Using gps telemetry to explore mechanisms of 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 nomadism and fission-fusion population structures
  + Seasonally driven: changes in food availability, maternity roosts

Most models assume closed populations, not metapopulation dynamics

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

Used telemetry data to estimate two parameters: probability of dispersal and probability of intermingling.

**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 two forms of interaction: dispersal and intermingling.

A diagram of activity and interlocutor

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Figure 2: Figure that shows how dispersal and intermingling are different

Dispersal : biweekly movement of individuals

Intermingling : homerange overlap

**Pathogen Persistence Simulations**

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

Use annual estimates of subpopulation connectivity from telemetry

Simulated across a range of population parameters

Compared models: telemetry data connectivity stochastic, telemetry data connectivity single mean, no connectivity

**RESULTS**

**Subpopulation connectivity**

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Figure: timeline of representative gps data across seasons/months

A map of bangladesh with black dots

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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**

MSIRN

MSIRS

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R0

R0

MSIRNI

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R0

Figure: persistence under differing disease conditions (population parameters fixed from brook and Daudet data)

* With data-backed estimates of parameter space boxed/marked

**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
* As population size decreases (extinction) – more infection? More spillover risk?

Using serology of eidolon with telemetry of Pteropus – okay for these reasons, but future fitting of models to Pteropus serology important because of a few key differences (roosting in trees instead of caves)

**SUPPLEMENT**

Equations

Population Trajectories under different models

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MSIRS

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