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A Spatial Multi Criteria Decision Analysis (SMCDA) to map the risk of avian influenza in Lazio and Toscana (central Italy)

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Abstract

Avian influenza (AI) is a global concern, affecting wild and domestic bird populations worldwide. Environmental conditions facilitating the presence of wild birds and a consistent domestic bird population contribute to the introduction and spread of AI within a territory. This study focuses on the identification of major risk areas for AI in the Lazio and Toscana Regions of central Italy using Spatial Multi-Criteria Decision Analysis (SMCDA). Through the integration of eleven risk factors regarding domestic bird farms and facilities, wild birds density, water bodies, and roads network, a suitability map for AI introduction and spread was generated. The findings reveal that approximately 30% of Lazio and 20% of Toscana are at high risk for AI introduction and spread. Notably, the implementation of rigorous biosecurity measures in intensive poultry industries has significantly prevented the occurrence of AI outbreaks, even in areas considered at risk. The study emphasizes the importance of informed decision-making in AI risk management, highlighting the potential applications of the SMCDA in prioritizing surveillance efforts and planning control programs. Furthermore, it underscores the need for continuous data updating and comprehensive preventive strategies to address the complex dynamics of AI transmission and safeguard both poultry and human health.

Keywords

Avian influenza, Surveillance, GIS, Risk factors, Spatial Multi Criteria Decision Analysis

Introduction

Avian influenza (AI), caused by infection with avian influenza Type A viruses, has a global distribution and includes both low and high pathogenic strains. Low pathogenic avian influenza (LPAI) causes reduced mortality rate and mild disease in birds. Some LPAI viruses can mutate into highly pathogenic avian influenza viruses (HPAI), which poses severe disease and high mortality risks to domestic bird populations (CDC, 2024). Various bird species, particularly water birds such as Anseriformes and Charadriiformes serve as AI reservoirs and spread the infection during migratory patterns in domestic bird population (WOAH, 2024). Multiple factors contribute to the introduction and spread of HPAI within a territory. The primary source of infection originates from migratory wild birds. As a result, the principal risk factors are closely related to environmental conditions that facilitate the presence of wild birds, including water bodies and migratory routes. The target species mainly consist of migratory waterfowl, including ducks, geese, swans, herons, storks, roosters, coots, grebes, and cormorants. Other species, such as various raptors (hawks, eagles, etc.), are of non-negligible importance due to their role as predators or scavengers, which may expose them to infected bird tissues. Another group of birds that may play a role in the spread of the virus are those acting as "bridge hosts". These species, including crows, sparrows, and pigeons exhibit a high tolerance for habitats modified by human

activity, which increases the likelihood of contacts with domestic birds and especially free-range poultry (Whitworth et al., 2007). Among waterfowl, the presence of the mallard is relevant. Mallards are partially sedentary and nesting species, often semi-wild, and display high ecological adaptability. They inhabit various environments such as coastal lagoons, marshes, large and small lake basins, rivers, and canals, making their presence a significant factor in the context of avian influenza transmission.

Proximity to rivers, lakes, ponds, and wetlands represents a risk factor due to the frequent presence of migratory wild water birds, primary carriers of AI. Water sources can also be contaminated by AI viruses, where it can survive for a long period (Ahmad et al., 2022). A systematic review identified the main risk factors for AI infection in poultry farms, which include environmental conditions (such as open water bodies, infections on nearby farms) and biosecurity measures at farm level (such as disinfection protocols and the presence of other species) (Wang et al., 2014). Additionally, infections in poultry can lead to the spillback of the virus to wild birds (CDC, 2024), with increasing spread of viral circulation. Emerging evidence suggests an increasing trend of AI infections in mammalian species. Recent outbreaks in Europe and America have affected a range of terrestrial and marine mammals, including farmed mink in Spain (Agüero et al., 2023), seals in the United States (Puryear et al., 2023), sea lions in Chile (Ulloa et al., 2023), and marine mammals and seabirds (dolphins, sea lions, sanderlings, pelicans and cormorants) in Peru (Leguia et al., 2023). Furthermore, detections of H5N1 in domestic animals such as cats in Poland (Domańska-Blicharz et al., 2023) and dogs in Italy (Moreno et al., 2023) underscore the potential risks of cross-species transmission. In the 2024, USA Food and Drug Administration and USA Centers for Disease Control and Prevention published the alert on spread of AI among dairy cattle in USA and the survival of virus in milk has been proved (Garg et al., 2024). These outbreaks raise concerns about the adaptability of the virus to infect humans and its potential ability to develop a pandemic.

In Italy, all poultry farms with a commercial scope or hosting more than 50 heads are identified and registered in the National Animal Registry (Banca Dati Nazionale, BDN). Backyard farms are defined as farms with fewer than 50 birds and no commercial purpose, and identification and registration in BDN of these farms are optional. In Lazio and Toscana Regions (central Italy), the farm and animal population are substantial, with over 1000 commercial farms hosting approximately 5,000,000 of heads and around 2000 backyard farms. Farms are not homogeneously distributed, with the Viterbo (VT) province standing out as a densely populated poultry area (DPPA). Many of these farms belong to same owner/company and are strictly connected (agistment) with large companies in northern Italy. The VT province is also identified as at risk for avian influenza by the Italian Ministry of Health in the National Avian Influenza Surveillance Plan (2024). Due to limited space for new farms in VT, the poultry industry is beginning to establish new farms in the nearby provinces. Backyard farms are scattered throughout the regions, without clustering in specific provinces.

In Italy, a total of 96 LPAI and 752 HPAI outbreaks have been reported since 2011. In northern Italy, multiple outbreaks are notified every year, with significant variation among years, while sporadic outbreaks occur in other areas of the country. The Geographic Information System (GIS) has become an increasingly important tool in recent decades for studying animal disease dynamics (Pfeiffer et al, 2008; Rinaldi et al, 2006). As GIS technology advanced, there has been a growing emphasis on modelling approaches for tracking animal movements, environmental assessment, and resource allocation. While these consistent opportunities rely on the availability of disease data, other techniques deal with risk assessment in situations of poor data or disease-free areas. Multi-Criteria Decision Analysis (MCDA) offers a comprehensive approach to bridging knowledge gaps in disease risk mapping, effectively integrating diverse sources of information on the disease and its epidemiology.

The aim of this study was to create suitability maps (vulnerability maps) for AI in Lazio and Toscana Regions. A Spatial Multi-Criteria Decision Analysis (SMCDA), a method designed to aid decision-making by assessing multiple criteria (i.e. risk factors) was used, integrating and analysing various layers of data and value judgments to generate actionable insights (decision map) (Malczewski, 2006; Papadopolou & Hatzichristos, 2019). This study contributes to enhancing preparedness for the impact of AI on both animal and human health. By mapping AI risk at local level, we aim to inform the application of effective AI prevention and control strategies, safeguarding health and economics of the poultry sector and supporting the Competent Authorities (CAs) in the process of the possible authorization of new poultry premises.

Material and methods

Identified risk factors for AI introduction/spread were imported as layers into a GIS project. Experts elicitations were performed to weigh each risk factor, and weights were determined through pairwise comparisons using the Analytical Hierarchy Process (AHP), by QGIS 2.8.8 plugin "Easy AHP". Additionally, each raster map was normalized using a specified fuzzification algorithm, implemented through tools such as "Fuzzy membership" in ArcGIS Pro® 3.3 and

Idrisi Taiga®. Finally, the integration of these normalized raster maps into the final suitability map was achieved through a linear weighted combination (LWC) method in ArcGIS Pro®3.3. The steps of the methodological flow adopted in the study are summarized in Figure 1.

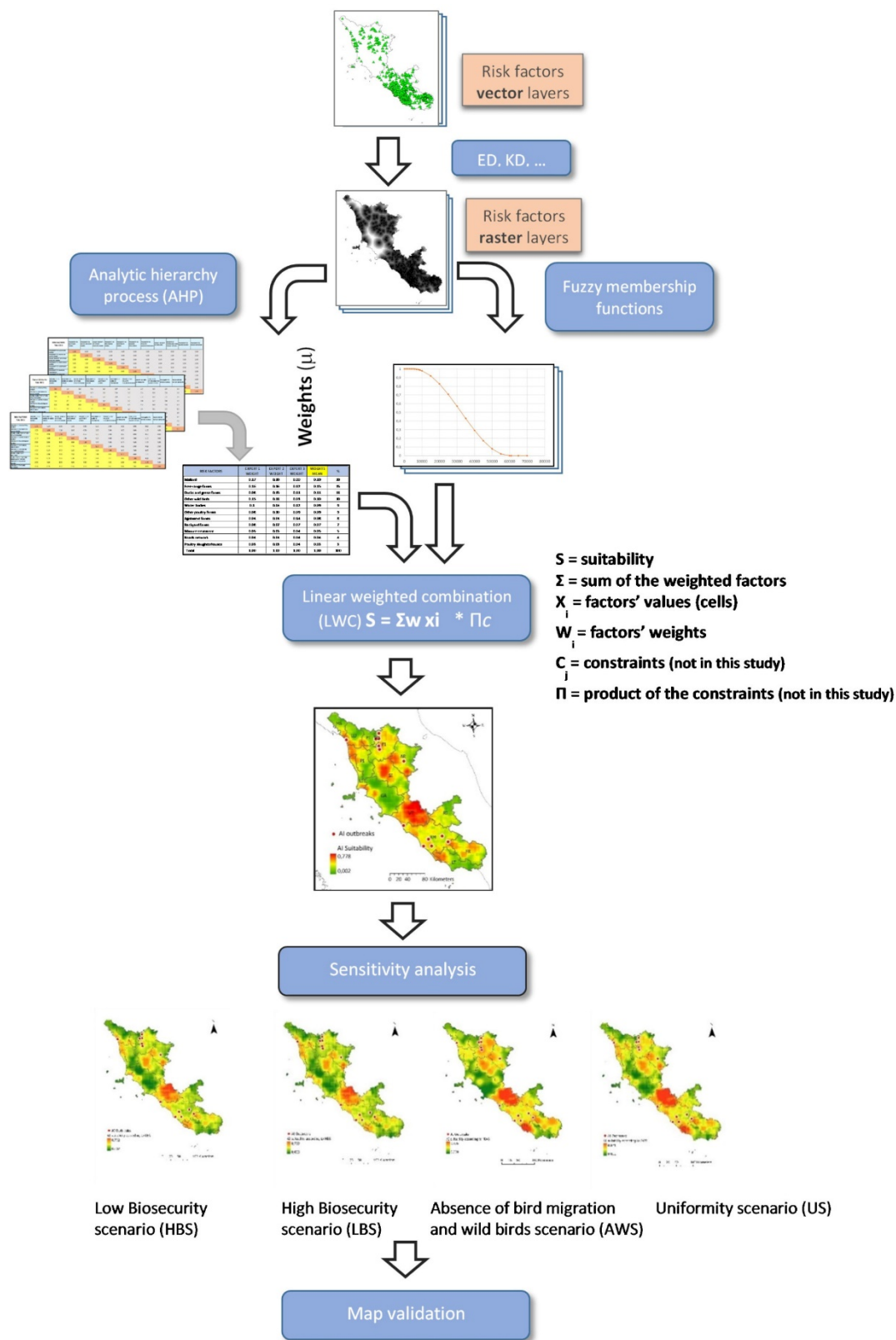


Figure 1. AI SMCD methodological flow.

Risk factors and data source

Risk factors associated with the introduction and spread of AI viruses in central Italy were identified through a comprehensive review of available information sources, including expert opinion (EO), literature searches, and analysis of historical data. A list of 11 risk factors was categorized into 4 groups:

- Domestic bird farms
- Wild birds
- Water bodies
- Road network and poultry farms facilities

Many of these factors primarily express proximity to potential primary sources of infection for domestic birds, both through direct and indirect exposure to wild birds. Additionally, anthropogenic factors like trade movements or lack of biosecurity measures, contribute to the spread of avian influenza between domestic bird farms.

Domestic bird farms

In this category, the species and the management were considered, as follows:

- backyard: farms with < 50 heads and no commercial purpose (N=2111)
- ducks or geese: farms hosting at least one animal of these species (N=12)
- free-range: farms hosting any bird species with partial or total access outdoors (N=266)
- agistment: farms belonging to avian sector companies of northern Italy, adhering to a management system where feed, veterinary care, animals supply and other necessities come from the company that manages other farms, then considered epidemiologically linked (N=185)
- other farms: farms housing domestic birds not covered in the other categories (N=1258).

Data were obtained by the BDN (October 2019). These categories were represented as point maps. Preprocessing was conducted to ensure the accuracy of spatial data (geographical coordinates). In case of missing coordinates, geocoding or determination of the municipality centroid were used.

Wild birds

AI-susceptible wild bird species (Table I) were considered, in 2 layers: Mallard (*Anas platyrhynchos*) and other wild bird species (Table I).

Data source:

- Mallard (*Anas platyrhynchos*). A vector map of mallard densities, provided by ISPRA (Istituto Superiore per la Protezione e la Ricerca Ambientale) data.
- Other wild bird species (N=34). The layer derived from the integration of 2 sources:

- presence data: 998 observations made between January 2011 and December 2019 (inaturalist.org, 2024). Citizen science platform for sharing biodiversity data;
- Directive 2009/147/EC on the conservation of wild birds.

Common name	Scientific name	Order	inaturalist	Directive 2009/147/EC	'Target species' (TS) 2010/367/UE
Goshawk	<i>Accipiter gentilis</i>	Accipitriformes	X	X	X
Sparrowhawk	<i>Accipiter nisus</i>	Accipitriformes	X	X	X
Buzzard	<i>Buteo buteo</i>	Accipitriformes	X	X	X
Marsh Harrier	<i>Circus aeruginosus</i>	Accipitriformes	X	X	X
Black Kite	<i>Milvus migrans</i>	Accipitriformes	X	X	X
Red Kite	<i>Milvus milvus</i>	Accipitriformes	X	X	X
Pintail	<i>Anas acuta</i>	Anseriformes	X		X
Shoveler	<i>Spatula clypeata</i>	Anseriformes		X	X
Teal	<i>Anas crecca</i>	Anseriformes	X	X	X
Wigeon	<i>Mareca penelope</i>	Anseriformes	X		X
Mallard	<i>Anas platyrhynchos</i>	Anseriformes	X	X	X
Garganey	<i>Spatula querquedula</i>	Anseriformes	X	X	X
Gadwall	<i>Mareca strepera</i>	Anseriformes	X	X	X
Greylag Goose	<i>Anser anser</i>	Anseriformes	X		X
Pink-footed Goose	<i>Anser brachyrhynchus</i>	Anseriformes	X		X
Common pochard	<i>Aythya ferina</i>	Anseriformes	X		X
Tufted pochard	<i>Aythya fuligula</i>	Anseriformes	X	X	X
Canada Goose	<i>Branta canadensis</i>	Anseriformes	X		X
Muscovy Duck	<i>Cairina moschata</i>	Anseriformes	X		X
Swan	<i>Cygnus olor</i>	Anseriformes	X	X	X
Turkish Fiston	<i>Netta rufina</i>	Anseriformes	X	X	X
Common Gull	<i>Chroicocephalus ridibundus</i>	Charadriiformes		X	X
Black-headed godwit	<i>Limosa limosa</i>	Charadriiformes	X		X
Golden Plover	<i>Pluvialis apricaria</i>	Charadriiformes	X		X
White stork	<i>Ciconia ciconia</i>	Ciconiiformes	X	X	X
Peregrine Falcon	<i>Falco peregrinus</i>	Falconiforms	X	X	X
Kestrel	<i>Falco tinnunculus</i>	Falconiforms	X	X	X
Coot	<i>Fulica atra</i>	Gruiforms	X	X	X
Magpie	<i>Pica pica</i>	Passeriformes	X	X	X
Grey Heron	<i>Ardea cinerea</i>	Pelecaniformes	X	X	X
Great Crested Grebe	<i>Podiceps cristatus</i>	Podicipediformes	X	X	X
Little Grebe	<i>Podiceps nigricollis</i>	Podicipediformes	X		X
Little Grebe	<i>Tachybaptus ruficollis</i>	Podicipediformes	X	X	X
Eagle Owl	<i>Bubo bubo</i>	Strigiformes		X	X
Cormorant	<i>Phalacrocorax carbo</i>	Suliformes	X	X	X

Table 1. Wild bird species considered.

Data for wild birds other than mallard from the Directive 2009/147/EC (annexed vectorial map of 10X10 km) were upscaled to 3X3 km. The integration vector layer was obtained using the vector layers from the Directive 2009/147/EC or alternatively from the inaturalist.org presence reports (observations) layer. In case of overlap between species, the individual contributions were then summed to obtain a final raster with the value of the species count.

Water bodies

Different vector layers were considered, including rivers, lakes, main water bodies near the borders of the regions,

such as Trasimeno lake or Tevere and Arno rivers (European environment agency, 2023).

Road network and poultry farms facilities

Roads can serve as potential routes for the transmission of the virus between farms, depending on poultry movements and their intensity and other factors including vehicles, equipment and people (Rivas et al., 2010; Stevens et al., 2013). The following main categories of roads were considered: highway, primary roads, secondary road and their junctions (Mapcruzin.com, 2024).

Other considered risk factors were facilities linked to poultry farms as manure treatment plants (where dung is recycled by industrial treatment for fertilizing land) and poultry slaughterhouses.

Generation of the risk factors raster maps

Two kinds of risk factor data layers are generated during the geoprocessing steps of the SMCDa: crisp sets - spatial data layers with clearly defined attributes (e.g. Euclidean distance to a feature) and fuzzy sets - strength of the association between each risk factor and the outcome. Through the fuzzy membership functions, crisp sets are converted in fuzzy sets, the appropriate rasters for the inclusion in the model (Stevens et al., 2013; La Sala et al., 2019). The crisp and fuzzy sets are in the format of raster, with a cell size of 3X3 km.

Crisp sets

Original data available as vector layers (points, lines or polygons as basic units) were converted to raster risk layers using a spatial function, as follows:

- Proximity-related risk factors are domestic bird farms, water bodies, road network and poultry farms facilities. In AI dispersal dynamics most, events are associated with transmission between domestic birds, covering relatively short distances (4 km) (Harvey et al., 2021). Raster were obtained from the input vector by calculating for each cell the Euclidean distance (ED) or straight-line, to the closest source location.
- Density (of heads). The density-related risk factors (Stevens et al., 2013) were obtained using kernel density estimation (KDE). This function assigns estimated kernel density values (heads density) to each pixel within a certain radius. It was calculated for the other poultry farms and the mallard species.
- Density of species. We considered as risk factor the number of other target wild bird species, other than mallard present on each cell (of 3X3 km) (Schreuder et al., 2022).

Fuzzy sets

Each layer (crisp sets) was converted into new rasters called fuzzy rasters, with values ranging from 0 to 1 (standardisation). This step was done assigning a degree of membership of the crisp sets to a membership function. The risk distribution function was based on EO and literature research (Harvey et al., 2021; Stevens et al., 2013). The fuzzy membership function used for most risk factors is the sigmoidal monotonic decreasing curve (small membership of tool "Fuzzy membership" in ArcGIS Pro® 3.3). It was used to model the risk decreasing as distance increases, reaching negligible risk at distances greater than threshold values. This model was used for a first group of domestic bird farms (backyard, free-range, duck and geese, agistment farms) and some facilities linked to poultry farms (Figure 2), as well as for road networks and water bodies (Figure 3) (Stevens et al., 2013; Paul et al., 2016). The increasing sigmoidal function (or large membership in ArcGis) was instead used for wild birds whose raw data are density (heads of mallard and number of other species) (Figure 4). A quadratic relationship was used for the density of the other domestic bird farms (the second group of poultry farms) (Figure 4) (Stevens et al., 2013) using the software Idrisi Taiga®.

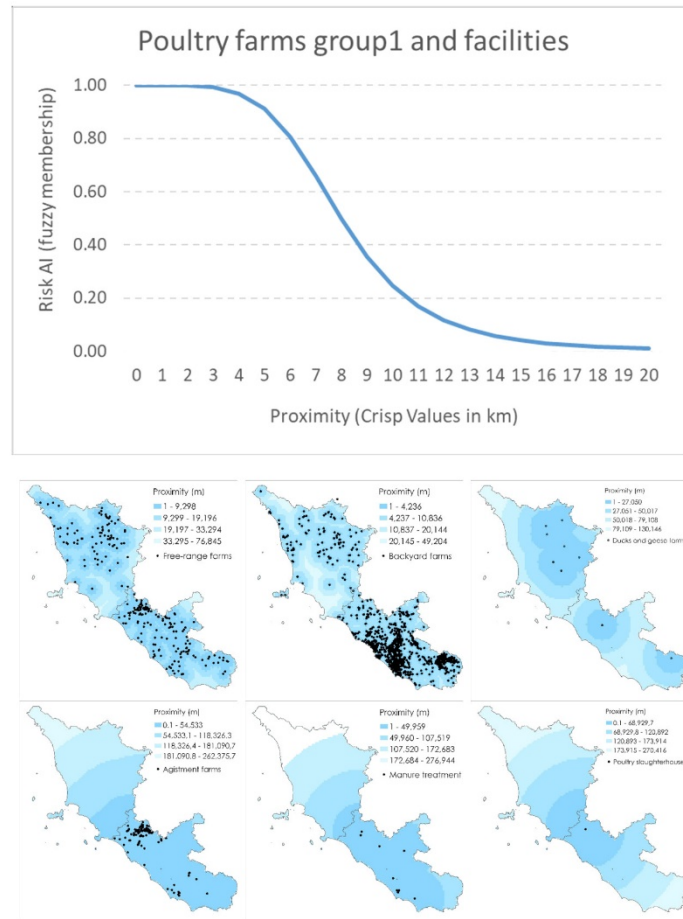


Figure 2. Proximity based factors: poultry farms group 1 and some poultry farms facilities (manure treatment and poultry slaughterhouses).

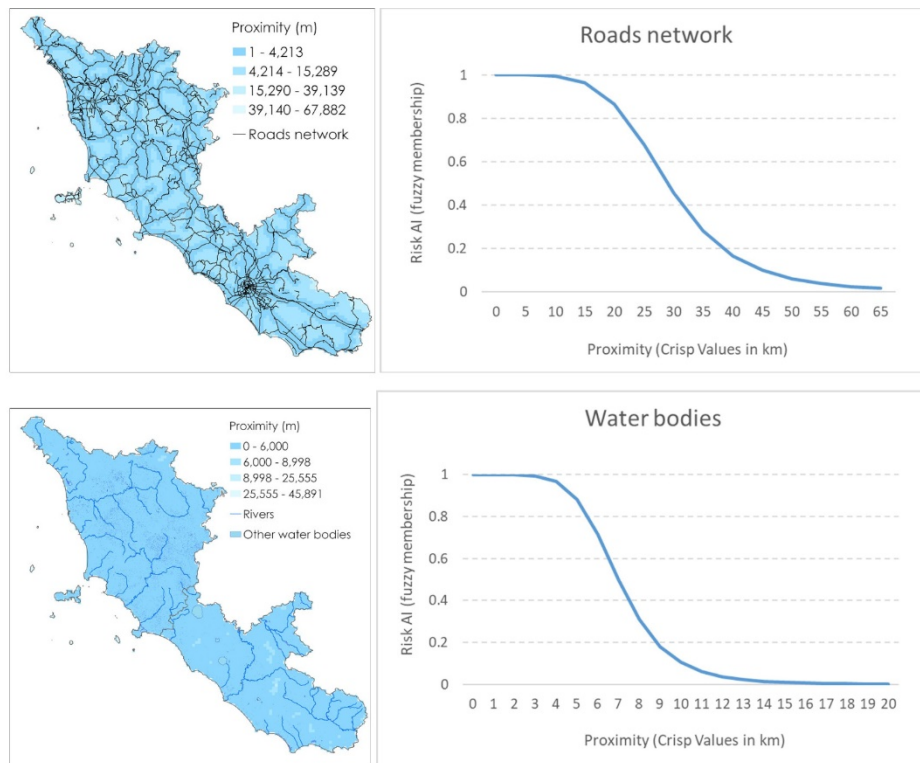


Figure 3. Proximity based factors: farm facilities and water bodies.

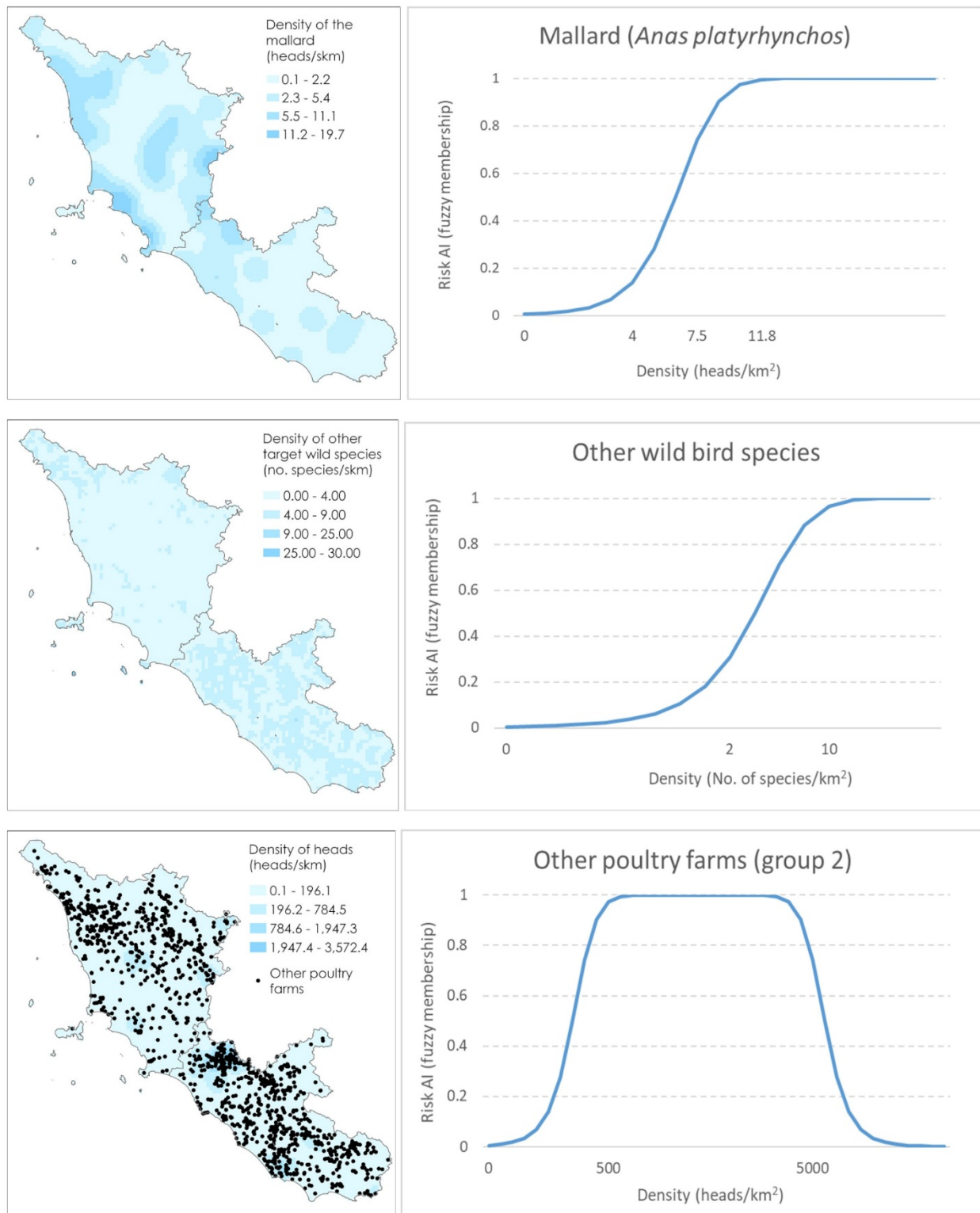


Figure 4. Density based factors: mallard, other wild bird species and other poultry farms.

Generation of weights - Analytic Hierarchy Process (AHP)

A weight for each risk factor was calculated, through the elicitation of 3 expert opinions. The selection of veterinary experts was based on their epidemiological and virological expertise on AI. The scoring of each risk factor was based on a seven-point scale, derived by Saaty et al. (1987), reported in Table II.

Less important			More important			
1/4 (=0.25)	1/3 (=0.333)	1/2 (=0.5)	1	2	3	4
very strongly less important	strongly less important	moderately less important	equally important	moderately more important	strongly more important	very strongly more important

Table II. AHP Scoring system.

The methodology employed is the Analytic Hierarchy Process (AHP), which derives ratio scales from pairwise comparisons between variables (Malczewski, 2000). Each variable was compared against all others, including itself, in a double-entry table. The weights were generated using the principal eigenvector of the pairwise comparison matrix. The results from the 3 tables were then integrated through arithmetic averaging, producing a single table of weighted values (Table III).

CATEGORIES	RISK FACTORS	EXPERT 1 WEIGHT	EXPERT 2 WEIGHT	EXPERT 3 WEIGHT	WEIGHTS MEAN
A - poultry	Free-range farms	0.16	0.16	0.12	0.15
	Ducks and geese farms	0.08	0.15	0.11	0.11
	Water bodies	0.10	0.06	0.12	0.09
	Agistment farms	0.04	0.04	0.14	0.08
	Backyard farms	0.08	0.07	0.07	0.07
B - wild and migratory birds	Mallard	0.17	0.19	0.20	0.19
	Other wild birds	0.15	0.11	0.03	0.10
C - water bodies	Other poultry farms	0.08	0.10	0.09	0.09
D - other farm facilities	Manure treatment	0.05	0.05	0.04	0.05
	Road network	0.04	0.04	0.04	0.04
	Poultry slaughterhouses	0.03	0.03	0.04	0.03
Total		1.00	1.00	1.00	1.00

Table III. AI risk factors weights.

The reliability of the comparisons among risk factors and of the decision-making process is ensured by the calculation of the CR (consistency ratio) index (from 0 to 1) through QGIS 2.8.8 and the Plugin Easy AHP softwares. Only if CR is ≤ 0.1 there is an acceptable level of consistency (Malczewski, 2000).

Suitability map

The suitability map for AI was created through a combination of weighted risk factors/layers (fuzzy raster and weights of each variable), at 3X3 km resolution, according to the equation:

$$S = \sum_{ij=1}^n (W_j RF_{ij})$$

where S is the final suitability estimate for each raster cell, W is the weight for risk factor j , and RF is the value of risk factor j for raster cell i .

$WLC = \text{FuzzyRaster1} * \text{Weight1} + \text{FuzzyRaster2} * \text{Weight2} + \dots + \text{FuzzyRaster11} * \text{Weight11}$

where WLC is for Weighted Linear Combination (Malczewski, 2000).

Sensitivity analysis

A sensitivity analysis was performed, investigating various scenarios to assess the robustness and reliability of different risk factors weights and the result of potential different risk maps.

Expert Opinion scenario (EOS)

The baseline scenario, with risk factors weights assigned by experts.

Low Biosecurity scenario (LBS)

Intensive, commercial farms usually have a high biosecurity level. The LBS scenario assumed a low biosecurity standard for this type of farming and at the same level of risk (0.100) for all the subcategories. As a result, the weights were recalculated for the other categories of poultry farms, while remained unchanged in water bodies and other farm facilities (roads, slaughterhouses and manure plants).

High Biosecurity scenario (HBS)

In non-intensive farms, such as backyard, biosecurity levels are generally lower than in intensive farms. In this scenario, all type of poultry farms were considered to have the same high level of biosecurity of intensive farms. The weights of categories other than poultry increased consequently.

Absence of wild bird migration scenario (AWS)

The weight of the target wild and migratory birds is assumed to be null (Howard et al., 2018; Nourani et al., 2017), to consider only the risk of the AI spread due to commercial farms and related structures/facilities.

Uniformity scenario (US)

There is no difference in risk weights among the factors. All factors are treated as equally important.

To compare the scenarios, a Pearson product-moment correlation matrix was calculated (Table V), using the 'rcor' function from the 'Hmisc' package of the R software.

Map validation

The map validation was assessed through a comparison with past AI outbreaks spatial distribution in the study area through descriptive and visual analysis and the spatial risk classes of the suitability map (Table VI, Figure 5), and through the Boyce Index using the ecospat.boyce package in R software. All maps produced in this study are consistent with the spatial scale shown in Figure 5. Additionally, each map uses the Universal Transverse Mercator (UTM) projection, Zone 32N, based on the World Geodetic System 1984 (WGS 84) coordinate system.

CATEGORIES	RISK FACTORS	EOS	LBS	HBS	AWS	US
A - poultry	Free-range farms	0.150	0.100	0.080	0.211	0.091
	Ducks and geese farms	0.110	0.100	0.080	0.155	0.091
	Other poultry farms	0.090	0.100	0.080	0.127	0.091
	Agistment farms	0.080	0.100	0.080	0.113	0.091
	Backyard farms	0.070	0.100	0.080	0.099	0.091
B - wild and migratory birds	Mallard	0.190	0.190	0.228	0	0.091
	Other wild birds	0.100	0.100	0.120	0	0.091
C - water bodies	Water bodies	0.090	0.090	0.108	0.127	0.091
D - other farm facilities	Manure treatment	0.050	0.050	0.060	0.070	0.091
	Road network	0.040	0.040	0.048	0.056	0.091
	Poultry slaughterhouses	0.030	0.030	0.036	0.042	0.091
Total		1.000	1.000	1.000	1.000	1.000

Table IV. AI risk factors weights in each scenario (EOS= expert opinion scenario; LBS= low biosecurity scenario; AWS= absence of wild birds migration scenario; US=uniformity scenario).

Results

Suitability map

AI suitability map for Lazio and Toscana Regions were produced (Figure 5). The value of suitability is expressed on a continuous scale (scale colour from green to red), with the lowest values indicating the least suitable cells. Half of the risk comes from the presence of poultry (0.5 category A), 38% from migratory birds (0.29 for wild birds, 0.09 for water bodies), and 12% from other farm facilities (Table III, Figure 6).

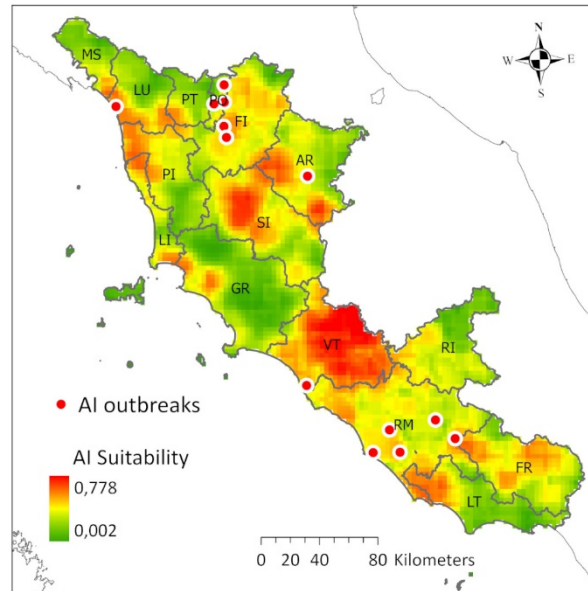


Figure 5. Avian Influenza suitability map (names of the provinces: AR=Arezzo; FI=Firenze; FR=Frosinone; GR=Grosseto; LT=Latina; LI=Livorno; LU=Lucca; MS=Massa-Carrara; PI=Pisa; PT=Pistoia; PO=Prato; RI=Rieti; SI=Siena; VT=Viterbo).

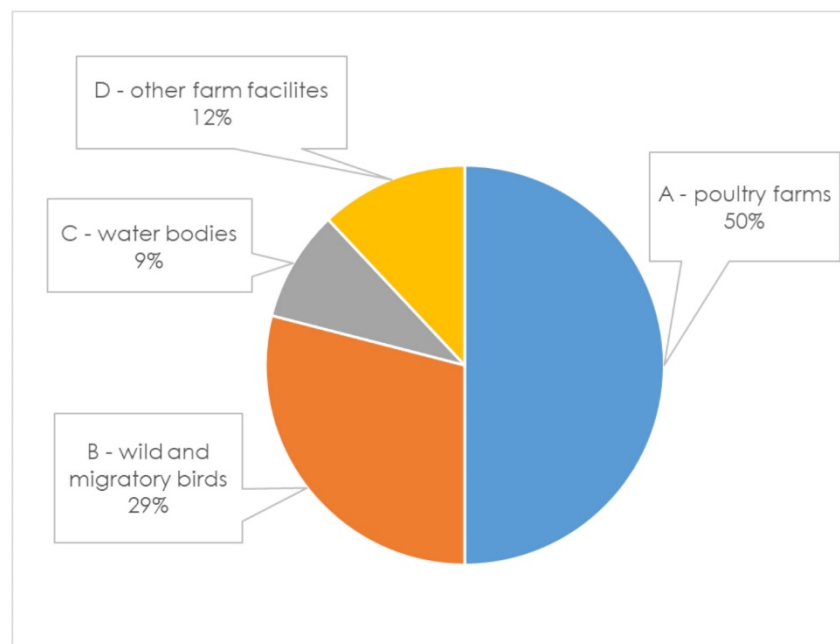


Figure 6. Risk factors weights distribution in EOS.

The suitability raster values were grouped into 4 risk classes using the quartile classification: 0.01 – 0.31 (low risk); 0.32 – 0.41 (low-medium risk); 0.42 – 0.49 (high-medium risk); 0.50 – 0.78 (high risk). In Lazio, the high and high-medium risk areas cover respectively 33 and 28%. The first one is located in the VT province and along the coastal area between Latina (LT) and Roma (RM) provinces with some minor inner areas in Frosinone (FR) province. In Toscana, high risk areas cover around 19% of the region and the medium-high risk area is equal to 24%). High-risk areas are primarily located along the coast with some inland spots. The largest is between Siena (SI) and Arezzo (AR)

while two smaller ones are in the northwest, including wetlands such as the “Padule del Fucecchio”), and the southeast zone.

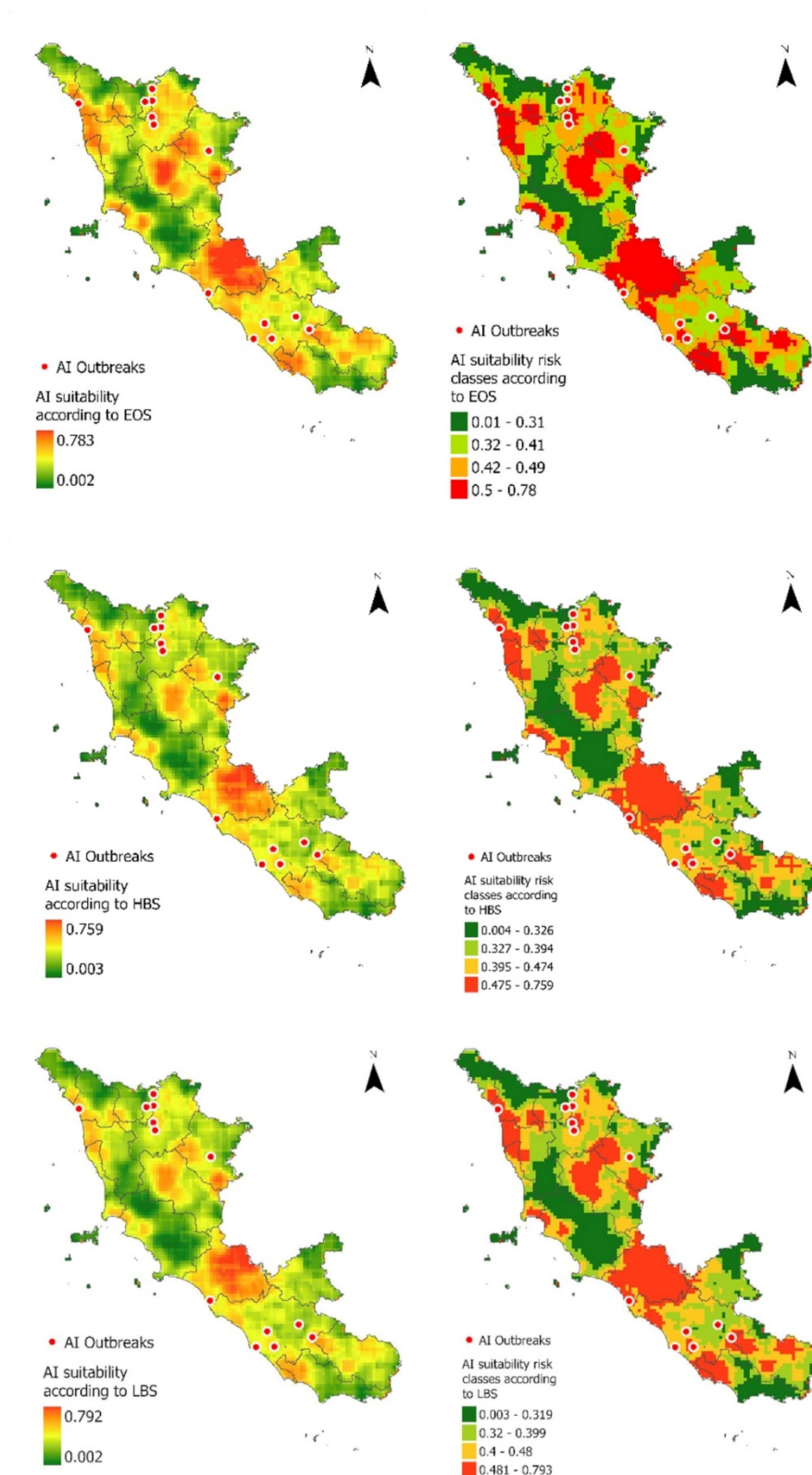


Figure 7. Avian Influenza suitability mp (Quartile classify method) with outbreaks.

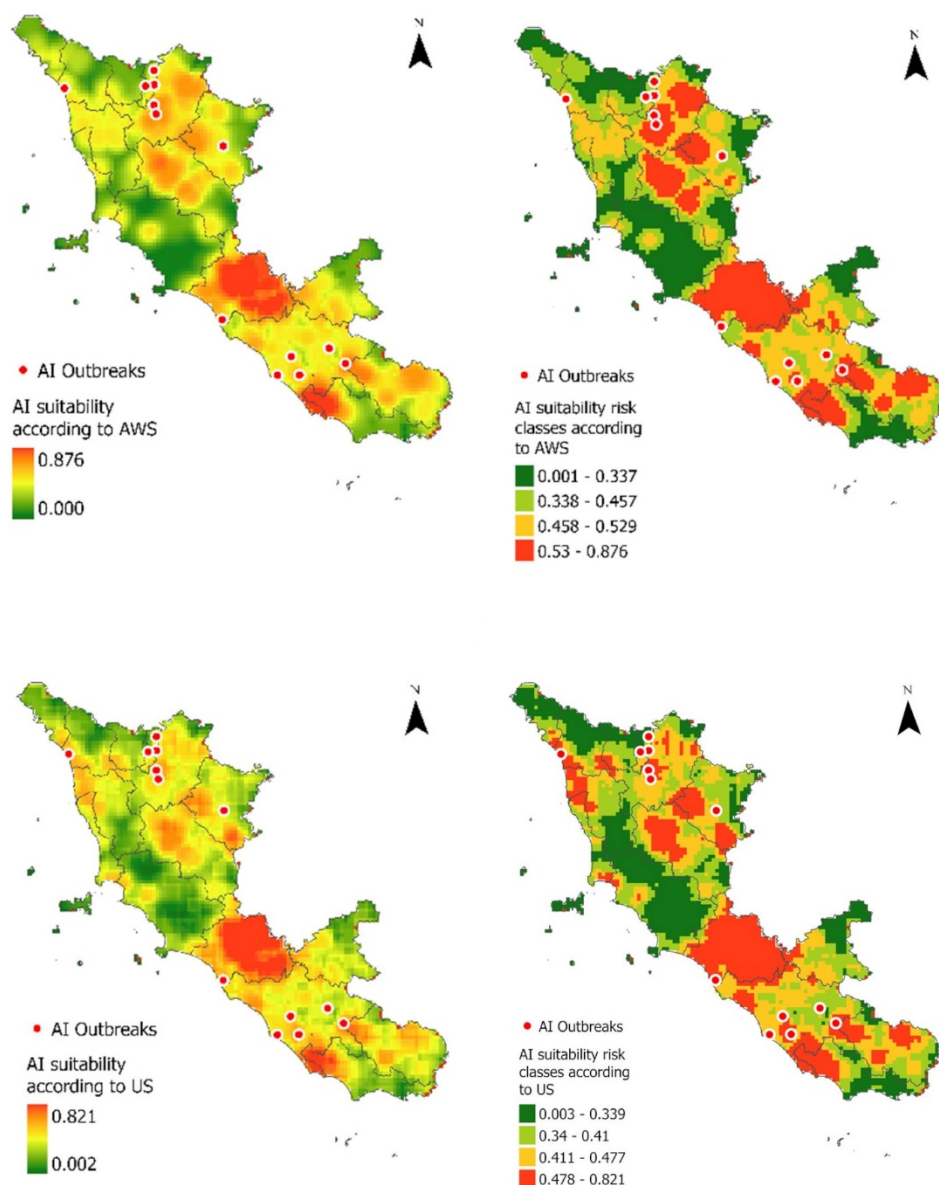


Figure 8. Avian Influenza suitability map (Quartile classify method) with outbreaks.

Sensitivity analysis

Two AI suitability maps were created for each scenario, the suitability distribution (left map) and its classification (right map), with the aim of identifying homogeneous risk areas, using the quartile method, as described above (Figures 7-8).

Since suitability is a continuous variable, a Pearson product-moment correlation matrix was calculated to evaluate the differences among scenarios (Table V). Each cell of the matrix represents the correlation between two variables, ranging from -1 and 1 (where 1 is a perfect positive relationship, -1 a perfect negative relationship, and 0 no linear relationship). The correlation matrix between raster maps was calculated with R software, using the 'rcor' function from the 'Hmisc' package. All the p-values are < 0.05. Alternative hypothesis: true correlation is not equal to 0.

	EOS	LBS	HBS	AWS	US
EOS	1				
LBS	0.989	1			
HBS	0.979	0.993	1		
AWS	0.878	0.860	0.806	1	
US	0.960	0.971	0.954	0.930	1

Table V. Correlation matrix between scenarios.

Map validation

During the period 2011-2023, a total of 13 AI outbreaks (8 HPAI and 5 LPAI) were reported in Lazio and Toscana Regions, 6 and 7, respectively. LPAI occurred in RM, VT, PO, and AR, while HPAI in RM, FI, LU, and PO. Twelve outbreaks occurred in domestic farms, while one involved wild birds (SIMAN, 2024). Overlapping these outbreaks to the EO suitability map, 7 out of 13 outbreaks fall into the high-medium risk suitability zone, 3 in the high-risk zone, 2 in low-medium risk zone and 1 in low-risk suitability zone (Table VI, Figure 5). The Boyce index estimated a good performance, resulting 0.6 (Boyce index ranges from -1 to + 1). The distribution of the model predictive power (predicted/expected ratio) is not the same for all suitability values. It reaches a peak for suitability values around 0.5 (Figure 9).

Risk classes	EOS		LBS		HBS		AWS		US	
	risk surface (%)	N. outbreaks	risk surface (%)	N. outbreaks	risk surface (%)	N. outbreaks	risk surface (%)	N. outbreaks	risk surface (%)	N. outbreaks
Low	24.3%	1	24.4%	1	24.4%	2	25.8%	0	24.0%	1
Low-medium	25.2%	2	25.7%	2	25.5%	1	24.7%	2	25.6%	2
High-medium	25.4%	7	24.8%	7	25.5%	7	26.1%	7	25.8%	6

Table VI. Distribution of AI outbreaks in risk classes.

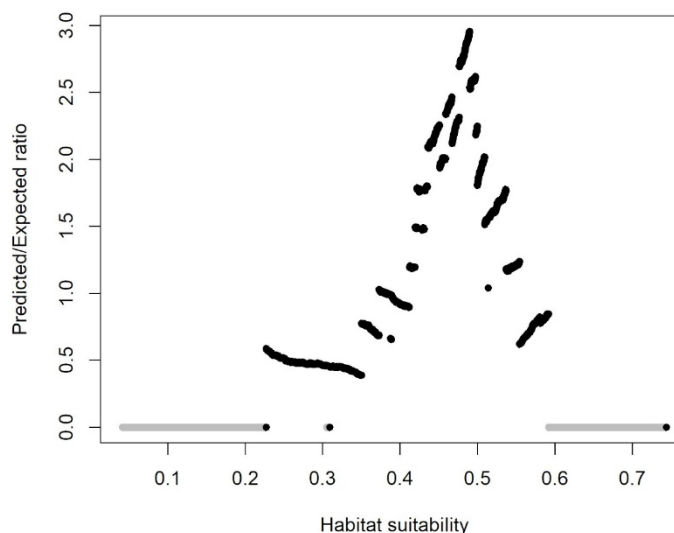


Figure 9. Predictive power (predicted/expected ratio) of the model (with a Boyce index = 0.6).

Discussion

Avian influenza is widely circulating in Europe, with numerous outbreaks affecting both wild and domestic animals. The significant impact on human and animal health, and its economic burden, emphasizes the critical need for data and models that provide policy makers with a knowledge-driven approach. In this context, the present SMCDA was developed to identify AI major risk areas in Lazio and Toscana, regions where the poultry industry is relevant. The

spatial risk assessment can assist CAs in designing risk-based surveillance programmes.

The AI Italian Surveillance Plan relies on risk factors, grouped in two categories, geographical/naturalistic and managerial/zootechnical, using a qualitative method, and assigned to administrative units, such as region or province, enabling different surveillance activities. This study analysed the same risk factors, but at a finer scale, enabling more precise targeting of active and passive surveillance. Individual farmers and their associations can use these results to enhance biosecurity measures based on the risk of their farms, while information campaigns can be better tailored to areas with a higher risk of AI introduction and spread. Regional risk maps should refine the National Surveillance Plan activities.

SMCDA is particularly valuable in areas with no surveillance data, as it can create preliminary risk estimates, but need to be periodically updated, such as input data change. This is particularly relevant for poultry population and outbreak occurrence. To our knowledge, this study represents the first application of this method to assess the AI risk in Europe.

Our findings showed that more than 30% of Lazio and about 20% of Toscana are at high-risk for AI. Over more than a decade, only 3 out of 13 outbreaks occurred in the high-risk areas. This may reflect the high level of biosecurity implemented by the intensive poultry industries and applied to farms in this area. This significant progress in preventing AI likely results from coordinated efforts to increase and implement biosecurity on farms, acknowledging the recognised AI risk by both the industry and the health sector stakeholders.

Sensitivity analysis

The main scenario (EOS) was evaluated through the sensitivity analysis using other scenarios. LBS represents a "worst case", where all poultry layers (category A) are assumed to have a low biosecurity level, thereby increasing their risk weights in poultry farms. This scenario helps to assess whether the EOS weights among different types of poultry farms is justified. In HBS it is possible to evaluate the increased weight of categories B, C and D, while AWS and US helps to consider the impact of wild birds and a uniform distribution of the risk. All scenarios yielded similar spatial risk class, confirming the reliability of the EOS. The significant agreement among the scenarios was also confirmed by the correlation matrix (Table V). The little differences are mostly on a local scale, depicting slightly different spatial risk patterns. Differences are observed in LBS and HBS, compared to EOS, resulting in a widening of the low-risk range (23 to 24%). In AWS, the contribution of wild birds was excluded, resulting in an even greater widening of the low-risk range (from 23 to 26%), albeit with a different pattern (no outbreak falls into it), yet 11 out of 13 outbreaks still fell within the 2 highest risk spatial classes. A possible explanation is that the viral circulation due to poultry might be more significant than that due to wildlife (perhaps indicative of a slight overestimation of this last contribution in EOS). In the US, we observe a significant number of outbreaks falling within the high-risk ranges. Even a significant reduction in the most important risk factor (wild avifauna) confirm the robustness of the model, with 10 outbreaks out of 13 falling in the 2 highest risk areas. In summary, the 5 scenarios have essentially identified the same areas of vulnerability in Lazio and Tuscany.

Map validation

Several methods are used in literature to evaluate the performance of habitat suitability models. Most of them, e.g. Receiver Operating Characteristic (ROC) curve are based on binary data (presence/absence) and cannot be applied with pure presence disease data. The AI outbreaks dataset used in this study was a presence-only data. The Boyce index is a presence-only metric for evaluating the predictions of species distribution models (Hirzel et al. 2006), which calculates the correlation between the frequency of observed presences and the model's predictions (i.e. the observed vs. expected proportion of occurrences), comparing with a random distribution. It ranges from -1 to +1, indicating a good (close to +1) or a random performance (close to 0) or a prediction worse than random (negative values). Despite a limited number of observations (outbreaks), the Boyce index indicated medium performance (0.6), with a maximum predictive power around 0.5 suitability value. This aligns with the descriptive analysis done (Figure 7, Table VI) in which the higher number of outbreaks (7) falls into the high-medium risk class (suitability 0.42-0.49).

Possible limitations of this study include several issues:

- the reliability of the database (BDN) regarding backyard farms, as not all of them are recorded in it;
- the need for regular updating of the model due to evolving data;
- the absence of accurate data regarding the biosecurity at farm level;

- the arbitrary choice of the 3X3 km grid cell to establish a common scale for mapping different risk factors;
- the choice of the risk distance pattern in poultry facilities (manure plant and slaughterhouses), where the same risk model used for domestic bird farms was applied (Figure 2) (Stevens et al., 2013). Similarly, for the mallard and other wild bird species, it was decided to adopt a risk pattern based on densities, derived by that of other poultry farms (Figure 3) (Stevens et al., 2013). An increasing sigmoid function was used (and not a quadratic one) as the increase in the risk of virus transmission is here simply associated with the density, without a limiting effect of high densities, which is instead typical of intensive farming and in particular determined by their higher level of biosecurity.
- the generalizability and the transferability of the AI risk map, both in spatial and temporal terms. Regarding the temporal dimension, a specific scenario (AWS), linked to climate change, was evaluated as a possible long-term effect on bird migrations. Reliable data on abundance, distribution and seasonal pattern of migrant birds are limited. While the model could theoretically be applied to larger areas, such as Italy, it would require adaptation and preliminary studies to account for new risk factors at national level, which was beyond the scope of this study.

This study provides a preliminary tool for assessing the risk of spatial spread of AI viruses in two regions of central Italy where the presence of AI is sporadic (13 outbreaks in 12 years) and therefore difficult to map if based only on virus detection. The validity of the model is guaranteed in terms of robustness (sensitivity analysis) and validation (Boyce Index) compared to data on the presence of the disease on the field (outbreaks).

The main result of this study is to provide valuable support for avian influenza risk management. It allows tailoring AI surveillance and control activities in specific areas, such as targeted information campaigns for different stakeholders. For example, several meetings with farmers in the area were conducted on biosecurity, and webinar for hunters were organised on AI epidemiology. The local health authorities are also engaged in educating poultry farmers and hunters about possible zoonotic risk.

A further potential use of this model is the authorization of new farms opening. The intensive poultry industry is growing and interested in building a network of structures close to each other and well connected by roads network. Unfortunately, these features also facilitate the potential spread of pathogens. CAs could benefit of these maps in granting authorizations, carefully evaluating the new farm location and its risk value. Despite the limitations, this model supports a knowledge-based approach. This study acknowledges the complexity of AI control measures, emphasizing the role of wild birds as carriers and highlighting the need for comprehensive preventive strategies. AI poses significant risks to both poultry and human health, highlighting the importance of proactive measures in managing and controlling AI impact.

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