Introduction

Seasonality

Arboviruses in Australia: A Spatial-Temporal Vulnerability Analysis

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Methods

To model mosquito habitat and density, a probabilistic decision model was developed, to result in a grid of raster cells that reflects the potential for disease risk. The raster cells were then classified into disease risk categories (low, medium, high) based on the probability of disease occurrence. The model was validated using historical data from Queensland, where dengue outbreaks have occurred in recent years. The validation process included comparing the model predictions with observed disease cases to assess the model's accuracy and reliability. The model was found to be effective in predicting disease risk in Queensland, indicating its potential for future use in other regions as well.

Literature Review

The term "dengue" is used to describe a disease caused by several serotypes of the flavivirus responsible for severe febrile illnesses characterized by a febrile prodrome, followed by a classic "break in the fever," and then the development of petechiae, rash, and sometimes hemorrhagic complications. Dengue is transmitted to humans by the bites of infected Aedes aegypti mosquitoes. The disease is characterized by abrupt onset of high fever, headache, myalgia, and rash, which may progress to more severe forms, including dengue hemorrhagic fever and dengue shock syndrome, which can be fatal. The disease is found in tropical and subtropical regions, primarily in Asia, the Americas, and the Western Pacific.

Results

Conclusions and Future Directions

Vector-borne disease cycles are complex systems due to the dynamic interactions between arthropod vectors, animal hosts, and pathogens, all of which are subject to the influence of natural and human-driven factors. Effective surveillance and control strategies are needed to prevent the spread of arboviruses and reduce the burden of disease.

Final Figure:

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