The role of connectivity in pathogen persistence in bat populations

**INTRODUCTION**

How do pathogens persist in populations? Role of between host transmission, particularly changes in that over time.

Why are bats special/interesting?

* Host pathogens of public health importance that can spill over
* Species traits such as nomadicism and fission-fusion population structures
  + Seasonally driven: changes in food availability, maternity roosts

Most models assume closed populations, not metapopulation dyanamics

We seek to 1) quantify seasonal changes in connectivity/contact rates in bat species, 2) examine the effects of these changes on viral persistence.

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.

Use model of demographic dynamics from etc.

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 with time to extinction of simulations (conditioned on invasion success) of each of the three models (1 year persistence) (100 year persistence) under different initial population immunity (?) and timing of introduction

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\*\*

**Discussion**

Spillover

* Three proposed hypotheses of variation in viral shedding (plowright et al 2016)
  + This is evidence for between-host contact being important, in addition to within host transmission dynamics
* CCS