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Modelling Human African Trypanosomiasis and the effects of domestic animals on transmission

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The Human African Trypanosomiasis (HAT) parasite, which causes African Sleeping Sickness, is transmitted by the tsetse fly as a vector. It has several possible hosts, including wild and domestic animals, who are not as negatively impacted by the disease as the human host. It has long been assumed that because domestic animals can be hosts for the parasite, that keeping domestic animals near human populations increases the spread of the disease. However, several parameters found in the literature, including the shorter lifespan of the male vector, and the female vector's preference for domestic animals, made us question this assumption.

We developed a differential equation compartmental model to examine whether increasing the domestic animal population can be used to deflect the infection from humans and reduce its impact. We have used numerical simulations and have examined the Basic Reproduction Number (R_0) for the model to quantify the effect of the domestic animal population on human infection. These analyses allow us to propose novel methods of controlling the impact of the disease on humans.

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