibility can include but are not limited to vector competence (*Aedes* are primary vectors where populations in such areas are more susceptible), climate and urbanization (warmer, humid climates boost mosquito breeding, raising susceptibility and urban areas with poor water storage practices facilitate *Aedes* proliferation), and demographics (older adults (>65 years) and infants are more susceptible to severe disease due to weaker immune responses or a lack of prior exposure) [7]. For example, the La Réunion outbreak (2024–2025) had a rapid spread (over 47,500 cases) in a population with waning immunity since the 2005–2006 outbreak [7]. The Mayotte outbreak (2025) indicated renewed susceptibility after the first local transmission since 2005–2006. The Caribbean outbreak (2013–2014) had a near-universal susceptibility that led to 1.2 million cases within a year [29].

2. Materials and method

2.1. Data

We used publicly available epidemiological surveillance data from the Brazilian Ministry of Health, accessed via the TABNET platform [39]. Specifically, we retrieved weekly confirmed cases of dengue and chikungunya reported to the national SINAN (Sistema de Informação de Agravos de Notificação) system from 2017 onward. Data were aggregated at the regional level to assess spatiotemporal dynamics and inter-regional synchrony.

Global situation was drawn from the European Centre for Disease Prevention and Control (ECDC), World Health Organization (WHO), and Pan American Health Organization (PAHO) datasets.

Further, for contextual comparison, we show the yearly totals of dengue and chikungunya cases in India and Colombia in the Supplementary Materials (Appendix Section C; data sources: Indian NCVBDC [40, 41], and Rico-Mendoza et al. [43]).

All datasets used are publicly accessible. Data processing and analysis were conducted in R.

2.2. Model construction

To simulate the long-term transmission dynamics of dengue virus (DENV) and chikungunya virus (CHIKV) in a human population with waning immunity, we developed an extended SEIR^{5}S compartmental model. This model generalizes the classical SEIR framework by including five sequential recovery compartments, thereby enabling immunity duration to attain a gamma distribution.

The model consisted of the following compartments: $S \to E \to I \to R \to R_1 \to R_2 \to R_3 \to R_4 \to S$. Susceptible individuals (S) become exposed (E) after effective contact with infectious individuals.

They then progress to the infectious stage (I), and upon recovery, enter a chain of five recovered states (R_1 to R_5), after which they return to the susceptible class. This sequential recovery structure mimics gamma-distributed immunity loss and allows for reinfection. The average durations of the latent (E) and infectious (I) periods were fixed at 14 days and 7 days, based on clinical literature. The total mean duration of immunity was assumed to be around 16 years for dengue and 64 years for chikungunya and was implemented via five equal-length stages in the recovered class. Initial conditions assumed that 80% of the population was susceptible at the beginning of 2017, reflecting partial immunity in an endemic setting.

To account for seasonal and interannual variability in transmission potential driven by mosquito activity, the transmission rate $\beta(t)$ for chikungunya was modeled as an exponential cubic spline:

$$\beta_c(t) = \exp(f_0(t))$$

Here, $f_0(t)$ is a natural cubic spline function with 25 evenly spaced knots spanning from January 2017 to epidemiological week 29 of 2025 (i.e., 9.5 years). This flexible formulation captures nonlinear temporal patterns in transmission due to environmental and vector dynamics.

For dengue, the transmission rate was modeled as

$$\beta_d(t) = \exp(f_0(t)) + \exp(f_1(t)) = \beta_0(t) + \beta_1(t) \tag{2.1}$$

Here, $f_1(t)$ is another natural cubic spline function with 6 evenly spaced knots. $f_1(t)$ accounts for the distinct component in the transmission rate of dengue than in that of chikungunya, given the fact that the reported prevalence of dengue is tenfold as high as that of chikungunya.

Model fitting was conducted using the `pomp` package in `R`, which implements partially observed Markov process (POMP) models.

2.3. Model for dengue

We use an SEIR type of model, even though we understand that dengue and chikungunya are vector-borne diseases. Note that Li et al. [44] used an SIR model for dengue.

$$\begin{aligned}
\frac{dS}{dt} &= 5\eta_d R_5 - \beta_d S I/N \\
\frac{dE}{dt} &= \beta_d S I/N - \sigma E \\
\frac{dI}{dt} &= \sigma E - \gamma I \\
\frac{dR_1}{dt} &= \gamma I - 5\eta_d R_1 \\
\frac{dR_i}{dt} &= 5\eta_d R_{i-1} - 5\eta_d R_i, \quad i = 2, 3, 4, 5 \\
\frac{dT}{dt} &= \phi\gamma I - \kappa T \\
\frac{dC}{dt} &= \theta\kappa T,
\end{aligned} \tag{2.2}$$

where η_d is set to be between (0.0572, 0.0615) per year, which means a mean duration of protection of $\sim$ 16 years, thus over a lifespan of 65 years, and the expected numbers of infections are four, each with one of the four serotypes of dengue. σ and γ are set at 26.071 per year and 52.143 per year, which mean a mean duration of 14 days for the latent period (including both internal and external, latent in

human and mosquito), and 7 days for the infectious period. ϕ is set at 0.15, which means only 15% of infections will see a doctor and leave a sample, and θ is set to be between (0.5, 0.99). The case-reporting ratio is equal to $\phi * \theta$. κ denotes the rate at which samples are processed. T and C denote the number of samples and positive results, respectively. This setting corresponds to the reported low case-reporting ratio, i.e., $\sim 1/12$. The recovered class (R) is set to have five stages such that the recovered duration attains a more biologically realistic gamma distribution.

2.4. Model for chikungunya

$$\begin{aligned}
\frac{dS}{dt} &= 5\eta_c R_5 - \beta_c S I/N \\
\frac{dE}{dt} &= \beta_c S I/N - \sigma E \\
\frac{dI}{dt} &= \sigma E - \gamma I \\
\frac{dR_1}{dt} &= \gamma I - 5\eta_c R_1 \\
\frac{dR_i}{dt} &= 5\eta_c R_{i-1} - 5\eta_c R_i, \quad i = 2,3,4,5 \\
\frac{dT}{dt} &= \phi\gamma I - \kappa T \\
\frac{dC}{dt} &= \theta\kappa T,
\end{aligned} \tag{2.3}$$

where η_c is set at $0.25\eta_d$ per year, which means a mean duration of protection of $\sim$ 64 years, thus over a lifespan of 65 years, and the expected numbers of infections is one, due to the fact that only one chikungunya serotype circulates. σ, γ, ϕ, and θ are the same as that of dengue. The recovered class (R) is set to have five stages such that the recovered duration attains a more biologically realistic gamma distribution.

We consider a transmission rate with common and distinct parts for dengue and chikungunya, which is an innovation.

The simulated cases are

$$\hat{C}_t^i = \int_{4 \text{ weeks}} \theta\kappa T dt,$$

where $i = 1, 2$ is the index of viruses and t is the index of time.

Denote the reported cases as C_t^i, and we assume

$$C_t^i \sim Negative\_Binominal(mean = \hat{C}_t^i, variance = \hat{C}_t^i(1 + \tau\hat{C}_t^i),$$

where τ is the over-dispersion parameter. The log likelihood is defined as

$$Loglik = \sum_{i=1}^{2}\sum_{t=1}^{n} \log\_density\_Negbinom(C_t^i | C_{1:(t-1)}^i, \Theta),$$

where Θ denotes the vector of estimated parameters and n denotes the total number of data points. In order to speed up the calculation, we aggregate weekly into a 4-week format. The second-order Akaike Information Criterion is defined as

$$AICc = -2Loglik + 2n_p(2n)/(((2n) - n_p - 1),$$

where n_p denotes the number of estimated parameters.

In Appendix Figure B.2, we show $AICc$ as a function of n_β, i.e., the number of knots in the common components, which justifies our choice of $n_\beta = 25$.

3. Results

3.1. Case trends in Southeast Asia

Figure 1(a) illustrates the monthly reported cases of malaria, dengue fever, and chikungunya fever in Hong Kong from 2009 to 2025. Dengue cases have shown an increasing trend over time, while chikungunya cases remain sporadic. A sharp spike in malaria cases was observed around 2022, though overall malaria incidence remained low.

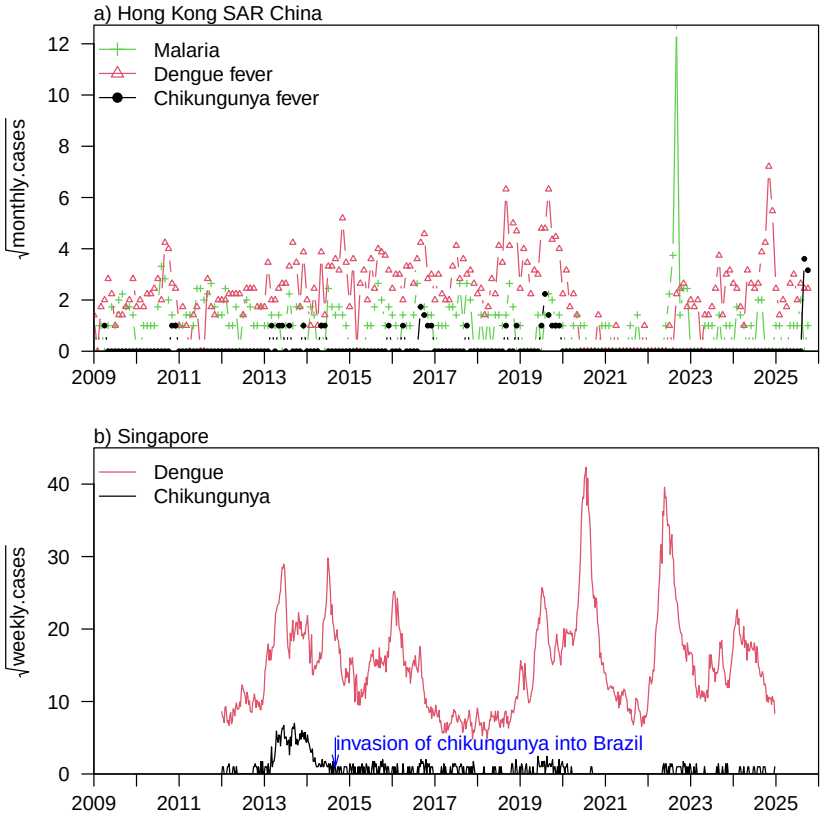

Figure 1. Reported cases of mosquito-borne diseases in Hong Kong SAR China and Singapore. Panel (a): Hong Kong data from 2009 to 2025. Panel (b): Singapore data from 2012 to 2024.

Hong Kong SAR China is a major travel destination in Asia. The top countries/regions whose citizens travel to Hong Kong include Mainland China, the Philippines, and various Southeast Asian nations. As such, data from Hong Kong shows a snapshot of the situation in this area.

Figure 1(b) illustrates the monthly reported cases of dengue fever and chikungunya fever in Singapore from 2012 to 2025. While dengue shows clear seasonal peaks with substantial outbreaks, chikungunya cases remain sporadic, mostly imported. Nevertheless, the peak in 2013–14 was ahead

of the first reported chikungunya cases in Brazil.

3.2. Serotype distribution and case-fatality patterns of dengue

Figure 2 shows the temporal dynamics of dengue virus serotype distribution in Singapore and Brazil and case severity in Brazil. In both Singapore and Brazil, serotype proportions fluctuate over time with shifts in dominance.

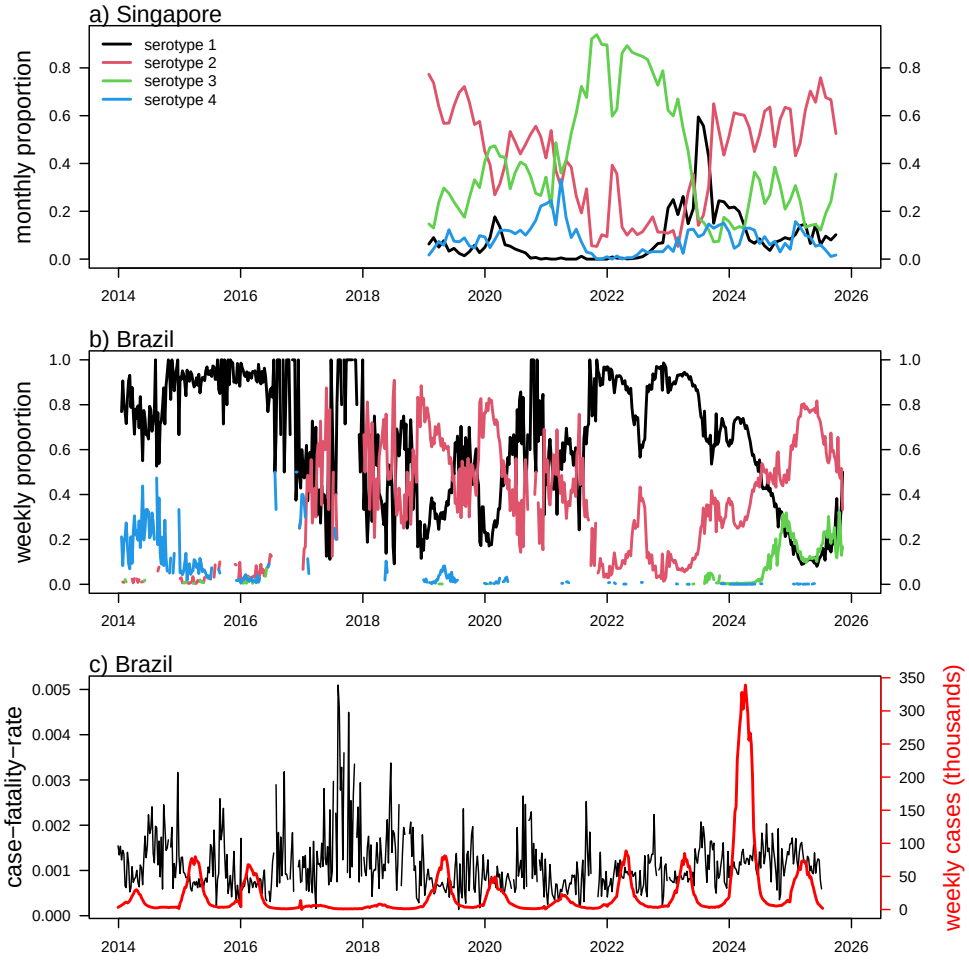

Figure 2. Temporal dynamics of dengue case severity and serotype distribution. (a) Monthly proportion of dengue virus serotypes 1–4 in Singapore, 2014–2025. (b) Weekly proportion of dengue virus serotypes 1–4 in Brazil, 2014–2025. (c) Case-fatality rate of dengue in Brazil with weekly reported dengue cases in thousands, 2014–2025.

Particularly, we note that serotype-2 proportions synchronized between Singapore and Brazil, unexpectedly. The correlation reached 0.7 with a time lag of 6 months, Singapore ahead of Brazil (see Figure B.1). The mechanism between this evident synchrony is unclear. This could be due to the emergence and spread of a serotype-2 strain with a transmission advantage. Long-term observation is warranted. The case-fatality rate tends to be high over the troughs of the dengue epidemics.

3.3. Age distribution of cases in Brazil

Figure 3 presents weekly reported cases of dengue (top panel) and chikungunya (bottom panel) in Brazil from 2017 to 2025, disaggregated by age group (after age standardization).

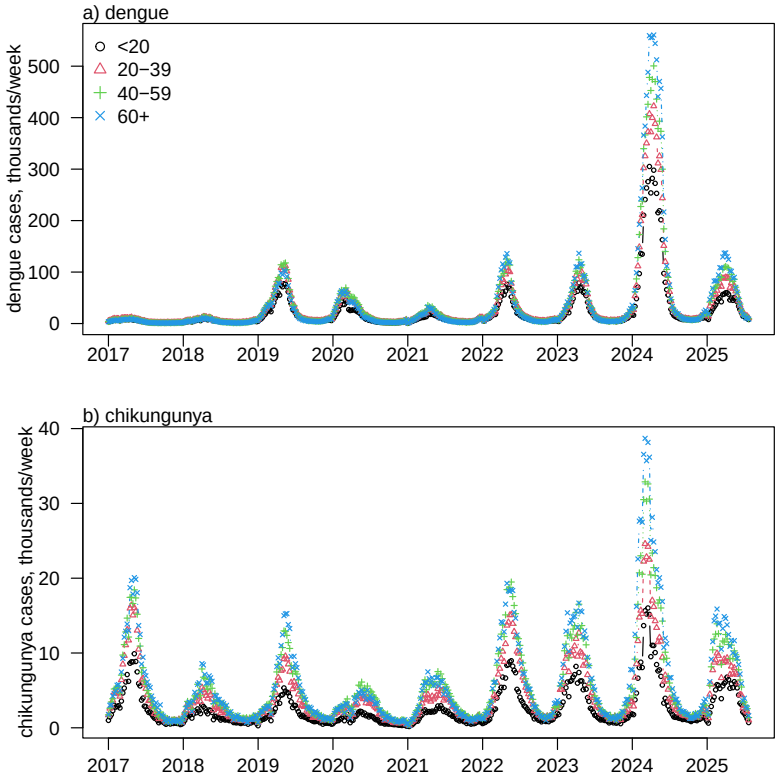

Figure 3. Age-specific weekly reported cases of dengue and chikungunya in Brazil, 2017–2025.

After age standardization, we found that the risk is relatively even across the three adult age groups (>20 years) for both dengue and chikungunya. Older ages tend to have slightly higher risk. The raw number of cases is high among working age group due to their large population size.

3.4. Regional heterogeneity in transmission in Brazil

To explore the spatial dynamics of transmission, we plot weekly dengue and chikungunya cases by region (North, Northeast, Central-West, Southeast, and South) in Figure 4(a) and Figure 4(b). For dengue, the Southeast region consistently records the highest number of cases, followed by the South region, in recent years. For chikungunya, regional dominance varies by year, with both the Northeast and Southeast regions showing significant transmission at different times.

To better visualize the trend, we show a comparison of cases in a region (black curve) versus their expectation (red curve) in Figure 5. The expectation is defined as the median level of cases in the other four regions but the focal region. We can see that the five regions show two distinct patterns for dengue, i.e., a low north pattern and high south-and-central pattern, while there is no clear pattern for chikungunya.

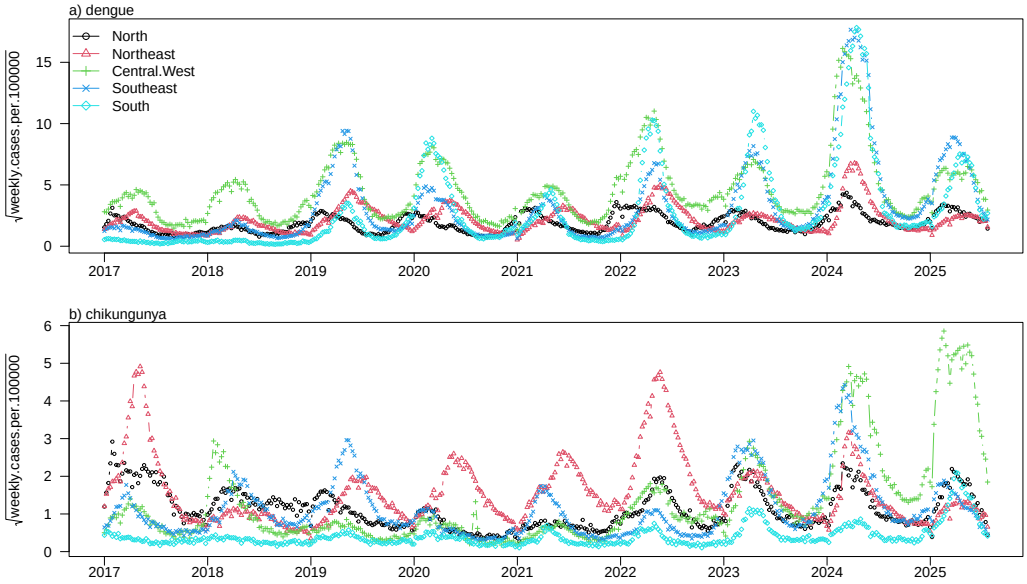

Figure 4. Regional trends in square-root weekly cases of dengue and chikungunya in Brazil, 2017–2025 (a),(b).

3.5. Infection attack rate in Brazil

We consider the dengue and chikungunya data from 2017 through epidemiological week 29 of 2025. Among them, over 6.4 million dengue cases were reported in the single year of 2024. Given the 2024 Brazil population as 212 million, the total dengue cases from 2017 account for 6.79% of the population and the 2024 epidemic accounts for 2.98% of the population. Table 1 shows the annual infection attack rate (IAR) of dengue in Brazil. Here we consider a reporting ratio of 1/12 (see [42]), which means that for every reported case, there were 12 infections (i.e., 11 infections unreported for a variety of reasons).

As shown in Table 2, an average of approximately 9% of the Brazilian population has been infected with dengue annually over the first eight years since 2017. However, 2024 stands out as an exceptional year, during which an estimated 36.42% of the population was infected. Assume the initial susceptible proportion is 80%, i.e., 20% of the population is immunized by prior infections by the beginning of 2017. Given that the reported infection rate is 6.79%, and assuming a 1/12 reporting ratio [42], the total infection attack rate (IAR) is estimated to be 81.51%, as presented in Table 2.

A study in the Philippines found that the average annual infection attack rate of dengue was 13% between 2014-2018 [45]. Relatively speaking, Brazil is a more developed country compared to the Philippines; an annual IAR of 9% is reasonable compared to 13% in the Philippines, as well as other climatic differences.

We assume a similar reporting ratio of chikungunya at 1/12, the same as dengue. Recall that in La Reunion outbreaks, 18% of chikungunya cases were reported. Then chikungunya infects 1% of the Brazilian population annually with an exception of 2.28% in 2024. These estimates are summarized in Table 2. External factors (such as the El Nino effect) may cause the exceptionally high cases for both chikungunya and dengue in 2024. The effect is higher for dengue than for chikungunya. As both viruses compete for susceptible hosts, a substantial dengue outbreak can attenuate the transmission dynamics of chikungunya.

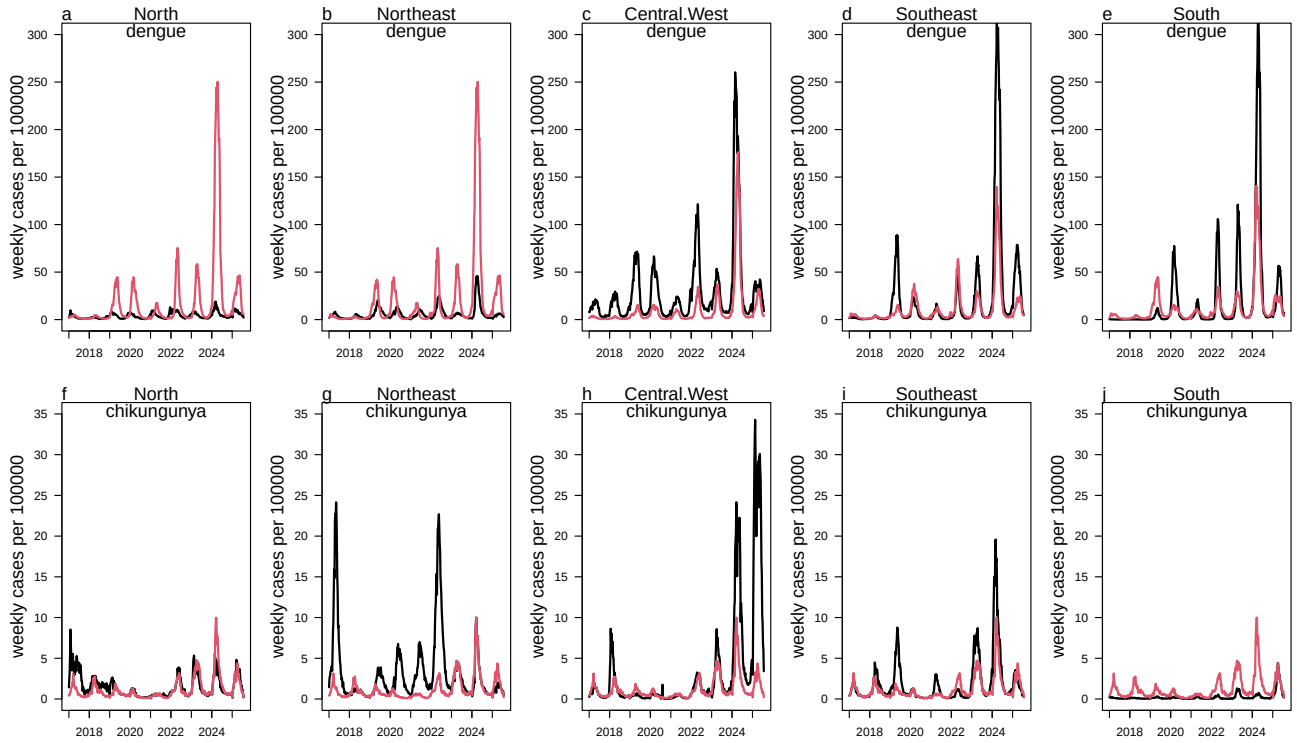

Figure 5. A comparison of cases in a region (black curve) versus their expectation (red curve). Top panels show dengue and bottom panels show chikungunya in five regions, respectively. The black curves show the reported cases. The red curves show the expectation, which is defined as the median level among the other four regions but the focal region.

Table 2. Estimated annual infection attack rate (IAR, percentage of the population) of dengue and chikungunya in Brazil, assuming a 1 : 12 case-infection ratio.

Year	2017	2018	2019	2020	2021	2022	2023	2024	2025*
Dengue (%)	1.38	1.50	8.80	5.41	3.01	7.89	8.54	36.42	8.57
Chikungunya (%)	1.40	0.67	1.01	0.58	0.73	1.55	1.40	2.28	1.07

*Through epidemiological week 29.

3.6. SEIR^{5}S model for dengue and chikungunya

We simplify our previous mosquito-human model (see [46, 47]) to be an SEIR^{5}S model. Susceptible individuals go through stages of being exposed, infective, five recovery stages, and return to susceptible. We use the five recovery stages $(R_1, ..., R_5)$ to model a gamma-like distribution recovery duration. We use this model for both viruses. The difference is the mean duration in recovered stages and the transmission rate $\beta(t)$. For dengue, the mean duration is around 16 years, while for chikungunya, it is around 64 years. This difference reflects the fact that one may be infected with dengue multiple times (each time with a different serotype), while it is mostly once with chikungunya. We assume the transmission rates of the two viruses have a common component and that of dengue has an extra component. We assume the transmission rate to be time-dependent. The

common transmission rate is modeled as an exp-cubic-spline function of time with 25 nodes evenly distributed over 9.5 years (from 2017 to 2025 week 29).

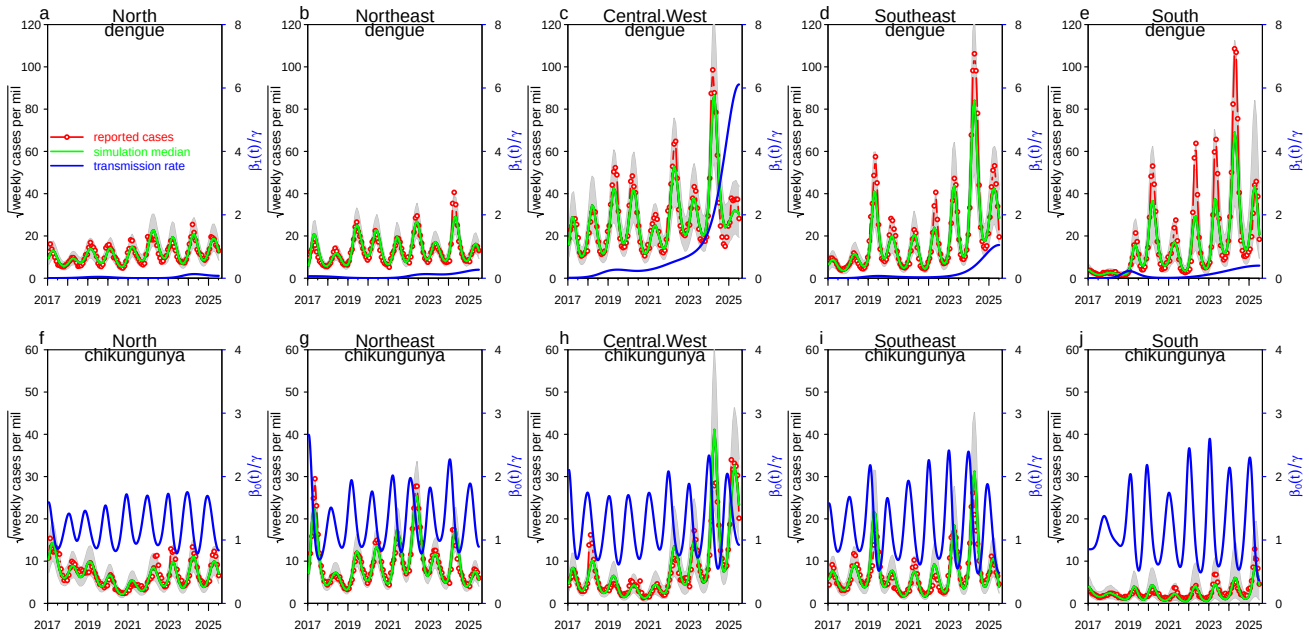

Figure 6. Simulation results of the SEIR^{5}S model for dengue (a)–(e) and chikungunya (f)–(j) in Brazil, 2017–2025, in five regions, respectively. The blue curves show the transmission rate. The top panel blue curves show the extra component of the transmission of dengue. The bottom panel curves show the common component of the transmission for both viruses. We show the transmission rate in the units of $1/\gamma$, and thus it can be interpreted as the time-varying basic reproductive number.

We assume the mean durations for the latent and infective states at 14 days and 7 days, respectively, to account for both latent periods in mosquitoes and humans. We assume the initial susceptibility is 80% at the beginning of 2017. Considering the regional heterogeneity of dengue and chikungunya transmission in Brazil, we focus on five geographic regions of Brazil and fit the model separately to weekly (4-weekly) national surveillance data using the R package POMP.

We find that, see in Figure 6, under the current setting, the transmission rate of dengue is similar in the North and Northeast for the two diseases. Dengue has a higher transmission rate in the Southeast, South, and Central-West than that of chikungunya in recent years. The transmission rate of dengue appears to have increased in 2025 across these three regions, especially after the major wave of 2024. This rise coincides with the expansion of dengue serotype-2 (Figure 2). Notably, dengue dynamics in the Southeast, South, and Central-West regions exhibit a stronger correlation compared with the other two regions (see Figure 4).

4. Discussion

This study compared chikungunya and dengue epidemics in Brazil from 2017–2025 using surveillance data and an SEIR^{5}S model. By examining spatiotemporal heterogeneity, age-specific burdens, infection attack rates (IARs), and inter-virus interactions, we highlight both shared and distinct features of their transmission dynamics.

Spatiotemporal heterogeneity Dengue epidemics, particularly the unprecedented 2024 outbreak, were highly synchronized across Brazilian regions, consistent with its strong force of infection and partial, serotype-specific immunity. Chikungunya showed lower synchrony and greater spatial variation, with alternating dominance of the Northeast and Southeast. These differences reflect distinct immunity profiles: dengue permits reinfection, while chikungunya infection typically provides long-lasting protection, limiting recurrent epidemics.

Age-specific burden While dengue imposed a larger acute burden, chikungunya's chronic sequelae, including long-term arthritis, represent significant socioeconomic costs concentrated in the most productive age groups. But after age standardization, we found that the higher number of cases among working-age adults was mainly due to their larger population size, rather than higher individual risk. Severe outcomes, however, remained concentrated in infants and the elderly.

Infection attack rates Dengue's epidemic potential far exceeded that of chikungunya. The 2024 dengue epidemic infected an estimated 36% of Brazil's population, while chikungunya rarely exceeded 2% annually. Competitive interactions appear important: large dengue epidemics may temporarily suppress chikungunya by depleting susceptibles. This underscores the need to analyze co-circulating arboviruses jointly, rather than in isolation.

Model-based insights The SEIR^{5}S model successfully captured epidemic trajectories by incorporating waning immunity and temporary cross-protection. Dengue transmission rates were consistently higher in the Southeast, South, and Central-West, aligning with surveillance data. The rise in dengue transmission in 2025 coincided with expansion of serotype-2, illustrating the influence of viral evolution on epidemic potential.

Global implications Dengue serotype-2 dynamics showed unexpected synchrony between Singapore and Brazil, suggesting long-range viral spread or shared climatic drivers. Note that the chikungunya outbreak in Singapore was also a herald wave of the invasion of chikungunya in Brazil and other South American countries. The 2025 resurgence of chikungunya in multiple continents highlights its continued global threat, particularly under climate anomalies such as El Niño. These findings stress the importance of coordinated surveillance and early warning systems.

Limitations IAR estimates depend on assumed under-reporting ratios that vary between viruses and regions. Dengue cases are more often laboratory confirmed, potentially biasing comparisons. Our model does not explicitly include vector ecology, climate drivers, or human mobility. Finally, surveillance underestimates the chronic burden of chikungunya sequelae.

Public health implications Strengthened surveillance and integrated vector control are critical. Improved differential diagnosis is essential in co-circulating regions. Vector interventions should be regionally tailored, and Infants and the elderly should be given priority consideration as they have the highest probability of suffering from serious diseases. Sustained investment in community-based prevention and global coordination will be vital to mitigate recurrent arboviral epidemics.

5. Conclusions

We find that the 2013 chikungunya outbreak in Singapore preceded the invasion of chikungunya into Brazil in September 2014. The monthly dengue serotype 2 in Singapore preceded that in Brazil by half a year. In this sense, Singapore has acted as a sentinel for Brazilian mosquito-borne disease dynamics.

Regarding the modeling and fitting of dengue and chikungunya transmission, we introduce an innovative framework in which the transmission rate is decomposed into a shared component (reflecting the common mosquito vector) and a disease-specific component for dengue (reflecting viral characteristics and serotype differences). We found that the disease-specific component (i.e., extra component for dengue) was needed in Central-West, South and Southeast, but not in North and Northeast. The mechanism behind these differences deserves further study.

While dengue remains Brazil's dominant arbovirus threat, chikungunya imposes a distinct and underestimated burden. Differences in epidemic synchrony, immunity, and chronic health outcomes demand integrated surveillance, modeling, and vaccination strategies. Addressing these complementary threats will be central to reducing the long-term health and socioeconomic toll of arboviruses in Brazil and worldwide.

Use of AI tools declaration

The authors acknowledge the assistance of ChatGPT in the early stages of literature retrieval and topic clarification. In particular, AI assistance was used to help identify and synthesize relevant references related to chikungunya epidemiology and transmission. All final interpretations and writing were conducted by the authors.

Author contribution

He Daihai, Fan Guihong: conceptualization, methodology, software, supervision, writing, reviewing and editing. He Linxi, Wen Li: data curation, writing original draft preparation. Sun Ningkui: visualization, investigation, writing, reviewing and editing. Li Qiong, Wang Weiming: funding, software, validation, writing, reviewing and editing.

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Conflict of interest

The authors declare that there is no conflict of interest.

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Appendices

A. Severity of dengue in Brazil

Figure A.1 shows the temporal trends in the proportion of reported dengue cases classified as "alarme" (warning signs) and "grave" (severe) in Brazil from 2017 to 2025. The proportion of "alarme" cases is noticeably lower during the COVID-19 pandemic period (2020–2022), while exhibiting pronounced seasonal patterns in other years. "Grave" cases remain consistently low and stable over time. It looks like the % of "alarme" grew in 2024–2025 more than the % of "grave" did. 2024–2025 saw bigger waves of dengue in Brazil. We would suspect at least some role of improved case-detection in 2024–2025.

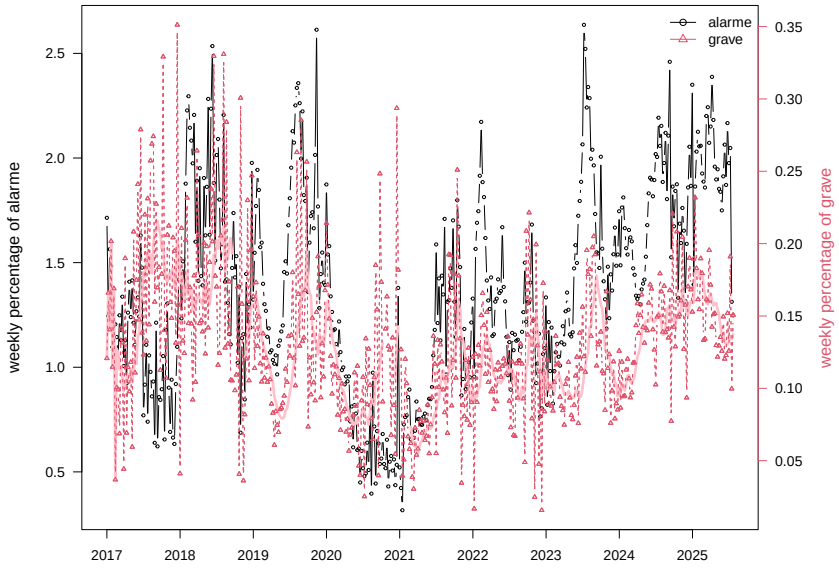

Figure A.1. Proportion of dengue cases classified as "alarme" (warning signs) and "grave" (severe) in Brazil from 2017 to 2025.

B. Unexpected synchrony of serotype-2 between Singapore and Brazil

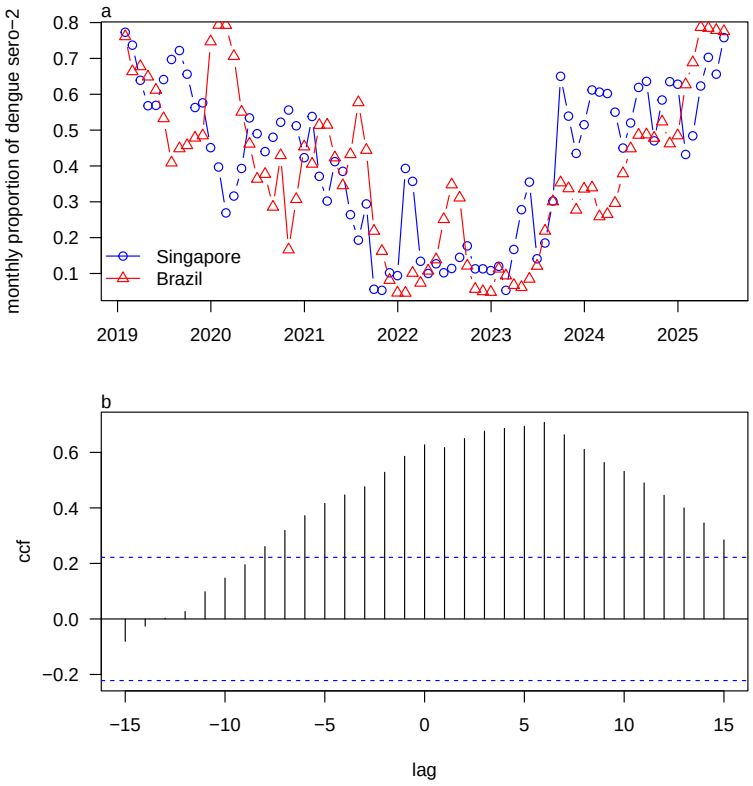

Figure B.1. Proportion of dengue serotype-2 in Brazil and Singapore and the results of ccf of the two proportions.

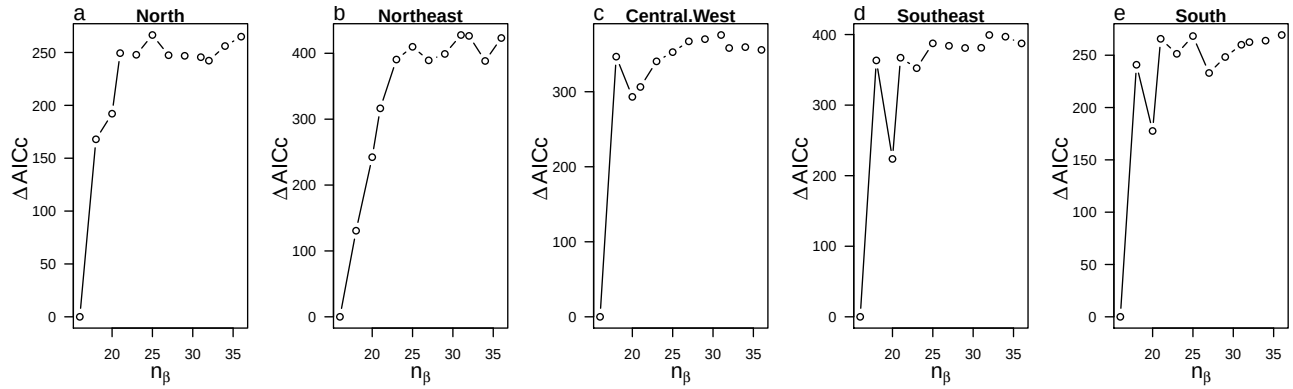

Figure B.2. The second-order Akaike information criterion (AICc) as a function of the number of knots in the common component of transmission rate in five regions. We show the difference between the maximum AICc and all AICc for each region.

Figure B.1 shows the comparison of serotype-2 proportions in Singapore and in Brazil. Brazil seems to follow the trend in Singapore with a lag of 6 months. The bottom panel shows the results of ccf, R function.

C. Yearly total of dengue and chikungunya in India and Colombia

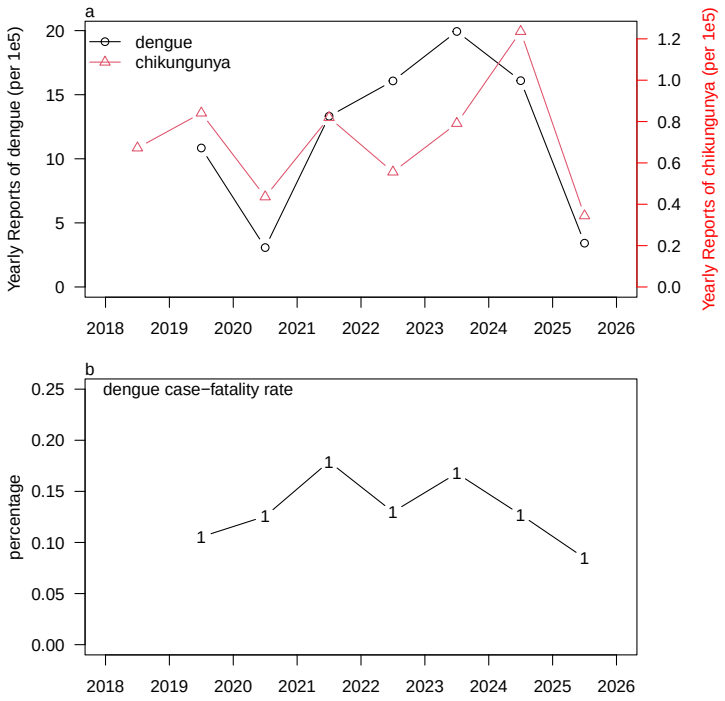

Figure C.1. Trends of dengue and chikungunya cases in India from 2018 to 2025. Panel (a) shows annual reported dengue incidence and chikungunya incidence. Panel (b) presents the annual dengue case–fatality rate.

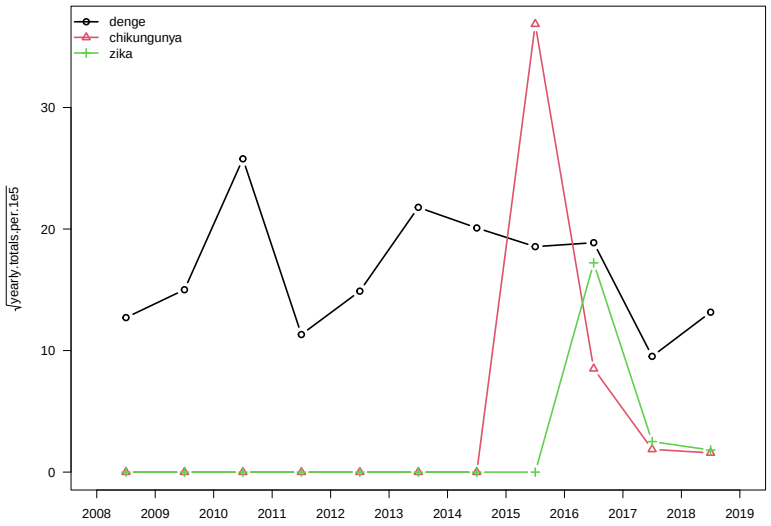

Figure C.2. Reported cases of mosquito-borne diseases in Columbia.