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Within-Herd Transmission Dynamics for Bovine Tuberculosis in British Cattle: A Parametric Bootstrapping Approach

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Bovine Tuberculosis (bTB) is an infectious respiratory disease caused by the bacterium Mycobacterium bovis ssp. bovis. Cattle herds in the UK are subject to regular whole herd tests (WHT) for the disease and detected animals slaughtered. Despite regular testing, bTB remains a persistent problem in the UK and the economic costs associated with bTB between 2004 and 2011 is ~£1bn.

We present a simple model of bTB incorporating the latent stages of the disease and assuming no knowledge of the transmission parameters or the sensitivity of the tests we perform a bootstrapping operation to the model to infer the parameters for 1 & 4 year testing areas of the UK.

The Model & Assumptions

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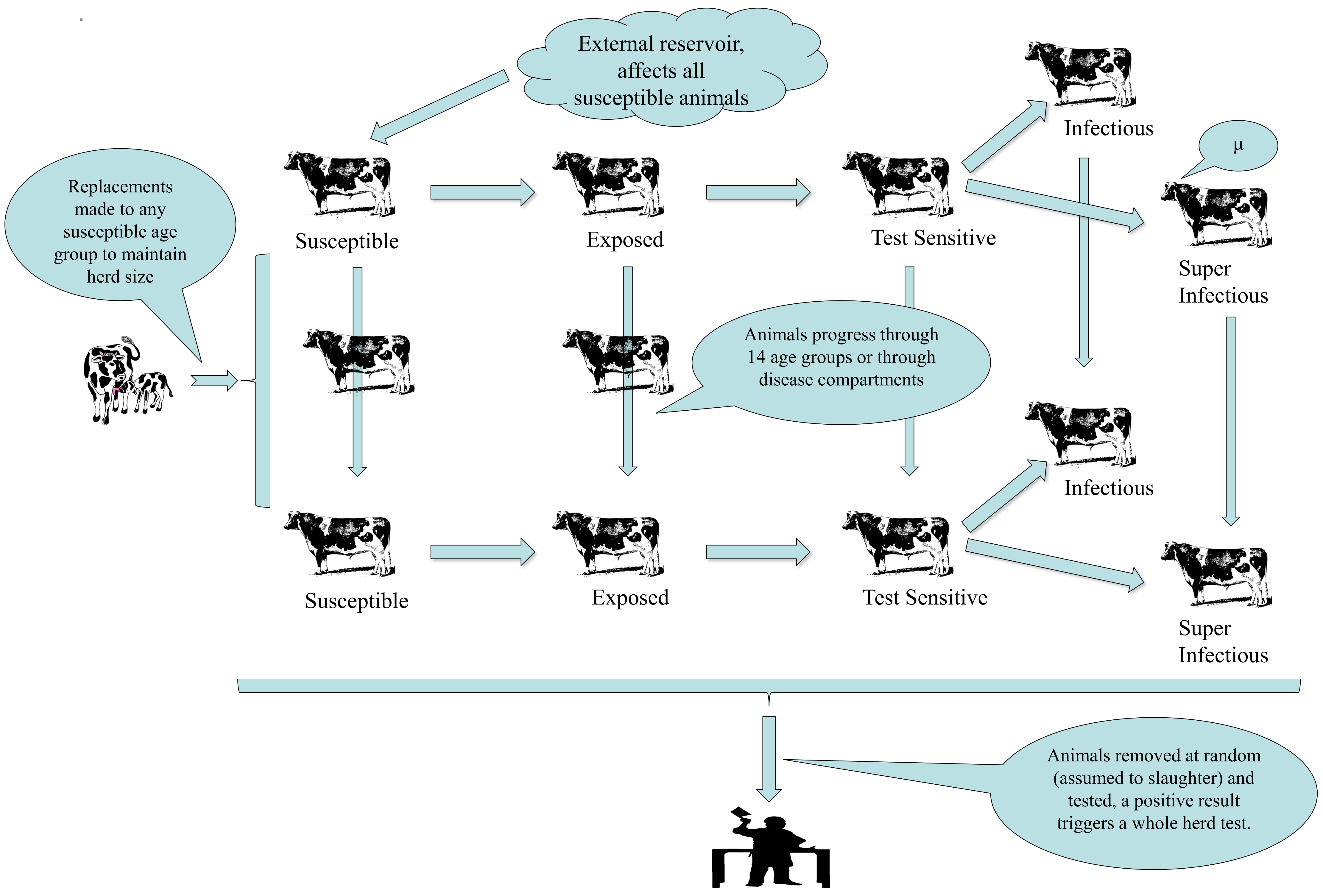

Notes

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- Start with a single infected animal in the herd.
- Test each animal in the herd at regular intervals (1 or 4 years).
- If a breakdown occurs, test every 2 months until successive clear tests.
- Assume that a proportion of the herd are super-infectious. i.e. the transmission parameter is scaled relative to 'normal' infectious animals
- Assume a proportion of herds simulated have scaled up transmission parameter (super-spreader herds)
- No reservoir for 4 year areas.

Methods & Results

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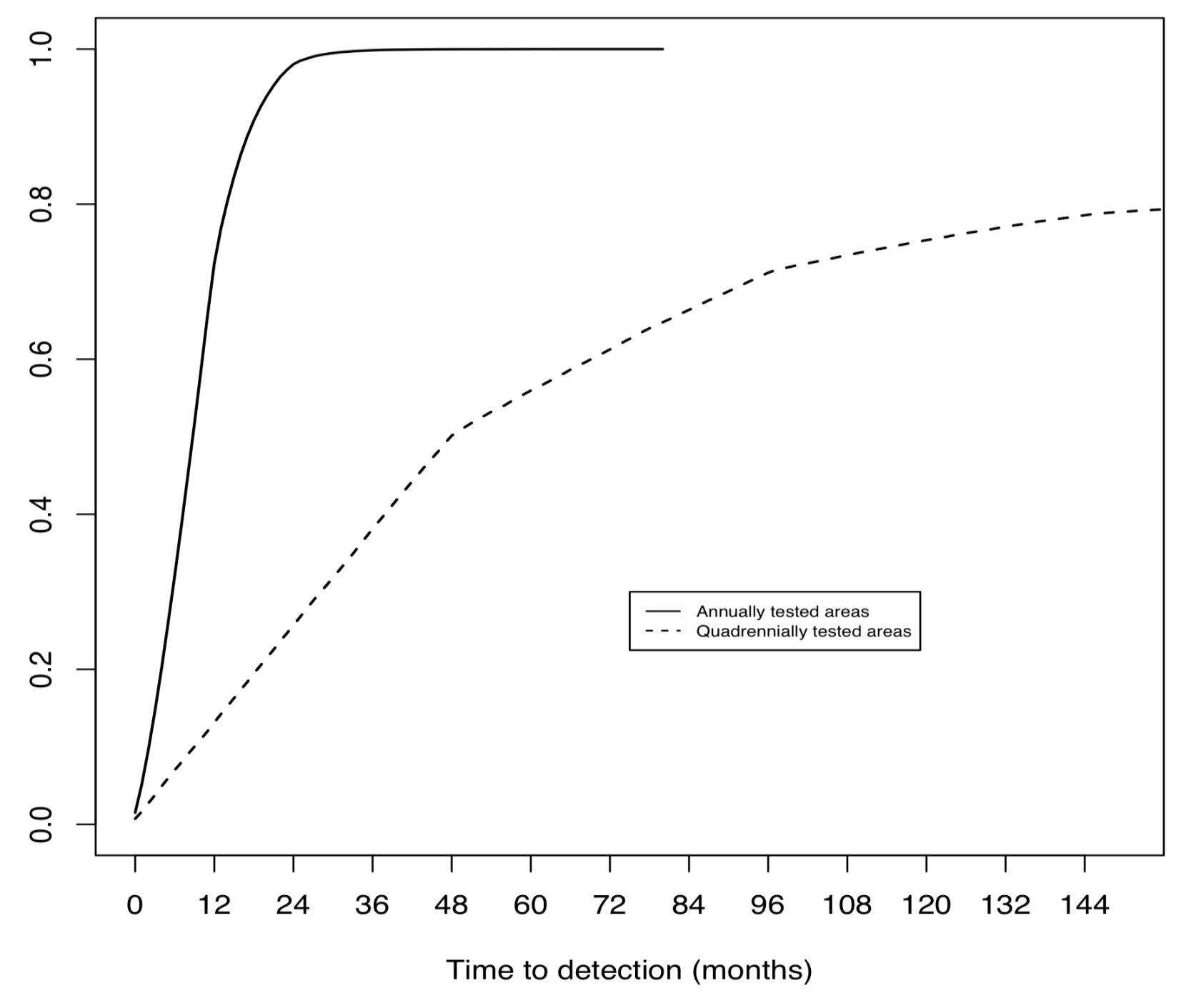
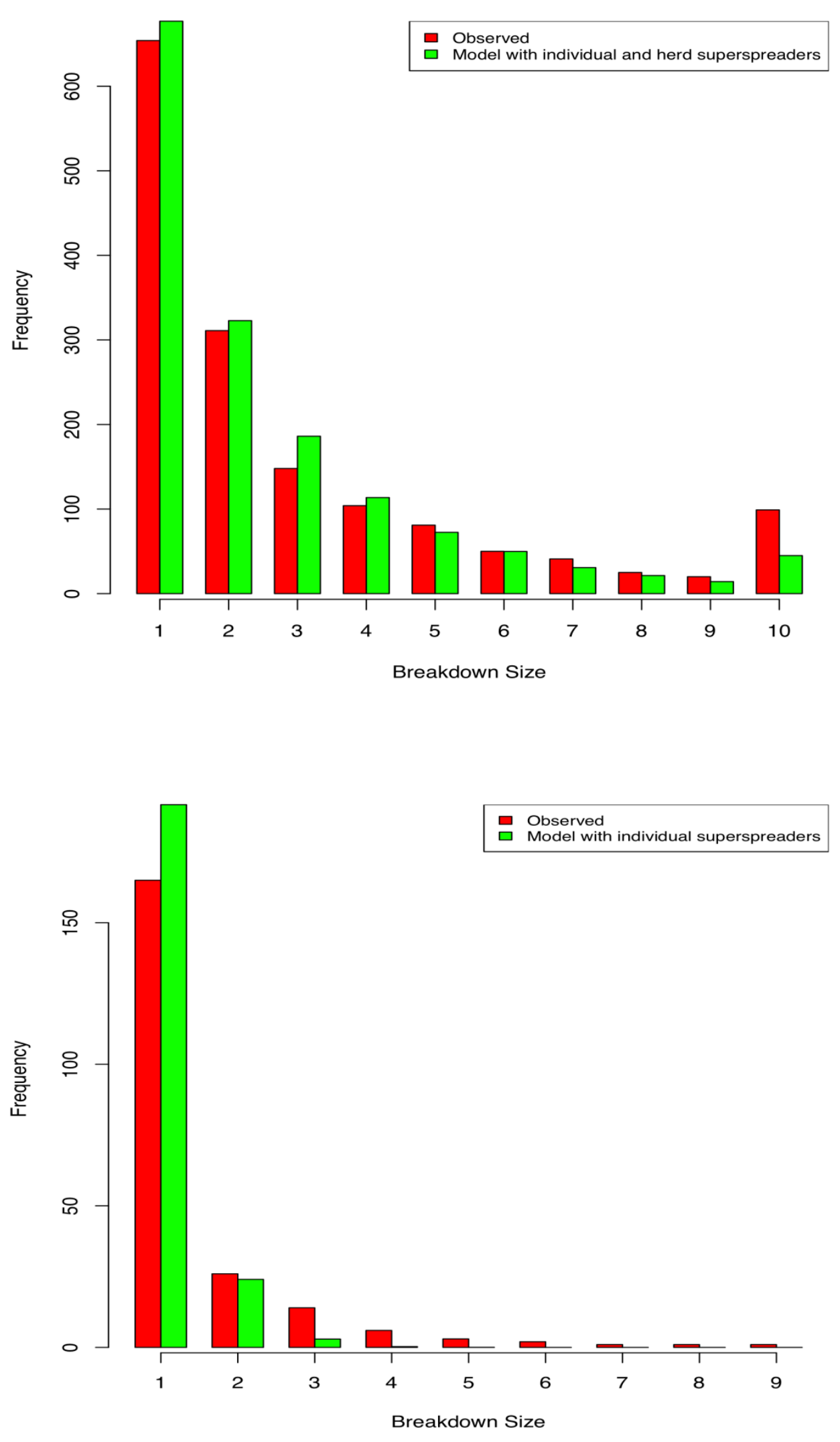
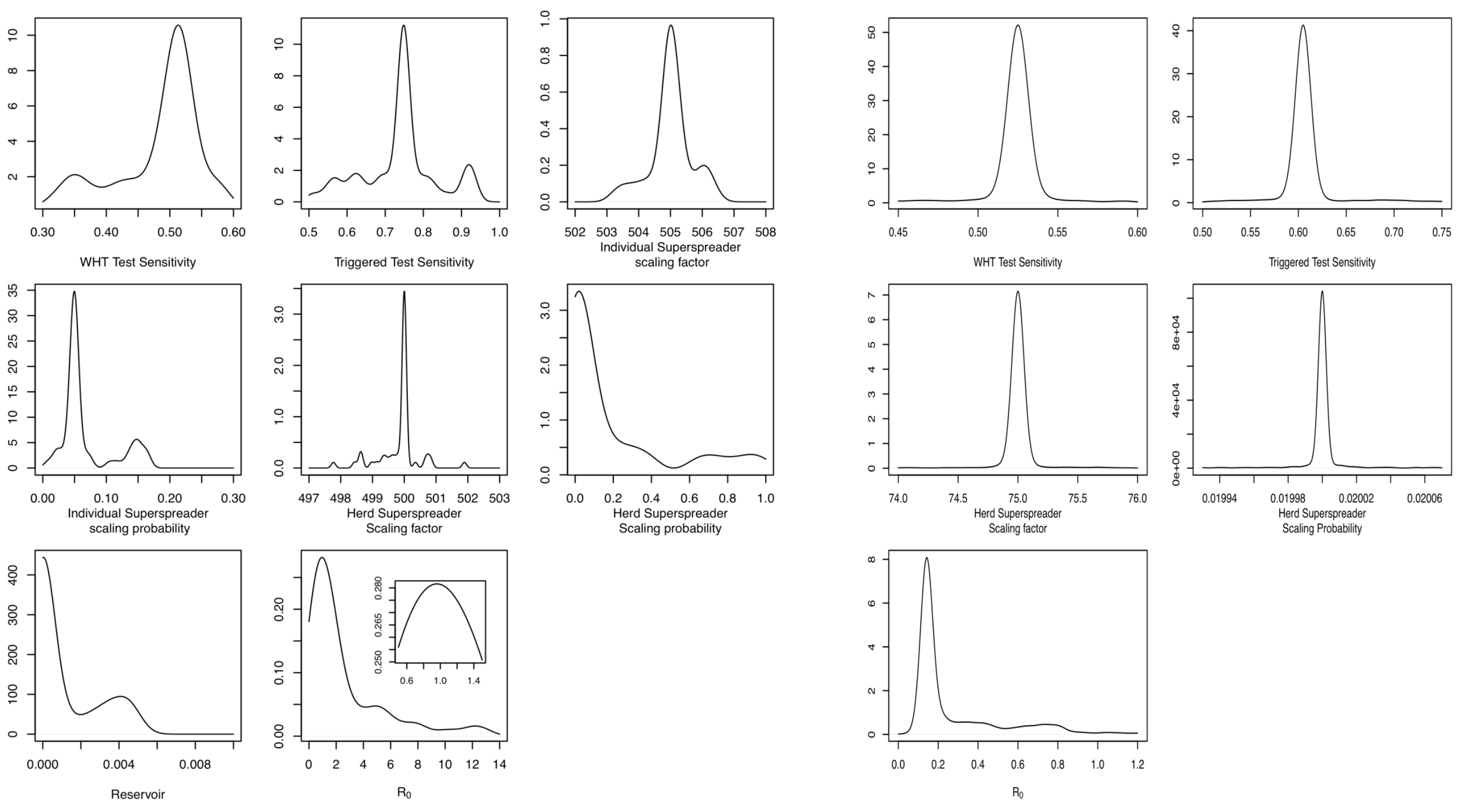
- MCMC walk through parameter space to maximize the likelihood based on breakdown size (number of reactors in a breakdown) at first detection.
- Super infectious animals and super-spreader herds important to explain outbreaks in annual testing areas.
- Super infectious animals alone enough to explain outbreaks in 4 year areas.
- Sensitivity of the WHT is poor (50-55%) and allows for infection to persist in the herd.



Cumulative time to detection in a herd in 1 year and 4 year testing areas for the preferred model in each case. Initially a single infected animal is introduced into the herd and the infection is allowed to spread until a positive test results in a breakdown. Both models agree that ~ 50% of infection is detected at the end of the testing period (either 1 year or 4 year). The lower detection rates for 4 year testing areas is due to post-mortem detection rather than routine herd testing.



Breakdown size (number of reactors in a breakdown) distribution for 1 year (top) and 4 year (bottom) areas using the appropriate model in each case. We maximize a likelihood based on this multinomial distribution.



Posterior kernel density estimates for the parameter distributions for the preferred model for 1 year (left) & 4 year (right) testing areas. Using an AIC score, adding individual and herd super-spreaders to the model provides the best fir to the observed breakdown distribution while simply adding individual super-spreaders was sufficient for 4 year areas.

The maximum likelihood estimate for R0 is much less than 1.0 for low risk areas and approximately 1.0 for high risk areas but with a substantial tail on the distribution that lies above one. Therefore a large proportion of herds could sustain disease transmission.

However, in the absence of super-spreaders or high transmission herds (not shown here) the value of $R_0 < 1$, highlighting the importance of super-spreaders in the model fit.

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