



Padova MEETING

20-21 May 2026

Modelling Pathogen Transmission in Wildlife: From Ecological Complexity to Mitigation Strategies

Pierre Nouvellet (University of Sussex - UoS)

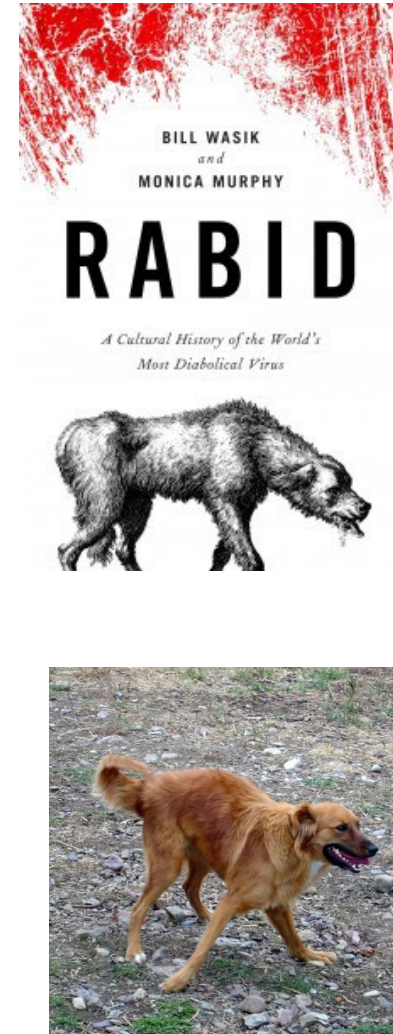


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Overview

- **Wildlife** play a **critical role** in the emergence, maintenance, and spread of infectious diseases
- But, **Ecological complexity** poses major **challenges** for epidemiological analysis.
- **Quantitative modelling can help understand pathogen transmission** processes in wildlife systems and guide **effective mitigation strategies**.
- **Through case studies**, present work integrating **ecological data, and surveillance records** to estimate key transmission parameters and identify **drivers of pathogen** persistence.



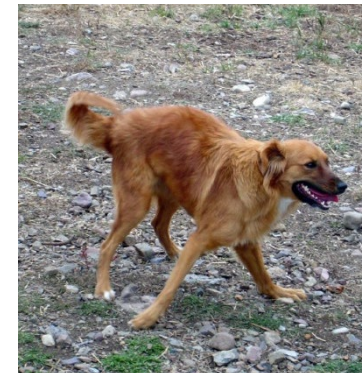
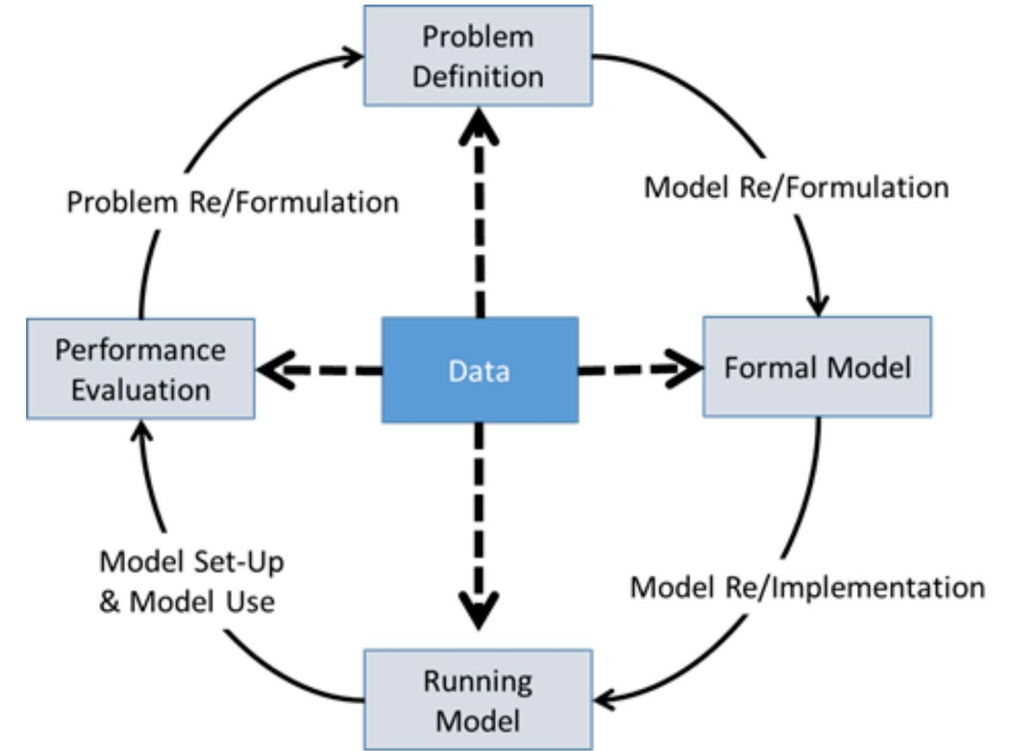
Overview

Why mathematical models:

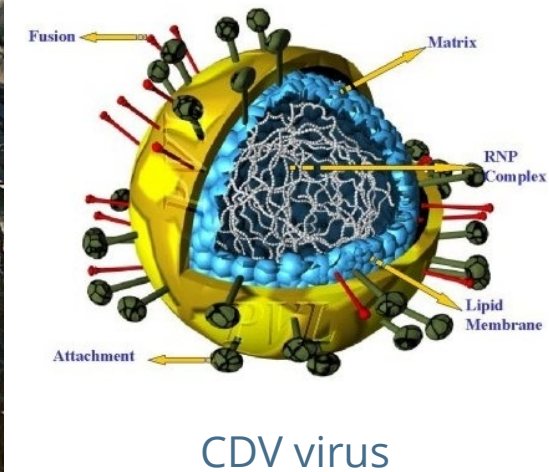
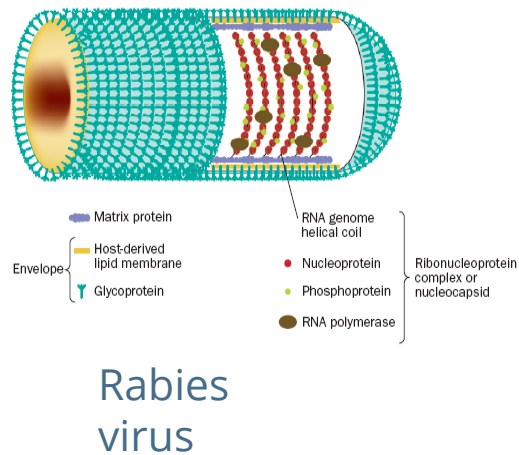
- Organise thinking
- Generate testable predictions
- Guide policies

Confronting models with data

- Fundamental aspect of modelling! – Models need to be fed with data...
- But analysis of data is also greatly enhanced by modelling
- Require statistical modelling of dynamical systems



Rabies and canine distemper virus epidemics in the red fox population of northern Italy (2006-2010).

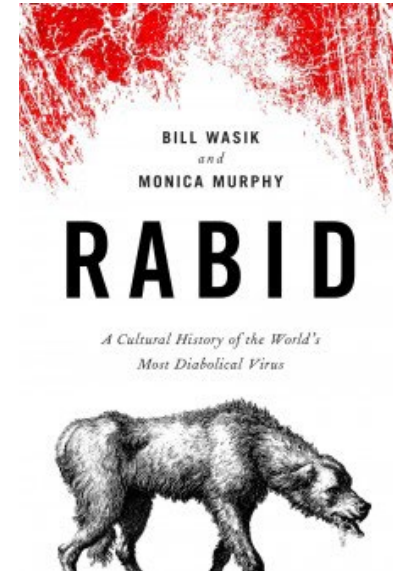


P. Nouvellet, C. Donnelly, M. De Nardi, C Rhodes, P De Benedictis, C Citterio, F Obber, M. Lorenzetto, M. Dalla Pozza, S Cauchemez, G Cattoli 2013 PLoS One

Overview

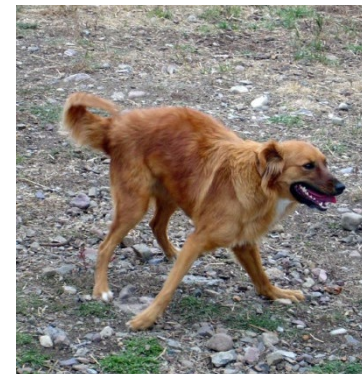
Rabies: zoonosis affecting all mammals

- Fatal acute encephalitis
- large human burden

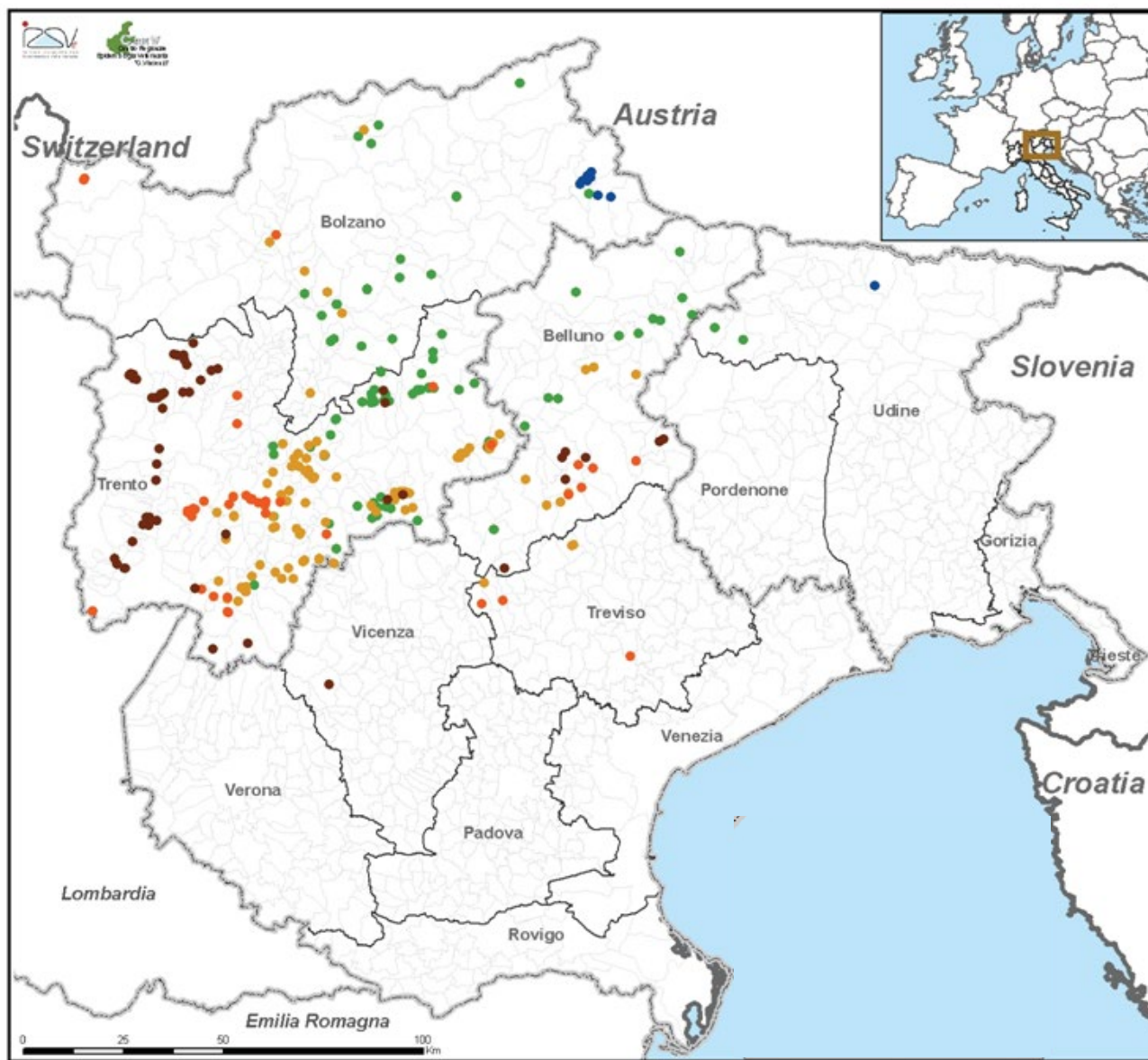


CDV: affecting some mammals (not human)

- Gastrointestinal, respiratory and neurological symptoms
- Dynamic of transmission much less studied



Epidemiological data

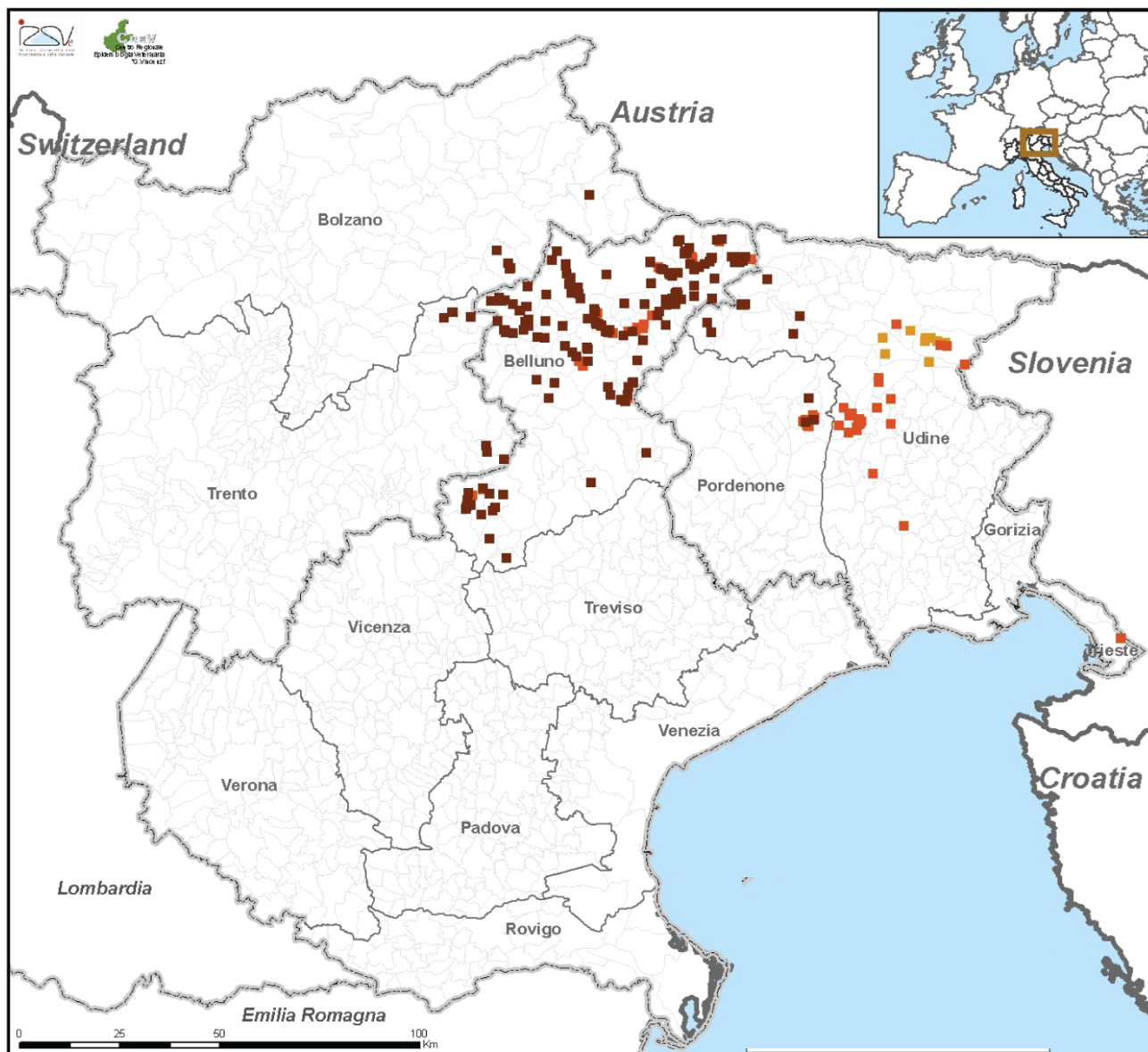


Legend

CDV

- Positive 2006
- Positive 2007
- Positive 2008
- Positive 2009
- Positive 2010

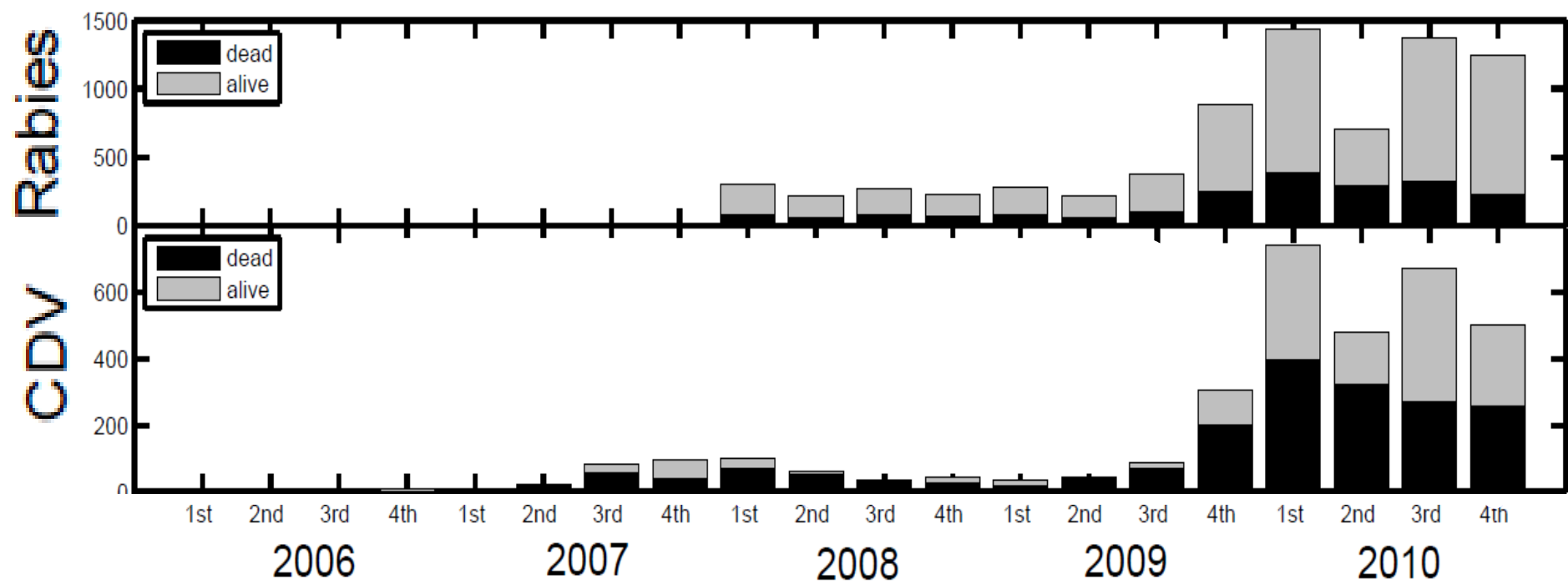
Epidemiological data

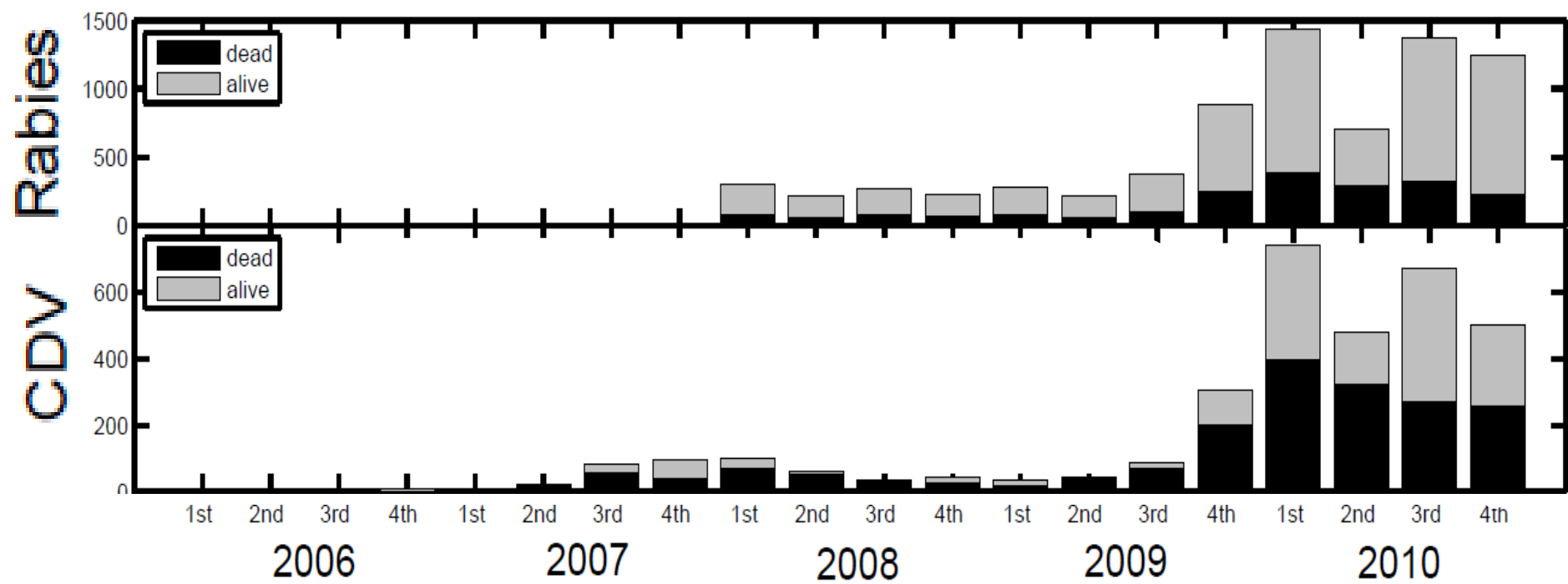


Legend

Rabies

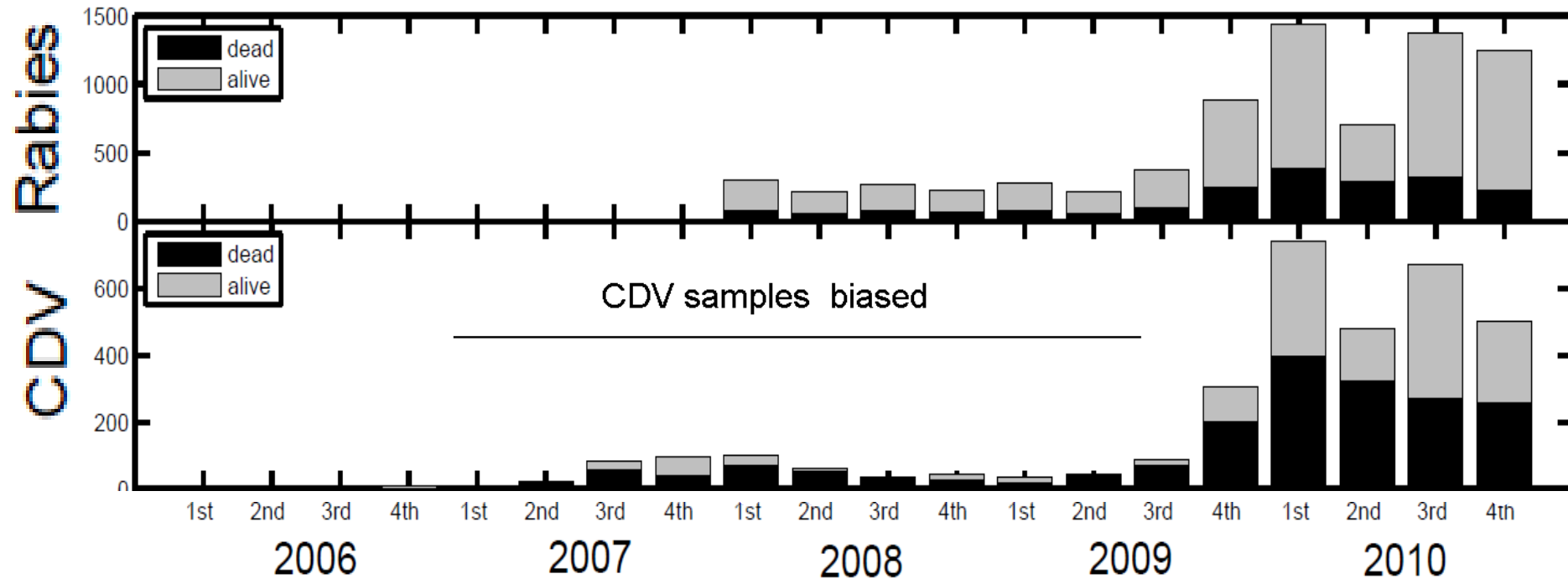
- Positive 2008
- Positive 2009
- Positive 2010





Presentation of the problem

Challenge when monitoring wildlife disease:



Presentation of the problem

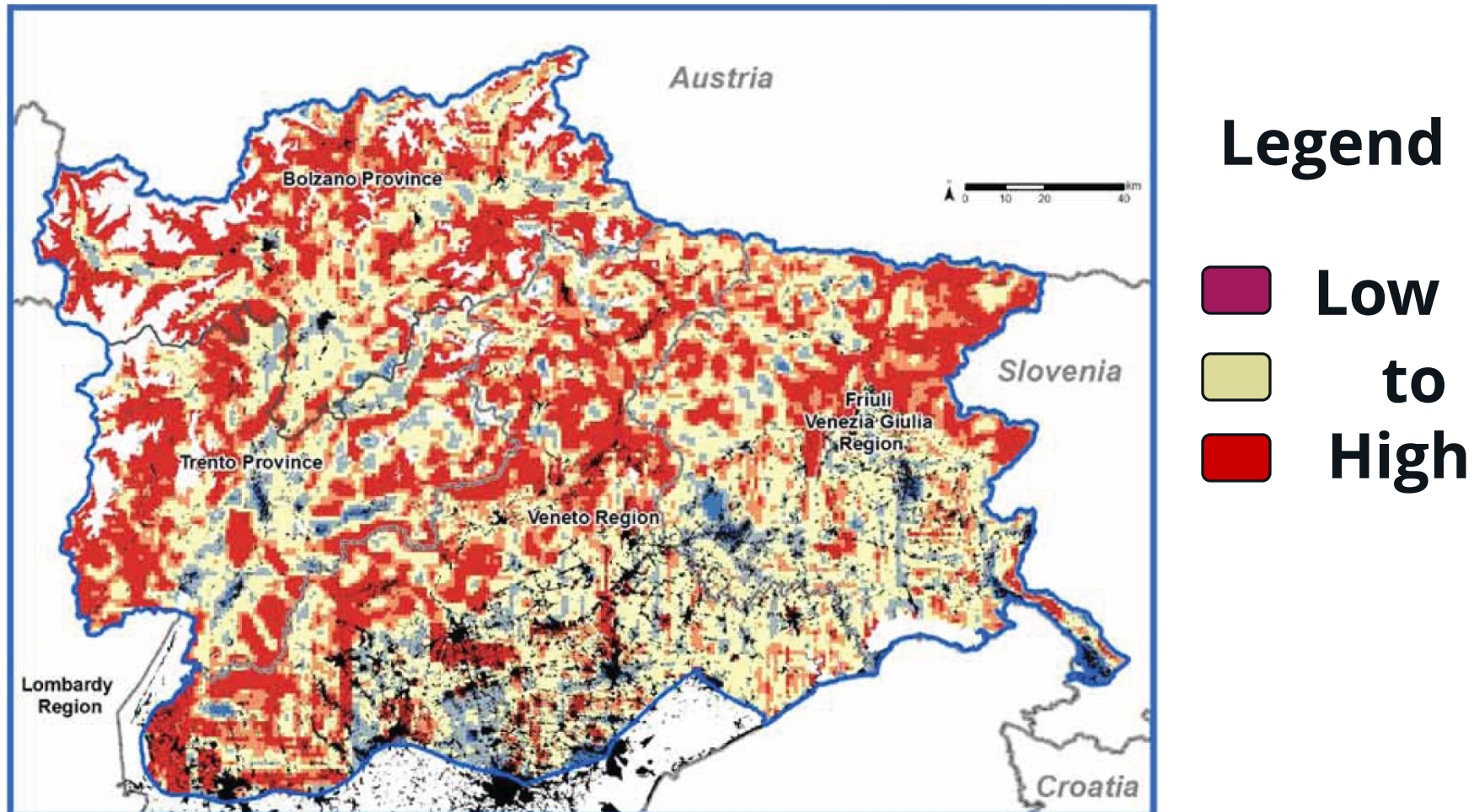
- Early 2010, campaign of oral vaccination against fox rabies



Thanks to Mirco Piccin, Corpo de poliza provinciale, Belluno

Presentation of the problem

- Early 2010, campaign of oral vaccination against fox rabies

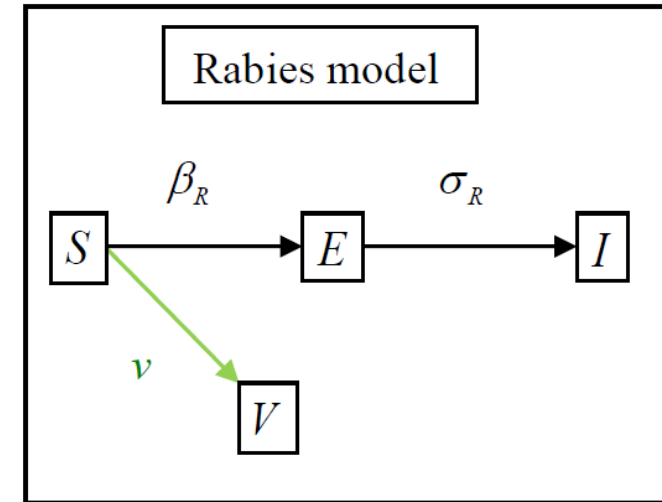


1. Estimate the incidence of both diseases
2. Quantify the parameters of transmission for both diseases
3. Assess the impact of the vaccination strategy against rabies

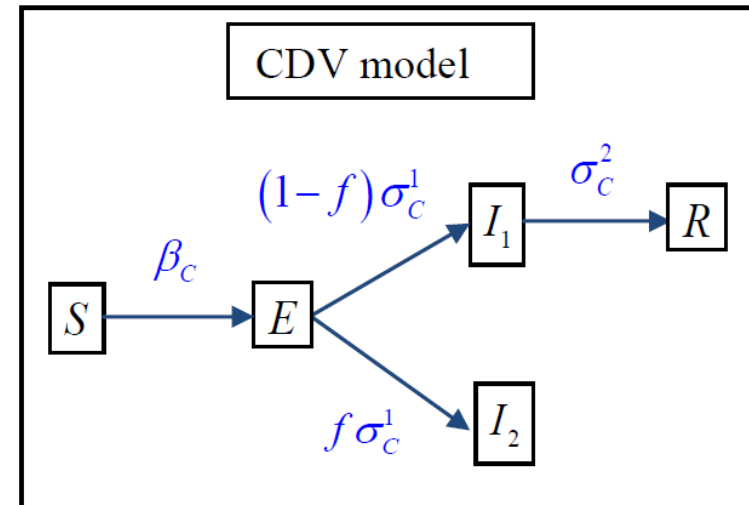
Results

We construct 2 compartmental models:

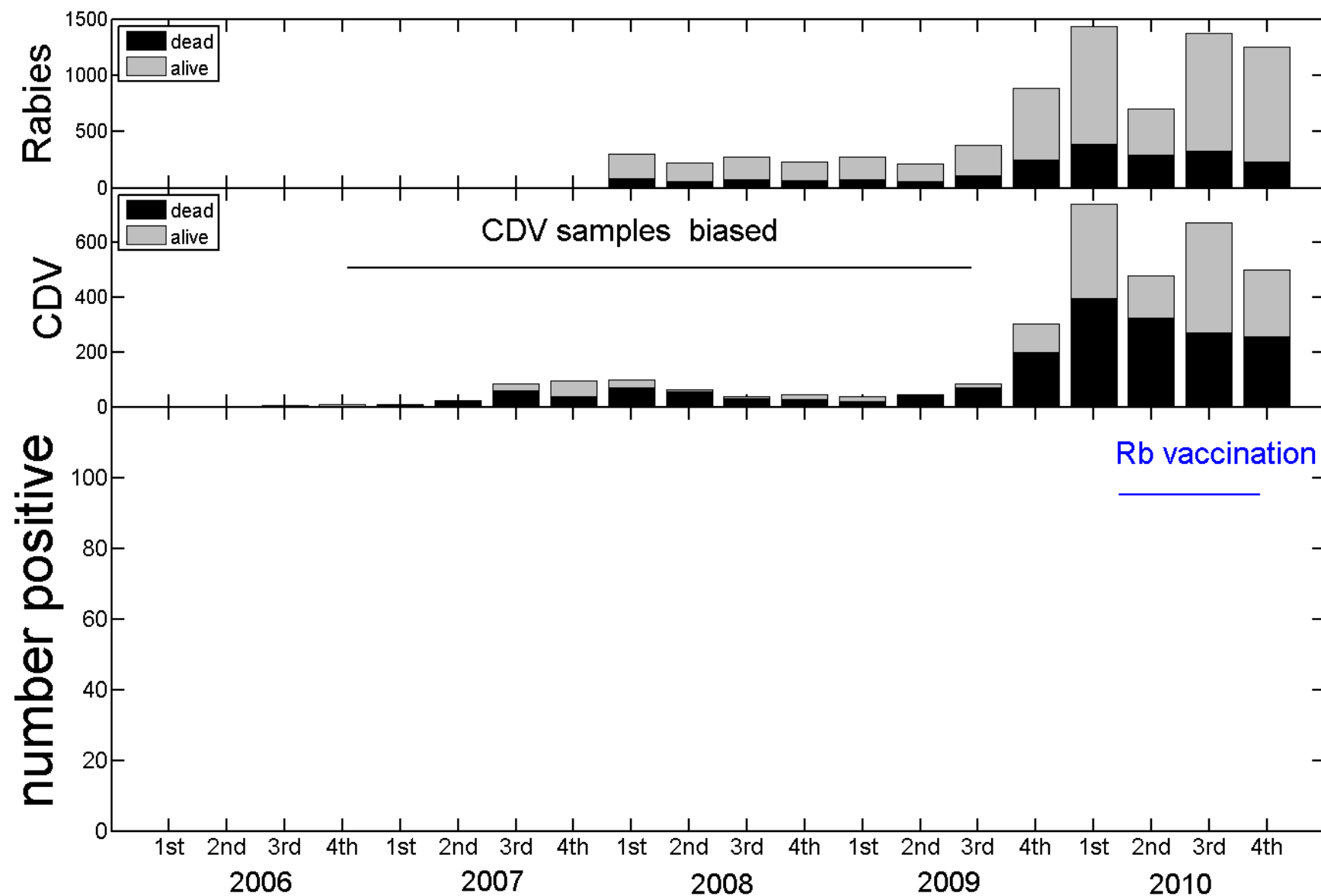
- Rabies model: as in seminal
Anderson *et al.* 1984 *Nature*



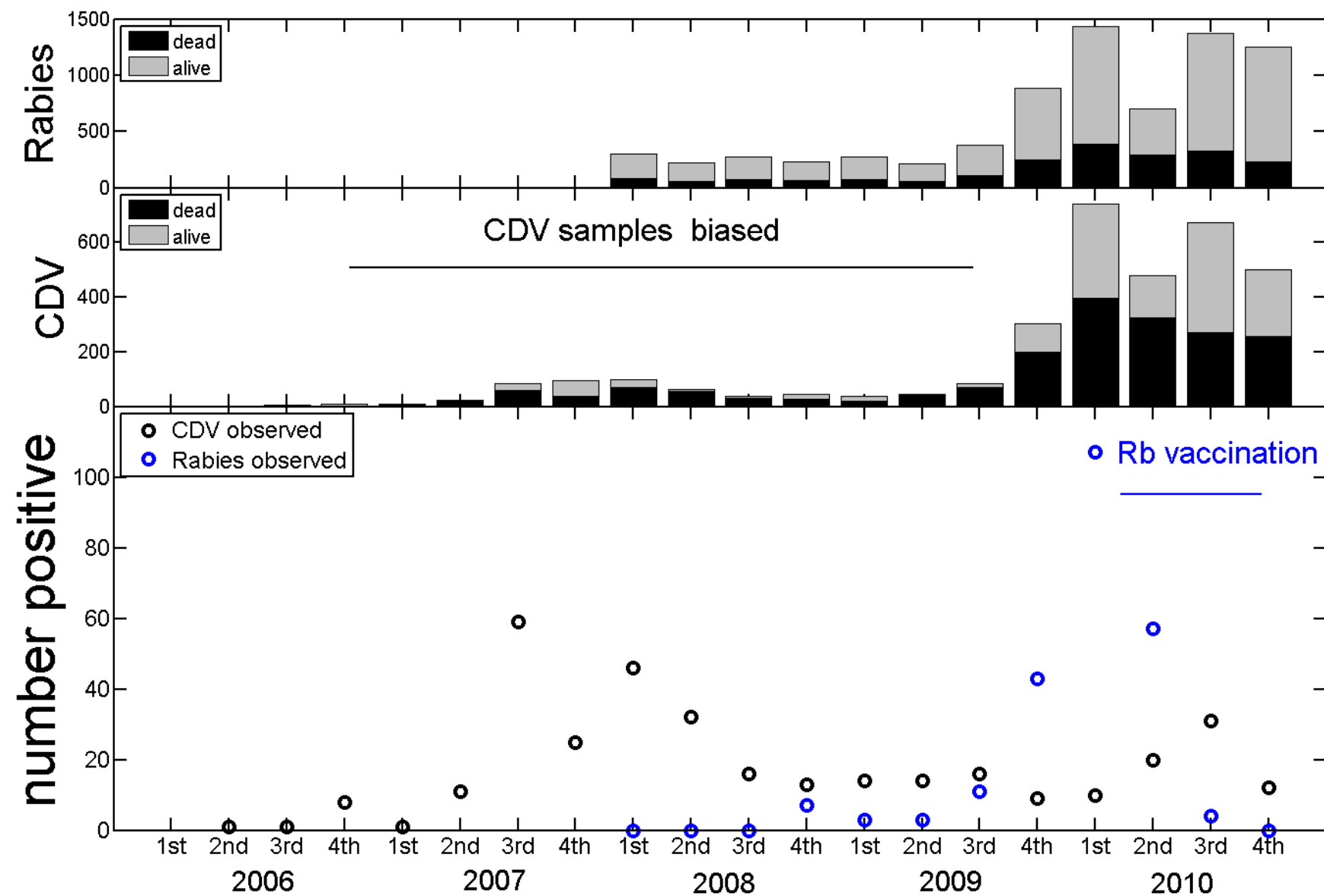
- CDV model: modified SEIR model



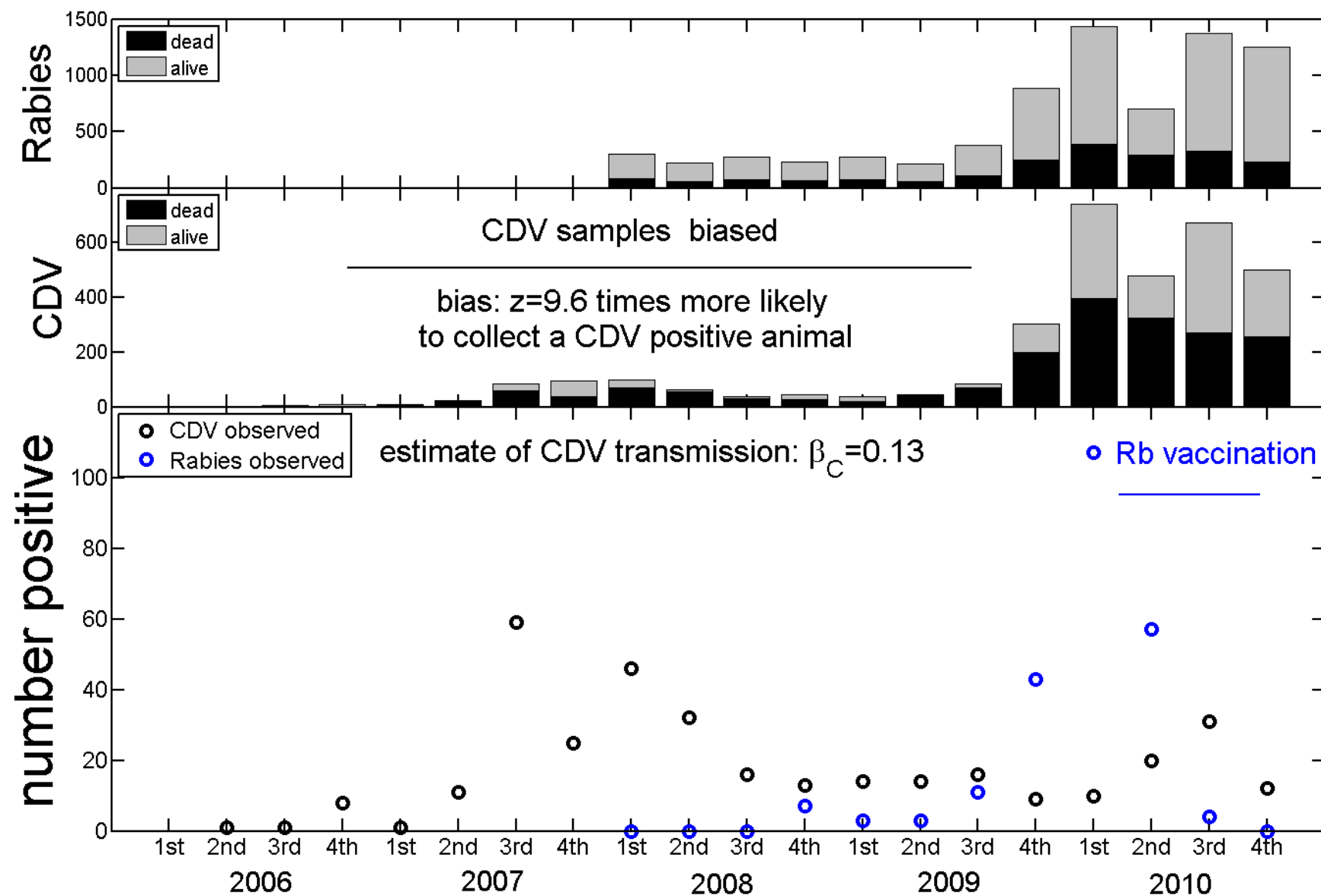
Results



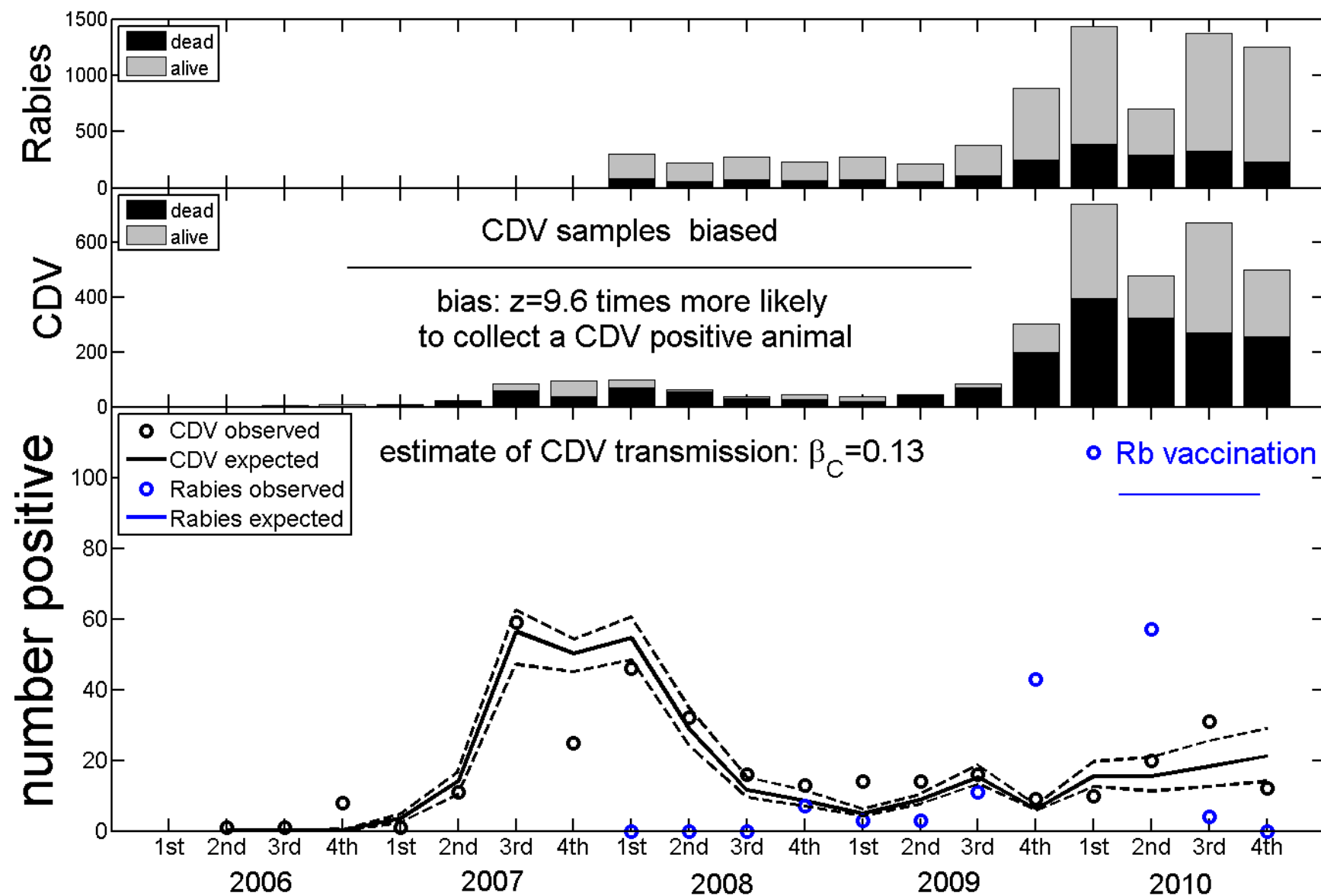
Results



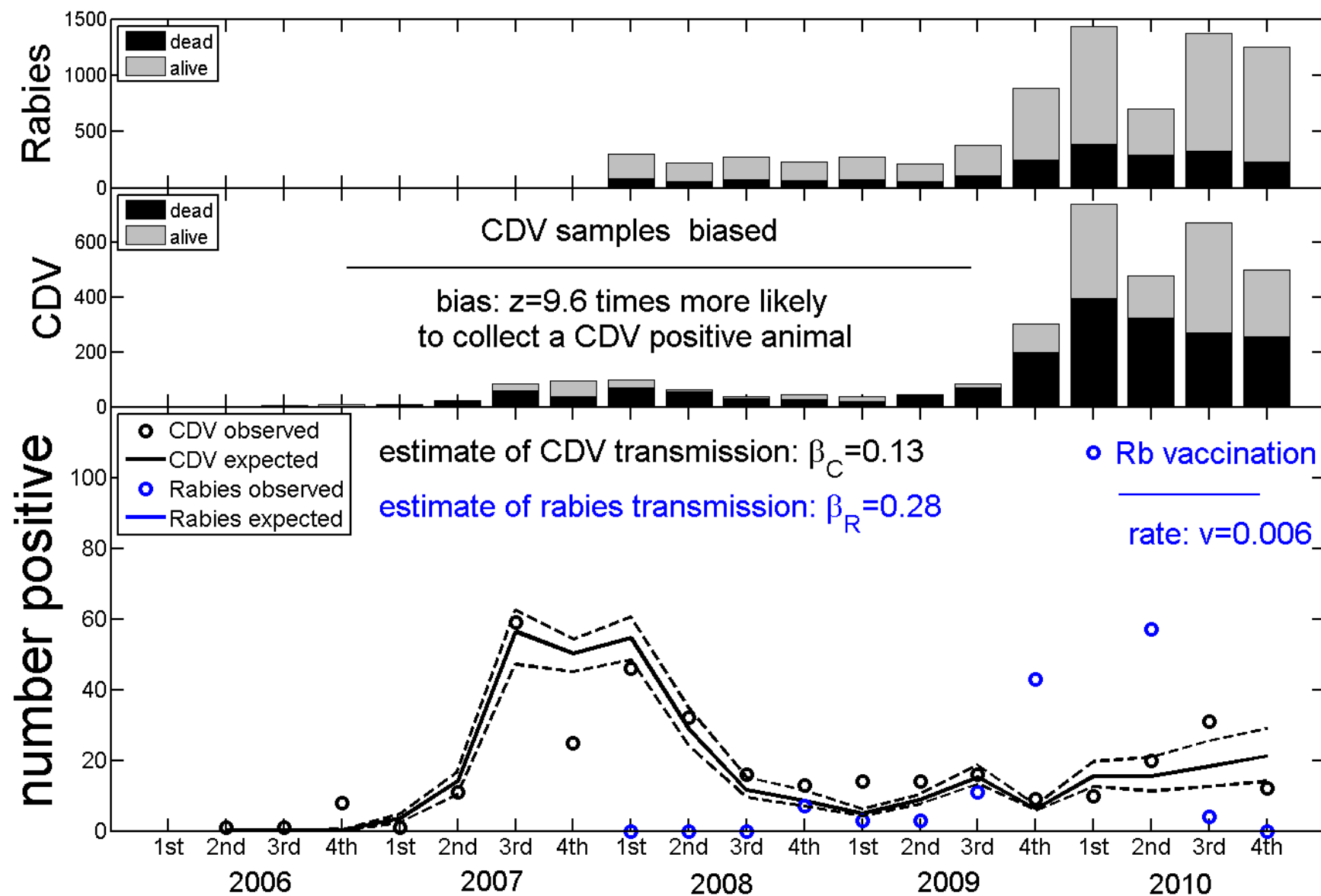
Results



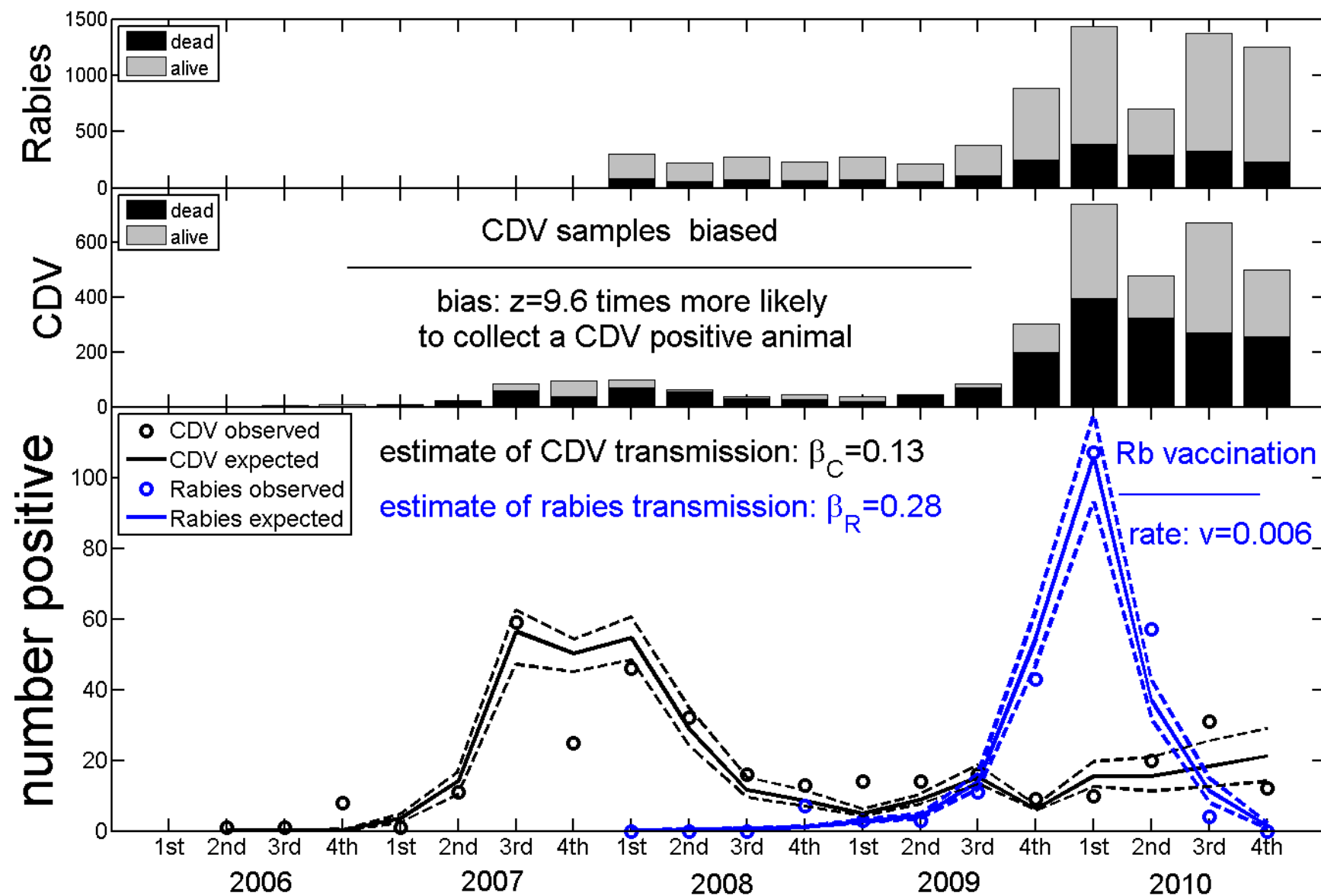
Results



Results

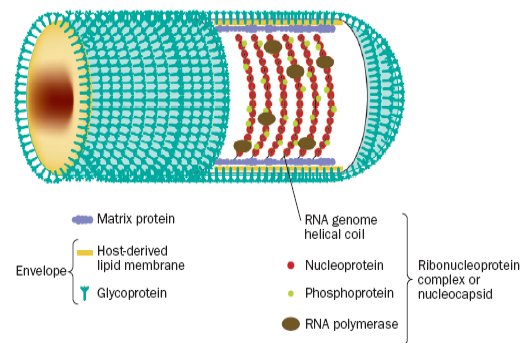


Results



- Able to translate prevalence of infection among dead and living animals to incidence in the population
- This allowed us to estimate:
 1. Rabies transmission: 1 every 3 days;
CDV transmission: 1 per week
 2. Bias in early CDV collection: 10x more likely to collect CDV+ fox
 3. Vaccination estimated to cover 70% of foxes

Transmission dynamics of lyssavirus in *Myotis myotis*: mechanistic modelling study based on longitudinal seroprevalence data



Rabies
virus



Y. Kim, S. Leopardi, D. Scaravelli, B. Zecchin, P. Priori, F. Festa, P. Drzewnioková, P. De Benedictis, P. Nouvellet, 2023, Proc. R. Soc. B.

Kim et al. 2022 Transmission dynamics of lyssavirus in Myotis myotis: mechanistic modelling study based on longitudinal seroprevalence data. Proceedings B.

- Investigated the transmission dynamics of lyssavirus in *Myotis*
- Available data – 2 maternal colonies, between 2015-2022
 - Ecological – maternity colony size,
 - Virological – RT-PCR,
 - Serology - rapid fluorescent inhibition test to detect neutralizing antibodies EBLV-1.
- Aim: characterise pathogen's life history and its dynamics
 - Use modelling to integrate data source into common framework.

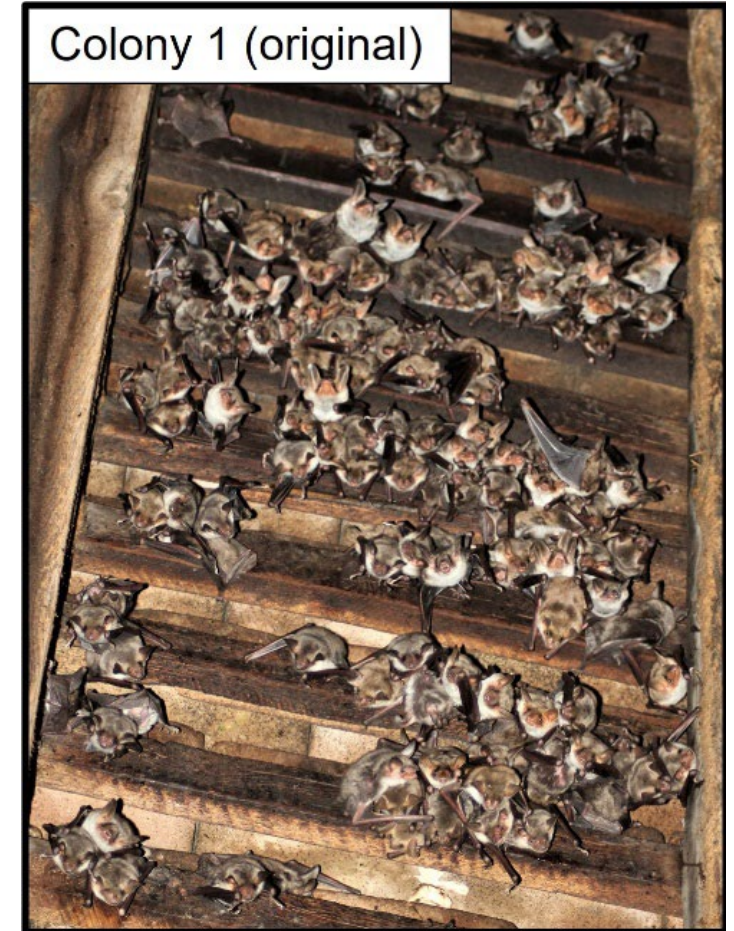


Case study on bat lyssavirus in Italy



Kim et al. 2022 Transmission dynamics of lyssavirus in *Myotis myotis*: mechanistic modelling study based on longitudinal seroprevalence data. *Proceedings B*.

- Investigated the transmission dynamics of lyssavirus in *Myotis*
- Available data – 2 maternal colonies, between 2015-2022
 - Ecological – maternity colony size : **yearly size + size of birth cohort assumed**
 - Virological – RT-PCR: **356 samples across whole period and colonies**
 - Serology - rapid fluorescent inhibition test to detect neutralizing antibodies EBLV-1: **837 samples across colonies, and 27 sampling events, sample ranged between 72-291 per year,**



Case study on bat lyssavirus in Italy



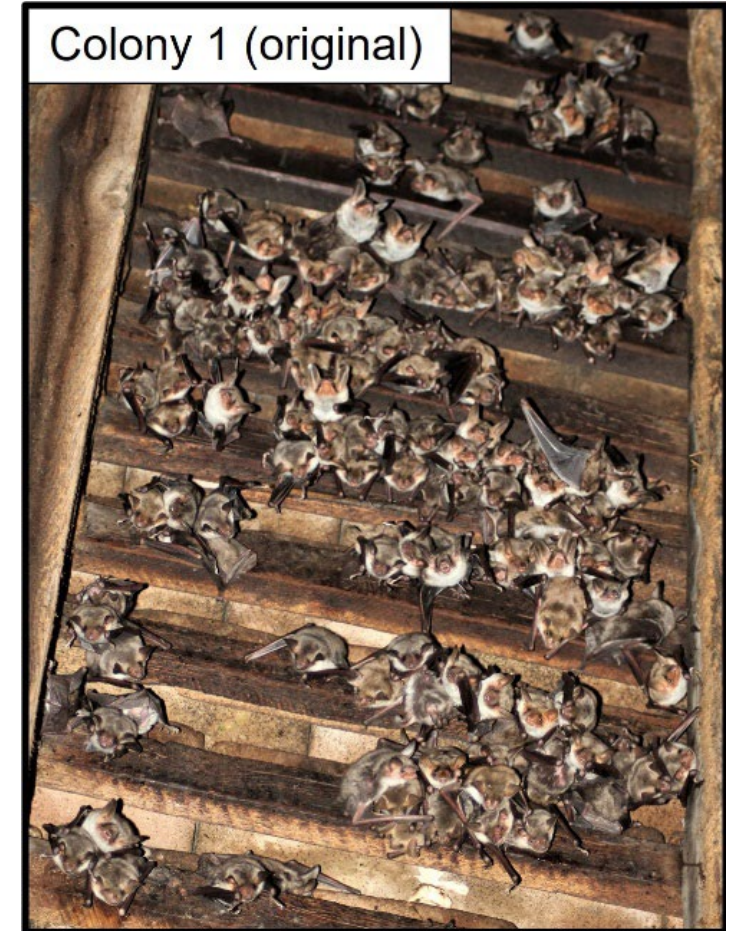
Kim et al. 2022 Transmission dynamics of lyssavirus in Myotis myotis: mechanistic modelling study based on longitudinal seroprevalence data. Proceedings B.

Aim: characterise pathogen's life history and its dynamics

Various hypotheses – 8 main hypotheses, evaluated over 40 model variants to identify those which are consistent with observations.

Some examples:

- *Is transmission frequency or density dependent?*
i.e. the more bats, the more contact between per bats (density vs frequency),
- *How disease life-history change over time (incl. during hibernation)?*
Transmission? Infectiousness period?
- *Are there significant death from infections, and are individual surviving after being infectious?*
- *Evidence for maternal immunity?*



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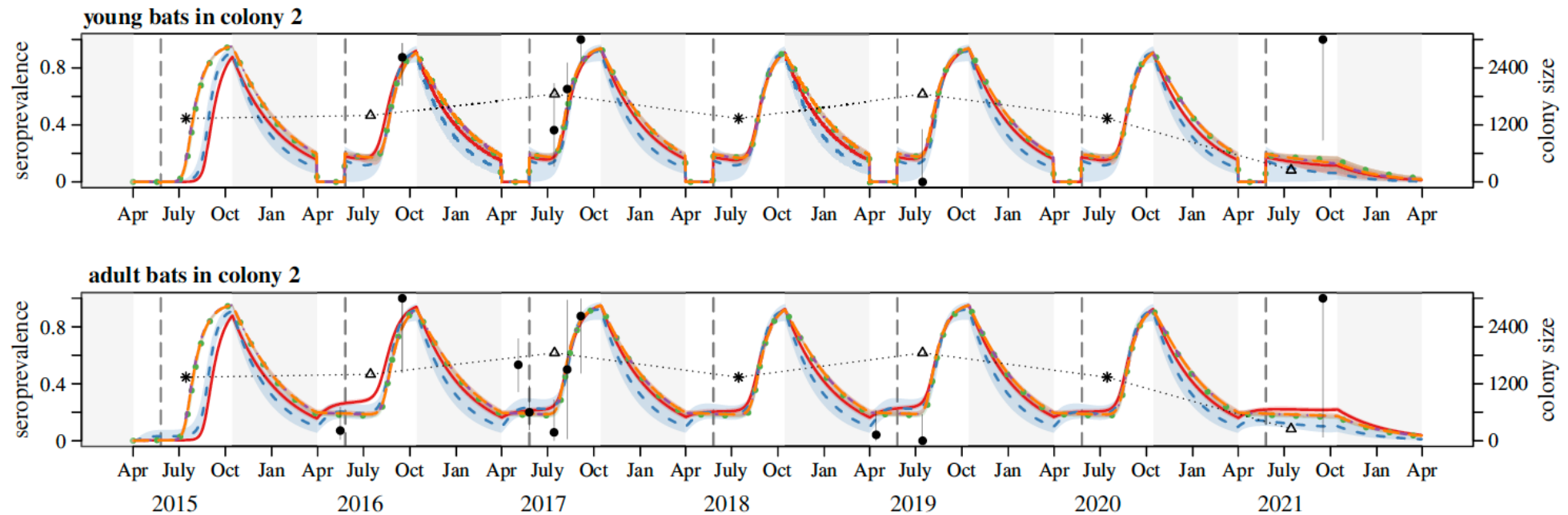
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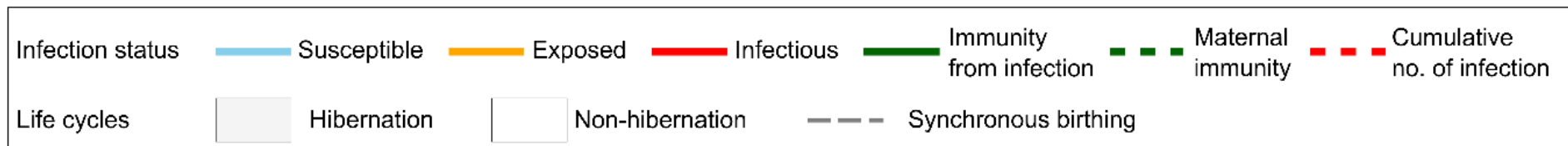
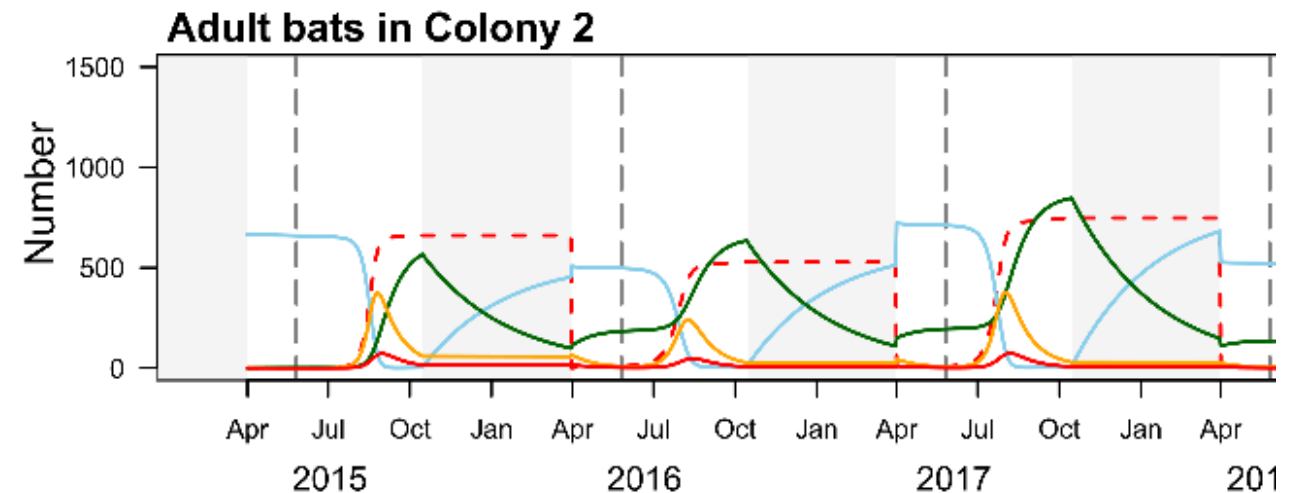


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Kim et al. 2022 Transmission dynamics of lyssavirus in *Myotis myotis*: mechanistic modelling study based on longitudinal seroprevalence data. *Proceedings B*.

- Aim: characterise pathogen's life history and its dynamics
 - Use modelling to integrate data source into common framework.
- Model also used to predict periods of high viral circulation
 - Attempt to inform sampling to actually detect/isolate virus.



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Various hypotheses – 8 main hypotheses, evaluated over 40 model variants to identify those which are consistent with observations.

Key results: in all models that fit the data:

- Density-dependent transmission;
- Highest transmission between synchronous birthing and hibernation;
- Lowest transmission (possibly none) during hibernation;
- Increase in the rate of immunity loss during hibernation;
- presence of maternity immunity;
- Still unclear whether actively infectious (i.e. exposed and infectious) bats survive. i.e. possibility of micro-exposure inducing immune response but no clinical infection

model	baseline and alternative hypotheses	SEIR (final models in bold)			SEID/SER (final models in bold)		
		DIC	DIC ^a	model weight ^b	DIC	DIC ^a	model weight ^b
baseline model	density-dependent transmission transmission rate (β) no transmission during hibernation ($\beta = 0$) β changes in a stepwise manner at the start of the following life cycle events: 1) maternity colony forming, 2) synchronous birthing, 3) hibernation rate of becoming infectious (τ), rate of recovering and becoming immune (γ in SEIR, ϑ in SEID/SER) τ , γ , and ϑ are constant non-zero during hibernation τ , γ , and ϑ are zero during hibernation rate of immunity loss (σ) changes in a stepwise manner at the start of hibernation. no recrudescence	283.8	47.2	0.00	277.7	41.1	0.00
model 1	frequency-dependent transmission	318.9	82.3	0.00	324.9	88.3	0.00
model 2.1	β changes following a sinusoidal curve until hibernation.	236.6	0	0.59	239.2	2.6	0.16
model 2.2	β is constant until hibernation.	377.0	140.4	0.00	354.6	118	0.00
model 3.1	σ changes throughout each year following a sinusoidal curve	280.8	44.2	0.00	269.1	32.5	0.00
model 3.2	σ is constant throughout each year	335.2	98.6	0.00	299.9	63.3	0.00
model 4	no maternal immunity	291.9	55.3	0.00	314.3	77.7	0.00
model 5	τ , γ , and ϑ are constant non-zero throughout the year	240.8	4.2	0.07	243.4	6.8	0.02
model 6.1	model 5 + β changes following a sinusoidal curve until hibernation, no transmission during hibernation ($\beta = 0$)	240.8	4.2	0.07	257.4	20.8	0.00
model 6.2	model 5 + β changes following a sinusoidal curve throughout the year, including during hibernation ($\beta \neq 0$)	261.8	25.2	0.00	264.0	27.4	0.00
model 6.3	model 5 + β during hibernation is estimated separately from other periods ($\beta \neq 0$)	240.8	4.2	0.07	243.3	6.7	0.02
model 6.4	model 5 + β is constant throughout the year, including during hibernation ($\beta \neq 0$)	415.0	178.4	0.00	355.8	119.2	0.00
model 7	bats with immunity become infectious again at the rate of ρ	283.9	47.3	0.00	NA		
model 8	death from infection at the rate of χ	283.9	47.3	0.00	NA		

^aDifference from the lowest DIC (i.e. 236.6 from SEIR model 2.1).

^bModel weights were obtained using $\exp(-\text{DIC}/2)$ and standardised over all models compared (sum to 1) [54].



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Conclusions

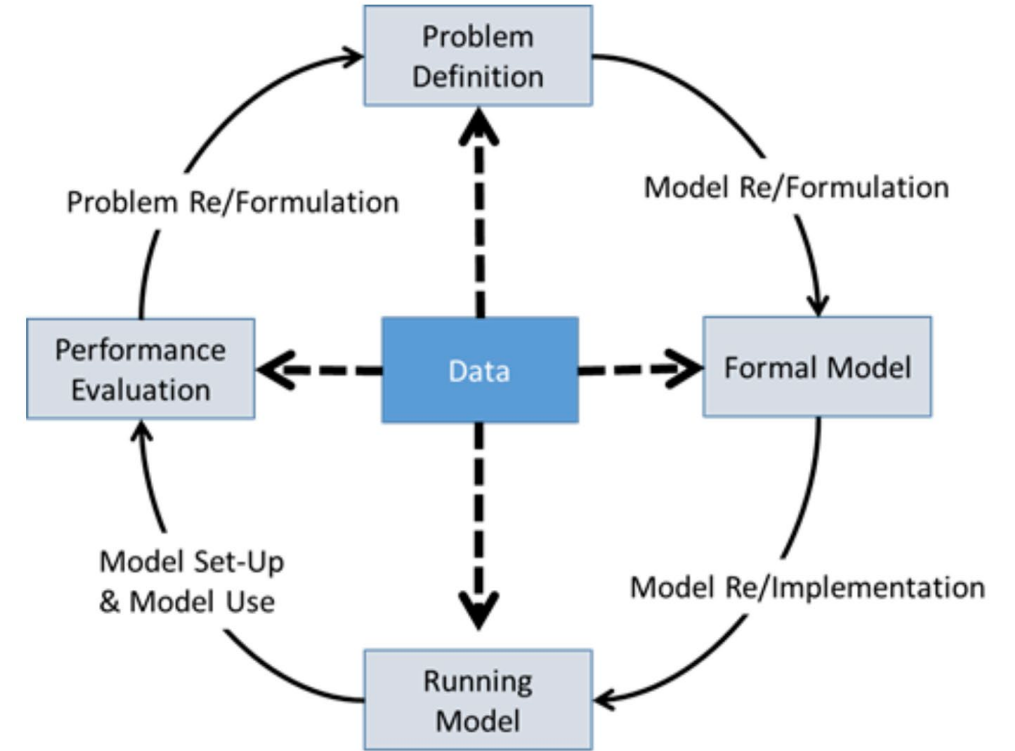
Conclusions

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