Modelling Zoonoses in Rodent Communities

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Introduction

Rodents are reservoirs of zoonotic diseases, posing a significant threat to human health. Understanding rodent ecology and population dynamics is therefore important for mitigating human zoonotic hazards. Trapping studies have improved our understanding of zoonotic epidemiology, however, capturing known reservoirs to the exclusion of other rodent species limits inference on broader eco-epidemiological questions. Detailed information on rodent communities could be used to understand how global changes in habitat suitability and climate influence the dynamic ecosystems from which zoonotic diseases emerge and are maintained. Currently, there is no standard method for reporting rodent trapping data. This project aims to establish a high-resolution rodent community seroprevalence database by collating published data on rodent abundance and pathogen prevalence, and provide a standard for its reporting going forward. These data will facilitate robust inference on the eco-epidemiological predictors of rodent-borne disease, helping to shape our understanding of zoonotic disease risk in a changing world.

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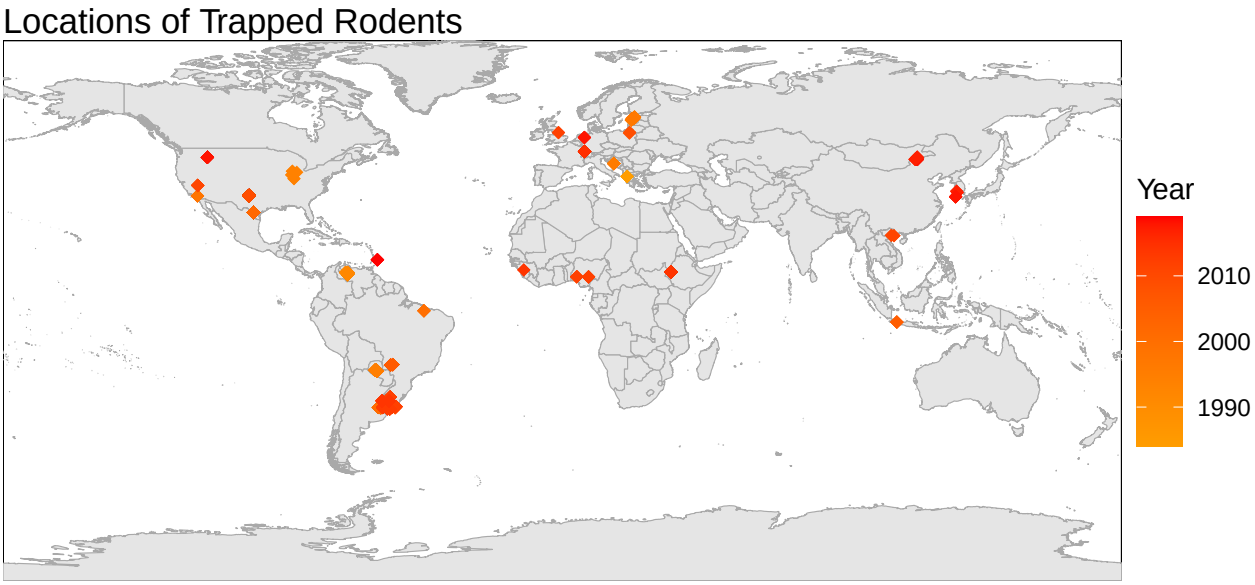
David Simons' paper: Simons et al. (2023).

Methods

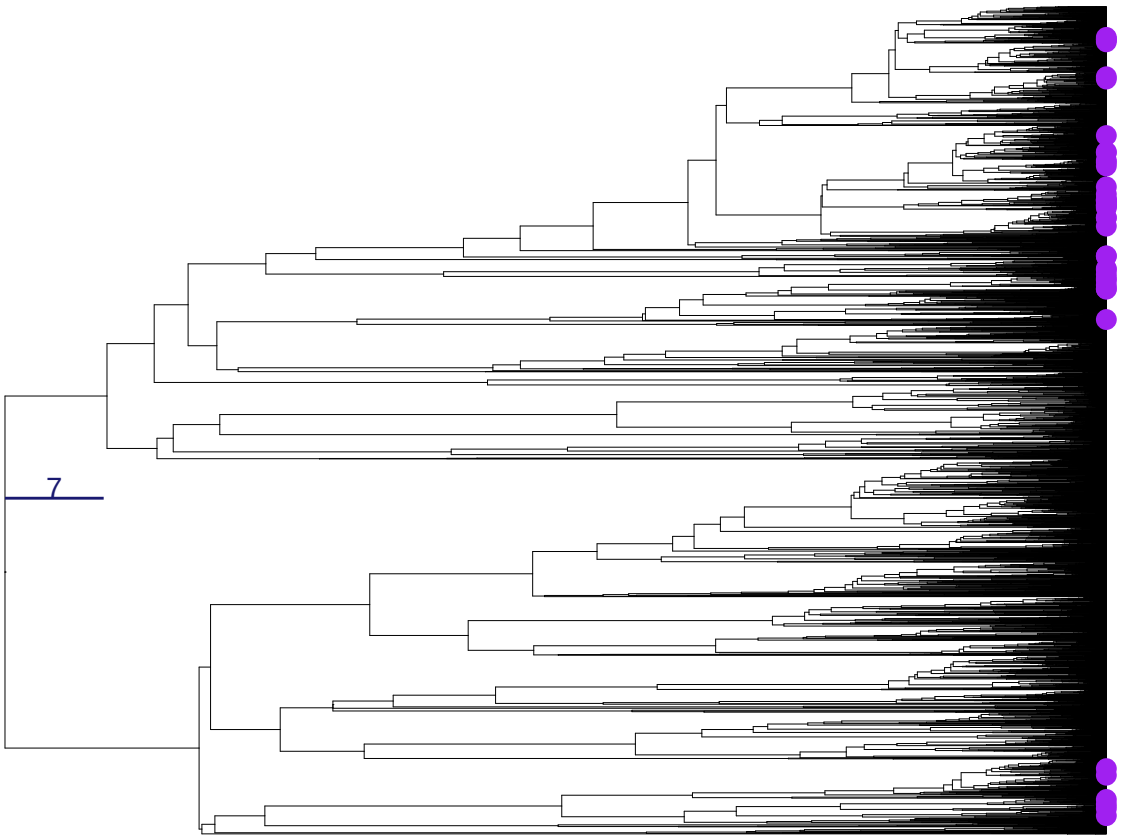
These are the methods.

Here is a world map displaying locations of our sampled rodents:



Rodent phylogeny

Here is the mammal tree with our host species higlighted



Data papers

We collected data from the following papers for use in this analysis: Burns et al. (2018), Cabrera et al. (2023), Dietrich et al. (1997), Fernandes et al. (2015), Fulhorst et al. (2002), Jameson et al. (2013), Kosasih et al. (2011), Ledina et al. (2002), LeDuc, Antoniades, and Siamopoulos (1986), Mauldin et al. (2013), Milazzo et al. (2013), Nemirov et al. (1999), Zhang et al. (2024), Seijo et al. (2003), Sheikh Ali et al. (2014), Suárez et al. (2003), Williams et al. (1997), Williamson et al. (2021).

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