Summary:
Modelling to infer the role of animals in *gambiense* human African trypanosomiasis transmission and elimination in DRC

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Abstract

Gambiense human African trypanosomiasis (gHAT) has been targeted for elimination of transmission (EoT) to humans by 2030. Although the deadline of this ambitious goal is rapidly approaching, there remain fundamental questions about the presence of non-human animal transmission cycles and their potential role in slowing progress towards, or even preventing, EoT. In this study we focus on the country with the most gHAT disease burden, the Democratic Republic of Congo (DRC), and use mathematical modelling to assess whether animals may contribute to transmission in specific regions, and if so, how their presence could impact the likelihood and timing of EoT.

By fitting two model variants – one with, and one without animal transmission – to the human case data from 2000–2016 we estimate model parameters for 158 endemic health zones of DRC. We evaluate the statistical support for each model variant in each health zone and infer the contribution of animals to overall transmission and how this could impact predicted time to EoT.

We conclude that there are 24/158 health zones where there is moderate or high statistical support for some animal transmission. However, – even in these regions – we estimate that animals would be extremely unlikely to maintain transmission on their own. Animal transmission could hamper progress towards EoT in some settings, with projections under continuing interventions indicating that the number of health zones predicted to be on track for EoT by 2030 reduces from 68 to 61 if animals are included in the model. With supplementary vector control (at a modest 60% tsetse reduction) added to medical screening and treatment interventions, the predicted number of health zones meeting the goal increases to 147 for the model including animals. This is due to the impact of vector reduction on transmission to and from all hosts.

Introduction

In this article, we take two different model variants for transmission of gambiense human African trypanosomiasis (gHAT) and fit them to longitudinal data (2000–2016) across endemic health zones

of the Democratic Republic of Congo (DRC). We use statistical methods to assess whether there is more support for a model with animal transmission or for one without in each health zone. We also use the fits to assess whether animals are able to maintain transmission on their own and to predict how the time to reach elimination of transmission (EoT) might change if animals contribute to onward infections.

Methods

We used two previously developed variants of the Warwick gHAT model; both include low-risk and high-risk humans and capture systematic non-participation high-risk groups in the population. The key difference is that one model has animals which can acquire and transmit infection to and from tsetse, and the other has animals as dead-end hosts which do not contribute to the transmission cycle of gHAT. The models take into account previous improvements in medical, diagnostic and control systems, in the same way as described in previous work [1].

We fit to human case data from 2000–2016 in 158 health zones of DRC where there are sufficient data points (at least 13 instances of an active screening OR a passive case detection for the health zone). We then assess whether the model with or without animal transmission has better statistical support. After fitting we also assessed the impact that including animal transmission made to our EoT model predictions under different intervention strategies.

Results

We see that there is most support for the model with animal transmission in some health zones of former Equateur and Kasai Oriental provinces – these are locations where there has been low, but persistent case reporting for several years (see Fig 1). Despite this, there is strong statistical evidence that any animal transmission could not be sustained on its own in any health zone.

Fig 2 shows predictions of case reporting and transmission for two health zones (high-incidence Bokoro health zone in former Bandundu province and low-risk Tandala health zone in former Equateur province) under continuation of active screening with mean coverage from 2012–2016 and passive screening. We see that, whilst Tandala has similar results between the model variants with and without animal transmission, Bokoro has substantially more estimated underlying new human infections each year. If we include vector control in the model (with 60% vector reduction) from 2020 in Bokoro, we see that new infections are predicted to decline rapidly under either model variant (see Fig 3). The results of all 158 health zone level fits and projections under various strategies are available online (see Animal Fitting GUI, `https://hatmepp.warwick.ac.uk/animalfitting/v1/`).

Conclusion

Health zones in which there was evidence in support of the model with animal transmission are concentrated in the former provinces of Equateur and Kasai Oriental. These health zones had low levels of on-going passive detection throughout the data period while active screening activities also took place, particularly in the early 2000s. This may suggest that if similar patterns arise in other health zones – such that they reach low prevalence but not zero case reporting – support for the animal reservoir model may increase across DRC. Despite this, the present analysis suggests that animals alone are not likely to be capable of maintaining transmission, however, the presence of animal transmission could slow down progress towards the EoT goal.

Under the model without animal transmission the expected number of health zones achieving EoT by 2030 is 43%, while it is 39% with animal transmission. If it was possible to implement vector control on a large-scale across DRC from 2020, with a 60% annual reduction in tsetse population,

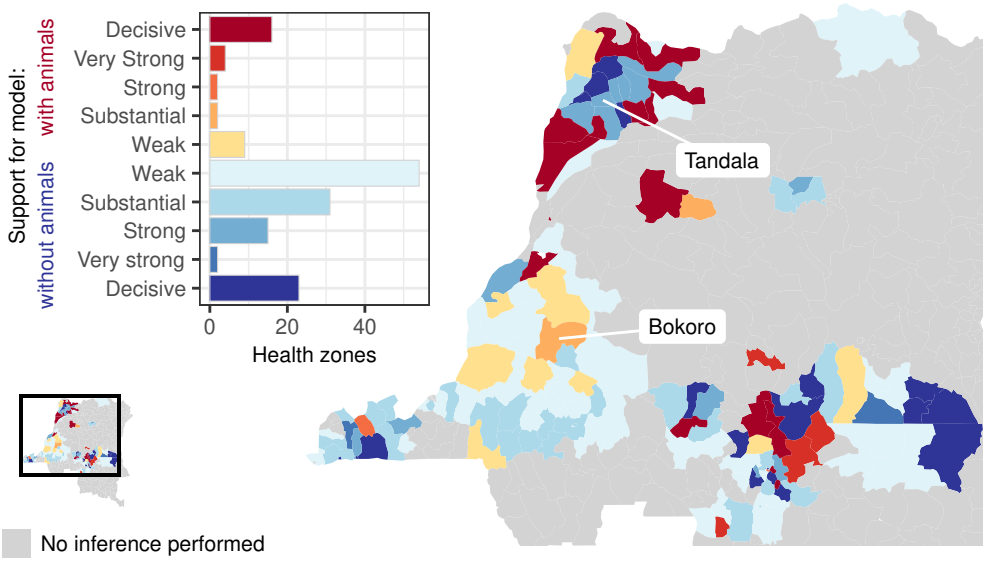

Figure 1: Support for model either with or without animals contributing to transmission of gHAT. The red and orange colours have more statistical support for the model with animal transmission, whereas blue colours have more support for the model without animal transmission.

then the predicted number of health zones reaching EoT by 2030 is 94% and 93% under models without and with animal transmission, respectively. This shows the benefit of targeting the tsetse as a means of preventing transmission to and from all hosts.

References

[1] Ronald E. Crump, Ching-I Huang, Edward S. Knock, Simon E. F. Spencer, Paul E. Brown, Erick Mwamba Miaka, Chansy Shampa, Matt J. Keeling, and Kat S. Rock. Quantifying epidemiological drivers of *gambiense* human African Trypanosomiasis across the Democratic Republic of Congo. *PLOS Computational Biology*, 17(1):1–23, 01 2021.

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Acknowledgments

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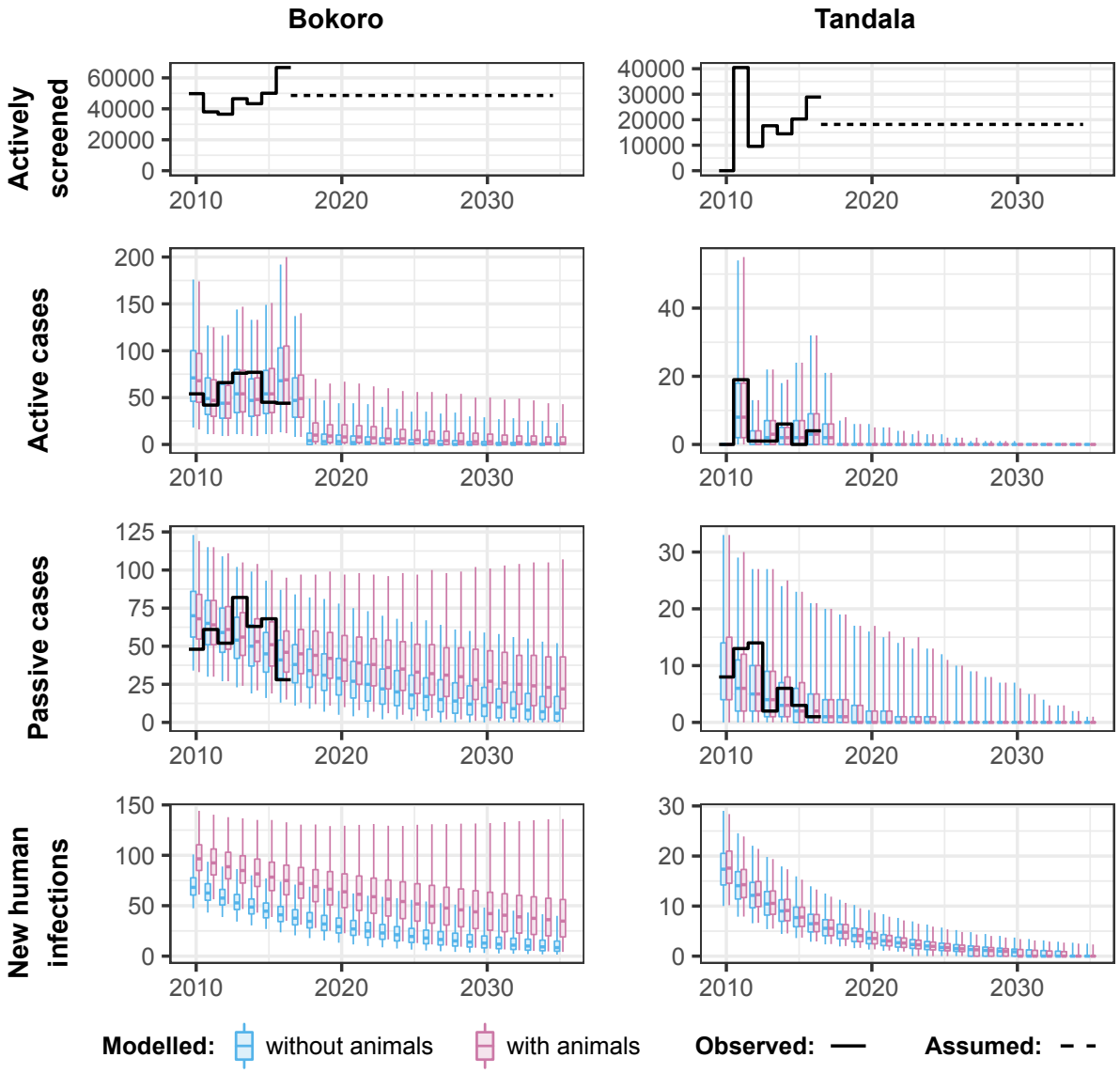

Figure 2: Forward projections for Bokoro and Tandala health zones for models with and without animals contributing to gHAT transmission. Within each health zone, future active screening is assumed to be at the average level of screenings from 2012–2016, while passive screening continues at the 2016 level of effectiveness. In Bokoro, and other health zones in the former province of Bandundu, the specificity of active screening was assumed to increase to 100% in 2018.

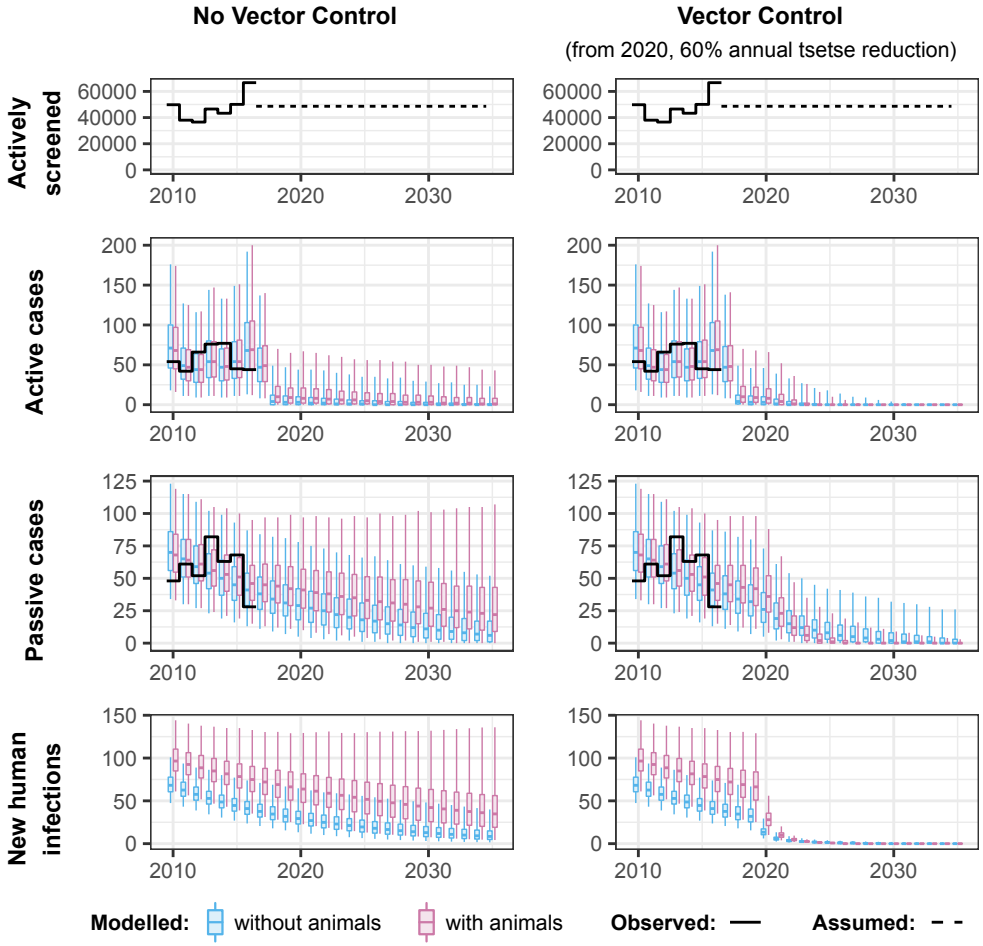

Figure 3: Forward projections in Bokoro health zone for models with and without animals contributing to gHAT transmission and with or without Tiny Target-based vector control from 2020. Future active screening is assumed to be at the average level of screenings from 2012–2016 while passive screening continues at the 2016 level of effectiveness. In Bokoro, and other health zones in the former province of Bandundu, the specificity of active screening was assumed to increase to 100% in 2018.

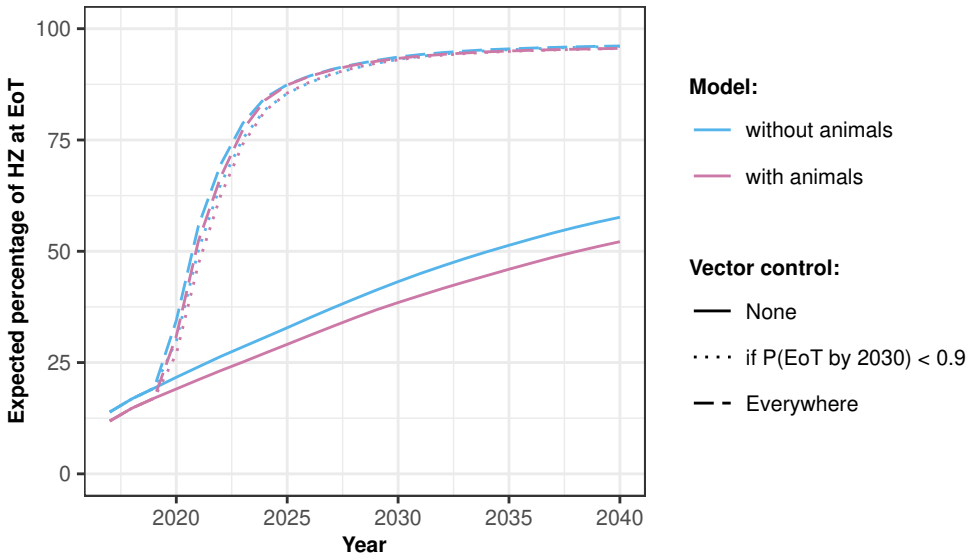

Figure 4: The percentage of health zones studied expected to have reached elimination of transmission (EoT) against year. Vector control (VC) was either simulated in none (solid lines), all (dashed lines), or a subset of health zones in which the probability of reaching EoT by 2030 without VC was less than 0.9 (dotted lines; VC was simulated in 76% of health zones in the model without animal transmission and in 79% of health zones in the model with animal transmission as the remaining health zones had at least 90% probability of EoT without VC).