Modelling the spillover risk of HPAI from wild birds to cattle in Denmark

A spatiotemporal risk assessment using two modelling approaches

Speakers: You Chang & Yangfan Liu
Section for Animal Health and Welfare

@CPHCattle Seminar 2026, 14-04-2026

UNIVERSITY OF COPENHAGEN

Ongoing HPAIV outbreak in U.S. cattle -- infecting >1000 Cattle Herds

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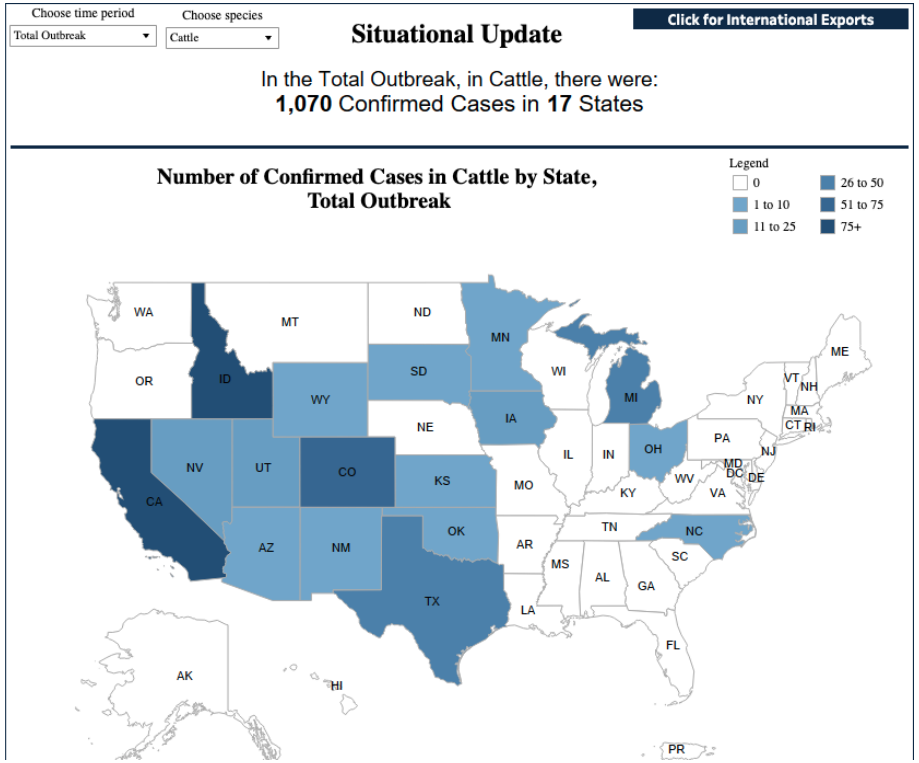
NEWS EXPLAINER | 08 April 2024

Bird flu outbreak in US cows: why scientists are concerned



MAY 9, 2024 | 6 MIN READ

How Bird Flu Caught the Dairy Industry Off Guard

Understanding how avian influenza jumped into cows can help shape the path to stopping the virus's spread

BY MEGHAN BARTELS

NEWS | 08 May 2024

Bird flu in US cows: where will it end?

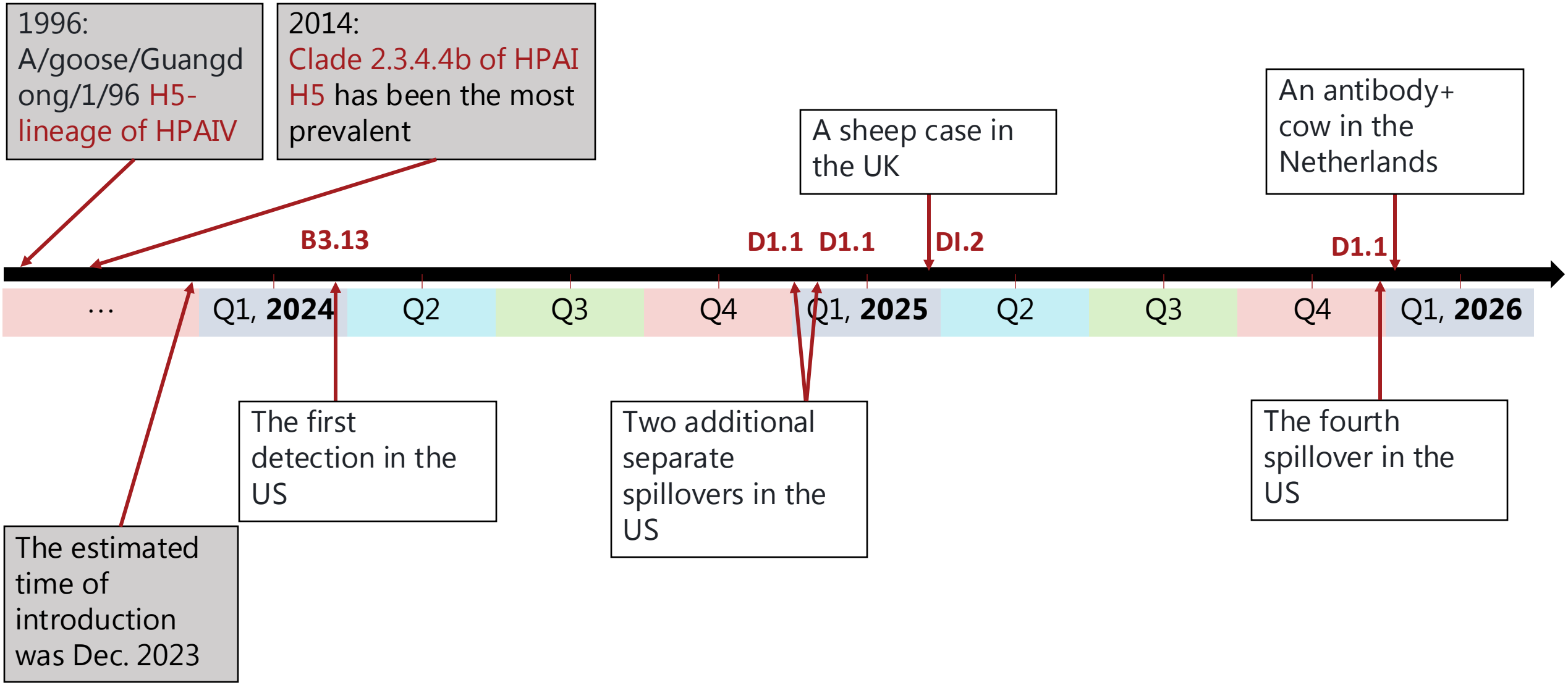
Scientists worry that the H5N1 strain of avian influenza will become endemic in cattle, which would aid its spread in people.

American cows now have bird flu, too – but it's time for planning, not panic

Devi Sridhar

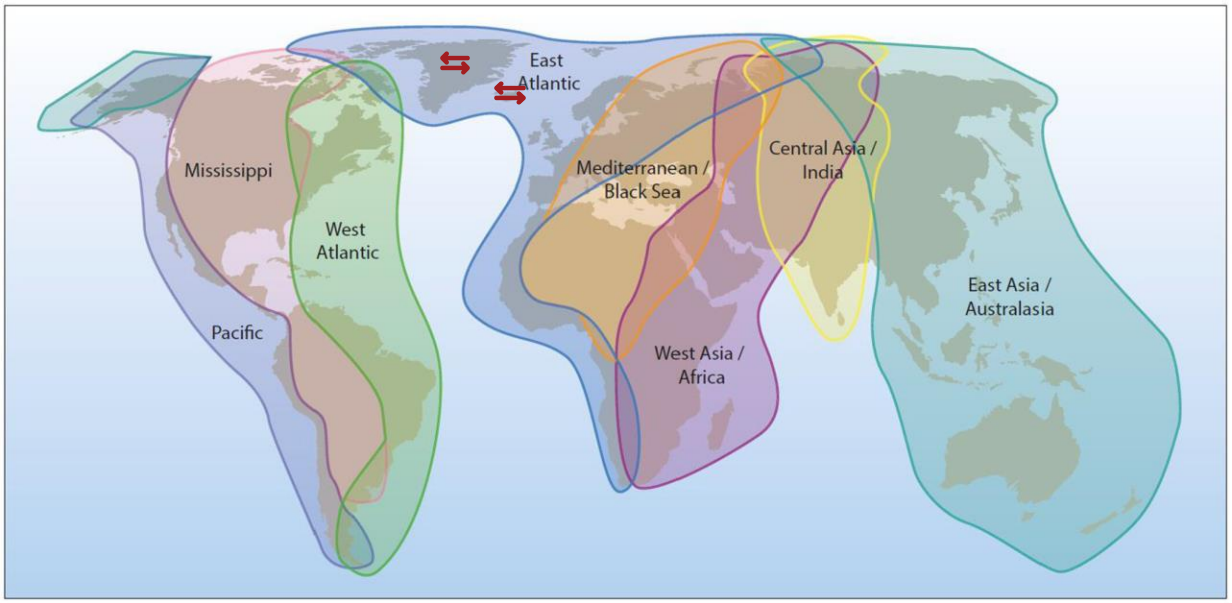
Vladimir Zapletin/Getty Images

Timeline of HPAIV striking cattle/ruminants

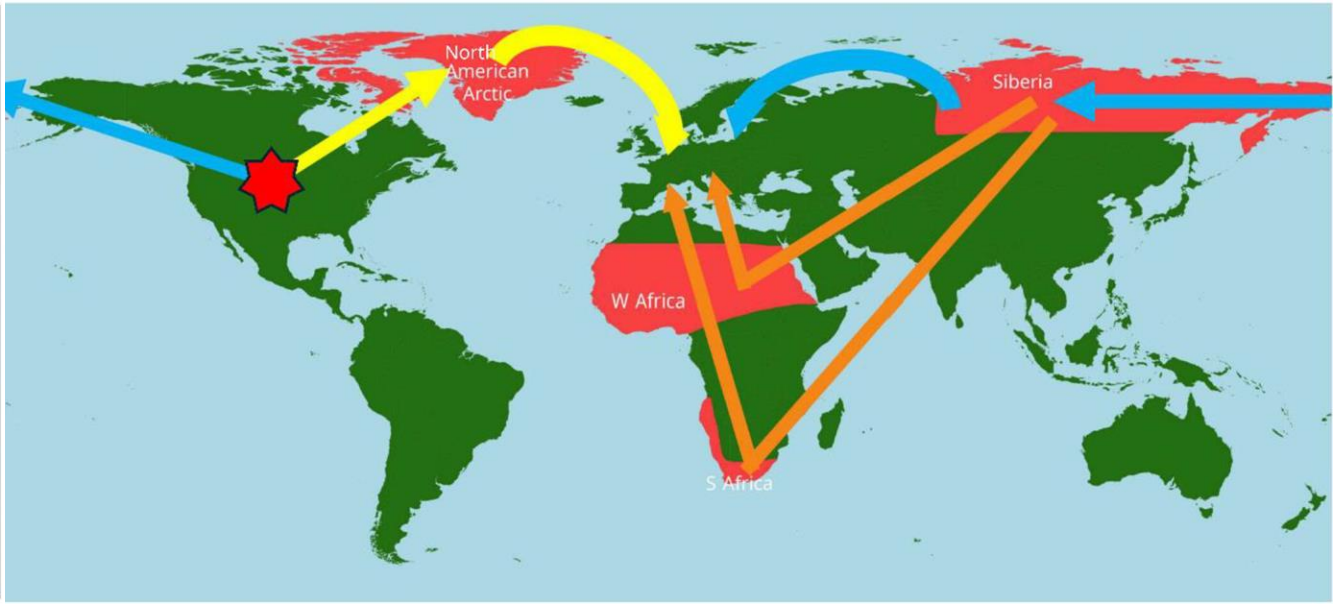


Why Denmark? Why now?

The general global migratory flyways of wild waterbird populations

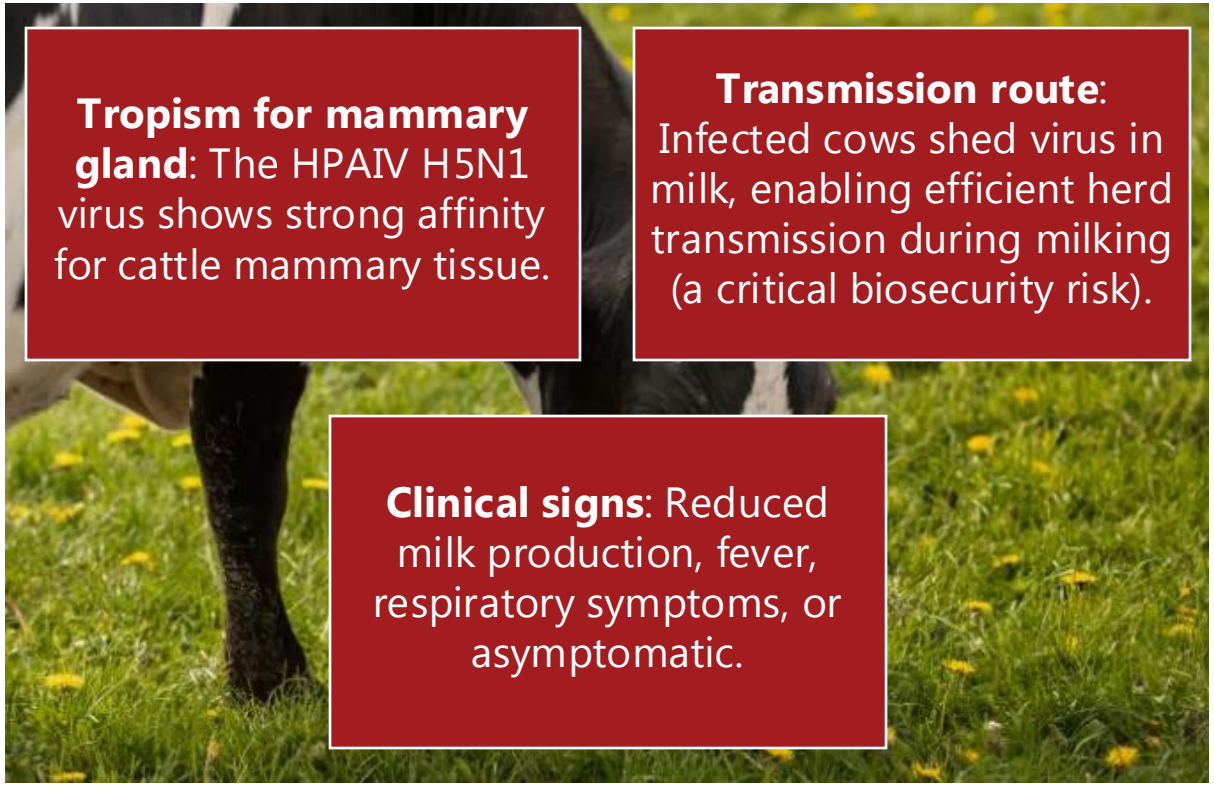


The possible routes of the virus by migratory waterbirds from the USA to Europe



Source: https://efsa.onlinelibrary.wiley.com/doi/10.2903/j.efsa.2025.9508

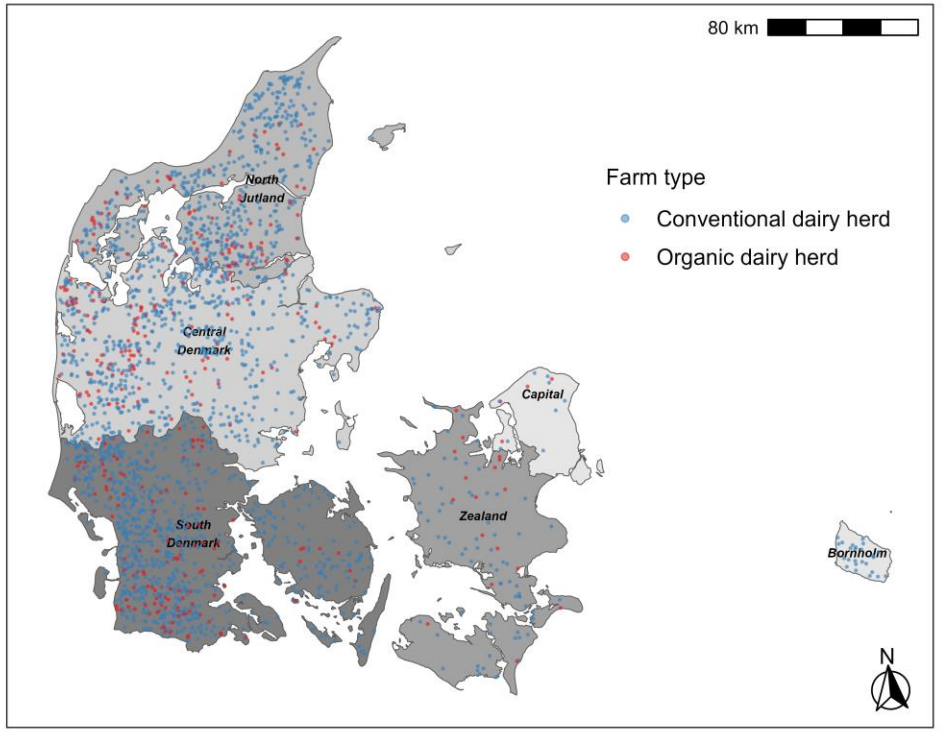
Why Denmark? Why now?



Tropism for mammary gland: The HPAIV H5N1 virus shows strong affinity for cattle mammary tissue.

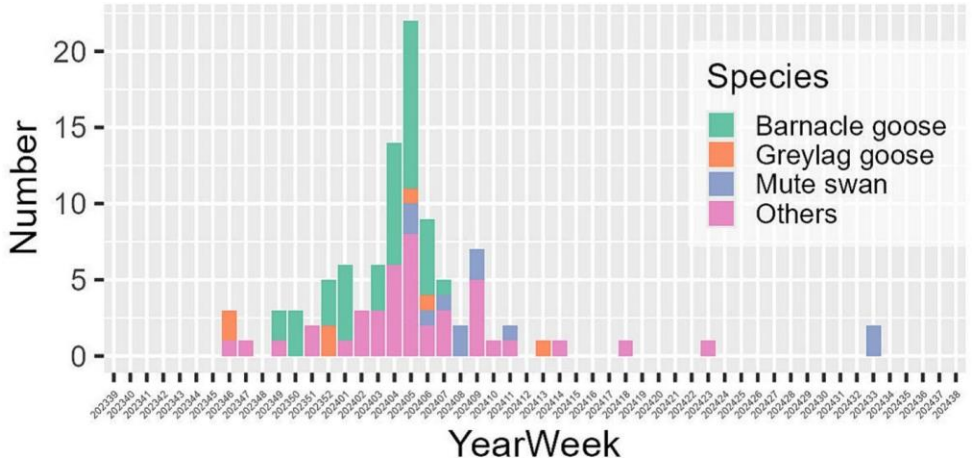
Transmission route: Infected cows shed virus in milk, enabling efficient herd transmission during milking (a critical biosecurity risk).

Clinical signs: Reduced milk production, fever, respiratory symptoms, or asymptomatic.



Data source: Danish Central Husbandry Registre

The 2023/24 season



Data source: https://ai.fvst.dk/

The power of two: a dual-approach for evaluating spatiotemporal HPAI risk to Danish dairy cattle

Objective: A spatiotemporal risk assessment to identify high-risk area period when uncertainty exists.

Validation, not variation, with two distinct, parallel-track approaches.

Styrelsen for Fødevarer, Landbrug og Fiskeri

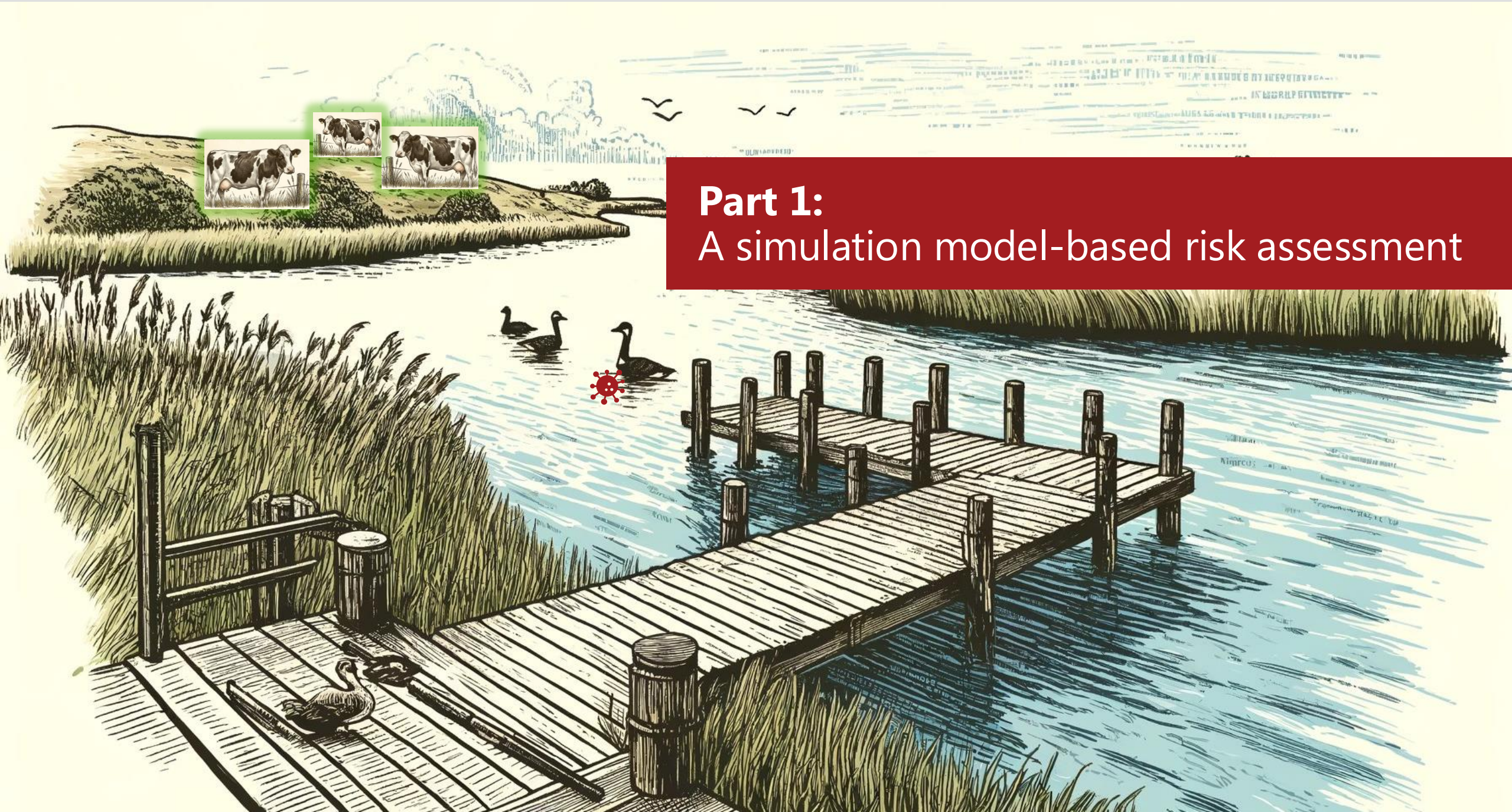
Simulation model

- **Foundation**: rooted in a PhD project since 2021
- **Focus**: explicit simulation of biological processes
- **Output**: Baseline understanding of the spatiotemporal risk

Kvægafgiftsfonden Mælkeafgiftsfonden

Integrated mechanistic model

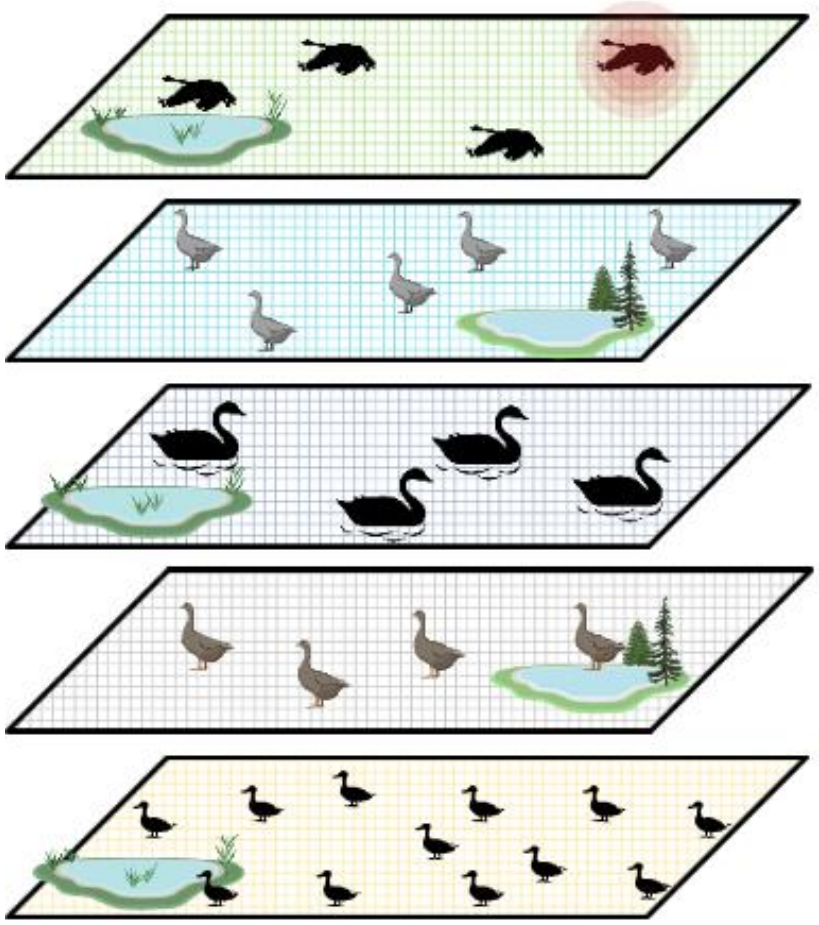
- **Foundation:** Project proposal submitted immediately the first cattle case in U.S.
- **Focus:** integrating a mechanistic model with existing models
- **Output:** spatially and temporally spillover risk



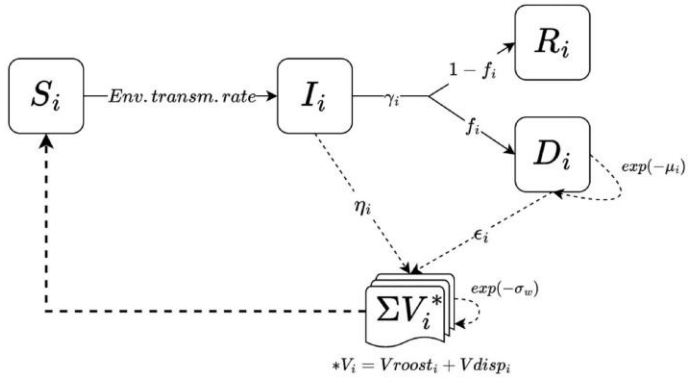
Part 1:
A simulation model-based risk assessment

Methods: An explicit stochastic simulation-based modelling

Grid-based bird abundance



- **Mechanistic model**: Susceptible-Infectious-Recovered-Dead-Environment (SIRD-V)



- **Core equation:**

$$Env.transm.rate_i = F\left(\frac{\ln(2)}{ID_{50,i}}, time\right) \times C(weight_i, time)$$

Source: https://doi.org/10.1016/j.ecolmodel.2025.111019

Methods: View the contaminated environment as a risk for dairy cattle

- Model initialisation

Round	Population Handling (N)	Infectious Birds (I)	Environment (V)	Primary Driver
1	All susceptible	**Proportion of infectious birds**	–	
2	**Round-1-end SIR**	–	**Round 1 carryover**	
3 (final output)	**Round-2-end SIR**	–	**Round 2 carryover**	

- Environmental contamination throughout the year

Methods: Explore uncertainty in cattle susceptibility

The infectious dose (ID_{50}) for HPAIV in cattle is currently unknown. To address this critical uncertainty, we evaluated three distinct scenarios.

High Susceptibility

$\boldsymbol{ID_{50}: 1}$

Assumes cattle are highly susceptible, requiring a very low viral dose to become infected. Represents a 'best-case' scenario for virus transmission.

Poultry-like Susceptibility

$\boldsymbol{ID_{50}: 5 \times 10^2}$

Assumes susceptibility is similar to that of poultry. This is considered the most plausible and realistic scenario.

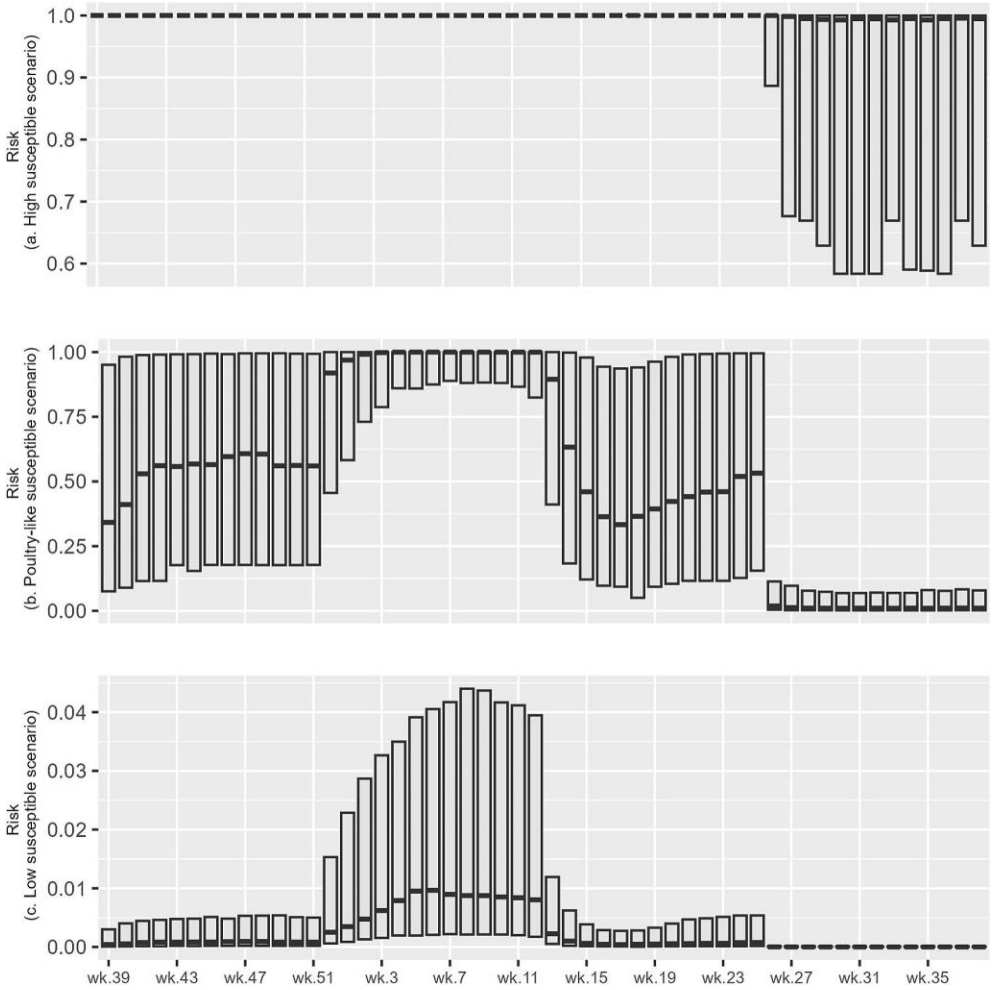
Low Susceptibility

$\boldsymbol{ID_{50}: 5 \times 10^5}$

Assumes cattle are relatively resistant, requiring a very high viral dose. Represents a 'worst-case' scenario for virus transmission.

$$\text{Risk}_{scenario} = 1 - exp(-(\frac{ln(2)}{ID_{50,scenario}}) * V_{grid})$$

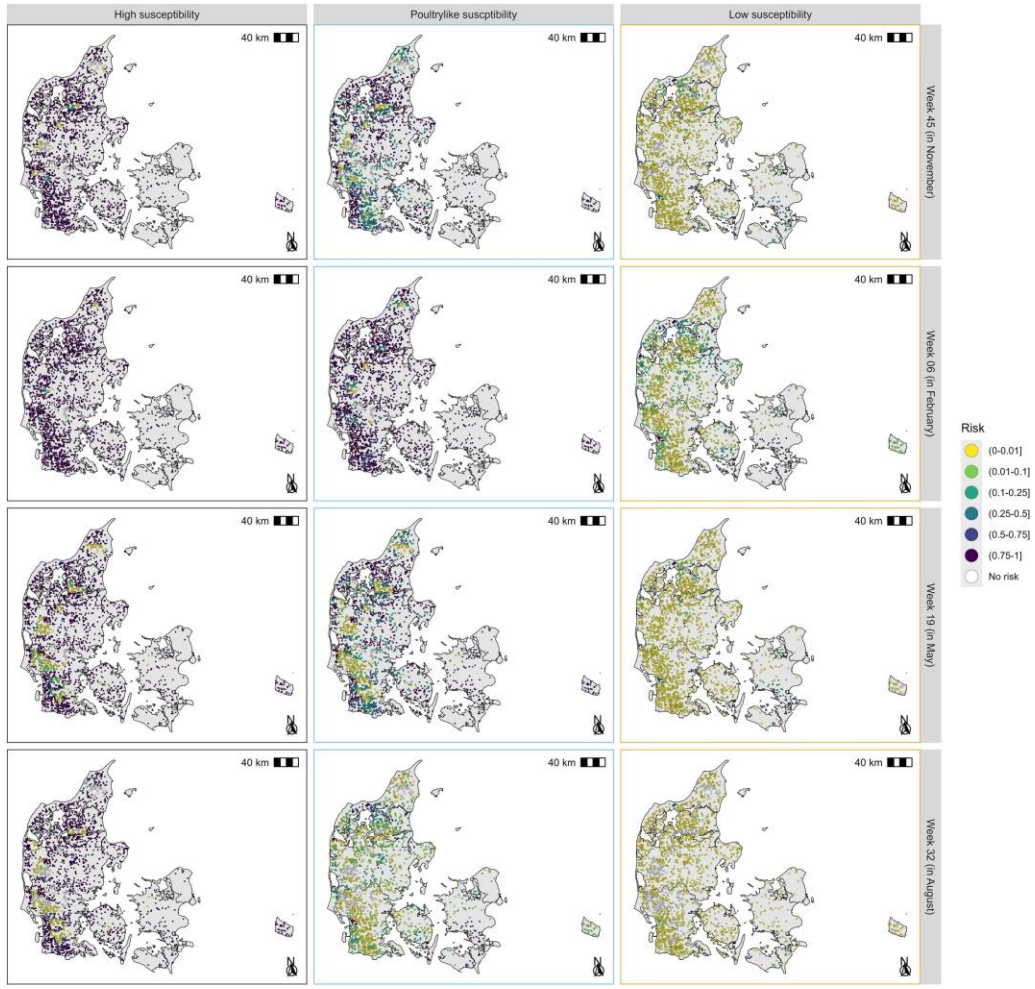
Results: Temporal dynamics



Weekly spillover risk distribution of dairy herds under three scenarios

- **Four risk stages**: the risk rises sharply in late winter, peaks in early spring, declines from late April, and remains very low in summer.
- **Highest risk period**: Jan.-Mar. (Weeks 52-12).
- The "Poultry-like" scenario (middle panel) best illustrates a strong seasonal fluctuation.

Results: Spatial hotspots



Risk Map in the middle week of each risk stage under three scenarios

- **Northern Jutland**: key waterfowl habitat near Limfjord.
- **Southern Zealand**: strategic location on major bird migration corridors.
- **Jutland coastal area**: coastal proximity drives elevated introduction risk.

Results: Impact of uncertain risk cutoffs

High Susceptibility > 90% of dairy herds were at risk during the winter/spring

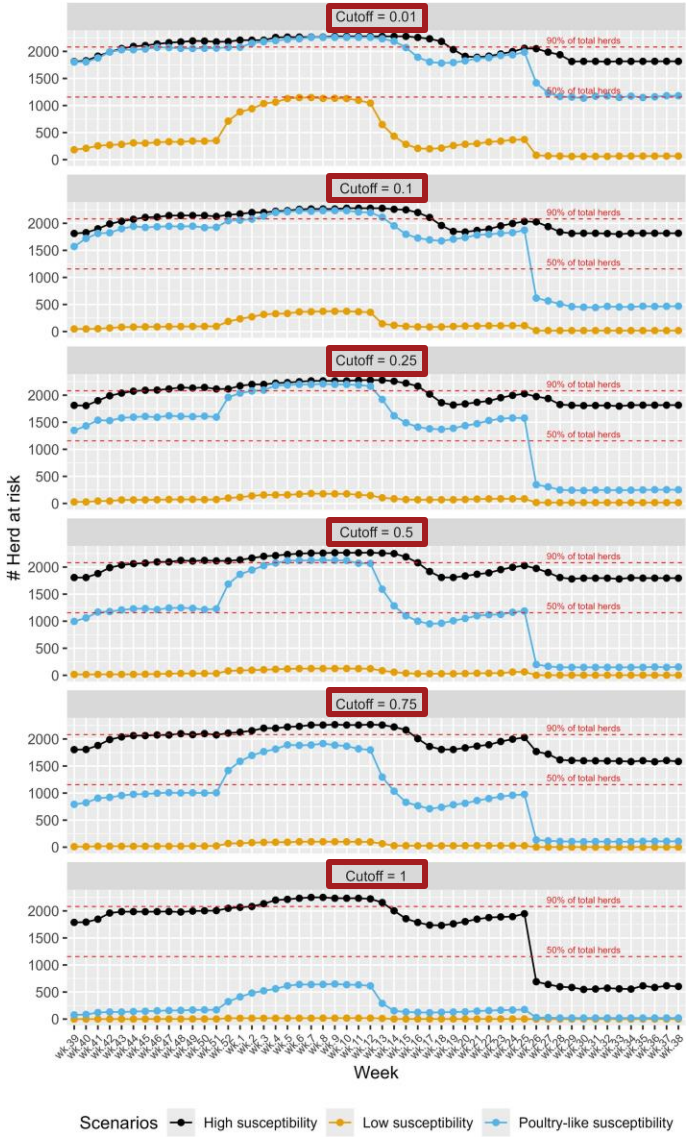
- The majority of farms are at-risk year-round, regardless of the cutoff applied.

"Poultry-like" Susceptibility Cutoffs did not affect the proportion of herds-at-risk much, except at 0.01

- Shows pronounced seasonal variation with peaks in winter and spring.

Low Susceptibility Always a small number of dairy herds were at risk

- Relatively few farms are classified as at-risk, even when using low cutoff values.

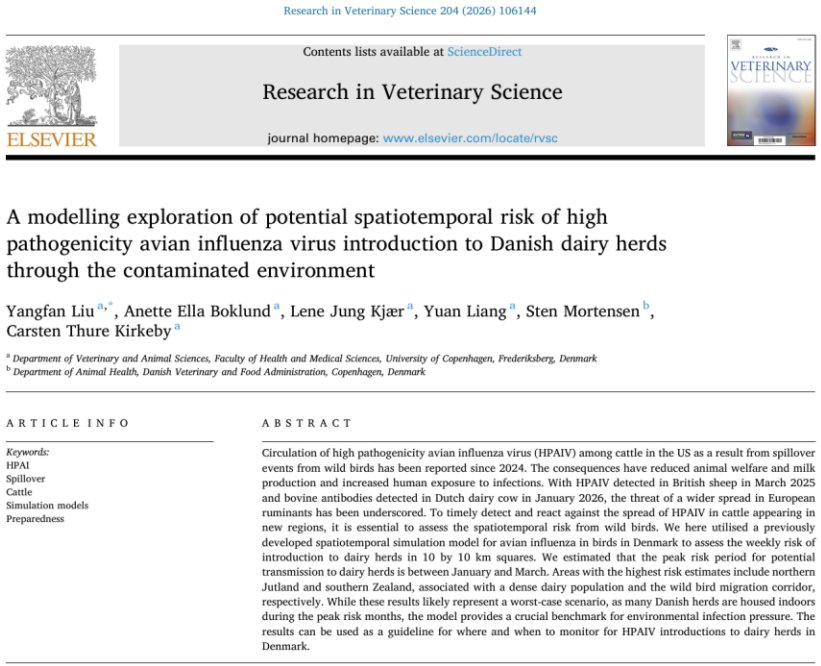


Discussions: part 1

- This study provides a fine-scale spatiotemporal risk map for HPAIV spillover from wild birds to dairy cattle in Denmark.
- **Implications**:
  - Optimise surveillance
  - Targeted biosecurity
- **Limitations**:
  - Uncertainty of the infectious dose
  - Overestimation of the indoor risk during winter
  - Simplified transmission in 10 km × 10 km geo-grid
  - Limited scope: no within-herd or between-herd transmission (only assesses spillover from wild birds)

Acknowledge

- Anette Boklund
- Lene Jung Kjær
- Yuan Liang
- Sten Mortensen
- Carsten Kirkeby
- **Voluntary bird enthusiasts**
- **Bird data managers**



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A modelling exploration of potential spatiotemporal risk of high pathogenicity avian influenza virus introduction to Danish dairy herds through the contaminated environment

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ABSTRACT

Circulation of high pathogenicity avian influenza virus (HPAIV) among cattle in the US as a result from spillover events from wild birds has been reported since 2024. The consequences have reduced animal welfare and milk production and increased human exposure to infections. With HPAIV detected in British sheep in March 2025 and bovine antibodies detected in Dutch dairy cow in January 2026, the threat of a wider spread in European ruminants has been underscored. To timely detect and react against the spread of HPAIV in cattle appearing in new regions, it is essential to assess the spatiotemporal risk from wild birds. We here utilised a previously developed spatiotemporal simulation model for avian influenza in birds in Denmark to assess the weekly risk of introduction to dairy herds in 10 by 10 km squares. We estimated that the peak risk period for potential transmission to dairy herds is between January and March. Areas with the highest risk estimates include northern Jutland and southern Zealand, associated with a dense dairy population and the wild bird migration corridor, respectively. While these results likely represent a worst-case scenario, as many Danish herds are housed indoors during the peak risk months, the model provides a crucial benchmark for environmental infection pressure. The results can be used as a guideline for where and when to monitor for HPAIV introductions to dairy herds in Denmark.

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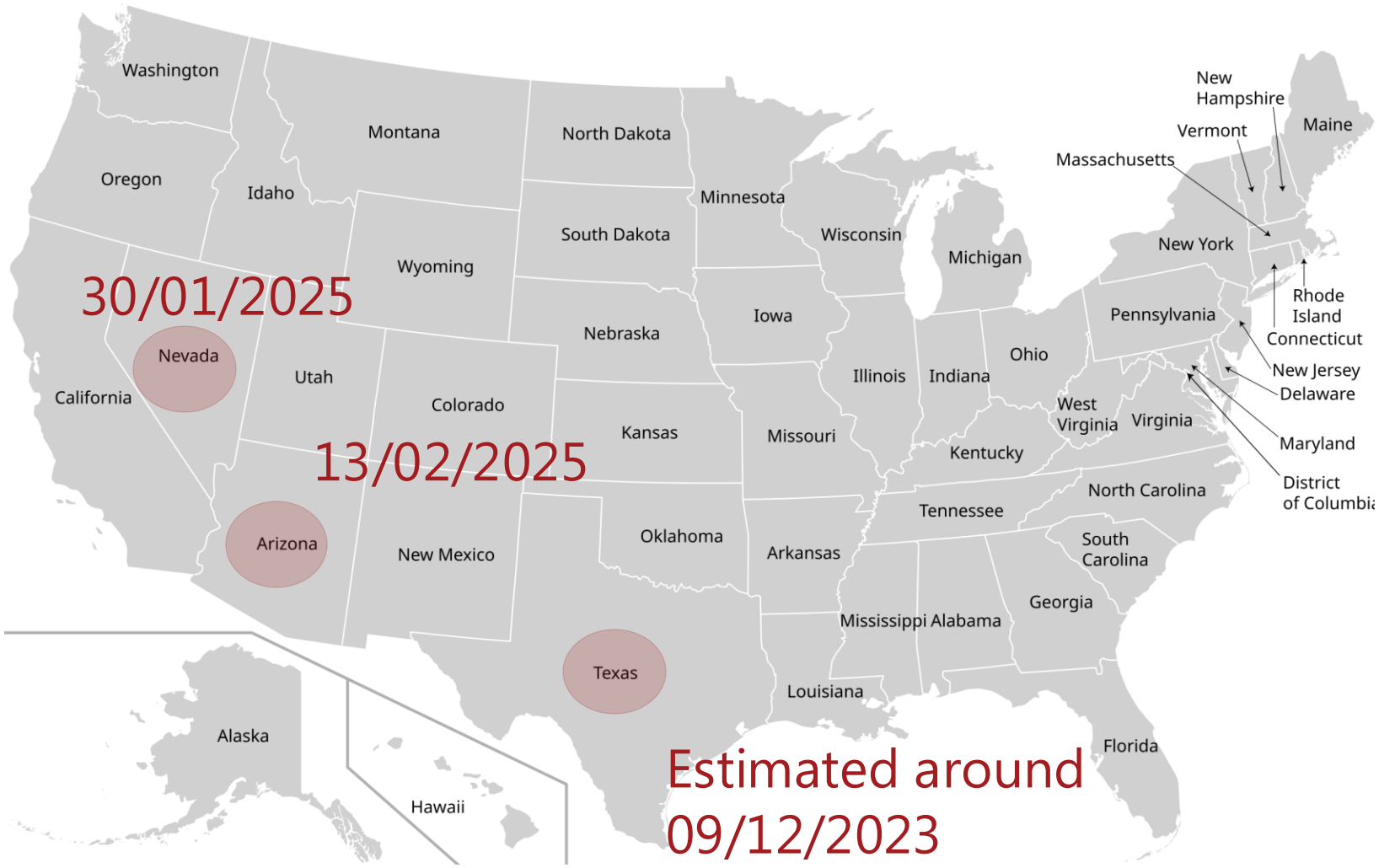
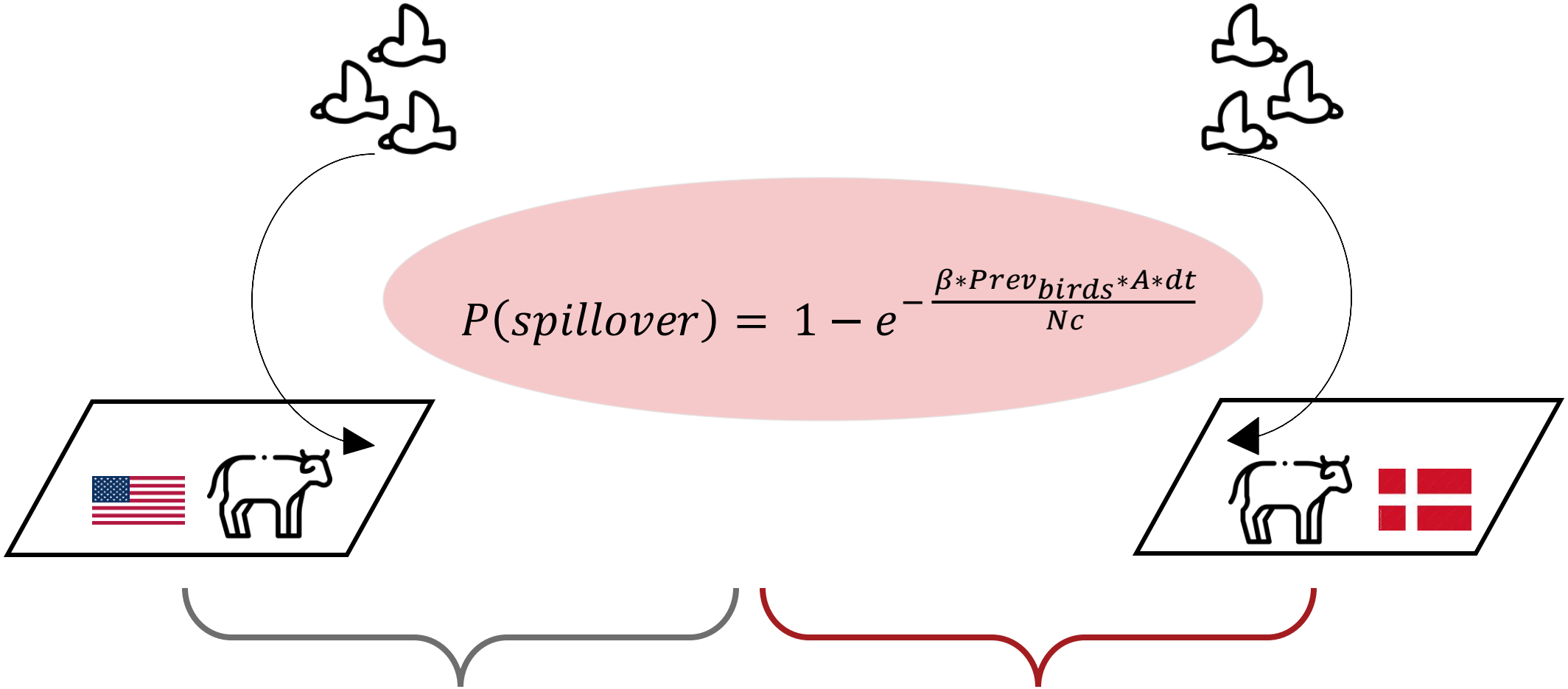
Part 2:

Integrated mechanistic model for spatiotemporal risk assessment

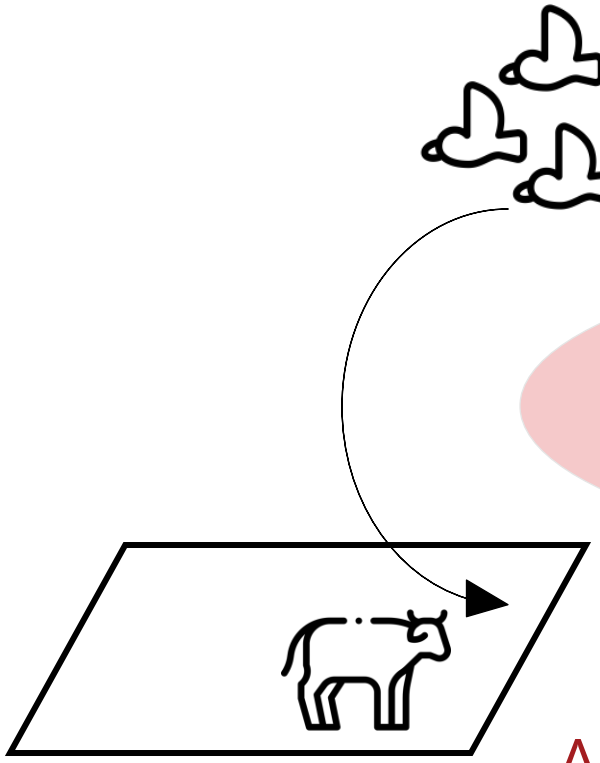
3 Spillover events from wild birds to cattle in US



Method: model diagram



Method: model diagram



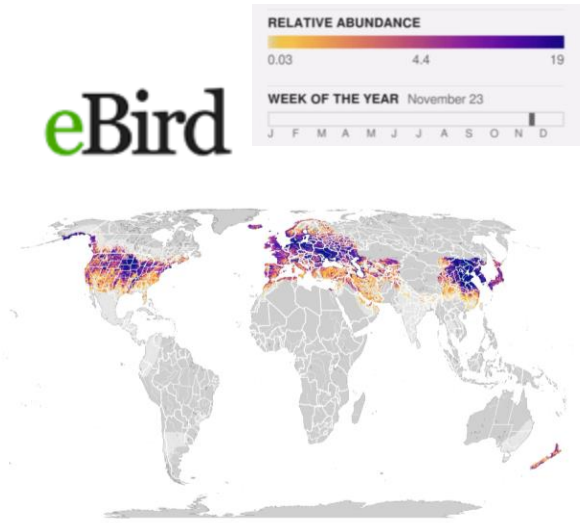
$$P(spillover) = 1 - e^{-\frac{\beta * Prev_{birds} * A * dt}{Nc}}$$

Assumption: Frequency dependent contact

β: transmission rate parameter from wild bird to cattle
$Prev_{birds}$: prevalence of HPAIV in wild birds during outbreak
A: wild bird abundance
dt: time interval (unit week)
Nc: cattle number
Expected cases in a cell in a week = $Nc * P(Spillover)$

Tools and Data

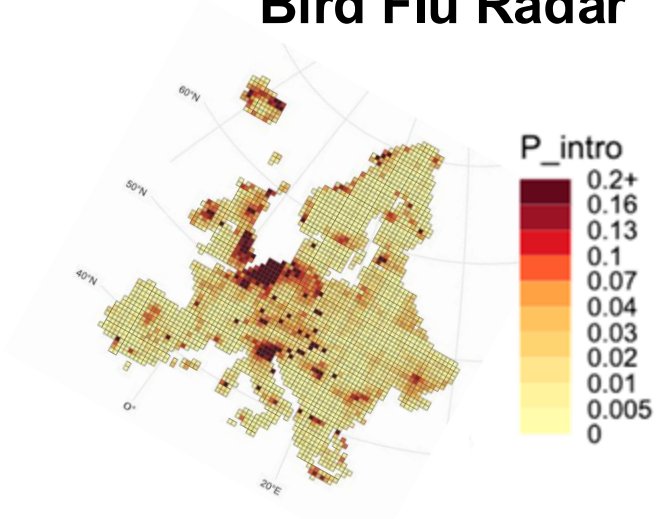
A)



Relative abundance of wild birds at global level

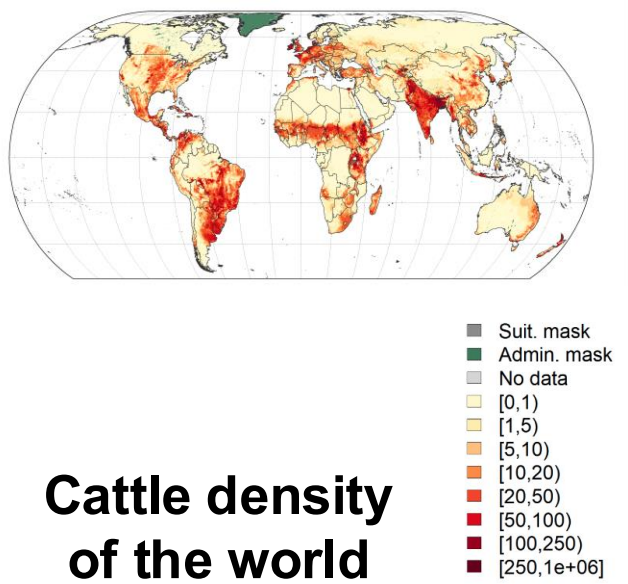
B)

Bird Flu Radar



Probability of HPAIV in wild birds at EU level

C)

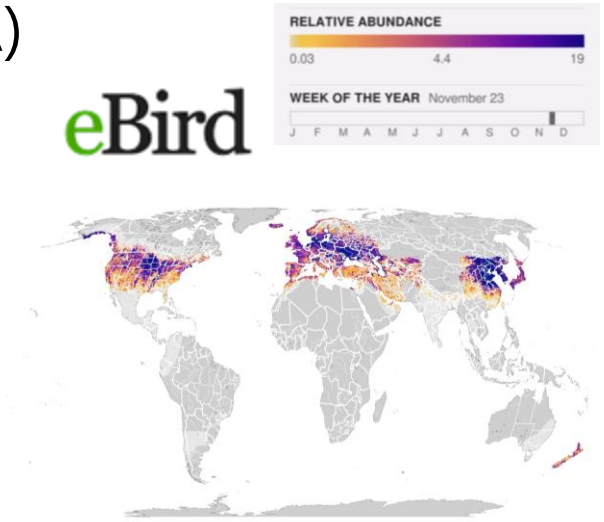


Cattle density of the world

D) **Danish Central Husbandry Registration (CHR)**

Brief description of eBird

A)

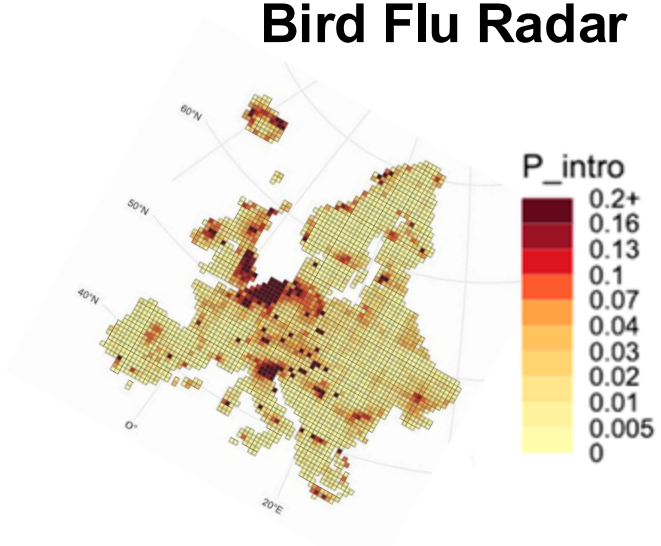


Relative abundance of wild birds at global level

- Machine learning models
- High spatial, temporal resolution
- Three groups of variables:
  - 5 observation effort variable
  - 3 temporal predictors
  - 76 environmental predictors from remote sensing data to describe bird habitat association across diverse landscapes, elevations and topographies.
- Extract all the waterfowls in US and DK (**54 species**)

Brief description of Bird Flu Radar

B)

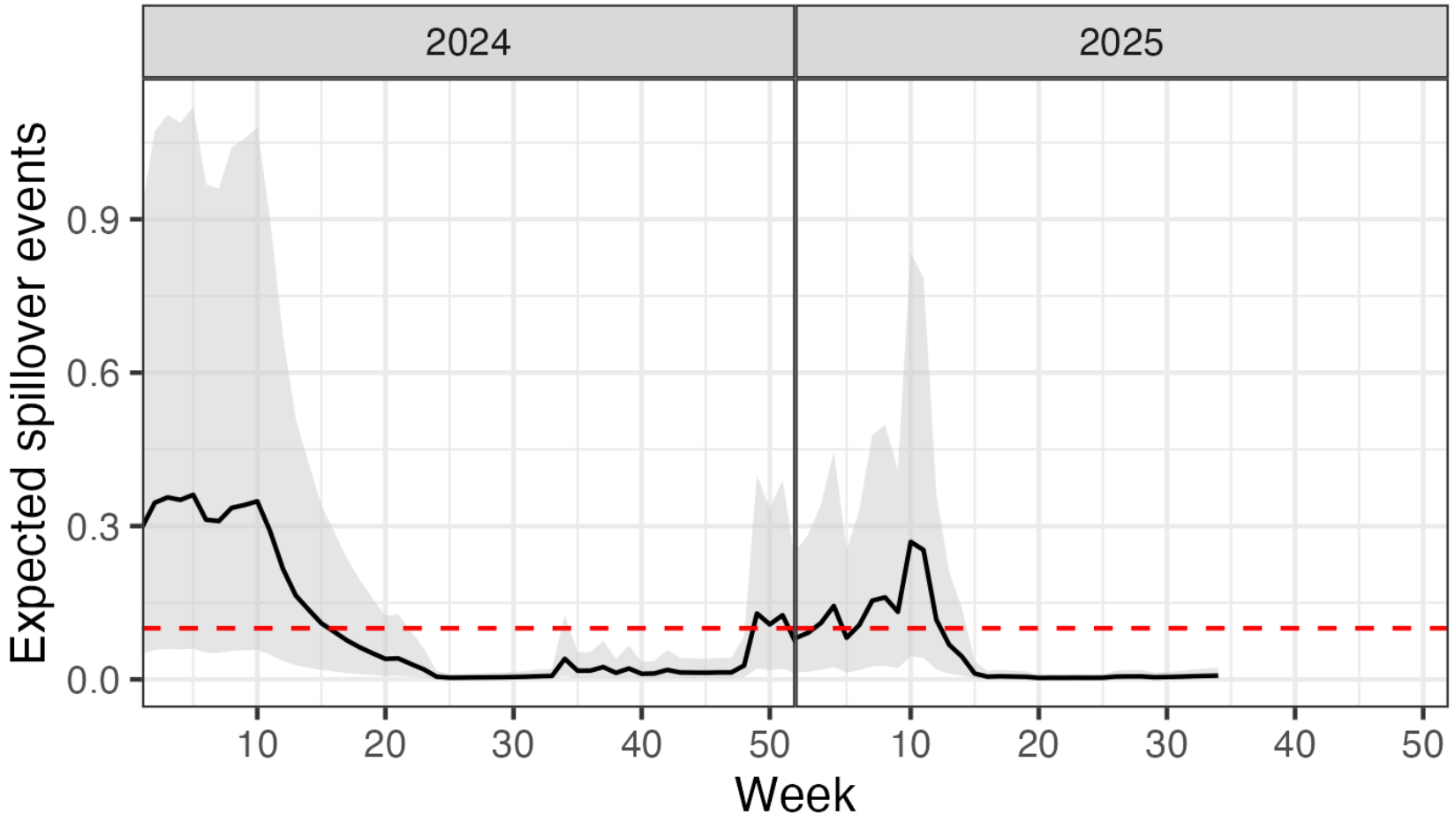


Probability of HPAIV in wild birds at EU level

- Predicts the weekly likelihood of HPAIV presence in wild birds
- Combines 3 models
  - Bird abundance model
  - Migration model
  - Scenario tree (optimize the threshold probability using ADIS and EMPRES-i databases)

	Threshold probability	Sensitivity	Specificity
	0.015	0.85	0.57
	0.03	0.79	0.66
★	**0.045**	0.73	0.73
	0.065	0.66	0.80

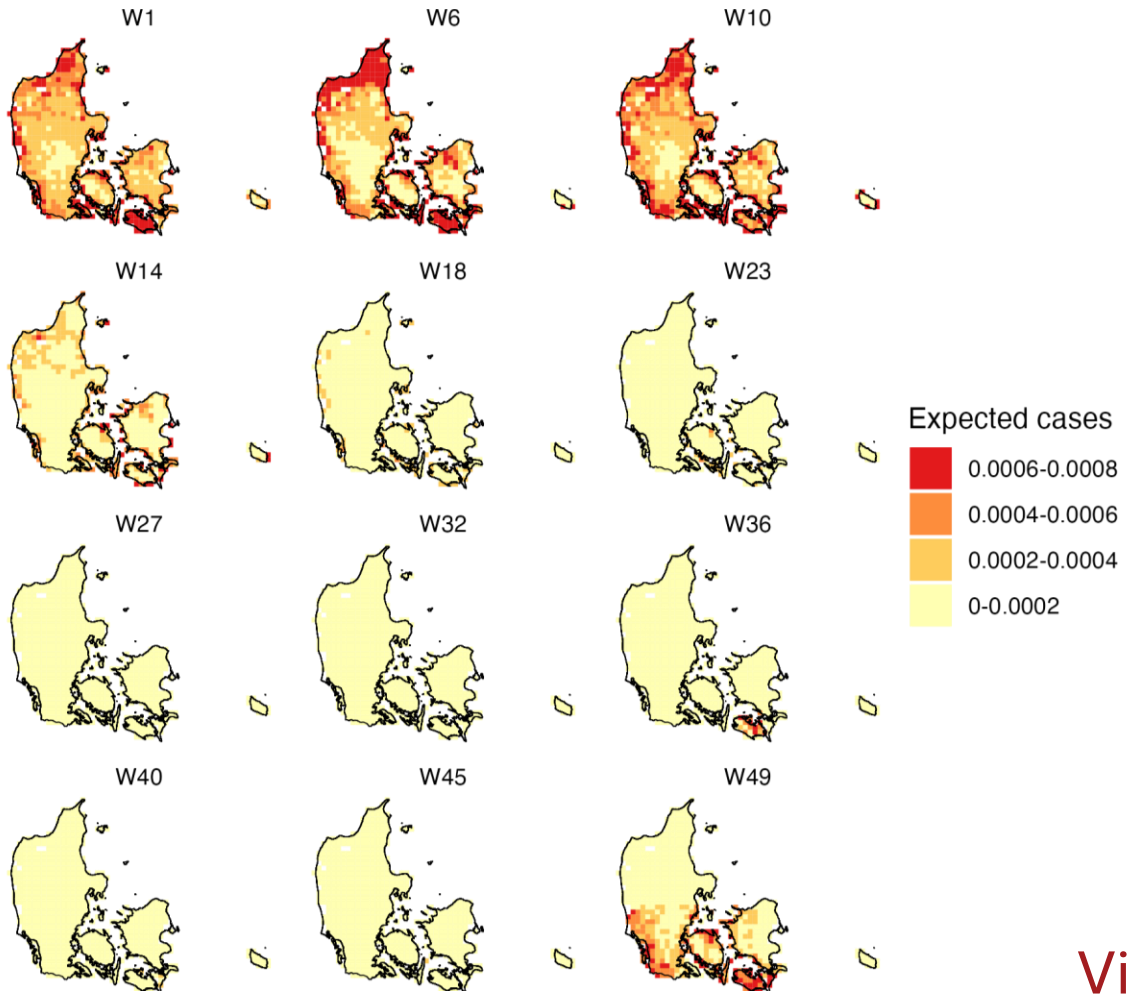
Results: Temporal dynamics



- **Winter (weeks 50–10 / Dec–Mar)**
- Low risk in **summer months**
- Weekly expected cases ~ 0.3 in high risk season

Consistent with Yangfan's prediction

Results: Spatial distribution



High-risk areas:

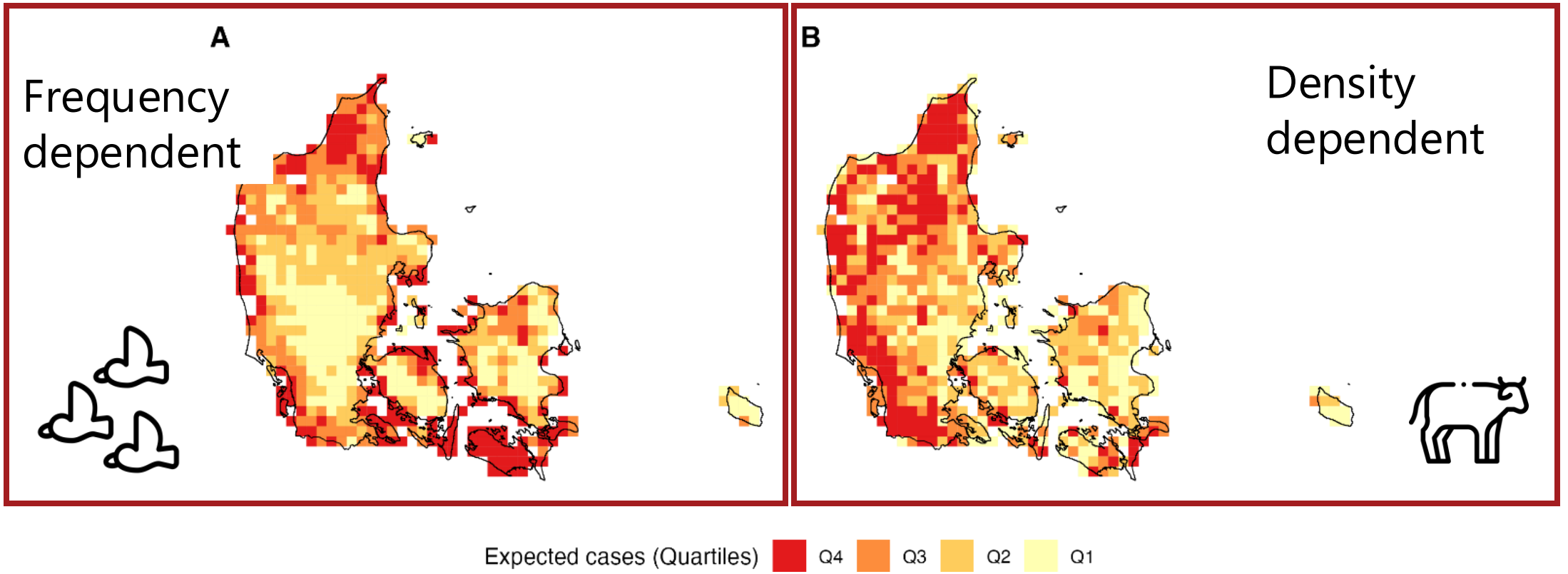
Coastal regions

Near German border

Visually different with Yangfan's prediction

Why?

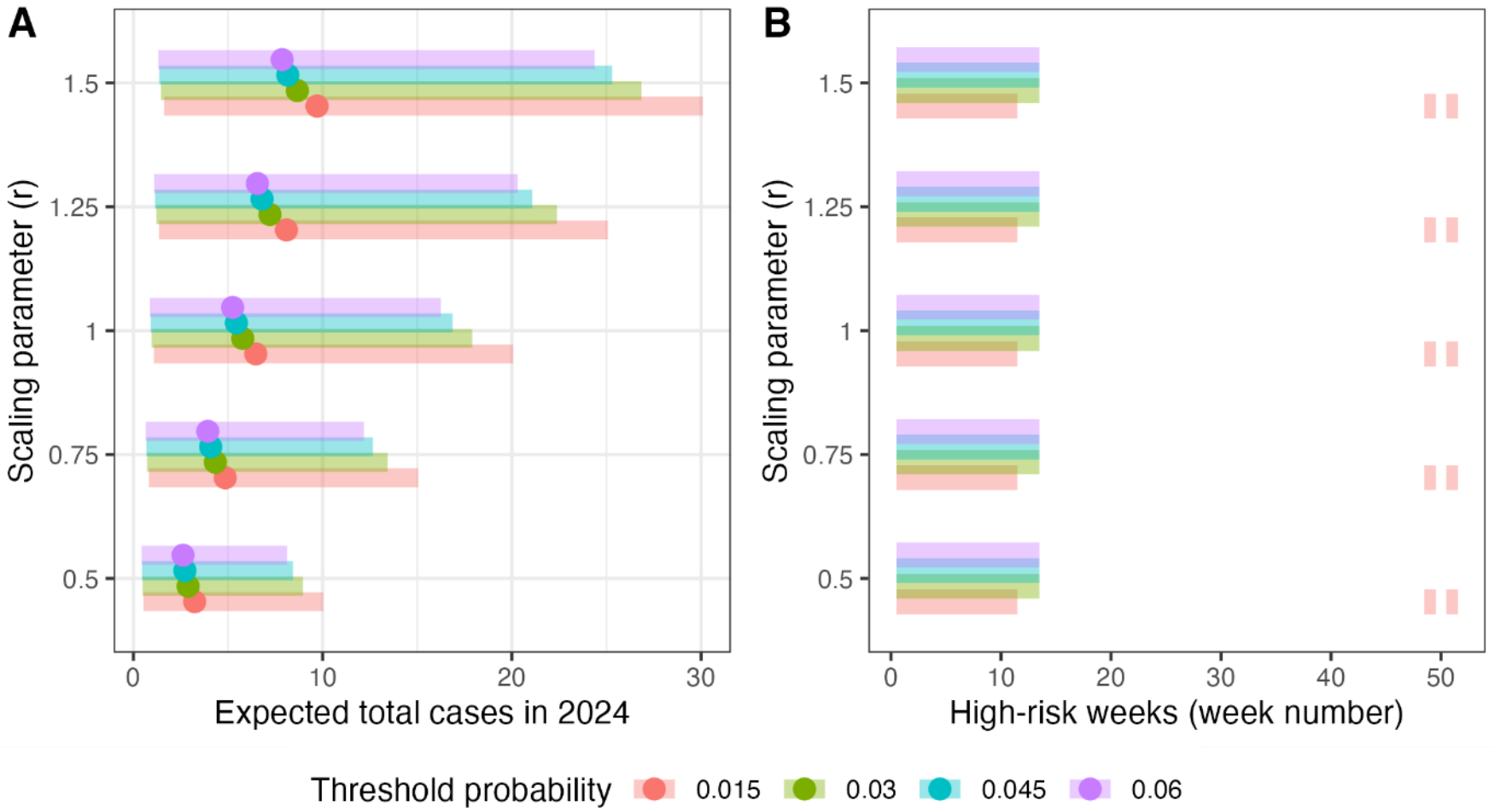
Results: Structural sensitivity analysis



Spatial distribution shifts to high cattle density areas

(the assumption of Yangfan's model)

Results: Parameter sensitivity analysis



20 parameter sets

Can influence the absolute number of expected cases

but does not affect the temporal pattern of spillover risk

Discussions: part 2

- **High risk season**: winter week 50-10
- **High risk areas**: Danish coastline, near German boarder

Key assumption: a frequency-dependent bird-cattle contact, spatial risk depends on contact structure

Absolute expected cases can be influenced by:

- Underreported U.S. data → underestimate $\hat{\beta}$ and risk
- Prevalence in U.S. and Danmark (Sensitivity analysis)
- Difference in cattle husbandry and biosecurity

Sensitivity analysis show the impact of these on the absolute value

More details

Preventive Veterinary Medicine
Volume 251, June 2026, 106844

Modeling the spillover risk of highly pathogenic avian influenza from wild birds to cattle in Denmark: A data-driven risk assessment framework

You Chang [a], Jose L. Gonzales [b], Erik Rattenborg [c], Mart C.M. de Jong [d], Beate Conrady [a]

Department of Veterinary and Animal Sciences

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19 March 2026

Bird Flu Risk to Danish Cattle – New Tool Can Warn Farmers Before Infection Spreads

DENMARK | WILD ANIMALS | FARM ANIMALS | VIRUS | GLOBAL HEALTH | NATURE AND ENVIRONMENT

VIRUS Bird flu can infect both cows and humans. Researchers from the University of Copenhagen have developed a tool that can predict where and when the risk of infection is highest.

Acknowledgement

Mælkeafgiftsfonden Kvægafgiftsfonden




SEGES

WAGENINGEN UNIVERSITY & RESEARCH

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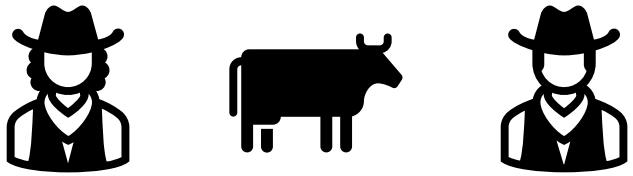
Conclusion and comparison

	Model 1 (Yangfan)	Model 2 (You)
Objective	A spatiotemporal risk assessment to identify high-risk area and high-risk period	
Result	Temporal patterns of **two models** shared high similarity Spatial pattern differs: Density-dependent model of **model 2** has the similar pattern as **model 1**	
Output unit	Expected cell-based risk for individual cattle herds per week	Expected cases per cell per week
Method	Stochastic simulation model with explicit mechanistic assumptions	Integrated mechanistic model calibrated using U.S. data
Assumption	Density-dependent transmission between contaminated environment and cattle, accounting for dilution factor	Frequency-dependent contact between wild birds and cattle
Limitation	**Both models** only assessed the risk of introduction. Further movement of cattle herds was not considered in the models.	
	Expert opinion on infectious dose, extrapolate spillover for poultry to spillover for cattle	U.S. derived parameter and scaled to Danish context

Take away

- Even low expected cases justify preparedness due to **high impact**
- The potential occurrence depends on the actual **threshold for spillover events** in Danish context
- Focus on **high-risk regions + seasons**
- **Framework** can serve as:
  - Early warning tool
  - Decision support for surveillance design



Questions ?

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