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Models for the spread of *Wolbachia* in mosquito populations

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The vector-borne Dengue fever poses a major health issue in tropic environments, which includes areas such as far-north Queensland. Historically, attempts at curtailing the spread of dengue have focused on controlling the size and spread of mosquito populations that carry the virus. Several factors make this an astronomically difficult task to accomplish on any reasonable scale, however, and so more novel methods of suppressing dengue outbreaks are being explored. One such method is the introduction of bacteria called *Wolbachia* into mosquito populations, which prevents mosquitoes from passing on viruses to humans. A *Wolbachia* invasion has strong potential to completely saturate mosquito populations due to a mechanism called cytoplasmic incompatibility. The mathematical modelling problem here becomes twofold-first, the task of inferring the position of mosquito populations, and then the modelling of *Wolbachia* spreading through these populations. Here, we will be discussing the effects and mechanisms of *Wolbachia* in more detail, including the phenomenon of cytoplasmic incompatibility. Next, recent developments in modelling mosquito populations such as the use of semi agent-based models will be outlined, within the context of predicting the spread of *Wolbachia*.

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