Inference of a Bovine Respiratory Disease mechanistic model

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Impact of Data Quality and Stochasticity on Parameter Estimation of a Bovine Respiratory Disease Propagation Model

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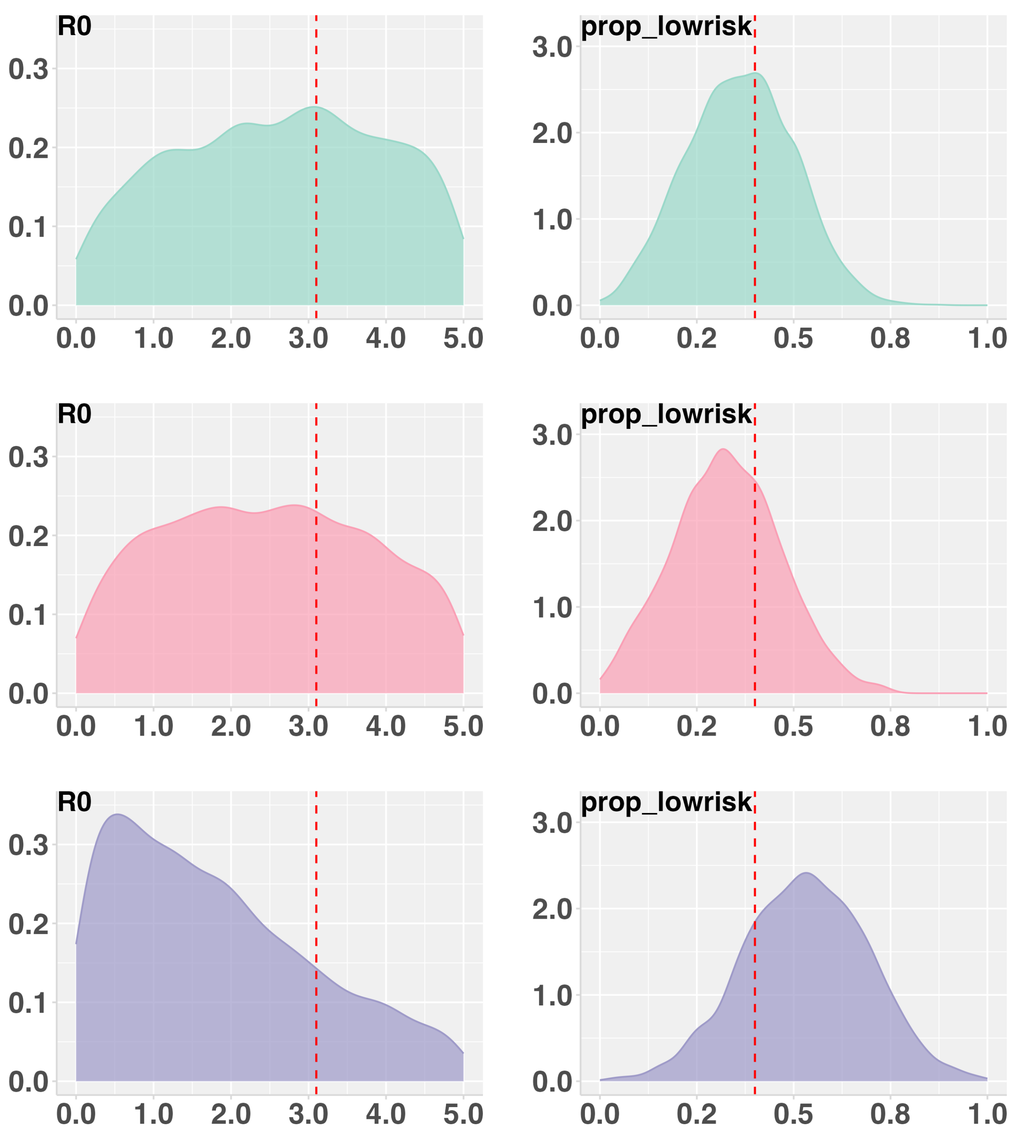
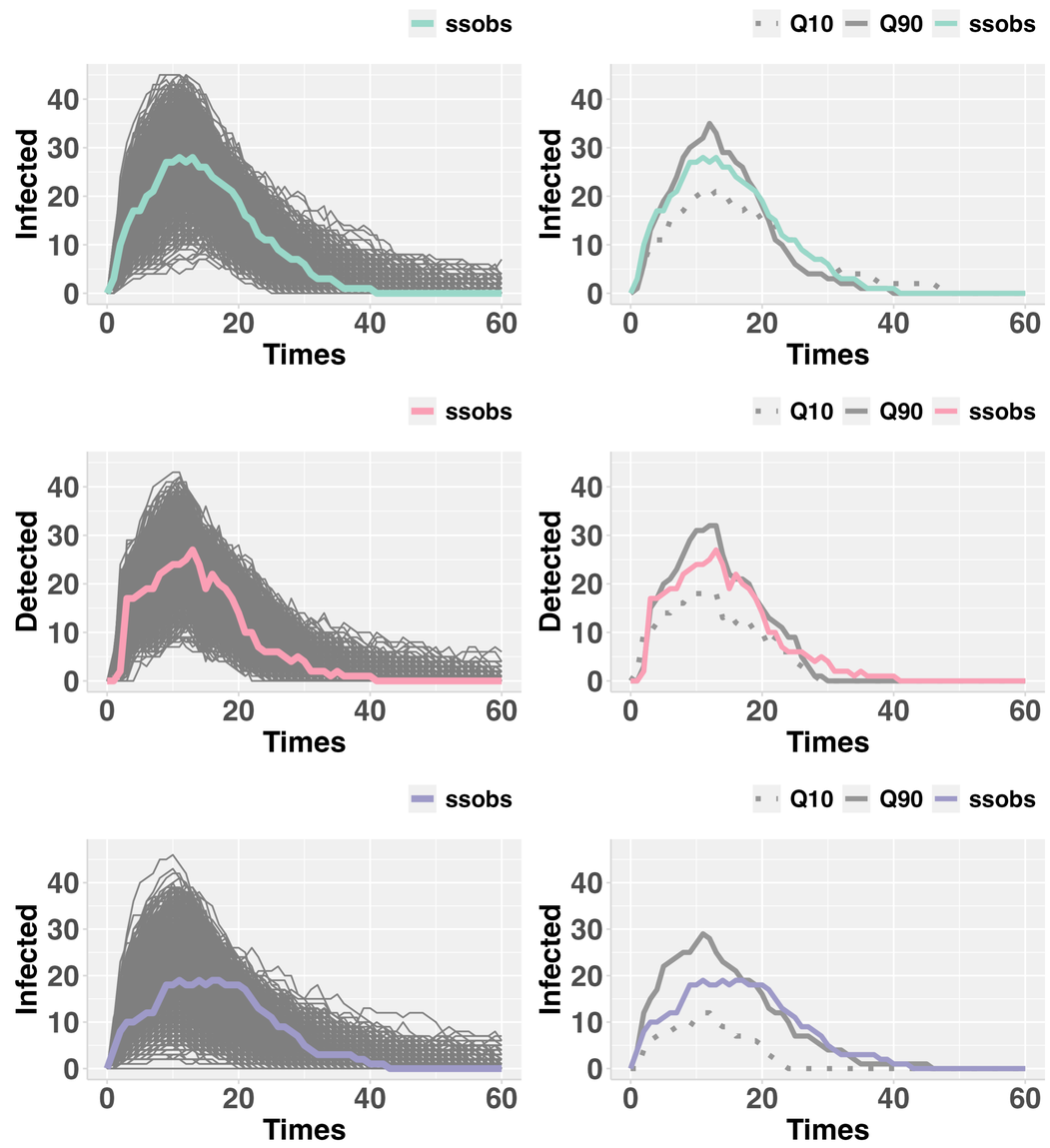
Bovine Respiratory Disease (BRD), a significant enzootic disease affecting young cattle, leads to economic losses, animal welfare concerns, and increased reliance on antimicrobial usage. To better understand and anticipate BRD occurrence on-farm under diverse conditions, INRAE developed a stochastic epidemiological model[1] using the EMULSION framework[2]. Accurate calibration of such a model is crucial for reliable predictions, which is often complicated by the heterogeneous and incomplete nature of available data, as well as model stochasticity. This study aims to assess the impact of these factors on parameter inference.

Results



Density of the 3000 last parameter set accepted, which form the posterior of parameters R_0 and prop_lowrisk; Vertical lines correspond to the target parameter values; the observed trajectory being respectively the F1, F2 and F3.



First column: trajectories obtained from the 3000 accepted particles (gray) and observed trajectories; Second column: quantile trajectories (Q10: dotted line; Q90: solid line) obtained from the 3000 accepted particles (gray), observed trajectories being colored.

Methods

- **Approximate Bayesian Computation** method based of **Sequential Monte Carlo** approach (ABC-SMC[3]) applied to the BRD model, using the **new R package BRREWABC[4]** developed at INRAE.
- **Parameters estimated:** transmission rate (R_0); initial proportion of low risk (*prop_lowrisk*) animals in a batch
- **Data:** synthetic data.
- Pathogens: Bovine Respiratory Syncytial Virus (BRSV)
- **Scenarios: F1**: large unique batch of 50 animals and complete observed data (summary statistics: all infected animals); **F2**: large unique batch of 50 but data degradation (summary statistics: all animals detected as infected); **F3**: 5 batches of 10 to increase biological stochasticity (summary statistics: all infected animals).
- Individual risk level of animal exposed to BRD: low vs. high risk.
- Monitoring periods: 30 days with a time step of 12 hours.

Conclusion

Robustness of inference: the posterior distributions consistently included the parameter values used to generate the synthetic data (observed data), demonstrating the model robustness even when estimated values deviated from initial parameters.
Stochastic nature & data quality: the inherent model randomness and data quality can lead to significant variations between simulations, explaining why some estimated values differ from the initial ones without indicating model inefficiency.
Reliable predictions: despite variations due to stochasticity, the model successfully produced trajectories that closely matched observed data, affirming the reliability of inference procedures.

References
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2. Picault et al. 2019. EMULSION: transparent and flexible multiscale stochastic models in human, animal and plant epidemiology. PLoS Comput Biol e1007342.
3. Del Moral et al. 2006. Sequential Monte Carlo samplers. J R Stat Soc B 68, 411-436.
4. Beaunée. 2024. BRREWABC: Batched Resilient and Rapid Estimation Workflow through Approximate Bayesian Computation. https://github.com/GaelBn/BRREWABC

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