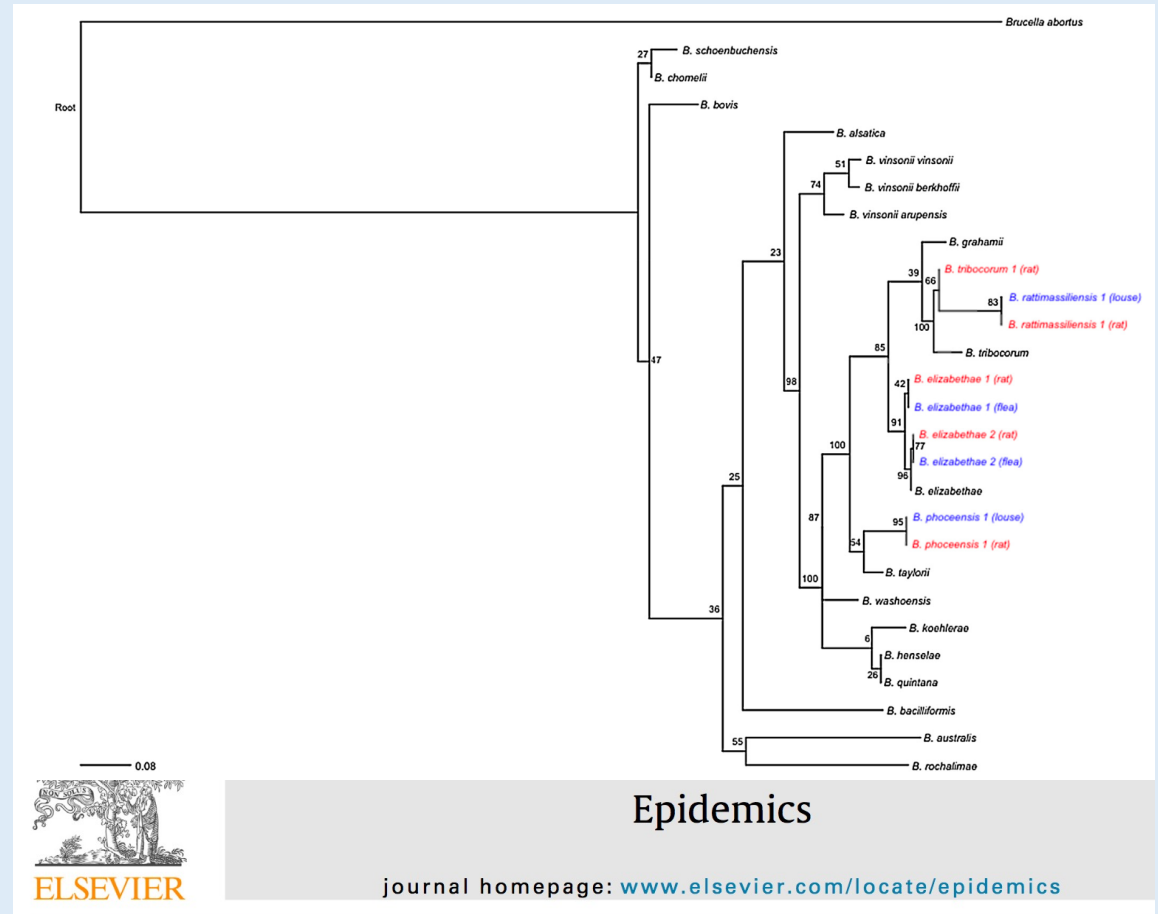# Transmission dynamics and host-parasite-vector relationships in rodent-borne *Bartonella* spp.

- **Background:** *Bartonella* spp. is an erythrocytic bacterial pathogen of Malagasy rodents with different genotypes which could demonstrate unique transmission mechanisms.

- **Statistical Question:** Is the occurrence of *S. fonquerniei* on Malagasy *R. rattus* related to (a) the indoor/outdoor locality in which the rat is trapped, (b) abundance of *E. gallinacea,* and (c) the abundance of *X. cheopsis* on the same rat?

- **Mechanistic Question:** How can we explain the prevalence of different genotypes of *Bartonella* spp. by age class in Malagasy *Rattus rattus?*

- **Acknowledgements:** Christian and Sophia (readers); Gwen (presentation)

Cara Brook, University of Chicagp

Epidemics

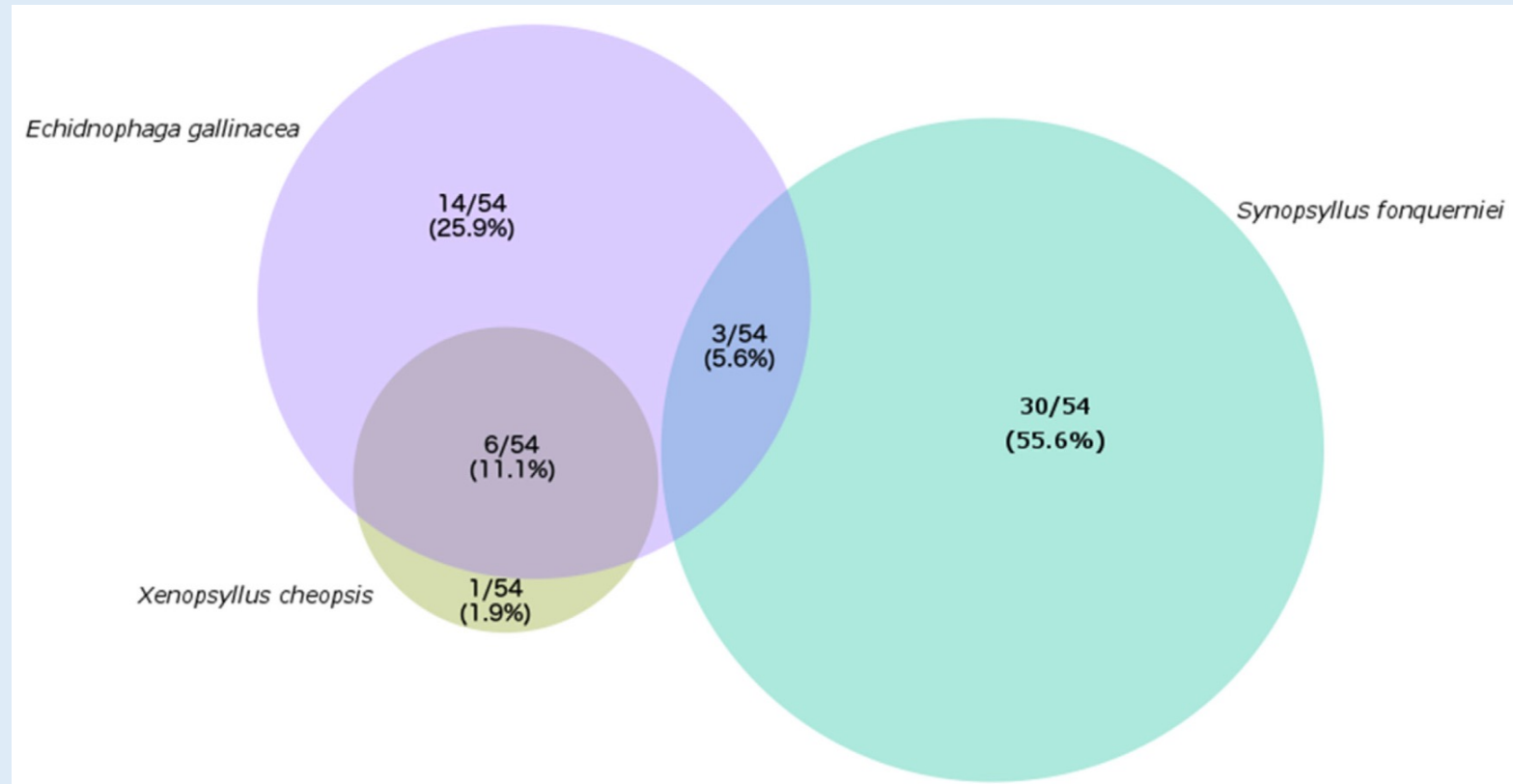journal homepage: www.elsevier.com/locate/epidemics

Elucidating transmission dynamics and host-parasite-vector relationships for rodent-borne *Bartonella* spp. in Madagascar

Cara E. Brook [a,*], Ying Bai [b], Emily O. Yu [a], Hafaliana C. Ranaivoson [c,d], Haewon Shin [e], Andrew P. Dobson [a], C. Jessica E. Metcalf [a,1], Michael Y. Kosoy [b,1], Katharina Dittmar [e,1]

Statistical Question:
Is the occurrence of *S. fonquerniei* on Malagasy *R. rattus* related to (a) the indoor/outdoor locality in which the rat is trapped, (b) abundance of *E. gallinacea,* and (c) the abundance of *X. cheopsis* on the same rat?
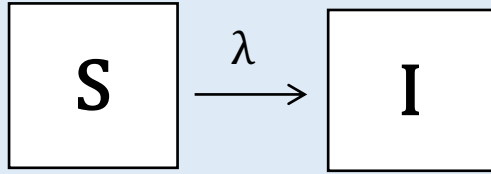
- **Response Variable:** pres/abs *S. fonquerniei*

- **Predictor Variables:** abundance of
  E. gallinacea (numeric); abundance
  of *X. cheopsis* (factor);
  indoor/outdoor locality (factor)

- **Family:** "binomial"

- **Link:** logit

- **Hypothesis:** *S. fonquerniei* occurrence
  is related to low abundance of
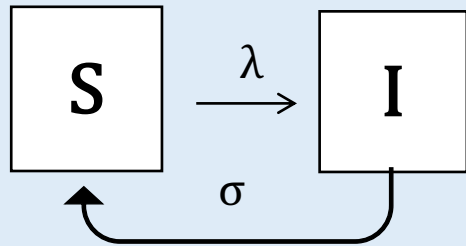 *X. cheopsis* & outdoor status locality

- **R code:**

glm(pres/abs *S. fonquerniei* ~ abundance *X. cheopsis* + abundance *E. gallinacea* + indoor_outdoor, family="binomial", data = madarat)

Mechanistic Question:

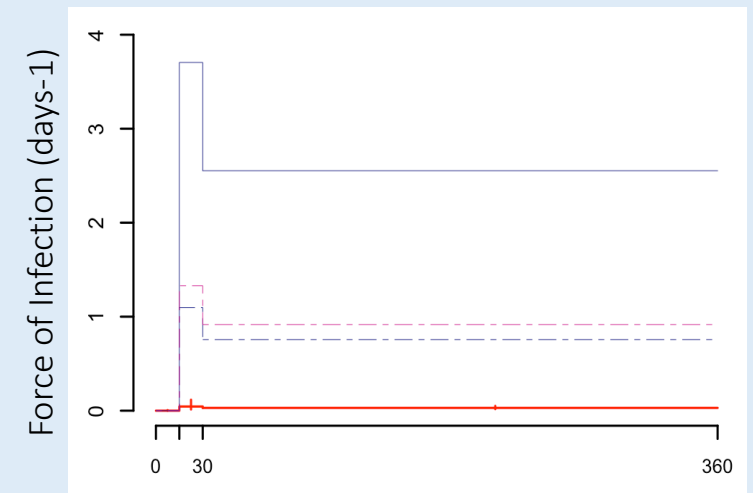How can we explain the prevalence of different serotypes of *Bartonella* spp. by age class in Malagasy *Rattus rattus?*
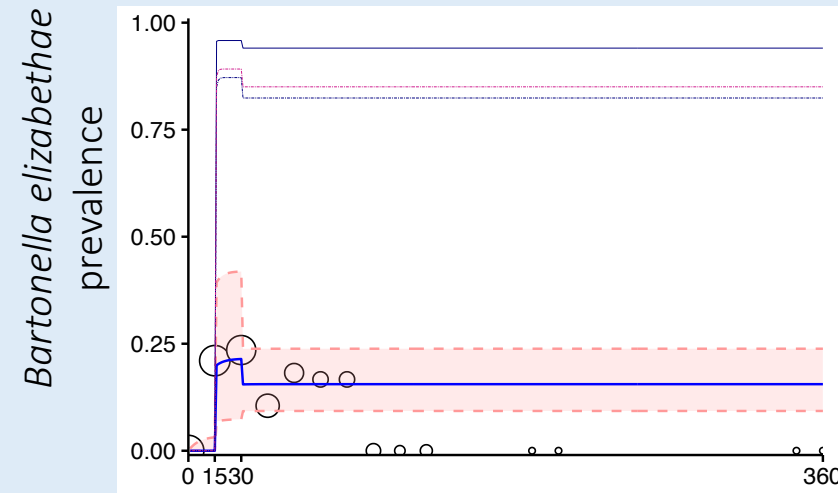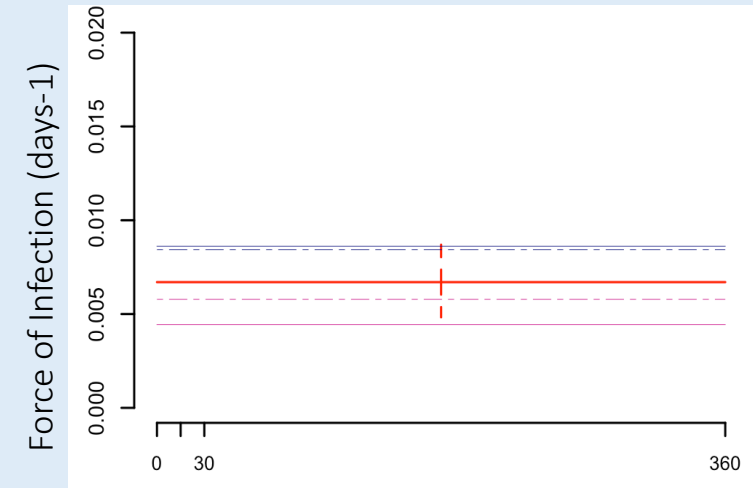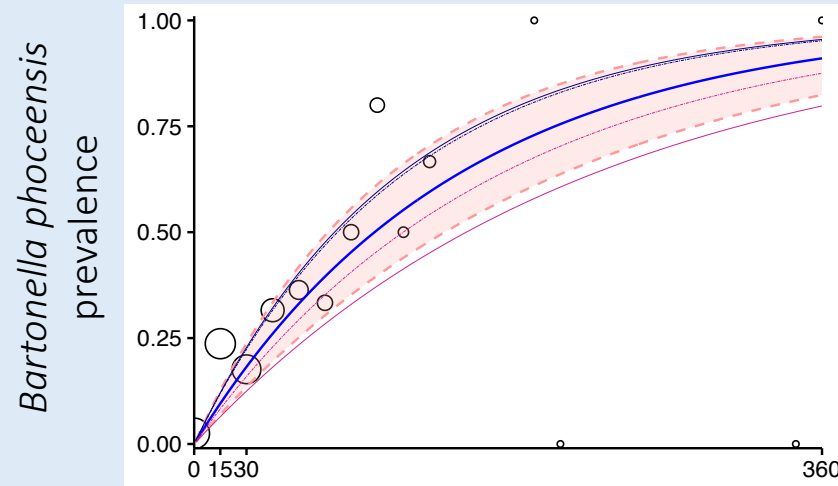
S = susceptible rats
I = infectious rats

λ = force of infection;
σ = rate of waning immunity

$$\frac{dI(a)}{da} = \lambda(a)\big(1 - I(a)\big)$$

$$\frac{dI(a)}{da} = \lambda(a)\big(1 - I(a)\big) - \sigma I(a)$$

Next Steps:

1. Conduct further field studies in lowland regions of Madagascar to determine whether the distribution of *B. elizabethae* is limited to the highland range of *S. fonquerniei*

2. Conduct serological tests on *R. rattus* blood to attempt to identify a whether *Bartonella* spp. negative rats are recovered or susceptible.

3. Fit relevant mechanistic transmission models to age-seroprevalence data.

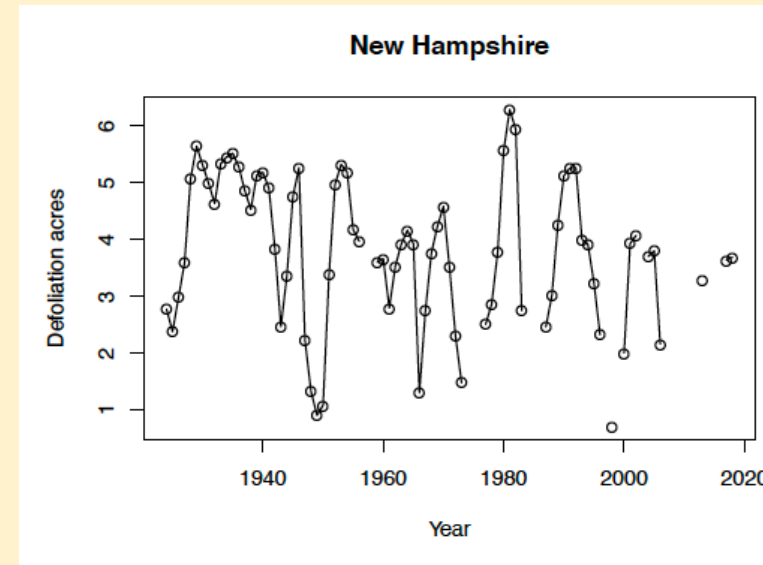# Investigating coinfections in the spongy moth-fungus-virus system

Background: The spongy moth, *Lymantria dispar,* is an invasive lepidopteran (family: Lymantriidae) that defoliates hardwood trees across North America. Its population dynamics are driven by epizootics (epidemics in animals) of two fatal, environmentally-transmitted pathogens: a fungus, *Entomophaga maimaiga,* and a baculovirus, *Ld-nucleopolyhedrovirus.* Coinfections are detected in nature, but we do not understand what factors drive the presence of coinfection, or how coinfections influence spongy moth population dynamics.

Statistical Question: What is the relationship between environmental factors (rainfall, relative humidity, temperature) and the presence of coinfections?

Mechanistic Question: How do coinfections drive spongy moth population dynamics?

Sophia Horigan, University of Chicago

New Hampshire

Defoliation acres / Year

Statistical Question:

What is the relationship between environmental factors and the presence of coinfections?

Response Variable: cumulative number of coinfections in a population

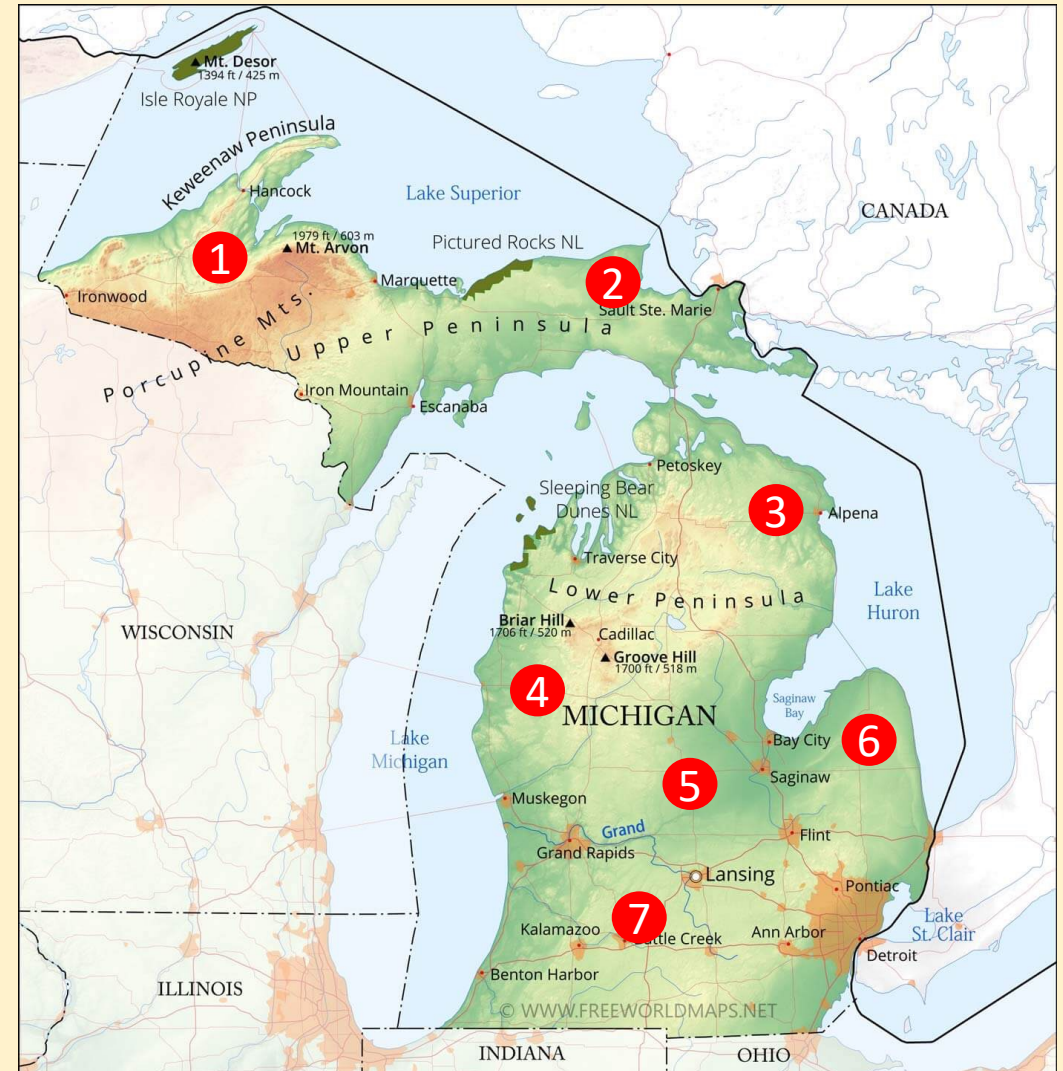**Predictor Variable:** temperature, relative humidity, rainfall, site

Family: "poisson"

Link: log

Hypothesis: Sites with higher rainfall, higher humidity, and moderate temperatures will have a higher number of cumulative coinfections.

R code:
glmer(cum. # coinfections~rainfall + temperature + relative humidity + (1| site), family = "poisson", data=infection.data)

Sophia Horigan, University of Chicago

Mechanistic Question:
How do coinfections drive spongy moth population dynamics?

States
S – susceptible caterpillars
$I_{f,E}$ – early fungus infected
$I_{f,L}$ – late fungus infected
$I_{v,E}$ – early virus infected
$I_{v,L}$ – late virus infected
I_{fv} – coinfected
F – fungal spores in the environment
V – viral particles in the environment

Parameters
β_f – fungus transmission
β_v – virus transmission
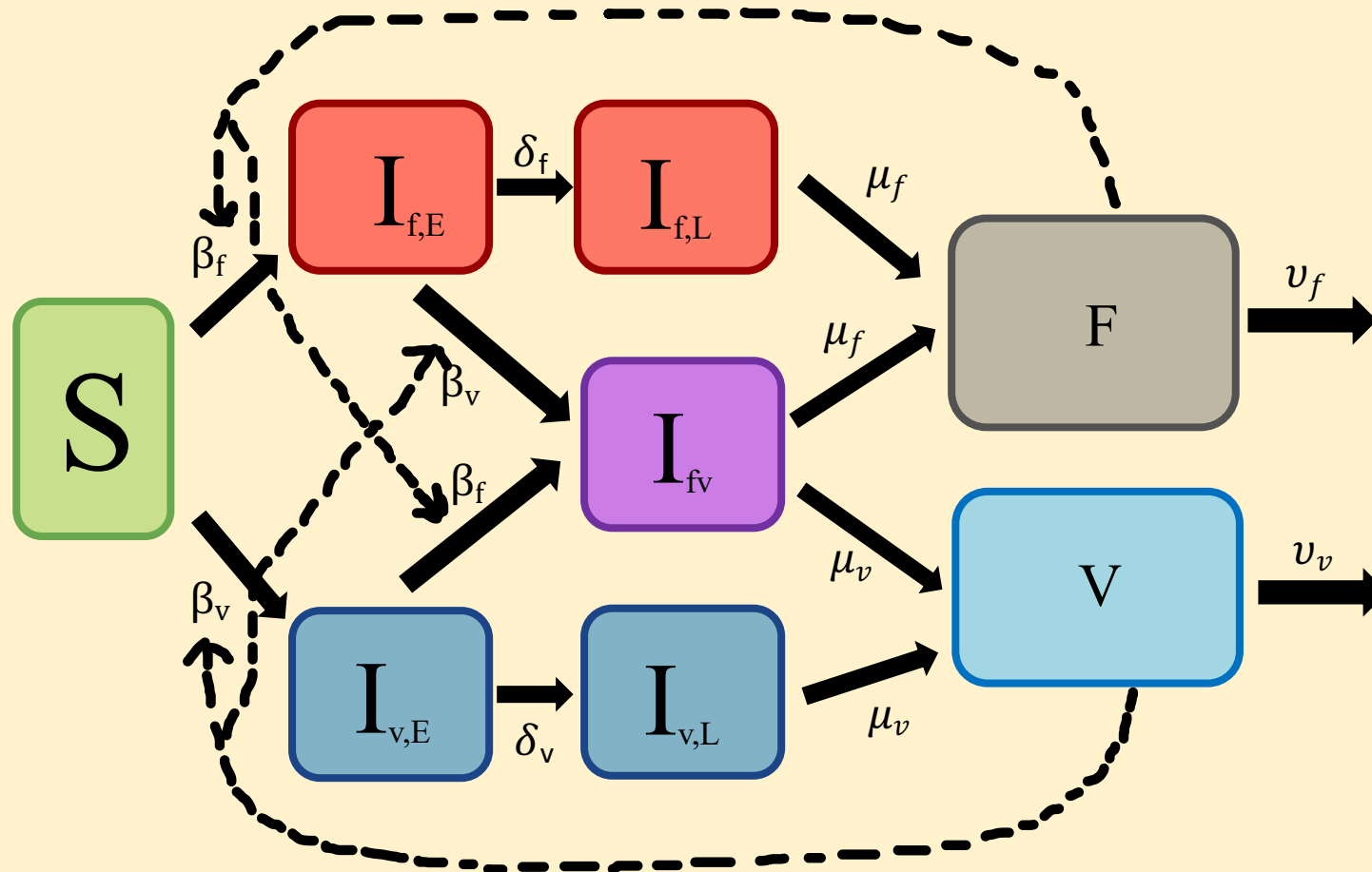δ_f – progression to late fungus infection
δ_v – progression to late virus infection
μ_v – conversion of dead insect to virus particles
μ_f – conversion of dead insect to fungal spores
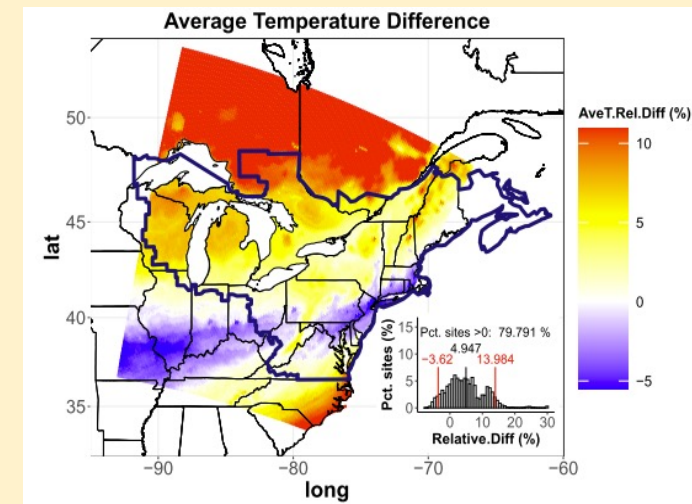υ_f – fungal spore decay
υ_v – viral particle decay

Investigating coinfections in the spongy moth-fungus-virus system

Next Steps:

1. Conduct field sampling at all sites for at least two more years to get infection data across a range of annual weather conditions.

2. Fit the mechanistic model to field data.

3. Extend the model to long-term dynamics by incorporating spongy moth reproduction and pathogen overwintering dynamics.

4. Use the long-term model to predict the future of spongy moth populations under climate change.

Sophia Horigan, University of Chicago

Age mediated viral shedding in Malagasy fruit bats

Background: Previous work in our lab has shown that age class and sex of bats impacts seroprevalence for henipaviruses and filoviruses. However, we do not know how viral shedding in bats from active infections impact age-seroprevalence.

Statistical question: How does age class drive viral load in Malagasy fruit bats?

Mechanistic question: How does viral shedding differ between juvenile and adult Malagasy fruit bats?

Acknowledgement to people who have evaluated these models:
Cara Brook, Sophia Horigan (readers); Nuzha (presentation)

Disentangling serology to elucidate henipa- and filovirus transmission in Madagascar fruit bats

Cara E. Brook,[1,8] Hafaliana C. Ranaivoson,[2,3] Christopher C. Broder,[4] Andrew A. Cunningham,[5] Jean-Michel Héraud,[2] Alison J. Peel,[6] Louise Gibson,[5] James L. N. Wood,[7] C. Jessica Metcalf,[1,†] and Andrew P. Dobson[1,†]

Gwen Kettenburg, UChicago

Statistical question: How does age class of Malagasy fruit bats mediate viral load?

Hypothesis: Adult bats shed more virus than juvenile bats

Response variable: presence/absence of coronavirus, filovirus, lyssavirus, and/or henipavirus

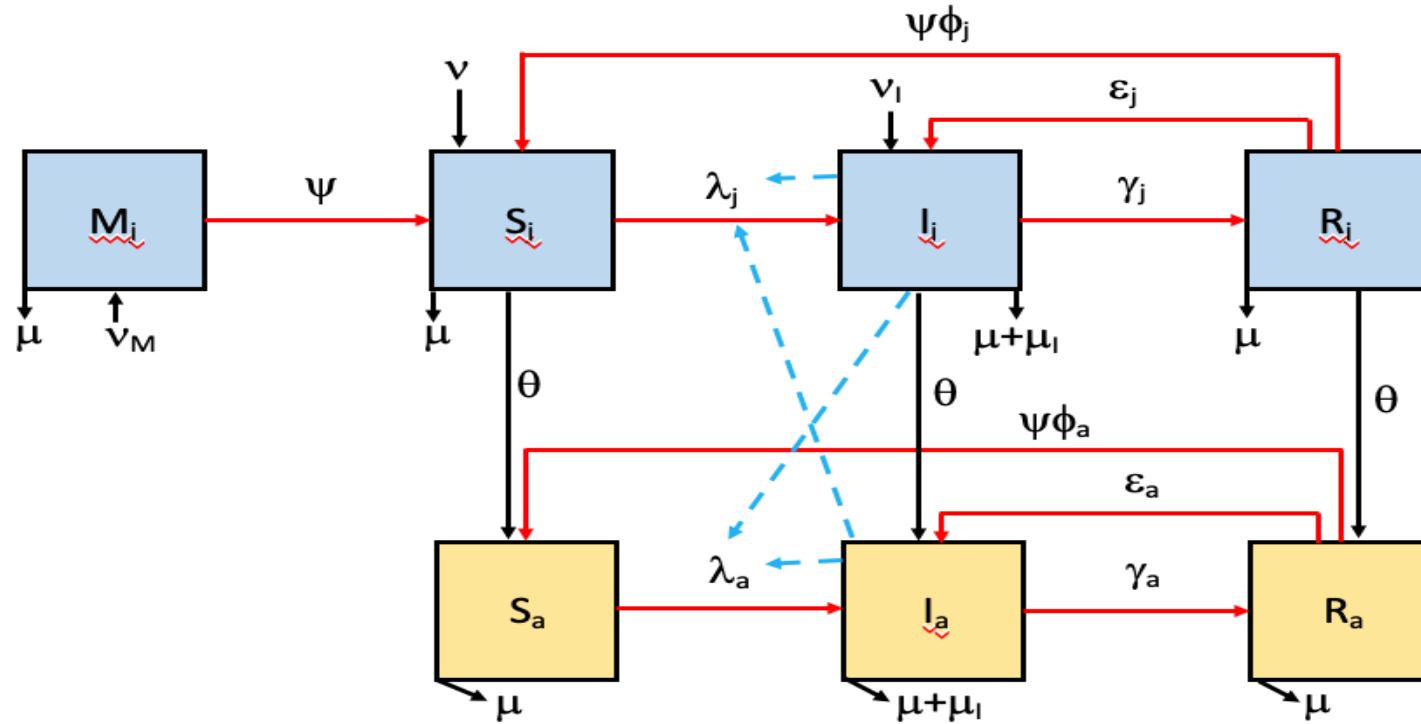**Predictor variable:** age, bat species, virus family

Distribution: "binomial"

Linker: logit

Species	Viral family	PCR pos/neg ratios	Age
E. dupreanum	Coronavirus	10/90 n=100	Each indiv. has an age associated with it
	Filovirus	0/100 n=100	Each indiv. has an age associated with it
	Lyssavirus	12/68 n=100	Each indiv. has an age associated with it
	Henipavirus	25/75 n=100	Each indiv. has an age associated with it
R. madagascariensis	Coronavirus	8/92 n=100	Each indiv. has an age associated with it
	Filovirus	2/98 n=100	Each indiv. has an age associated with it
	Lyssavirus	17/83 n=100	Each indiv. has an age associated with it
	Henipavirus	0/100 n=100	Each indiv. has an age associated with it
P. rufus	Coronavirus	9/91 n=100	Each indiv. has an age associated with it
	Filovirus	0/100 n=100	Each indiv. has an age associated with it
	Lyssavirus	10/90 n=100	Each indiv. has an age associated with it
	Henipavirus	0/100 n=100	Each indiv. has an age associated with it

R function: glmer(presence/absence virus~age+(1|bat/virus), family="binomial", data=mada.bat.age.virus.shedding
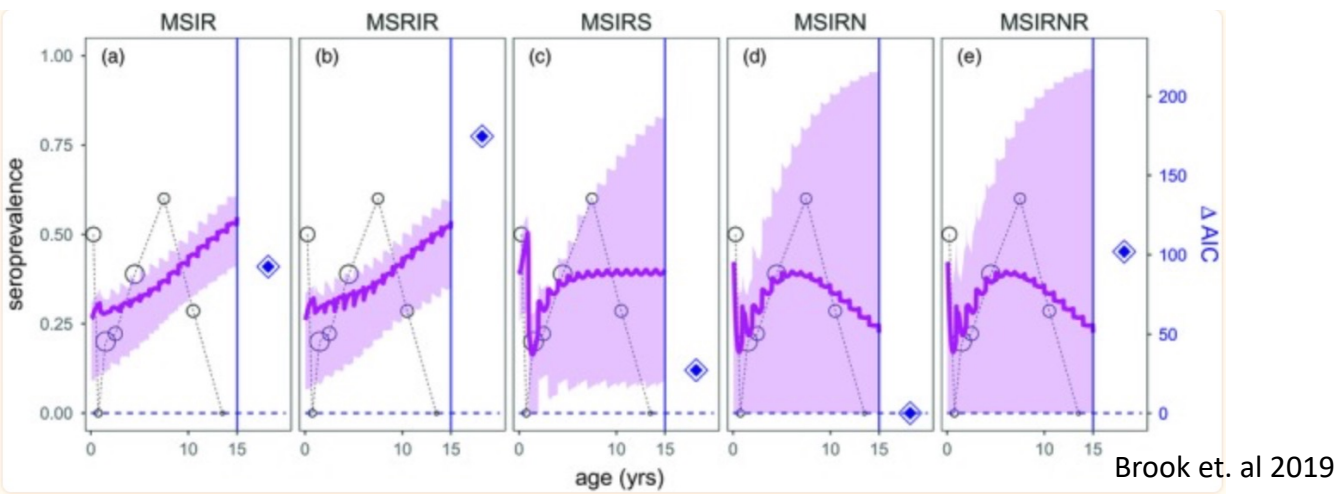
Nest virus family in bat fam as rndm effect for glmer

Mechanistic question: How does viral shedding differ between juvenile and adult Malagasy fruit bats?

Brook et. al 2019

Parameter	Description
M	Maternally immune
S	Susceptible
I	Infectious/infected
R	Recovered

Parameter	Description
ν	Births
ν_M	Births from maternally immune adults
ν_I	Births from infected/infectious adults
μ	Deaths
μ_I	Deaths from infection
λ_j	Virus transmission rate in juveniles
λ_a	Virus transmission rate in adults
	Recovery rate in juveniles
γ_a	Recovery rate in adults
ψ	Maternal antibody waning
N_j	Juvenile population size
N_a	Adult population size
ϕ_j	Antibody waning, susceptible again in juveniles
	Antibody waning, susceptible again in adults
ε_j	Persistently infected or latent in juveniles, infected->infectious or latent->infectious
ε_a	Persistently infected or latent in adults, infected->infectious or latent->infectious
θ	Aging rate from juvenile to adult

Next steps:

- Generate family level PCR data for coronaviruses, lyssaviruses, filoviruses, henipaviruses (presence/absence data)
- Use Sanger sequencing from positive hits to design specific virus primers
- Generate qPCR data for above viruses (quantitative data)
- Fit relevant mechanistic model to relevant age-qPCR data for each viral family.