From mechanistic models to decision-support tools

Generating user-friendly web application from artificial intelligence and software engineering methods

Sébastien Picault, G. Niang, V. Sicard, B. Sorin, S. Assié, P. Ezanno

INRAE, BIOEPAR, Dynamo – August 28, 2024

Challenges in mechanistic models & tools

Developing & revising mechanistic models:

- is essential to understand, anticipate and control pathogen spread in contrasted situations
- takes time (conceptualization + software implementation)
- computer code deprives non-computer scientists of their ability to check and revise assumptions ("black box")

Using models:

- requires a broad expertise (code handling + large number of parameters + large number of outputs)
- often leads to "generic" results (stochasticity + scenarios but also "average" calibration)

Developing decision-support tools based on mechanistic models:

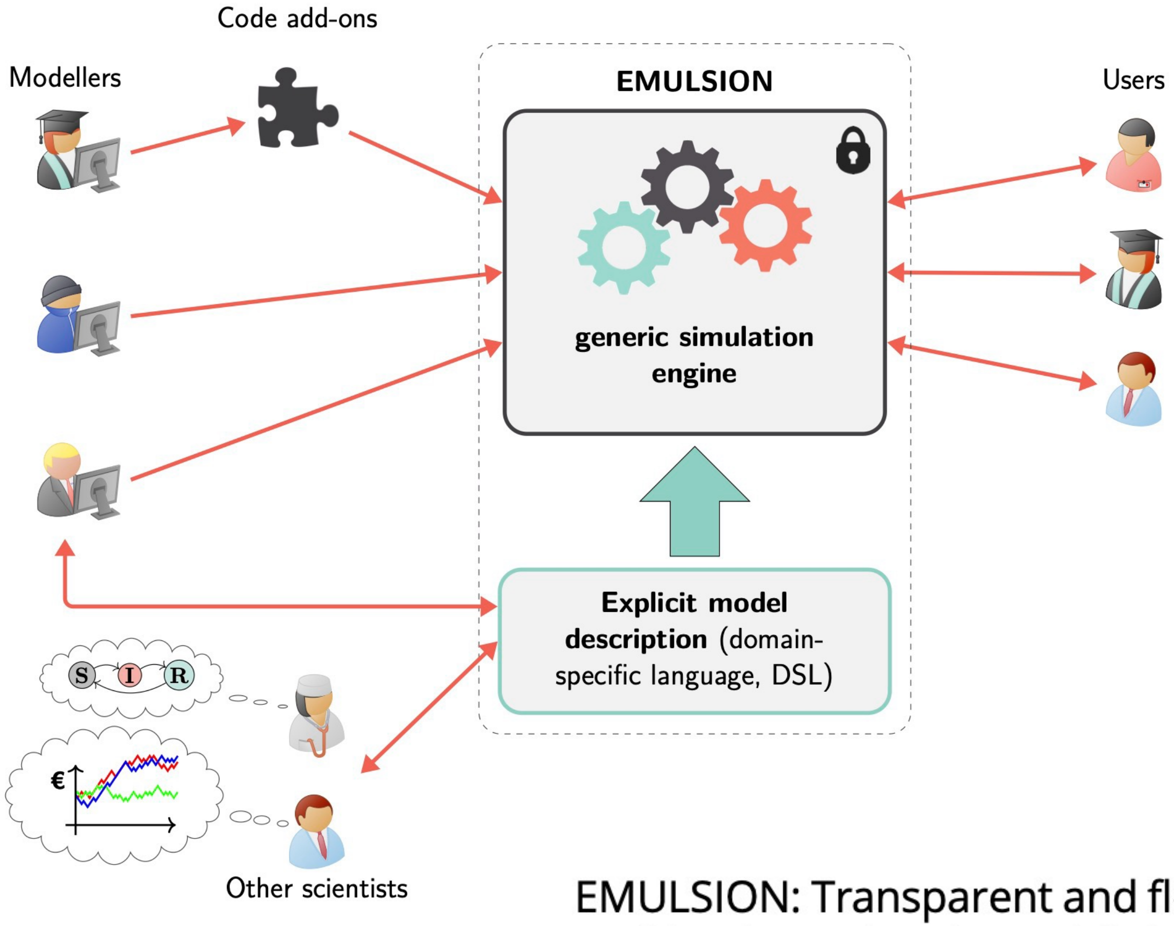
- requires further software developments (to target relevant use cases and provide meaningful outcomes)
- requires evolvability (tool features + model updates)

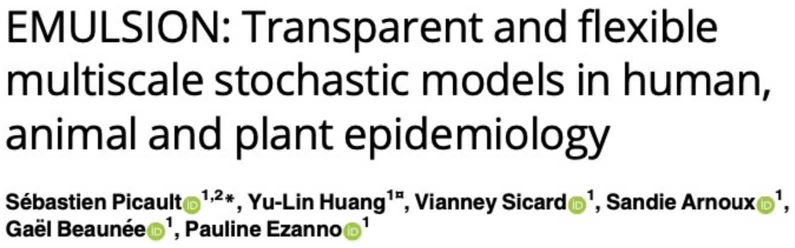
EMULSION: AI methods to foster the co-construction of models

- declarative language for epi models
- explicit models
  - → structured text: readable, revisable
  - → co-construction with non-modellers
- no (little) programming code
  – provides built-in calculation processes
- gains time, reliability, evolvability

AI → multi-level agent-based systems
knowledge representation

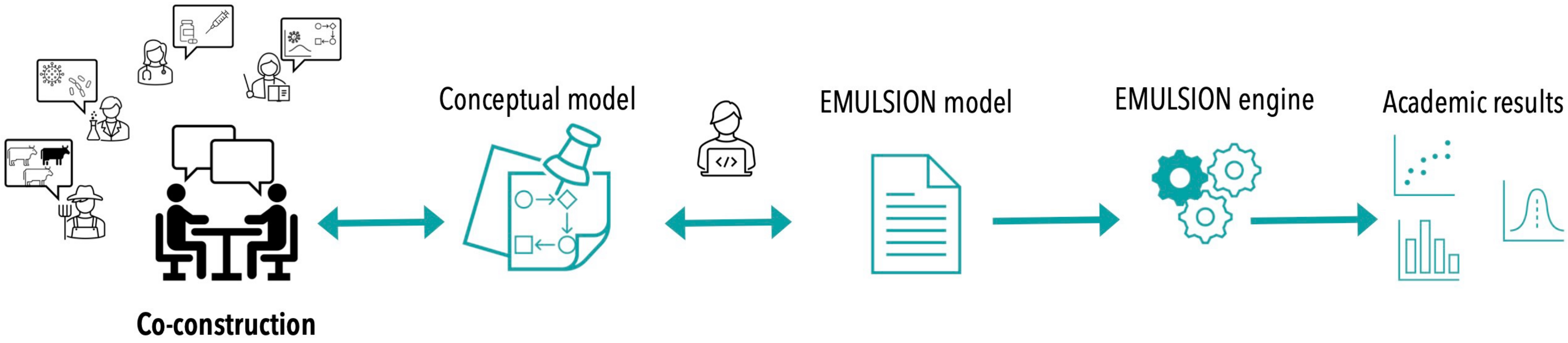
Software Engineering → dedicated language




EMULSION: Transparent and flexible multiscale stochastic models in human, animal and plant epidemiology

Sébastien Picault[1,2]*, Yu-Lin Huang[1¤], Vianney Sicard[1], Sandie Arnoux[1], Gaël Beaunée[1], Pauline Ezanno[1]

PASTE: from models to web tools


Co-construction

Conceptual model

EMULSION model

EMULSION engine

Academic results

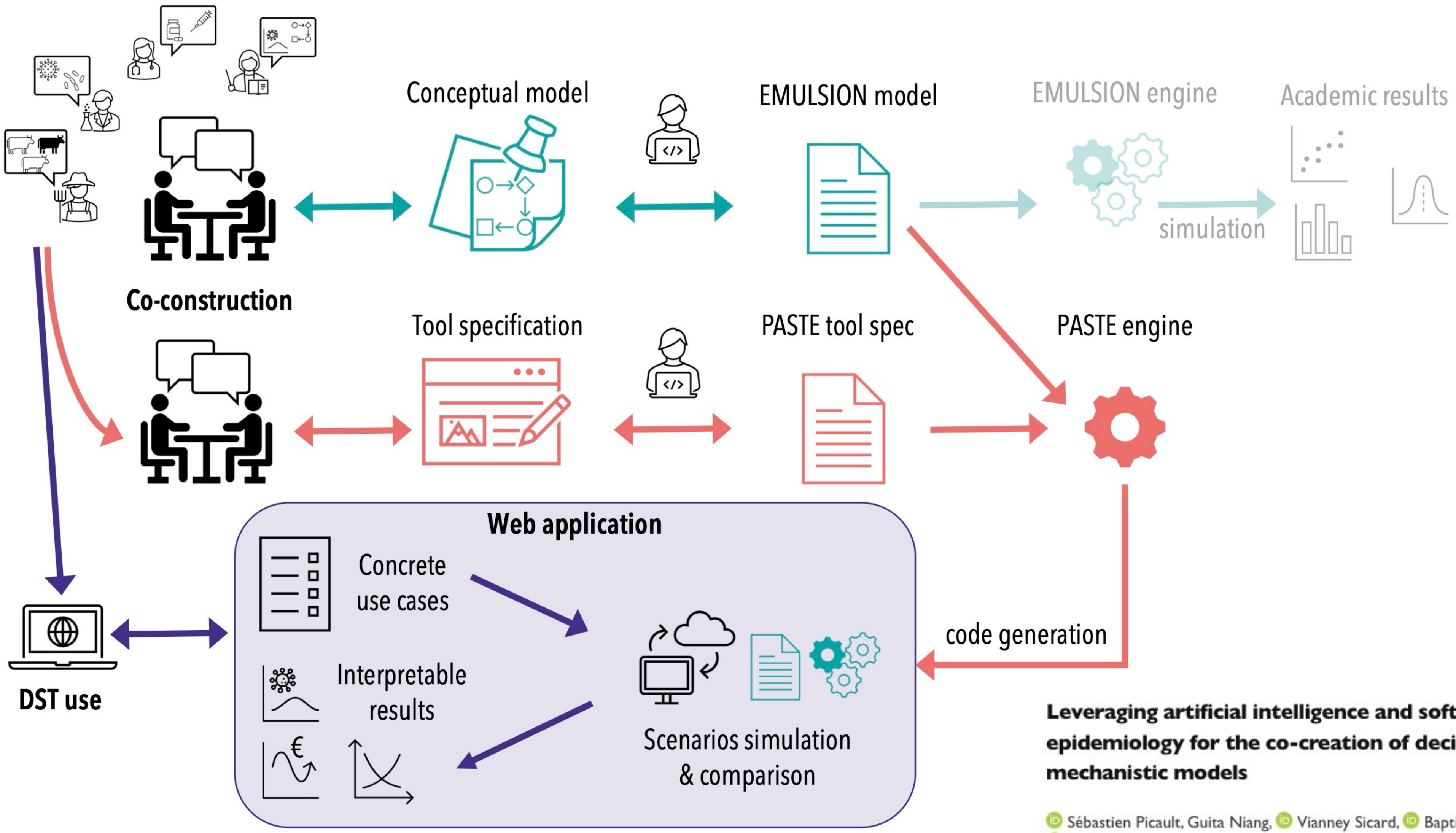
using EMULSION for co-constructing models → based on a dedicated language

- human-readable
- machine-readable

core of a decision-support tool = specific way of using a model

→ build a dedicated language !

PASTE: from models to web tools

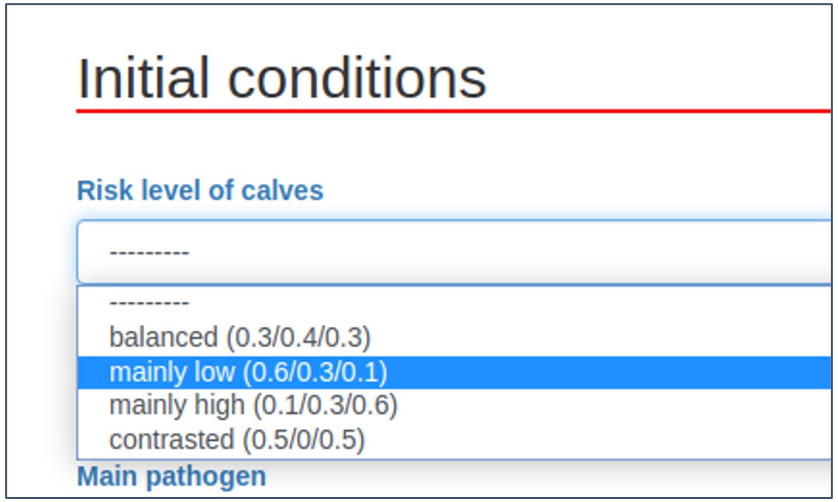


Leveraging artificial intelligence and software engineering methods in epidemiology for the co-creation of decision-support tools based on mechanistic models

Sébastien Picault, Guita Niang, Vianney Sicard, Baptiste Sorin-Dupont, Sébastien Assié, Pauline Ezanno

doi: https://doi.org/10.1101/2023.09.03.555060

PASTE: Deployment & utilisation

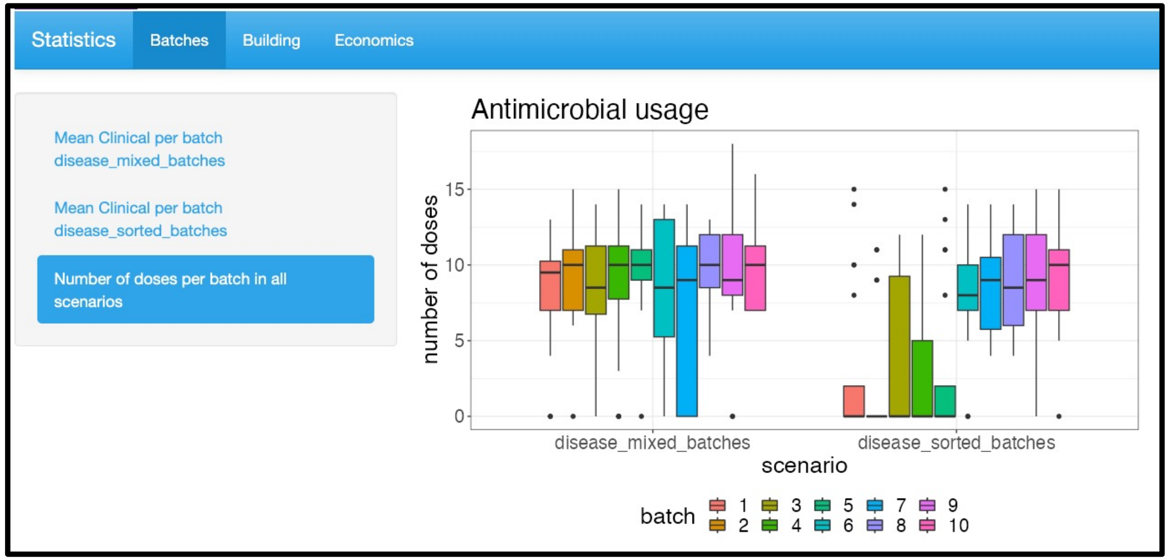


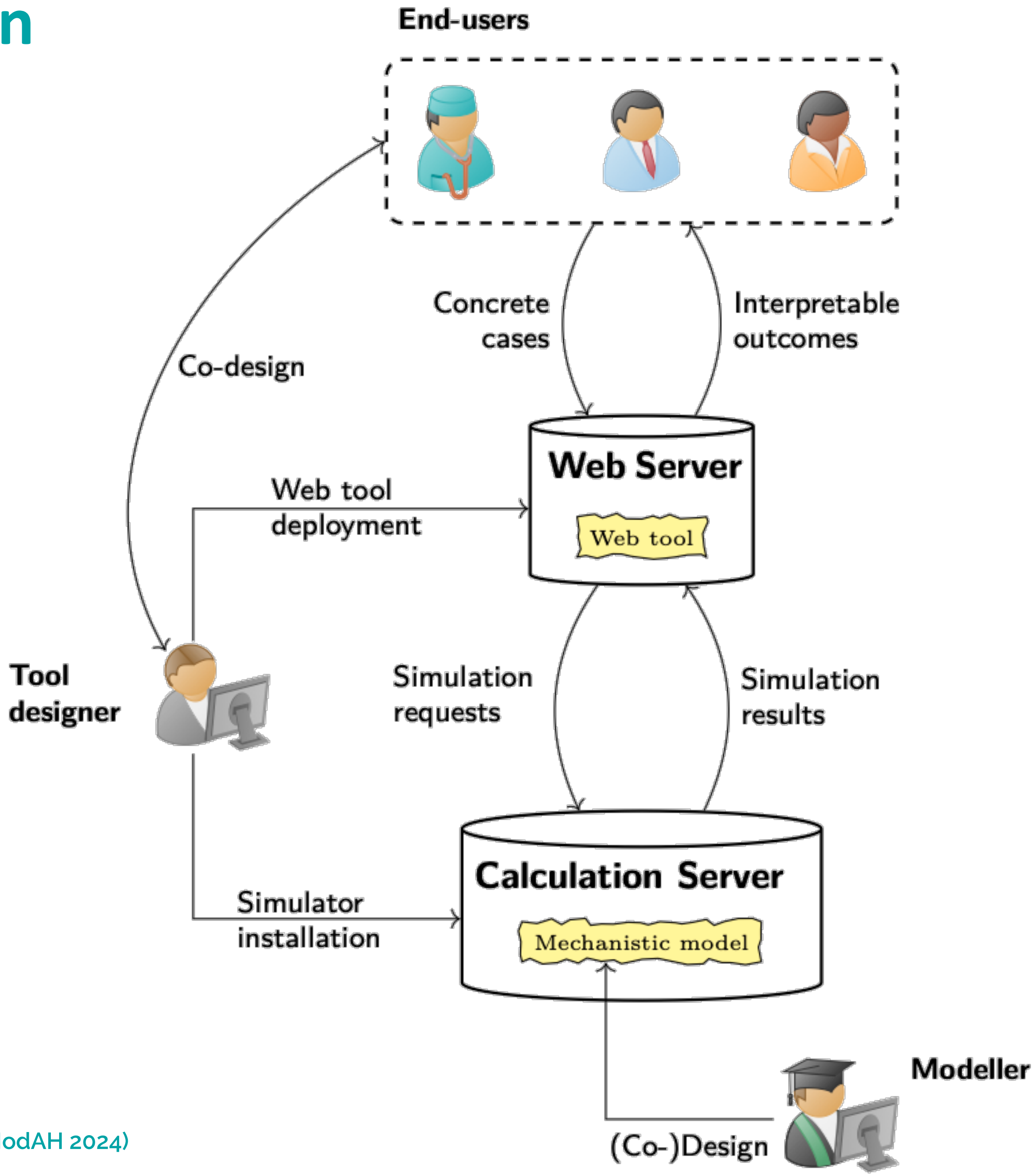
Initial conditions

Risk level of calves

- ---------
- balanced (0.3/0.4/0.3)
- mainly low (0.6/0.3/0.1)
- mainly high (0.1/0.3/0.6)
- contrasted (0.5/0/0.5)

Main pathogen





End-users

Concrete cases

Interpretable outcomes

Co-design

Web Server

Web tool

Web tool deployment

Tool designer

Simulation requests

Simulation results

Calculation Server

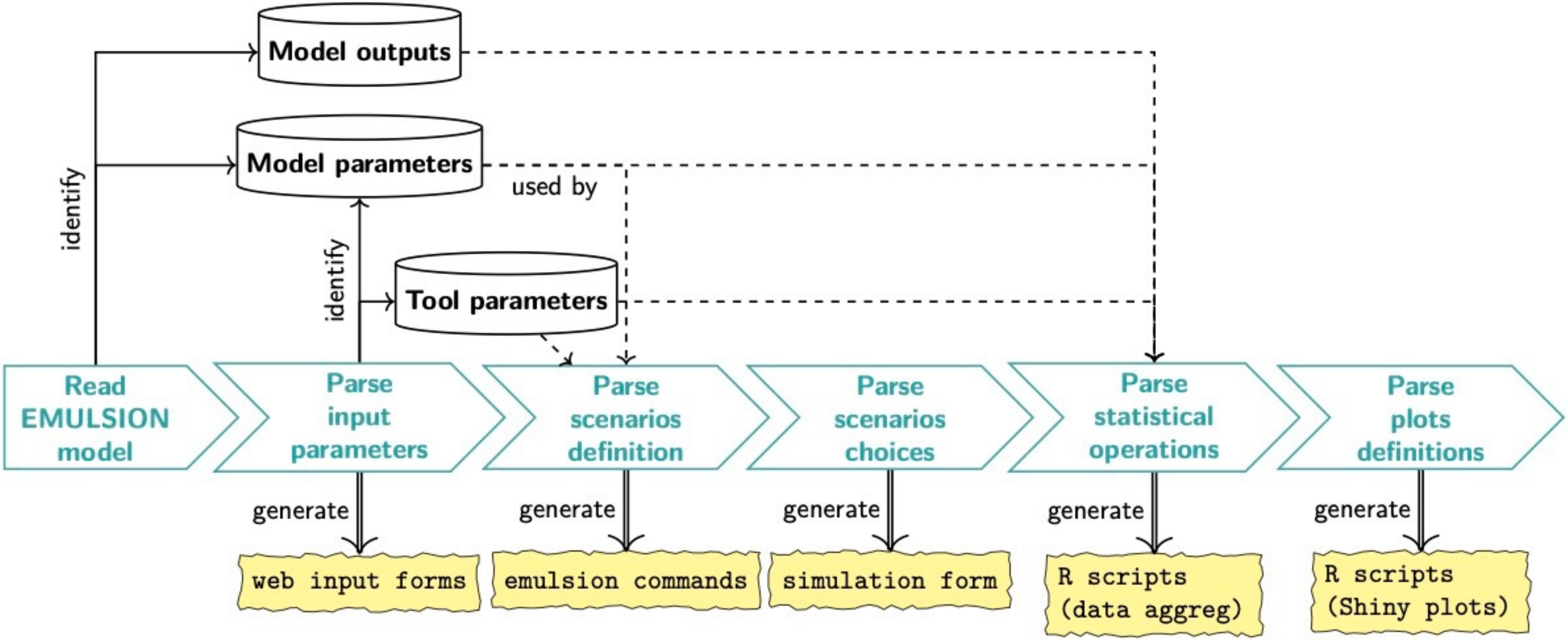
Mechanistic model

Simulator installation

Modeller

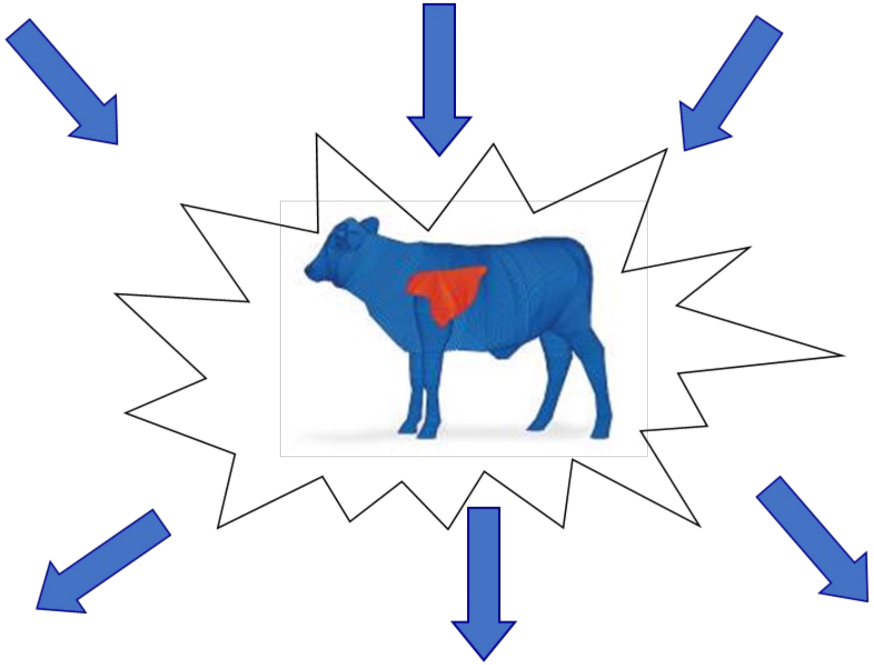
(Co-)Design

PASTE: workflow for automated web code generation



Application: controlling BRD in young beef cattle

Bovine Respiratory Disease (BRD)



Pathogens

Environment

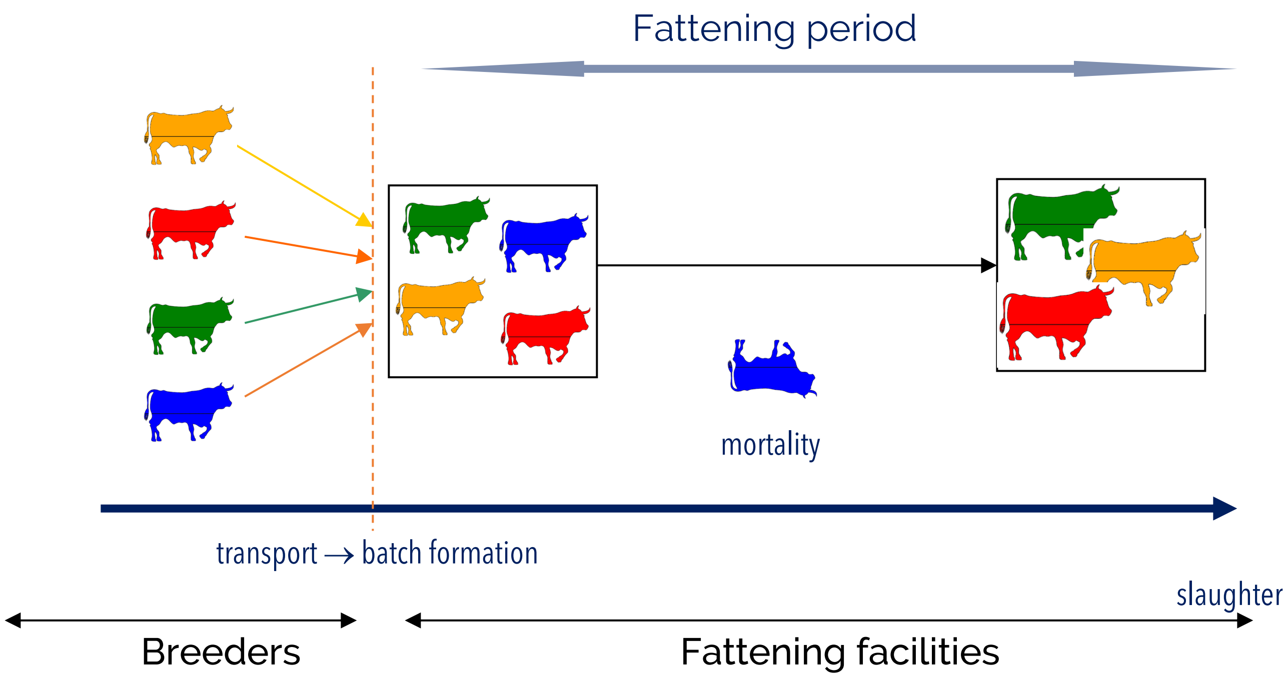
Farm management,
stress

Economic losses
Mortality

Welfare

Antibiotic
usage

Fattening farms



Fattening period

mortality

transport → batch formation

slaughter

Breeders

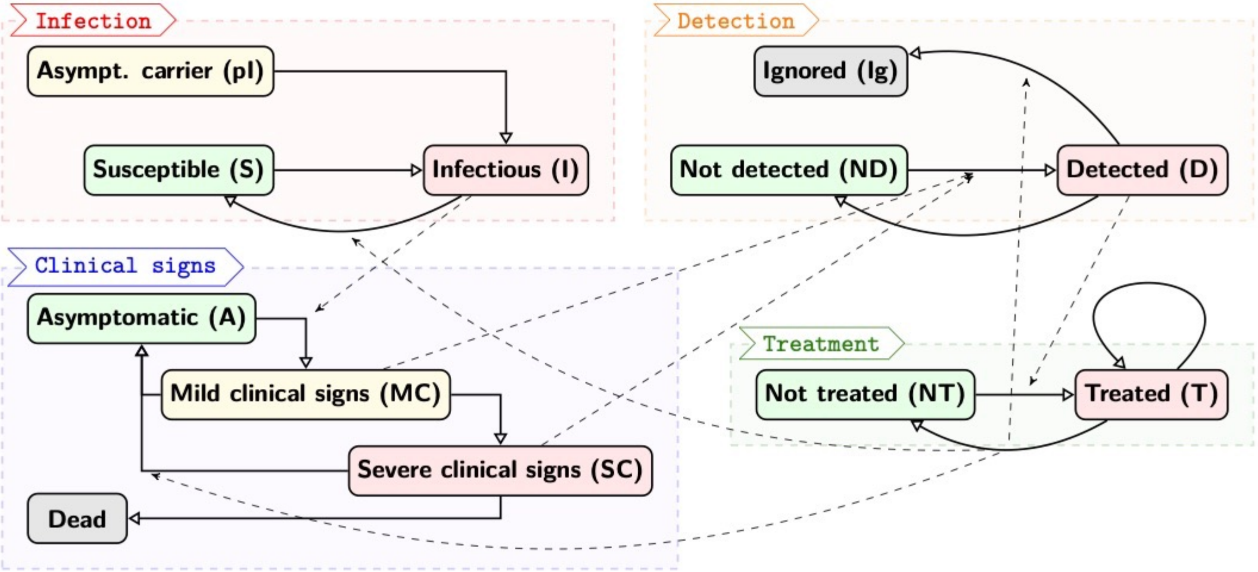
Fattening facilities

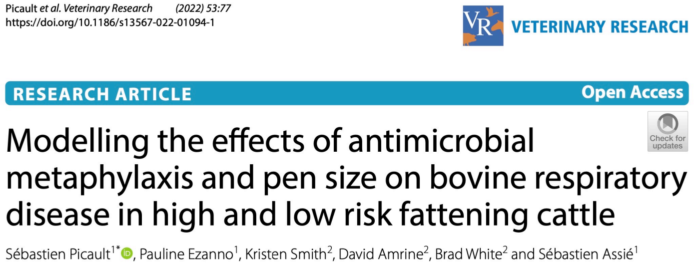
(source : S. Assié)

Modelling BRD onset, detection and treatment

Gather several relevant processes

- infection: pathogens, transmission, infection duration…
- disease: onset of mild / severe clinical signs, mortality…
- detection: visual appraisal, hyperthermia, sensors…
- treatment: individual vs. collective




Picault *et al. Veterinary Research* (2022) 53:77
https://doi.org/10.1186/s13567-022-01094-1

VETERINARY RESEARCH

RESEARCH ARTICLE Open Access

Modelling the effects of antimicrobial metaphylaxis and pen size on bovine respiratory disease in high and low risk fattening cattle

Sébastien Picault[1]*, Pauline Ezanno[1], Kristen Smith[2], David Amrine[2], Brad White[2] and Sébastien Assié[1]


Contents lists available at ScienceDirect

Preventive Veterinary Medicine

journal homepage: www.elsevier.com/locate/prevetmed

ELSEVIER

Modeling the effects of farming practices on bovine respiratory disease in a multi-batch cattle fattening farm

Baptiste Sorin-Dupont [a,*], Sebastien Picault [a], Bart Pardon [b], Pauline Ezanno [a,1], Sebastien Assié [a,1]

How to make these models usable ?

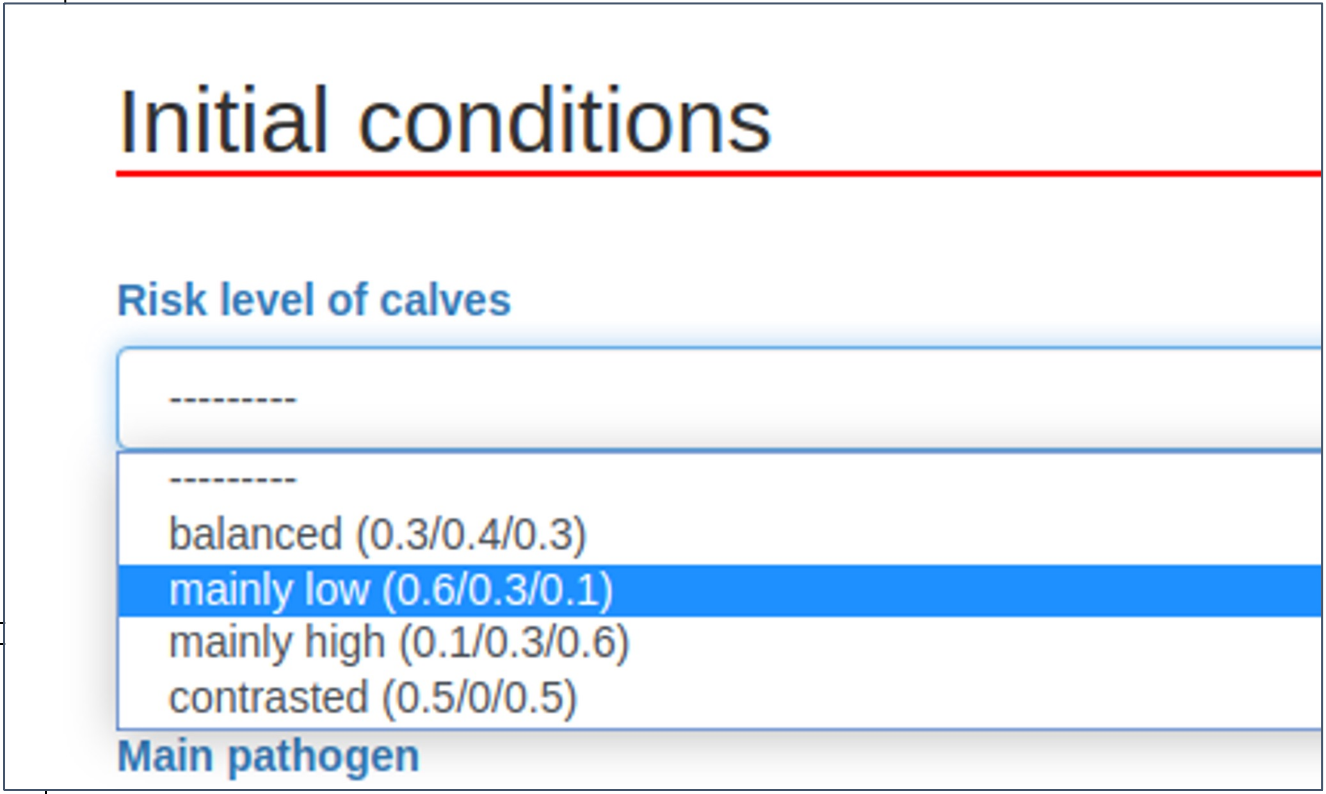
- in real farms
- by veterinarians / farmers
- autonomously

Overview of the generated BRD tool

```
input_parameters:

 - block_values:

     pathogen:
       - file_path: "input_files/pathogens.csv"

     batch_isolation:
       - file_path: "input_files/biosecurity.csv"

     risk_level:
       - file_path: "input_files/risk_level.csv"
```

```
risk_level.csv

name,prop_lowrisk,prop_mediumrisk,prop_highrisk

balanced (0.3/0.4/0.3),0.3,0.4,0.3
mainly low (0.6/0.3/0.1),0.6,0.3,0.1
mainly high (0.1/0.3/0.6),0.1,0.3,0.6
contrasted (0.5/0/0.5),0.5,0.0,0.5
```

BRD model parameters



Initial conditions

Risk level of calves

----
balanced (0.3/0.4/0.3)
mainly low (0.6/0.3/0.1)
mainly high (0.1/0.3/0.6)
contrasted (0.5/0/0.5)

Main pathogen

Identify relevant parameter groups & values

Identify tool-specific parameters

Overview of the generated BRD tool

```yaml
statistics:
   for_each_scenario:
     - mean_C:
         - desc: "Animals with severe clinical
    signs (mean, q05, q95)"
         - target_variable: [ "metapop_total_C" ]
         - groupby: [ "step" ]
         - summarise:
             - mean
             - perc_0.5:
                 value: "quantile(..., 0.05)"
                 desc: "5th percentile"
             - perc_0.95:
                 value: "quantile(..., 0.95)"
                 desc: "95th percentile"

    comparison_of_scenarios:
      ...
```

generated R code

```r
mean_C <- data  %>%  group_by(step)   %>%
summarise(
   mean_metapop_total_C=mean(metapop_total_C),

    perc_0.5_metapop_total_C=quantile(metapop_total_C,
      0.05),

    perc_0.95_metapop_total_C=quantile(metapop_total_C,
       0.95))
```

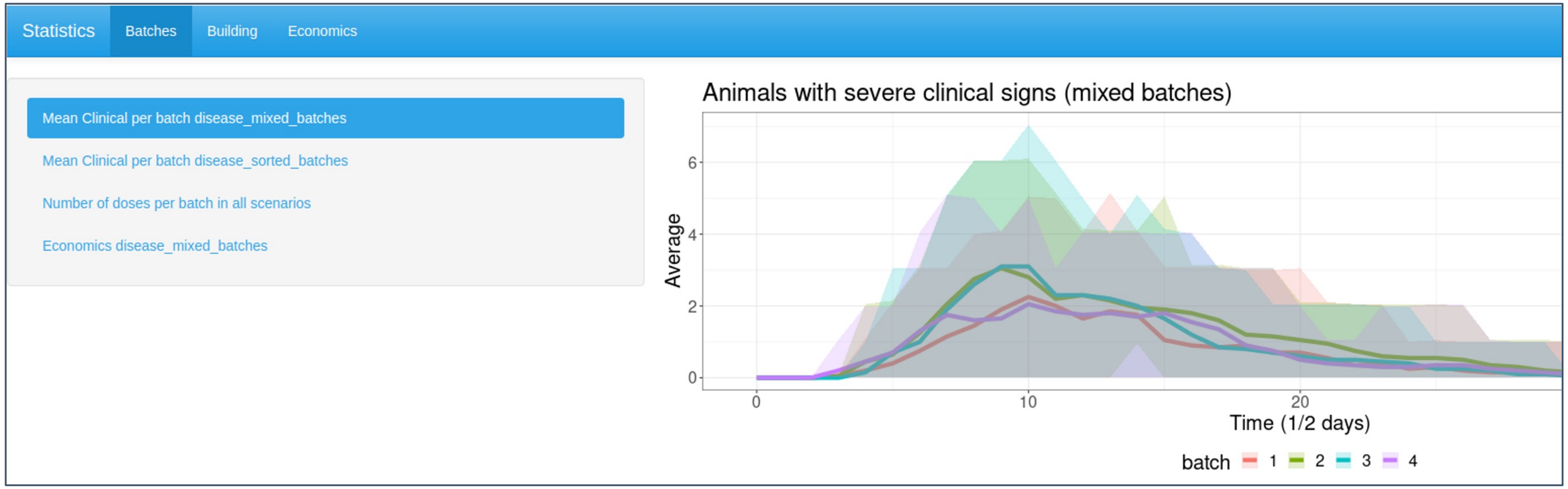
Specify generic
treatment workflows

Compare scenario
outcomes

Overview of the generated BRD tool

```
graphics:
 plot_mean_C_disease_mixed:
   - data: "mean_C"
   - on_page: ["Batches"]
   - label: ["Mean Clinical per batch"]
   - single_graph: "yes"
   - scenario: ["disease_sorted_batches"]
   - plot_variables:
       x: "step"
       y: "mean_total_C"

   - plot_type:
       - line:
           plot_variables:
             colour: "scenario_name"
           plot_options:
             size: "2"
       - ribbon:
           plot_variables:
             ymax: "perc_0.95_metapop_total_C"
             ymin: "perc_0.5_metapop_total_C"
             fill: "batch"
           plot_options:
             alpha: "0.2"
   - plot_annotations:
       title: "Animals with severe clinical signs (mixed batches)"
       x_title: "Time (1/2 days)"
       y_title: "Average"
```

generated R shiny app + ggplot



Identify and organize meaningful outputs

Perspectives

Finalisation of a tool for BRD:

- realistic parameterization of the economic gains / losses + relevant interventions (Théo Salles & Baptiste Sorin)

Application to other diseases/species:

- developing a model for *Mycoplasma hyopneumoniae* (IRTA) ← → sketching a tool for pig diseases management

Extending the language & tool features:

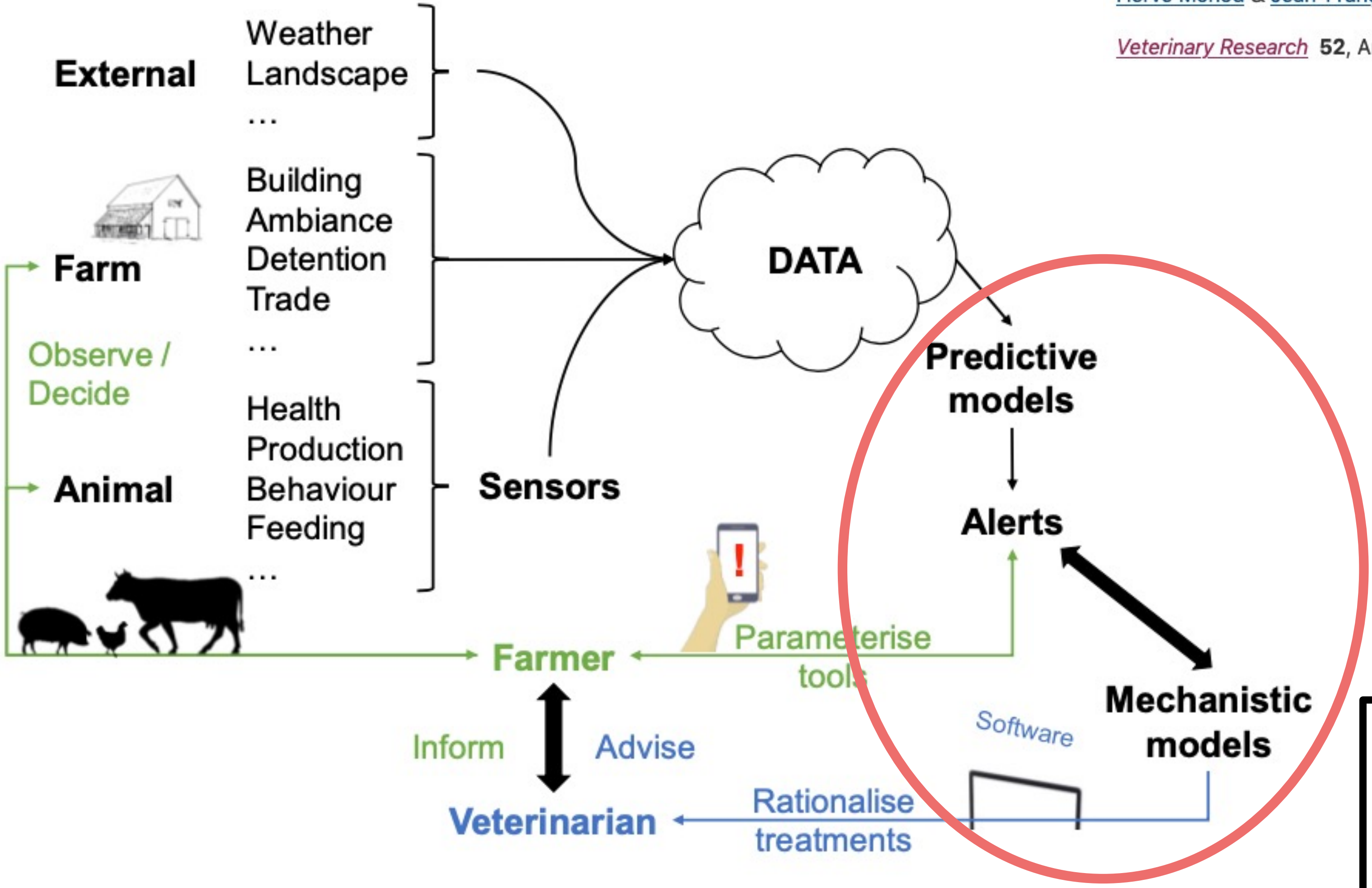
- Metrics for scenario comparisons, intervention prioritization & recommendations
- Integration of real-time data to inform the model & update scenarios

Connecting models with data

Research perspectives on animal health in the era of artificial intelligence

Pauline Ezanno, Sébastien Picault, Gaël Beaunée, Xavier Bailly, Facundo Muñoz, Raphaël Duboz, Hervé Monod & Jean-François Guégan

Veterinary Research **52**, Article number: 40 (2021) | Cite this article



Data-based models

- Predictive models built from data
- "Health alerts" often lack specificity
- Short time scales (hours/days)

Mechanistic models

- Challenge in model calibration
- Comparison of scenarios, even counterfactual
- Broader time scales (weeks/months)

Take-home messages

- Artificial intelligence and software engineering methods leveraged together help automate model & tool design

- Knowledge representation methods provide explicit & readable representations of model & tool components to foster co-construction

- Generic, modular & extensible approaches → adaptable to various pathosystems, diseases, species…

Thank you for your attention!

Open-source software!

https://sourcesup.renater.fr/www/emulsion-public

https://forgemia.inra.fr/dynamo/software/paste-public-release

One step further: incorporating real-time data