Project title: Modelling the best use of sleeping sickness diagnostics under existing and emerging tools

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Background

Human African trypanosomiasis (HAT, sleeping sickness) is a parasitic infection transmitted by tsetse vectors to humans in West and Central Africa. After developing disease, many infections are fatal. During the mid-1900s the burden of disease was reduced through mass screening and treatment programmes, although diagnosis and treatment were both extremely challenging. In the 1990s after decades of limited intervention, record numbers of people were diagnosed with HAT and a new surge of effort with new intervention tools began to bring infection under control. Since this time, a range of new diagnostics have become available and new treatments have improved patient outcomes. In 2012 the World Health Organization (WHO) set a target to have fewer than 2000 cases of HAT globally by the year 2020 and now there is a subsequent goal of zero transmission (elimination) by 2030. To date, progress towards these goals is promising, however at extremely low prevalence intervention strategy will have to adapt to make the best use of diagnostic tools to identify remaining patients and then to confirm elimination of infection.

Aim of project:

The team at ITM have been working for many years on diagnosis of *Trypanosoma brucei gambiense* (the causative agent of sleeping sickness). In the 1970s they developed the "CATT test", one of the key tests which has been used since the 1990s in screening, as well as a Rapid Diagnostic Test (RDT) "Sero-K-SeT" used frequently in intervention programmes. The team are now currently developing new diagnostics to be used in peri- and post-elimination settings.

Two key questions form this project:

(i) *How can we use currently available diagnostics to reach elimination?*

By using a previously developed and parameterised model of HAT, the impact of using different tests on infection dynamics can be explored using numerical simulation. Should we use single tests or combinations of tests in screening (in series or in parallel)? Are there infection prevalence or population size thresholds for which the optimal diagnostic algorithm is different? Does our choice of diagnostic tools change with the mode of screening; if someone is ill and self-presents in a local health facility do we use the same test as in mass screening? What impact does the cost of the test have?

(ii) *What diagnostic characteristics should a new tool ideally have to confirm absence of infection (post-elimination)?*

There is no current guidance on how to verify that elimination has been meet for sleeping sickness (or for a range of other diseases targeted for elimination). Ideally lots of people in previously endemic regions would be tested to have high certainty not infection remains; we need to find a balance between misdiagnosing people (false positive) and thinking we have failed to meet the target, and underdiagnosing people (false negative) and declaring elimination too soon. The new "iELISA" test under development by ITM is designed to have better accuracy than most available HAT tests. Philippe will provide plausible sensitivity/specificity parameter pairs for iELISA so that an these different characteristic profiles can be analysed in the post-elimination setting.

References/reading:

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