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Temperature-driven model for the abundance of Culex mosquitoes

Vector-borne diseases account for more than 17% of all infectious diseases worldwide and cause more than 1 million deaths annually. Understanding the relationship between environmental factors and their influence on vector biology is imperative in the fight against vector-borne diseases such as dengue, malaria, and West Nile virus. We develop a temperature-driven abundance model for West Nile vector species, *Culex pipiens* and *Culex restuans*. Temperature dependent response functions for mosquito development, mortality, and diapause were formulated based on results from published field and laboratory studies. Preliminary results of model simulations compared to observed mosquito traps counts from 2004-2014 demonstrate the capacity of our model to predict the observed variability of the mosquito population in the Peel Region of southern Ontario over a single season. The proposed model has potential to be used as a real-time mosquito abundance forecasting tool and would have direct application in mosquito control programs. This work is supported by CIHR, PHAC, and NSERC, under the supervision of Professors Neal Madras and Huaiping Zhu.