

1116-VW-269 **Marshall Hampton*** (mhampton@d.umn.edu), Duluth, MN 55812. *Probabilistic models of Trypanosome RNA tails.*

Trypanosomes cause a variety of diseases, most notably sleeping sickness and Chagas disease. Trypanosomes are very unusual unicellular parasitic flagellate protozoa; one of the strangest features being that their mitochondrial genome is essentially encrypted, requiring massive editing by their minicircle DNA. In addition, mitochondrial RNA transcripts have complicated 3' tail additions incorporating uridine (U) as well as adenine (A). Unique features of these parasites are important as they could provide good novel drug targets.

Based on new circularized RNA deep sequencing data, we present different probabilistic approaches to modeling the structure of these RNA tails, and how the models can inform biological interpretation. (Received August 19, 2015)