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Sequential modeling of the effects of mass drug treatments on Anopheline-mediated lymphatic filariasis infection in Papua New Guinea

Inherent bioecological complexity in transmission dynamics and parameter uncertainty complicate the prediction of extinction endpoints for complicated parasitic systems, such as the vector-borne macroparasitic disease, lymphatic filariasis (LF). One source of this difficulty is the limited quantity and quality of data used to develop and parameterize numerical models of parasite transmission, implying that model fitting methods that can be used to sequentially update or refine initial parameter estimates will be essential for reducing extant uncertainty regarding values of transmission/infection endpoint/breakpoints within and between endemic localities.

Here, we extend a newly developed numerical modelling and Bayesian Melding calibration framework in order to fit our previously developed deterministic LF transmission model to human age-infection prevalence data recorded from several village communities in Papua New Guinea that underwent annual mass drug treatments. Specifically, we examine: 1) whether transmission controlling parameters remained stable (from baseline estimates) in the face of the specific interventions implemented in each of these communities, 2) if it was possible to use the model fits from each intervention period to reliably perform backward extrapolations to reconstruct baseline age-infection patterns, 3) whether it was possible to use post-intervention infection data to estimate LF transmission/infection endpoints consistent with those estimated using baseline only data, and 4) if such a modelling and fitting framework can allow better estimates of drug treatment-related parameters.

We show that transmission parameters obtained by fitting the model to data from baseline versus each intervention period remain stable throughout the whole study period. This result enabled us to reliably reconstruct the observed baseline data in each community. Estimates of worm breakpoint values from both direct as well as back-fits to baseline data also showed little variation. The employed updating procedure showed a shift towards higher and less variable values for the worm but not the microfilaria killing parameter.

This work demonstrates that biological parameters governing the transmission process of LF in endemic communities may not change appreciably during an intervention period. This result implies that endpoint values for this disease, which is currently being targeted for global elimination, can be successfully estimated by model fitting of post-intervention monitoring data, if the drug regimen parameters and population coverage values, along with information on the frequency and number of treatments, are available for any given endemic community.