Istituto Zooprofilattico Sperimentale delle Venezie

MODAH 3 Modelling in Animal Health

Unraveling the Role of Wild-Domestic Interface in the Spread of High Pathogenicity Avian Influenza

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MODAH 2024

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Avian Influenza

Major economic impact

2021-2022 epidemic in Italy

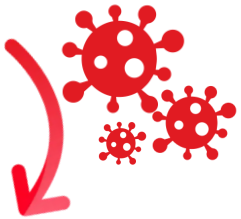
- 317 Domestic outbreaks
- 500 million euros losses

Threat to public health

- Risk of spillover to mammals and humans

Eco-epidemiology

- Anseriformes and Charadriiformes maintenance hosts
- Over 90 species involved
- Spillover events from wild birds to domestic bird species



Introduction

- **Wild-domestic interface**
  - Direct interactions between waterfowl and poultry
  - **More complex interface (reservoir species, bridge species and environment)**

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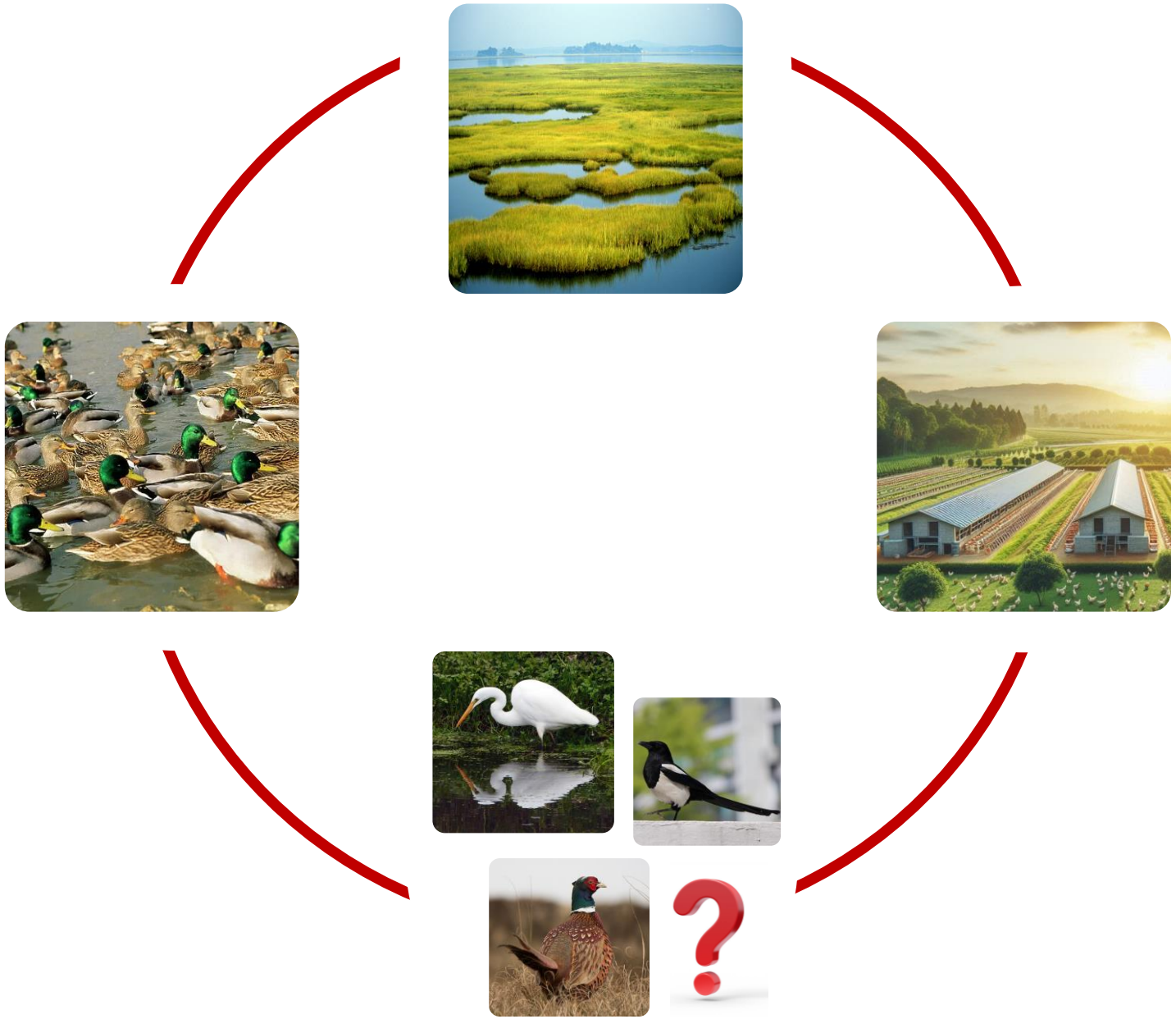
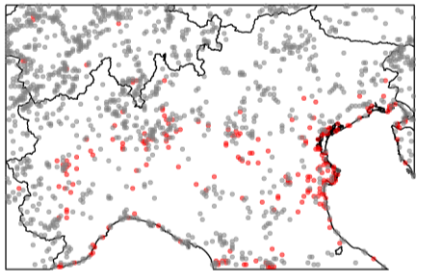
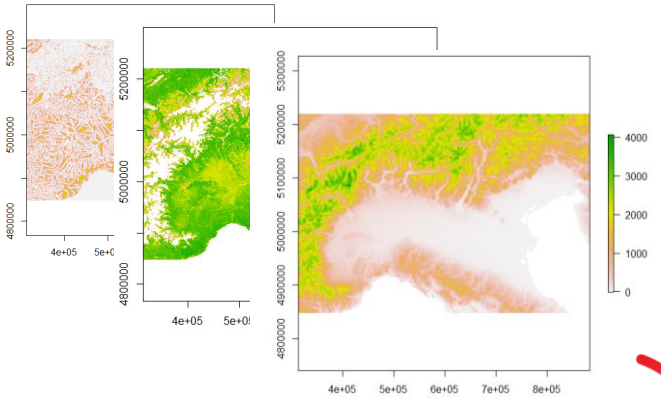


Objectives

Species observations



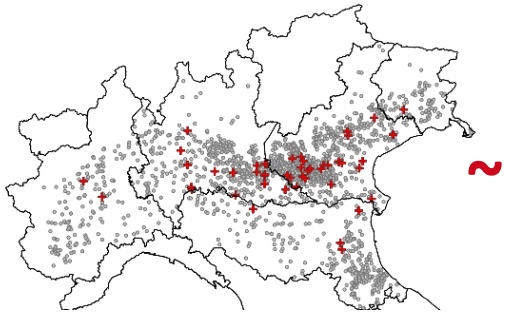
Environmental variables



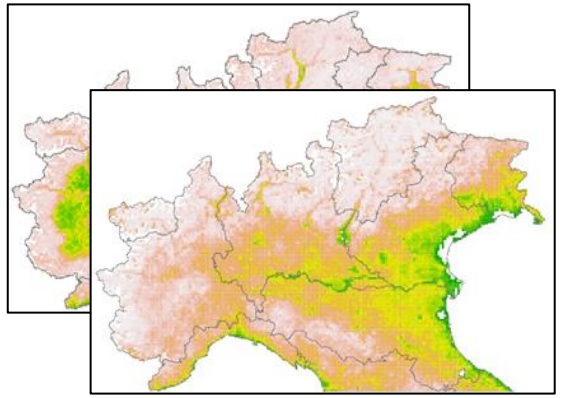
Phase 1

- Construction of Wild Birds Species Distribution Models

Outbreaks occurrences 2017-2018



Species distribution maps



Phase 2

- **Wild birds distribution and new AI oubreaks emergence associations**
- **Spatial prediction of new outbreaks**

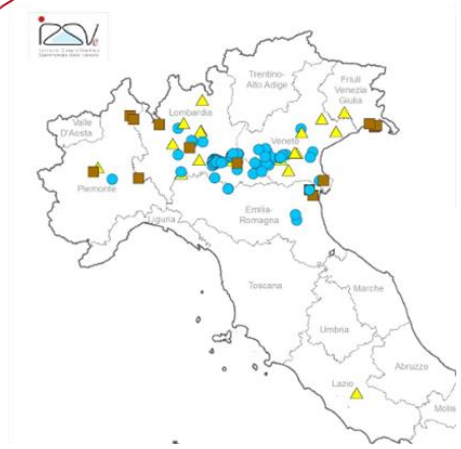
Study area and species selection

- Analysis of the bird community in in the proximity of 10 poultry farms in North of Italy in 2019(1)

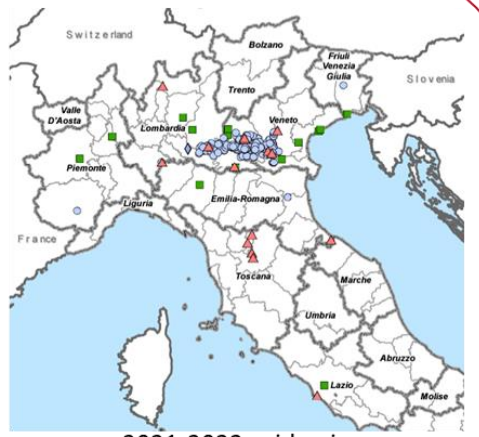
Camera traps
40 species

- Characterize bird communities
- Identify the species that get closest to poultry farms

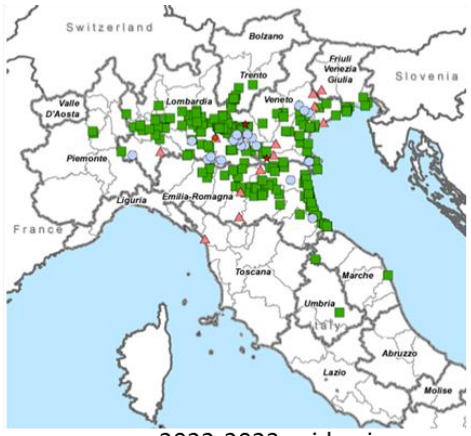
Study area



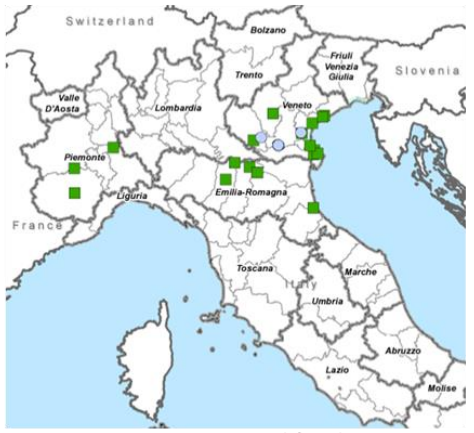
2017-2018 epidemic



2021-2022 epidemic



2022-2023 epidemic



2023-2024 epidemic

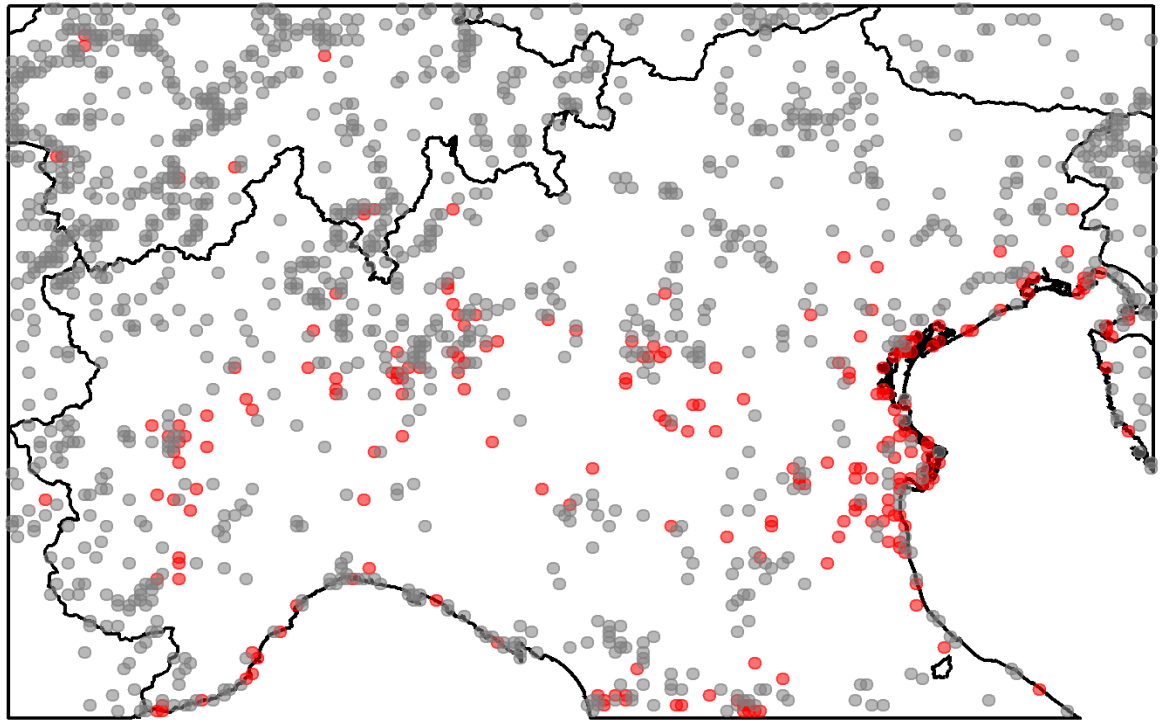
(1) L. Martelli et al., "Study of the Interface between Wild Bird Populations and Poultry and Their Potential Role in the Spread of Avian Influenza," Microorganisms, vol. 11, no. 10, p. 2601, Oct. 2023, doi: 10.3390/microorganisms11102601.

Data collection – Phase 1

- **Wild bird occurrences data collection**
  - 2019
  - Complete checklists

eBird

Species occurrence data



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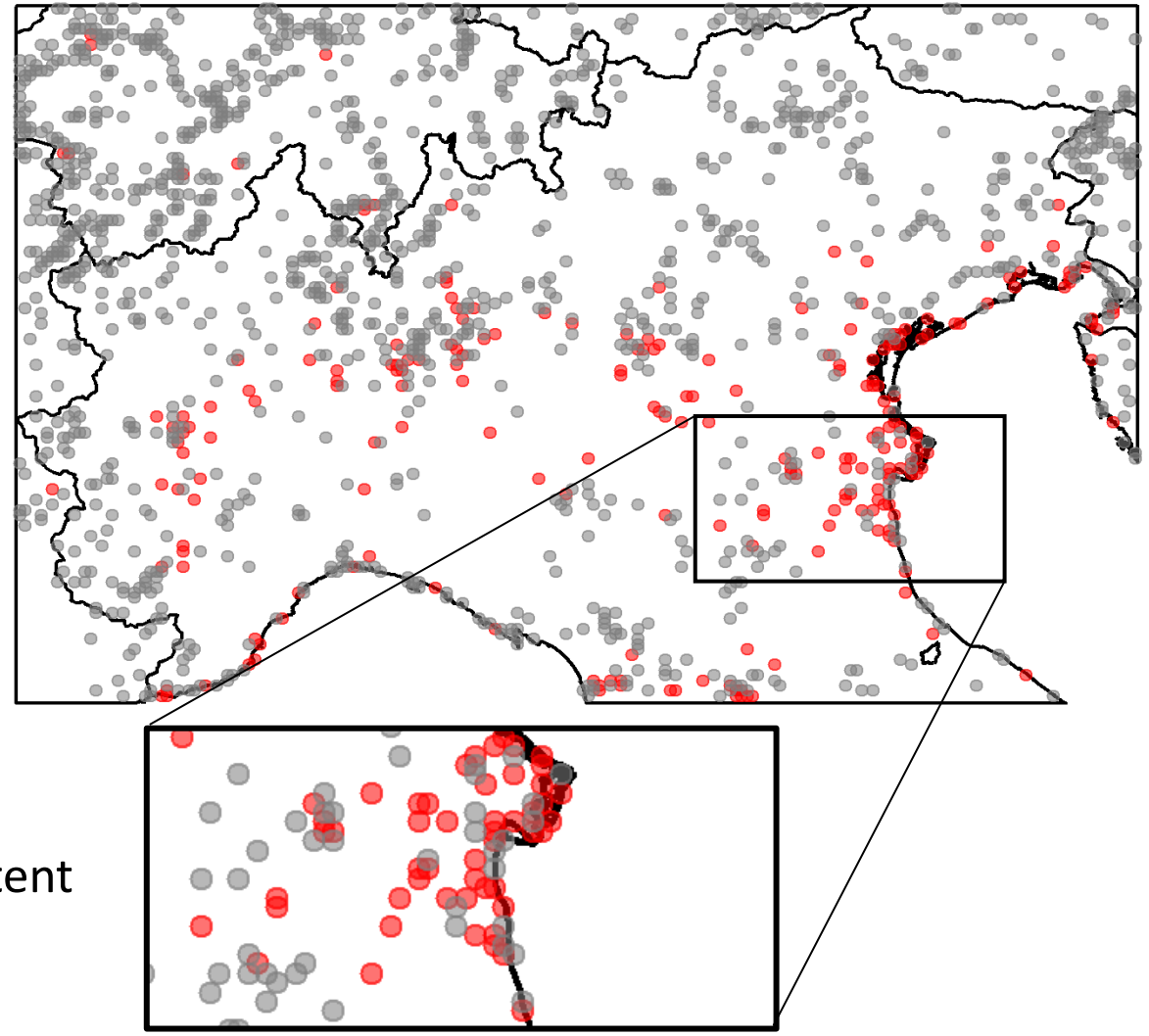
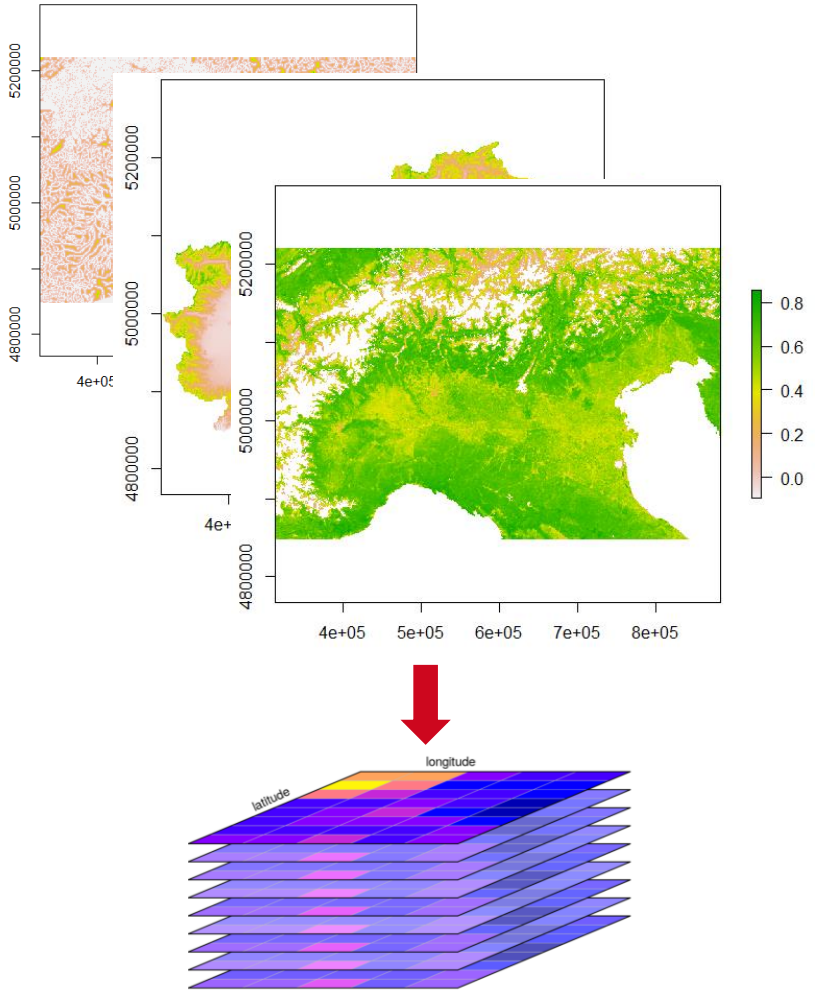


  - Occurrences considered at a consistent spatial unit level (3 km x 3 km cells)

Data collection – Phase 1

- **Environmental variables**
  - Environmental Data for Veterinary Epidemiology platform (EVE)[2]
  - Biovars
  - 15 additional quantitative variables from Corine land cover's levels



(2) M. Mazzucato et al., "An integrated system for the management of environmental data to support veterinary epidemiology," Front. Vet. Sci., vol. 10, Mar. 2023, doi: 10.3389/fvets.2023.1069979.

Data collection – Phase 2

- **Domestic outbreaks data**

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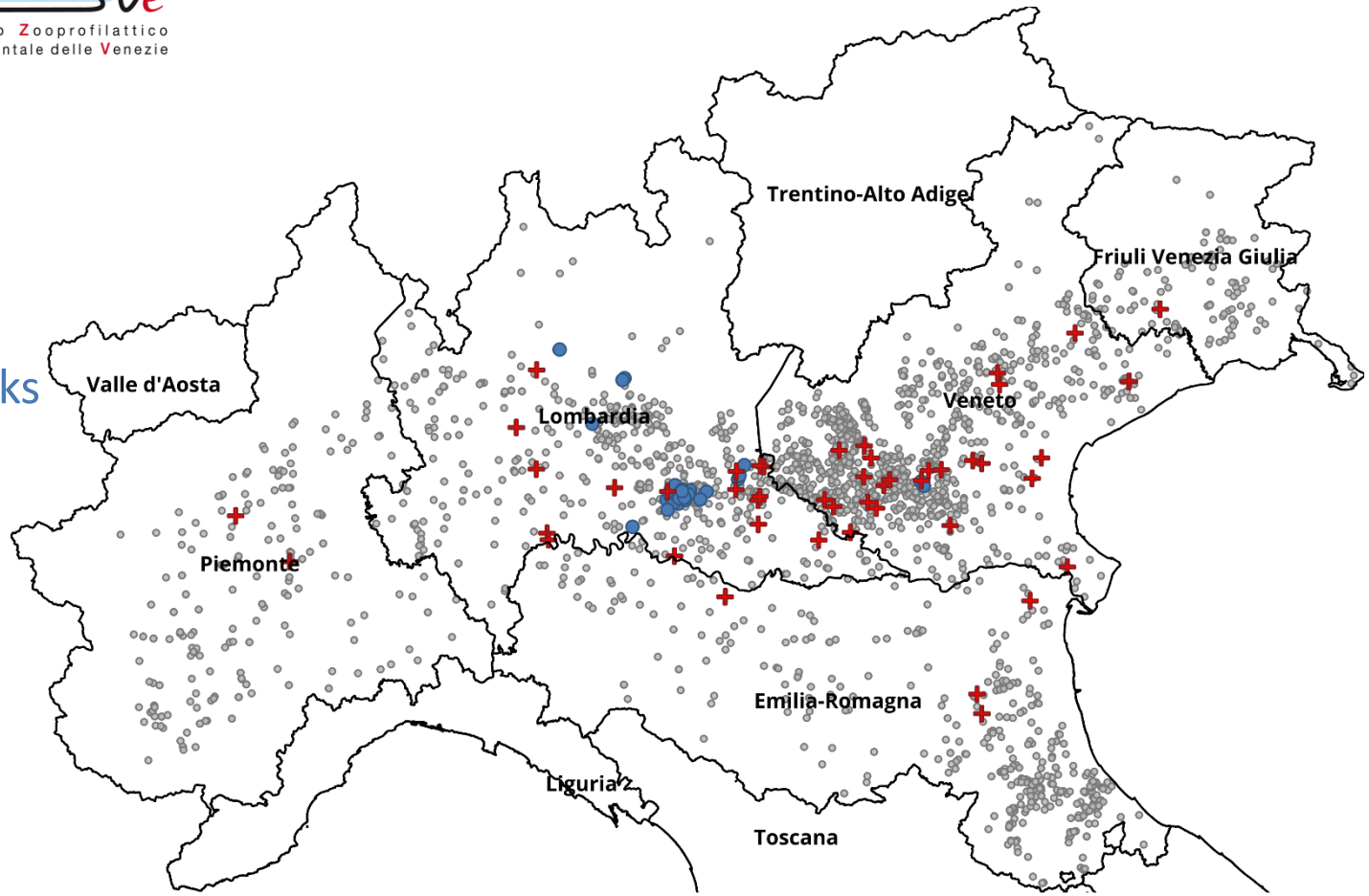
- 2017-2018 epidemic – 83 outbreaks
- 49 primary outbreaks – 34 secondary outbreaks
- 2203 farms not diagnosed as AIV positive during the HPAI H5N8 epidemic

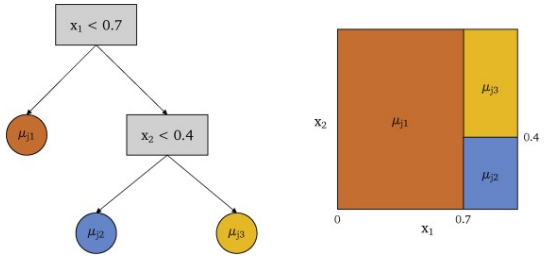


Species distribution models (SDM)

- **BART: Bayesian Additive Regression Trees**

Machine learning

Decision tree



$$f(\cdot) = \sum_{j=1}^{m} g(\cdot;\, T_j,\, M_j) + \epsilon; \qquad \epsilon \sim \mathcal{N}\left(0,\, \sigma^2\right).$$

Diagnostic metrics — Cutoff

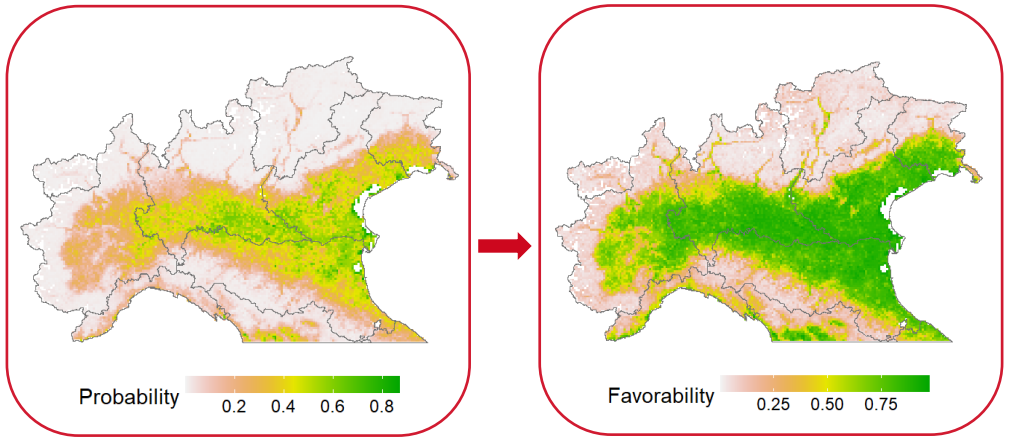
- Area Under the Receiver Operating Characteristic Curve — 0.7
- True skills Statistics — 0.4
- Miller Calibration Slope — >0.5 & <1.5

22/40 species

- **Favorability**

$$F = \frac{\frac{P}{(1-P)}}{\frac{n1}{n0} + \frac{P}{(1-P)}}$$

Probability → **Favorability**

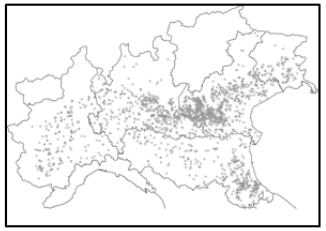


Domestic outbreaks probability prediction

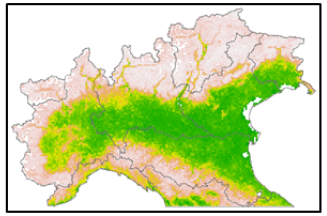
- **Univariable ensemble models**

Occurrences (n=49)

Absences (n=2203)

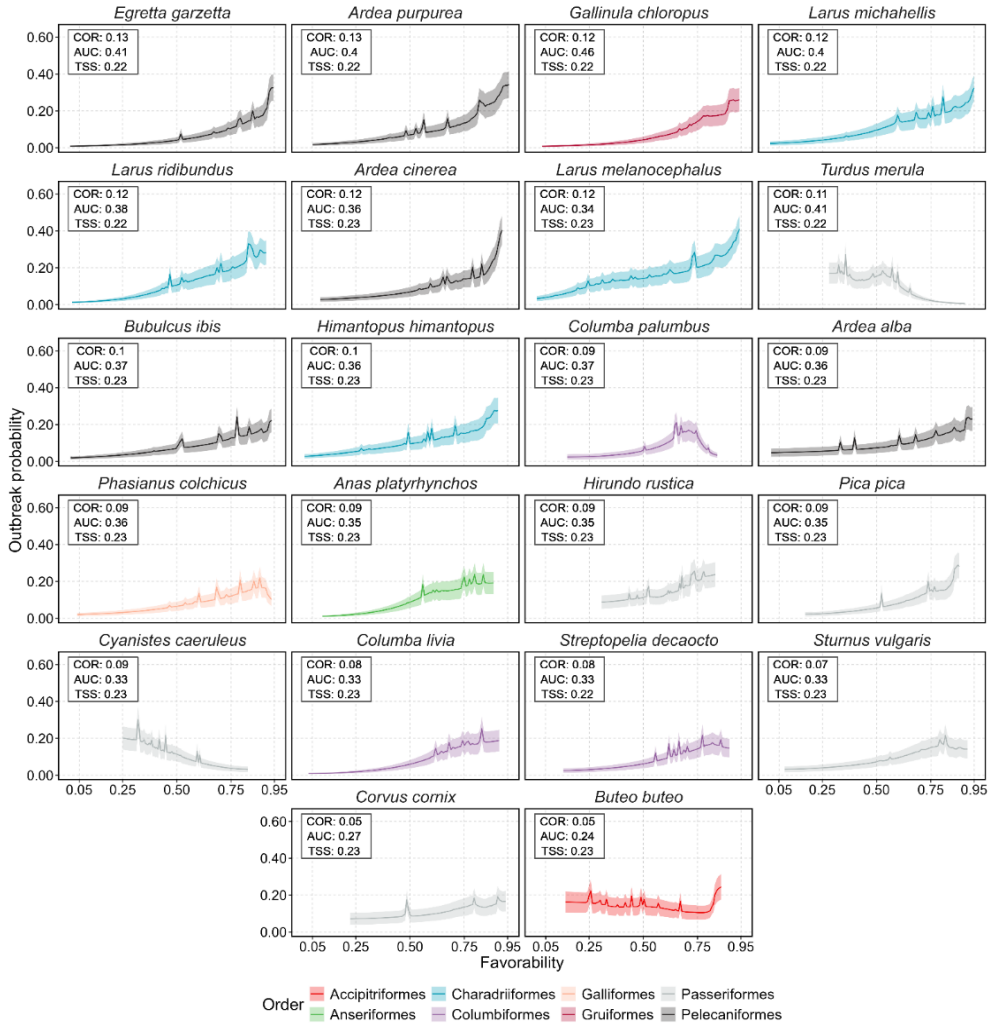


Predictors (n=1, species)



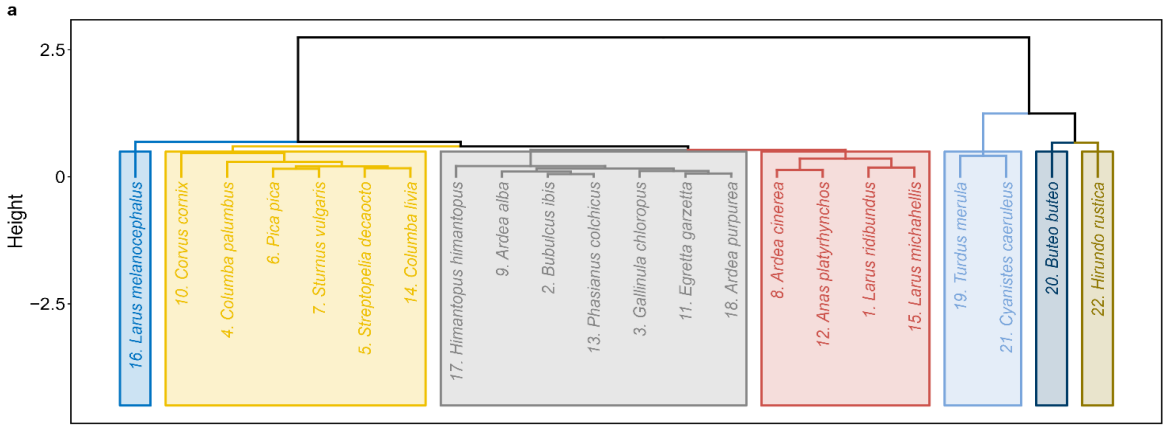
5 algorithms ensemble model

- Generalized Linear Model (GLM)
- Generalized Additive Model (GAM)
- Random Forest (RF)
- Boosted regression tree (BRT)
- Maximum entropy (MaxEnt)

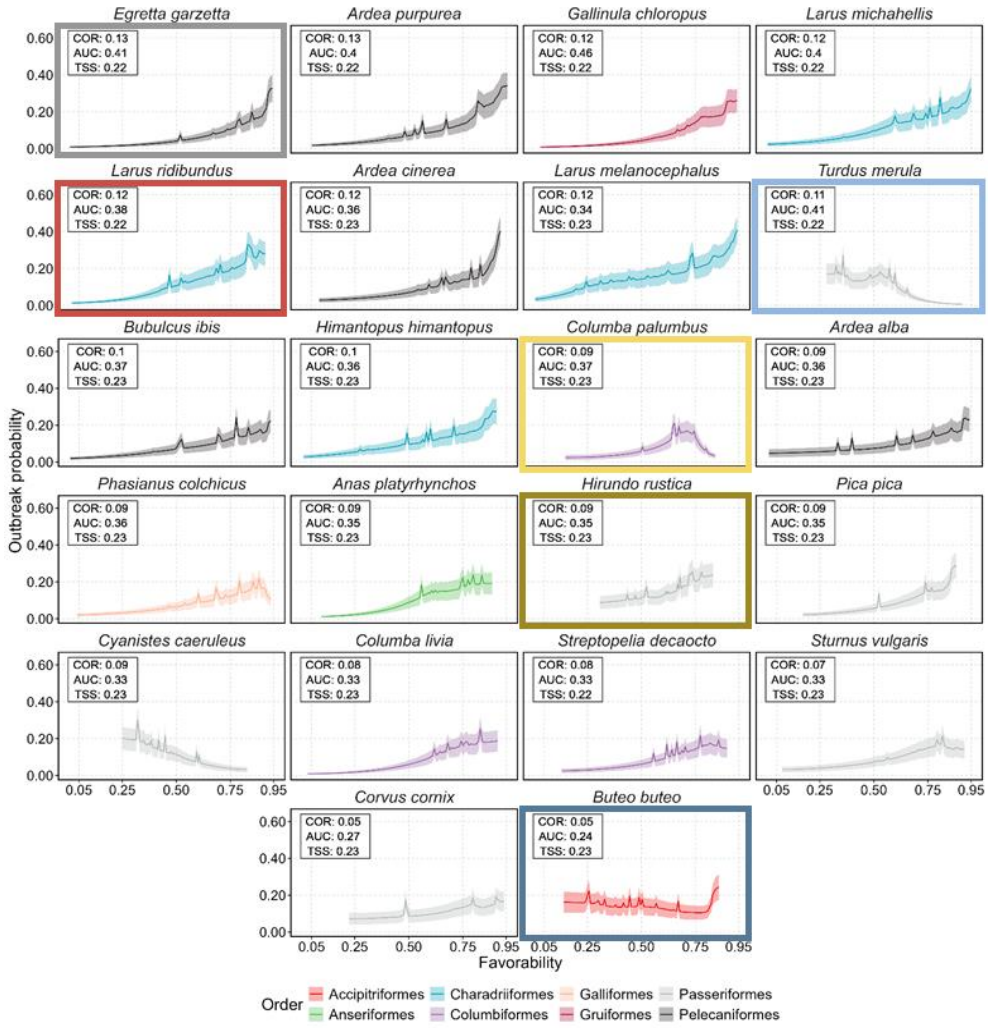


Domestic outbreaks probability prediction

- **Cluster analysis**



- 7 clusters
- Best regressors from each Cluster used as predictors

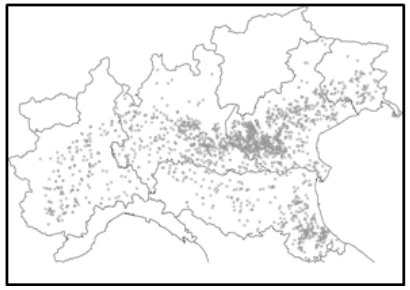


Domestic outbreaks probability prediction

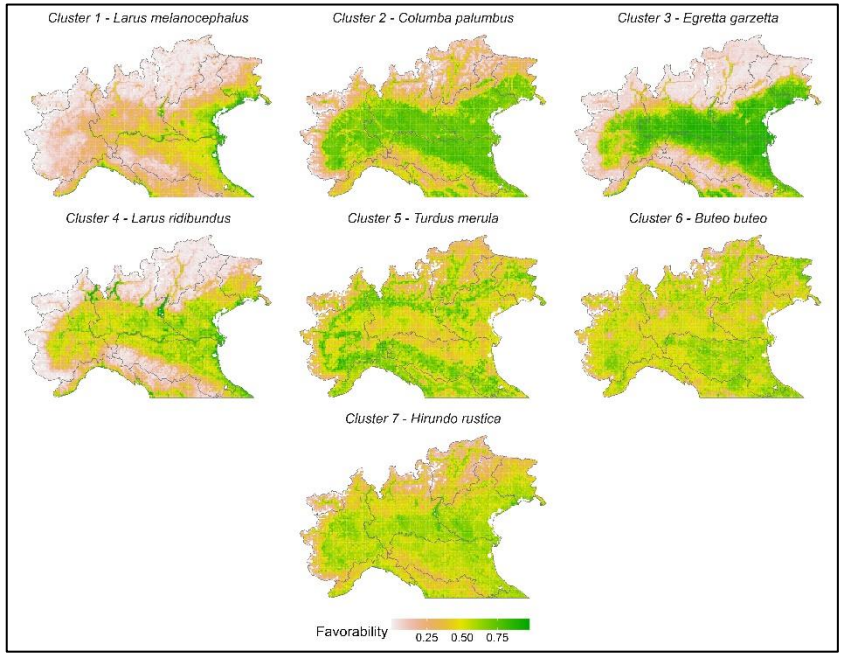
- **Multivariable ensemble model**

Occurrences (n=49)

Absences (n=2203)



Predictors (n=7, species)



5 algorithms ensemble model

- Generalized Linear Model (GLM)
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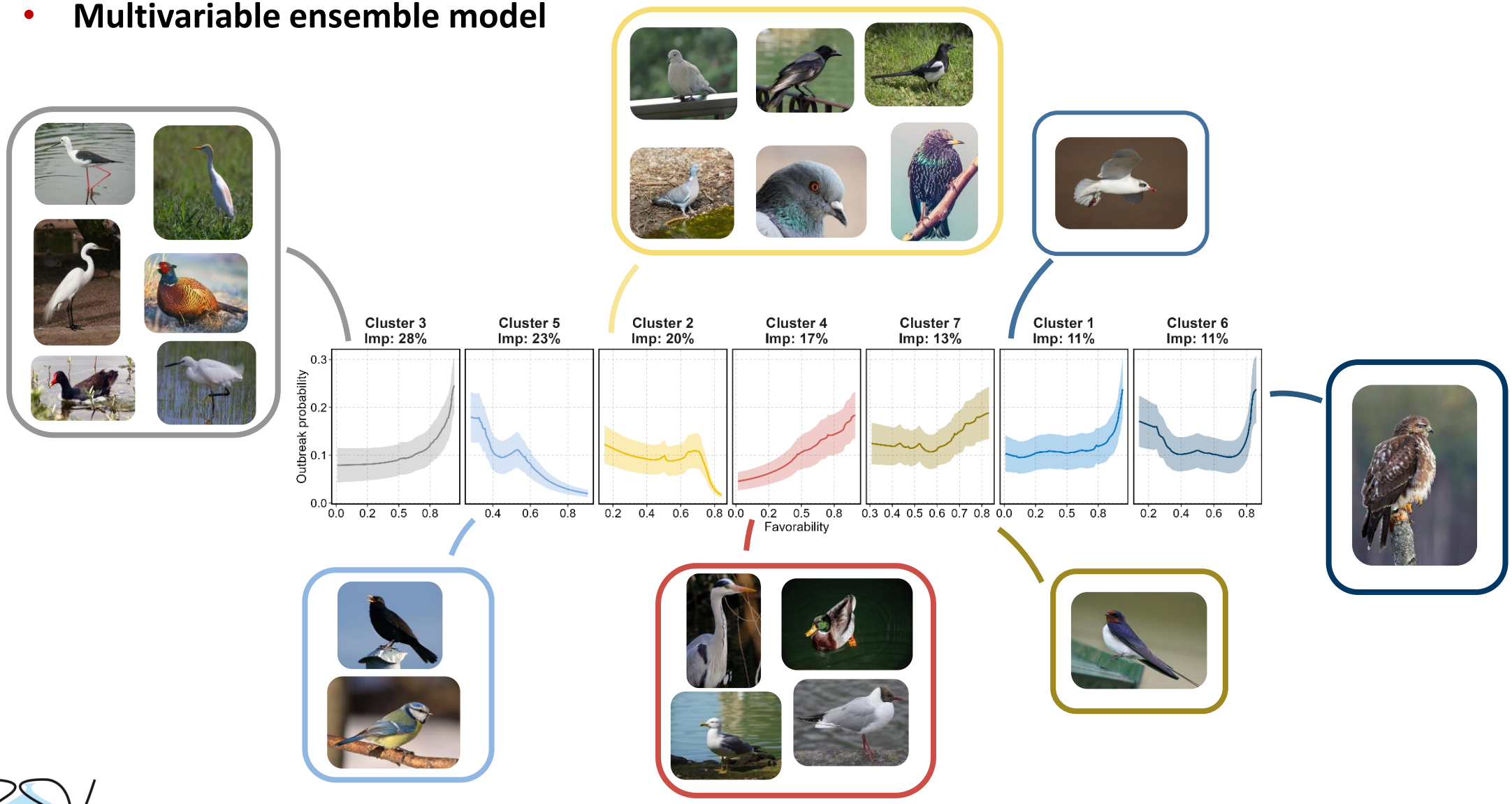
- Maximum entropy (MaxEnt)

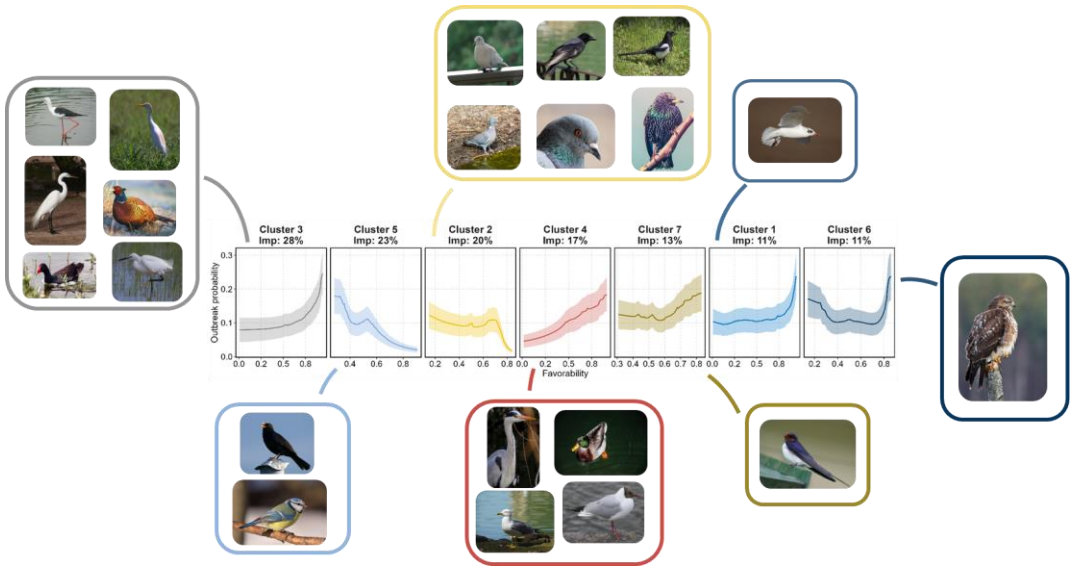
Domestic outbreaks probability prediction

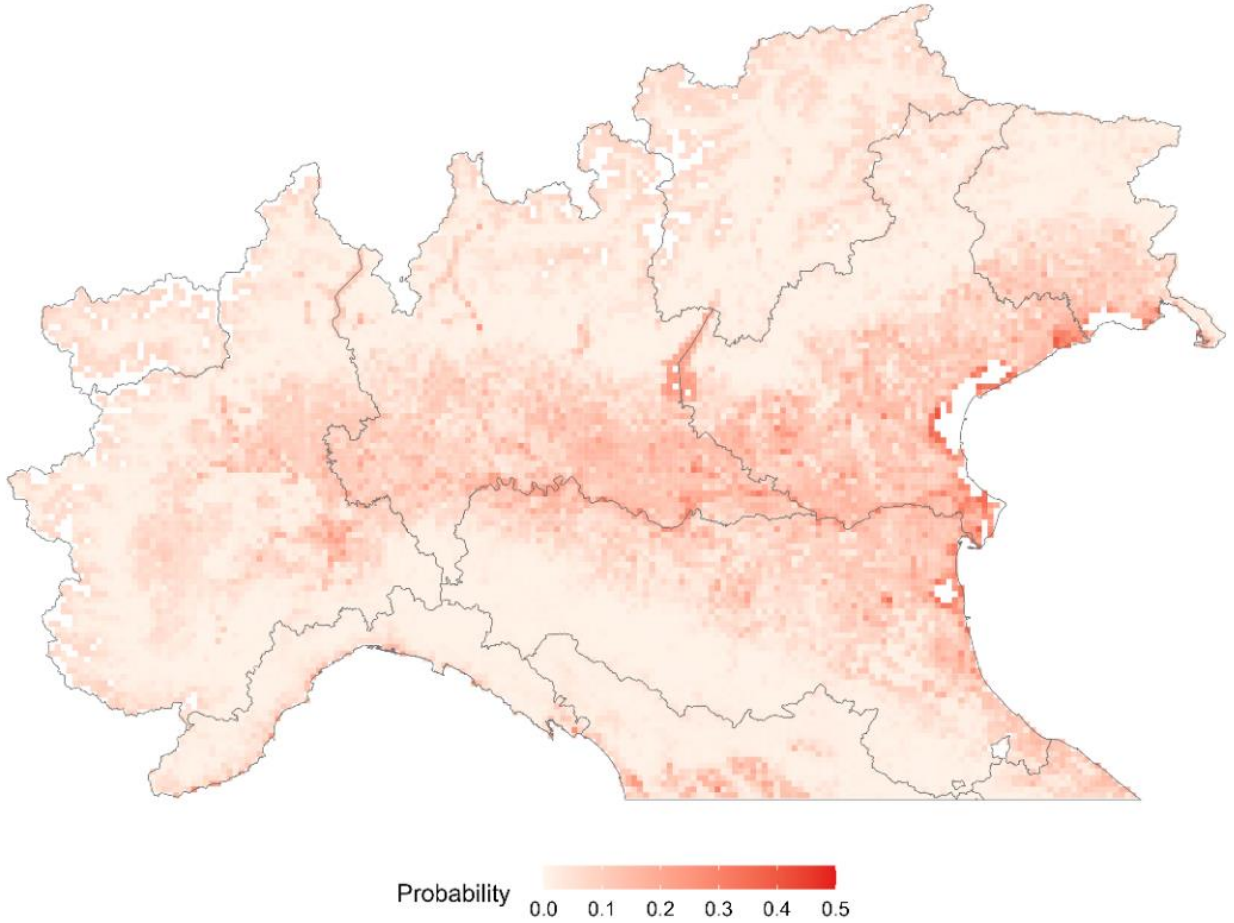
- **Multivariable ensemble model**



Domestic outbreaks probability prediction

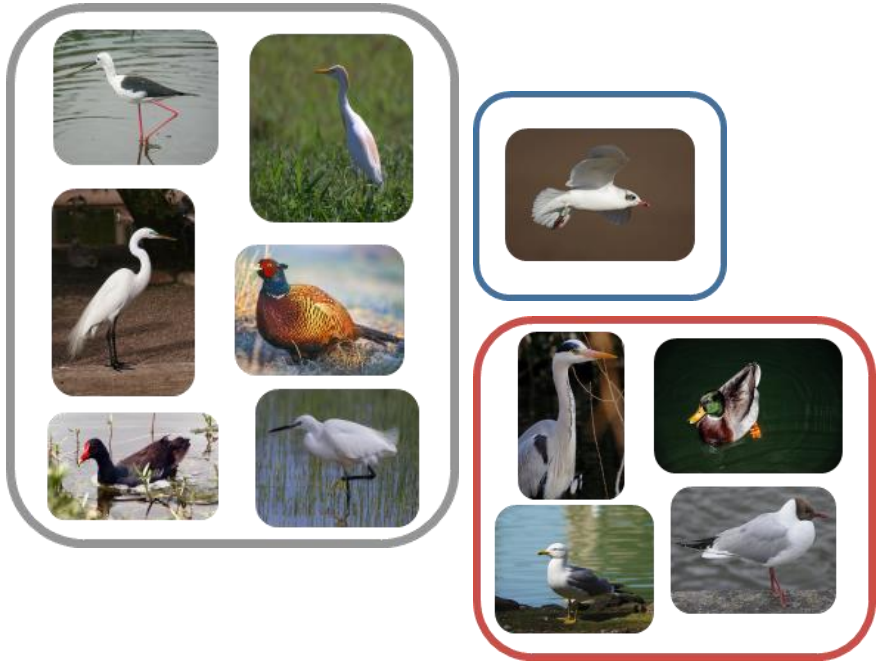
- **AI Outbreaks prediction map**





Conclusions

- Waterbirds are confirmed to have a role in the AI spillover events
  - **Manteinment hosts** were of lesser importance in explaining the phenomenon
  - **Ardeidae family** showed the highest importance and association



- Common Pheasant could have a role in the AIV transimission
- Synanthropic terrestrial birds' role cannot be excluded

Future perspectives

- Virus shedding patterns and transmission dynamics

- Dedicated data collection
- Model approaches capable to account for species interactions

- Assessment of the role of the environment in the maintenance and transmission of AIVs among wild birds

- **Acquisition of new knowledge in AI eco-epidemiology**
- **Refine surveillance approaches to facilitate AI early warning and early detection**

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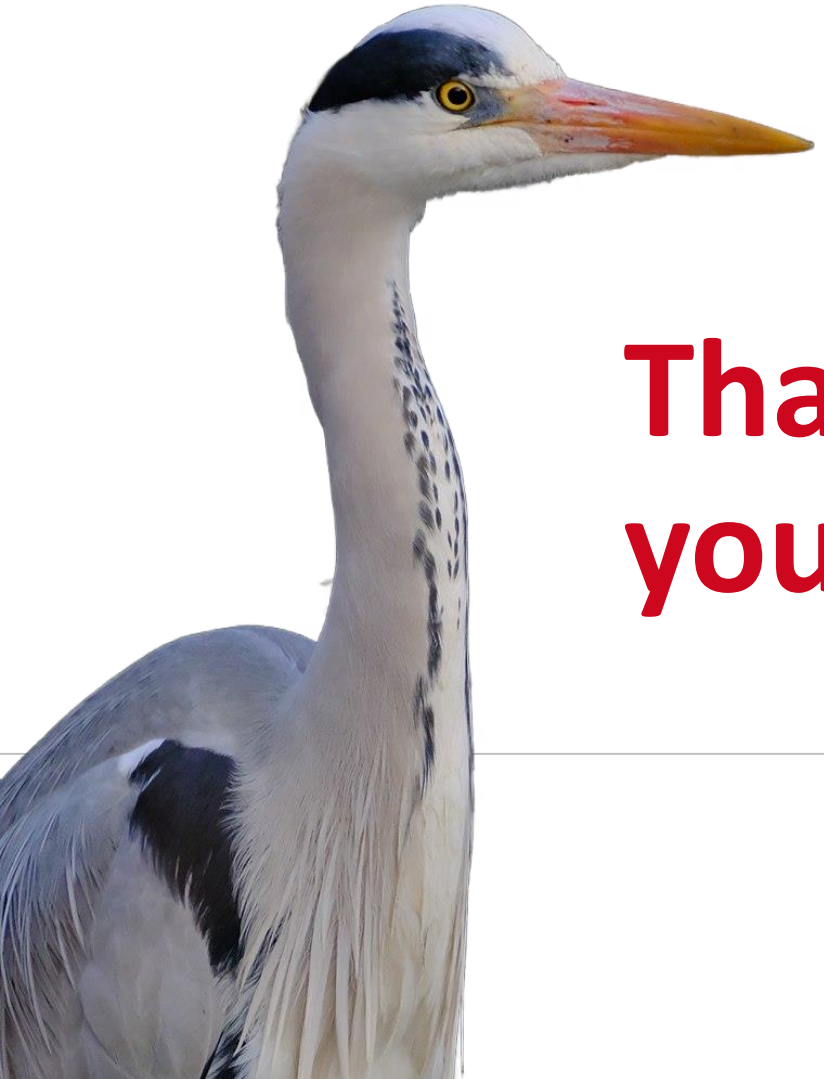

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Thank you for your attention

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