

# SpREAD: Spatio-temporal Rodent Community Ecology And Disease Database.

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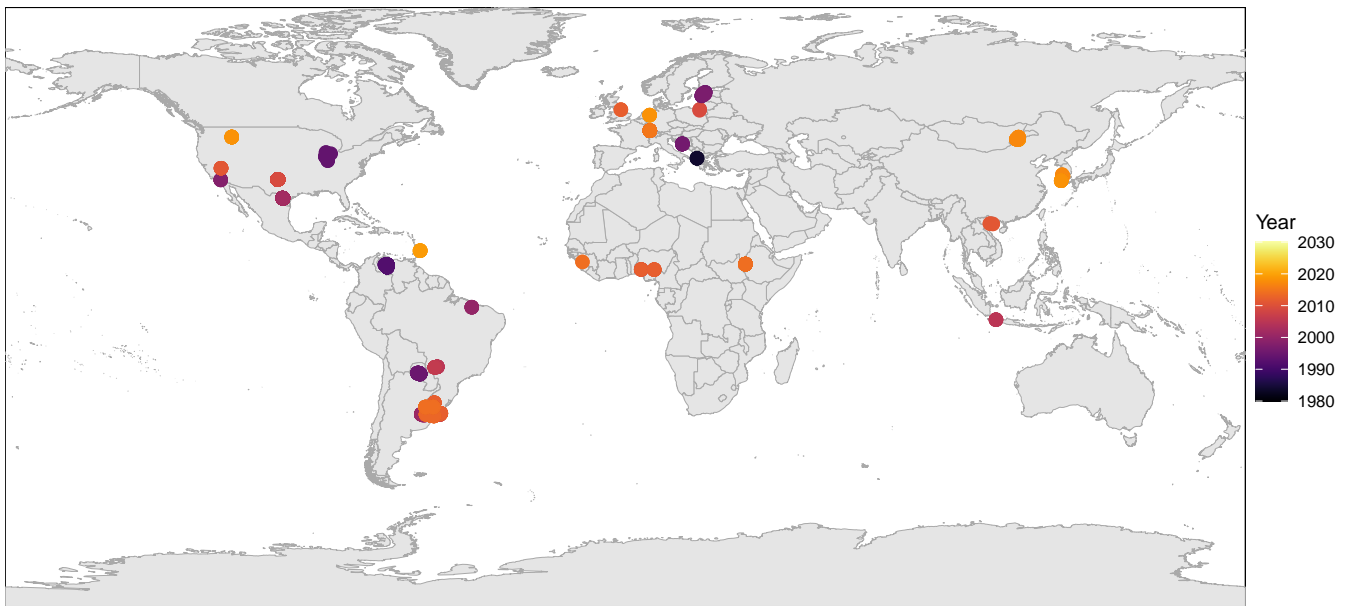


Figure 1: The geographic locations of trapped rodents included in our study. The colour of points denotes the year sampled.

## This information is for researchers interested in co-authorship

SpREAD is a project being carried out by the Infectious Disease Systems Ecology Group of the Natural History Museum, London. SpREAD aims to aggregate many previous rodent community trapping studies to a common resolution, to achieve the sample size necessary for robust infection dynamics modelling in rodent communities. It is a database inspired by previous efforts to gather data from scientific papers (Simons et al. 2023) and other open databases such as PREDICTS (Hudson et al. 2017).

The secondary aim of SpREAD is to provide a much-needed format for the reporting of trapping studies on rodent communities going forwards. It is sometimes not feasible to include fine-scale data in publications, so data reported in these studies have often been highly summarised (e.g yearly) and do not include all information about the location and serology of the trapping. This complete data could be added to the SpREAD database, and reporting the fine-scale data would be as easy as citing the database publication.

The database would serve as a convenient data-hosting service, and clear labelling of data points with the publication of origin and authors would promote collaboration and opportunities for future projects. The full dataset would be

available for anyone to use in their research, making the most out of the resources and effort put in by scientists in the field. The SpREAD database will serve as a community-driven tool to be continually added to, ever improving in its completeness and utility.

## Requirements for inclusion

The minimum requirements for data to be included in the SpREAD database are as follows:

1. **Date of trapping** (minimum resolution of a month)
2. **Duration of trapping** (or start and end date)
3. **Locality or coordinate location** of trapping site
4. **All captured rodents' abundances** are reported
5. **All individuals are tested** for at least one pathogen
6. **Type of test used and pathogen name** (at least family level e.g. hantavirus)

Desirable:

1. Indication of trapping method (e.g. grid area/number of traps/type of trap)
2. Indication of trapping effort (e.g. trap nights)

If you are interested in co-authoring this paper and providing your data, please submit it via **this link** or paste this in your browser: <https://forms.gle/BhRf5SP36EHwJYPV9>.

If you do not have access to the data but know someone who does, please pass this email/document along.

## The SpREAD database as of Sept. 2024

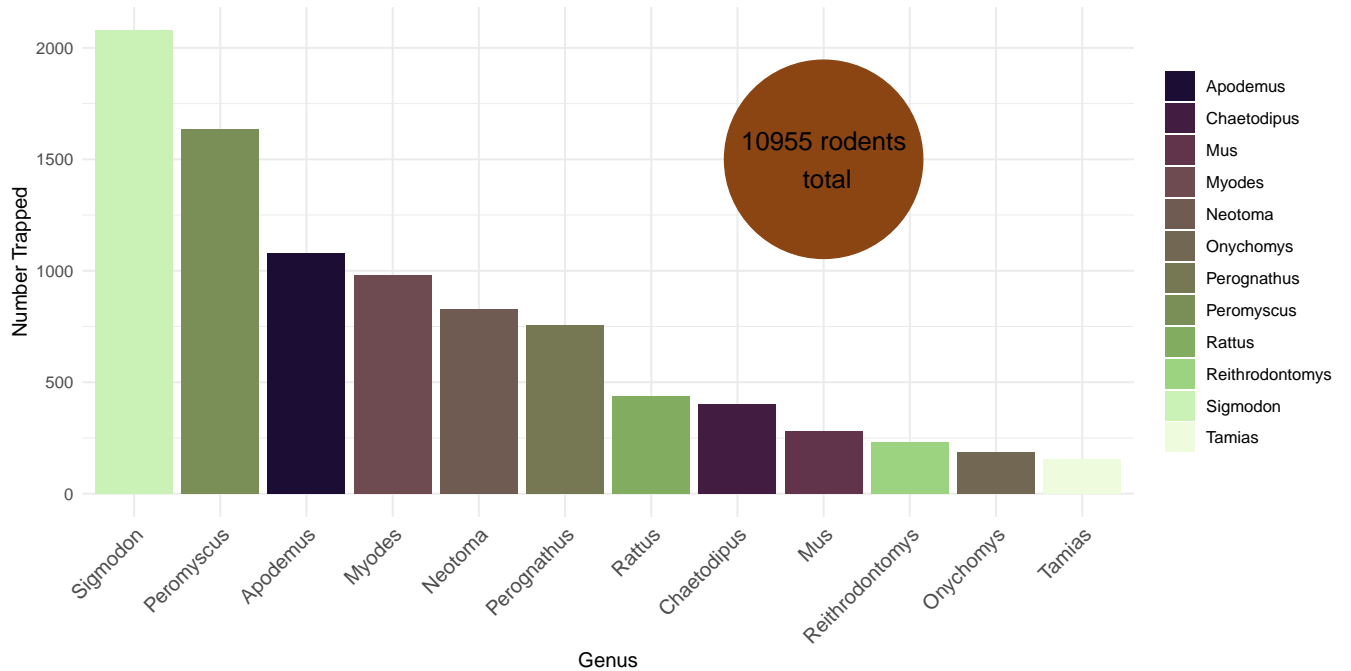


Figure 2: The number of hosts trapped for each genus

Through extraction of data from 27 published articles (so far), we have gathered data on 189 unique rodent communities across 5 continents (fig. 1). These are comprised of 10,955 rodents, of which 480 were positive for a pathogen of interest. The most common rodents found were of the *sigmodon* (cotton rats) and *peromyscus* (deer mice) genera (fig. 2). The most prevalent viruses were Sin Nombre Virus, Catarina Virus and Puumula Orthohantavirus, all belonging to the family *hantaviridae* (fig. 3).

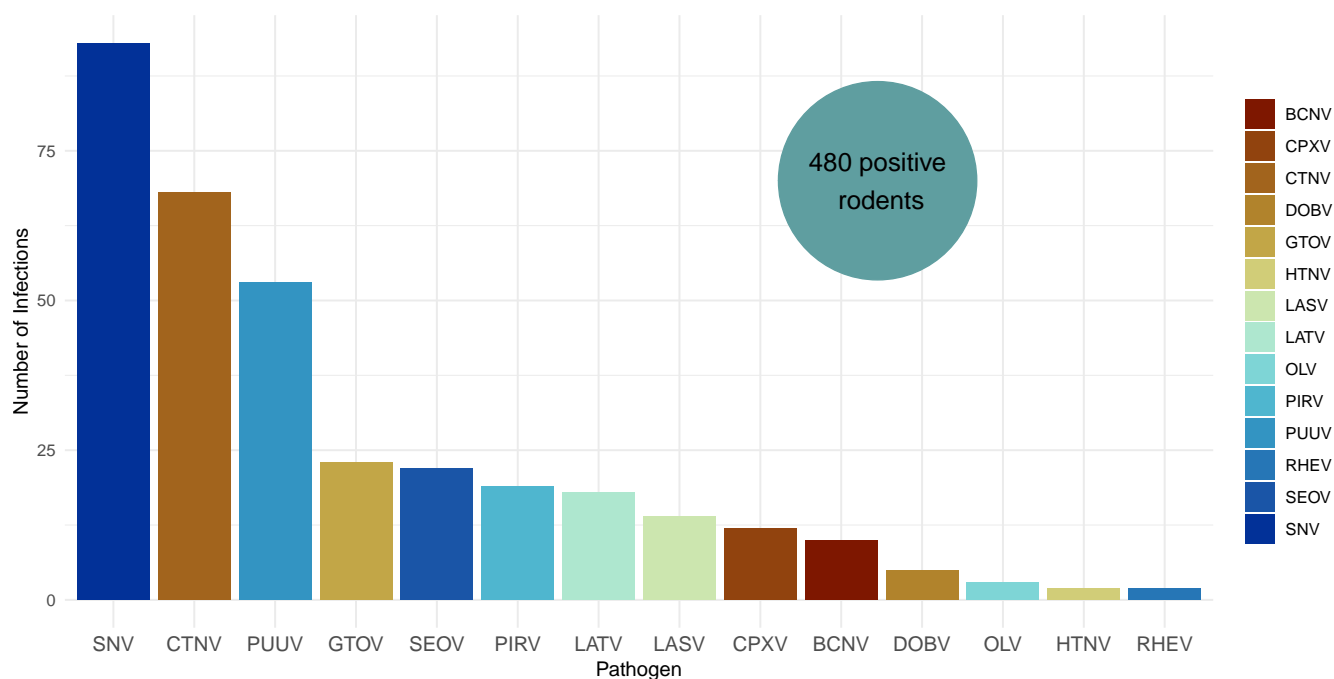


Figure 3: The number of infections for each virus tested

## References

- Hudson, Lawrence N, Tim Newbold, Sara Contu, Samantha LL Hill, Igor Lysenko, Adriana De Palma, Helen RP Phillips, Tamera I Alhusseini, Felicity E Bedford, and Dominic J Bennett. 2017. “The Database of the PREDICTS (Projecting Responses of Ecological Diversity in Changing Terrestrial Systems) Project.” *Ecology and Evolution* 7 (1): 145–88.
- Simons, David, Lauren A Attfield, Kate E Jones, Deborah Watson-Jones, and Richard Kock. 2023. “Rodent Trapping Studies as an Overlooked Information Source for Understanding Endemic and Novel Zoonotic Spillover.” *PLOS Neglected Tropical Diseases* 17 (1): e0010772.