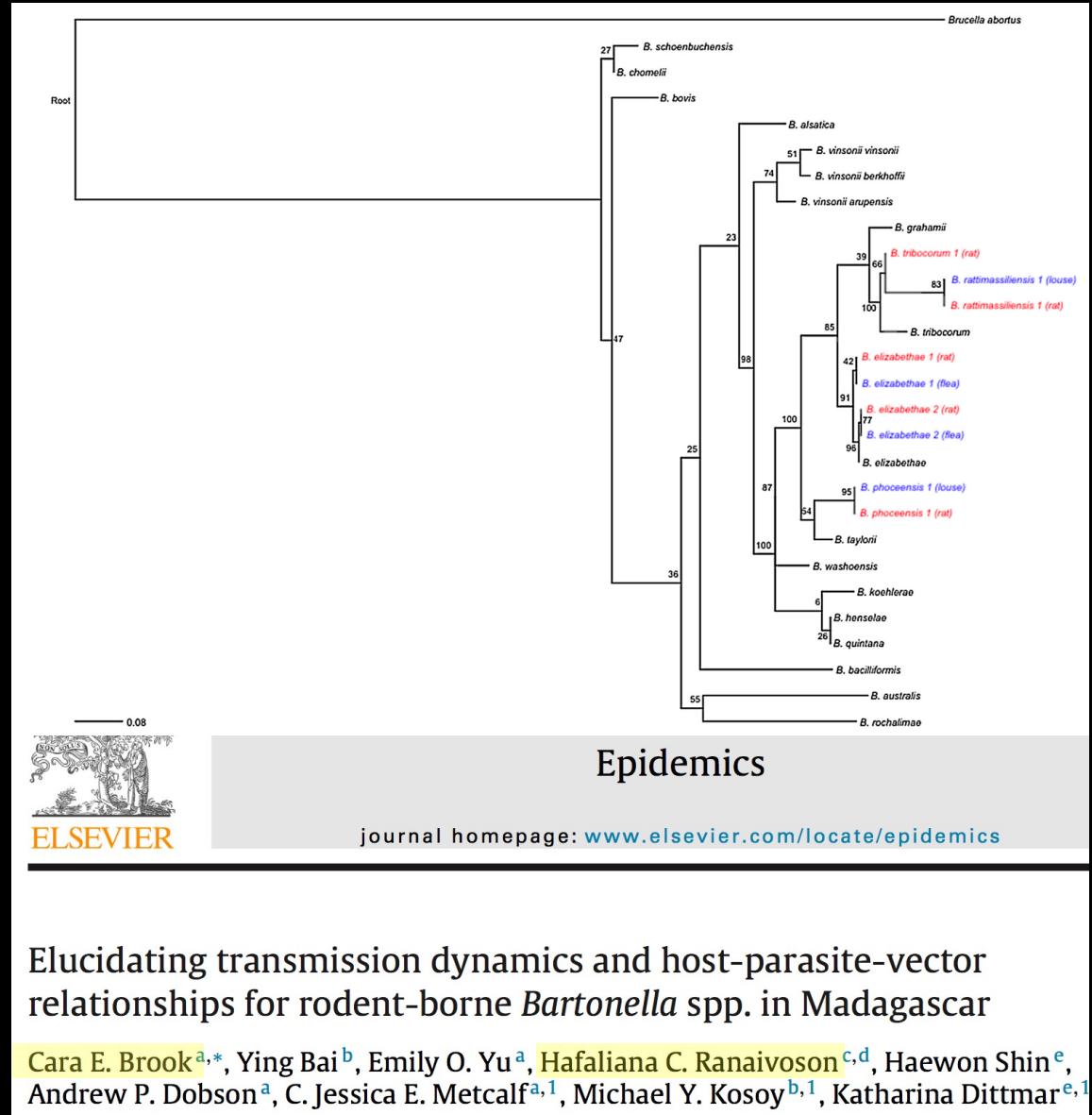


Transmission dynamics and host-parasite-vector relationships in rodent-borne *Bartonella* spp.

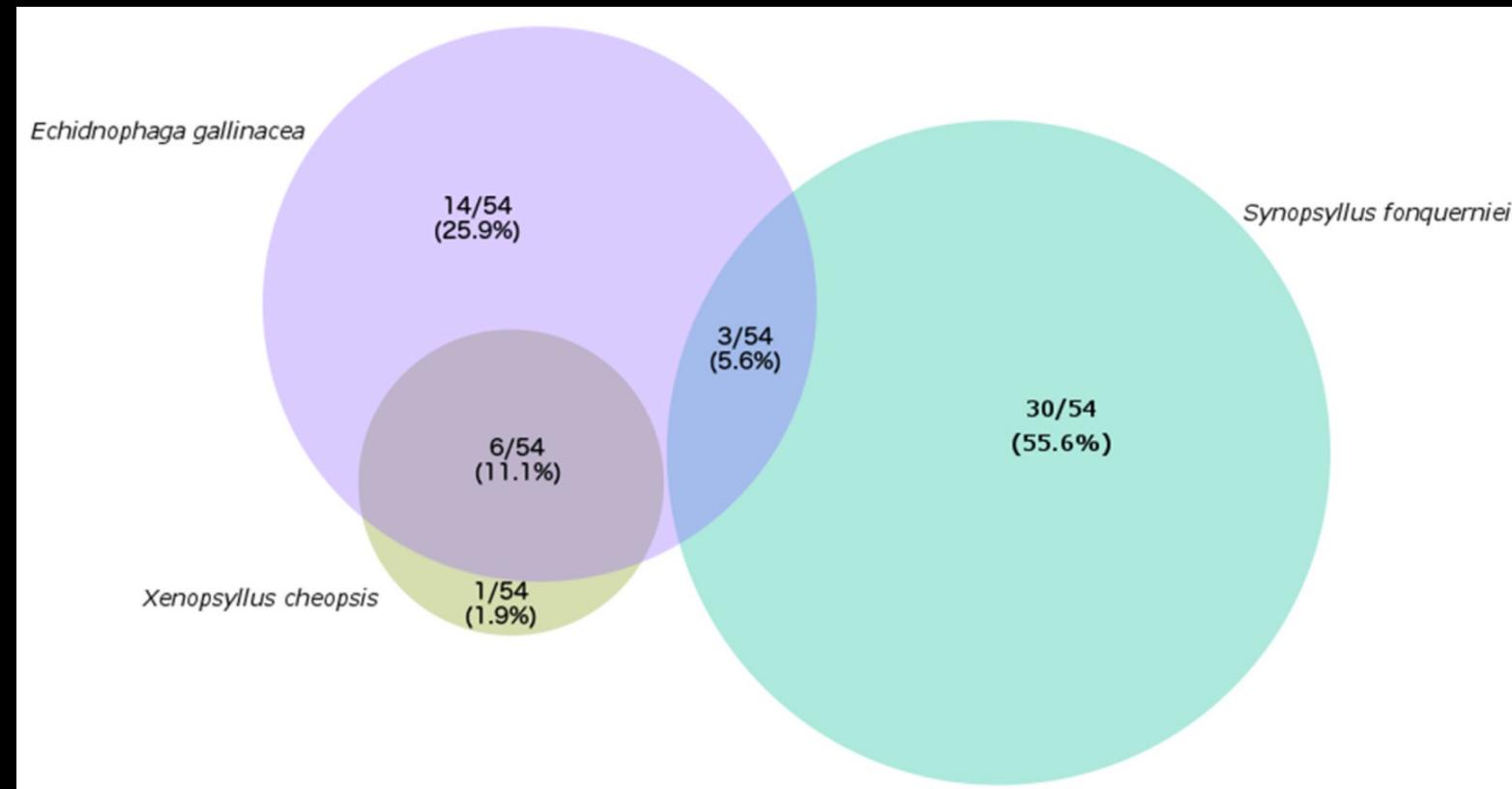
- **Background:** *Bartonella* spp. is an erythrocytic bacterial pathogen of Malagasy rodents with different genotypes which could demonstrate unique transmission mechanisms.
- **Statistical Question:** Is the occurrence of a given species of flea on Malagasy *R. rattus* related to (a) the rest of the ectoparasite community infesting the rat and/or (b) the locality in which the rat is trapped?
- **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)



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?

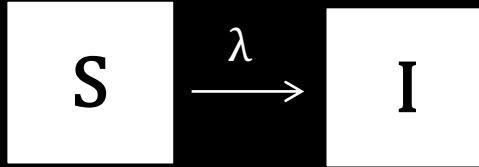
- **Response Variable:** pres/abs *S. fonquerniei*
- **Predictor Variables:** abundance of *E. gallinacea* (numeric); abundance of *X. cheopsis* (factor); indoor/outdoor locality (factor)
- **Family:** “binomial”
- **Link:** logit
- **Hypothesis:** *S. fonquerniei* occurrence is related to low abundance of *X. cheopsis* & outdoor status locality
- **R code:**



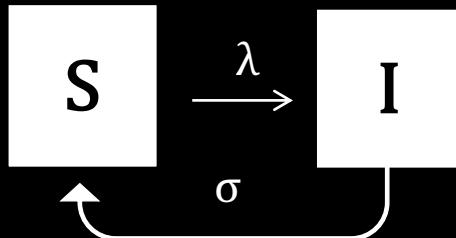
```
glm(pres/abs S. fonquerniei ~ abundance X. cheopsis + abundance E. gallinacea + indoor_outdoor, family="binomial", data = madarat)
```

Mechanistic Question:

How can we explain the prevalence of different serotypes of *Bartonella* spp. by age class in Malagasy *Rattus rattus*?



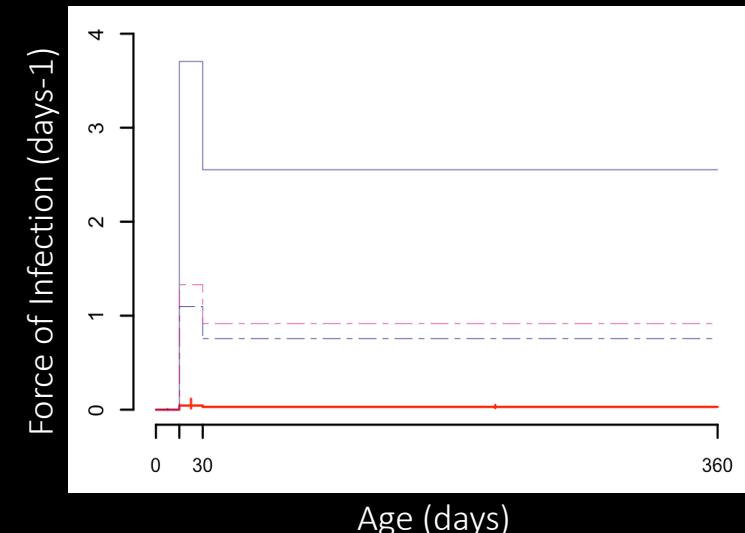
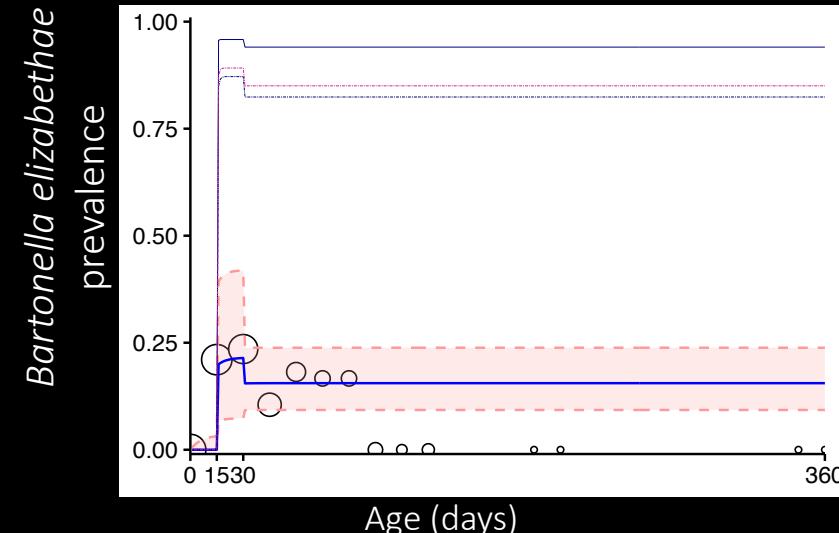
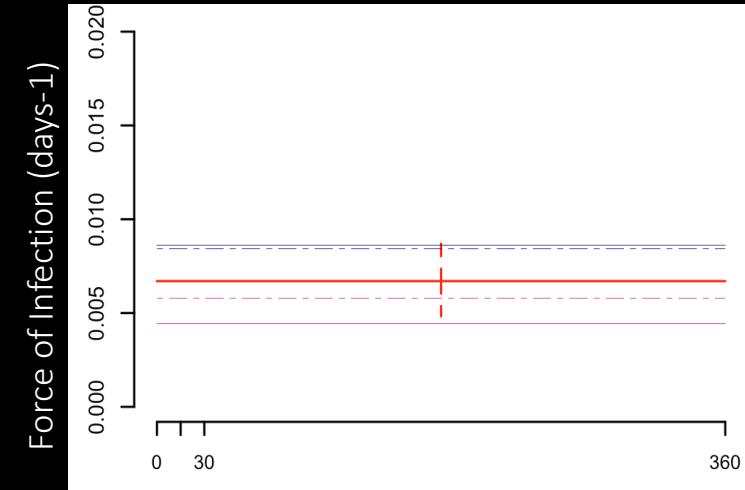
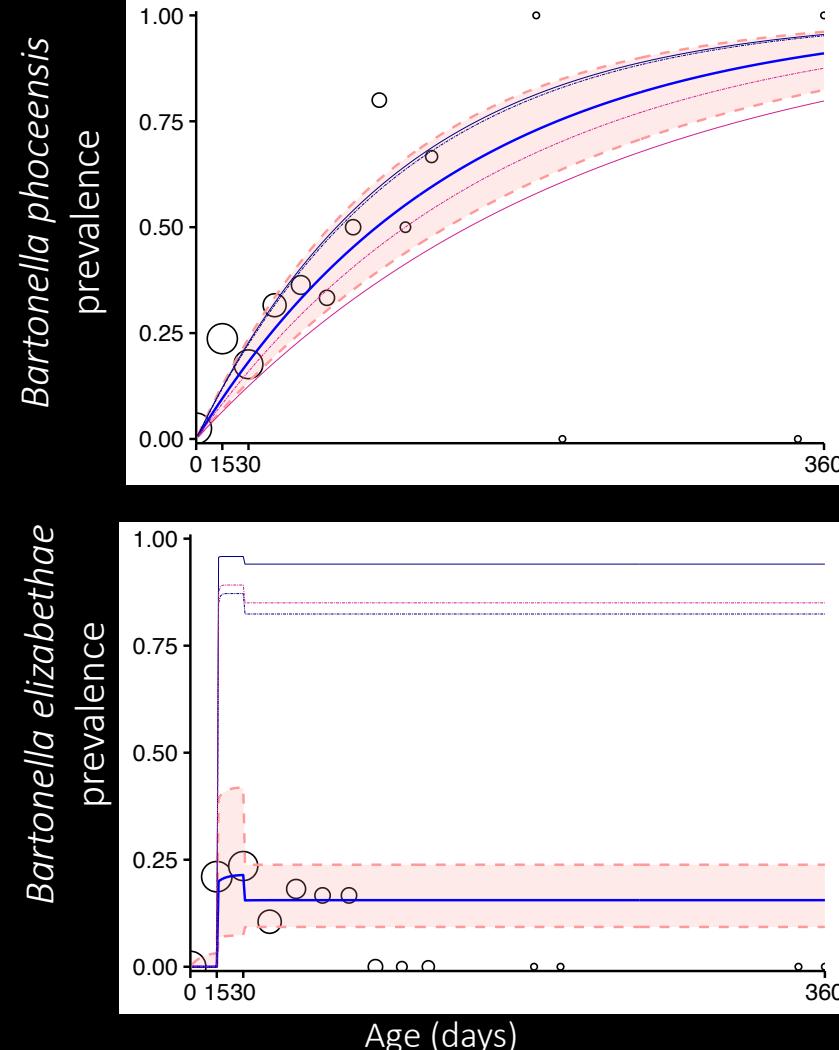
$$\frac{dI(a)}{da} = \lambda(a)(1 - I(a))$$



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

S = susceptible rats
I = infectious rats

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



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. fonquernei*
2. Conduct more thorough sampling of *R. rattus* ectoparasite community to augment data suggesting that *Polyplax* sp. lice may serve as a vector for *B. phoceensis*
3. Conduct serological tests on *R. rattus* blood to attempt to identify whether *Bartonella* spp. negative rats are recovered or susceptible.
4. Fit relevant mechanistic transmission models to age-seroprevalence data.

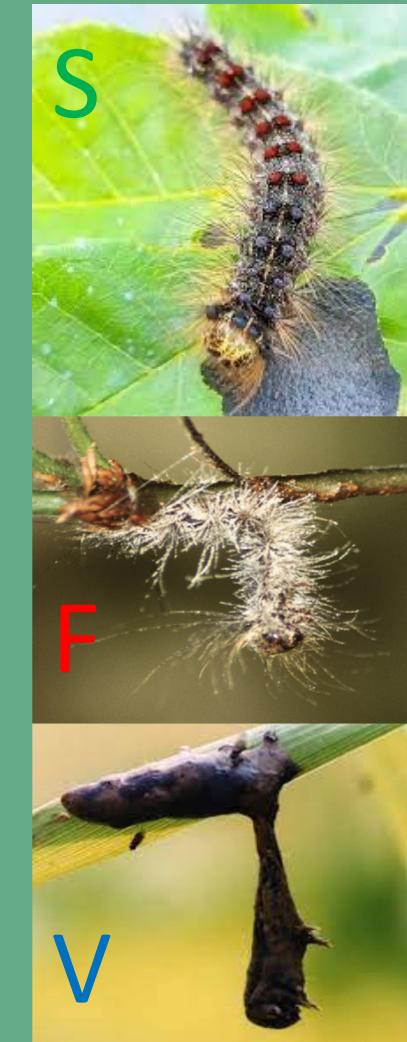
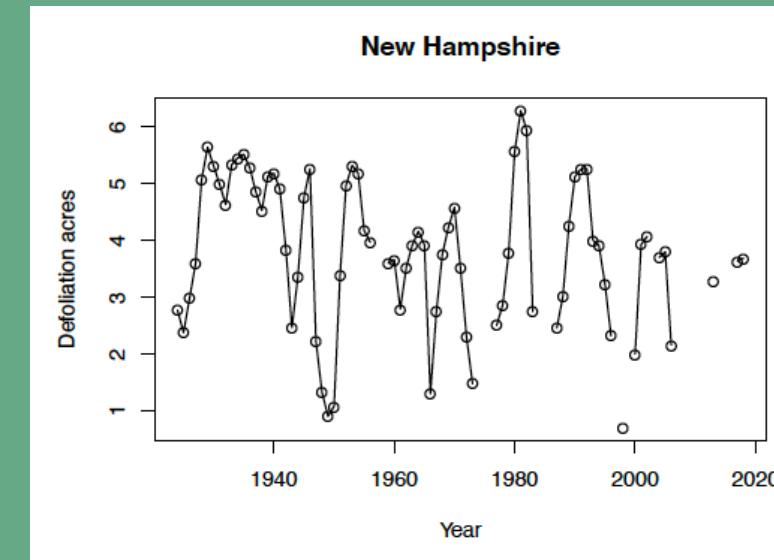


Investigating coinfections in the spongy moth-fungus-virus system

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?



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

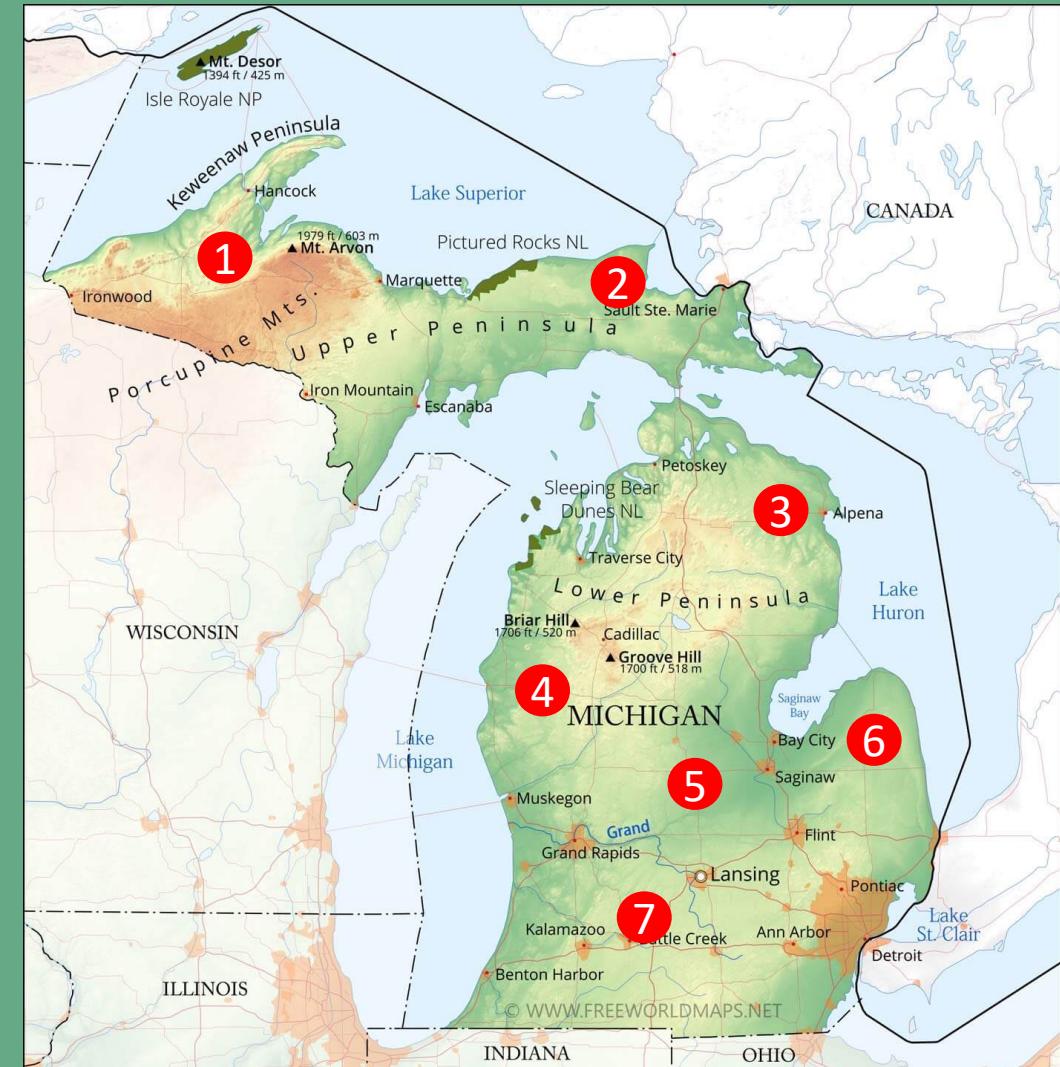
Family: "poisson"

Link: log

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

R code:

```
glm(cum. # coinfections~rainfall + temperature + relative  
humidity + (1| site), family = "poisson", data=infection.data)
```



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

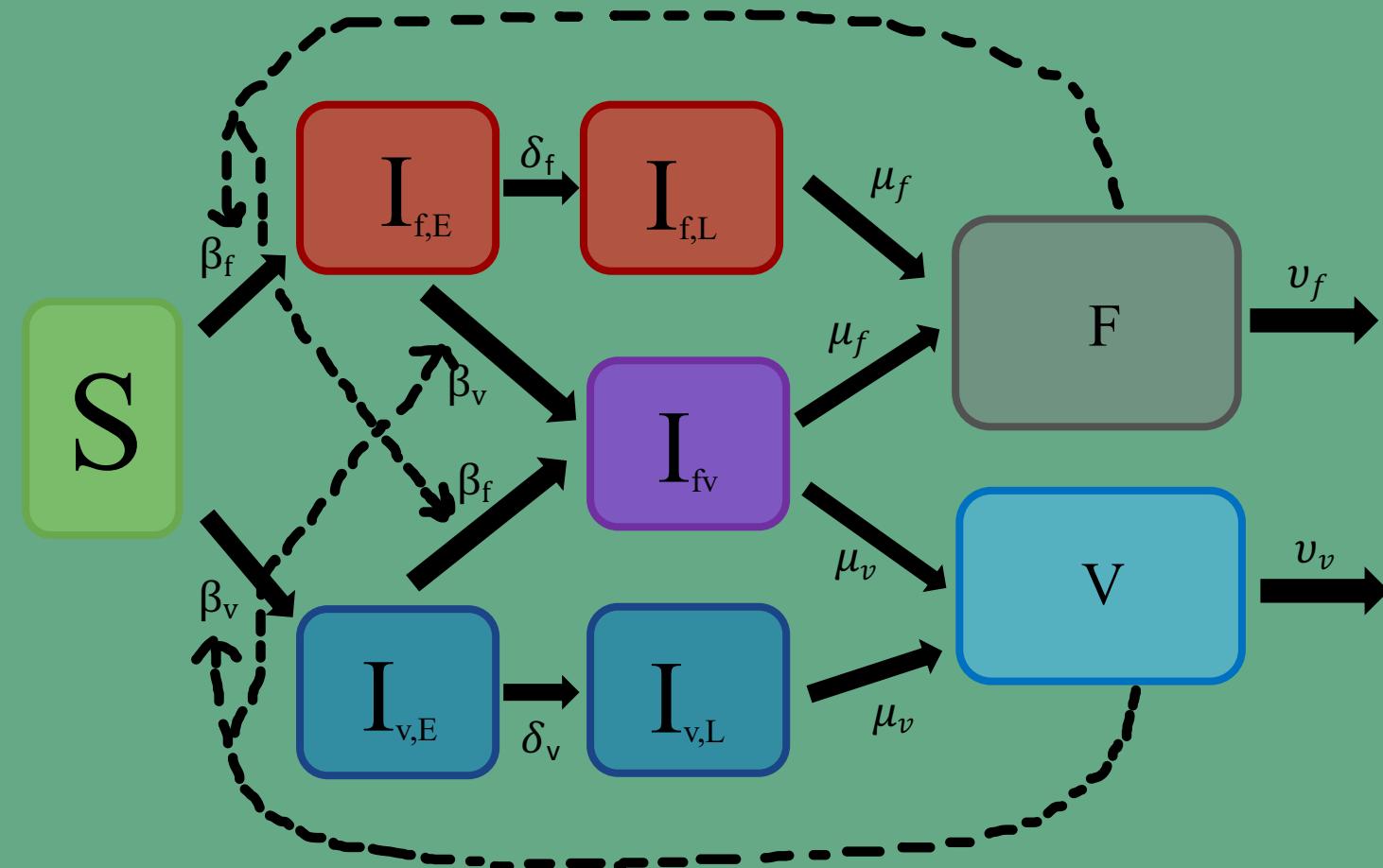
δ_v – progression to late virus infection

μ_v – conversion of dead insect to virus particles

μ_f – conversion of dead insect to fungal spores

v_f – fungal spore decay

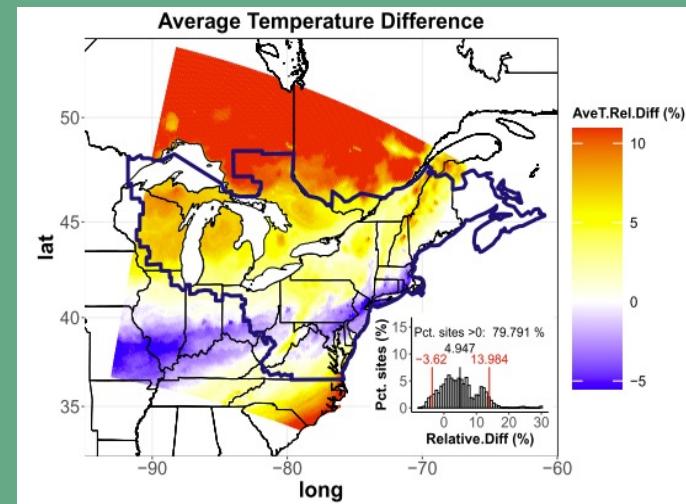
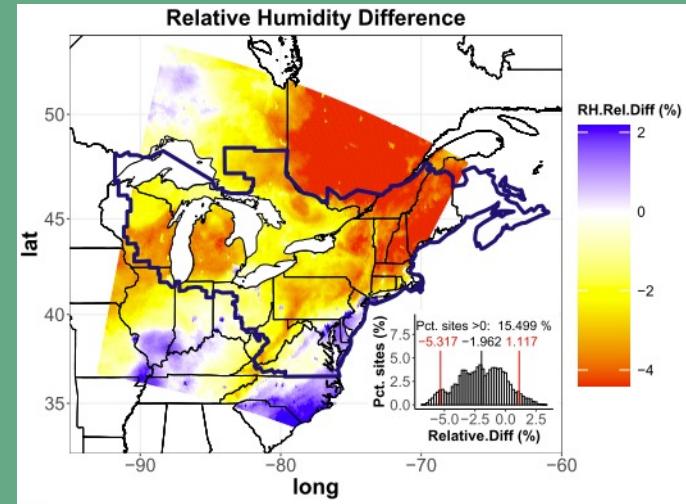
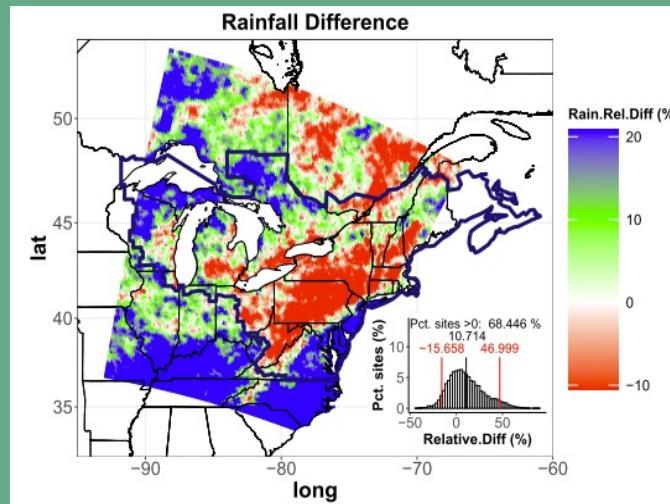
v_v – viral particle decay



Investigating coinfections in the spongy moth-fungus-virus system

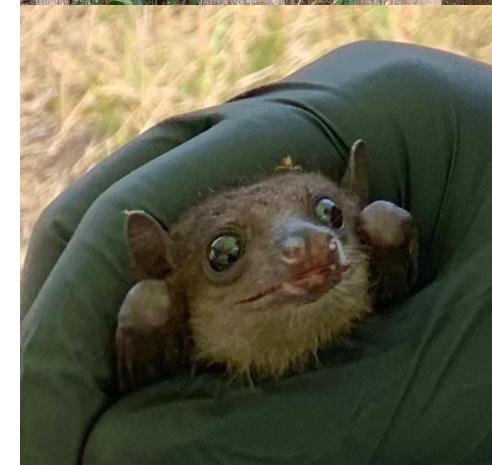
Next Steps:

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 both the field and experimental 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.



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: DAIDD 2021 (mechanistic model), Cara Brook, Sophia Horigan (statistical model)

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, †}

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”

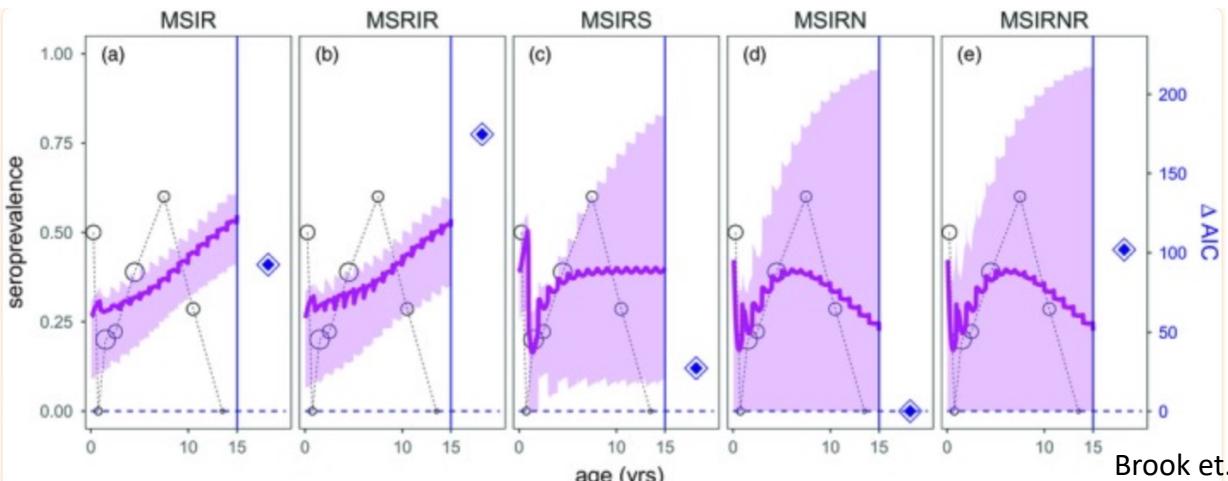
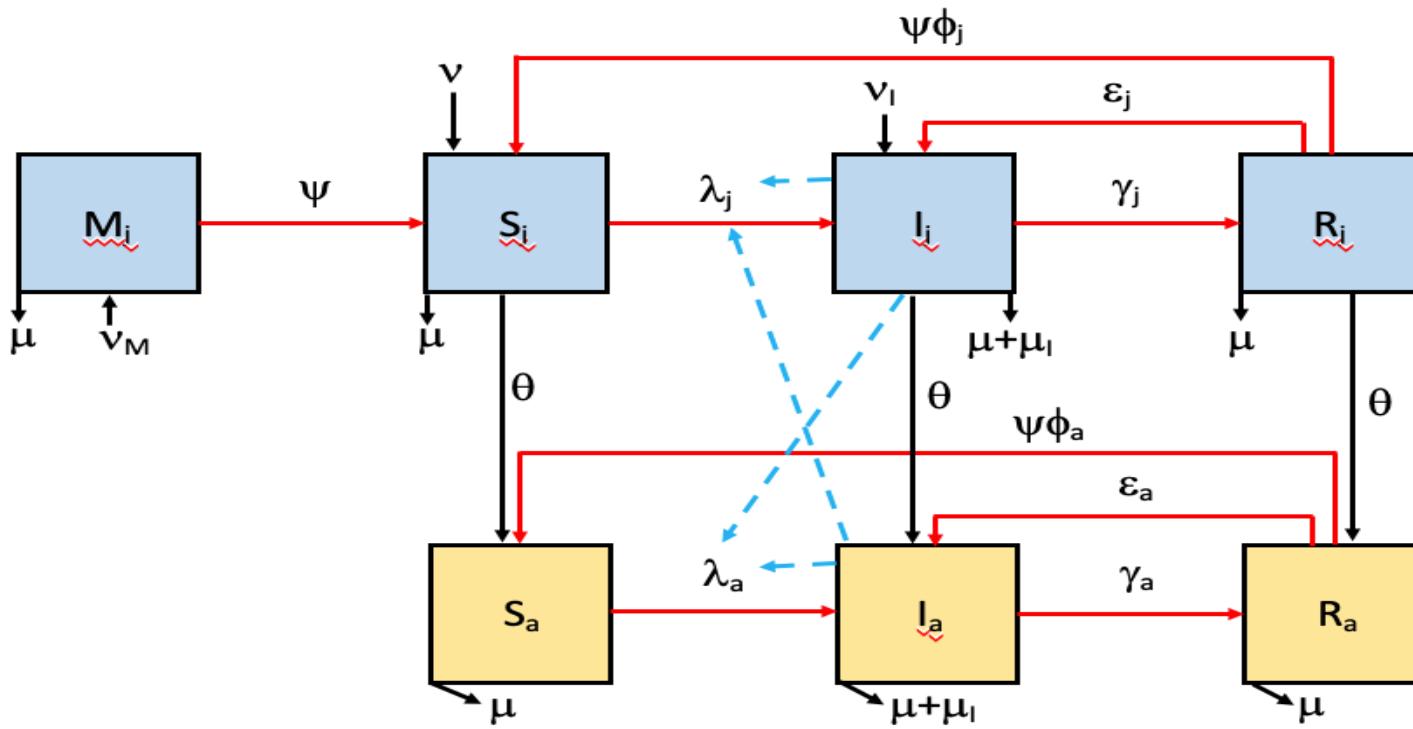
Linker: logit

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

Species	Viral family	PCR pos/neg ratios	Age
<i>E. dupreanum</i>	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
<i>R. madagascariensis</i>	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
<i>P. rufus</i>	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

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
v	Births
v_M	Births from maternally immune adults
v_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
γ_j	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
ϕ_a	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.

