

Arboviruses in Australia: A Spatial-Temporal Vulnerability Analysis

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Hanna Y. Ehrlich¹, Siobhan M. Mor⁴, Magaly Koch^{2,3}, Elena N. Naumova²

¹ School of Arts and Sciences, Tufts University, USA

² Faculty, Department of Civil and Environmental Engineering, Tufts University, USA

³ Research Associate Professor, Center for Remote Sensing, Boston University, USA

⁴ Faculty, Veterinary Science and Marie Bashir Institute of Infectious Diseases and Biosecurity/

School of Public Health, The University of Sydney, Australia

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Introduction

Three of the most common and clinically important arboviruses in Australia of today include Ross River Virus (RRV), Barmah Forest Virus (BFV), and dengue. These mosquito-borne diseases have exhibited an upward trend in Australia since 2002 (Fig. 1). Concern has arisen that these numbers will only continue to increase as a result of global warming and climate change. There is a growing body of evidence that insect vectors will escalate in distribution and activity, and in turn give rise to increases in the rates of arbovirus disease (Parham et al. 2015). Vector-borne disease risk is "a function of spatial and temporal patterns of vector breeding habitats and factors that affect distribution" (Dale et al. 1998). The identification of ecological patterns and parameters that affect vector distribution, as well as spatial-temporal dynamics of disease transmission, are necessary to predict and prevent the rise of arbovirus in Australia.

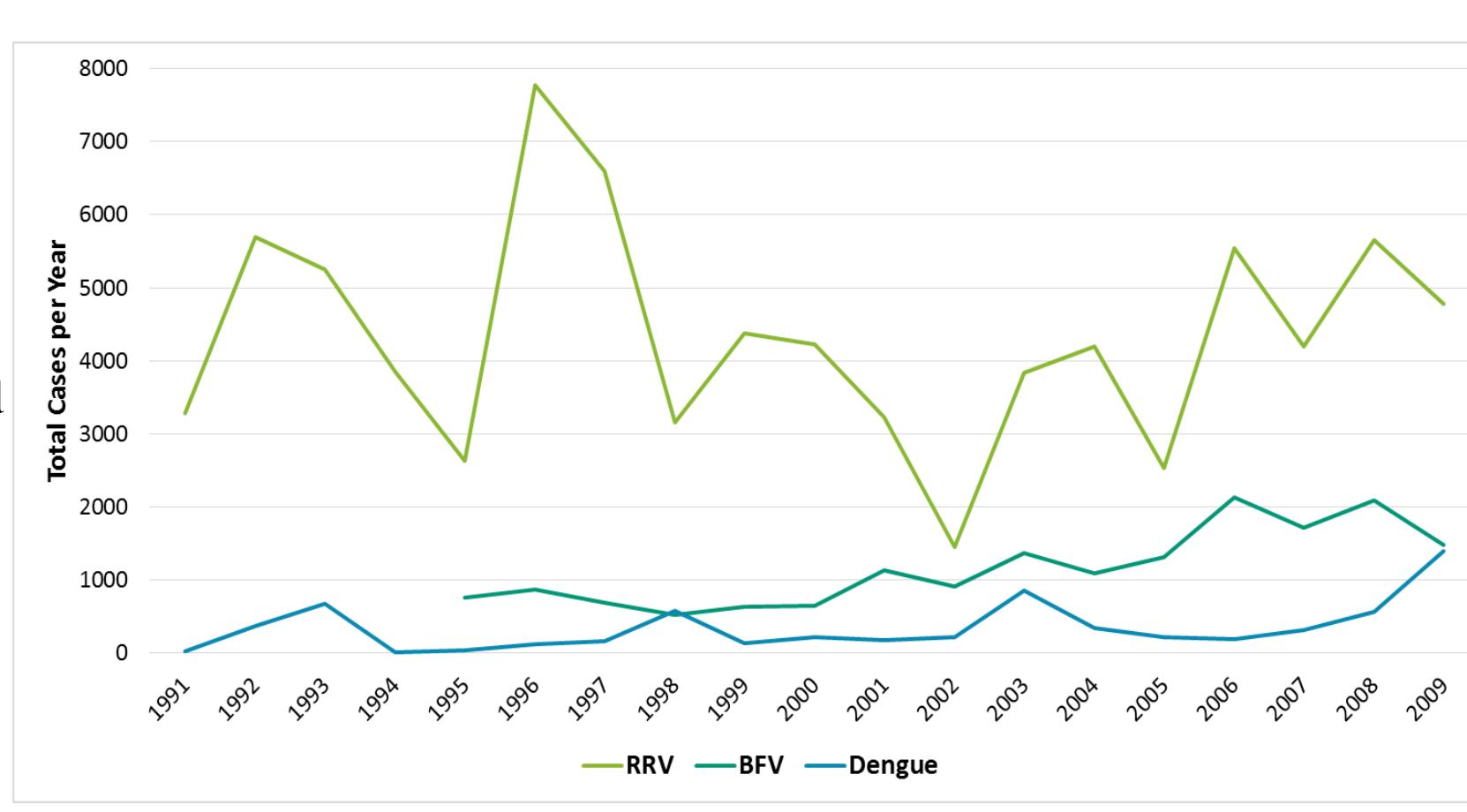


Figure 1. Annual case counts for three arboviral diseases in Australia.

RRV, BFV, and dengue differ significantly in their transmission scope (Table 1). RRV and BFV are both endemic to mainland Australia; dengue exhibits periodic epidemic activity currently limited to Queensland. While RRV and BFV have several mosquito genera implicated in their transmission, dengue has only one resident vector species. Further, RRV and BFV are zoonotic with wildlife reservoirs, whereas humans act as the only reservoir host for dengue. Although RRV and BFV are responsible for a greater number of annual infections than dengue in Australia, dengue will be the primary focus for the spatial analysis in this study, due to its singular vector species and reservoir host.

Arthropod Virus	Arthropod Vectors	Reservoir	Affected States	Year of Emergence/Discovery	Total Cases 1991–2010*	Mean Yearly Cases
Ross River (RRV)	<i>Culex annulirostris</i> , <i>Ochlerotatus vigilax</i> , 33 others	Marsupials, rats, bats	Mainland Australia	1963	86,014	4,301
Barmah Forest (BFV)	<i>Culex annulirostris</i> , <i>Aedes vigilax</i> , <i>Ochlerotatus camptorhynchus</i> , 10 others	Marsupials	Mainland Australia	1974	18,323	1,145
Dengue	<i>Aedes aegypti</i>	Humans	Queensland	1873	7,177	359

Table 1. Selected disease information on RRV, BFV, and Dengue.

*Data available beginning in 1995 for BFV

Seasonality

Seasonal fluctuations in vector-borne diseases are an established epidemiological phenomenon. Because seasonal patterns are so closely and commonly associated with meteorological and environmental factors, it is critical to understand the seasonality of a disease over time in order to determine the long-term effects of climate on disease incidence (Jaigi et al. 2009). BFV, RRV, and dengue all display seasonal patterns yearly and over time, with RRV exhibiting the most constancy over time and dengue the most variability (Fig. 2).

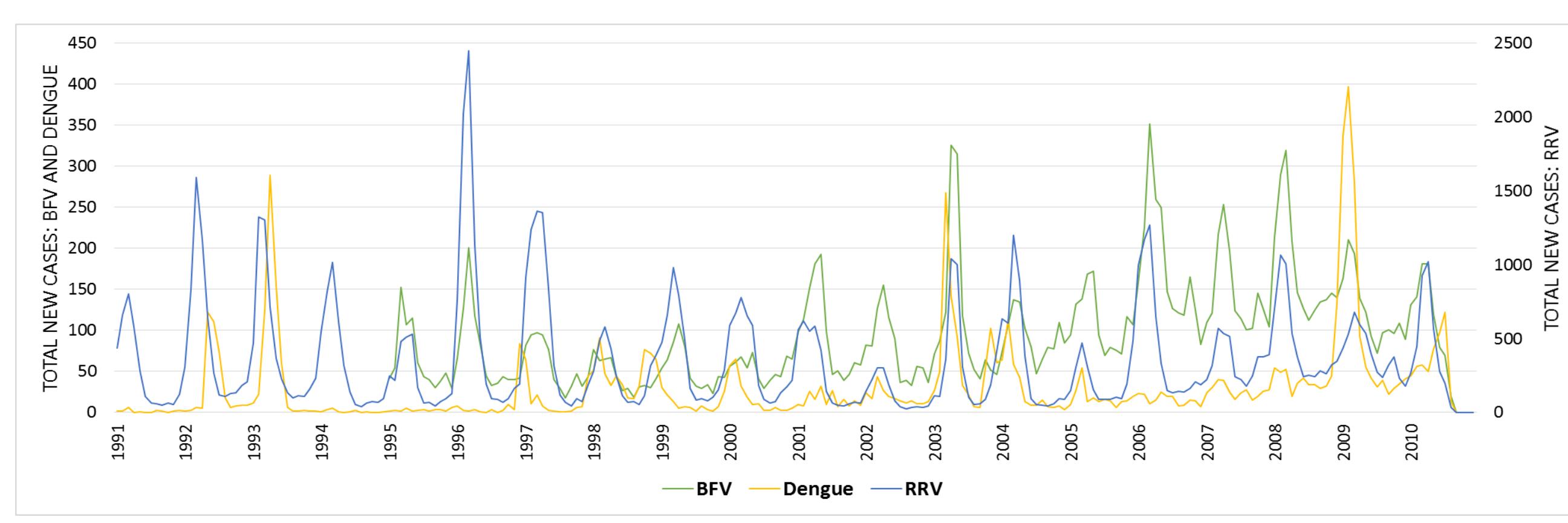


Figure 2. Time-Series for RRV, BFV, and Dengue.

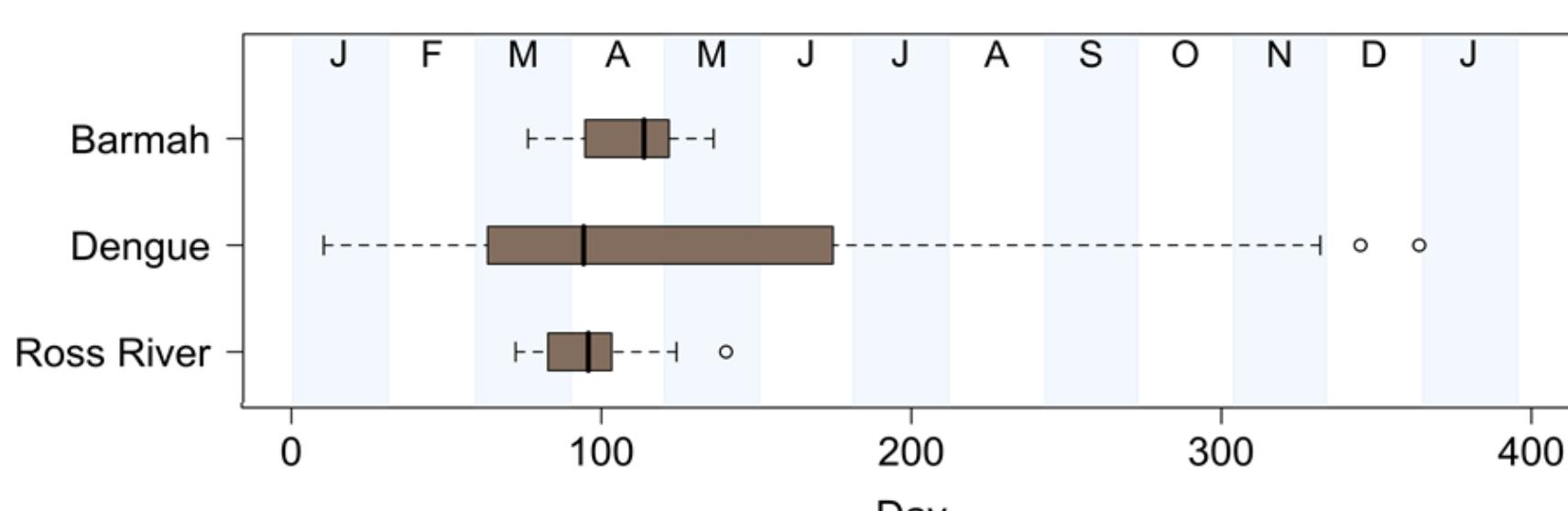


Figure 3. Estimation of Annual Peak Timing: Distribution of the Primary Peak.

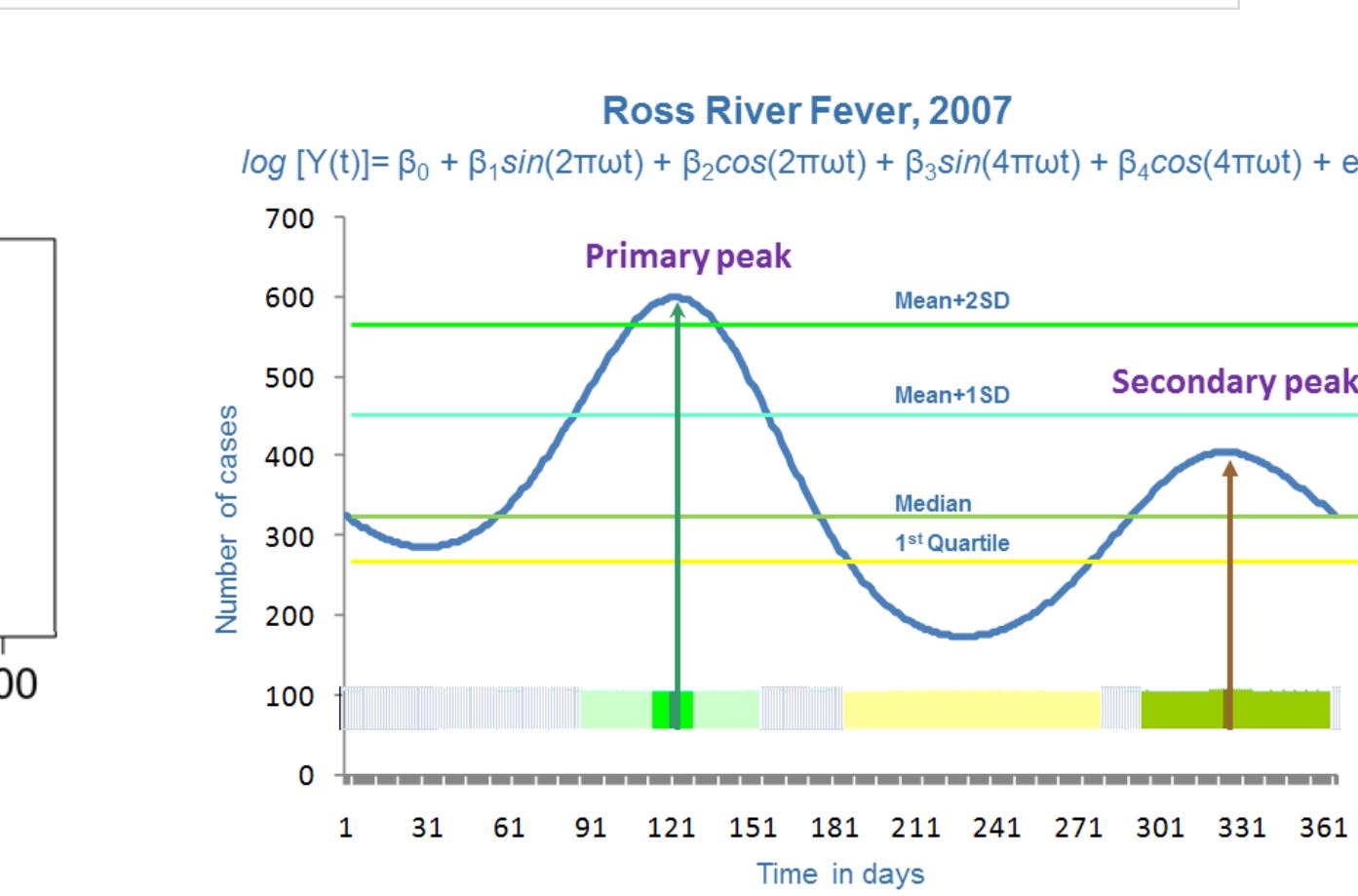


Figure 4. RRV in 2007 with incorporation of 4 harmonics.

S.M. Mor and E.N. Naumova (2011) more rigorously investigated the inter-annual and seasonal disease fluctuations of RRV, BFV, and dengue in Australia. By employing a harmonic regression, they estimated annual peak timing and determined that all three arboviruses exhibited a consistent peak around April of each year (Fig. 3). Fig. 3, above, demonstrates the overlapping and narrow distribution of peak timing for RRV and BFV in contrast to the more variable and complex pattern of dengue, which may actually exhibit 5-8 year periodicity (Fig. 2). Novel to their findings was the identification of a transient secondary peak in some years, with increasing prevalence of the secondary peak for RRV and BFV in the latter half of the time-series. RRV, for example, showed an unprecedented secondary peak in 2007 (Figs. 4 and 5a). Dengue, on the other hand, displayed more erratic patterns in its peaks (Fig. 5b). The unusual secondary peak in RRV in 2007 and the outbreak of dengue in 2009 (the largest in 50 years) highlights the need to examine possible correlations of disease seasonality with environmental parameters.

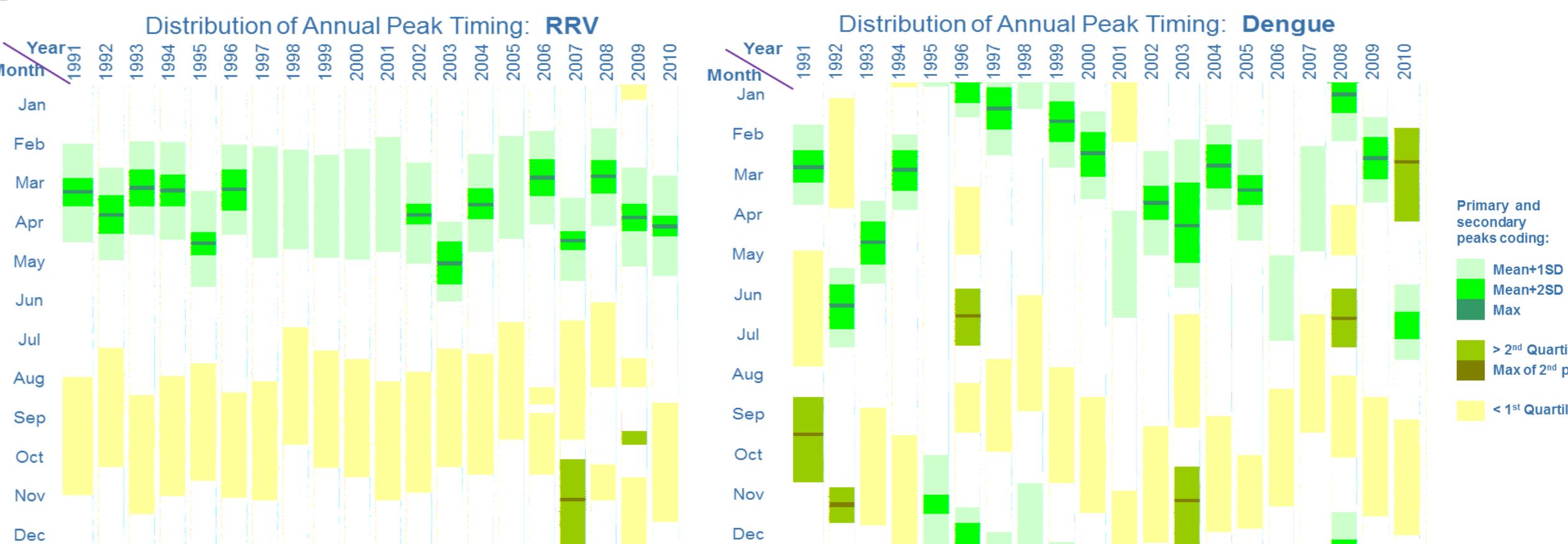


Figure 5. Distribution of daily fluctuations in reported cases predicted by the model with highlighted annual peaks over entire study period for (a) RRV, left, and (b) dengue, right.

Conclusions and Future Directions

Vector-borne disease cycles are complex systems due to the necessary interactions between arthropod vectors, animal hosts, and pathogens, all of which are under the influence of various environmental factors. Fortunately, the integrative features of Remote Sensing and GIS technology can prove incredibly helpful in better understanding these spatial and temporal relationships. In this study, GIS was used to elucidate spatial patterns that are important in the risk for and ecology of arthropod-borne diseases. The final risk maps (Figs. 7 and 8) are modifiable to emphasize/deemphasize specific variables, especially in light of climate change. For instance, warmer and drier conditions limit *Aedes aegypti* flight dispersal to <100 m, increasing the influence of population density (a proxy for domestic water-storage container density) on vector breeding (Jardine et al. 2014).

It is important to note that the habitat suitability map was based on thirty-year climatic averages and therefore does not speak to the potential effects of microclimatic or seasonal fluctuations and variability on disease incidence. Hence, the resultant risk maps can instead be used as general predictors of vector distribution and transmission potential, and the areas at highest risk can be subsequently analyzed more in-depth. For example, the final risk map (Fig. 8) indicates the coast of Queensland is at high risk for dengue, and it has been previously established that the majority of dengue cases have originated in Queensland (Hasan et al. 2013). With the assumption that most of the dengue cases came from Queensland, we performed a preliminary analysis relating monthly anomalies in weather variables (rainfall and precipitation) in Queensland to disease case data, with particular focus in discovering explanatory climatic variables for the 2009 outbreak (Fig. 9). While previous research from Hasan et al. (2013) established positive associations between temperature, rainfall, and dengue incidence in Queensland, we aimed to see if any climatic anomalies could better explain the epidemic. The results are inconclusive thus far.

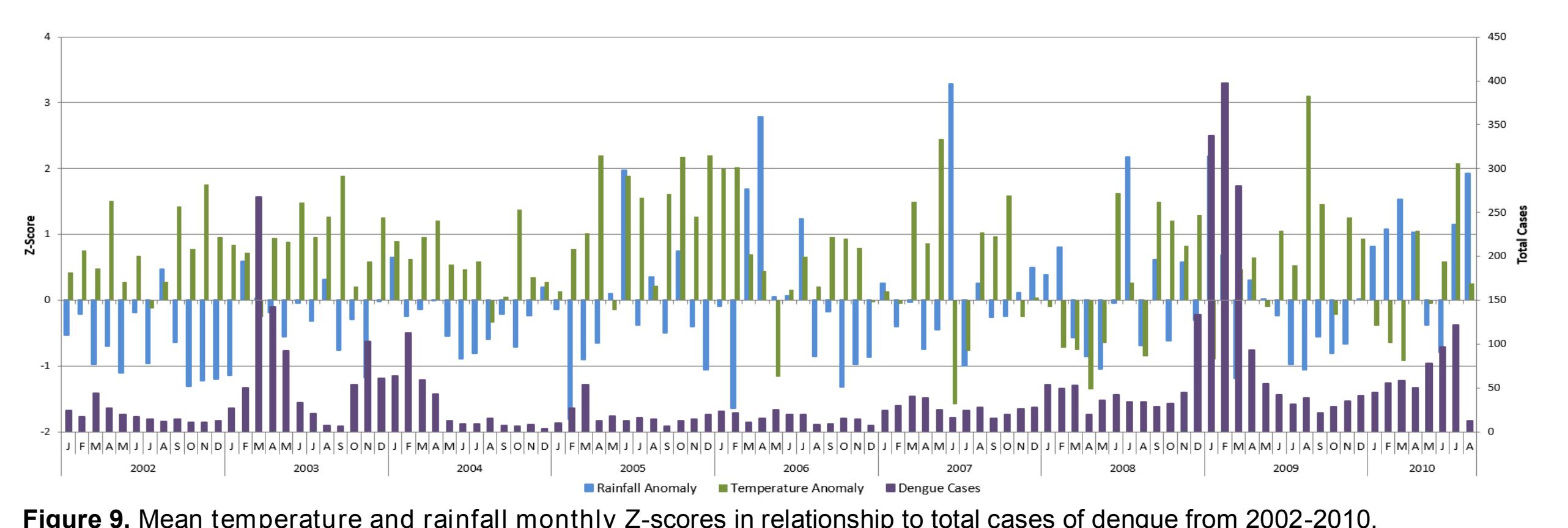


Figure 9. Mean temperature and rainfall monthly Z-scores in relationship to total cases of dengue from 2002–2010.

Looking forwards, statistical analyses can be used to further investigate correlations and time-lags between weather data, disease incidence, and anomalies thereof. Similar analyses to this study can be then conducted for RRV and BFV. One potential exciting research direction may be to use climate data to explore short-term and long-term meteorological parameters correlated with the recent appearance of secondary disease peaks in RRV and BFV. These analyses are beyond the scope of this study, which ultimately represented an exploratory approach to relating human case data with seasonality and climate variability.

Literature Review

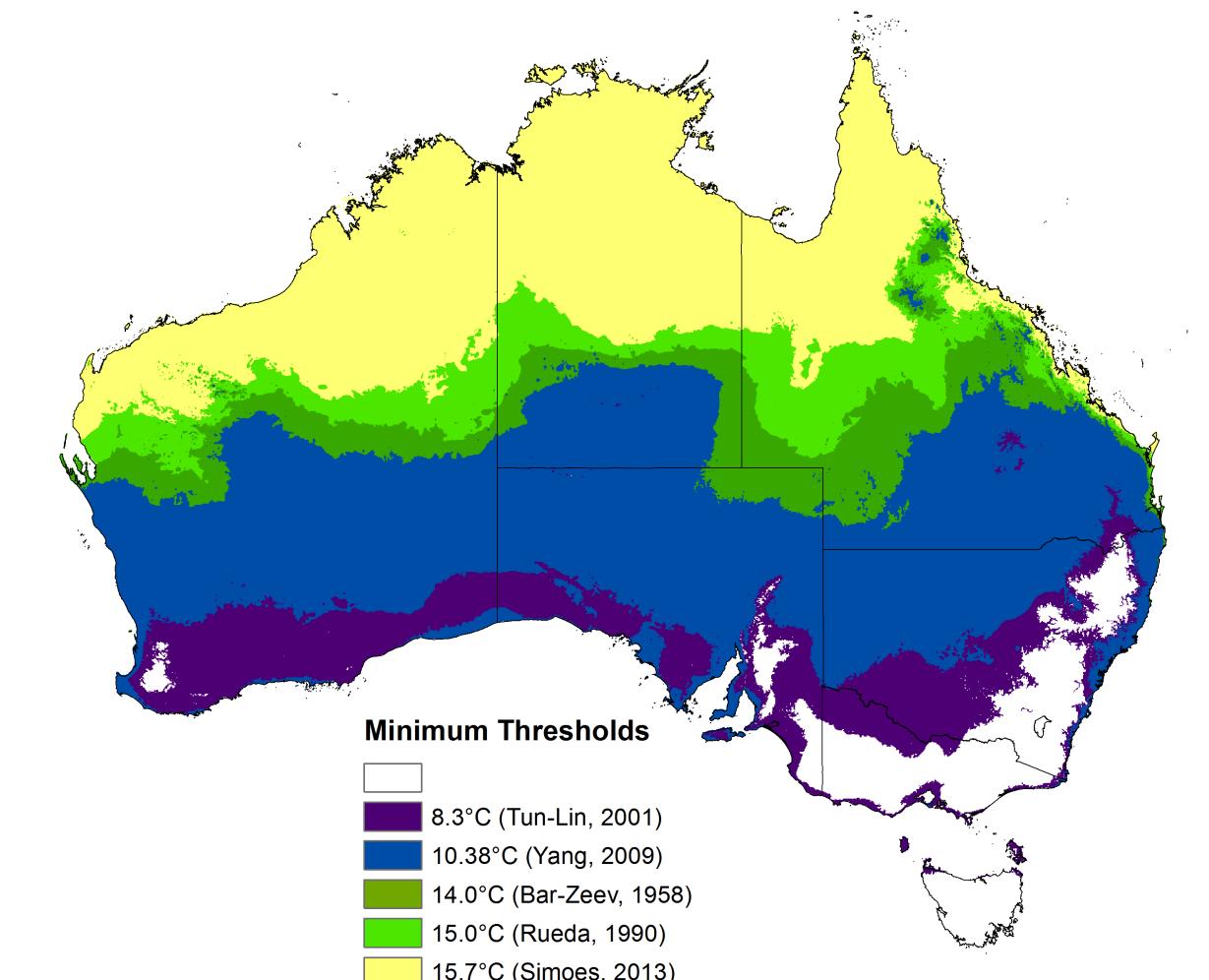


Figure 6. Minimum survival thresholds determined in a sampling of studies.

To model mosquito habitat and thereby predict dengue vulnerability, we needed to determine the climate factors that most influence establishment of the vector species, *Aedes aegypti*, in an area. In other words, (1) what regions of the country are most at risk for dengue, and (2) based on which environmental parameters? These questions proved difficult to answer due to major variability in the literature.

Two types of studies were reviewed: experimental research on climatic thresholds for *Ae. aegypti* survival, and GIS analyses mapping dengue transmission. There are hundreds of experimental studies investigating how environmental parameters are associated with *Ae. aegypti* survival and development; of the many environmental factors, temperature has been most frequently studied (Brady et al. 2014). Yet the attempts to model the effects of temperature on population persistence and ability to transmit dengue have used highly variable methods, such as: conditions (laboratory, field); specific temperature parameter (minimum/maximum/mean, air, water); region and climate; and effects being tested (physiology, morphology, longevity, fecundity, abundance, dispersal, viral load). As a result, studies aimed at determining minimum temperature thresholds for mosquito survival have produced significantly different results (Fig. 6).

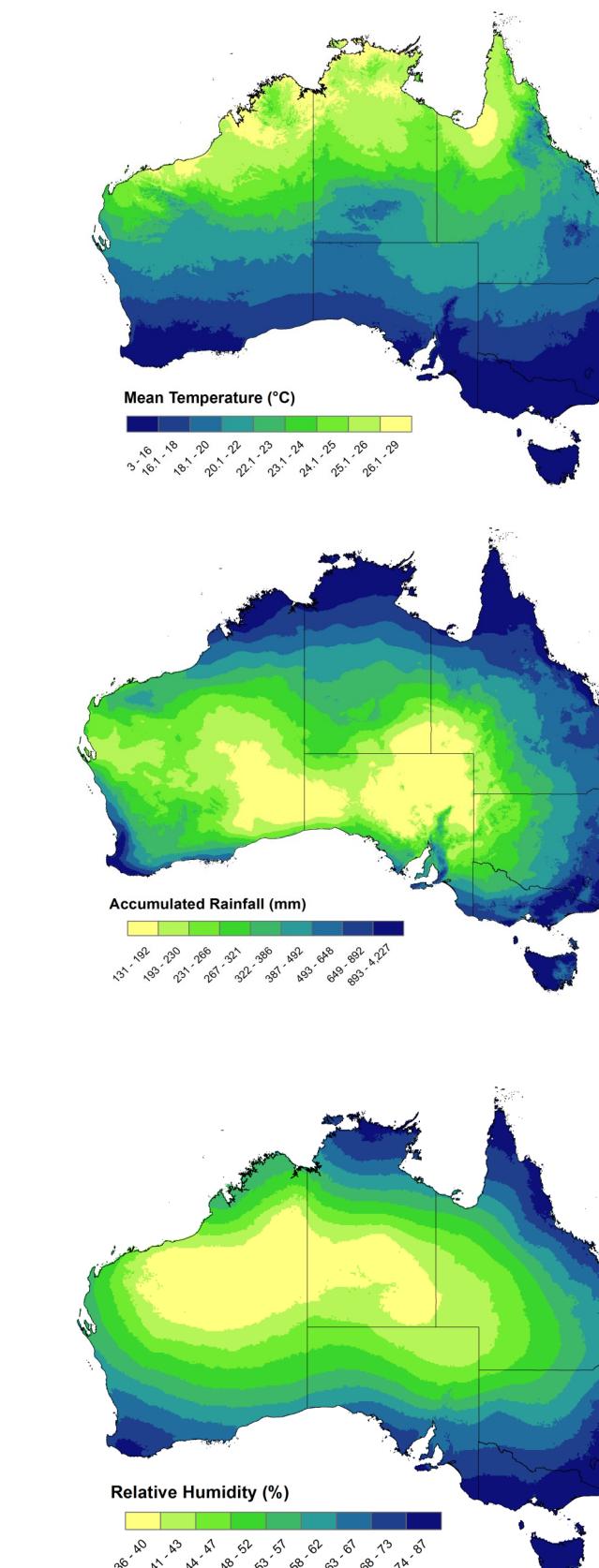
Perhaps because of inconsistencies in the literature, GIS analyses aimed at predicting mosquito habitat have also employed a wide variety of methods and often achieved contradictory results. Beebe et al. (2009) employed theoretical limits of six environmental parameters to map *Aedes* distribution in Australia but found their results inconsistent with the known distribution of dengue. Bhatt et al. (2013) incorporated six human factors, such as urbanization and relatively poverty, in addition to seven environmental parameters with results that under-estimated the distribution of dengue. Interestingly, Hales et al. (2002) modeled dengue transmission on a global scale with 89% accuracy using humidity as the only explanatory variable.

Methods

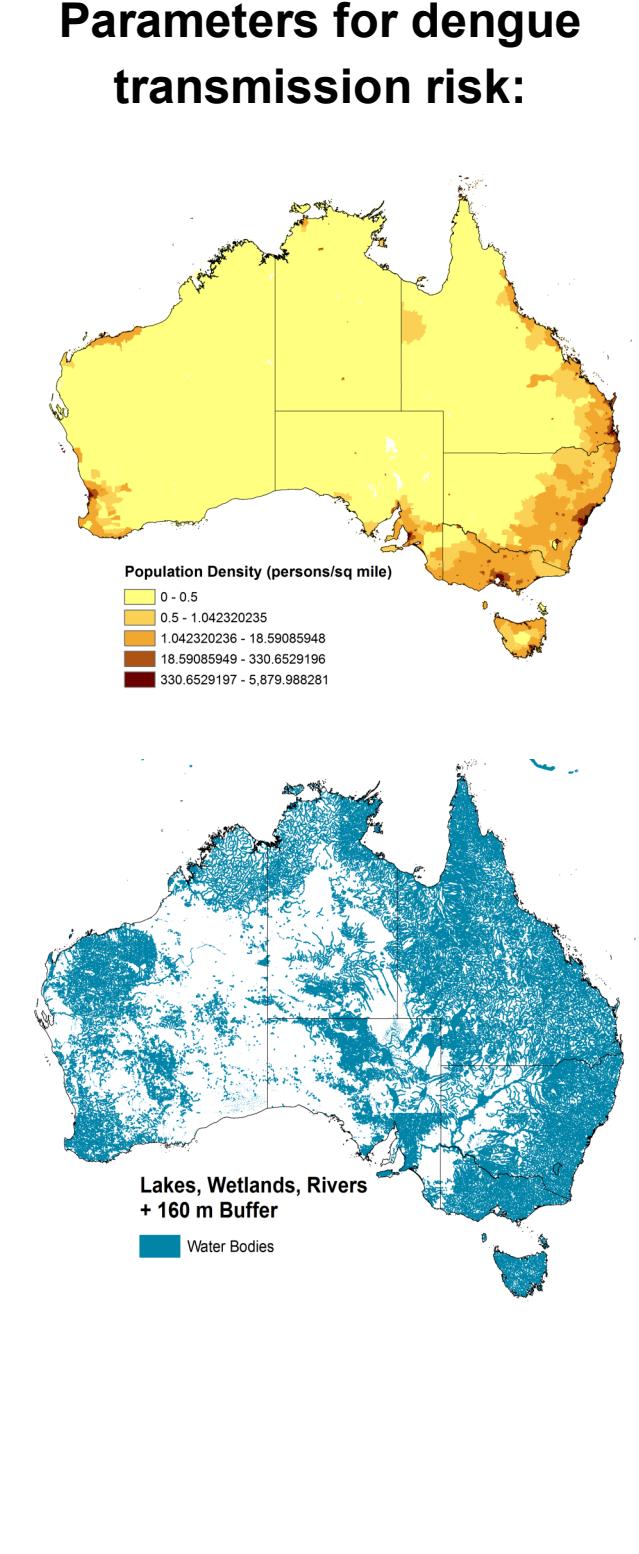
The algorithms applied in creating the risk map were adapted from Koliivas (2006). Areas in Australia deemed as suitable mosquito habitats were defined with a GIS overlay of temperature, precipitation, and humidity—the three primary meteorological factors positively associated with mosquito abundance. Favorable ranges for these parameters were considered rather than survival thresholds due to the variability in the literature on specific survival thresholds, and the more general agreement on optimal conditions. Referring literature on favorable conditions for *Aedes* rearing, cutoffs were chosen to be: 500 mm mean annual rainfall, 20°C–30°C mean daily temperature, and 55% relative humidity. These cutoffs/ranges were chosen based on studies within Australia or in regions of similar climate when possible. Climate grids were obtained from Australia's Bureau of Meteorology (BOM); all three parameters represented average conditions spanning 1961–1990. Each layer was reclassified to a binary with 0 (if below the lower limit) and 1 (if above the lower limit). Upper limits were not applicable in Australia. Temperature, rainfall, and humidity were then overlaid respectively (Koliivas 2006). The regions with overlaps of all three variables were classified as most suitable for potential mosquito establishment.

Zooming in on the region with the highest habitat suitability, a map was created for areas at highest risk for dengue transmission based on breeding ground and host availability. Two additional parameters were considered for this secondary map: hydrography and population density. A study conducted in the locally-relevant state of Queensland (Muir 1998) determined maximum flight dispersal of *Ae. aegypti* in the field to be 160 m; thereby, a buffer of that distance was created around all rivers, lakes, and wetlands in Australia. Hydrography was sourced from WWF (Lehner et al. 2006). The buffered hydrography was overlaid on the aforementioned most-suitable-habitat layer and reclassified as medium risk. Finally, populated areas were included using a gridded population density map (CIESIN 2005) and defined as areas with >0.5 persons per square mile. Populated areas were then reclassified with the same 0/1 binary and overlaid to create the final dengue risk map.

Parameters for habitat suitability:



Parameters for dengue transmission risk:



Results

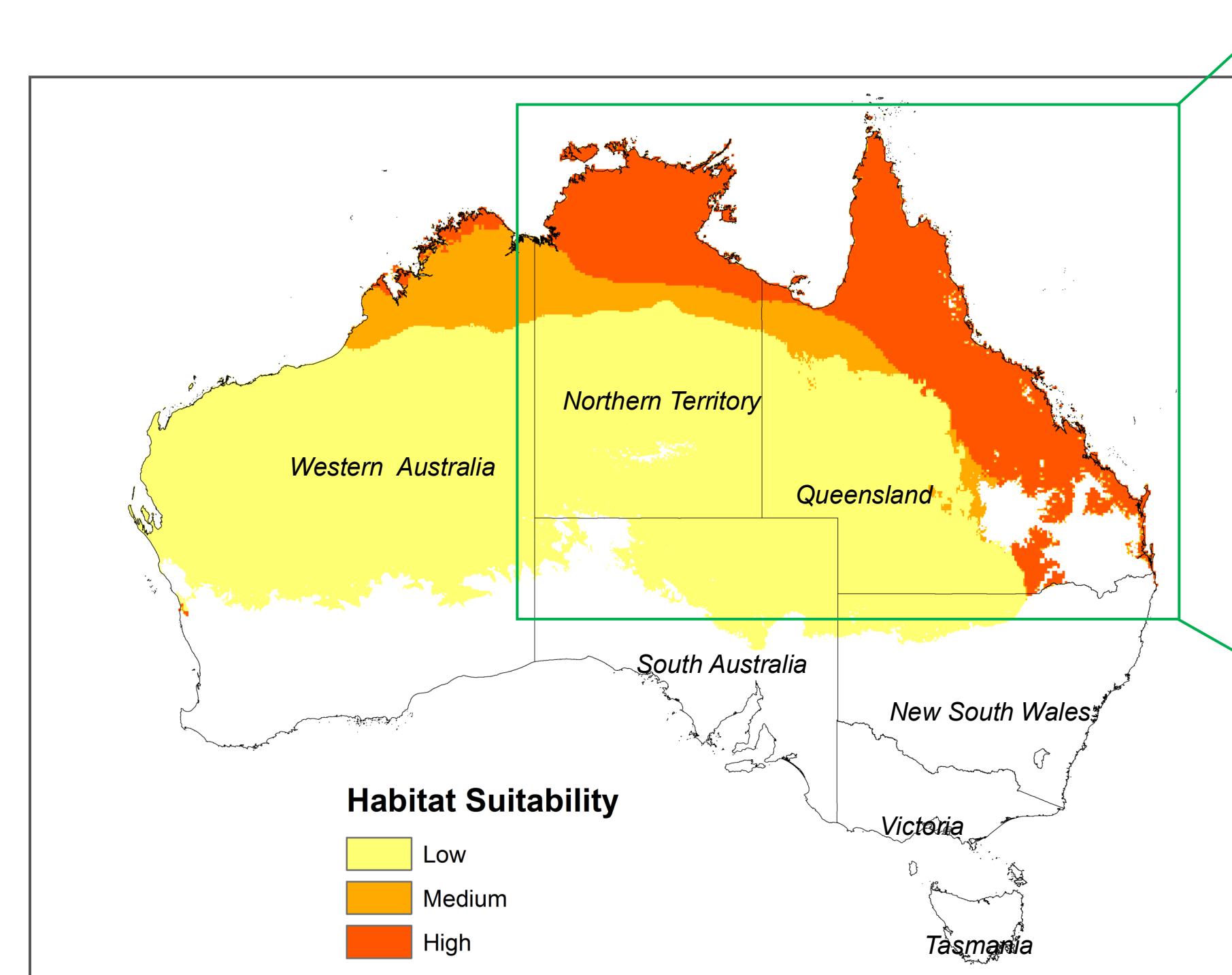
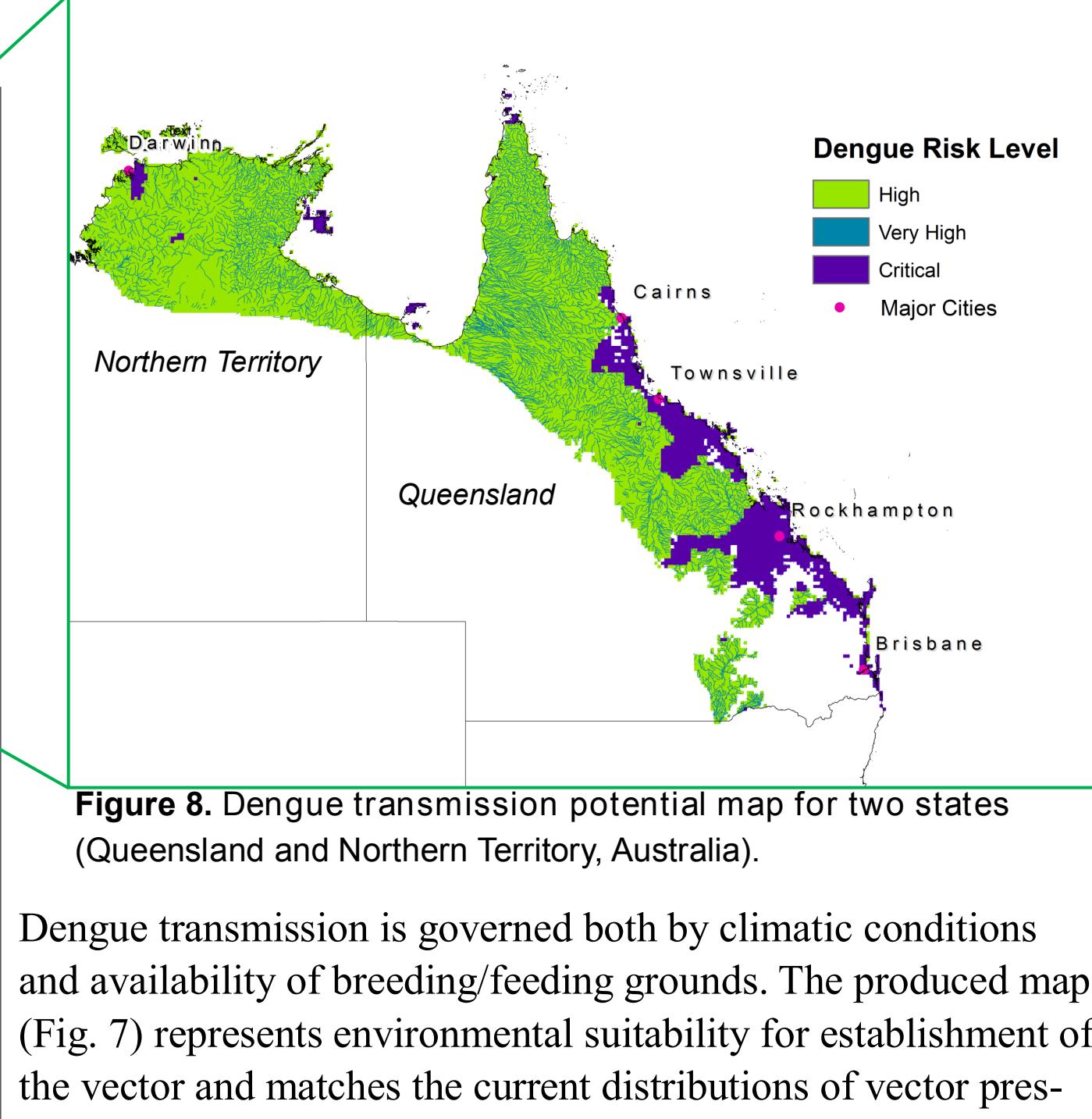


Figure 7. *Aedes aegypti* habitat suitability map.



Dengue transmission is governed both by climatic conditions and availability of breeding/feeding grounds. The produced map (Fig. 7) represents environmental suitability for establishment of the vector and matches the current distributions of vector presence. The zoomed-in map (Fig. 8) represents the breeding areas and host availability necessary to support an epidemic. A qualitative validation of the final map is required here due to a lack of data on vector distribution or geocoded case data. The areas deemed at highest risk for dengue (Fig. 8) coincide with the most recent dengue outbreaks in the past twenty years. For example, 2014–2015 has experienced two major outbreaks in Darwin and Tully (a city in between Cairns and Townsville), both of which are within 'critical risk' areas on the final map ("Current Dengue Outbreaks" 2015).

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