

Exploring modelling approaches to address the dynamic nature of animal health

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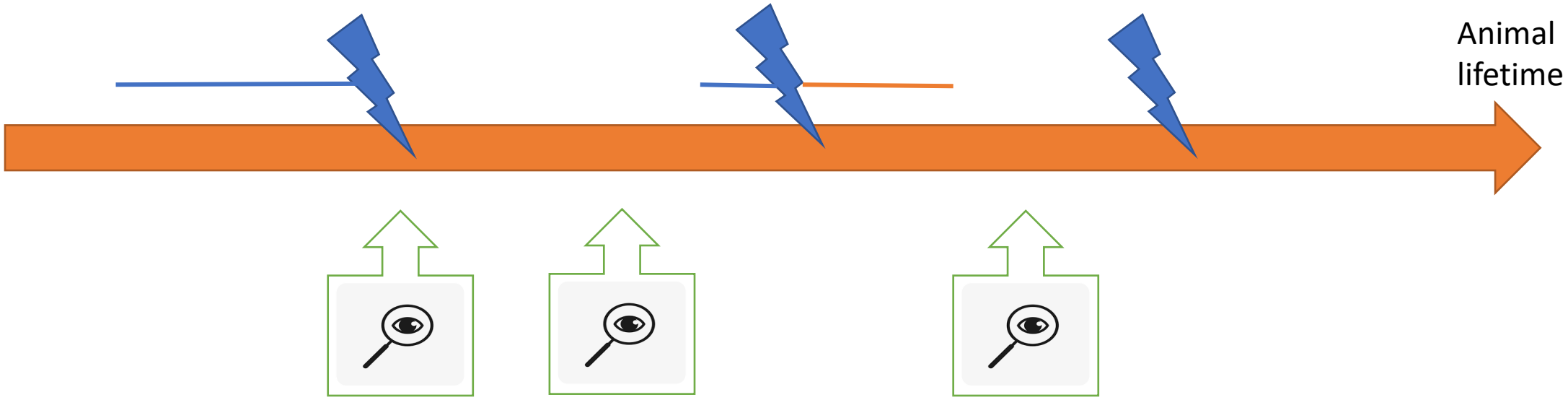
What are we missing when studying health traits?



- Only ponctual health checks (veterinary visits, monthly SCS…)
- Some health events may be entirely missed
- Early warning signs are not considered (enough), same for after effects

➔ Missing the dynamic nature of animal health!

How to access this dynamic nature?

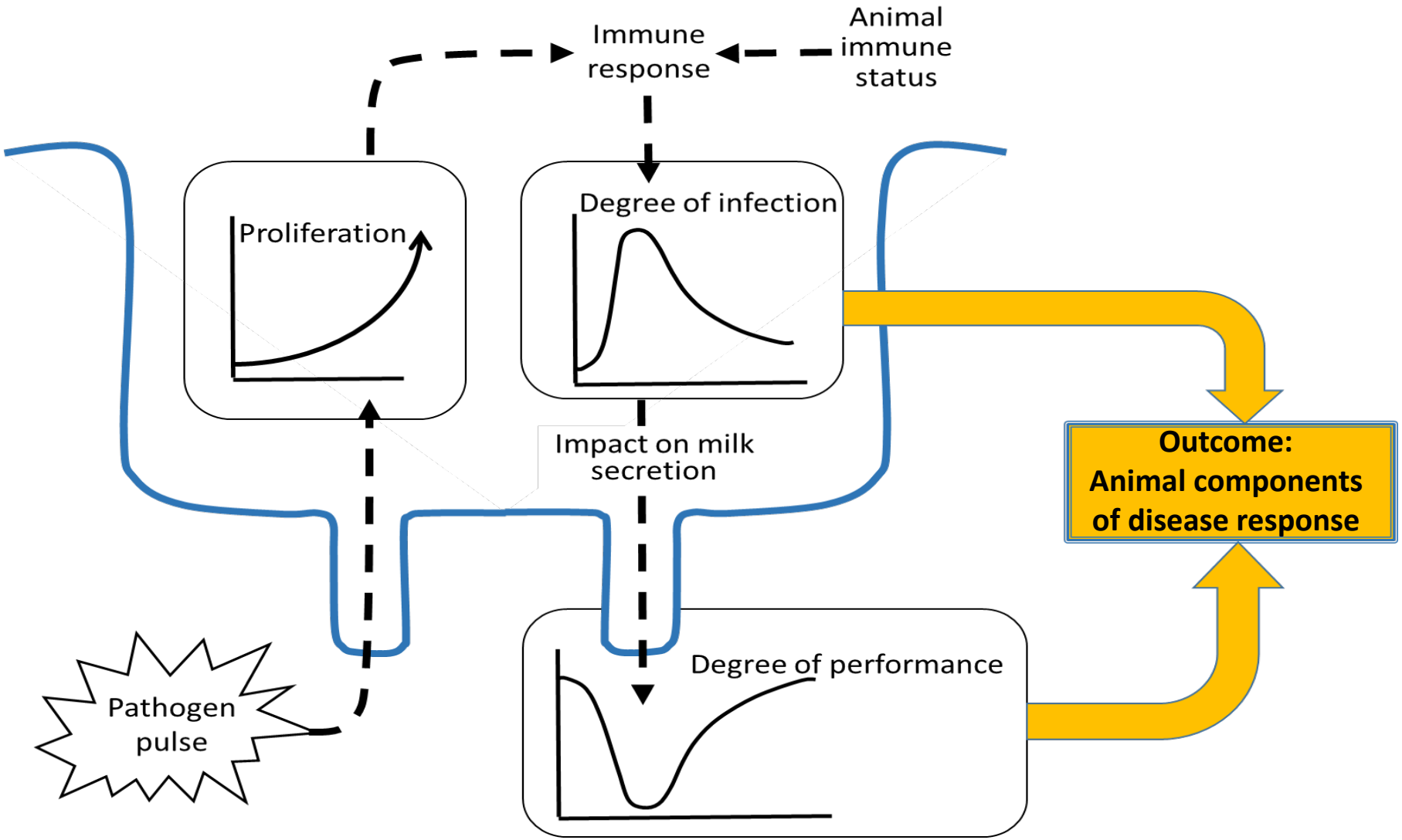
- By using continuous monitoring of performances or behavior:
  - ➔ it works (Poppe et al. 2020 ; Lardy et al. 2023)
  - ➔ consequences of health rather than health itself
  - ➔ early detection or resilience
- By using continuous monitoring of traits directly related to infection or immune response and modelling approaches
  - ➔ development of PLF (ex: OCC, herd navigator, O-CMT…)
  - ➔ existing models for the interaction between inflammatory cells and bacteria (Detilleux et al. 2006)
  - ➔ use of modelling to access to the animal immune capacity

Objective of this work

Propose a model that can be used to derive genetic components linked to the dynamic of the ability to deal with a disturbance

➔ Example of a mammary infection event

General concept



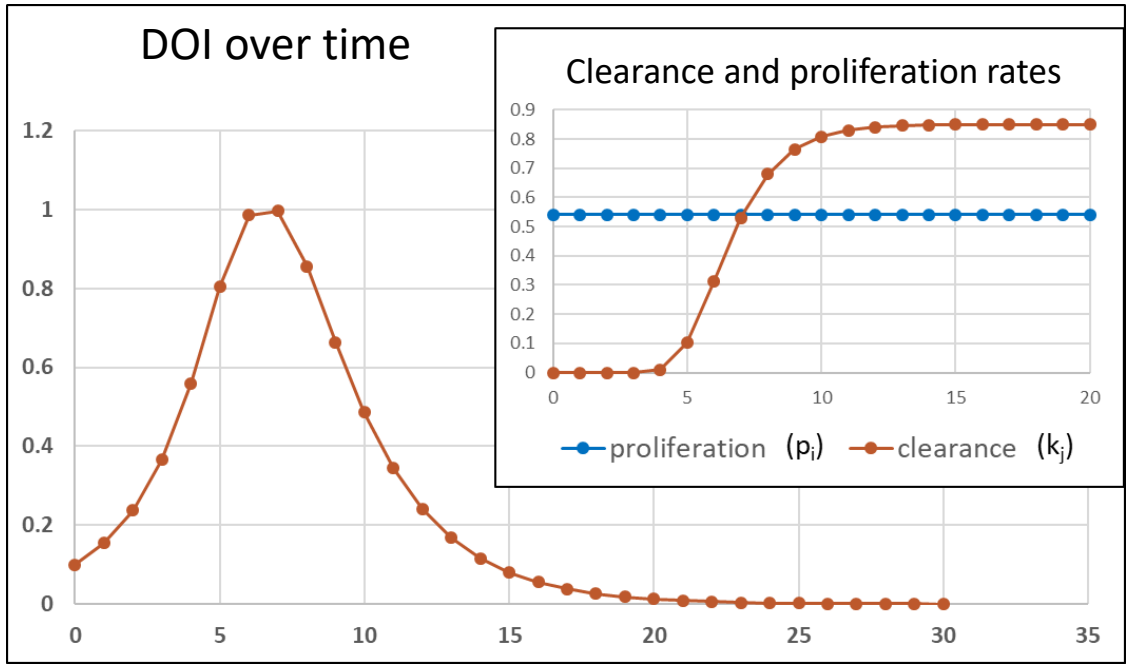
Degree of infection (DOI)

- Scaled parameter from SCC: varies from 0 (no infection) to 1 (max level of infection), varies with time
- Depends on the pathogen proliferation rate (kp) and clearance of the pathogene by the animal (xac)

$$\frac{\mathrm{d}x_{\mathrm{DOI}}}{\mathrm{d}t} = k_{\mathrm{p}} \cdot x_{\mathrm{DOI}} - x_{\mathrm{ac}} \cdot x_{\mathrm{DOI}}$$

- Gompertz model for clearance

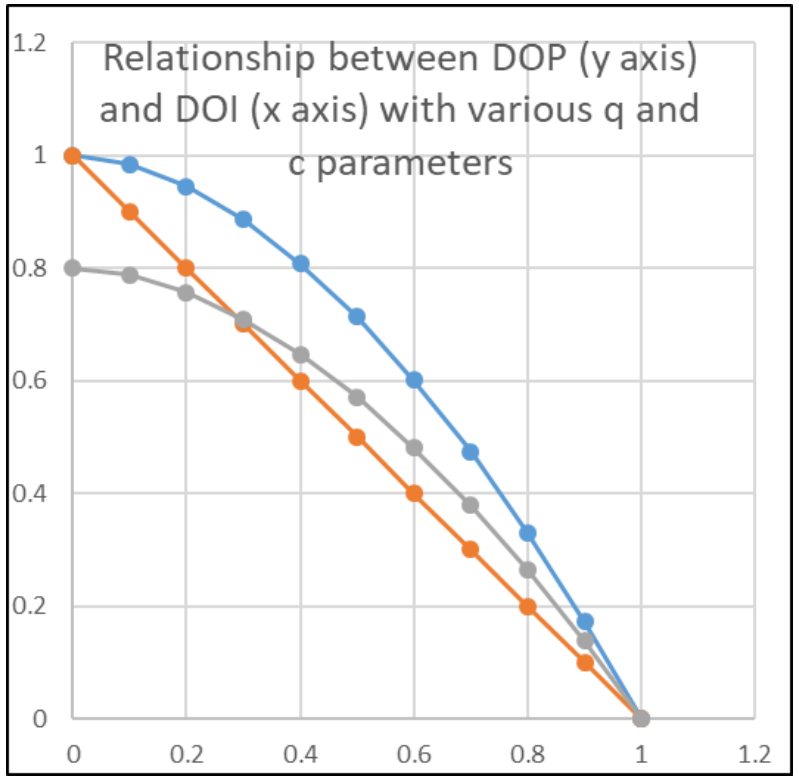
$$x_{\mathrm{ac}} = A \cdot \exp\left[-\exp\left(-B \cdot (t - T)\right)\right]$$



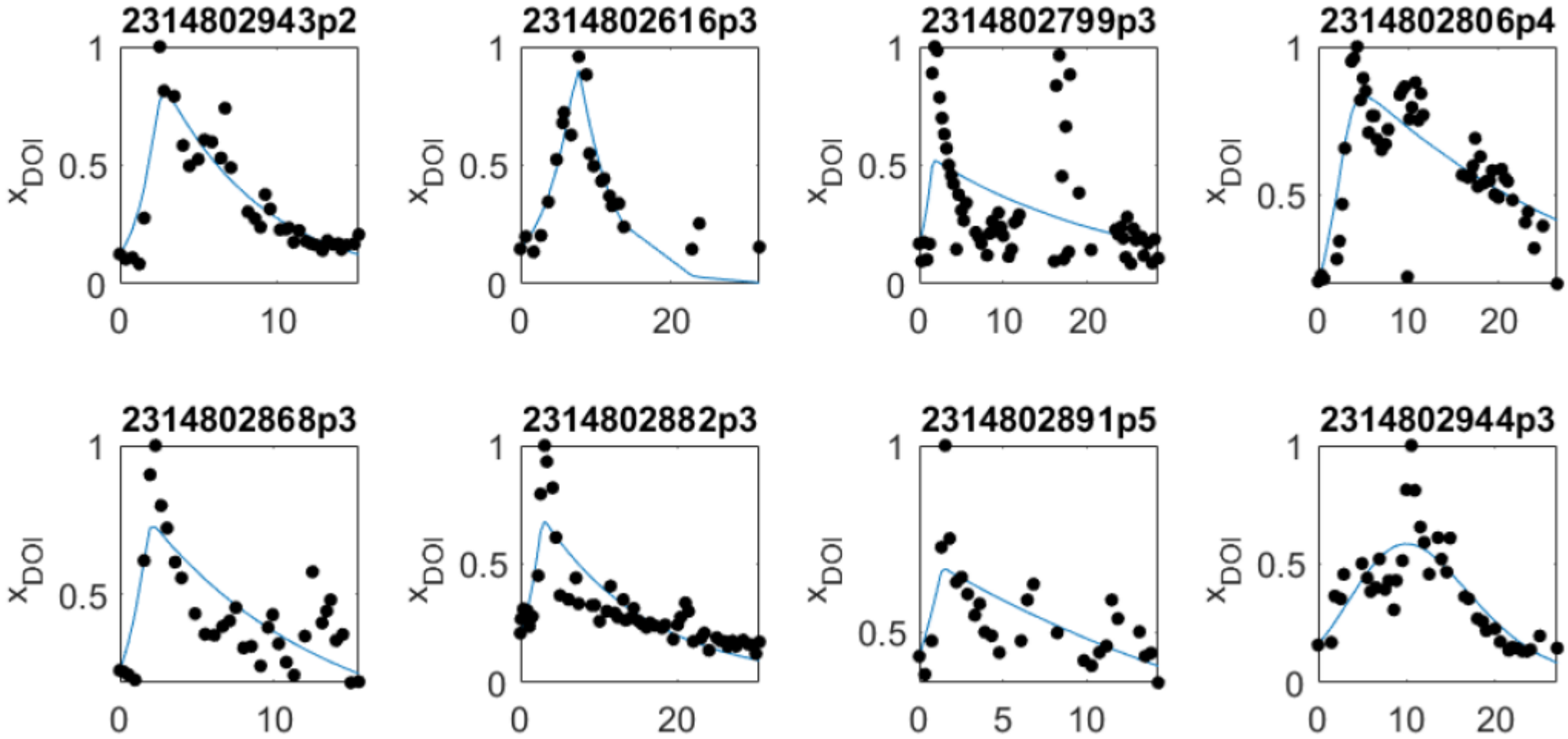
Degree of performance

- Same principle as DOI (0 to 1)
- Consequence of DOI
- Able to take into account a lag, the animal tolerance and potential after effects

$$DOP_t = (1-c)(DOI_{(t-lag)}{}^{q})$$



How does it work with real data?



What to use for this model for?

- NOT to predict the animal response to a given event
- To test general hypotheses in immunology prior experimentations
- For genomic prediction
  - ➔ Need for an extra step not included yet (animal components NE genetic components, h^2 and rg estimations…)
  - ➔ Need for a reference population
  - ➔ what trait(s) do we want to select for?
- Other perturbations than infection (heat stress?)

What's next?

- First paper to be submitted shortly with the concept
- Additional developments and tests on-going
- Data collection to access the genetic part
- WANTED: open to collaboration

Thank you for your attention

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