

Risk assessment of human exposure to HPAI after vaccination of layer hens

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Problem statement: In the Netherlands, Highly pathogenic avian influenza (HPAI) is year-round present in wild birds and incursions in poultry farms occur regularly. Vaccines have been developed that protect against transmission and disease¹. Detection is primarily based on passive detection. Vaccinated flocks might only be partially protected, when not all animals have sufficiently high titre against the circulating strain. Spread is slower within partially protected flocks which extends the time until detection. Due to the delayed detection of HPAI, the exposure of humans to the HPAI might increase, increasing the risk of zoonotic spill-over.

Aim: Calculate the potential change in human exposure to high pathogenic avian influenza after vaccination of layer hens for ...

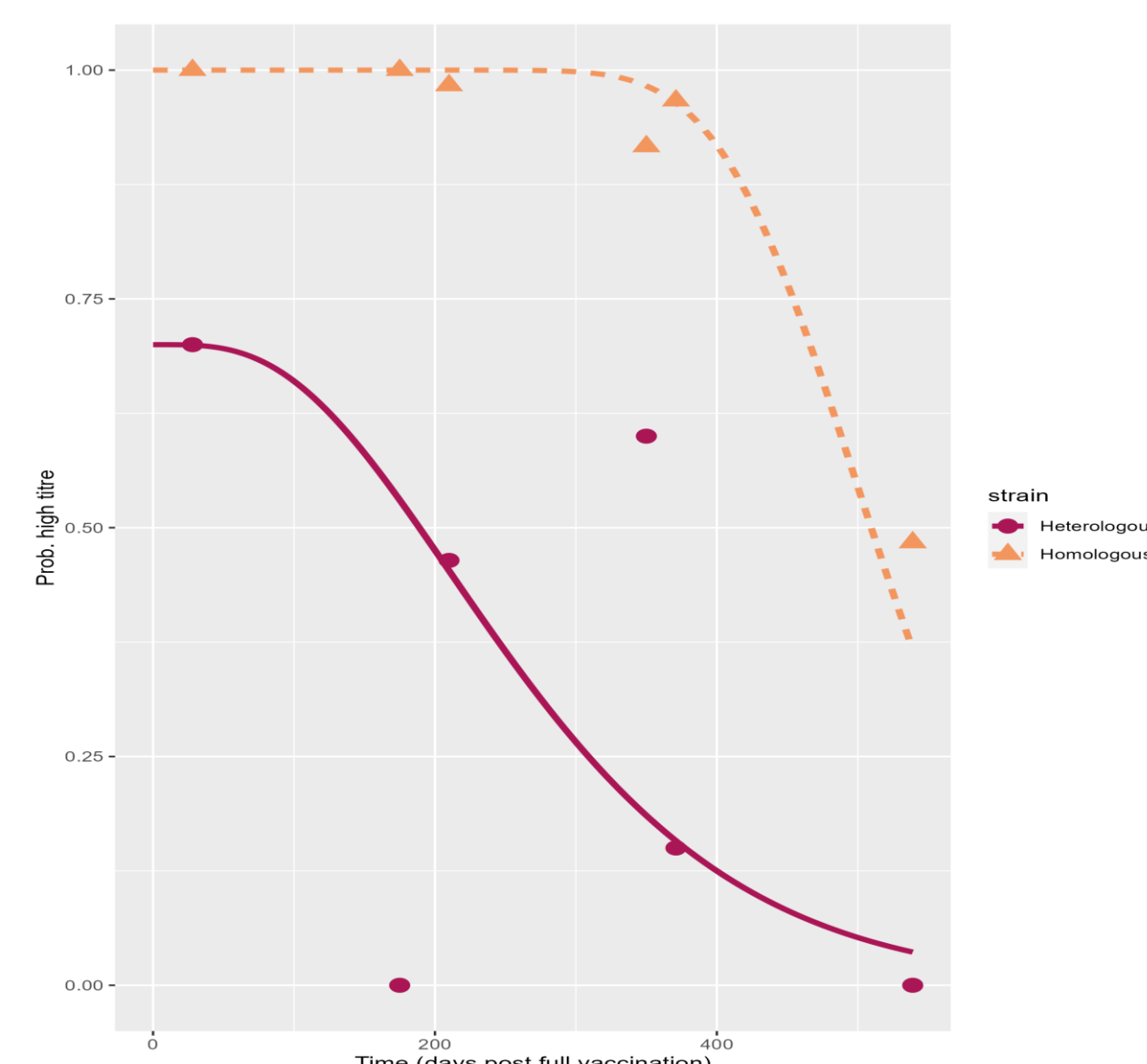
- An outbreak on a single farm
- Epidemic in the Netherlands

Within Farm model:

- Stochastic two-type SIR model
 - H(igh) = sufficient HI titre
 - L(ow) = insufficient HI titre
- Transmission depend on HI titre¹:

$$\begin{pmatrix} R_{LL} & R_{HL} \\ R_{LH} & R_{HH} \end{pmatrix} = \begin{pmatrix} 3.93 & 0.23 \\ 3.93 & 0.23 \end{pmatrix}$$

- Detection based on dead birds
 - Passive: 2 consecutive days $\geq 0.5\%$ of flock
 - Active: Weekly bucket sample
- Immune waning²



Immune waning with hetero- and homologous vaccine²

Between Farm model:

- Spatially explicit stochastic SIR³

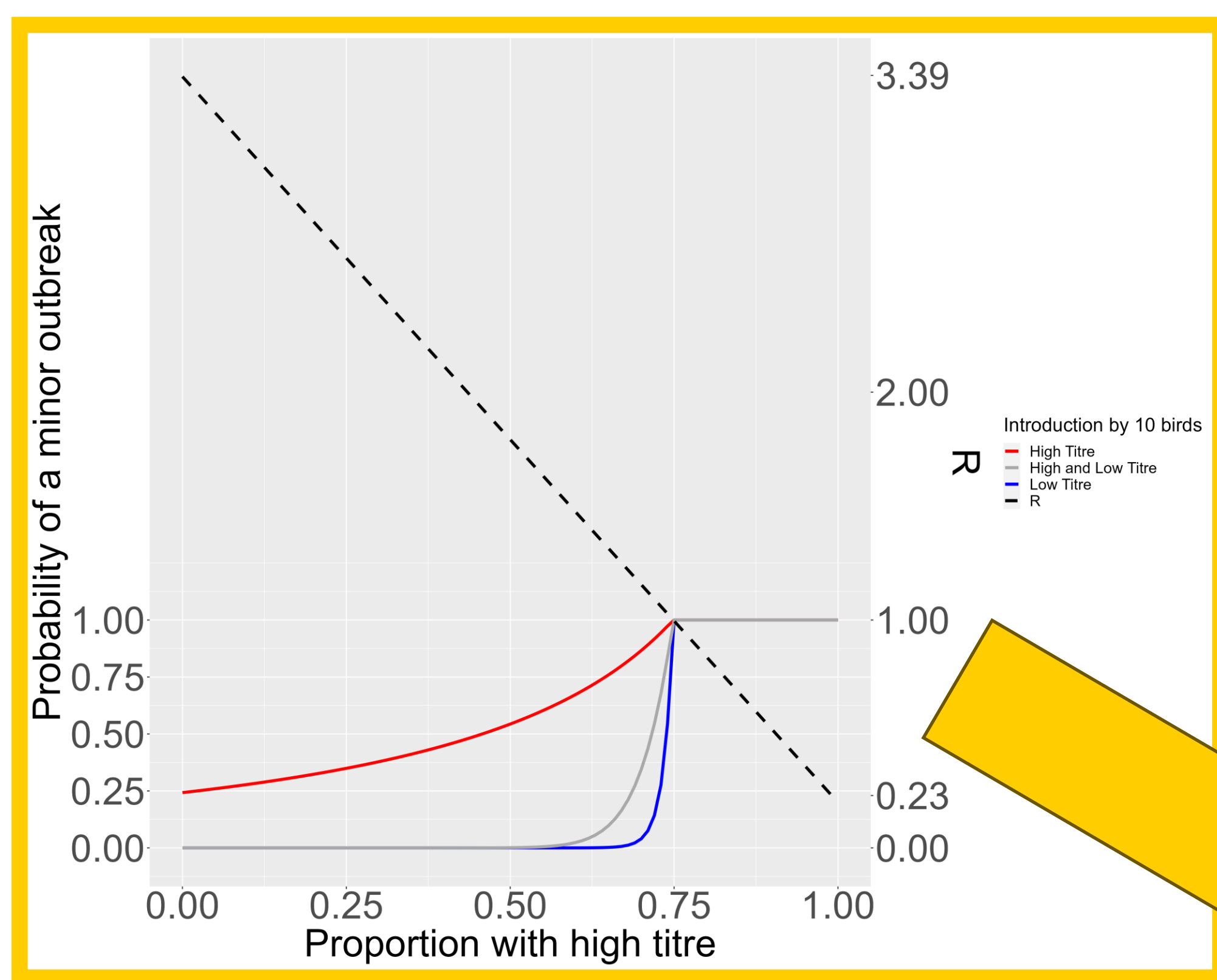
$$h(r_{ij}) = \frac{h_0}{1 + \left(\frac{r_{ij}}{r_0}\right)^\alpha}$$

- Within-farm model used for
 - Probability of major outbreak
 - Time-until-detection
 - Human exposure after introduction

Human exposure model:

- Exposure proportionate to transmission between birds
- Within-farm exposure = sum of total exposure from all birds until detection or fade-out
- Between-farm exposure = sum of exposure over farms
- Report difference with baseline scenario

Probability of a minor outbreak (see Box 1):



Box 1: Probability of a minor outbreak⁴

Let f_i be the offspring probability generating function for type i :

$$f_i(u_i, u_j) = \frac{a_i + \left((1-u_i) \frac{N_i}{N} R_{ii} + (1-u_j) \frac{N_j}{N} R_{ij} \right)^{a_i}}{a_i}$$

With N is population size, a is the shape variable of the gamma-distributed infectious period and R is the reproduction number.

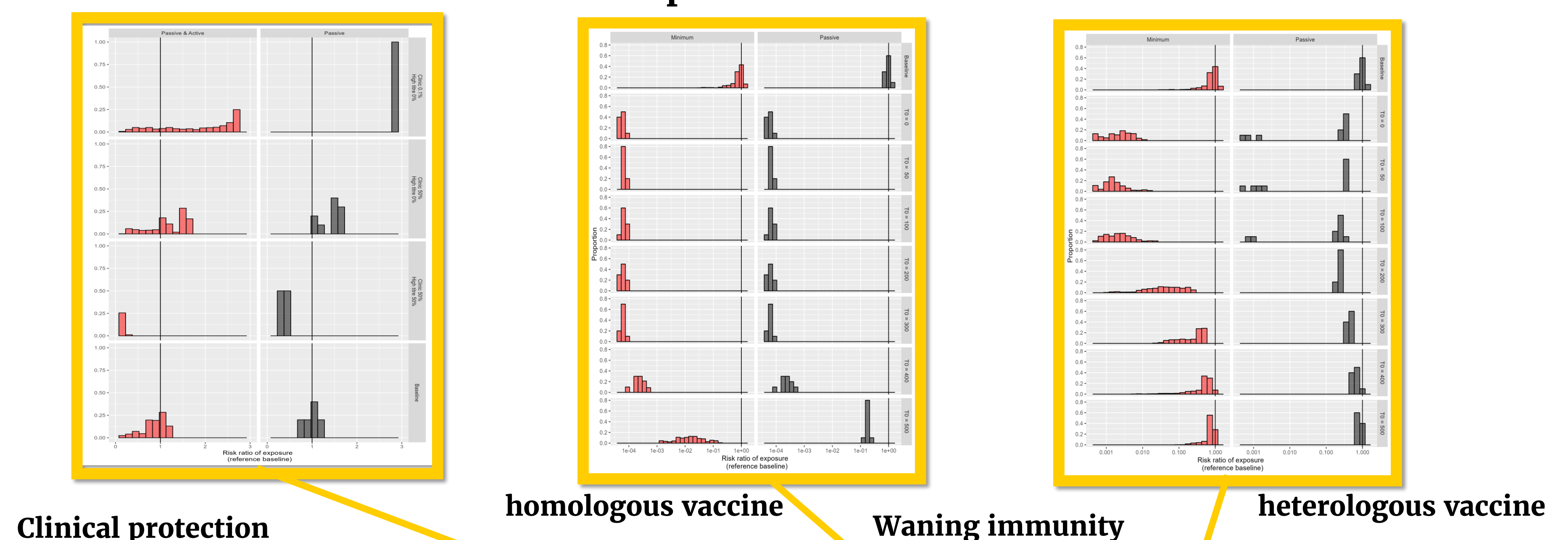
The probability of extinction q_i when introducing type i is found by solving

$$q_i = f_i(q_i, q_j), q_j = f_j(q_i, q_j)$$

Assuming independence of each branch in this branching process starting with I_i initial infectious animals:

$$P_{minor} = q_i^{I_i} q_j^{I_j}$$

Human exposure in a farm



50% of infected birds show clinical signs
0% protection against transmission

Uniformly distributed time of introduction



Ratio human exposure country-level Ref. median baseline scenario

Conclusion: Vaccination is not expected to increase human exposure even with prolonged detection times.

Recommendation: Test model assumptions in field experiment before large-scale implementation of vaccination strategies.