The role of connectivity in pathogen persistence in bat populations

**INTRODUCTION**

How do pathogens persist in populations?

How can subpopulation dynamics impact pathogen persistence?

Why are bats special/interesting?

* Host pathogens of public health importance
* Move extensively across landscape and intermingle
* Seasonal changes in many patterns, including movement

We seek to quantitatively explore the role of [seasonal changes in] subpopulation connectivity in pathogen persistence in bats.

**METHODS**

**Study System**

Fruit bats in Madagascar. Known metapopulation of *Pteropus rufus* in Mangoro River Valley. Well studied – population estimates, know they have a lot of viruses, know what habitats they use.

**Subpopulation Connectivity**

We deployed a total of eight gps telemetry devices on representative individuals from each subpopulation.

Table: tagged bats (lat lon, sex, weight, time of tag, number of records)

**Model**

Use models of candidate transmission dynamics from Brook et al 2019.

We added stochasticity.

We expanded these modified SIR models into metapopulation models, allowing for connectivity.

Figure 2: Model diagram with subpopulation connectivity clearly marked?

**Pathogen Persistence Simulations**

Use parameter estimates from Brook et al 2019 in candidate models.

Use annual estimates of subpopulation connectivity from

Simulation tests: introduce a range of pathogen types (different params) in different subpopulations and at different times, see if persistence can be achieved.

**RESULTS**

**Subpopulation connectivity**

Figure: timeline of representative gps data across seasons/months

Figure: some figure showing average and sd of subpop connect across the year (a visual summary of whatever time scale I put into the model)

**Pathogen Persistence**

Figure: for each different pathogen tested (a ‘coronavirus’, a ‘henipavirus’, a ‘filovirus’), panel simulation of each of the three models (1 year persistence) (100 year persistence) – or just pathogens where persistence was achieved?

Table: Short- and long-term probability of persistence for each pathogen-introduction-model pairing

\*\*3 pathogens x 3 subpop introductions x 2 times of year (wet vs dry season) x 3 models x 2 simulation lengths = 108 total simulations\*\*