Schistosomiasis is a debilitating parasitic disease that infects 230 million people. Mass drug administration (MDA) has successfully decreased disease burden, however, there is increasing evidence of treatment failure. Exploring drivers of treatment failure is difficult without measures of ‘true’ infection status.

Due to the inaccessible anatomical locations of worms, indirect diagnostics are used as infection status and intensity proxies. However, differences in specificity and sensitivity cause discrepancies between observed egg (Kato-Katz) and antigen-based (POC-CCA) diagnostic levels. These are enhanced post-treatment, affecting drug monitoring and evaluation efforts as well as transmission estimates.

Hidden Markov models (HMM) are probabilistic models that handle unobserved variables. In this case, the ‘true’ infection status of individuals is unobserved. Previous studies have modelled infection status and clearance and re-infection dynamics, using HMMs parameterised with Kato-Katz and POC-CCA.

By combining additional imperfect diagnostic methods, we can leverage HMMs to improve estimates of ‘true’ prevalence over time. Alongside longitudinal Kato-Katz and POC-CCA data from high and low endemic sites in Uganda, we performed quantitative PCR on stool samples and hatched parasite larvae from stool. We further developed HMMs to differentiate infected and transmitting but infected, but not transmitting. We then parameterised our HMMs with these additional diagnostics to investigate schistosomiasis infection dynamics across different transmission settings, over time and pre- and post-MDA.