Model Fitting and Comparison

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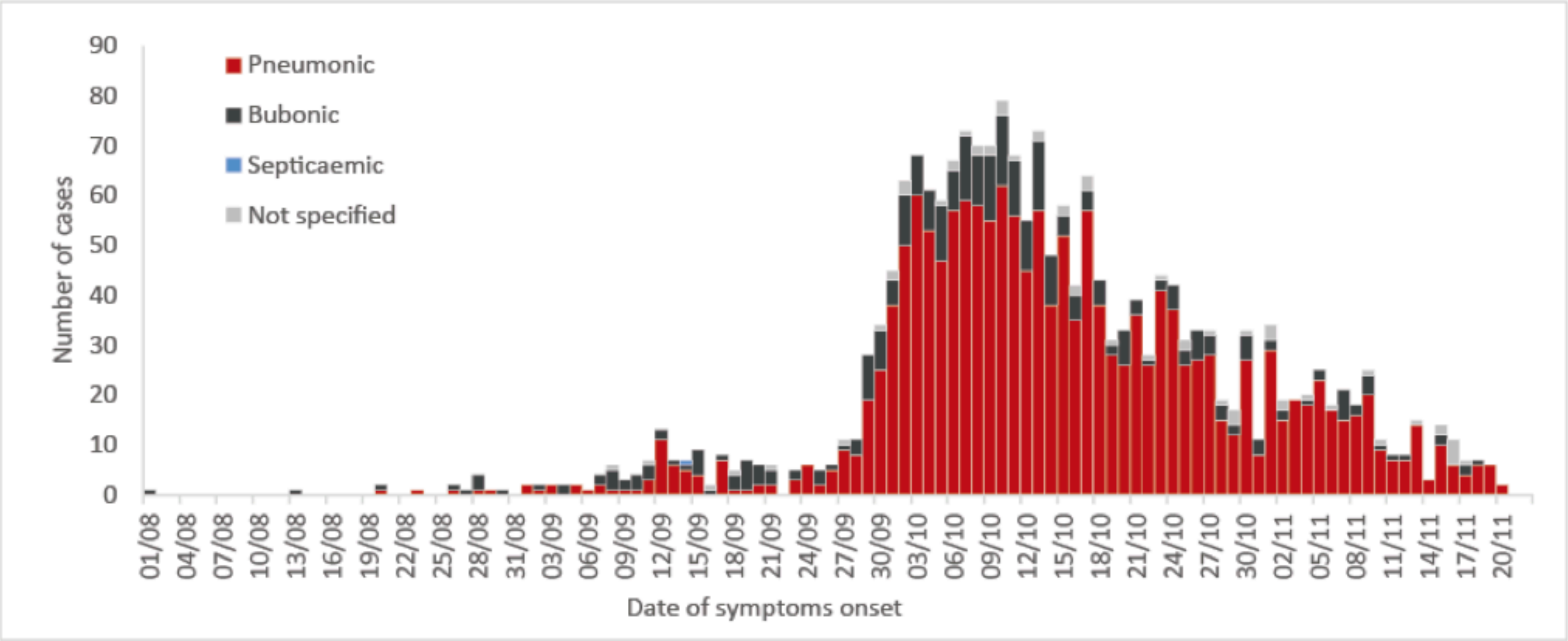
E2M2 2020

Ranomafana, Madagascar

Which model is best?



http://www.who.int/csr/don/27-november-2017-plague-madagascar/en/

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Least squares

Log likelihood

AIC

(uses least squares or log-likelihood but penalizes by number of fitted parameters)

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Log likelihood

AIC

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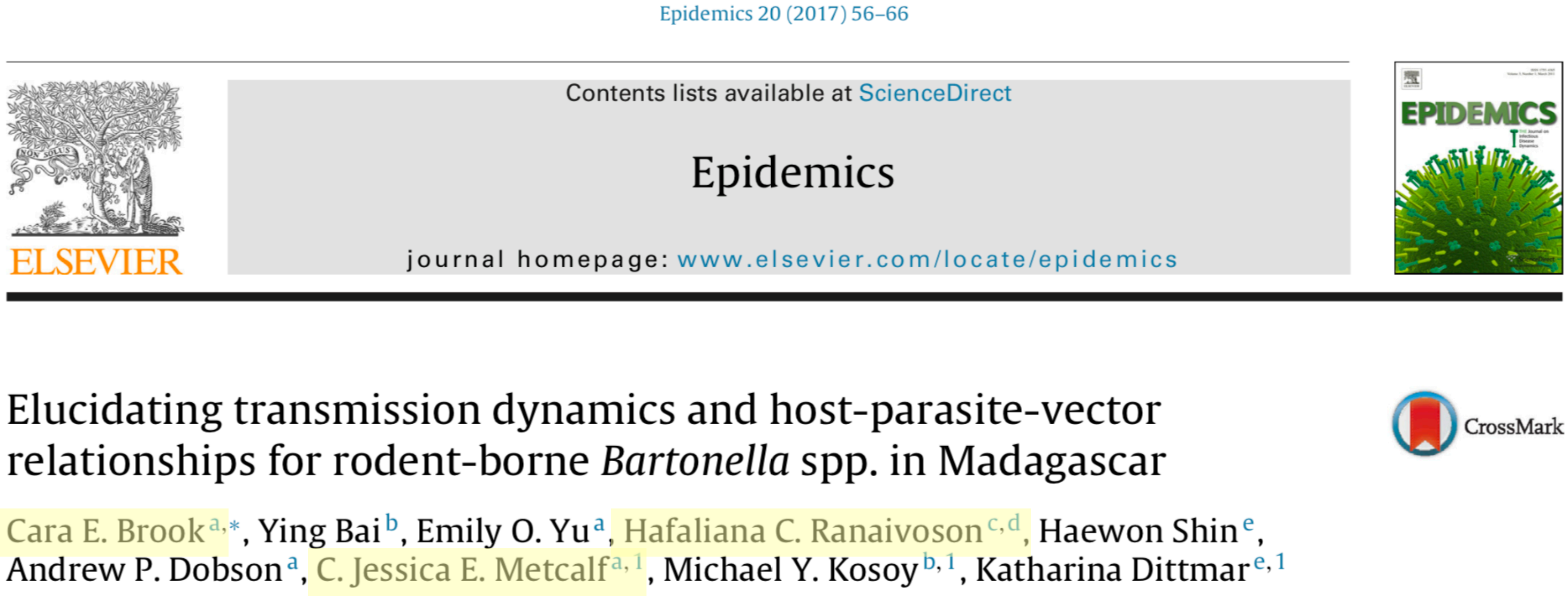
The R function ‘optim’ can be used to minimize these measures of model difference from the data.

An example of model selection: *Bartonella spp.* in Madagascar rats



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ELSEVIER

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

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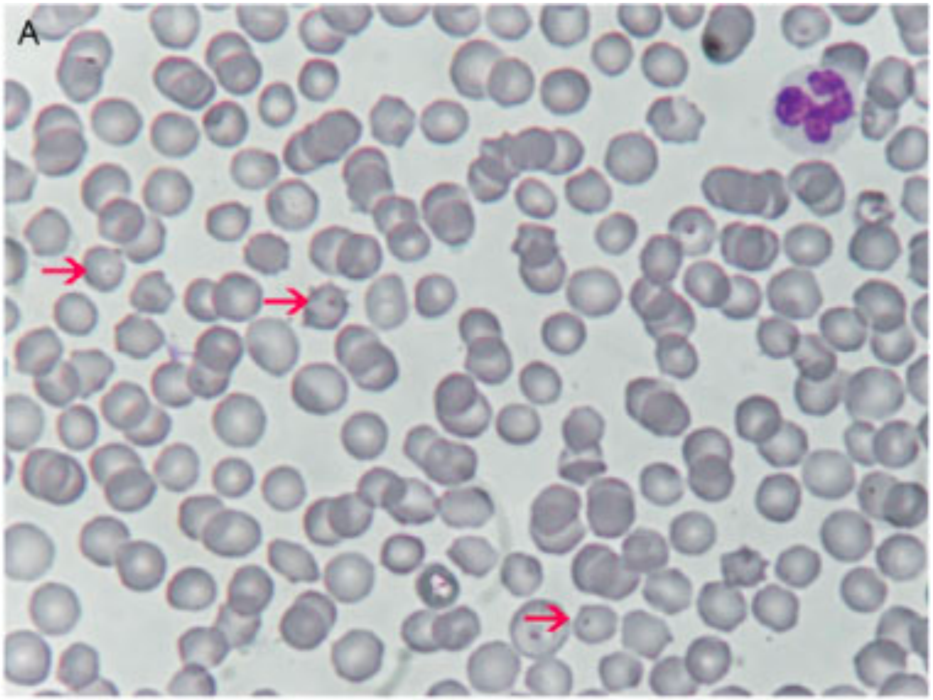
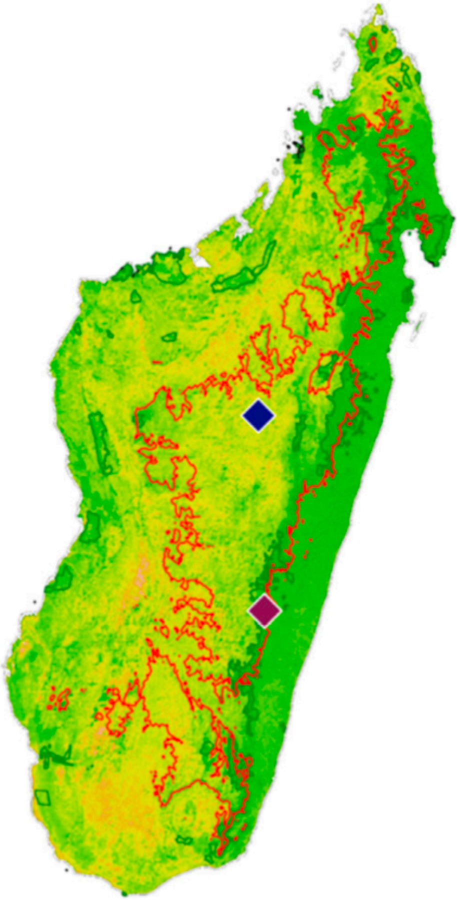
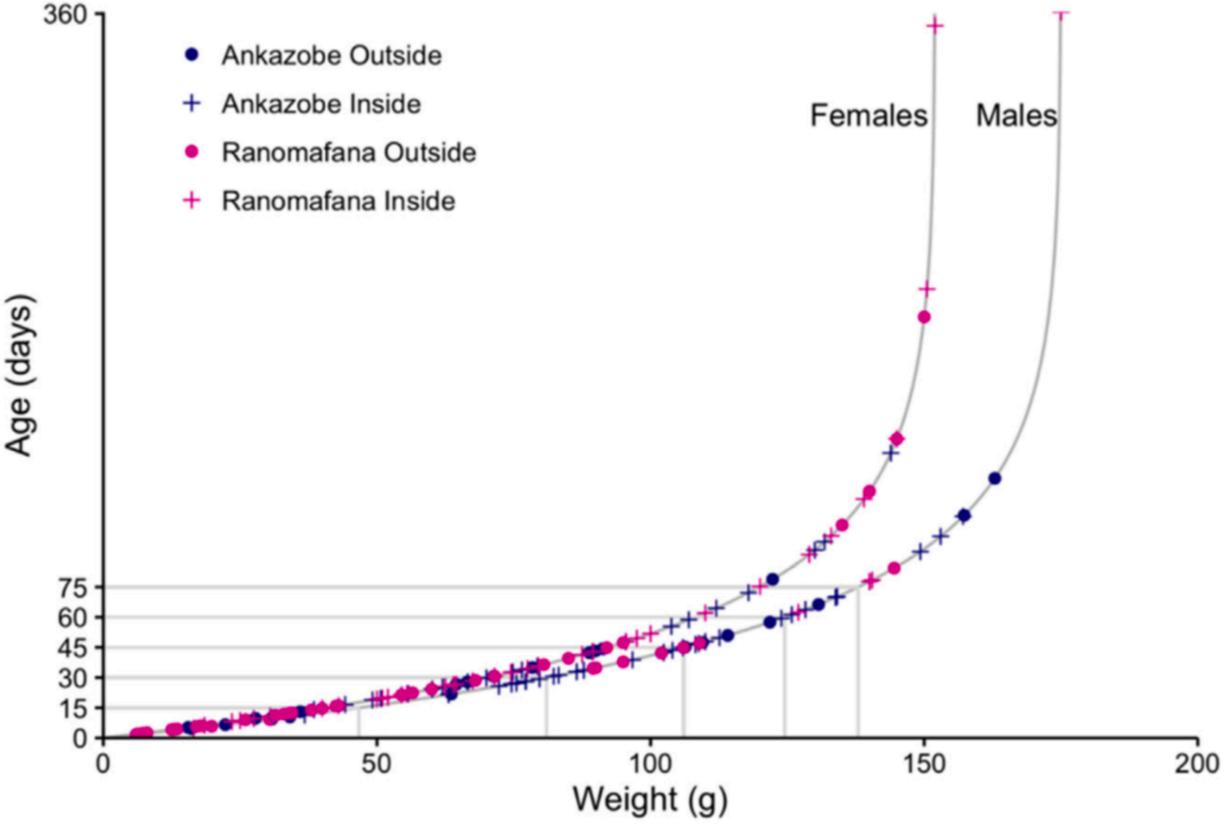
Bartonella spp.

- persistent erythrocyctic bacteria that are sometimes zoonotic
- vectored by ticks, fleas, sand flies, mosquitoes
- at least 8 human-infecting species
  - *Bartonella bacilliformis* = Carrion’s disease
  - *Bartonella henselae* = cat scratch fever
  - *Bartonella quintana* = trench fever

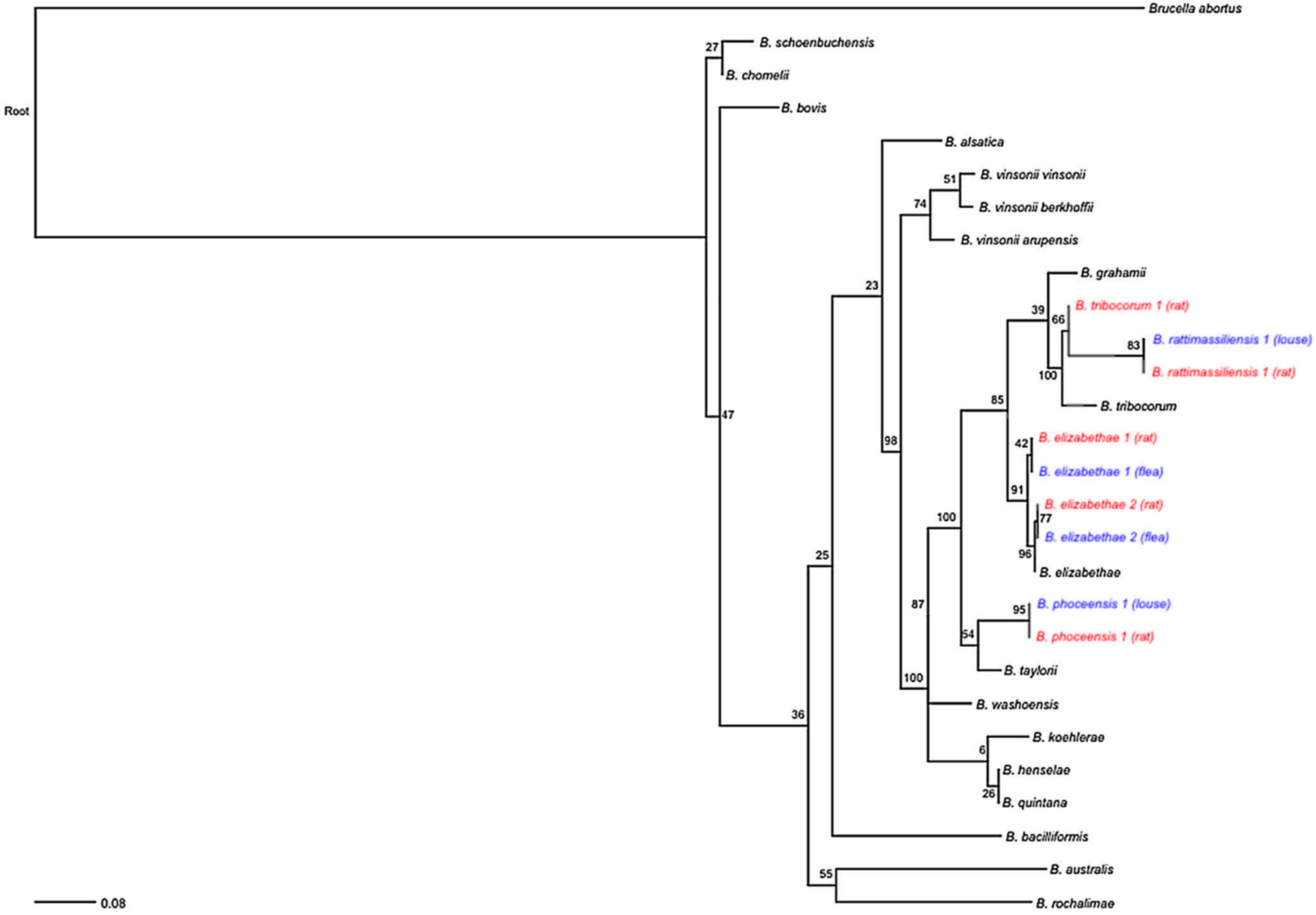


We first collected samples from rats in two sites Madagascar.





Statistically, we demonstrated an association between genotypes of *Bartonella* spp. found in rats and their ectoparasites.



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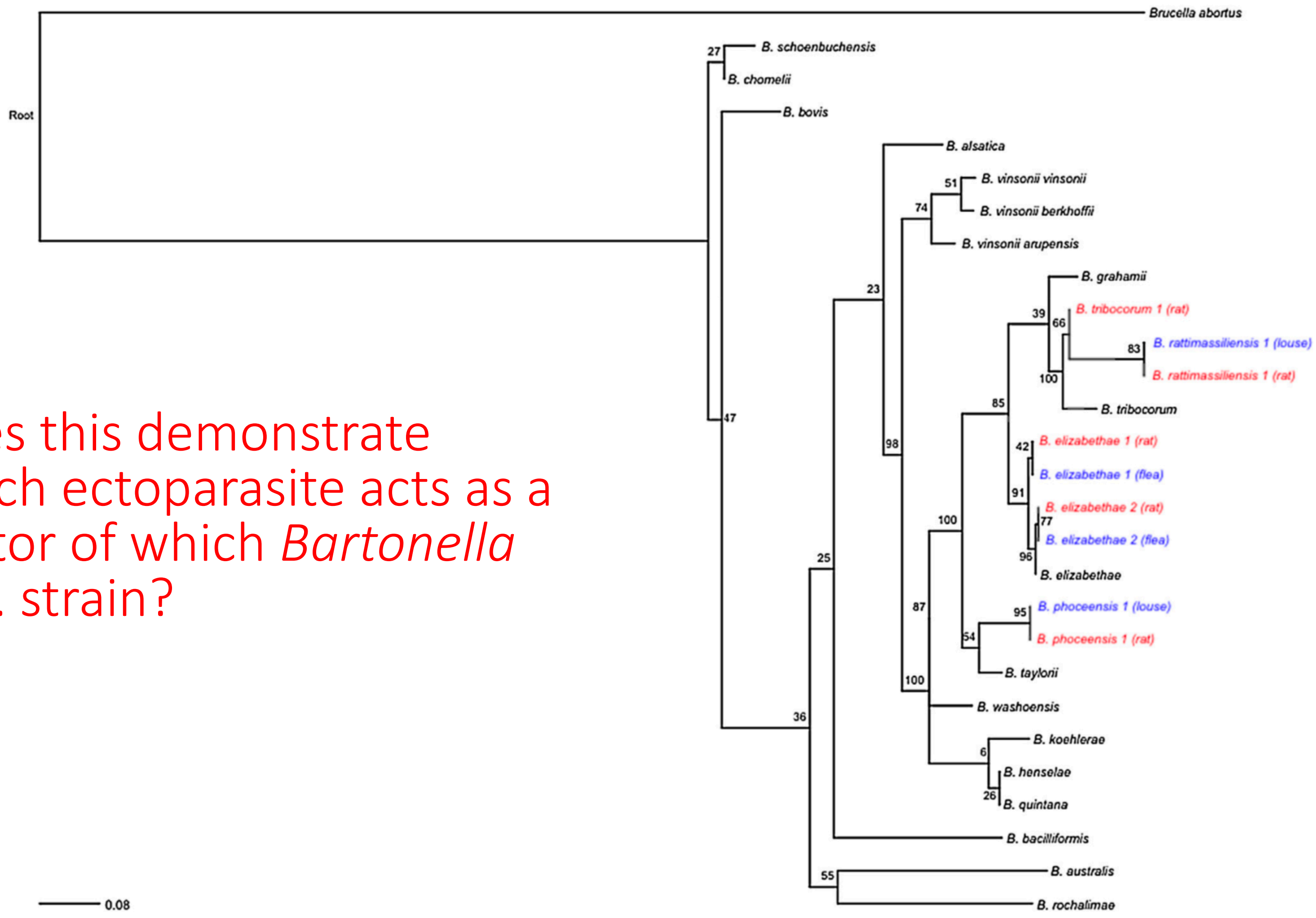
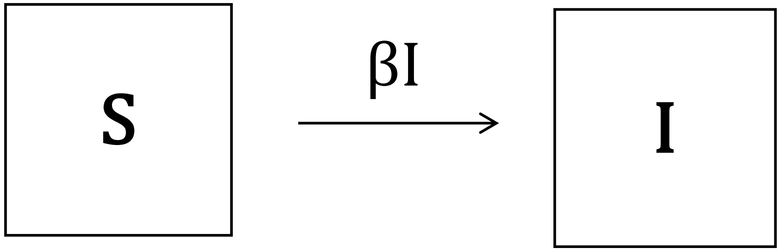


Does this demonstrate which ectoparasite acts as a vector of which *Bartonella* spp. strain?

Then, we asked: *How does the rate of becoming infected vary with age?*

Age-prevalence data allows for powerful inference into the dynamics of pathogen transmission.



for a persistent, non-immunizing infection

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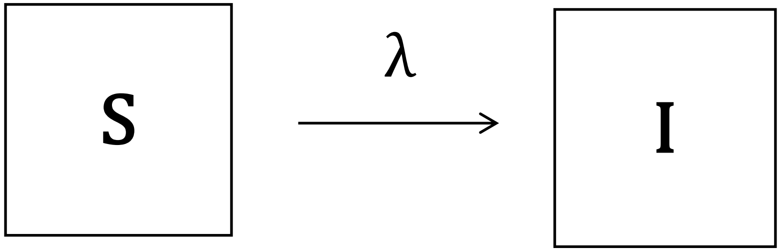
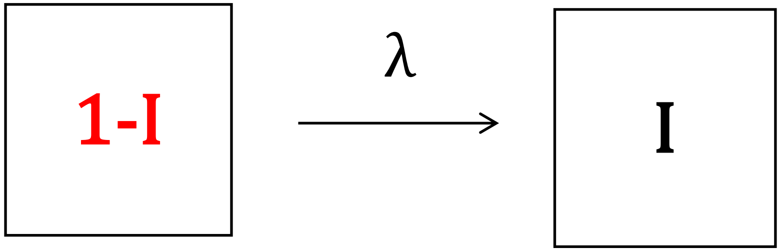


$$S \xrightarrow{\lambda} I$$

where λ, the force of infection, is the per capita rate at which susceptible hosts become infected

Age-prevalence data allows for powerful inference into the dynamics of pathogen transmission.

with a persistent infection, we can assume that, if not infected, you must be susceptible….



$$1-I \xrightarrow{\lambda} I$$

where λ, the force of infection, is the per capita rate at which susceptible hosts become infected

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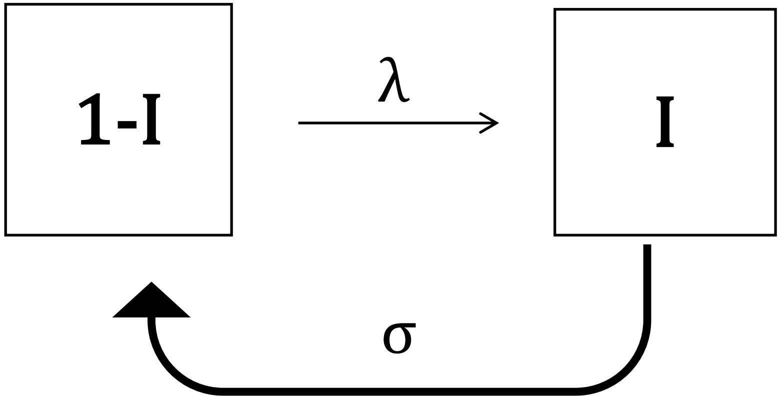

and σ is the rate of recovery from infection

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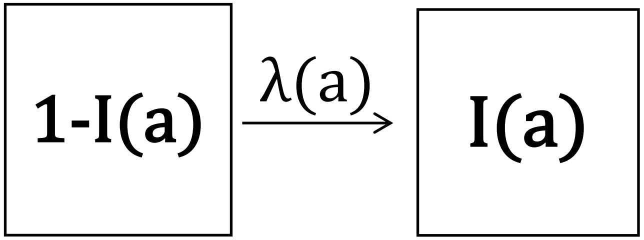
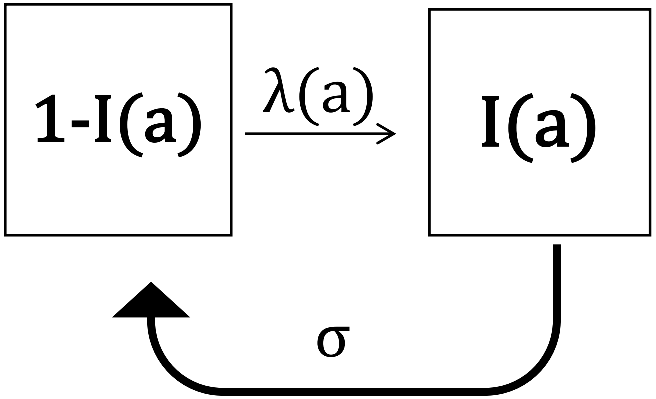
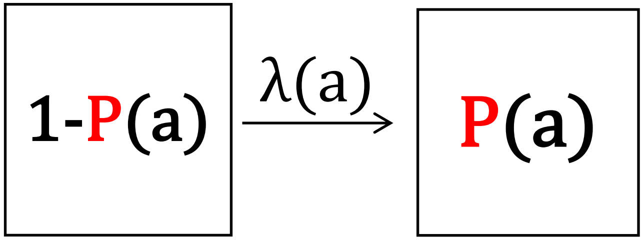


$$\frac{dI(a)}{da} = \lambda(a)\left(1 - I(a)\right)$$



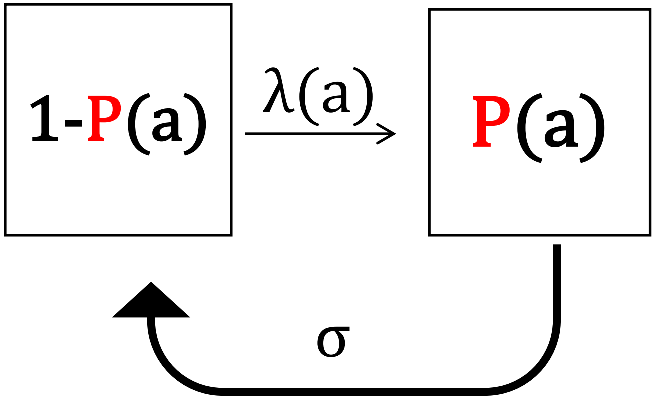
$$\frac{dI(a)}{da} = \lambda(a)\left(1 - I(a)\right) - \sigma I(a)$$

Age-prevalence data allows for powerful inference into the dynamics of pathogen transmission.



$1-P(a)$ $\xrightarrow{\lambda(a)}$ $P(a)$

$$\frac{d\,P(a)}{da} = \lambda(a)\,(1 - P(a))$$



$1-P(a)$ $\xrightarrow{\lambda(a)}$ $P(a)$

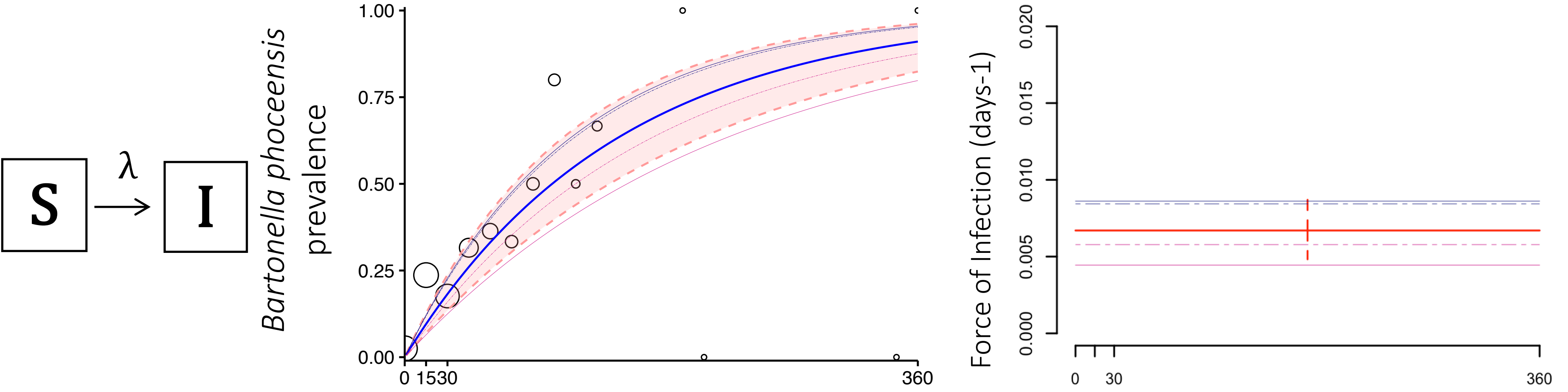
σ

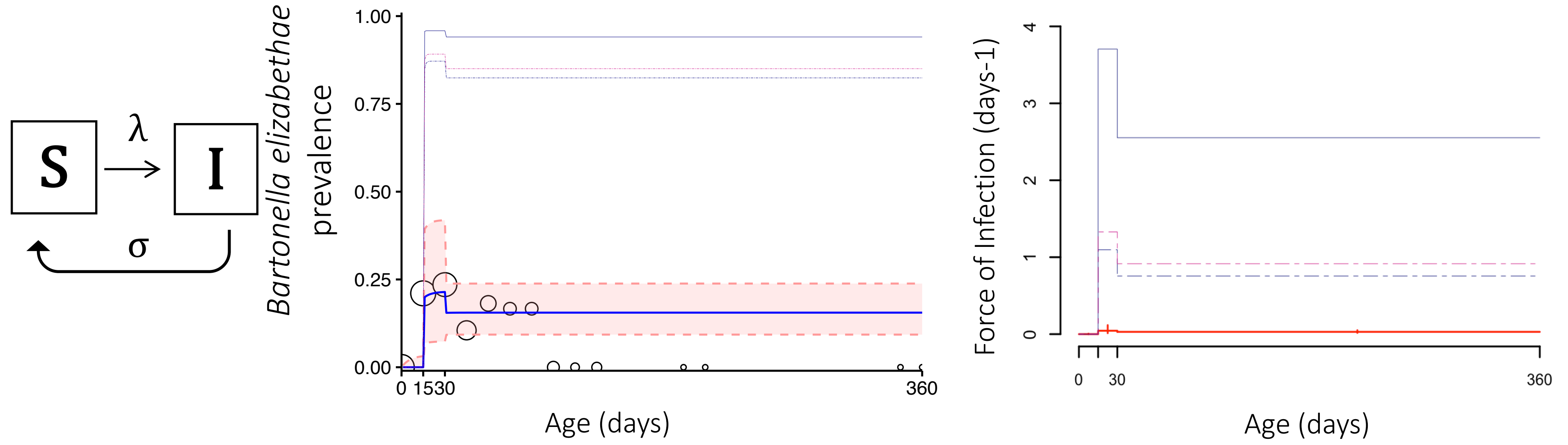
$$\frac{d\,P(a)}{da} = \lambda(a)\,(1 - P(a)) - \sigma(a)P(a))$$

similar techniques can also be applied to age-seroprevalence data for immunizing infections

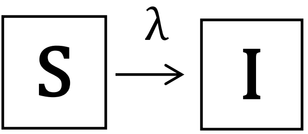
Let’s see which model works best for your data!

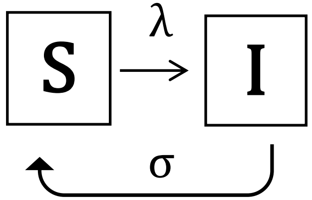
We found that an SI model offered the best fit to *B. phoceensis* data while the SIS model offered the best fit to the *B. elizabethae* data.

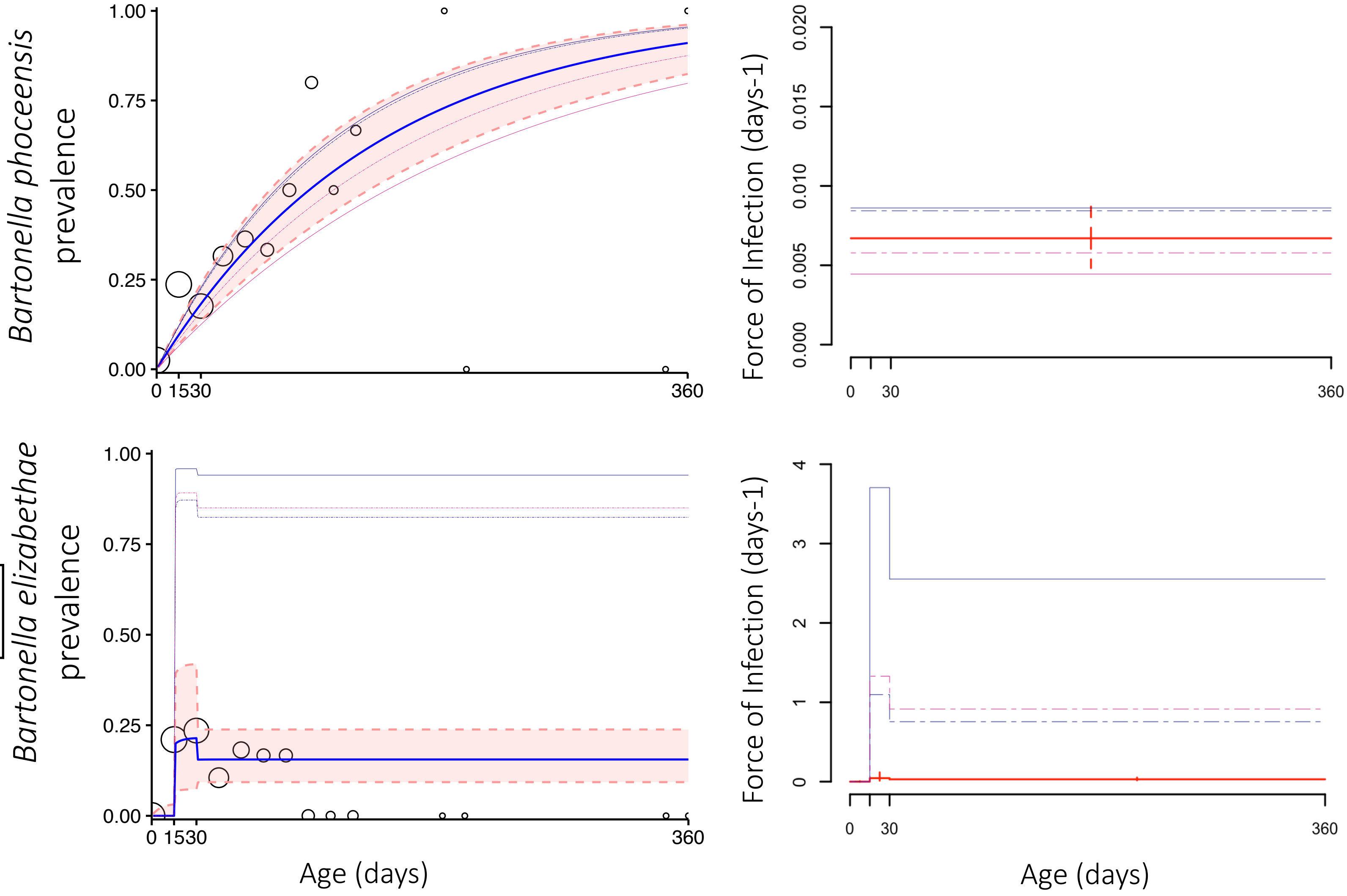


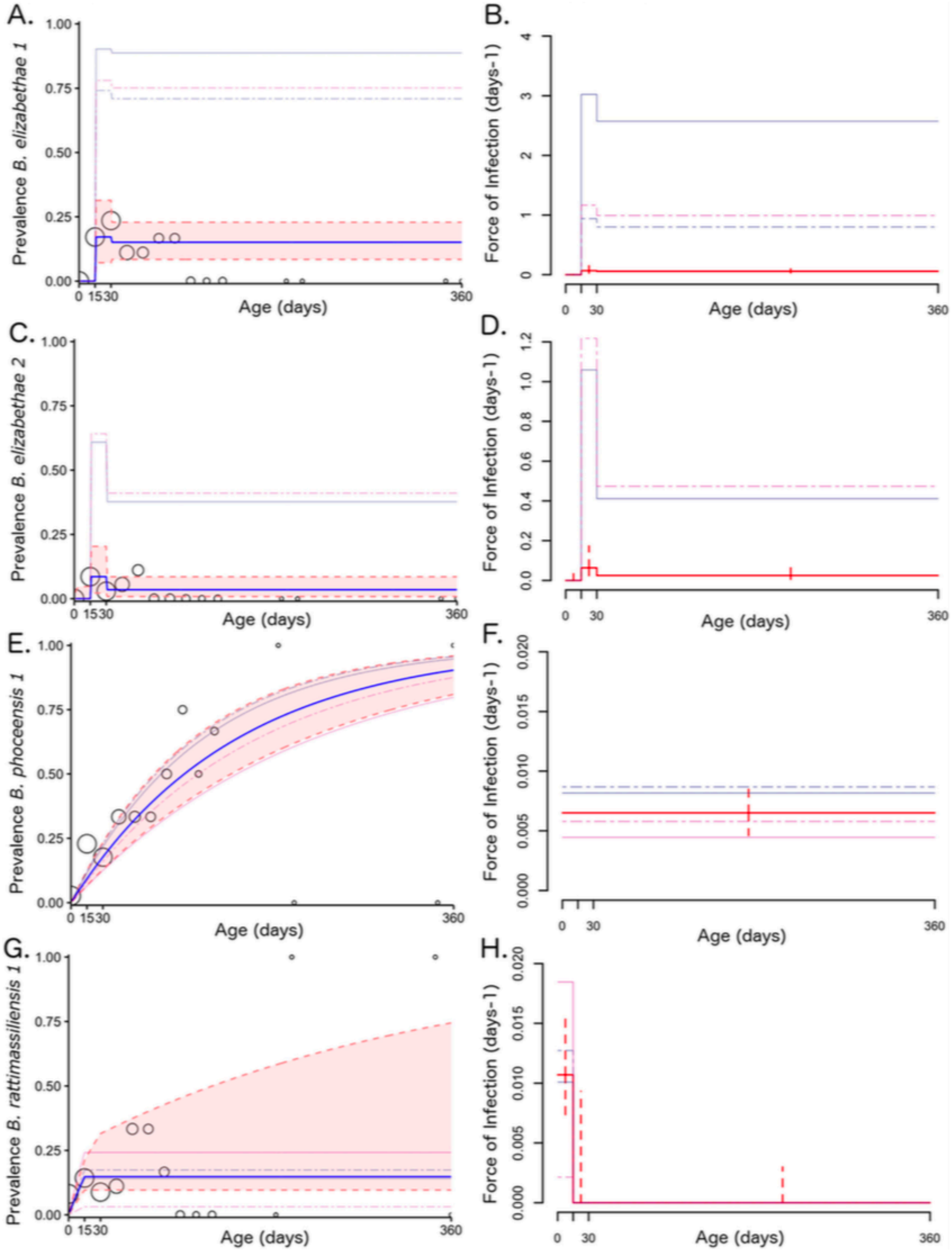


The age-structured FOI identifies age cohorts most influential in an epidemic. Juveniles showed the highest FOI.








A.
Prevalence B. elizabethae 1
1.00
0.75
0.50
0.25
0.00
0 1530
360
Age (days)
B.
Force of Infection (days-1)
4
3
2
1
0
0 30 360
Age (days)
C.
Prevalence B. elizabethae 2
1.00
0.75
0.50
0.25
0.00
0 1530
360
Age (days)
D.
Force of Infection (days-1)
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0 30 360
Age (days)
E.
Prevalence B. phoceensis 1
1.00
0.75
0.50
0.25
0.00
0 1530
360
Age (days)
F.
Force of Infection (days-1)
0.020
0.015
0.010
0.005
0.000
0 30 360
Age (days)
G.
Prevalence B. rattimassiliensis 1
1.00
0.75
0.50
0.25
0.00
0 1530
360
Age (days)
H.
Force of Infection (days-1)
0.020
0.015
0.010
0.005
0.000
0 30 360
Age (days)