

Spatio-Temporal Dynamics of Infection: HAT as a case study

Background

Human African trypanosomiasis (HAT), commonly called sleeping sickness, is caused by *Trypanosoma* spp. and transmitted by tsetse flies (*Glossina* spp). HAT is usually fatal if untreated and transmission occurs in foci across sub-Saharan Africa. Mathematical modelling of HAT began in the 1980s with extensions of the Ross-Macdonald malaria model and has since consisted, with a few exceptions, of similar deterministic compartmental models. These models have captured the main features of HAT epidemiology and provided insight on the effectiveness of the two main control interventions (treatment of humans and tsetse fly control) in eliminating transmission.

WHO (World Health Organization) has collated data on the testing and treatment of individuals for HAT in Africa – the so-called “HAT Atlas” (http://www.who.int/trypanosomiasis_african/country/foci_AFRO/en/).

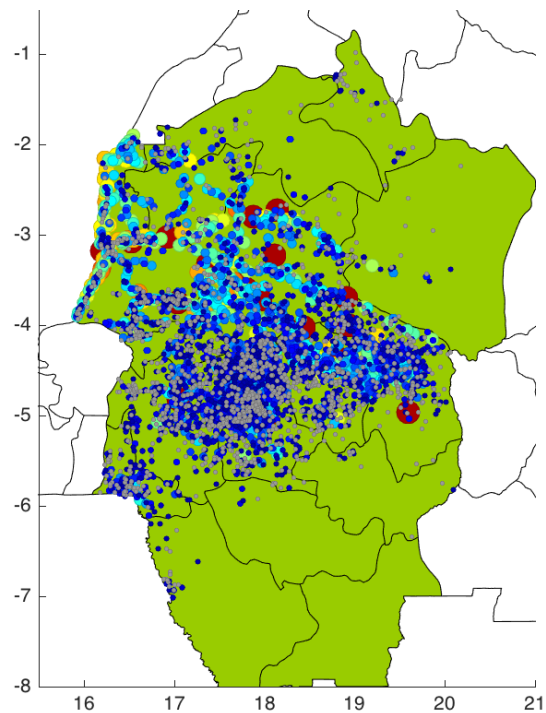
Working closely with WHO and the Gates Foundation, we have gained access to these records for the Bandundu regions of DRC.

The Problem

The aim of this project would be to explore the spatio-temporal dynamics of detected cases – accounting for underlying screening levels and population size. It is to be hoped that this approach will provide deeper insights into the spread of this Neglected Tropical Disease, the underlying transmission potential and the routes to elimination.

The project could use a number of tools and techniques: from model fitting to statistical analysis to simulation and prediction.

The researcher would join a growing team in WIDER, looking at the elimination of 9 Neglected Tropical Diseases as part of the WHO 2020 goals.



References.

Rock, K.S., Torr, S.J., Lumbala, C., Keeling, M.J. (2015) Quantitative evaluation of the strategy to eliminate human African trypanosomiasis in the Democratic Republic of Congo. *Parasites & Vectors*. **8** 1131

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<http://www.ntdmodelling.org/>