The hidden burden of bovine tuberculosis in Irish cattle

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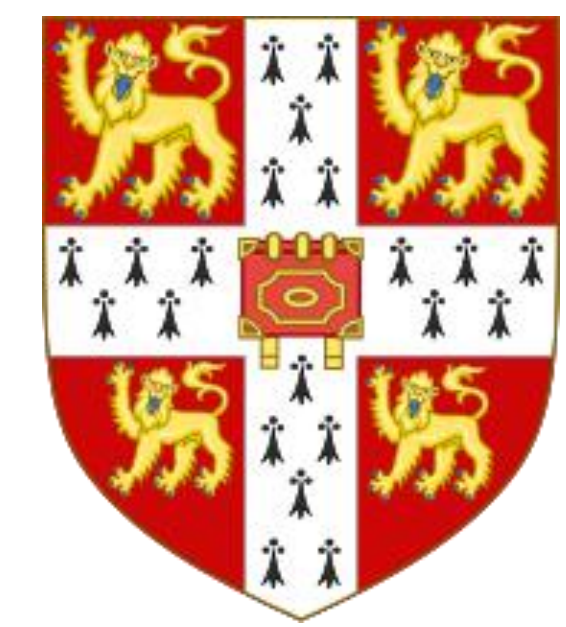
Introduction and aims

In Ireland, *M. bovis* is the most prevalent of the *Mycobacterium tuberculosis* complex bacteria in animals, causing bovine tuberculosis (bTB) in cattle and wildlife. Because of its zoonotic potential and impacts on livestock health, and the need to maintain access to international markets for cattle product exports, there has been a national eradication programme in place since 1954. Despite early reductions in bovine tuberculosis in cattle, progress of late has plateaued, and bovine tuberculosis incidence has increased from 3.27 per cent of herds with new outbreaks in 2016 to 4.89 per cent in 2023. The current eradication programme has cost approximately €2 billion over the past twenty years, and increasing levels of bTB threaten our cattle product export market access which, in 2022, was worth €9.45 billion. Uncertainties relating to complex multi-species epidemiology of bTB, highly imperfect diagnostic testing, in association with robust stakeholder debate about cattle and wildlife related control measures, create disease control challenges.

To improve our understanding of *M. bovis* transmission within herds, to estimate where in the diagnostic testing process infected cattle are being missed, and to enable exploration of the potential impact of interventions, we built a within-herd transmission model.

Methods and preliminary results

We simulated introduction, spread and detection in 9,137 Irish cattle herds, with bTB breakdowns (outbreaks) ending between 2015 and 2020. Demographic, movement, spatial and neighborhood bTB burden data were incorporated, and the processes of the Irish diagnostic and control system were integrated. Stochastic, continuous-time model outputs were fitted to data using approximate Bayesian computation.

Key metrics for model calibration and validation included breakdown recurrence patterns, case counts, and whether the breakdown was initially detected by routine slaughterhouse inspection for lesions, or by skin testing.
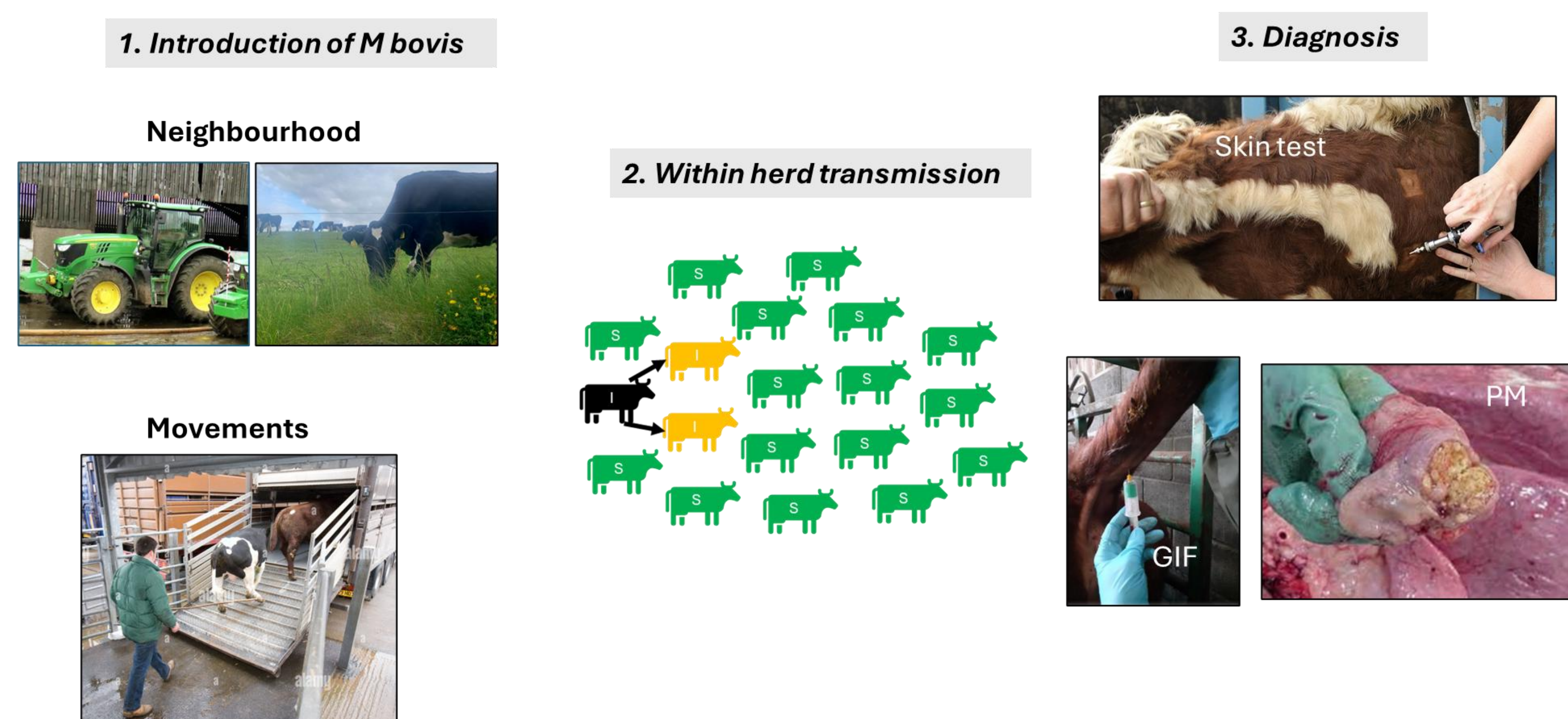

Figure 1: Introduction, within herd transmission, diagnosis and controls were modelled.

Figure 3: Simulated causes of breakdown recurrence within three years from current best-fit model. Dots represent simulation outputs from a weighted sample of 100 discrete collections of parameters (particles) in the end round of approximate Bayesian computation. These are summarized by the boxplots.
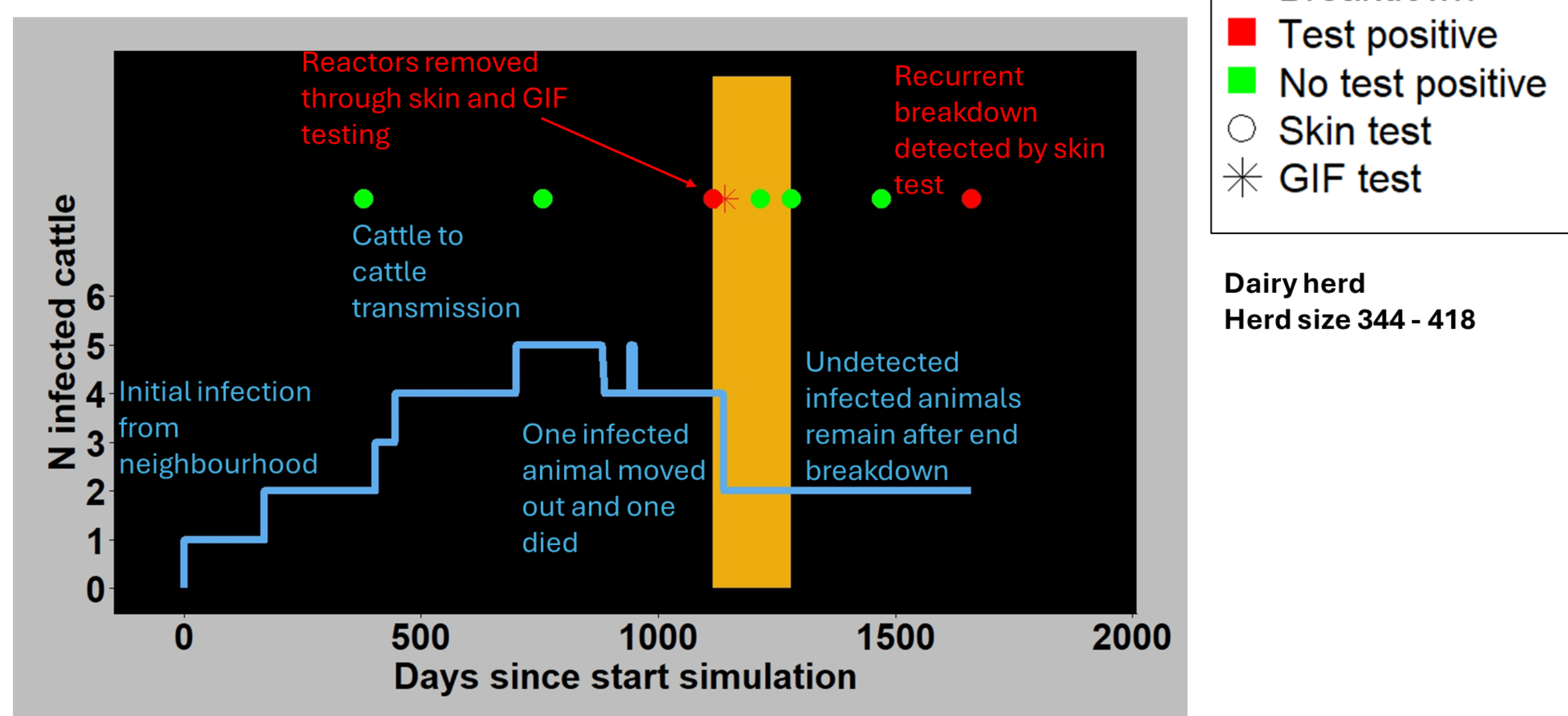

Figure 2: Example model output showing introduction, within herd transmission, a positive test initiating a breakdown (trade restrictions and extra testing), retained infected cattle, and a recurrent breakdown . This is one of many repeat simulations of a single herd.
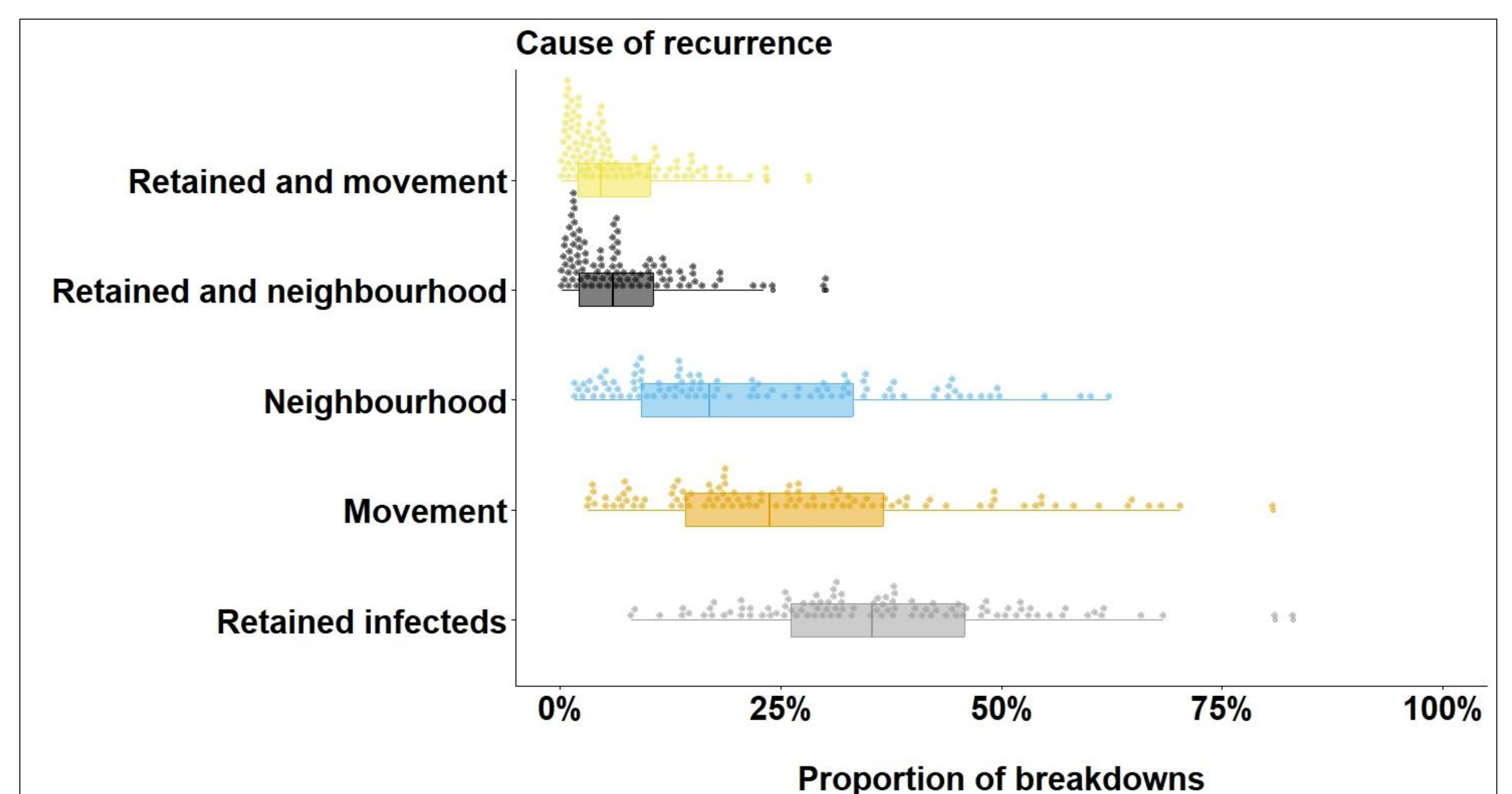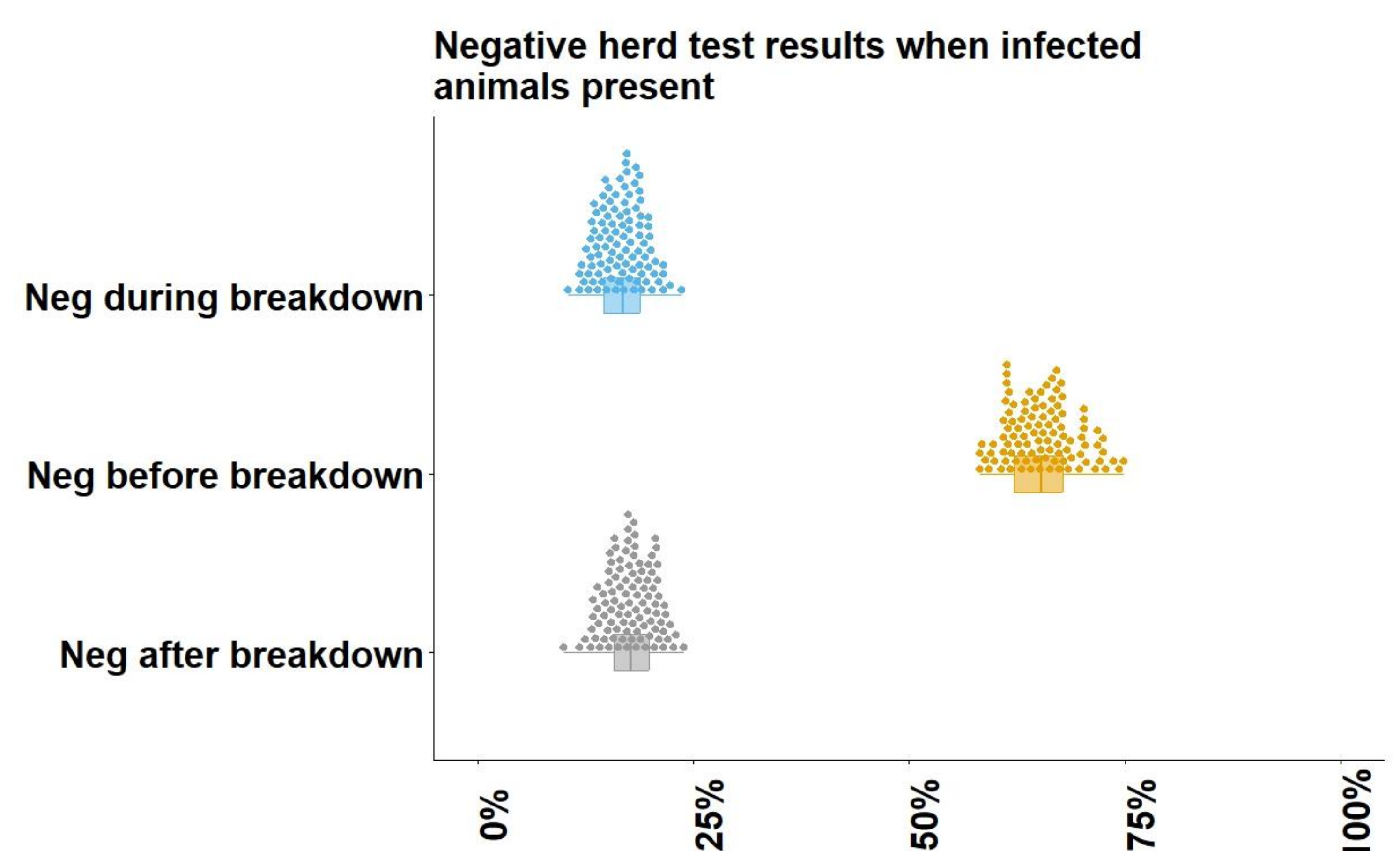

Figure 4: Negative herd level diagnostic tests occurring (proportions) before, during and after initial outbreak (breakdown) detection) from current best fit model.

Conclusions to-date

- Most infected cattle are being missed by the diagnostic testing system in advance of initial breakdown detection.
- Retained infected cattle are the most dominant driver of recurrent breakdowns but repeat introductions from inward movements and the farm neighbourhood also play important roles.