

SPREAD: Spatio-temporally Precise Rodent Community Ecology And Disease Database.

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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>.

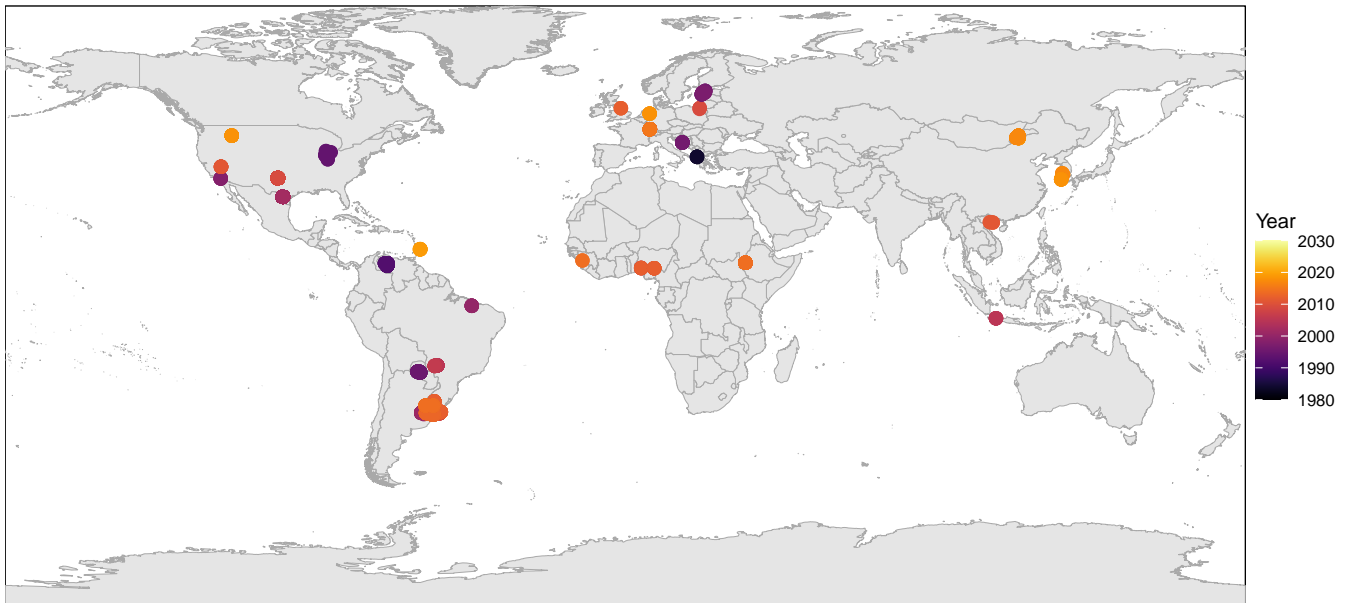


Figure 1: The geographic locations of trapped rodents included in our study. The colour of points denotes the year sampled.

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 completeness and utility.

Requirements for inclusion

scientificName	startDate	endDate	locality	decimalLatitude	decimalLongitude	individualCount	trapEffort	pathogenName	testUsed	positives
Myodes glareolus	04-04-2024	07-04-2024	Site 1	-45.73666	110.25633	25	60	Sin Nombre Virus	ELISA	2
Rattus norvegicus	04-04-2024	07-04-2024	Site 1	-45.73666	110.25633	2	60	Sin Nombre Virus	ELISA	0
Myodes glareolus	15-06-2024	18-06-2024	Site 2	-45.10563	107.83911	110	60	Sin Nombre Virus	ELISA	12
Rattus norvegicus	15-06-2024	18-06-2024	Site 2	-45.10563	107.83911	43	60	Sin Nombre Virus	ELISA	1
Mastomys natalensis	15-06-2024	18-06-2024	Site 2	-45.10563	107.83911	6	60	Sin Nombre Virus	ELISA	0
Myodes glareolus	25-07-2024	28-07-2024	Site 3	-42.73342	112.26327	70	60	Sin Nombre Virus	ELISA	20
Rattus norvegicus	25-07-2024	28-07-2024	Site 3	-42.73342	112.26327	14	60	Sin Nombre Virus	ELISA	0
Mastomys natalensis	25-07-2024	28-07-2024	Site 3	-42.73342	112.26327	38	60	Sin Nombre Virus	ELISA	13

Figure 2: Example of included data, individual level data (one row per rodent) is also accepted. This table is to demonstrate resolution, **data do not have to match this format**.

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. **Precise coordinates for all trapping locations** (if sites not recorded, indication of trapping area in kmsq)
4. **All captured species' abundances** are reported (separately for each trapping session and site)
5. **All individuals are tested** for pathogen(s) of interest.
6. **Diagnostic assay 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)

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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

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).

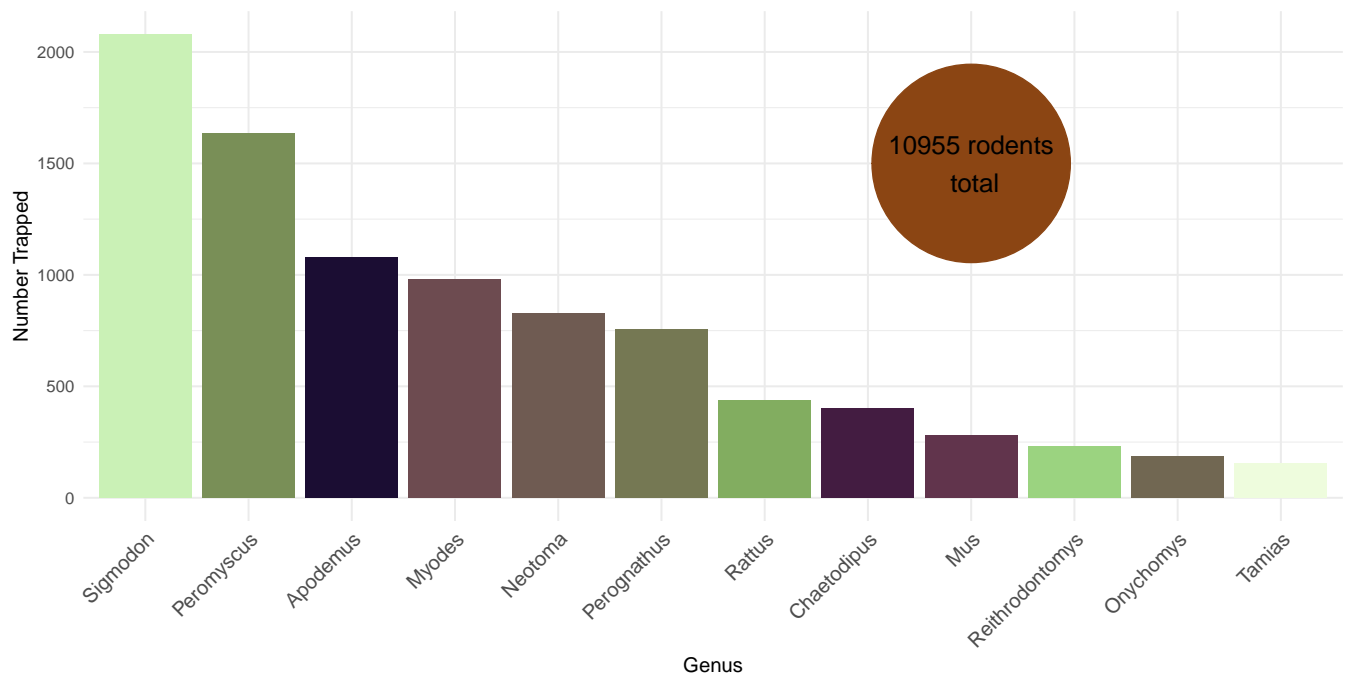


Figure 3: The number of hosts trapped for each genus

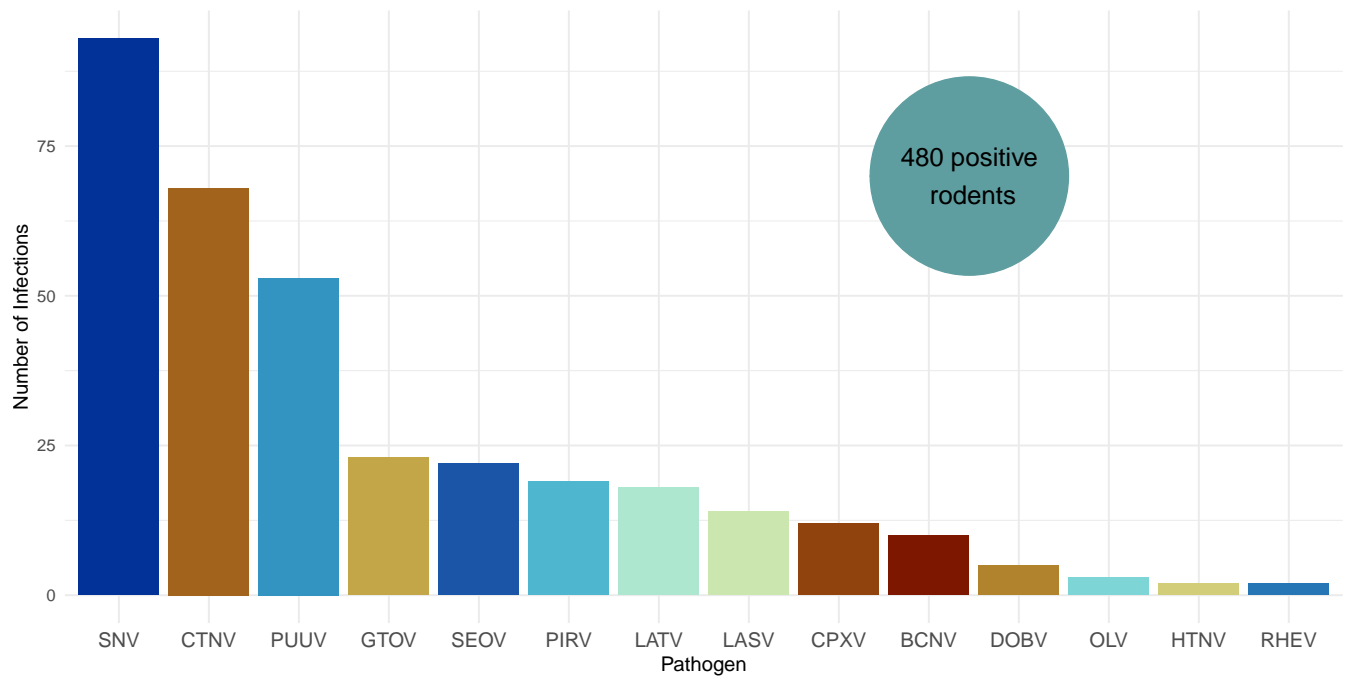


Figure 4: The number of infections for each virus tested

References

- Hudson, Lawrence N, Tim Newbold, Sara Contu, Samantha LL Hill, Igor Lysenko, Adriana De Palma, Helen RP Phillips, Tamera I Alhousseini, 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."

