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A multi-scale, multi-paradigm epidemiological modelling language for investigating Q Fever regional infection dynamics

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Understanding Q fever spread

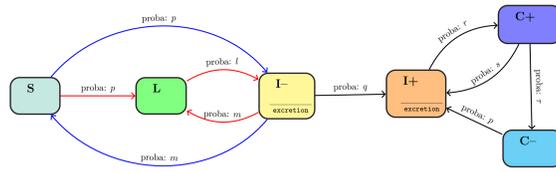
The regional spread of Q fever, an endemic cattle zoonosis, relies upon airborne transmission and between-herd trade movements. Our goal was to better understand the contribution of each pathway to yearly herd incidence by coupling within- and between-herd dynamics.

To accelerate model design, explore multiple assumptions at each scale with a reduced amount of code to write, and enhance reliability, reusability and reproducibility, we used a generic framework, EMuLsion, which provides a domain-specific language (DSL) for explicitly describing all components of epidemiological models, and relies upon a multi-level agent-based architecture to encompass existing modelling paradigms [1].

Exploring model assumptions

Within-herd level

- simplification of previous model [2]
- intermittent shedding: **return to S** vs. **latent state**

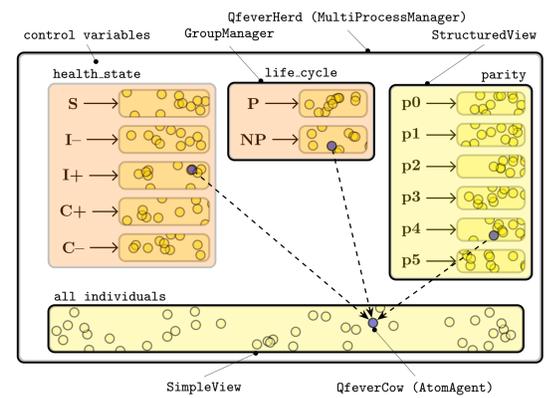


Between-herd level

- heterogeneity in herd characteristics
- external risk at purchase
- Ermak-Stockie vs. Gaussian aerial dispersion

Within-herd Q fever model

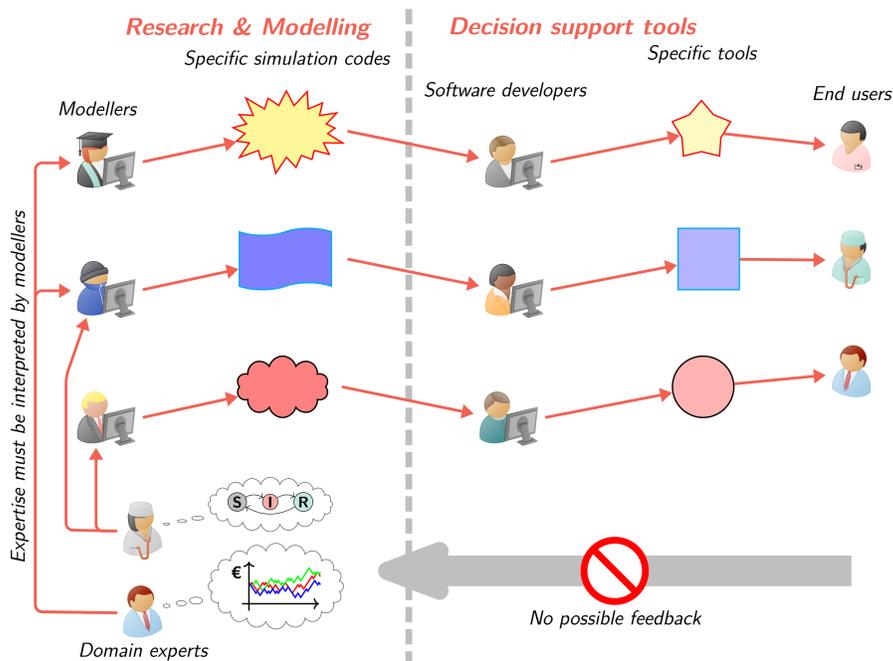
Automated agents aggregation based on concerns: an hybrid approach



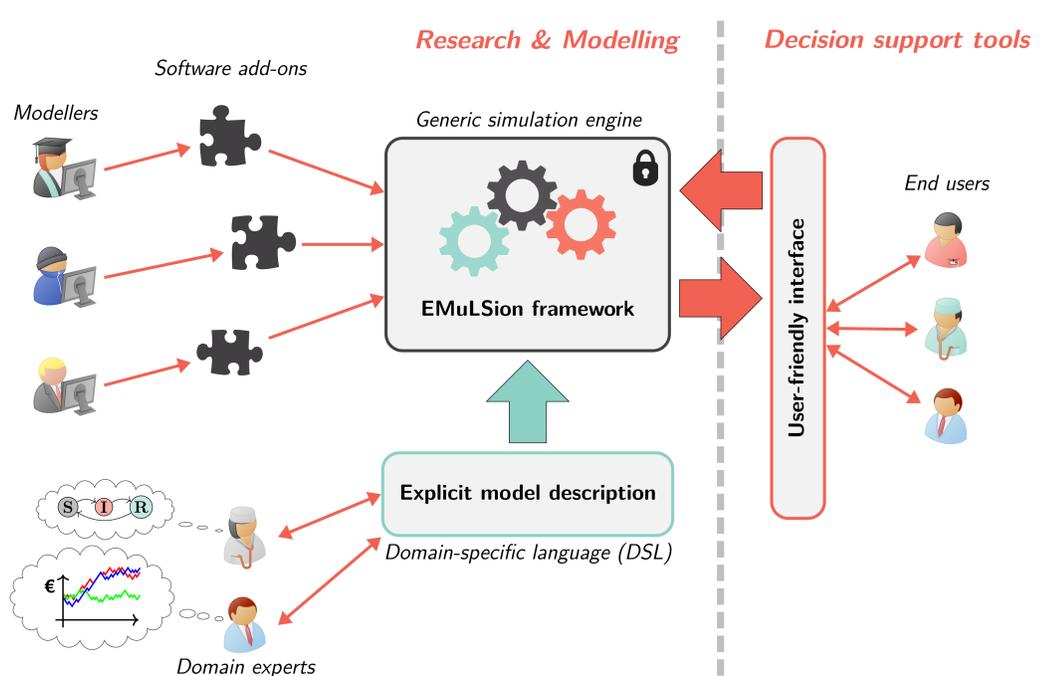
individual states preserved + efficient computation

The EMuLsion approach: involving experts and users throughout model design

Classical situation: ad-hoc programs

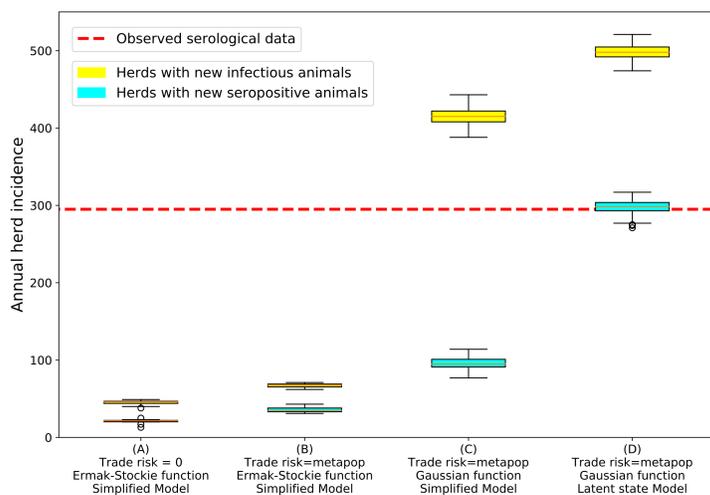


EMuLsion: Domain-Specific Language + Simulation framework

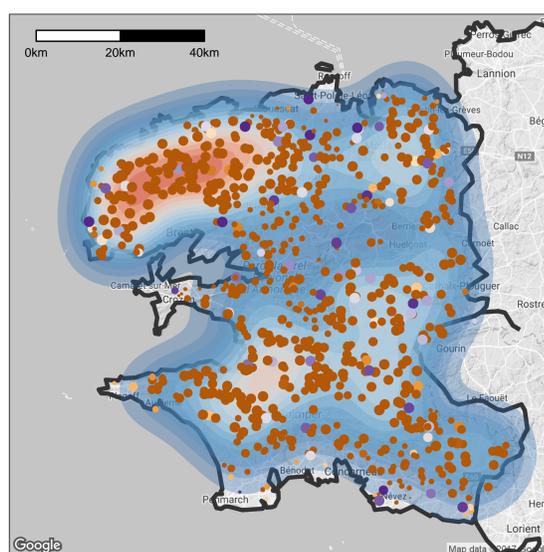


Model calibration at regional scale and influence of herd density

- within-herd model calibrated on previous model [2]
- between-herd model calibrated on observed annual herd incidence



Distribution of annual herd incidence as output of different models based on the combination of variants of three main features.



Map of Finistère with the density of initially infected herds (2012) and the location of herds infected in at least one run. Color shows the proportion of infections caused by wind vs. trade movements.

Future work

- extend DSL + framework to other diseases
- develop modelling standard in epidemiology
- automatize production of decision support tools

References

- [1] S. Picault, Y.-L. Huang, V. Sicard, and P. Ezanno (2017). Enhancing Sustainability of Complex Epidemiological Models through a Generic Multilevel Agent-based Approach *26th Int. Joint Conf. on Artificial Intelligence*.
- [2] A. Courcoul, H. Monod, M. Nielsen, D. Klinkenberg, L. Hogerwerf, F. Beaudou, and E. Vergu (2011). Modelling the effect of heterogeneity of shedding on the within herd *Coxiella burnetii* spread and identification of key parameters by sensitivity analysis *J. Theor. Biol.* **284**(1):130–141.

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