Anthropogenic Roosting and Virus Richness in Bats

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INTRODUCTION:

- Bats are a very diverse group of mammals known to host many pathogens of increasing domestic animal and human health concern.
- It is crucial to identify factors that may explain this variation in pathogen diversity.
- Known traits associated with viral diversity include:
  - IUCN status
  - population structure
  - longer lifespan
  - larger group size
  - geographic distribution in the eastern hemisphere
- **Bat roosting ecology, especially the ability to roost in anthropogenic structures, is often not included in past models owing to a sparsity of standardized data. Omitting this information could impact the prediction of spillover risk.**

OBJECTIVE:

Using a novel roosting ecology dataset, this study is a species-level analysis that uses a machine learning approach to investigate if anthropogenic roosting:

1. is important in predicting viral richness
2. improves identification of undetected but likely bat reservoir species

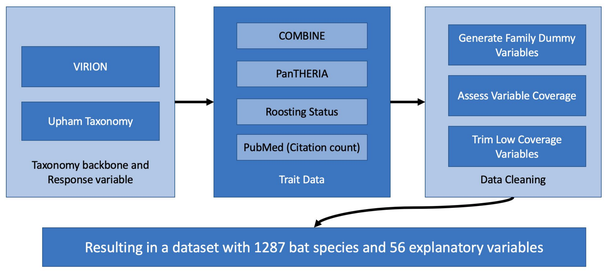
METHODS:

Classifying bat roosting status

Anthropogenic roosting bat species are defined as having record of roosting in any human-made structure (houses, bridges, attics, mines, etc.).

- **Categories**
  - This explanatory variable of interest is a binary variable of 0 and 1 (0 = natural roost, 1 = roosts in anthropogenic structures)
- **Sources**
  - IUCN
  - Walker's Bats of the World 1994 edition
  - Google Scholar
  - Animal Diversity Web
- **Incomplete or missing roost information**
  - Will be considered as NA if:
    - IUCN states natural history or roosting status unknown/data deficient
    - Cannot find evidence of known roosting sites within the first 10 pages of GS or having no relevant search results

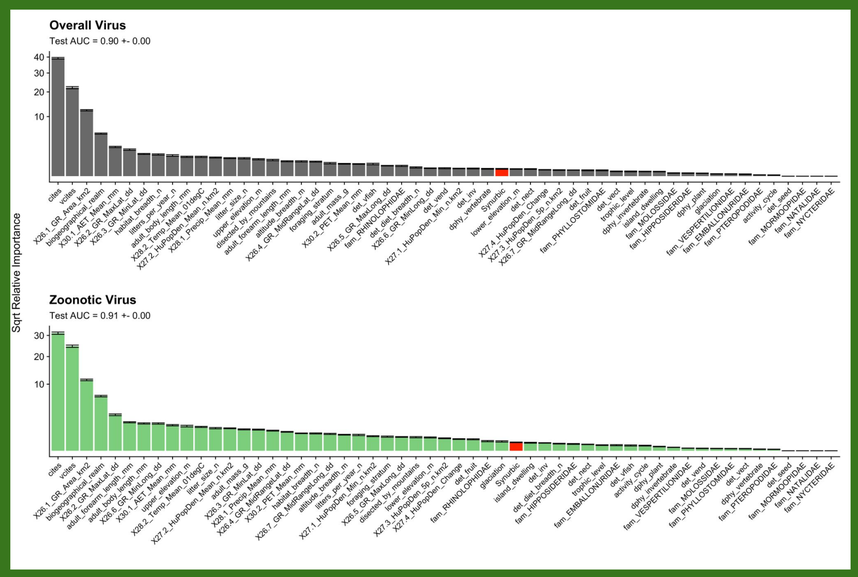
Dataset Building:



Analysis:

- For preliminary analysis, both overall virus and zoonotic virus response variables were turned into binary variables (0 for non-host and 1 for host).
- Boosted regression tree (BRT) models were run for both response variables, using a Bernoulli distribution for 50 partitions each of a 70:30 training/test split.
- Resulting variable importance and test AUC were averaged to view mean variable importance and standard error across models.

Preliminary findings suggest that anthropogenic roosting status is *less important* in predicting virus bat hosts than human population density, but more important than most family, diet, and foraging traits.

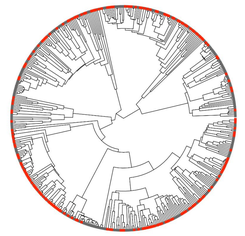


Scan to view/download data sources and additional info

Scan to view Briana's Website or go to babetke.github.io

PRELIMINARY RESULTS:

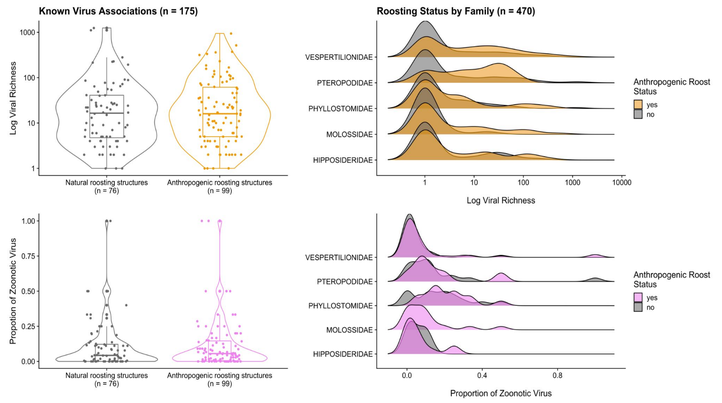
- Current coverage of the roosting status variable is 40% with 544 bats identified and 470 non-NA values.
- Of the 470 bat species with a value (either 0 or 1), 57.7% were found to roost exclusively in natural structures and 42.3% were found to roost in anthropogenic roosting structures.
- These anthropogenic structures included bridges, attics, mines, and overhangs of buildings.
- Preliminary roosting status data represent 11 bat families and show the highest percentage of anthropogenic roosting species to be Molossidae (69.7% roosting in anthropogenic structures). Second highest is Vespertillionidae at 42%.



Roosting Status: Natural (Grey) Anthropogenic (Red)

Family	Natural	Anthropogenic	Total	Percent
CRASEONYCTERIDAE	1	0	1	0
EMBALLONURIDAE	16	6	22	27.27
FURIPTERIDAE	1	1	2	50
HIPPOSIDERIDAE	35	35	70	50
MEGADERMATIDAE	1	4	5	80
MOLOSSIDAE	20	46	66	69.7
MORMOOPIDAE	1	1	2	50
NATALIDAE	2	0	2	0
PHYLLOSTOMIDAE	53	29	82	35.37
PTEROPODIDAE	47	9	56	16.07
VESPERTILIONIDAE	94	68	162	41.98

- Preliminary analysis of known viral associations, 45.5% bats were found to not roost in human-made structures whereas 54.4% were found to roost in human-made structures.
- Boxplots suggest negligible differences in viral richness and proportion of zoonotic viruses, between natural and anthropogenic roosting bats.
- Ridgeplots reveal relationships between viral outcomes and roosting status are distinct across bat families.
- Members of the Phyllostomidae and Hipposideridae do not show differences whereas anthropogenic roosting species in the Vespertilionidae, Pteropodidae, and Molossidae have greater virus richness than their natural-roosting counterparts.



DISCUSSION:

This work emphasizes the need to characterize and synthesize species traits that relate directly to the wildlife-human interface, such as the use of anthropogenic structures as roosts, where spillover occurs.

Further study consists of:

- Improving coverage of roosting structure
- Change the response variables to the number of viruses and proportion of zoonotic virus rather than binary variables.
- Comparing performance/prediction between models that don't contain roosting status to those that do.