The spread of rabies in Ethiopian wolves: from field data to transmission parameters

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BACKGROUND

- The Ethiopian wolf: an endangered species threatened by regular outbreaks of rabies
- In 2008 - 2009: nearly half of the animals of the Web Valley died from rabies
- Quantification of the spread of infection: an important step towards effective control planning
- Epidemic process: only partially observed making parameter inference hard
- Is Approximate Bayesian Computation a method of interest?

OBJECTIVE

To assess rabies transmission in Ethiopian wolves during the 2008-2009 outbreak using Approximate Bayesian Computation (ABC)

A few words about ABC

- Bypass exact likelihood calculations by matching simulated to observed data
- The simplest ABC framework: rejection samplers (Figure 1)

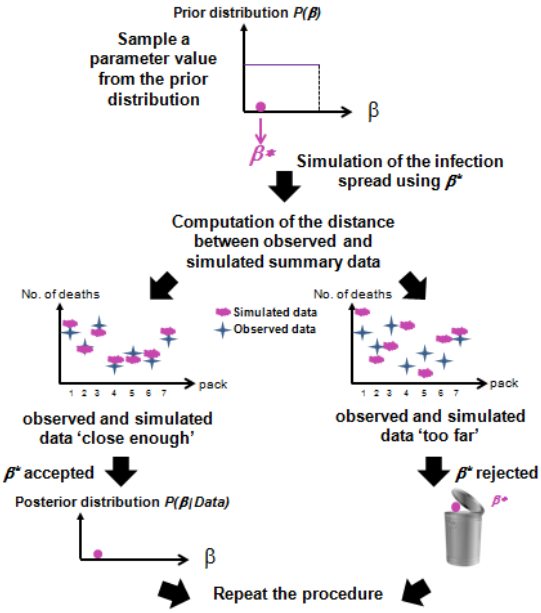

Figure 1: schematic representation of ABC rejection for one parameter

- Here: minimally informative priors for β_w and β_b. Summary statistics: number of carcasses per group of packs, duration of outbreak, and time between the first carcass and the first carcass in a neighboring pack. 80,000 simulations, the 100 leading to the smallest distance between observed and simulated summary statistics kept for inference. Algorithm of Beaumont *et al.* (2002) based on local linear regression.

DATA & METHODS

Field data

- pre and post-outbreak pack compositions, date and place of vaccination events and carcass recoveries

⇒ 72 wolves in 7 packs, 35 carcass recoveries over a 5-month period, 13 animals vaccinated

Modelling

- spatially explicit stochastic SEIR model for infection spread within a metapopulation of 7 packs
- inclusion of natural mortality, vaccination and uncertainty about home packs of carcasses
- mean incubation and infectious period fixed to respectively 22 days and 3 days

⇒ Two parameters to infer using ABC: the within (β_w) and between neighboring pack (β_b) transmission rates. Then computation of the basic reproduction number (R_0) of the infection

⇒ Before inferring β_w and β_b from the real data set, check on the method accuracy and robustness using simulated data from known parameter values

RESULTS

Check on the method accuracy and robustness

⇒ good inference for β_w and β_b (Figure 2). The data set was generated with β_w=0.04 and β_b=0.008.

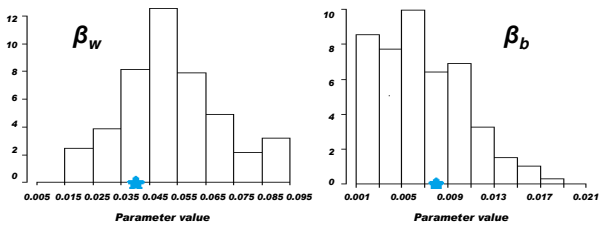

Figure 2: posterior distributions of β_w and β_b obtained with the ABC procedure (see 'A few words about ABC' for details). The blue stars represents the real parameter values. Priors distributions were uniforms between 0 and 0.1 for β_w and between 0 and β_w/2 for β_b.

Assessment of rabies transmission during the 2008-2009 outbreak

- Median β_w: 0.041 (95% CI: 0.020-0.070)
- Median β_b: 0.0054 (95% CI: 0.0011-0.0105)

⇒ The median within-pack transmission was approximately 8 times higher than the median between pack transmission, consistent with behavioral studies

⇒ The mean R_0 was 2.5 (sd: 2.05), in agreement with previous estimates for the 2003 rabies outbreak

CONCLUSION

• ABC seems a useful method to assess infection transmission parameters in wildlife where data are scarce

• Besides biological insights following the estimation of rabies transmission parameters in Ethiopian wolves, these outputs will be used to calibrate a simulation model to assess the effectiveness of different vaccination strategies in those populations

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