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# Better targeting treatments against Bovine Respiratory Disease by combining dynamic generalized linear models and mechanistic modelling

## ModAH

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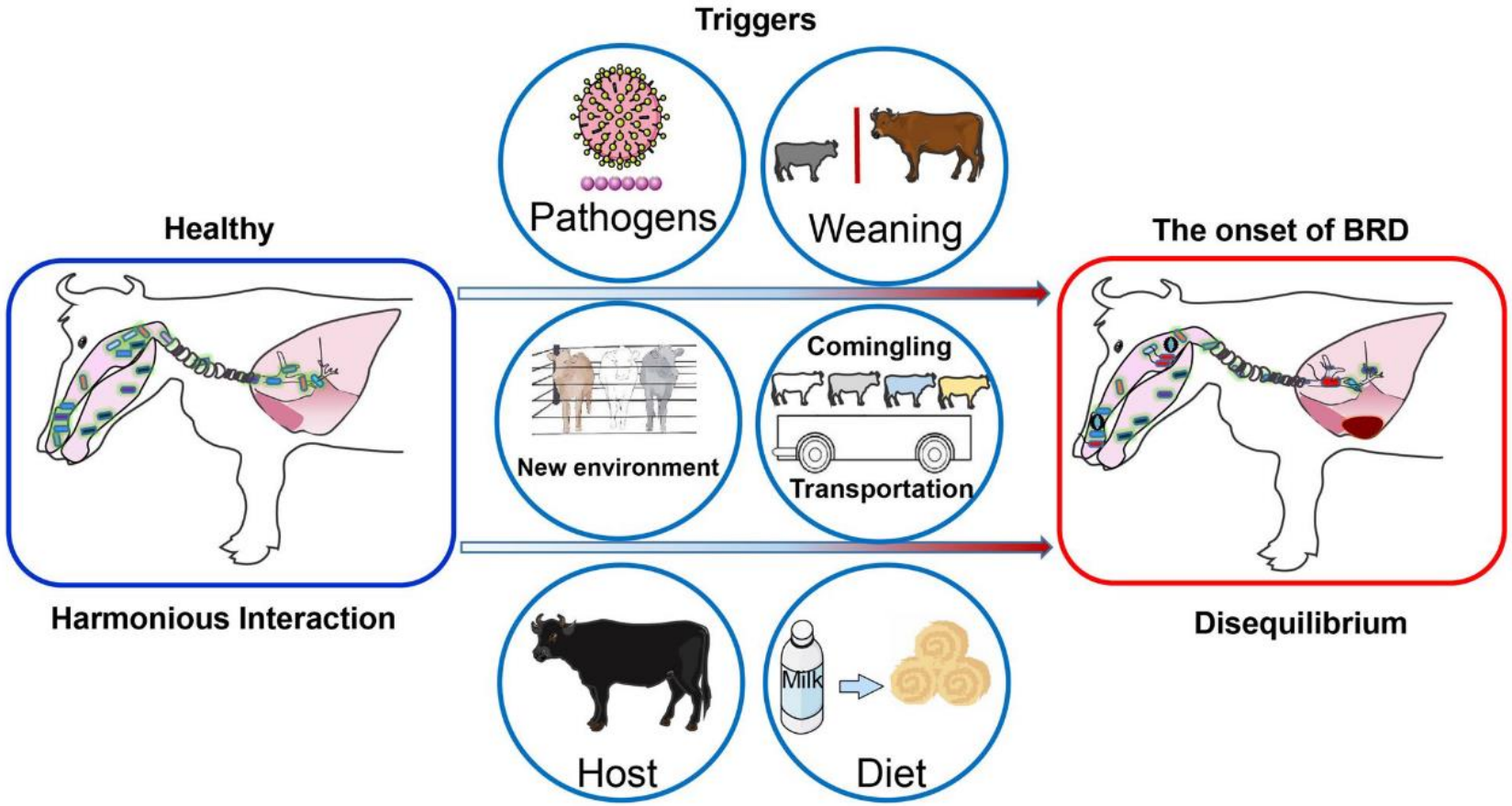
# Bovine Respiratory Disease (BRD)



# How to efficiently control BRD ?

Vaccination

Stress reduction

Treatment

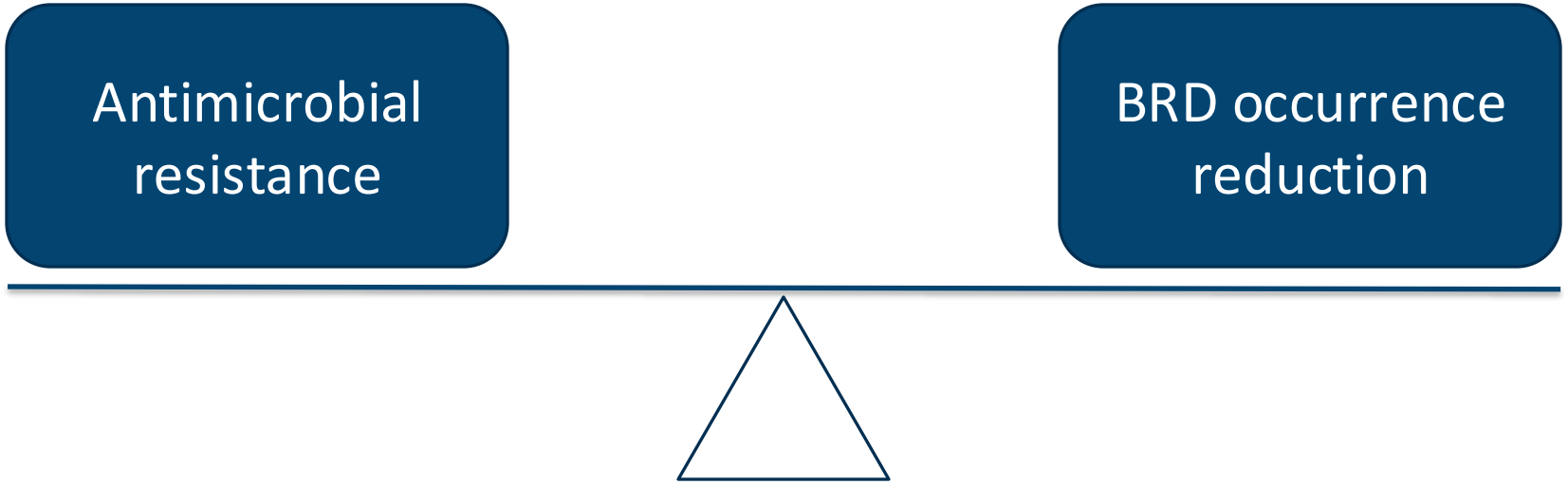
# BRD treatment strategies

If D>0.1*Total

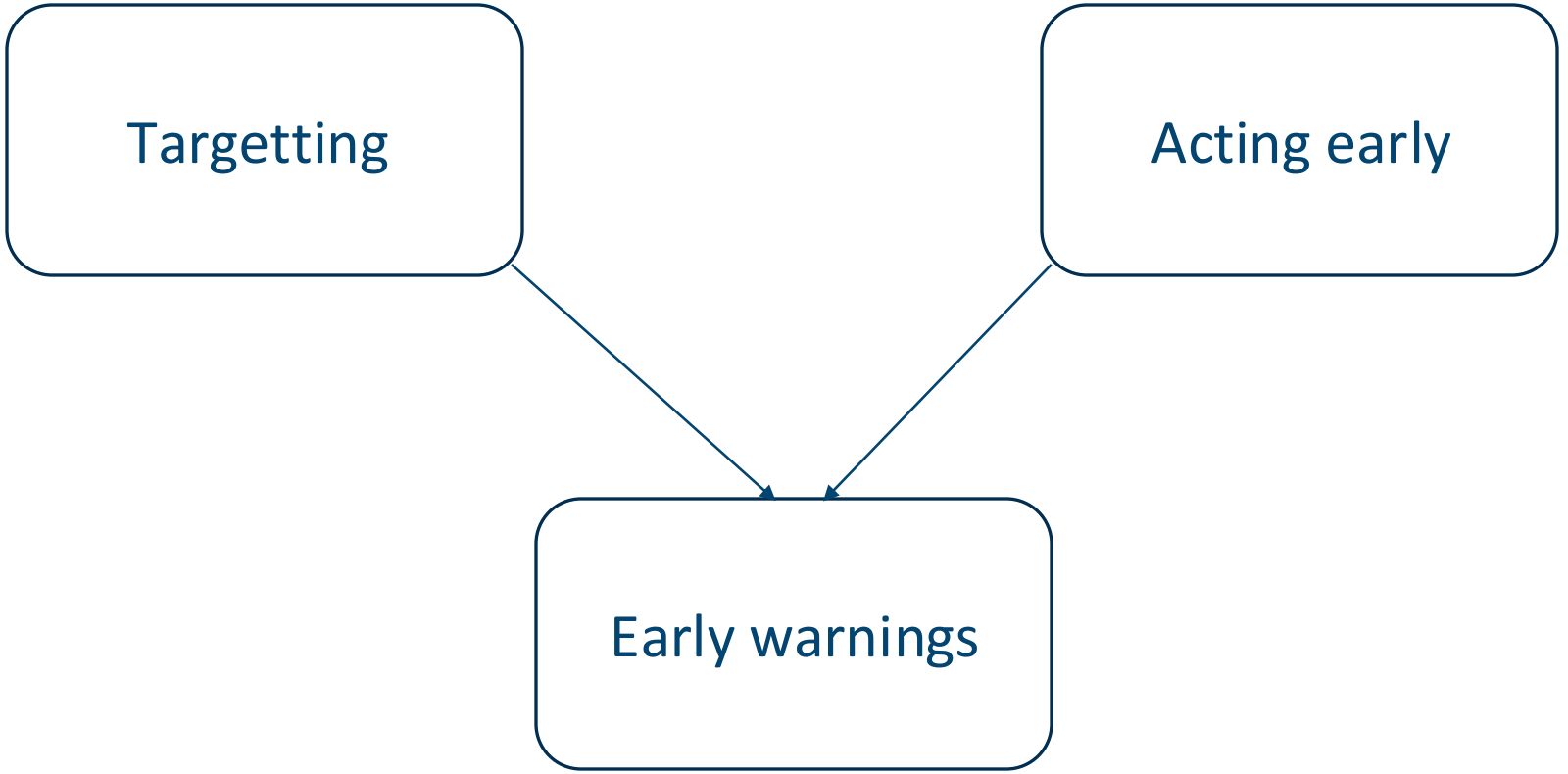
Individual treatment

Collective treatment

# BRD treatment : a trade-off

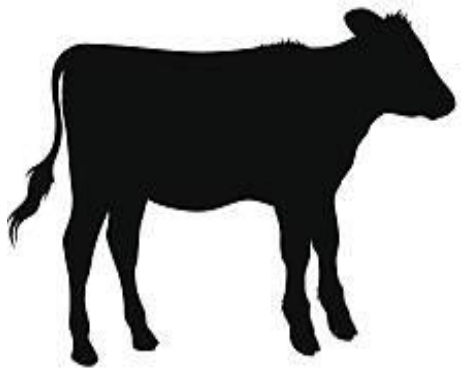


# How to treat better ?

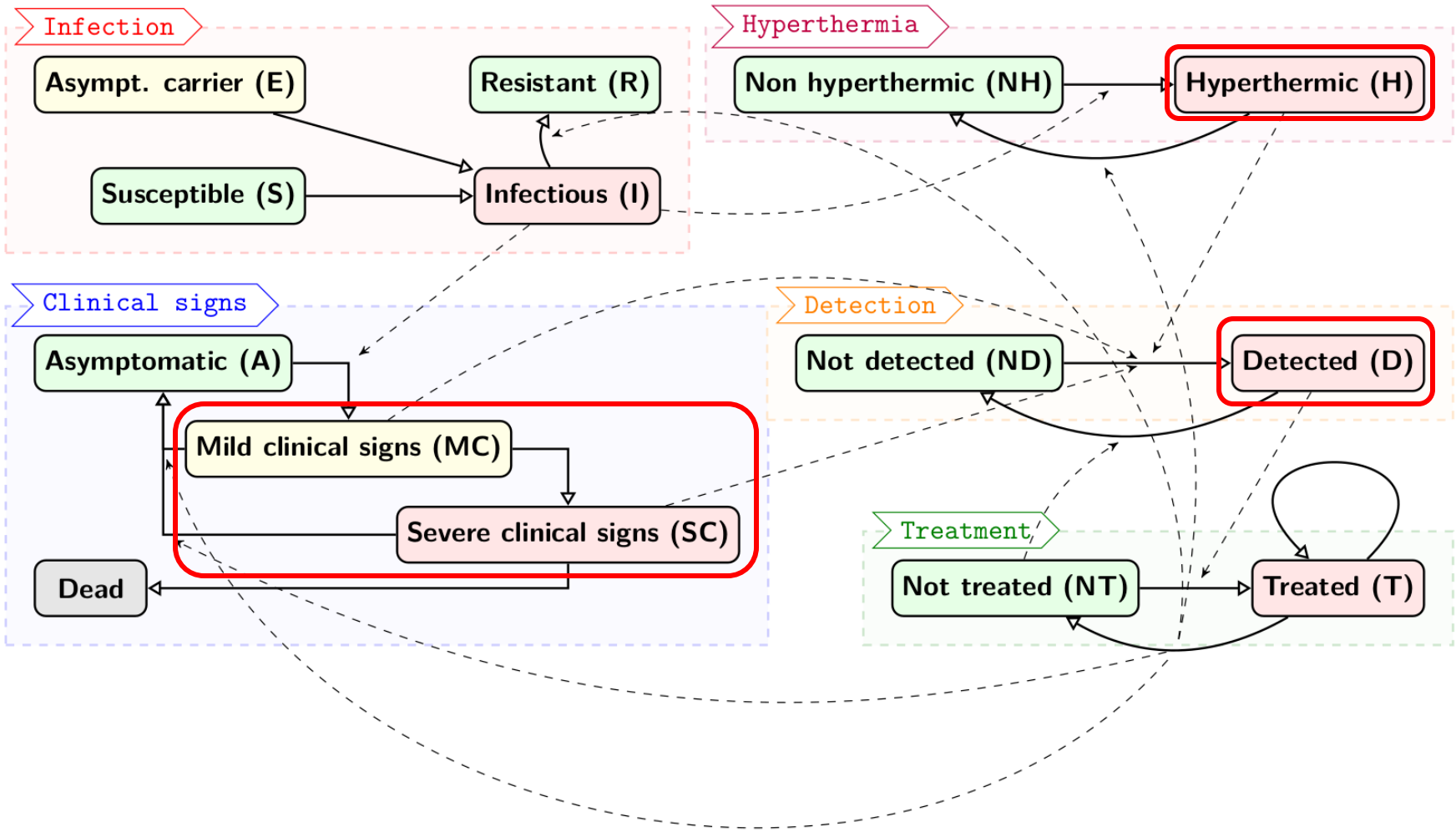


# Aim

Create a proof of concept for a decision support tool for farmers and veterinarians that can help them to better decide when collective treatment for BRD should be performed, according to different scenarios.



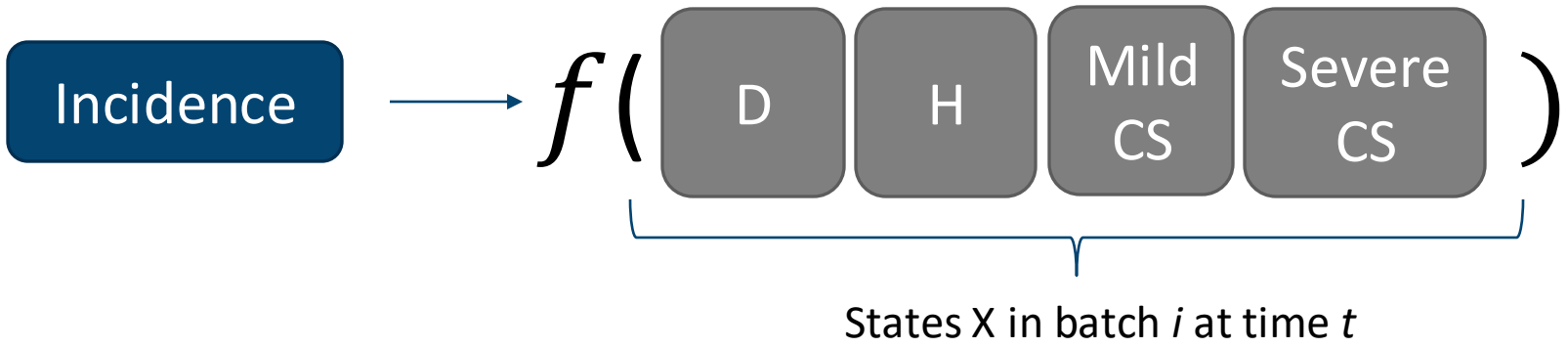
# The mechanistic model



# Dynamic Generalized Linear Models (DGLM)

- Particular case of state space models
- Multivariate hierarchical Binomial
- Estimates the underlying parameter vector $\theta_t$ from observed data and prior information

# Dynamic Generalized Linear Models (DGLM)




$R_{Xjt}=y_{Xjt}/N_{Xjt}$

$y_{Xjt} \sim B(p_{Xjt}, N_{Xjt})$

$\eta_{Xjt}=log(p_{Xjt}/(1-p_{Xjt}))$

$\eta_{Xjt}=\mu_{1t}+\delta_{jt}+\beta_X$

$p_{Xjt}$: Probability of entering state X in batch $j$ at time $t$

$\mu_{1t}$: True risk of infection in batch 1

$\delta_{jt}$ : deviation between batch 1 and batch $j$ at time $t$

$\beta_X$: observation bias

# Dynamic Generalized Linear Models (DGLM)

## Observation equation

$\eta_t = F_t' \theta_t \Rightarrow p_{Sit} = 1/(1+e^{-Ft' \theta t})$

- $\theta_t$ : risk of infection in each batch and observation biases.
- $F_t'$: design matrix

## System equation

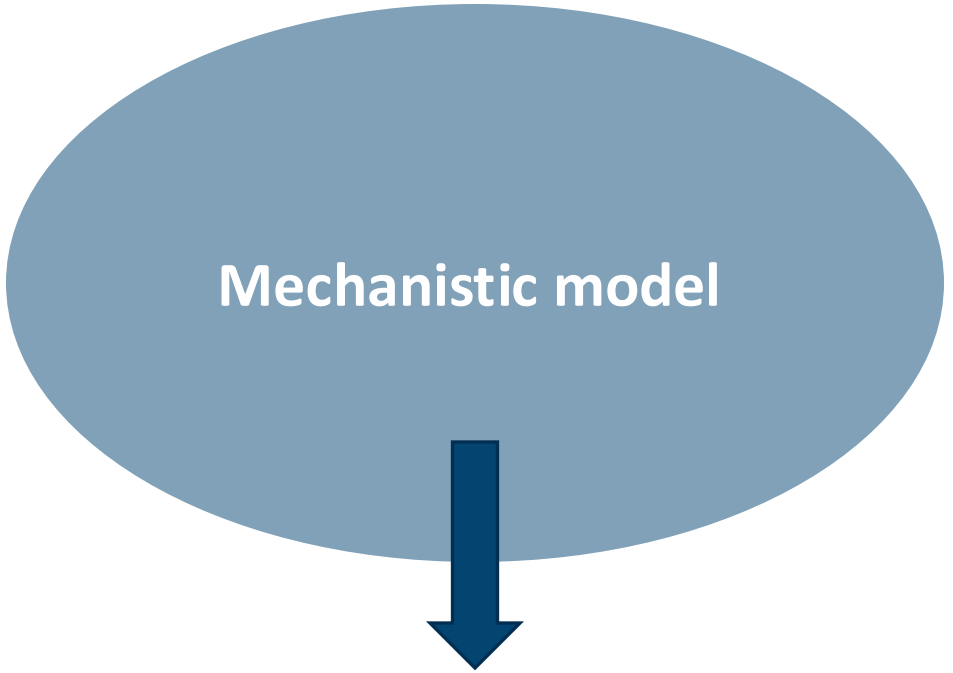
$\theta_t = G_t \theta_{t-1} + w_t,\ w_t \sim [\underline{0}, W_t]$

- The system matrix ($G_t$) serves to update the expected values.
- The variance-covariance matrix $W_t$ describes how the risks are expected to change over time.

# DGLM update

1. **Bayesian updating**
2. **Generate predicted probabilities**
3. **Estimate risk of infection** → Warning if too high 
4. **New observations**
5. **Forecast error computation**

# Coupling both methods




Simulation model for BRD:
- Synthetic data
- Interventions

# Coupling both methods

**Dynamic generalized linear model (DGLM)**

Early warning system

**Mechanistic model**

Simulation model for BRD:
- Synthetic data
- Interventions

# How does it work?

**Mechanistic model**

Data per time step

| step | SMH | RMH | IMH | EMH | NH | H | A | MildC | C | Dead | U | D | NT | T | level | agent_id |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 1 | 6 | 0 | 0 | 14 | 20 | 0 | 20 | 0 | 0 | 0 | 20 | 0 | 20 | 0 | batch | 1 |
| 1 | 10 | 0 | 1 | 9 | 19 | 1 | 19 | 1 | 0 | 0 | 19 | 1 | 19 | 1 | batch | 2 |
| 1 | 10 | 0 | 1 | 9 | 18 | 2 | 19 | 1 | 0 | 0 | 20 | 0 | 20 | 0 | batch | 3 |
| 1 | 12 | 0 | 0 | 8 | 19 | 1 | 20 | 0 | 0 | 0 | 20 | 0 | 20 | 0 | batch | 4 |
| 1 | 6 | 0 | 1 | 13 | 19 | 1 | 19 | 1 | 0 | 0 | 20 | 0 | 20 | 0 | batch | 5 |
| 1 | 8 | 0 | 1 | 11 | 19 | 1 | 19 | 1 | 0 | 0 | 20 | 0 | 20 | 0 | batch | 6 |
| 1 | 9 | 0 | 5 | 6 | 14 | 6 | 15 | 5 | 0 | 0 | 20 | 0 | 20 | 0 | batch | 7 |
| 1 | 8 | 0 | 3 | 9 | 17 | 3 | 17 | 3 | 0 | 0 | 20 | 0 | 20 | 0 | batch | 8 |
| 1 | 8 | 0 | 1 | 11 | 19 | 1 | 19 | 1 | 0 | 0 | 20 | 0 | 20 | 0 | batch | 9 |
| 1 | 7 | 0 | 0 | 13 | 19 | 1 | 20 | 0 | 0 | 0 | 20 | 0 | 20 | 0 | batch | 10 |

Run in:

EMULSION

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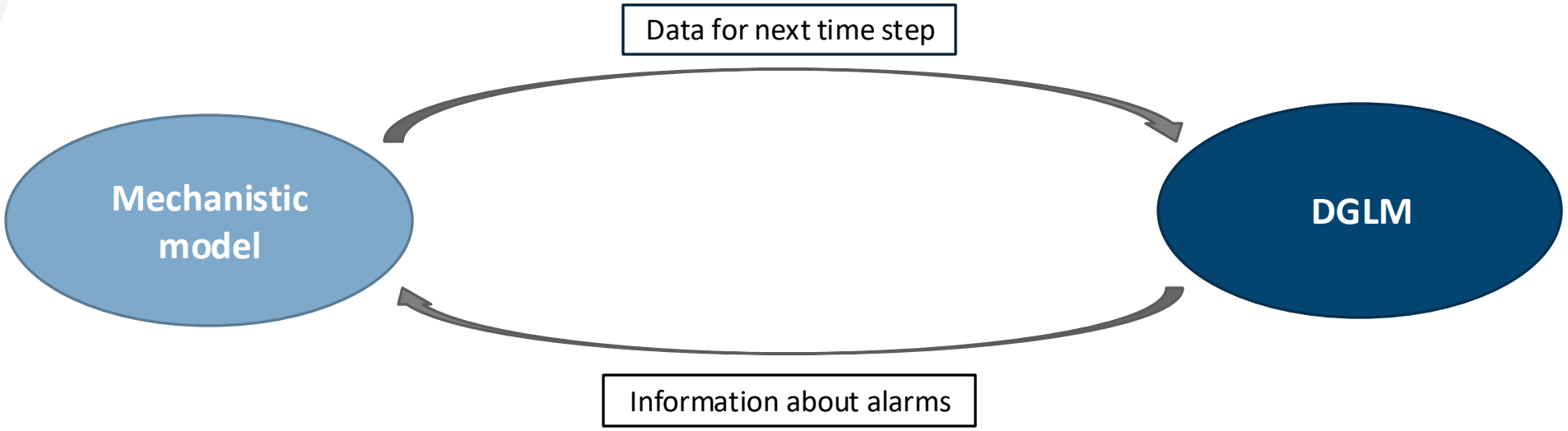
# How does it work?

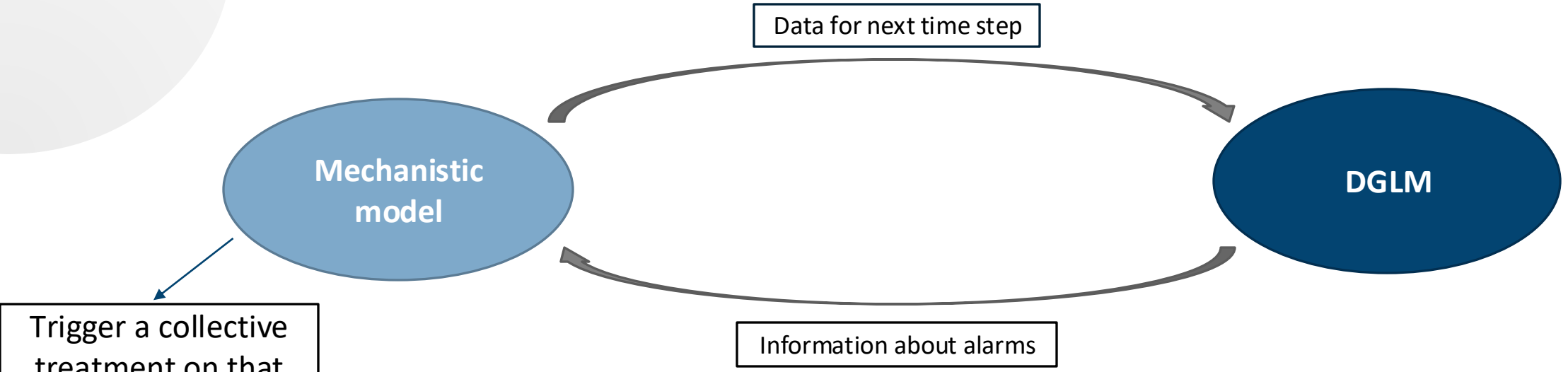



Run in:

- EMULSION
- R script
- Python

| Time | Batch1 | Batch2 | Batch3 | Batch4 | Batch5 | Batch 6 | Batch7 | Batch8 | Batch9 | Batch10 |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | FALSE | FALSE | FALSE | FALSE | FALSE | FALSE | FALSE | FALSE | FALSE | FALSE |

# How does it work?




| Time | Batch1 | Batch2 | Batch3 | Batch4 | Batch5 | Batch6 | Batch7 | Batch8 | Batch9 | Batch10 |
|---|---|---|---|---|---|---|---|---|---|---|
| 1 | FALSE | FALSE | FALSE | TRUE | FALSE | FALSE | FALSE | FALSE | FALSE | FALSE |

# Scenarios

Risk levels [$P_H$, $P_M$, $P_L$] :

- Low [0.9,0.1,0]
- Medium [0.1,0.9,0]
- High [0,0.1,0.9]
- Balanced [0.3,0.4,0.3]

Treatment:

- Individual
- Collective, proportion-based (T=0.1)
- Collective, DGLM based (T=0.05)

Batches:

- Random
- Risk level sorting

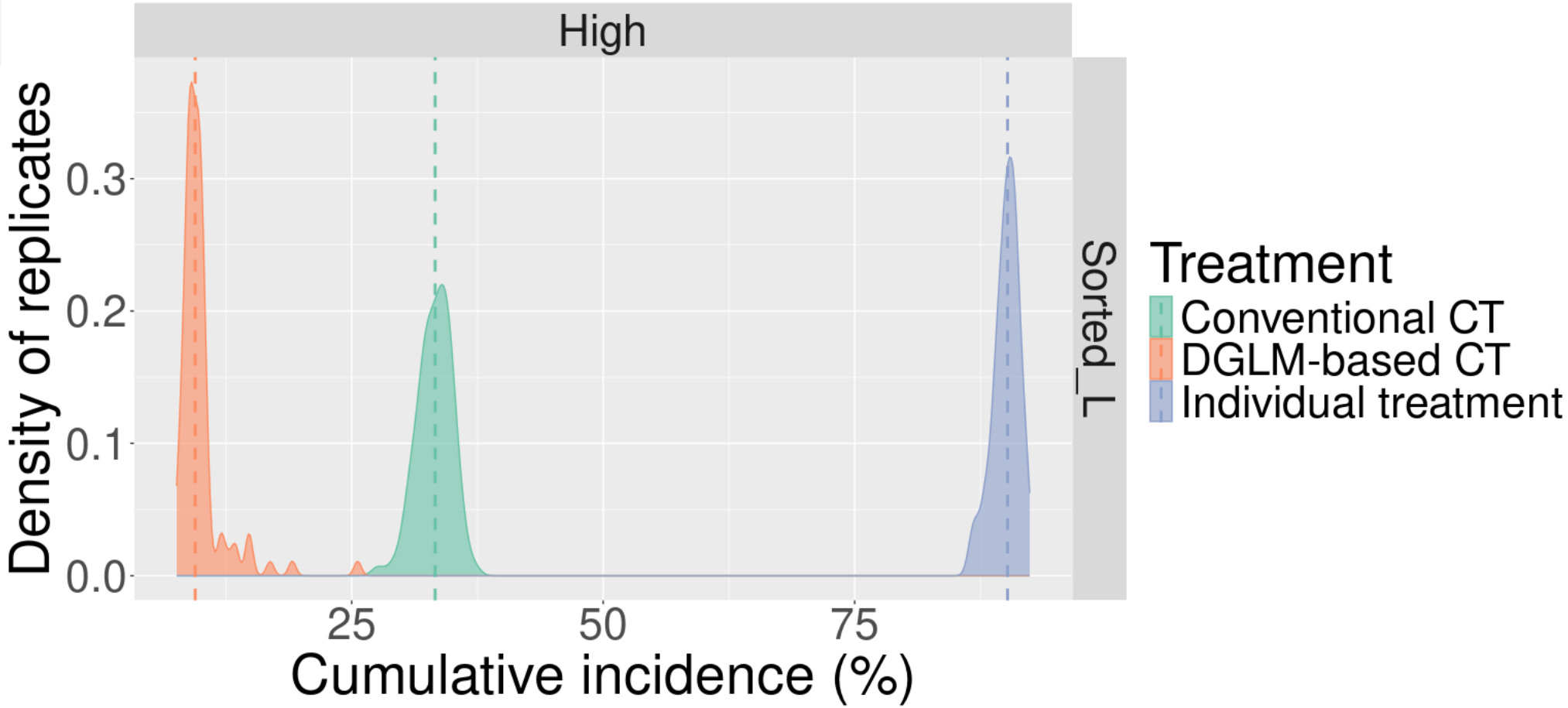
Batch size:

- Large (100)
- Small (20)

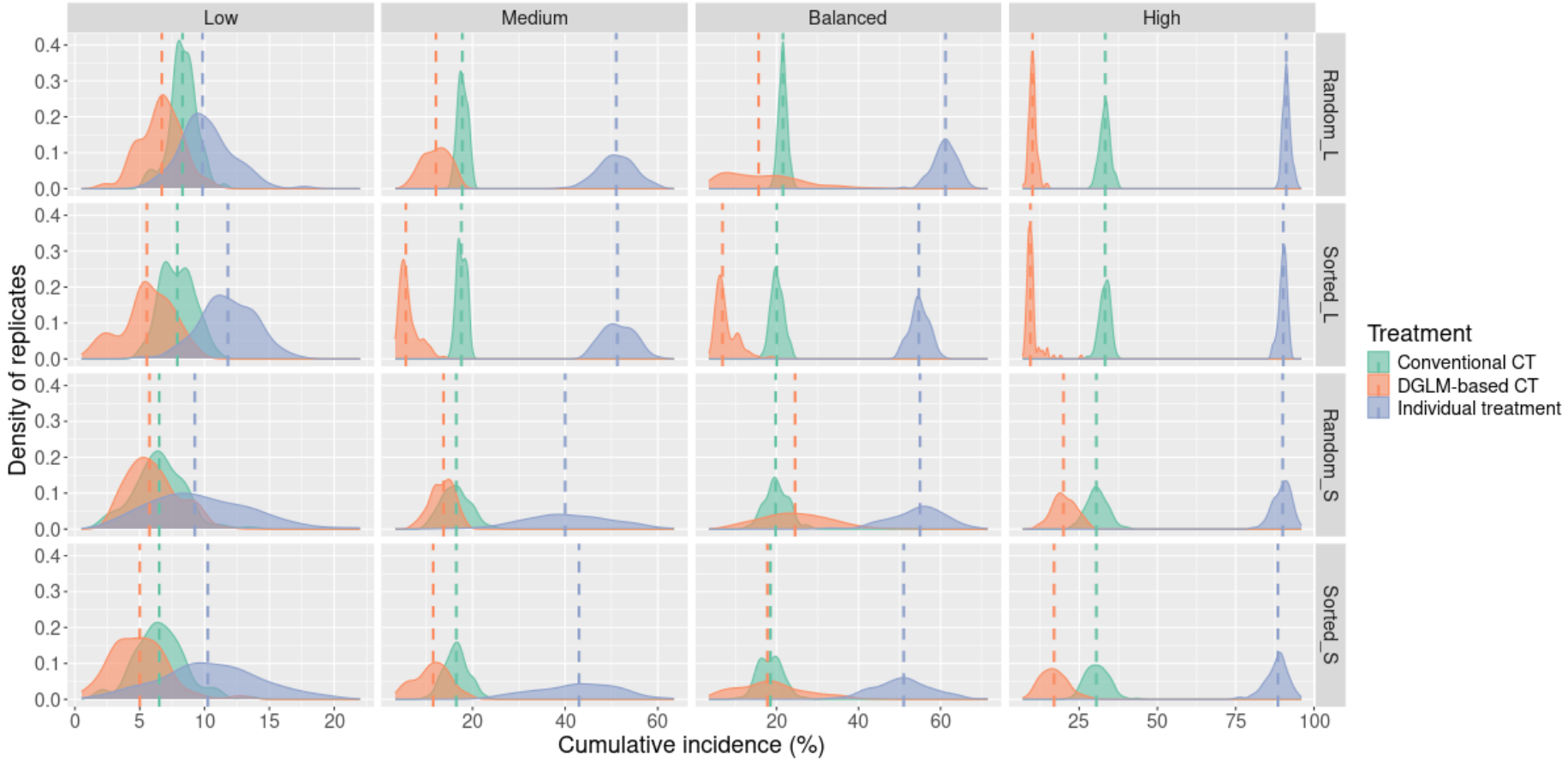
--> 48 scenarios (200 stochastic replicates)

Outputs: Incidence, Antimicrobial use, Estimated risk, Empirical risk

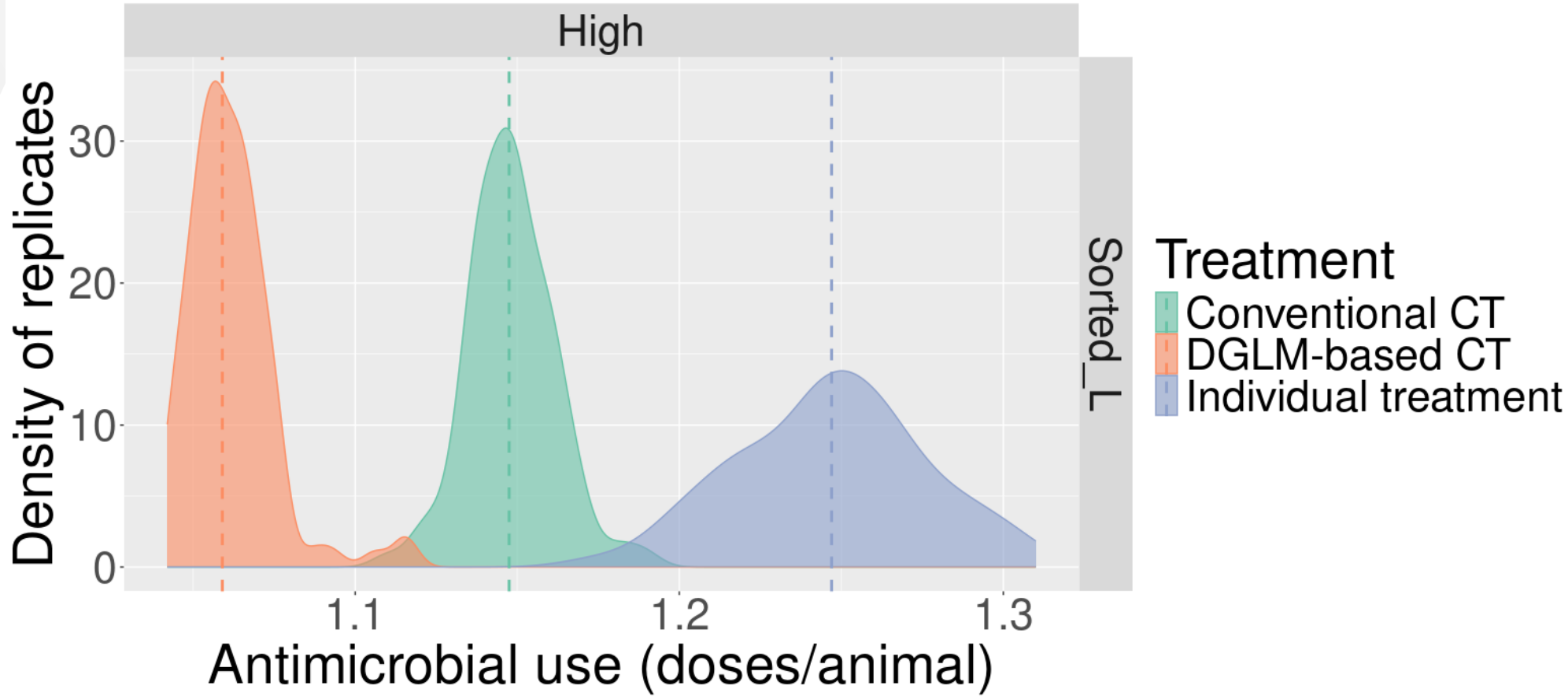
# Results


High
Density of replicates
0.3
0.2
0.1
0.0
25
50
75
Cumulative incidence (%)
Sorted_L
Treatment
Conventional CT
DGLM-based CT
Individual treatment

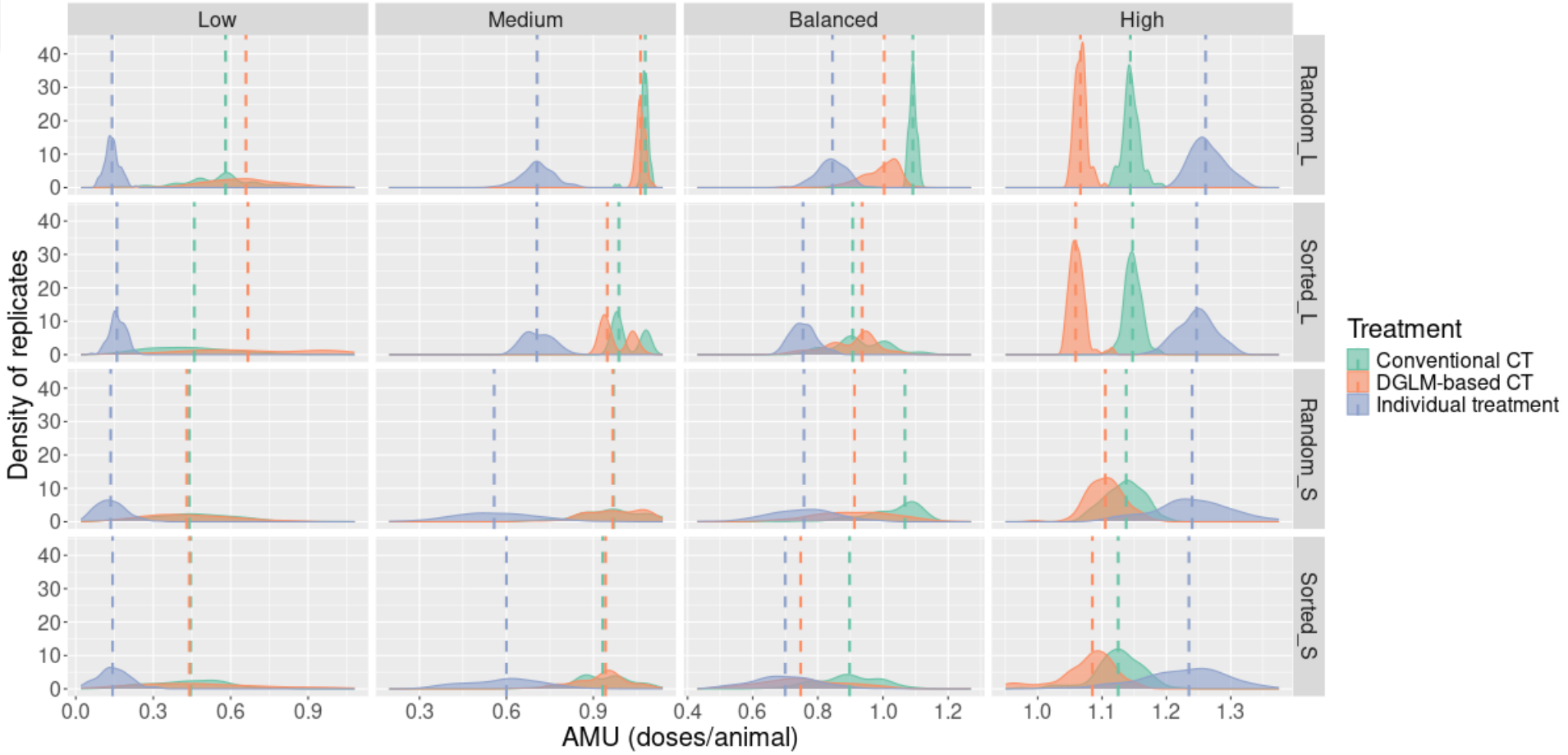
# Results


Low
Medium
Balanced
High
Random_L
Sorted_L
Random_S
Sorted_S
Density of replicates
Cumulative incidence (%)
Treatment
Conventional CT
DGLM-based CT
Individual treatment

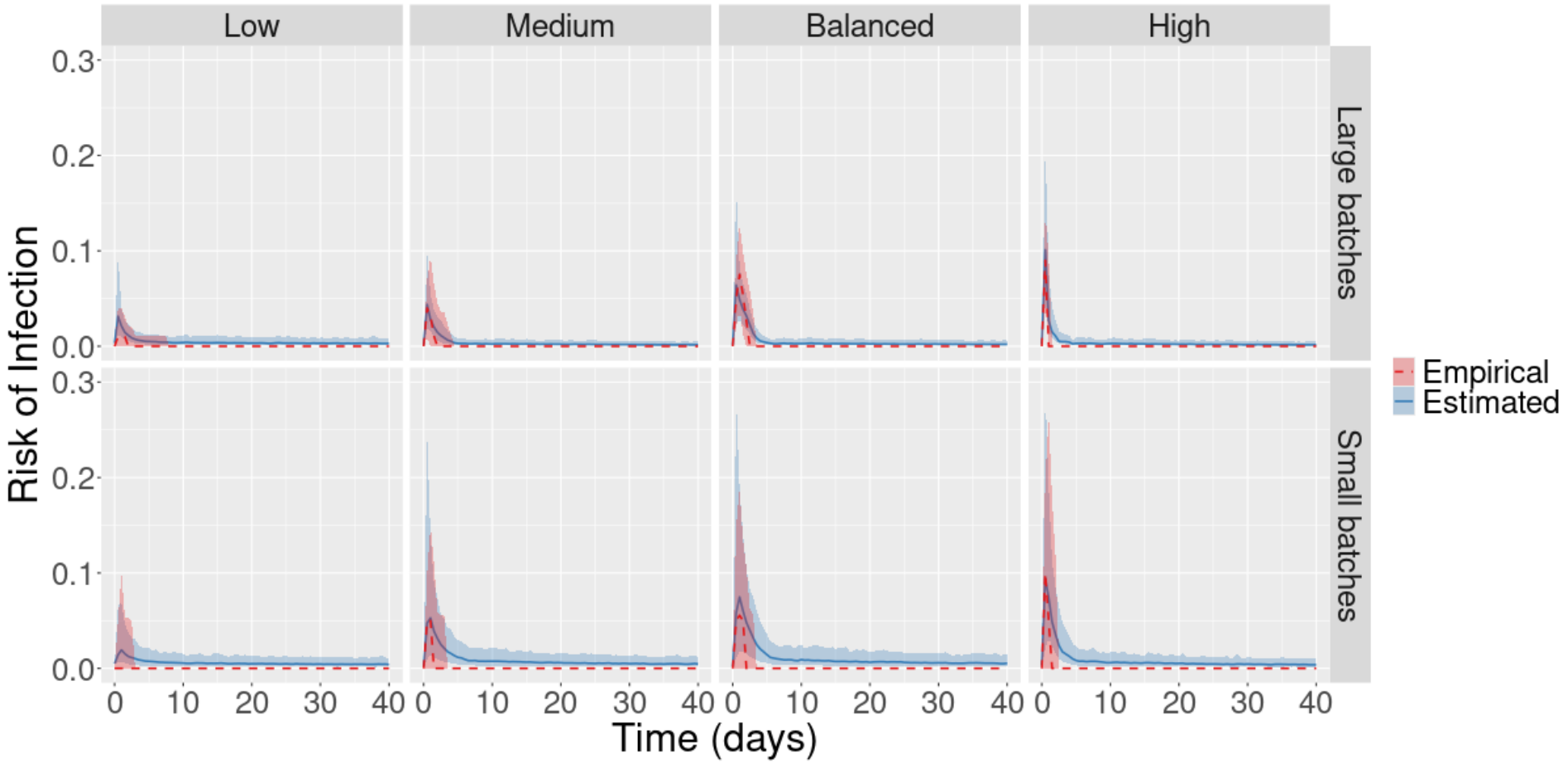
# Results


High
Density of replicates
30
20
10
0
1.1
1.2
1.3
Antimicrobial use (doses/animal)
Sorted_L
Treatment
Conventional CT
DGLM-based CT
Individual treatment

# Results


Low
Medium
Balanced
High
Random_L
Sorted_L
Random_S
Sorted_S
Density of replicates
AMU (doses/animal)
Treatment
Conventional CT
DGLM-based CT
Individual treatment

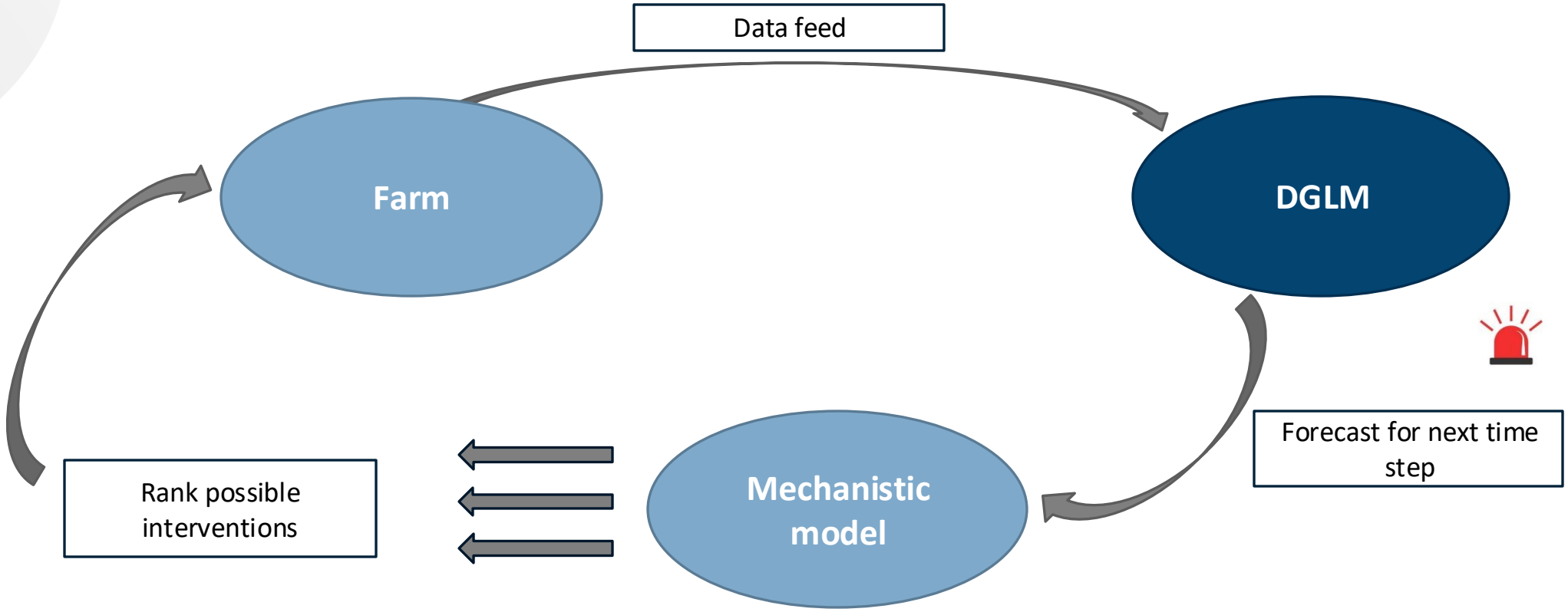
# Results


Low
Medium
Balanced
High
Large batches
Small batches
Risk of Infection
0.0
0.1
0.2
0.3
0
10
20
30
40
Time (days)
Empirical
Estimated

# Take-home messages

- First coupling of DGLM and mechanistic model in veterinarian epidemiology
- DGLM allows triggering timely interventions in higher risk scenarios
  - Reduction in both incidence and AMU
  - Best results for large pens
- Risk overestimation in Low-risk scenarios

# Perspective: real data application



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brings together 19 partners from 11 countries



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# Thank you for your attention!

## Questions?

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