

<https://doi.org/10.1038/s44482-026-00015-9>

# Forecasting of dengue importation risk in Brazil using deep learning and mobility networks

Check for updates

Xiang Chen &amp; Paula Moraga

Timely anticipation of dengue spread is essential for public health planning, particularly in large endemic countries where transmission is shaped by both local conditions and human mobility. While most early warning systems focus on local forecasts, they often neglect how cases in one location may influence risk elsewhere through spatial movement. Here, we present a generalizable framework that integrates short-term dengue incidence forecasts with a multimodal mobility network to estimate the relative importation pressure index between all 5,570 municipalities in Brazil. By coupling a climate-informed long short-term memory (LSTM) model with a composite mobility matrix spanning road, river, and air transport, we generate dynamic, city-level surfaces of predicted importation risk for 2024. Results reveal spatially structured corridors of transmission, strong asymmetries between source and sink cities, and wide variation in states' dependence on internal versus external seeding. This framework advances dengue surveillance by capturing spatial spillover effects in real time and offers a modular architecture for forecasting importation risk across diseases and settings.

Timely forecasting of vector-borne disease spread is a cornerstone of epidemic preparedness, especially in regions where rapid human mobility and climate suitability intersect to amplify transmission risk. Dengue remains a persistent and expanding global health threat, with more than 100 countries reporting local transmission and an estimated 390 million infections annually<sup>1</sup>. In Latin America, Brazil carries one of the world's highest burdens, experiencing recurrent epidemics and pronounced spatial heterogeneity in transmission patterns<sup>2</sup>. Although dengue spreads locally via mosquito-human contact, its broader geographic dispersion is strongly shaped by human movement: infected individuals traveling between locations can indirectly seed new outbreaks or intensify ongoing ones, particularly in regions with susceptible populations and favorable environmental conditions<sup>3</sup>.

A growing body of research has examined how mobility contributes to dengue dynamics at global, regional, and subnational scales. Internationally, studies have modeled the risk of dengue importation using air travel networks, showing that passenger flows from endemic countries—combined with origin-country incidence and travel volume—strongly predict where imported cases are detected<sup>4–6</sup>. Machine learning approaches have enhanced predictive accuracy by incorporating network centrality and destination vulnerability<sup>7</sup>. Within countries, mobility has been shown to drive internal dengue spread. In Brazil, network-based analyses have demonstrated that expansion of transportation

infrastructure and intercity travel increased vulnerability in previously unaffected states<sup>8</sup>. Longitudinal studies have uncovered seasonal waves of dengue propagating from west to east, shaped by the interaction of human mobility and climatic patterns<sup>9</sup>. Elsewhere, mobile phone data have been used to trace real-time population flows and forecast dengue invasion with high spatial precision<sup>10</sup>. More recent work has combined environmental suitability and movement data to model long-term dengue expansion, showing that spatial barriers constrain early spread, while mobility networks dominate transmission in later stages<sup>11</sup>. Together, these findings underscore the central role of mobility in both introducing dengue to new areas and sustaining its geographic expansion.

Despite these advances, most operational early-warning frameworks continue to treat locations as epidemiologically independent, even when strong intercity coupling is expected. Forecasting models—including autoregressive approaches, hierarchical statistical models, and neural networks—typically predict local incidence based on historical cases and environmental covariates, rarely accounting for how predicted cases in one location may influence risk elsewhere through human movement. Moreover, most mobility-informed models emphasize retrospective analyses rather than real-time, spatially structured forecasts that could directly inform public health response.

In this study, we introduce a generalizable framework that integrates short-term incidence forecasts with a mobility-weighted importation model

Computer, Electrical and Mathematical Sciences and Engineering Division, King Abdullah University of Science and Technology (KAUST), Thuwal, Saudi Arabia.

e-mail: [xiang.chen@kaust.edu.sa](mailto:xiang.chen@kaust.edu.sa)

to estimate the expected flow of infections between locations. The forecasting and mobility components are modular: any model capable of generating time-indexed incidence estimates can be coupled with an origin-destination mobility matrix to compute the relative contribution of each source location to the importation pressure faced by each destination. This flexible structure facilitates integration with existing early warning pipelines.

We apply this framework to Brazil at high spatial resolution, modeling importation risk across all 5,570 municipalities. Our approach combines a multimodal mobility network—capturing road, river, and air transport flows—with climate-informed long short-term memory (LSTM) forecasts of dengue incidence. By integrating these components, we generate a dynamic surface of predicted importation risk and decompose it into internal (within-city) and external (between-city) contributions. This allows us to identify persistent exporter municipalities, quantify each location's reliance on external seeding, and map stable corridors of mobility-driven transmission.

This work advances existing research in several ways. It extends dengue importation modeling from international and state-level contexts to a national, city-level scale within a large endemic setting. It moves beyond retrospective inference by embedding mobility directly into a prospective forecasting pipeline. And it offers interpretable attribution of spatial risk via source-destination decomposition. While demonstrated in Brazil, this framework offers a generalizable tool for spatially structured epidemic intelligence, with potential relevance for other emerging infectious diseases shaped by human mobility.

## Results

### Overview of Dengue Burden and Forecasting Setup

We begin by describing the historical and forecasted burden of dengue across Brazil's 27 federal units. Figure 1 visualizes monthly dengue incidence rates (DIR) from 2010 to 2024, aggregated by state. The heatmaps reveal strong seasonal patterns and substantial spatiotemporal heterogeneity. Dengue activity typically peaks between February and May, but the timing and intensity of epidemics vary considerably across regions and years. Notably, the heatmap clearly shows the exceptional magnitude of the 2024 dengue surge in Brazil, with record incidence rates observed across many states. States in the Northeast and Central-West often experience early-season outbreaks with high intensity, whereas southern and Amazonian states display more sporadic or delayed peaks<sup>12,13</sup>.

Several states exhibit increasing epidemic magnitude in recent years, culminating in projected surges for 2024, particularly in the Southeast and parts of the North. These patterns provide critical context for assessing importation dynamics, as regions with rising or early incidence may act as dominant sources of spatial spread.

To generate prospective case forecasts, we use a climate-informed deep learning model at the municipality level. Specifically, a long short-term memory (LSTM) network<sup>14,15</sup> is trained on 14 years of weekly dengue case counts and climate data (2010–2023) for each of Brazil's 5,570 municipalities. Forecasts are produced for all 52 weeks of 2024 using a sliding-window strategy: after every four-week forecast block, the model is retrained using a fixed historical window to maintain temporal consistency. This approach balances short-term adaptability with long-range stability. To quantify predictive uncertainty, we apply a conformal prediction method<sup>16–19</sup> calibrated on recent residuals to generate 95% uncertainty intervals. These forecasts serve as the input to the mobility-based importation model detailed in the following sections. Summary forecasting performance metrics (e.g., MAE, MAPE, RMSE) across municipalities are provided in the Supplementary Information (Supplementary Table 1).

### National Landscape of Predicted Importation Risk

To assess how dengue risk propagates through Brazil's national mobility network, we estimate city-level importation pressure for all 5,570 municipalities across 2024.

For each municipality and week, the importation signal reflects the aggregated contribution of predicted infections arriving from all

connected cities. This quantity is computed by considering each origin city's projected case count by its population (as a proxy for infection prevalence) and scaling by the directional mobility intensity from origin to destination. The resulting importation surface captures spatial spillover effects and highlights municipalities at heightened risk due to external exposure. The full mathematical formulation is provided in the Methods section.

Figure 2 presents the monthly evolution of predicted dengue importation risk across all Brazilian municipalities. Several consistent spatial patterns emerge. First, importation risk intensifies sharply from February to May, peaking during the canonical dengue season, followed by a gradual decline from May onward. This timing mirrors the typical dengue transmission cycle but reveals how spatial spillover interacts with seasonality at fine geographic resolution.

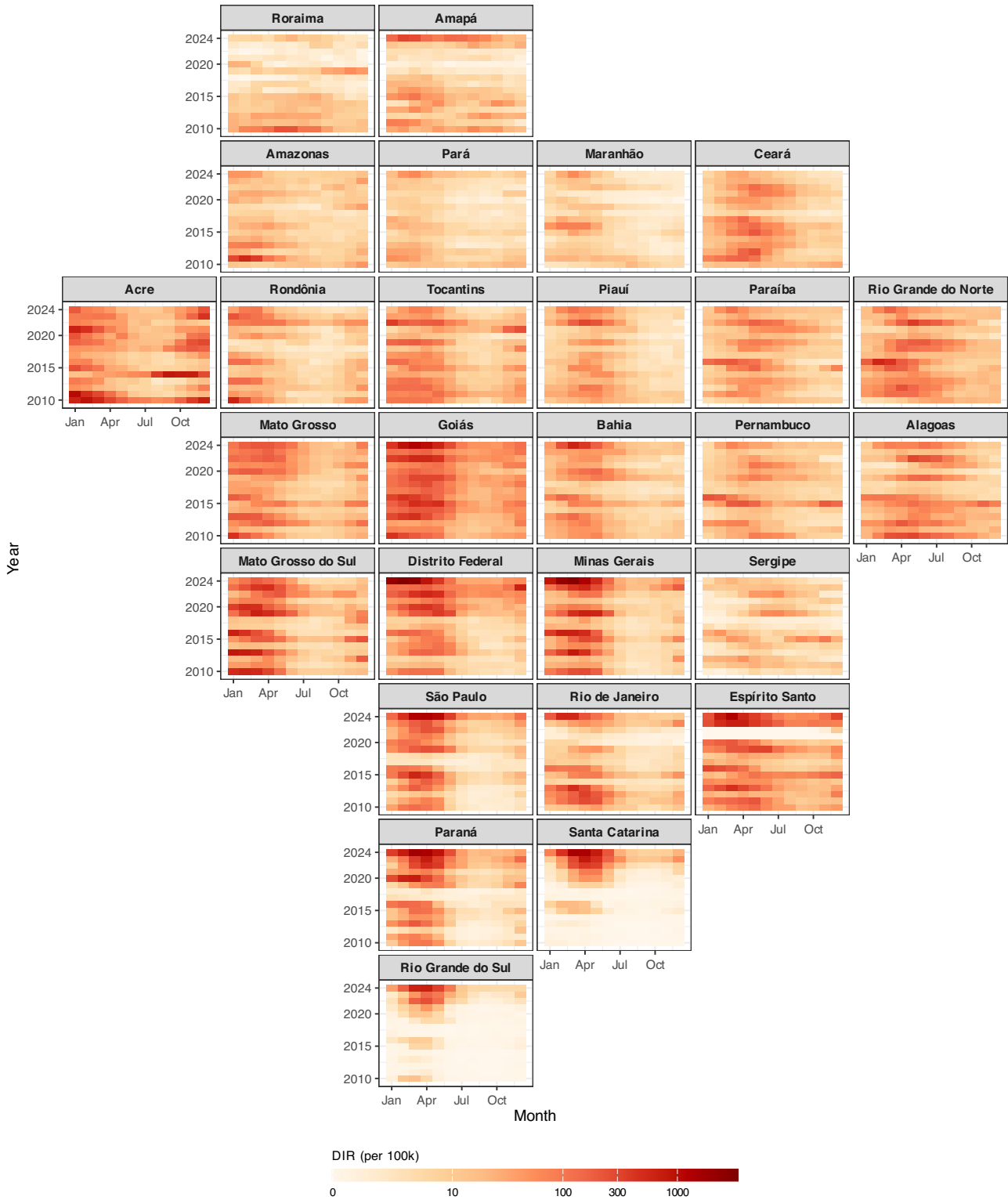
Second, high-risk zones are not uniformly distributed. Dense urban centers and major transit hubs—including parts of São Paulo, Rio de Janeiro, Goiás, and the Distrito Federal—exhibit persistently elevated importation pressure. These areas function as both sources and sinks within Brazil's interconnected mobility web. In contrast, certain remote municipalities in the Amazon basin and interior South experience comparatively low external exposure, either due to geographic isolation or weaker transport links.

Third, seasonal shifts in risk are not homogeneous across the country. Northern and northeastern states tend to show early importation signals (January–March), reflecting their historical epidemic timing and upstream role in seeding transmission elsewhere. Southern states such as Paraná and Santa Catarina exhibit a delayed and more attenuated importation profile, consistent with their lower endemicity and cooler climate.

It is critical to interpret the predicted importation signal as a measure of external seeding pressure driven by connectivity and forecasted incidence at origin locations, not as a direct measure of realized importation events or subsequent local transmission risk. An imported case only leads to a local outbreak if the destination environment is receptive—meaning conditions are favorable for the infection to spread from the human host to local mosquito vectors, which then transmit it to the susceptible population<sup>10,20</sup>. Such receptivity depends on factors including the presence of competent *Aedes* vectors, suitable climatic conditions, and local host susceptibility, which are not mechanistically modeled in the importation component of our framework. Key factors defining receptivity include the presence of competent *Aedes* populations<sup>21,22</sup>, adequate local temperature and rainfall, and high levels of host susceptibility<sup>23–25</sup>. Therefore, a city with high predicted importation pressure but currently unfavorable environmental conditions (e.g., during a dry, cold period) may absorb imported cases without a significant epidemic increase. Conversely, a single imported case into a highly receptive city can trigger a large outbreak<sup>26</sup>. This framework specifically isolates the external pressure component, which must be considered alongside the internal, environmentally-driven receptivity for a complete risk assessment.

To complement the monthly analysis, we also compute the total importation pressure accumulated over the full year. The resulting map, included in the Supplementary Material (Supplementary Fig. 1), highlights structural hotspots of spatial exposure—primarily large urban municipalities and major transit corridors—that sustain high levels of connectivity to dengue-affected regions throughout the season. Additionally, maps of the lower and upper bounds of the monthly 95% uncertainty intervals (Supplementary Fig. 2 and Supplementary Fig. 3) provide a visual summary of predictive uncertainty, offering bounds on possible importation scenarios under forecast variation.

This analysis reveals important spatial asymmetries in exposure. Some municipalities—despite having modest local incidence—receive substantial imported pressure due to strong connectivity with high-burden regions. Conversely, cities with large projected case counts may experience limited external importation if they are weakly coupled to the mobility network. These divergences underscore the limitations of relying solely on local case



**Fig. 1 | Monthly dengue incidence rate (DIR) across Brazil's 27 federal units from 2010 to 2024.** Each panel shows the DIR (per 100,000 population), aggregated at the state level and visualized monthly across 15 years. Rows represent years, columns represent months, and darker shades indicate higher incidence.

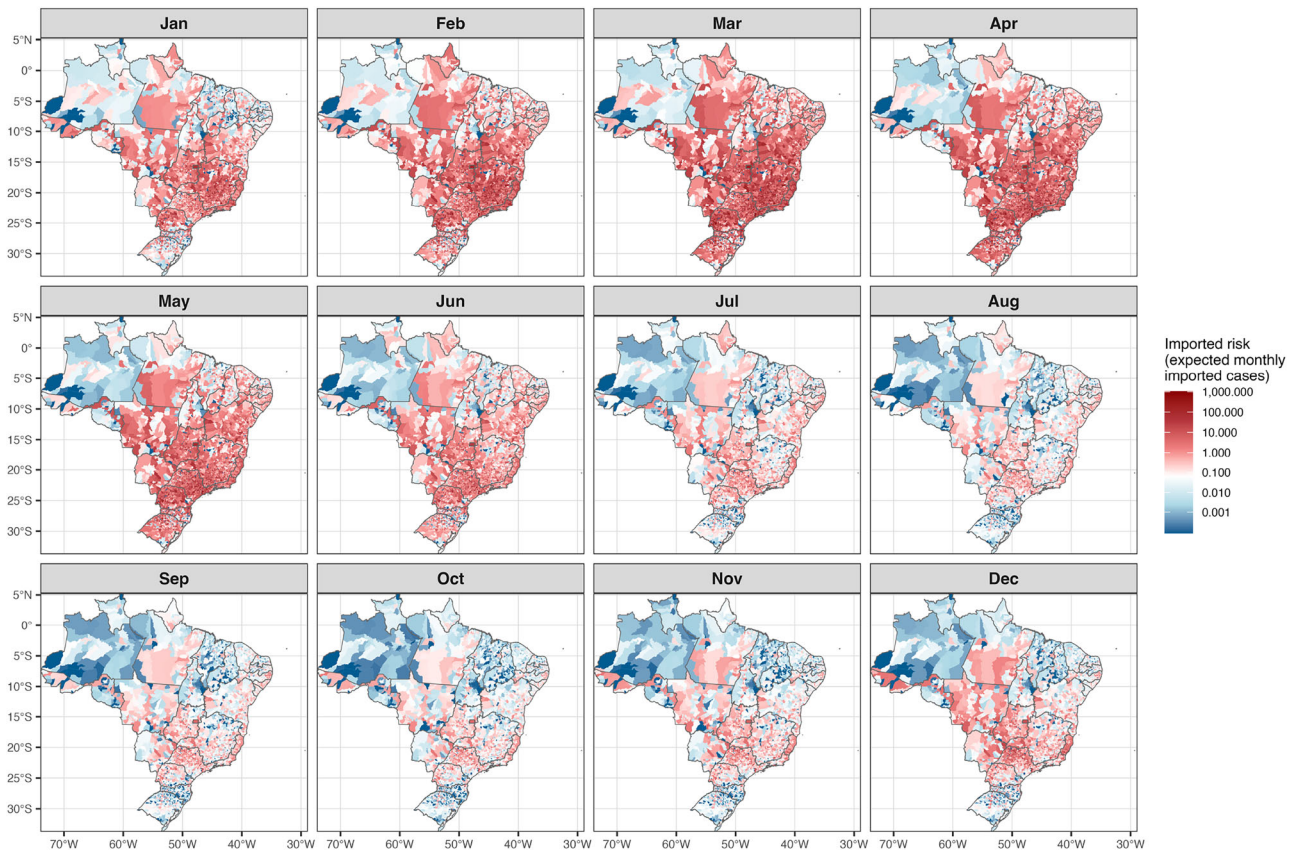
forecasts and highlight the added value of mobility-adjusted importation modeling for anticipatory surveillance and targeted intervention planning.

**Internal vs. External Importation Dynamics Across States**

To examine the spatial composition of dengue importation risk, we aggregated origin-destination flows from the municipality level to the scale of Brazil's 27 federal units. For each destination state, we computed the total

annual importation signal by summing incoming flows from all other municipalities and then decomposed this signal into internal contributions (originating from within the same state) and external contributions (originating from other states). This analysis enables a macroscopic view of how mobility-driven transmission varies across Brazil's regional units.

Figure 3 presents the national network of importation flows as a circular diagram. Self-loops reflect the volume of internally sourced



**Fig. 2 | Monthly dengue importation risk across Brazil’s 5,570 municipalities for the year 2024.** Colors indicate the expected monthly dengue importation risk per municipality, computed as connectivity-weighted forecasted per-capita incidence

from connected origin municipalities. Values are log-scaled to visualize both low and high transmission settings. Red tones reflect increasing importation pressure; blue tones indicate minimal risk.

importation, while ribbons connecting states depict dominant cross-border pathways. The structure reveals a set of high-volume corridors linking southeastern and central states—such as São Paulo, Minas Gerais, Goiás, and the Distrito Federal—with strong bidirectional flows and recurrent seeding events. Peripheral or sparsely connected states, by contrast, show weaker outgoing connections and often act primarily as import receivers.

To quantify these patterns, we calculated for each state the proportion of total importation attributable to its own municipalities versus other states, and identified the five largest external contributors. This decomposition uncovers striking heterogeneity in importation dependency. Several large states exhibit highly self-contained profiles—for instance, São Paulo (SP), Minas Gerais (MG), and Paraná (PR) each receive over 80% of their importation pressure from within-state circulation. These states act as both major epidemic hubs and strong internal propagators, suggesting that their mobility structures reinforce localized spread. In contrast, other states display heavy reliance on cross-border seeding. The Distrito Federal (DF), with no internal municipalities, is entirely dependent on external importation—primarily from Goiás (43.4%), Minas Gerais (23.9%), and São Paulo (12.4%). Roraima (RR), located in the northern Amazon basin, receives over one-third of its importation signal from DF and Amazonas (AM) combined. Tocantins (TO) and Rondônia (RO) similarly depend on concentrated flows from a small set of source states, often tied to their geographic centrality or limited internal mobility infrastructure. Intermediate cases also emerge: states such as Bahia (BA), Maranhão (MA), and Ceará (CE) exhibit roughly 40–80% internal sourcing, with the remainder coming from a mix of regional and long-range external links. These hybrid profiles reflect complex transmission dynamics influenced by both endemic circulation and spatial exposure.

The full breakdown of internal vs external importation shares and dominant contributors for each federal unit is provided in Supplementary

Table 2. Together, these results clarify the distinct spatial roles that states play in Brazil’s dengue network—as relatively self-sustained systems, regional exporters, or downstream importers—offering a diagnostic tool for targeting intergovernmental coordination, regional surveillance, and mobility-informed intervention strategies.

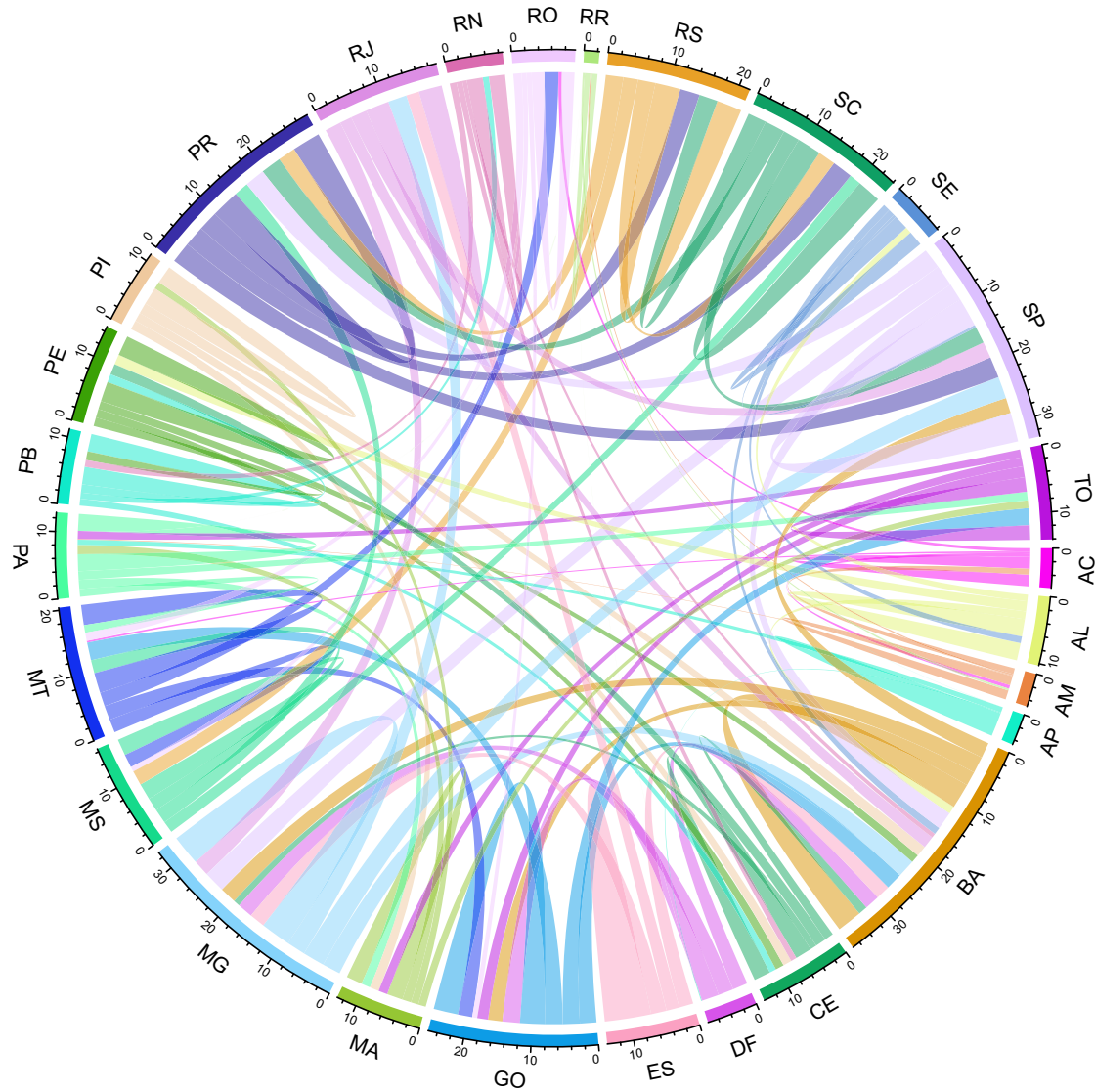
### City-Level Source-Sink Dynamics of Dengue Risk

To characterize the spatial asymmetry of dengue transmission across Brazil, we quantified the net importation balance for each of the 5,570 municipalities. For each city, we computed the difference between its exported and imported risk, where exported risk reflects how local infections are amplified by outbound mobility, and imported risk captures the cumulative pressure arriving from all connected cities. This formulation isolates the direction and magnitude of each municipality’s role in the national source-sink landscape.

Positive values indicate net exporters—municipalities that act as sources of dengue importation—while negative values denote net importers, or sinks. Supplementary Fig. 4 provided in Supplementary information shows the spatial distribution of the top 100 exporter and importer municipalities across Brazil in 2024, highlighting the cities that most strongly shape national source-sink dynamics.

Nationally, the distribution of net flow reveals a strongly right-skewed structure: while the majority of cities experience negative net flow (median:  $-0.69$ ; mean:  $0$ ), a small number of highly connected urban centers exhibit large positive net export values. In total, 67.0% of municipalities are net importers, while 29.7% function as exporters—highlighting a pronounced source-sink hierarchy in Brazil’s dengue mobility network.

The top exporting cities include major metropolitan hubs such as Campinas (SP), Belo Horizonte (MG), and Brasília (DF), each with net export values exceeding  $+1,000$ . These municipalities are among the most



**Fig. 3 | Annual dengue importation flows across Brazilian states in 2024.** Each segment represents one of the 27 federal units. Self-loops indicate internal (within-state) importation, while ribbons between states depict dominant external sources.

Tick marks around each segment show the relative magnitude of log-scaled outgoing flows; they do not correspond to raw case counts. The diagram highlights the structure and relative intensity of major importation pathways across states.

densely populated in the country and sit at the center of regional mobility webs. Other notable exporters include São José do Rio Preto (SP), Contagem (MG), and Joinville (SC), all of which function as second-tier nodes funneling risk to surrounding areas.

Conversely, the strongest importers include Curitiba (PR), Rio de Janeiro (RJ), and southern municipalities in Minas Gerais, Rio Grande do Sul, and Bahia. These cities absorb large volumes of incoming risk while contributing comparatively little outward flow, reflecting their location downstream in major mobility corridors and their relatively limited regional connectivity.

To further explore the spatial concentration of sources and sinks, we identified the 100 highest-exporting and 100 highest-importing municipalities, and tabulated their state-level distribution. Minas Gerais (MG), Paraná (PR), and São Paulo (SP) together account for over 60% of the top exporters, indicating that these states anchor the national risk-export network. At the same time, MG, SP, and Rio Grande do Sul (RS) also dominate the list of top importers—underscoring their dual role as both origin and destination nodes within Brazil’s densely interconnected system.

These results confirm that Brazil’s dengue mobility structure follows a hub-and-spoke topology, in which a relatively small number of highly mobile, high-prevalence cities act as consistent exporters of risk. Most

municipalities, however, lie at the periphery of this system and function as net receivers—underscoring the importance of upstream risk mitigation and early outbreak detection in urban centers that disproportionately shape national transmission dynamics. Full rankings of municipal net flow are provided in Supplementary Data 1.

### Discussion

This study presents a scalable framework for quantifying dengue importation risk across Brazil’s 5,570 municipalities by integrating short-term local case forecasts with a multimodal mobility network. By combining projected incidence and directional connectivity, we reveal how spatial spillover dynamically shapes exposure beyond what local forecasts can capture. The resulting importation surface enables attribution of risk to specific source regions and identifies key transmission corridors and urban centers that drive the broader epidemic landscape. We also decompose flows at both municipal and state levels, uncovering asymmetric source-sink dynamics and clarifying which locations are vulnerable to external seeding.

Our findings are consistent with and extend prior work on mobility-driven infectious disease spread. Past studies have demonstrated the importance of human movement for dengue introduction and amplification at both international and national scales. Air travel-based models have

shown that dengue importation correlates with passenger flows and origin-country burden<sup>4,5</sup>. Within-country analyses in Brazil and other endemic settings have traced seasonal waves and interregional spread using gravity models or mobile phone data<sup>8–10</sup>. Our work builds on this foundation by producing real-time, city-level forecasts of importation risk that account for intercity coupling and mobility-based exposure, providing a forward-looking lens for surveillance and response.

Several components of the framework offer novel advantages. First, it operates at national scale with full municipality-level granularity, allowing spatially resolved insight into risk propagation. Second, the mobility surface integrates road, river, and air transport infrastructure, yielding a structurally grounded representation of human connectivity across Brazil. Third, the forecasting module uses climate-informed LSTM networks with calibrated uncertainty bounds to generate robust, week-by-week incidence predictions. Most importantly, the architecture is modular: any forecasting model or mobility matrix can be substituted, making the approach widely adaptable across diseases, geographies, and data availability settings.

Finally, we used the full 2010–2023 dengue and climate record as the training period. This choice is natural because 2010 marks the start of consistent weekly municipal-level surveillance in InfoDengue<sup>27</sup>. In data-driven forecasting models, longer historical windows provide essential information about multi-year dengue cycles, climate variability, and large outbreak regimes—patterns that cannot be learned from short fragments. Our rolling moving-window framework further enhances robustness by repeatedly retraining the model over overlapping temporal segments, ensuring that results are not tied to any particular subset of years. Using 2010–2023, therefore, leverages the maximum reliable information while maintaining methodological coherence and predictive stability.

From a public health perspective, this framework offers actionable insights for epidemic preparedness in Brazil by differentiating between external seeding pressure and local transmission risk. The identification of cities with high predicted importation pressure is valuable for anticipatory resource allocation. However, these estimates must be interpreted in conjunction with a municipality’s receptivity, or the environmental and entomological suitability for local mosquito-borne spread<sup>10,20</sup>. Cities that experience high external importation but currently unfavorable environmental conditions (low mosquito presence) represent a future risk if conditions shift; they may be prioritized for intensified vector surveillance and community awareness campaigns to rapidly detect and contain any local transmission that may occur<sup>21–25</sup>. Conversely, highly receptive cities receiving any substantial importation signal warrant immediate targeted interventions, such as focused vector control, to prevent seeding new outbreaks. The decomposition of flows into internal versus external components at the state level clarifies the extent to which dengue dynamics are driven by self-sustaining transmission versus regional spillover, informing coordination across jurisdictional boundaries. Additionally, identifying recurrent exporter cities and corridors enables anticipatory monitoring of upstream sources before downstream epidemics unfold.

Our analysis also has limitations. First, the mobility matrix represents a static structural surface rather than real-time flow, and may not reflect temporal variations due to seasonality, behavioral shifts, unobserved travel, major mobility disruptions, or recent infrastructure development. Second, dengue case forecasts are subject to surveillance gaps and reporting inconsistencies, particularly in rural or under-resourced municipalities. Third, while we estimate relative importation pressure, the framework does not yield absolute infection counts attributable to imported cases. Fourth, the forecasting and importation components treat dengue in an aggregated manner and do not distinguish between viral serotypes or strains; differences in population immunity to circulating serotypes may therefore influence local outbreak potential following introduction. Finally, the framework does not mechanistically model vector-host interactions or local socioeconomic conditions—such as housing quality, sanitation, or population density—which can shape transmission dynamics and contribute to heterogeneous epidemiological profiles across municipalities. Future work

could incorporate slowly varying socioeconomic indicators as additional inputs or stratification layers, and could explore ensemble approaches that combine models with different structural assumptions to improve robustness across heterogeneous municipalities.

Nonetheless, the framework is readily extensible. On the forecasting side, our approach is compatible with a broad range of predictive models—including statistical time series models<sup>28–31</sup>, climate-driven mechanistic systems, or ensemble methods—allowing future integration of more complex epidemic drivers<sup>32–38</sup>. Likewise, mobility inputs can be updated with real-time origin-destination data from mobile phone traces or transportation logs. We point out that this method can be transferred to other countries or regions, and when similar population flow datasets are unavailable, a gravity-like model can be used for fitting<sup>39–42</sup>. Importantly, this modularity makes the system transferable to other mobility-sensitive diseases, and highly relevant for diseases transmitted person-to-person through social and travel networks, like influenza<sup>43</sup> and COVID-19<sup>44–46</sup>. This adaptability makes the framework suitable for use in other regions facing spatially structured epidemics.

## Methods

### Data Sources

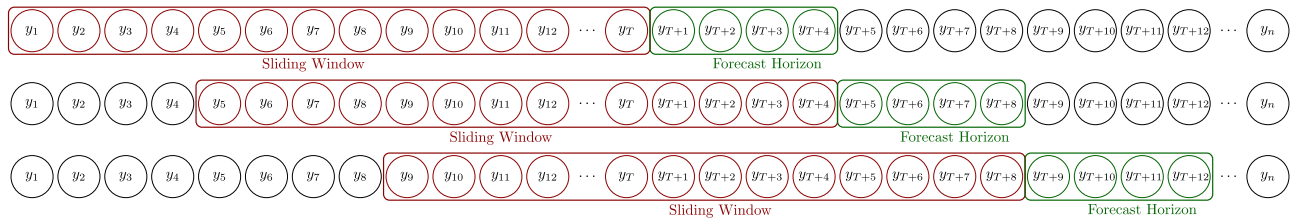
We used weekly dengue case reports from the InfoDengue platform spanning 2010–2024<sup>27</sup>, providing harmonized subnational surveillance across Brazil. Annual population estimates were drawn from DATASUS/TABNET<sup>47</sup>. Environmental covariates were derived from the ERA5 reanalysis<sup>48</sup> and aggregated to the municipal level. These included temperature indicators (minimum, mean, and maximum), precipitation metrics (minimum, mean, maximum, and weekly totals), atmospheric pressure (minimum, mean, and maximum), relative humidity (minimum, mean, and maximum), weekly thermal range, and the number of rainy days.

To describe human movement and estimate spatial spillover risk, we utilized a composite city-to-city mobility matrix derived from multimodal transport data assembled by<sup>49</sup>, encompassing road infrastructure, riverine routes, and scaled airline passenger flows. While this matrix does not reflect direct, instantaneous movement volumes, it captures the structural connectivity of Brazil’s transport system and serves as a crucial proxy for mobility intensity between municipalities. The final mobility matrix, **M**, represents a static, directional surface of connectivity strength,  $M_{ji}$  (flow from origin  $j$  to destination  $i$ ), based on the integration of three distinct transport modes. This was achieved by combining the number of connections from road infrastructure and riverine routes with high-volume commercial airline passenger flows. The passenger volumes were scaled and integrated with the connection counts to produce a hybrid measure of flow intensity across all city pairs. This composite approach ensures that the matrix captures both fine-scale, localized links (road/river) and long-distance connectivity (air), providing nationwide coverage and interpretability suitable for operational settings where detailed, time-varying origin-destination data are unavailable. We use this empirical mobility matrix directly in the importation calculation. Its interpretability and nationwide coverage make it suitable for real-time operational settings, especially where detailed origin-destination mobility data are unavailable. The spatial pattern of this composite matrix is illustrated in Supplementary Fig. 5.

### Framework Overview

We developed a scalable, mobility-aware framework to quantify the importation risk of dengue across Brazil’s 5,570 municipalities. This framework quantifies dengue importation risk by combining predicted local incidence at potential source locations with the spatial intensity of human connectivity between cities. For each destination municipality  $i$  and week  $t$ , the importation signal is defined as:

$$\text{Importation}_{i,t} = \sum_{j \in \mathcal{N}_i} \text{Mobility}_{ji} \times \frac{\widehat{\text{Cases}}_{j,t}}{\text{Population}_j} \quad (1)$$



**Fig. 4 | Sliding-window framework for multi-step dengue forecasting.** A fixed-length history window is used to predict 4 weeks ahead. The window then advances by 4 steps and the process is repeated, generating a sequential forecast across the full 2024 horizon.

This modular expression integrates two components: a short-term forecast of dengue incidence  $Cases_{j,t}$  for each origin  $j$ , and a composite intercity mobility score  $Mobility_{ji}$  that reflects directional movement intensity between locations. The term  $\mathcal{N}_i$  represents all cities with directed mobility connections to  $i$ . Normalizing by population yields a proxy for infection prevalence, allowing incidence to be transferred through the spatial network.

Importantly, the mobility matrix is not used to compute dengue incidence forecasts. Instead, forecasting and mobility enter the framework as distinct components: forecasts are generated first, and the mobility matrix is applied only downstream to translate predicted incidence at origin locations into importation risk at destination municipalities.

The framework is modular with respect to both the incidence forecasting model and the choice of spatial interaction weights. Any method capable of producing time-indexed incidence estimates can be used to obtain  $Cases_{j,t}$ , including statistical time-series models, machine learning approaches, or ensemble systems. Likewise, the mobility term  $Mobility_{ji}$  can be specified using different representations of spatial connectivity. When detailed mobility or empirically derived origin–destination matrices are unavailable, simpler alternatives such as distance-based adjacency weights or gravity-type kernels can be used to construct  $Mobility_{ji}$ , yielding a qualitatively similar interpretation of connectivity-modulated external exposure.

### Forecasting Model

Dengue incidence forecasts for each city-week pair were generated using a long short-term memory (LSTM) recurrent neural network<sup>14,15</sup>. The model was trained using a moving window strategy: for each 4-week prediction block in 2024, we used the preceding 14 years of weekly data (2010–2023) as training history. The window advanced in 4-week increments, allowing adaptation to recent trends while retaining long-range memory. Figure 4 illustrates this sliding-window structure, where a fixed-length input window is repeatedly shifted forward to produce sequential forecasts across the full 2024 horizon.

Input features included dengue case history and ERA5-derived climate variables. The LSTM architecture was intentionally kept compact to ensure scalability across all 5,570 municipalities. We used a single-layer LSTM with 64 hidden units, a dropout rate of 0.2, and the Adam optimizer with mean squared error loss. Training was capped at 30 epochs with early stopping, using a batch size of 64 and a fixed input window of 312 weeks. To determine a configuration that performs reliably across Brazil’s heterogeneous municipal profiles, we conducted hyperparameter tuning on a subset of representative cities spanning different incidence levels, population sizes, and climatic regions. This search explored the number of LSTM units, dropout rates, learning rates, and batch sizes, with the goal of identifying a single stable architecture rather than city-specific optima. Since the model is retrained hundreds of times across rolling windows and municipalities, a uniform configuration is preferable to heterogeneous, heavily optimized setups that may produce inconsistent behavior. Our focus was therefore on robustness and reproducibility rather than maximal predictive accuracy in any single city. Point predictions were accompanied by 95% prediction intervals computed via a conformal residual-based approach, using rolling-origin errors to construct quantile bounds<sup>16–19</sup>. To evaluate the predictive accuracy of the LSTM model across all municipalities and time steps, we

calculated the Mean Absolute Error (MAE), the Root Mean Squared Error (RMSE), and the Mean Absolute Percentage Error (MAPE). These metrics summarize the difference between the observed and the forecasted dengue incidence. The MAE provides the average magnitude of error, weighted linearly; the RMSE heavily penalizes large errors, as the errors are squared before averaging; and the MAPE provides a scale-independent measure of error relative to the observed value, expressed as a percentage. These forecast performance metrics serve as an essential basis for assessing the reliability of the importation risk estimates<sup>32–34</sup>.

While the framework allows flexible substitution of forecasting models, we selected LSTM due to its established performance in dengue forecasting and its compatibility with the dynamic nature of dengue-climate interactions<sup>32–37</sup>.

### Data availability

All data used in this study is open access and freely available from data repositories, see the “Methods” section for details.

Received: 30 November 2025; Accepted: 14 March 2026;

Published online: 04 May 2026

### References

1. Paz-Bailey, G., Adams, L. E., Deen, J., Anderson, K. B. & Katzelnick, L. C. Dengue. *Lancet* **403**, 667–682 (2024).
2. Gurgel-Gonçalves, R., Oliveira, W. K. D. & Croda, J. The greatest dengue epidemic in Brazil: surveillance, prevention, and control. *Rev. da Soc. Brasileira de Med. Tropical* **57**, e00203–2024 (2024).
3. Wesolowski, A. et al. Quantifying the impact of human mobility on malaria. *Science* **338**, 267–270 (2012).
4. Gardner, L. & Sarkar, S. A global airport-based risk model for the spread of dengue infection via the air transport network. *PLoS one* **8**, e72129 (2013).
5. Liebig, J., Jansen, C., Paini, D., Gardner, L. & Jurdak, R. A global model for predicting the arrival of imported dengue infections. *PLoS ONE* **14**, 1–18 (2019).
6. Poongavanan, J. et al. Dengue virus importation risks in Africa: a modelling study. *Lancet Planet. Health* **8**, e1043–e1054 (2024).
7. Salami, D., Sousa, C. A., Martins, M. dR. O. & Capinha, C. Predicting dengue importation into Europe, using machine learning and model-agnostic methods. *Sci. Rep.* **10**, 9689 (2020).
8. Lana, R. M., Gomes, M. F.dC., Lima, T. F. M. d, Honório, N. A. & Codeço, C. T. The introduction of dengue follows transportation infrastructure changes in the state of Acre, Brazil: A network-based analysis. *PLoS Neglected Tropical Dis.* **11**, 1–27 (2017).
9. Churakov, M., Villabona-Arenas, C. J., Kraemer, M. U., Salje, H. & Cauchemez, S. Spatio-temporal dynamics of dengue in Brazil: Seasonal travelling waves and determinants of regional synchrony. *PLoS Neglected Tropical Dis.* **13**, e0007012 (2019).
10. Wesolowski, A. et al. Impact of human mobility on the emergence of dengue epidemics in Pakistan. *Proc. Natl. Acad. Sci.* **112**, 11887–11892 (2015).
11. Harish, V. et al. Human movement and environmental barriers shape the emergence of dengue. *Nat. Commun.* **15**, 4205 (2024).

12. do Carmo, R. F., Silva Júnior, J. V. J., Pastor, A. F. & de Souza, C. D. F. Spatiotemporal dynamics, risk areas and social determinants of dengue in northeastern Brazil, 2014–2017: an ecological study. *Infect. Dis. poverty* **9**, 153 (2020).
13. Filho, A. S. N., Murari, T. B., Ferreira, P., Saba, H. & Moret, M. A. A spatio-temporal analysis of dengue spread in a Brazilian dry climate region. *Sci. Rep.* **11**, 11892 (2021).
14. Hochreiter, S. Long short-term memory. *Neural Computation MIT-Press* (1997).
15. Greff, K., Srivastava, R. K., Koutník, J., Steunebrink, B. R. & Schmidhuber, J. Lstm: A search space odyssey. *IEEE Trans. neural Netw. Learn. Syst.* **28**, 2222–2232 (2016).
16. Vovk, V., Gammernan, A. & Shafer, G. *Algorithmic learning in a random world*, vol. 29 (Springer, 2005).
17. Balasubramanian, V., Ho, S.-S. & Vovk, V. *Conformal prediction for reliable machine learning: theory, adaptations and applications* (Newnes, 2014).
18. Bracher, J., Ray, E. L., Gneiting, T. & Reich, N. G. Evaluating epidemic forecasts in an interval format. *PLoS computational Biol.* **17**, e1008618 (2021).
19. Colón-González, F. J. et al. Probabilistic seasonal dengue forecasting in Vietnam: A modelling study using superensembles. *PLoS Med.* **18**, e1003542 (2021).
20. Reiner Jr, R. C. et al. Time-varying, serotype-specific force of infection of dengue virus. *Proc. Natl. Acad. Sci.* **111**, E2694–E2702 (2014).
21. Liu-Helmersson, J., Stenlund, H., Wilder-Smith, A. & Rocklöv, J. Vectorial capacity of *Aedes aegypti*: effects of temperature and implications for global dengue epidemic potential. *PLoS one* **9**, e89783 (2014).
22. Kamal, M., Kenawy, M. A., Rady, M. H., Khaled, A. S. & Samy, A. M. Mapping the global potential distributions of two arboviral vectors *Aedes aegypti* and *Ae. albopictus* under changing climate. *PLoS one* **13**, e0210122 (2018).
23. Messina, J. P. et al. The current and future global distribution and population at risk of dengue. *Nat. Microbiol.* **4**, 1508–1515 (2019).
24. Mordecai, E. A. et al. Detecting the impact of temperature on transmission of Zika, dengue, and chikungunya using mechanistic models. *PLoS Neglected Tropical Dis.* **11**, e0005568 (2017).
25. Gardner, L. M., Bota, A., Gangavarapu, K., Kraemer, M. U. & Grubaugh, N. D. Inferring the risk factors behind the geographical spread and transmission of Zika in the Americas. *PLoS Neglected Tropical Dis.* **12**, e0006194 (2018).
26. Kraemer, M. U. et al. The global distribution of the arbovirus vectors *Aedes aegypti* and *Ae. albopictus*. *elife* **4**, e08347 (2015).
27. Codeco, C. et al. Infodengue: A nowcasting system for the surveillance of arboviruses in Brazil. *Rev. d. 'Épidémiologie et de. St.é Publique* **66**, S386 (2018).
28. Luz, P. M. et al. Time series analysis of dengue incidence in Rio de Janeiro, Brazil. *American Society of Tropical Medicine and Hygiene* (2008).
29. Cortes, F. et al. Time series analysis of dengue surveillance data in two Brazilian cities. *Acta Tropica* **182**, 190–197 (2018).
30. Silawan, T. et al. Temporal patterns and forecast of dengue infection in northeastern Thailand. *Southeast Asian J. tropical Med. public health* **39**, 90 (2008).
31. Buczak, A. L. et al. Ensemble method for dengue prediction. *PLoS one* **13**, e0189988 (2018).
32. Chen, X. & Moraga, P. Assessing dengue forecasting methods: a comparative study of statistical models and machine learning techniques in Rio de Janeiro, Brazil. *Tropical Med. health* **53**, 52 (2025).
33. Chen, X. & Moraga, P. Forecasting dengue across Brazil with LSTM neural networks and shap-driven lagged climate and spatial effects. *BMC Public Health* **25**, 973 (2025).
34. Chen, X. & Moraga, P. Dengue forecasting and outbreak detection in Brazil using LSTM: integrating human mobility and climate factors. *Infect. Dis. Model.* **11**, 338–354 (2026).
35. Roster, K., Connaughton, C. & Rodrigues, F. A. Machine-learning-based forecasting of dengue fever in Brazilian cities using epidemiologic and meteorological variables. *Am. J. Epidemiol.* **191**, 1803–1812 (2022).
36. Kakarla, S. G. et al. Weather integrated multiple machine learning models for prediction of dengue prevalence in India. *Int. J. Biometeorol.* **67**, 285–297 (2023).
37. Zhao, N. et al. Machine learning and dengue forecasting: Comparing random forests and artificial neural networks for predicting dengue burden at national and sub-national scales in Colombia. *PLoS neglected tropical Dis.* **14**, e0008056 (2020).
38. Majeed, M. A., Shafri, H. Z. M., Zulkafli, Z. & Wayayok, A. A deep learning approach for dengue fever prediction in Malaysia using LSTM with spatial attention. *Int. J. Environ. Res. Public Health* **2023**, 4130 (2023).
39. Wesolowski, A., O'Meara, W. P., Eagle, N., Tatem, A. J. & Buckee, C. O. Evaluating spatial interaction models for regional mobility in sub-Saharan Africa. *PLoS computational Biol.* **11**, e1004267 (2015).
40. Meredith, H. R. et al. Characterizing human mobility patterns in rural settings of sub-saharan africa. *Elife* **10**, e68441 (2021).
41. Kwon, O.-H., Hong, I., Jung, W.-S. & Jo, H.-H. Multiple gravity laws for human mobility within cities. *EPJ Data Sci.* **12**, 57 (2023).
42. Ramiadantsoa, T. et al. Existing human mobility data sources poorly predicted the spatial spread of SARS-CoV-2 in Madagascar. *Epidemics* **38**, 100534 (2022).
43. Charu, V. et al. Human mobility and the spatial transmission of influenza in the United States. *PLoS computational Biol.* **13**, e1005382 (2017).
44. Han, X. et al. Quantifying COVID-19 importation risk in a dynamic network of domestic cities and international countries. *Proc. Natl. Acad. Sci.* **118**, e2100201118 (2021).
45. Chang, M.-C. et al. Variation in human mobility and its impact on the risk of future COVID-19 outbreaks in Taiwan. *BMC Public Health* **21**, 226 (2021).
46. Badr, H. S. et al. Association between mobility patterns and COVID-19 transmission in the USA: a mathematical modelling study. *Lancet Infect. Dis.* **20**, 1247–1254 (2020).
47. Ministério da Saúde. População Residente - Estudo de Estimativas Populacionais por Município, Idade e Sexo 2000-2024 - Brasil. <http://tabnet.datasus.gov.br/cgi/deftohtm.exe?ibge/cnv/popsvs2024br.def> (2024).
48. (C3S), C. C. C. S. Era5: Fifth generation of ECMWF atmospheric reanalyses of the global climate. <https://doi.org/10.24381/cds.adbb2d47> (2017).
49. Oliveira, J. F. et al. Human mobility patterns in Brazil to inform sampling sites for early pathogen detection and routes of spread: a network modelling and validation study. *Lancet Digital Health* **6**, e570–e579 (2024).

## Acknowledgements

This research received financial support from The Letten Prize (<https://lettenprize.com/>), with a personal award to Paula Moraga. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

## Author contributions

X.C. and P.M. conceived and designed the study. X.C. collected and processed the data, and performed the experiments. All the figures and maps are drawn by X.C.; X.C. and P.M. were contributors in writing and revising the manuscript. All authors read and approved the final manuscript.

### Competing interests

Paula Moraga serves as a Guest Editor for the “Geospatial Artificial Intelligence in Public Health” Collection in *npj Digital Public Health*. She had no involvement in the peer-review or editorial decision-making process for this manuscript.

### Additional information

**Supplementary information** The online version contains supplementary material available at <https://doi.org/10.1038/s44482-026-00015-9>.

**Correspondence** and requests for materials should be addressed to Xiang Chen.

**Reprints and permissions information** is available at <http://www.nature.com/reprints>

**Publisher's note** Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.

**Open Access** This article is licensed under a Creative Commons Attribution-NonCommercial-NoDerivatives 4.0 International License, which permits any non-commercial use, sharing, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if you modified the licensed material. You do not have permission under this licence to share adapted material derived from this article or parts of it. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by-nc-nd/4.0/>.

© The Author(s) 2026