Istituto Zooprofilattico Sperimentale delle Venezie

31st Annual Meeting
of the National Reference Laboratories
for Avian Influenza and Newcastle Disease
of European Union Member States

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

L. Martelli, D. Fornasiero, J. A. Martínez-Lanfranco, A. Spada, Scarton, F. Scolamacchia, G. Manca, P. Mulatti

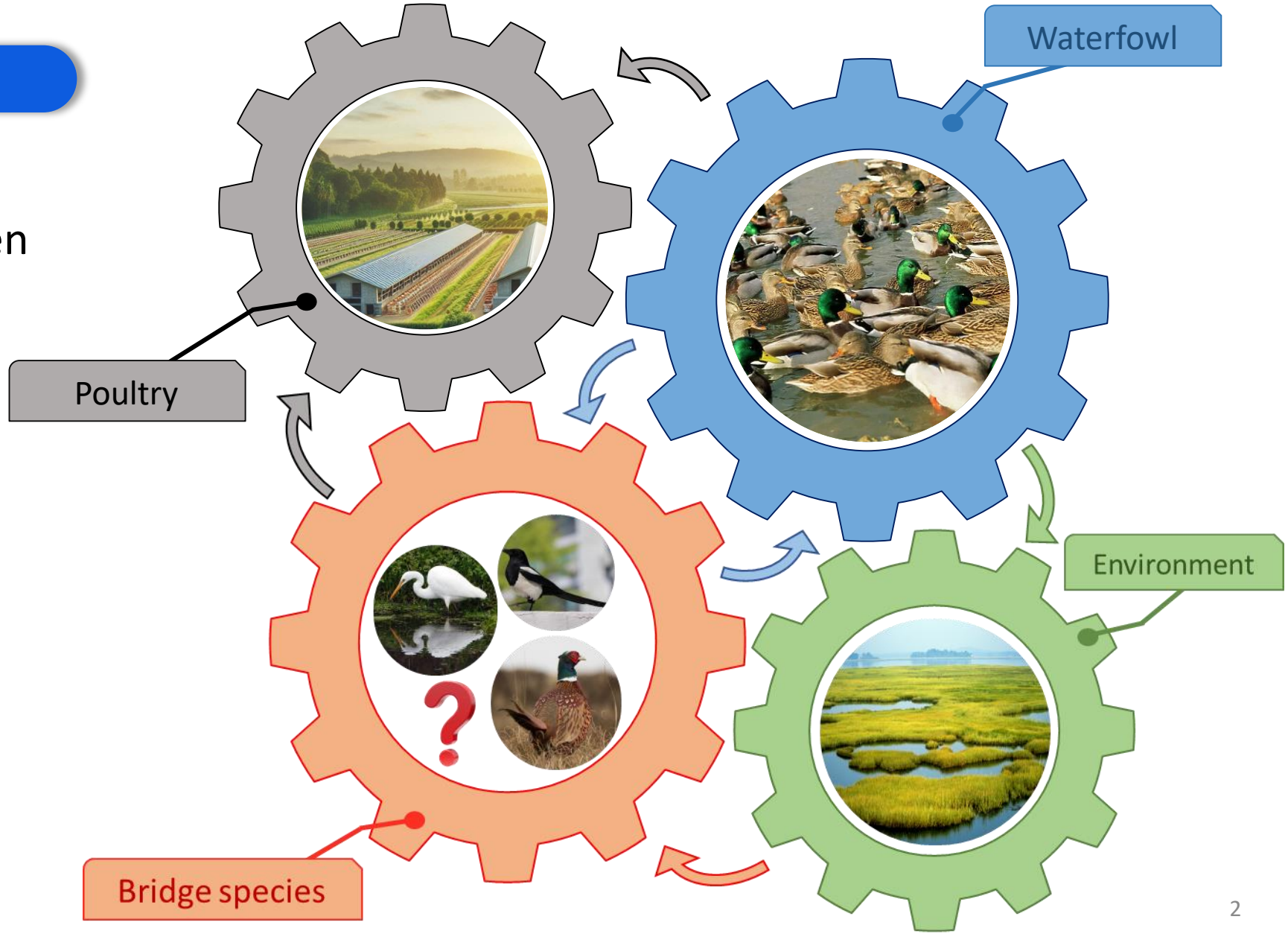
31st EURL Annual meeting
Friday, 17th October 2025

Introduction

Wild-domestic interface

- Direct interactions between waterfowl and poultry

- **More complex interface (reservoir species, bridge species and environment)**



Analysis of the Wild bird populations

Conducted in 10 farms in northeastern Italy in 2019

- Camera-trap survey

Camera traps
40 species

Wild-domestic interface

- Ornithological transects

Ecological analysis

Biodiversity levels

Article

Study of the Interface between Wild Bird Populations and Poultry and Their Potential Role in the Spread of Avian Influenza

Luca Martelli [1], Diletta Fornasiero [1,*], Francesco Scarton [2], Arianna Spada [2], Francesca Scolamacchia [1], Grazia Manca [1] and Paolo Mulatti [1,*]

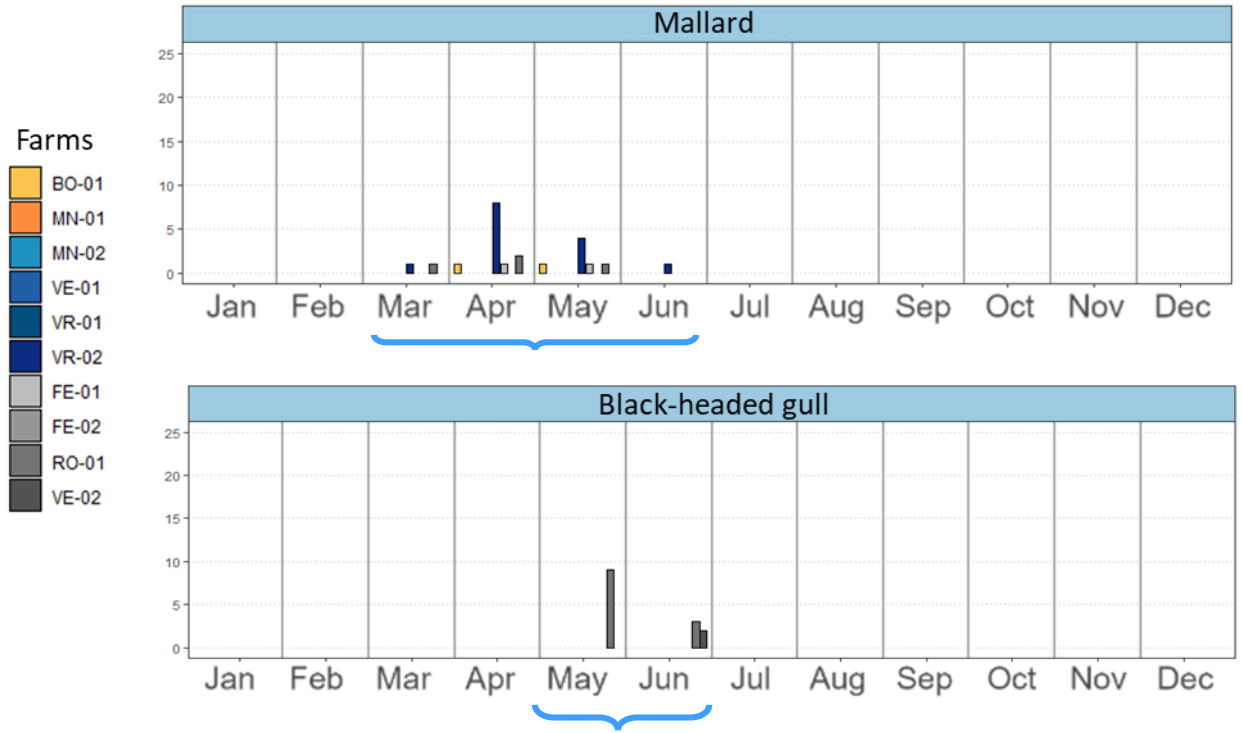
Analysis of the Wild bird populations

Conducted in 10 farms in northeastern Italy in 2019

- Camera-trap survey

Camera traps
40 species

Wild-domestic interface



Analysis of the Wild bird populations

Conducted in 10 farms in northeastern Italy in 2019

- Camera-trap survey

Camera traps
40 species

Wild-domestic interface

Analysis of the Wild bird populations

Bridge species

Susceptible to infection, capable of carrying and shedding the pathogen

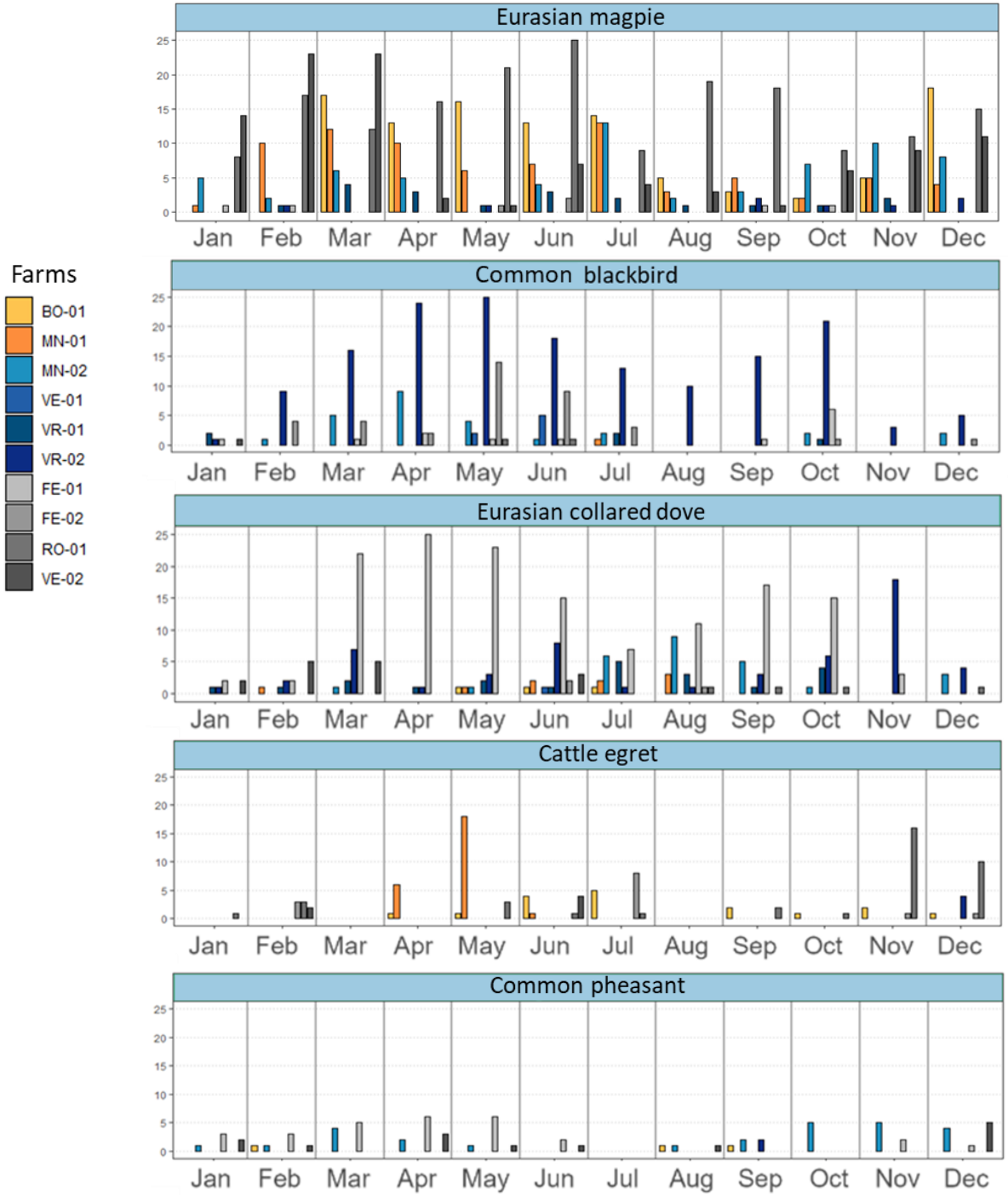
To mechanically carry the virus

Regularly frequents domestic poultry farming facilities

Shares habitat with maintenance hosts

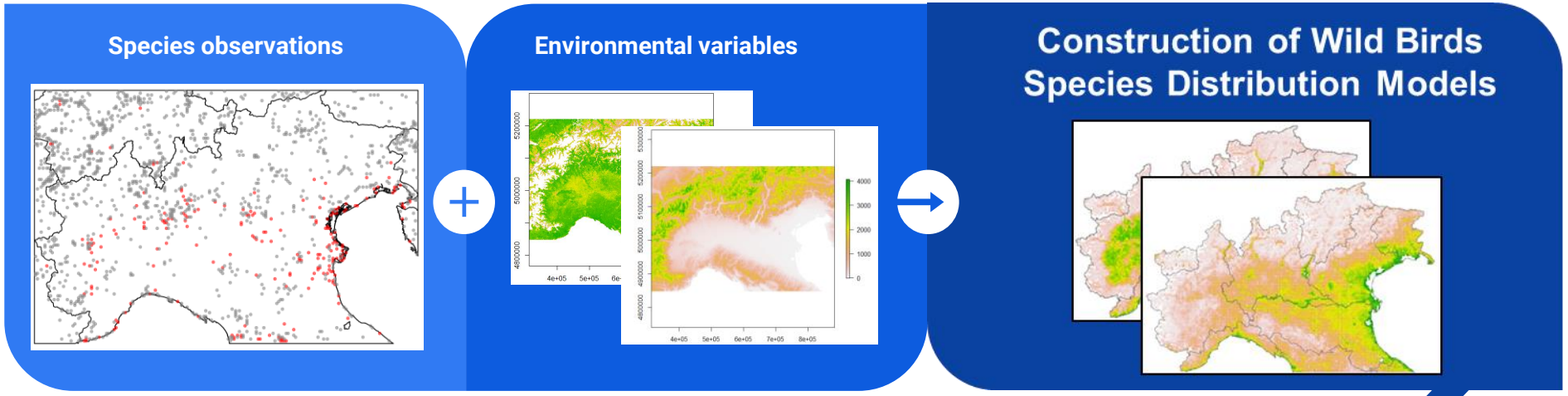
Epidemiological role

Helps compensate for the limited number of effective encounters between maintenance and target species

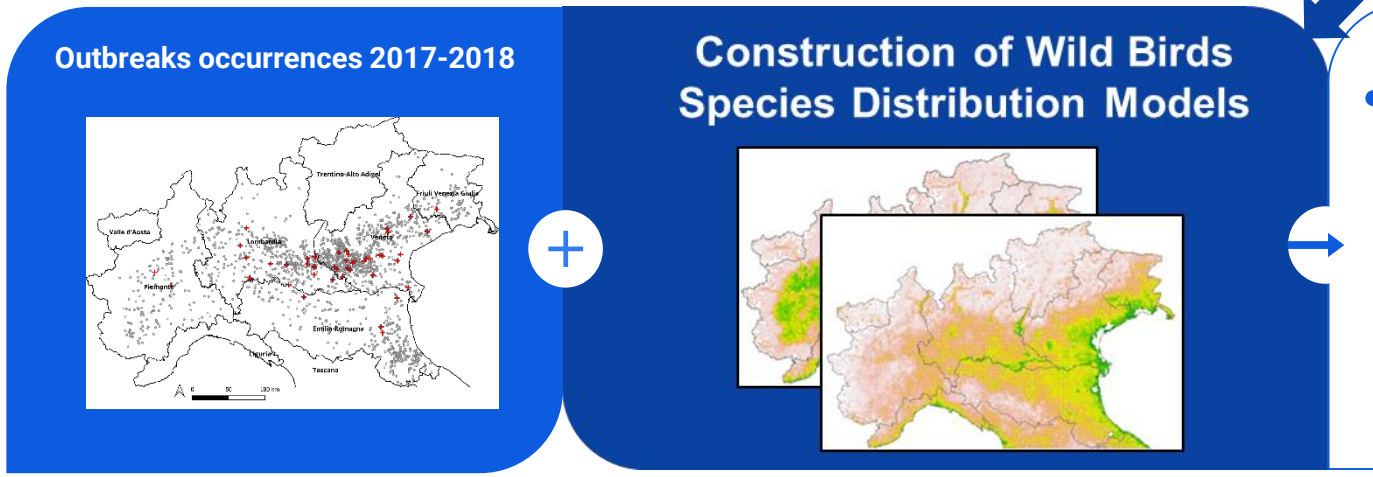


Objectives

- **Phase 1**



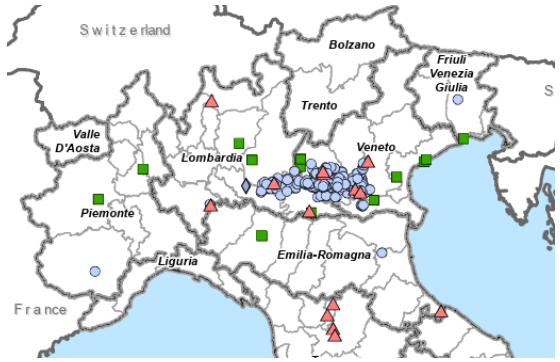
- **Phase 2**



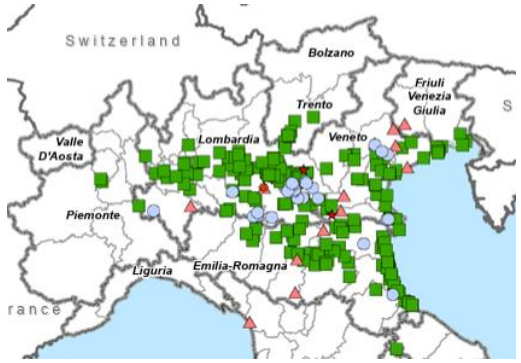
- **Wild birds distribution and new AI oubreaks emergence associations**
- **Development of a risk map**

Study area and species selection

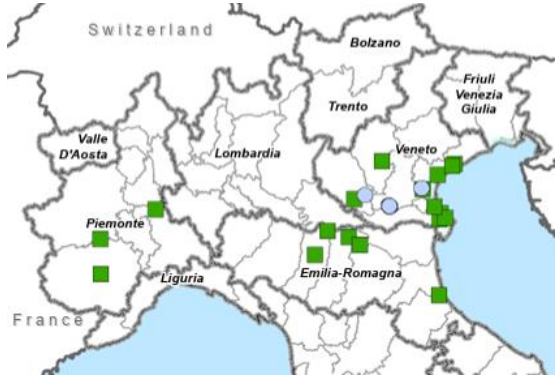
1. Study area



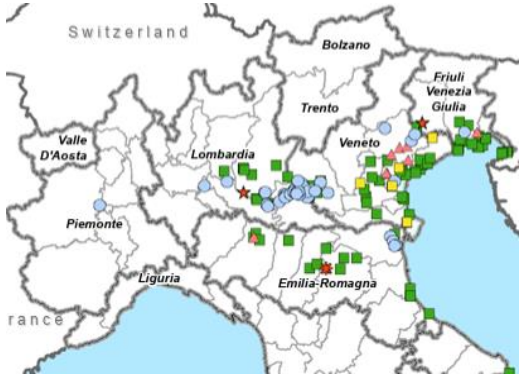
2021-2022



2022-2023



2023-2024



2024-2025

2. Species selection

- 40 species observed during the camera-trap survey
- 13 orders

Camera traps
40 species

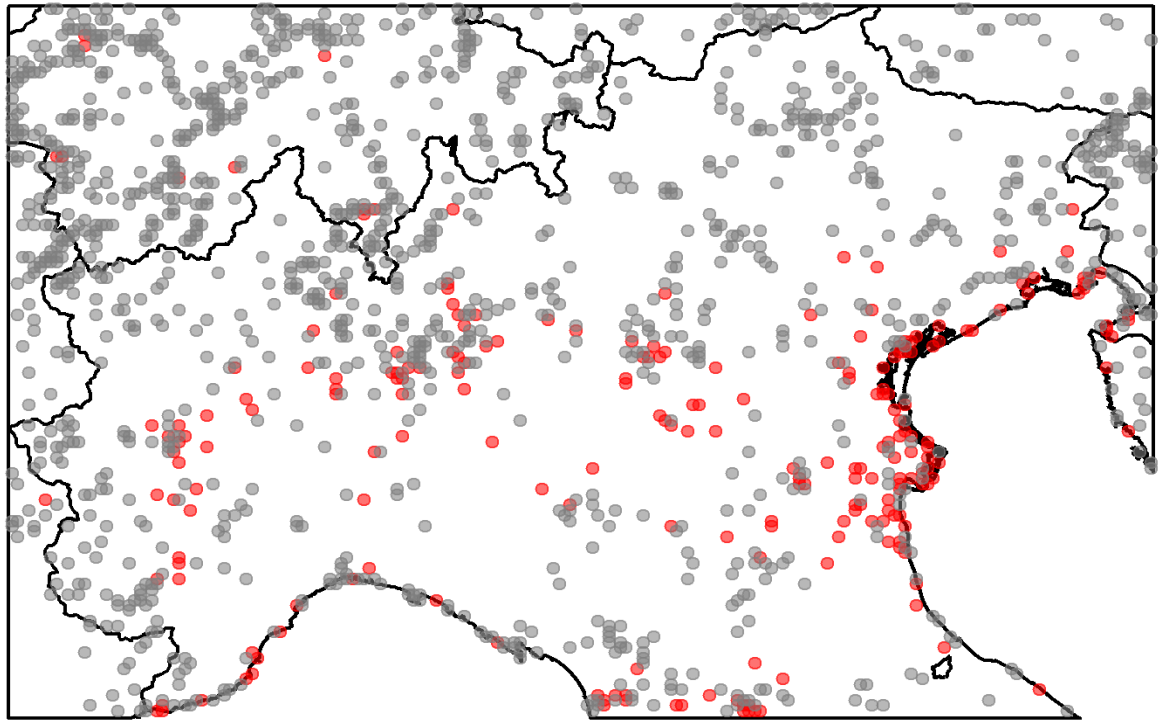
Data collection – Phase 1

Wild bird occurrences data collection

- 2019
- Complete checklists

eBird

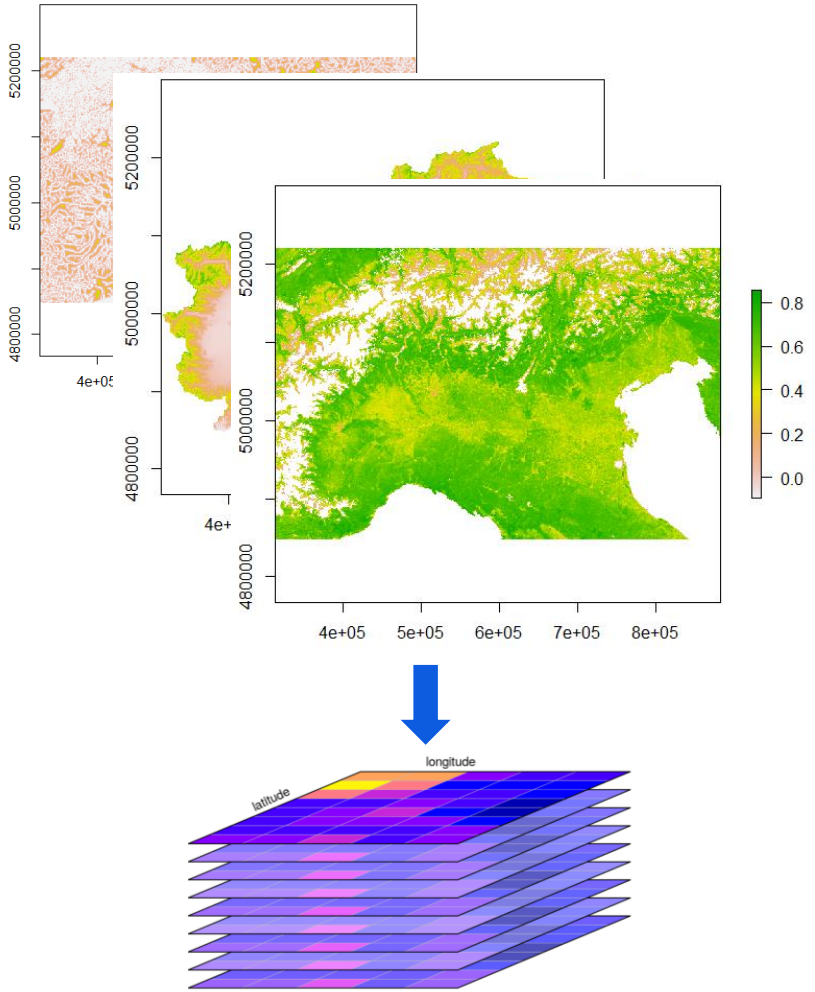
Species occurrence data



Data collection – Phase 1

Environmental variables

- Environmental Data for Veterinary Epidemiology platform (EVE)[1]
- Biovariables, land cover, elevation, distance from wetlands, vegetation index, etc.

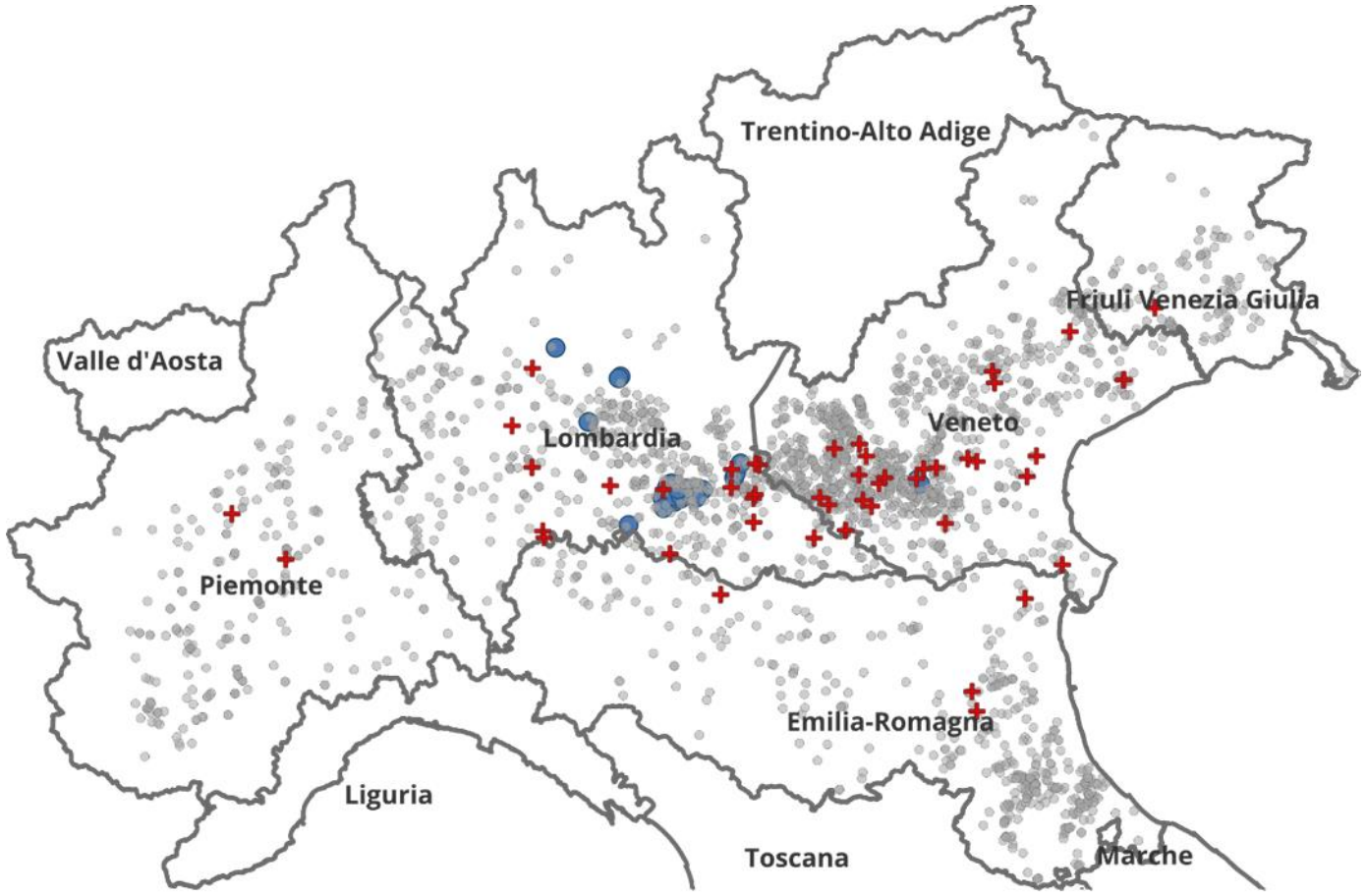


(1) M. Mazzucato et al., "An integrated system for the management of environmental data to support veterinary epidemiology," Front. Vet. Sci., vol. 10, Mar. 2023, doi: 10.3389/fvets.2023.1069979.

Data collection – Phase 2

Outbreaks data

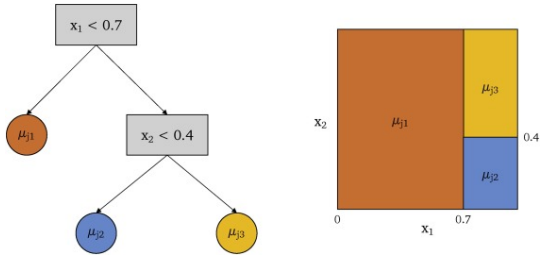
- 2017-2018 epidemic
- N= 83 AI outbreaks in poultry
- N= 49 primary outbreaks – N= 34 lateral spreads
- N= 2203 non AIV-positive farms during the HPAI H5N8 epidemic



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

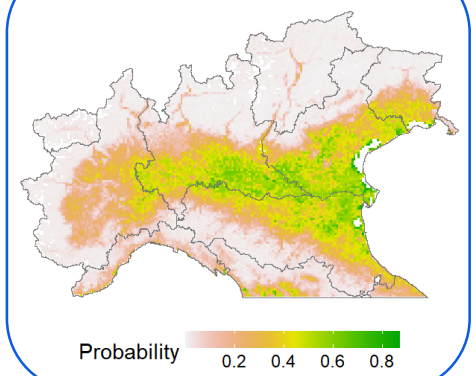
	Cutoff
○ Area Under the Receiver Operating Characteristic Curve	0.7
○ True skills Statistics	0.4
○ Miller Calibration Slope	>0.5 & <1.5

22/40 species

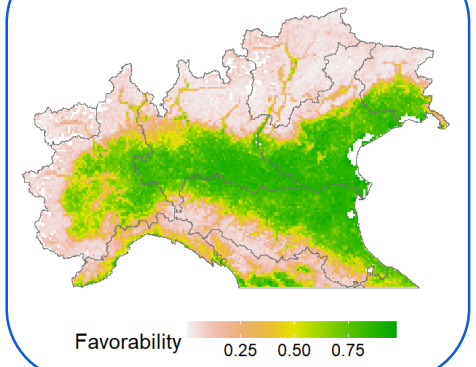
Favorability

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

Probability



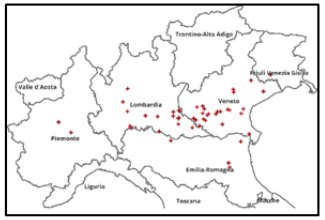
Favorability



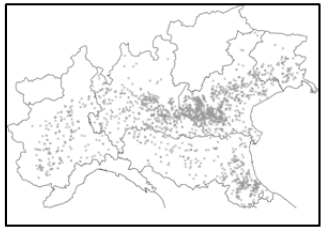
Domestic outbreaks probability prediction

Univariable ensemble models

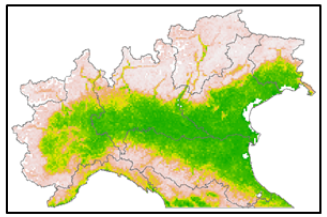
Occurrences (n=49)



Absences (n=2203)

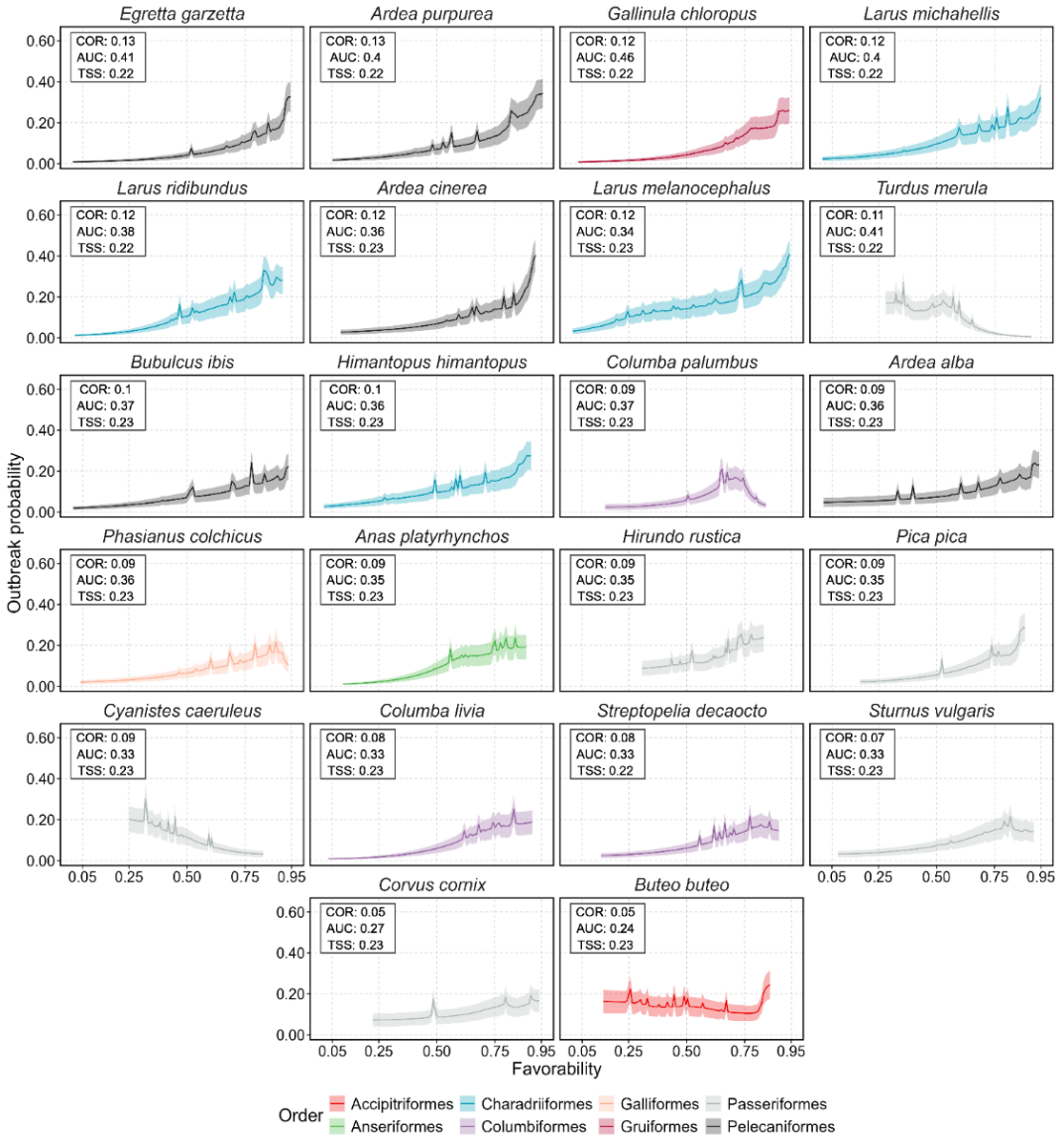


Predictors (n=1, species)



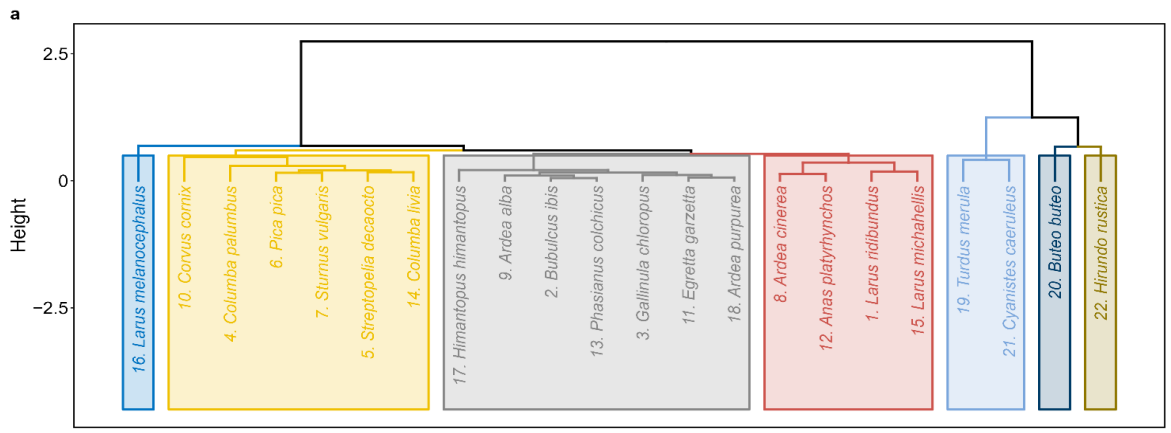
5 algorithms ensemble model

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

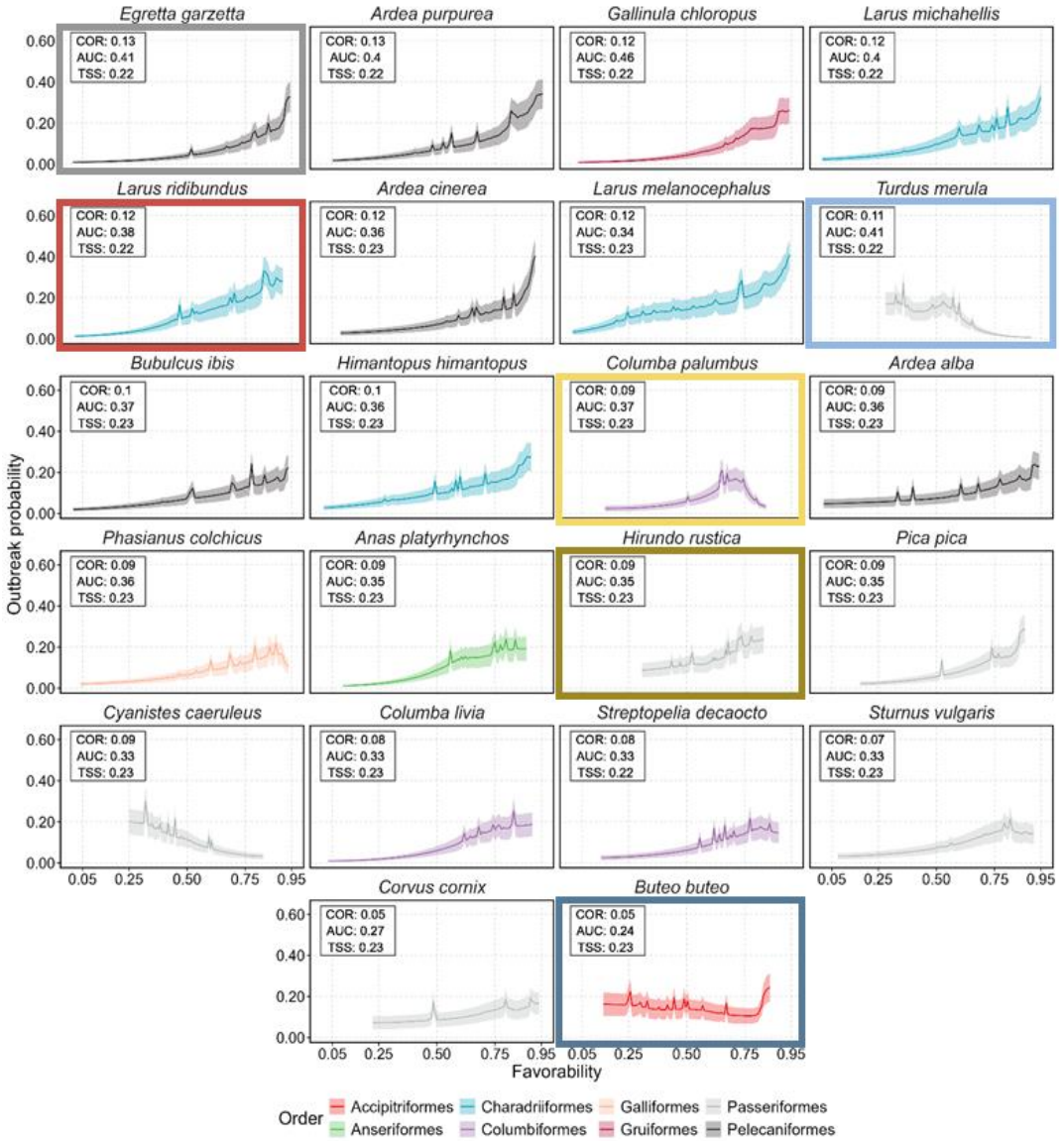


Domestic outbreaks probability prediction

Cluster analysis



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

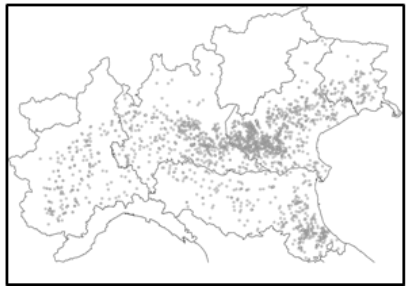


Domestic outbreaks probability prediction

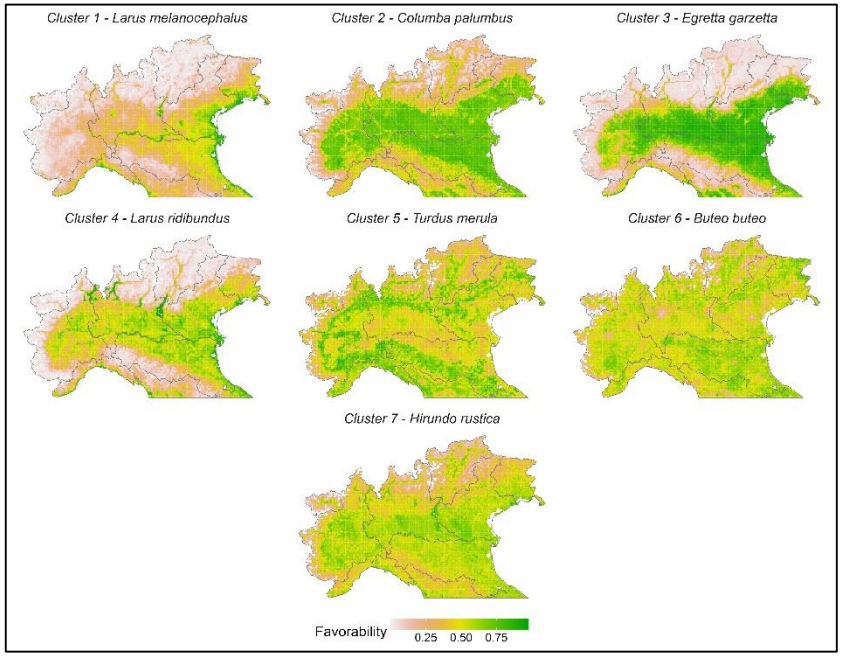
Multivariable ensemble model

Occurrences (n=49)

Absences (n=2203)



Predictors (n=7, species)

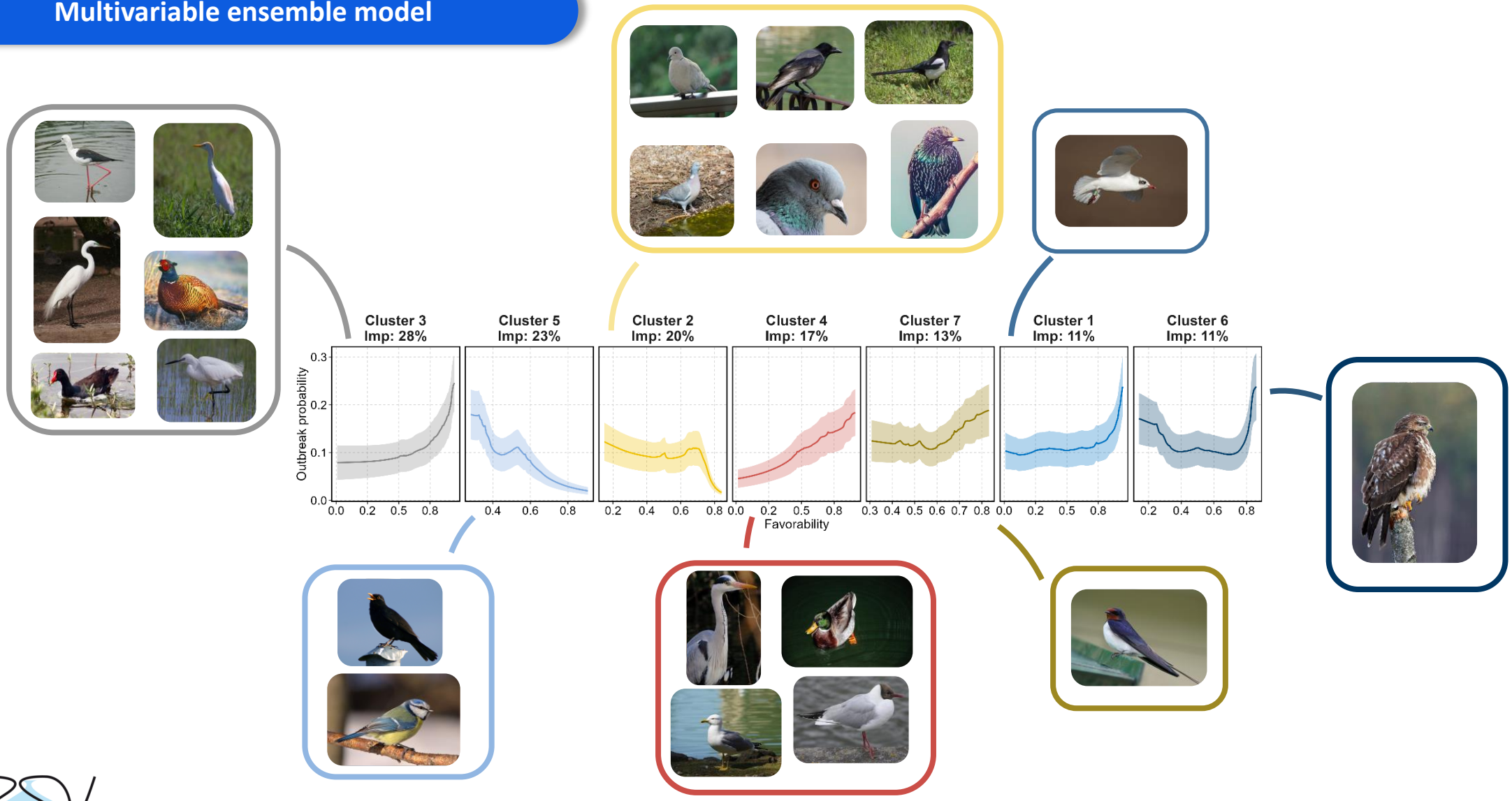


5 algorithms ensemble model

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

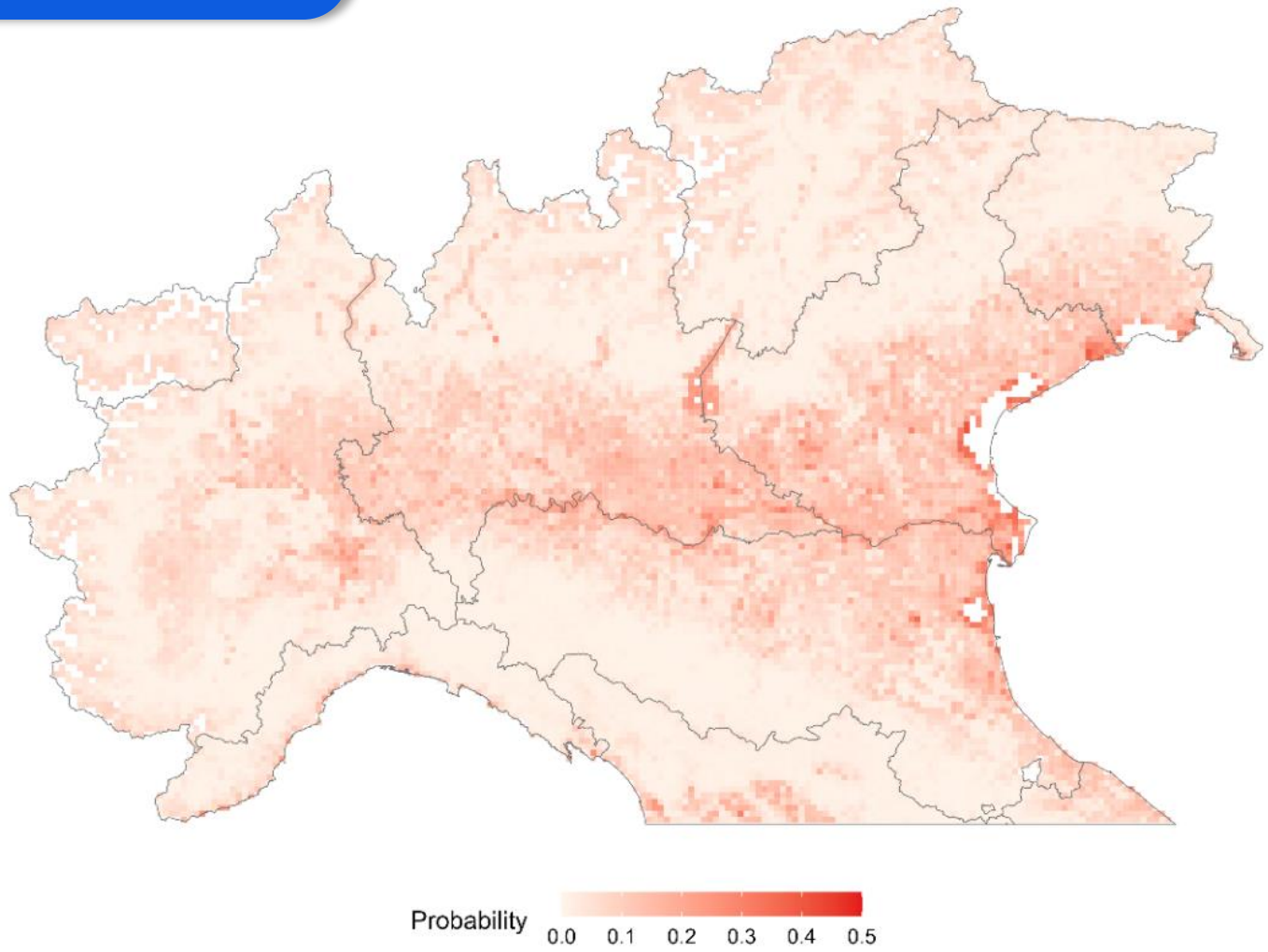
Domestic outbreaks probability prediction

Multivariable ensemble model



Domestic outbreaks probability prediction

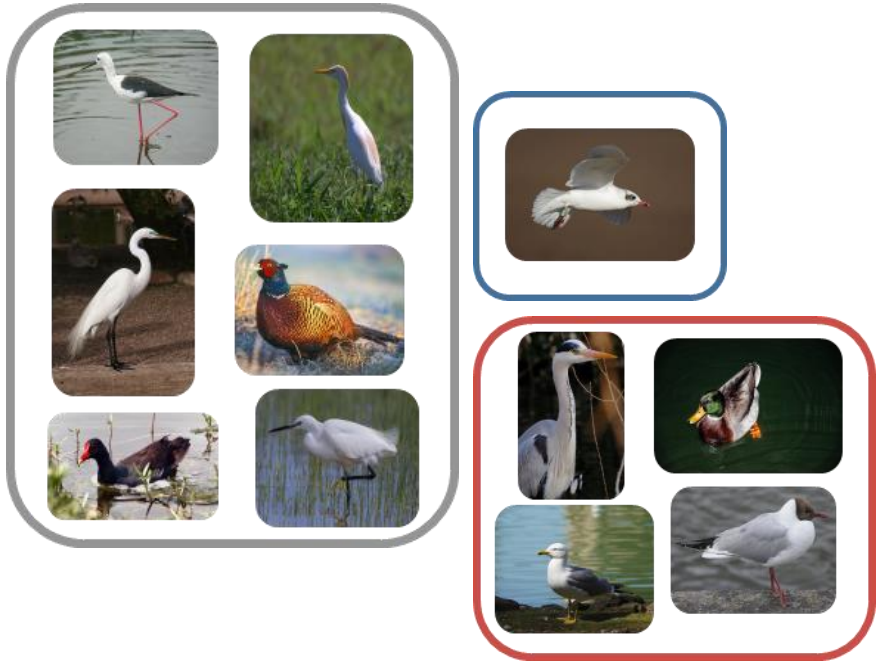
Multivariable ensemble model



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

Metodologies

- Virus shedding patterns and transmission dynamics

- 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

- Expantion of the study to backyard poultry

Update to the current situation

- Modification of the circulating viruses

- Wild birds ecology, distribution and abundances changes

Future perspectives

An example: Sacred ibis

- From sporadic to abundantly distributed in the study area
- Constantly growing population
- 2 confirmed cases in 2025 in Italy

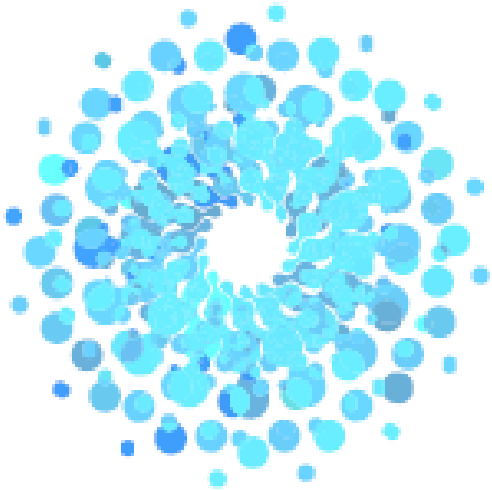
Epidemiology

Ecology

Broiler farm outbreak in the Province of Verona, 2024-2025 wave

Istituto Zooprofilattico Sperimentale delle Venezie

31st Annual Meeting
of the National Reference Laboratories
for Avian Influenza and Newcastle Disease
of European Union Member States



Thank you for your attention

Luca Martelli
lmartelli@izsvenezie.it