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Geostatistical modelling of Lymphatic Filariasis in Samoa using integrated human and mosquito surveillance data

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Abstract: Lymphatic filariasis (LF) is a vector-borne disease caused by infection with a helminth parasite. As most infected people are asymptomatic, surveillance and monitoring programs need to find ways to efficiently locate residual or new infections following rounds of triple-drug mass drug administration (MDA). This has traditionally relied on serosurveys which test human blood samples for either antigen (using a point-of-care rapid diagnostic test) or the presence of parasite microfilaria (identified under a microscope). In recent years, molecular xenomonitoring (MX) (testing vectors for the presence of pathogen DNA) has also proven to be a sensitive surveillance tool, capable of detecting changes in infection prevalence in less time than human based indicators (McPherson et al. 2022).

This study presents the first application of geostatistical modelling to group-tested MX data, integrating human antigen data and environmental covariates to map infection risk in humans and mosquitoes. We used data from a 2019 community survey in Samoa (McPherson et al. 2022, Mayfield et al. 2024) which took place between seven- and ten-months post-MDA. We tested 1,815 human participants for filarial antigen. We also trapped and tested 34,299 female mosquitoes for the presence of pathogen DNA. Traps were placed near the same households enrolled in the human survey, and left there for two days and mosquitoes were pooled before testing. Environmental and demographic variables were downloaded from online sources and compiled for each household or trap location. Bayesian geostatistical models run using a modified version of the PoolTestR package (McLure et al. 2021), were used to estimate risk surfaces for positive mosquitoes and antigen-positive humans separately and then integrated into a joint model.

Geostatistical models revealed marked spatial heterogeneity in LF risk across Samoa. Human antigen and infection prevalence *Aedes spp.* mosquitoes were highly correlated at nearby locations (correlation: 0.8, CrI 0.3-1.0), but correlation decayed rapidly as the distance between locations grew (correlation: 0.5 at 2km, <0.1 at 10 km). Consequently, while *Aedes* and human signals were highly correlated within villages, the pattern varied substantially between villages and regions. Infection prevalence in *Aedes* mosquitoes was lower on the island of Savai'i than on Upolu, though antigen prevalence in humans was similar or higher in Savai'i. However, within each island the two measures were highly correlated. Prevalence of human and mosquito infection markers were weakly associated with environmental covariates, however both measures increased with distance from major roads. Human antigen prevalence was higher on steeper terrain and in less densely populated areas, but prevalence in *Aedes* mosquitoes was not strongly associated with either variable. Strong spatial clustering but relatively weak associations with available environmental covariates meant that infection risks could not be reliably predicted far from existing sampling locations.

Integrating MX and human data in a geostatistical framework provides a powerful approach for LF surveillance with the potential to improve estimates of all infection markers and guide targeted surveillance efforts. The close correlation between signals in vectors and humans demonstrates the utility of MX as a proxy for infections in humans. The tight spatial clustering of infection markers underscores the need for future surveillance activities to be spread widely across all populated areas as infection prevalence can vary substantially over short distances. As Samoa moves toward LF elimination, joint geostatistical modelling can enhance decision-making in the programmatic endgame and serve as a model for surveillance of LF and other vector-borne diseases in other settings.

Keywords: *Lymphatic filariasis, molecular xenomonitoring, neglected tropical diseases, disease surveillance*

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