Effects of Human Mobility on the Spread of Disease-Transmitting Mosquitoes in Spain: Insights from Mobile Phone Data

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Abstract:

Motivation and Objective. Using mobile phone data in Spain, this study aims to (1) better define the association between human mobility and the dispersal of tiger mosquitoes (*Aedes albopictus*); and (2) build a predictive model that can forecast *Ae. albopictus* spreading into previously unaffected municipalities. This will enable more effective mosquito control measures and more accurate projections of possible disease spread.

Mosquito-borne diseases such as Zika, dengue, and chikungunya are not yet widespread in the EU, but local outbreaks are becoming more frequent, as highlighted by the European Centre for Disease Prevention and Control[1], and are triggered by imported cases in areas where vector mosquitoes are present(Trojánek et al., 2023). For most of these outbreaks, the primary vector (disease transmitter) is the tiger mosquito (*Ae. albopictus*). Without mosquitoes, the transmission rates between humans would be much lower.

Tiger mosquitoes are an invasive species that has been present in Spain for more than a decade and continues to spread. The favourable habitat conditions for these mosquitoes in Europe, further exacerbated by climate change, highlight the need for a deeper understanding of their dispersal mechanisms (Oliveira et al., 2021). This study aims to bridge the existing knowledge gap in mosquito dispersal models that traditionally focus on environmental habitat suitability but often overlook the critical role of human mobility. Recent evidence suggests the potential for mosquitoes to be transported by cars (Eritja et al., 2017); however, research on the influence of human mobility on mosquito dispersal is still in its nascent stages and relies on province-level survey data (Lucati et al., 2022) rather than high-resolution digital trace data at the municipality level.

Methods. To better understand the potential effect of human mobility on mosquito dispersal, we use high-resolution human mobility data and geolocated mosquito DNA samples to show the relationship between human flow intensity and genetic similarity of mosquitoes. By combining Mobile Network Data (MND) for 2019-2023[2] and survey data from the Economically Active Population Survey for 2011-2022[3], we construct accurate inter-municipality flows that include commuting and non-commuting trips. Mosquito DNA samples (2011-2015) are obtained from Lucati et al. 2022. Next, we use Bayesian multilevel models to link the genetic similarity of mosquito DNA samples with estimated mosquito fluxes driven by human mobility flows. Relying on the estimates from the previous step, we build a model to predict mosquito spread in previously unaffected municipalities given the inter-municipal flows in 2023. The final forecast model is validated using reports from the Mosquito Alert[4] citizen science project.

Results. Preliminary findings suggest a significant association between human travel patterns and the spread of disease-vector mosquitoes. Ae. albopictus DNA samples from pairs of municipalities with higher human mobility fluxes show higher similarity than those from municipality pairs with lower human mobility fluxes, even controlling for geographical distance (using both a linear distance function and a distance decay function to capture small-scale proximity). Moreover, these patterns seem to depend on the time of day of the human mobility fluxes, with fluxes that occur during the hours when we find *Ae. albopictus* most active (morning and late afternoon) having the largest impact on mosquito genetic

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[1] European Centre for Disease Prevention and Control, 2023-06-22, İncreasing risk of mosquito-borne diseases in EU/EEA following spread of Aedes species, URL: https://www.ecdc.europa.eu/en/news-events/increasing-risk-mosquito-borne-diseases-eueea-following-spread-aedes-specieshttps://www.ecdc.europa.eu/en/news-events/increasing-risk-mosquito-borne-diseases-eueea-following-spread-aedes-species

[2] released by the Spanish National Statistics Institute and the Spanish Ministry of Transport and Sustainable Mobility

[3] released by the Spanish National Statistics Institute

[4] https://www.mosquitoalert.com/en/https://www.mosquitoalert.com/en/, Mosquito Alert collects user-generated and expert-verified reports of tiger mosquitoes spotted in Spain and worldwide

distance (see Fig. 1). Therefore, we expect to see high-quality results in predicting and validating the forecast model to predict mosquito occurrence in previously unaffected municipalities using human mobility.

Originality/Value. This study is the first to use mobile phone data to study mosquito dispersal. Compared to studies based on Call Detail Records (CDR) data that rely on billable user-induced events, we use Mobile Network Data (MND) with proactive location pings, which allows for more accurate capture of human mobility patterns. Previous studies used CDR-based human mobility data to model disease dispersal with human case data as the outcome. We are modelling the mosquito itself, which is a critical part of the disease transmission process when it comes to mosquito-borne disease. Therefore, our model will help inform disease spread models. Our findings also contribute to the broader discourse on using mobile big data analytics for climate change adaptation and crisis management, emphasizing the value of interdisciplinary approaches in tackling complex global health challenges.
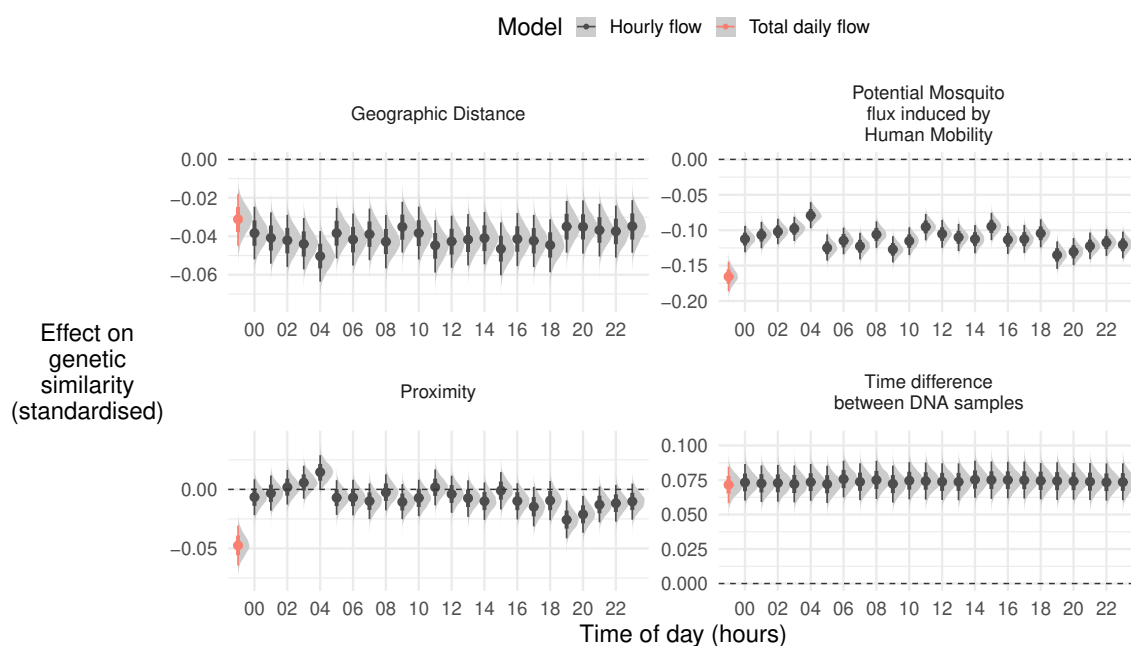

Figure 1. Standardised coefficients of Bayesian multilevel models predicting genetic similarity of pairs of mosquito samples. The full model (red) is estimated using full mean daily mobility flows, while all other models (black) are estimated using hourly slices of mobility. In the morning and evening hours, the effect of human mobility (top right panel) is higher, coinciding with peaks of both human mobility and mosquito activity times.

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