Geographic information systems applied to the international surveillance and control of transboundary animal diseases, a focus on highly pathogenic avian influenza

Vincent Martin, Lorenzo De Simone & Juan Lubroth

Summary

To respond to the lack of early warning in dealing with livestock diseases, the Food and Agriculture Organization (FAO) developed and launched the Emergency Prevention System for Transboundary Animal and Plant Pests and Diseases (EMPRES) programme in 1994. Emphasis was placed on the prevention of emergencies due to transboundary epidemic diseases of livestock of significant economic, trade and/or food security importance. EMPRES early warning activities, mainly based on disease surveillance, reporting and epidemiological analysis are supported by the EMPRES-i information system which enables integration, analysis and sharing of animal health data, combined with relevant layers of information, such as socio-economic, production and climatic data. Indeed, data integration, analysis and mapping represent a key step towards a better understanding of the distribution and behaviour, source and evolution of a disease (or infection) for the definition of appropriate cost-effective disease control strategies. With the emergence of highly pathogenic avian influenza (HPAI) H5N1 in South-East Asia and its rapid spread beyond its known original distribution range, through its EMPRES programme the FAO has invested time and resources in the implementation of several studies to reveal HPAI epidemiological features in specific ecosystems of Asia and advise member countries accordingly on the best disease control options. Some of the key findings are presented in this paper and illustrate the incredible potential of using geographic information systems as part of international early warning systems and their multiple applications in the surveillance and control of infectious diseases, such as HPAI.

Keywords

Early warning, EMPRES-i, Epidemiology, Food and Agriculture Organization, Geographic information system, Highly pathogenic avian influenza, Spatial analysis, Transboundary animal disease.

Sistemi informativi geografici applicati alla sorveglianza e controllo internazionali delle malattie transfrontaliere animali, con particolare riferimento all'influenza aviaria altamente patogena

Riassunto

In risposta alla mancanza di sistemi di early warning per le malattie degli animali da allevamento, l'Organizzazione Mondiale per

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l'Alimentazione e l'Agricoltura (FAO) ha sviluppato e reso operativo nel 1994 il programma EMPRES per la prevenzione di emergenze delle malattie animali e vegetali transfrontaliere. In quella circostanza si enfatizzò l'impegno sulla prevenzione delle emergenze a causa di malattie epidemiche transfrontaliere degli allevamenti animali di notevole importanza ai fini economici, commerciali e/o di sicurezza alimentare. Le attività di early warning di Empres, che si basano principalmente sulla sorveglianza e reportage delle malattie, e sull'analisi epidemiologica, sono supportate dal sistema informativo EMPRES-i che consente l'integrazione, l'analisi e la condivisione di dati relativi alla salute animale, in associazione con layers informativi appositamente selezionati, quali quelli socio-economici, produttivi, e climatici. Indubbiamente l'integrazione, l'analisi e la mappatura dei dati rappresenta un passo fondamentale verso una migliore conoscenza della distribuzione di una malattia (o di un infezione), del comportamento, dell'origine e dell'evoluzione della stessa al fine di definire delle misure di controllo delle malattie appropriate ed economicamente efficienti. In seguito all'emergenza dell'influenza aviaria altamente patogena (HPAI) H5N1 nel Sud-Est Asiatico e la rapida diffusione della stessa oltre l'allora noto range di distribuzione originale, la FAO ha investito attraverso il suo programma EMPRES tempo e risorse per l'implementazione di diversi studi di indagine sulle caratteristiche epidemiologiche del virus H5N1 in specifici ecosistemi in Asia, e, di conseguenza, per indirizzare i Paesi Membri verso le più opportune strategie di controllo della malattia. Alcuni risultati chiave di tali lavori sono presentati in questa pubblicazione dove viene sottolineato il grande potenziale dell'uso di sistemi informativi geografici quale parte integrante di sistemi di early warning internazionali e delle molteplici applicazioni degli stessi nella sorveglianza e controllo delle malattie infettive, quali l'HPAI.

Parole chiave

Analisi spaziale, *Early warning*, , EMPRES-i, Epidemiologia, Influenza aviaria altamente patogena, Malattie animali transfrontaliere, Organizzazione Mondiale per l'Alimentazione e l'Agricoltura, Sistema informativo geografico.

Introduction

By tradition, epidemiologists have used maps to study the relationships between time, location, environment and disease. Geographic information systems (GIS) offer an ideal framework to study these associations given the spatial analysis and visualisation capabilities. GIS is now used for a multitude of purposes, including surveillance and monitoring of vector-borne and water-borne diseases, environmental health, modelling exposure to electromagnetic fields, quantifying lead hazards in a neighbourhood, predicting child pedestrian injuries, and the analysis of disease policy and planning (1).

Managers of animal and public health administrations need timely information on the dynamics of disease and environmental data to implement appropriate action. Location and time reference are elements of information that characterise most epidemiological datasets. Knowledge of the new information offered by spatial and temporal analysis can greatly increase the effectiveness of response to potential animal health emergencies, including those can affect public health. GIS technology can support this process with tools that offer a description, analysis and interpretation of spatially-explicit disease data. This process employs many standard aspects of descriptive epidemiology but expands on these by systematically considering the pattern, statistical tests, alternative hypotheses and implications for intervention that contemporary animal health practice may require. The combination of GIS (which facilitates data manipulation) and spatial statistical tests (which can rigorously explore time-space patterns) provides an opportunity to more fully explore the way a disease is distributed in a population of animals in time and space. Spatial pattern of disease is fundamental to the understanding of current exposure and to the prevention of disease, regardless of whether the underlying process is contagious, environmentally influenced, or related to innate host factors.

The multidisciplinary aspects of GIS in regard to data collection, mapping and analysis may

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provide support to disease risk assessment, resulting in risk maps and relative maps of uncertainty of prediction. 'Turning data into information' is a well recognised expression that is used in GIS circles and also applies to the specific animal disease case (for instance, raw animal health data obtained from the veterinary service investigation reports, laboratory results and demographics, are entered into a GIS, with subsequent information produced as a graphic output in the form of maps with the corresponding descriptive statistic). Spatial analysis and the use of GIS for health in general have been reviewed by several authors (3, 5, 9, 10, 11, 12, 13, 14, 15). The literature suggests an heterogeneous variety of applications and an ever increasing number of available tools and capabilities of new software technology. However, in an attempt to give at least a defined body to the subject of GIS and spatial analysis, Gatrell and Bailey (2) provided a description of three general types of spatial analysis tasks, namely: visualisation, exploratory spatial data analysis and model building.

To respond to deficiencies in early warning and response systems in dealing with livestock diseases, in 1994, the Food and Agriculture Organization (FAO) developed and launched the Emergency Prevention System for Transboundary Animal and Plant Pests and Diseases (EMPRES) programme that placed emphasis on the prevention of emergencies due to transboundary epidemic diseases of livestock of significant economic, trade and/or food security importance (fao.org/ag/againfo/programmes/en/empres/home.asp). These diseases can spread easily to other countries and reach epidemic proportions and require co-operation between several countries in regard to control and management. The EMPRES early warning activities, mainly based on disease surveillance, reporting and epidemiological analysis are supported by the global animal health information system (EMPRES-i) which enables integration, analysis and sharing of animal health data combined with relevant layers of information, such as socio-economic, production and climatic data. Since the beginning of the highly pathogenic avian influenza (HPAI) crisis caused by the H5N1 strain in 2003/2004, priority has been given to the entry of all available information on HPAI outbreaks and cases in domestic poultry and wild birds into the EMPRES-i system that today contains thousands of records covering HPAI occurrences in Asia, Europe and Africa. Situation reports and risk analysis generated by the system are all presented in a GIS environment for the understanding and visual impact it offers.

With the emergence and rapid spread of HPAI in South-East Asia and beyond, the FAO conducted and coordinated a series of studies to further describe HPAI epidemiological features in specific ecosystems of Asia and thus advise affected countries accordingly on the most appropriate disease control strategies. Some of the key findings illustrate the broad potential of using GIS as part of international early warning systems and their multiple applications in the surveillance and control of infectious diseases such as HPAI.

Early warning information system for monitoring of avian influenza and other infectious diseases

To support the early warning and early reaction component of the EMPRES programme, the Web-based 'EMPRES-i' system was developed. EMPRES-i provides a platform that facilitates the exchange of information between animal health officers at the FAO headquarters and those in the field. It also enables inputs from co-workers, experts and other institutions involved in disease outbreak management and emergency response. The core of the system is a secure internet-based database using Oracle®, where users are granted different levels of access to the system (guest, manager, administrator) with different levels of privileges (viewing, editing and analysis).

EMPRES-i is designed to record, analyse and monitor data on major transboundary animal

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diseases (TADs). Priority diseases are as follows: HPAI, foot and mouth disease (FMD), Rift Valley fever (RVF), contagious bovine pleuropneumonia (CBPP), African swine fever (ASF) and rinderpest. From the beginning of FAO involvement in the HPAI crisis in 2004, emphasis has been placed on the entry into the system of all available information on the occurrence of avian influenza in domestic poultry and wild birds. Information is gathered from various sources. Official information, such as that from the World Organisation for Animal Health (OIE: Office International des Épizooties), World Health Organization (WHO) and Ministry of Agriculture (MoA) websites, are screened on a regular basis. Furthermore, additional information is provided directly from the European Commission or by governments. In addition to these official sources, data is drawn from electronic subscription lists, such as ProMed-mail, global public health intelligence network (GPHIN) or AI-watch and news items on avian influenza are traced though internet searches. Last, but not least of the important sources of information are the FAO country offices and their contact points in the field as well as OIE/FAO reference laboratories.

The main output of EMPRES-i consists in the delivery of timely and accurate situation updates as well as relevant risk analysis on TADs, which are distributed electronically (FAO *Avian Influenza Disease Emergency News* [*FAO AIDE News*], *HPAI Update*, *EMPRES Watch* messages, disease tracking list) to member countries and partner institutions.

The disease tracking list (DTL) is one example of disease information generated by EMPRES-i. The DTL is a biweekly summary of the HPAI epidemiological situation in space and time which captures both pending and unconfirmed events. Issued from epidemiological data entered into the system, it lists all confirmed outbreaks and pending investigations in domestic poultry and wild birds worldwide during the previous two weeks. It also displays the temporal evolution of the daily incidence of outbreaks over a one-year period. This list is shared with national and regional field staff as well as key partner

institutions which are requested to verify and validate unconfirmed events, follow-up and search for reliable sources of information.

Another key publication is the Emergency Centre for the Control of Transboundary Animal Diseases (ECTAD) *HPAI Update* which compiles information on HPAI outbreaks, suspicions of outbreaks/cases or other relevant issues observed over the previous two weeks. Mission reports, information from the field or from other organisations and institutions, as well as news reports, are edited and summarised to give the reader a brief overview of important events relating to HPAI. A map is featured on the first page showing HPAI occurrence locations, capturing confirmed outbreaks in poultry or cases in wild birds over a two-month window. *HPAI Update* is produced and distributed electronically three times a week (Monday, Wednesday and Friday). It was originally created to regularly update FAO officers on the current HPAI situation worldwide. In line with increasing demand and the impact it made, its distribution and access have been extended to FAO country offices, contact points in other international organisations (technical, political and financial) and partner institutions at universities, research and reference centres and certain supporting donor groups. As the *HPAI Update* does not only cover information on confirmed events but also on suspicions and rumours, distribution is currently limited to individuals at institutions who recognise their responsibilities and possible repercussions of any misused information.

The FAO *AIDE News*, on the other hand, provides an update on the avian influenza situation and is specially designed for public distribution. It is produced at least once a month and consists of a short situation analysis, country status regarding confirmed HPAI outbreaks and information on FAO missions and projects. Some of the above information is posted on the EMPRES and FAO avian influenza website, depending on its relevance to the target audience and the potential sensitivity of the information.

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Exploration of infectious disease epidemiological patterns using geographic information systems

Exploratory spatial data analysis

To provide a visual representation of disease distribution patterns and explore the relationships between location, environment and disease, EMPRES-i has been linked to a GIS application. The GIS environment offers the ideal framework for studying these associations because of its spatial analysis and visualisation capabilities and can contribute significantly to a better understanding of underlying epidemiological and ecological factors responsible for the emergence and spread of TADs. In addition, animal disease managers need timely information on the dynamics of disease and environmental data to implement appropriate actions. Location and time reference characterise most epidemiological datasets and knowledge of the new information offered by spatial and temporal analysis can greatly increase

potential for animal health action. The combination of GIS (which allows easy data manipulation) and spatial statistical tests (which offers a complete picture of time-space patterns) provides an opportunity to more fully explore the way a disease is distributed in a population of animals in time and space. Multidisciplinary efforts in GIS for data collection, mapping and analysis also provide support to disease risk assessment by providing risk maps and relative maps of uncertainty of prediction.

Through this GIS approach, HPAI disease observation data entered into EMPRES-i can be visualised as basic maps (Fig. 1) before being combined, for advanced disease analysis purposes, with additional geographical layers, such as land use, poultry density, remote-sensed imagery (Fig. 2) or other variables hypothesised as relevant to the epidemiology of the disease or ecology of the virus, host or environment (Fig. 3).

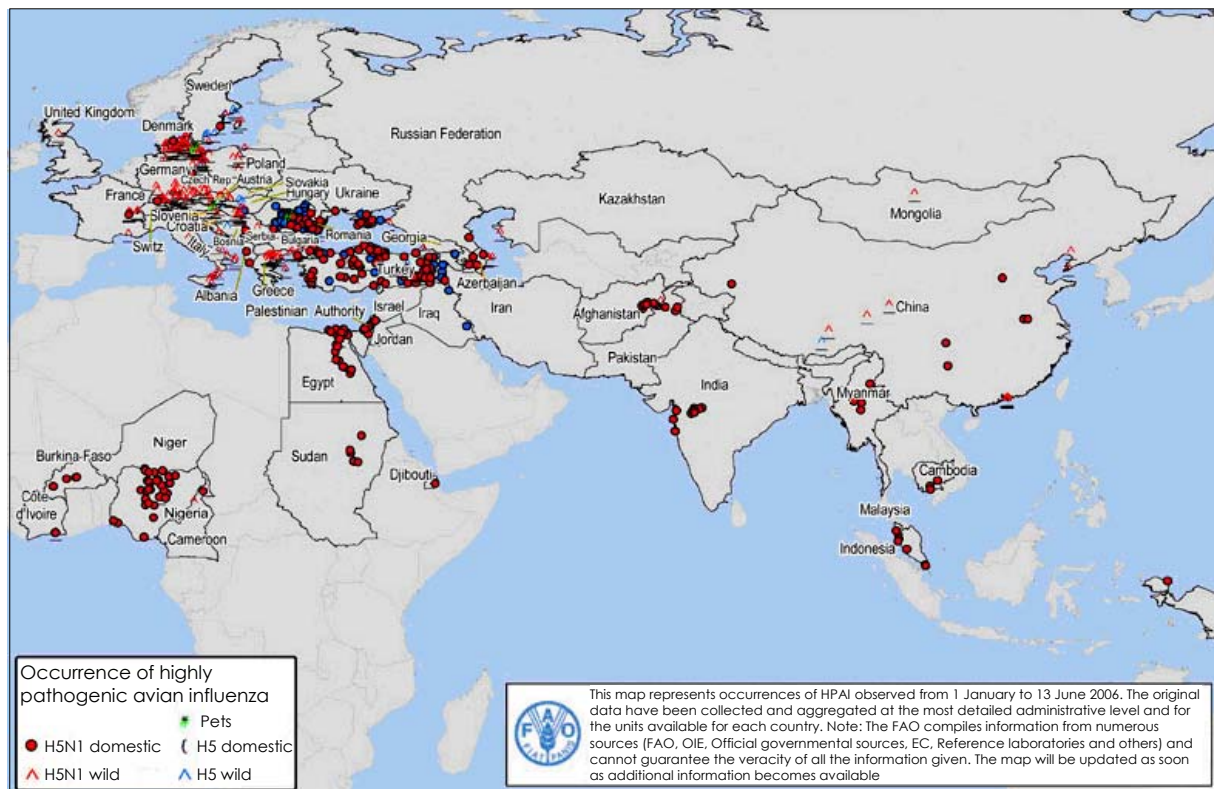Exploratory spatial data analysis (ESDA) represents a key step towards identifying

Figure 1
Distribution of highly pathogenic avian influenza, January-June 2006

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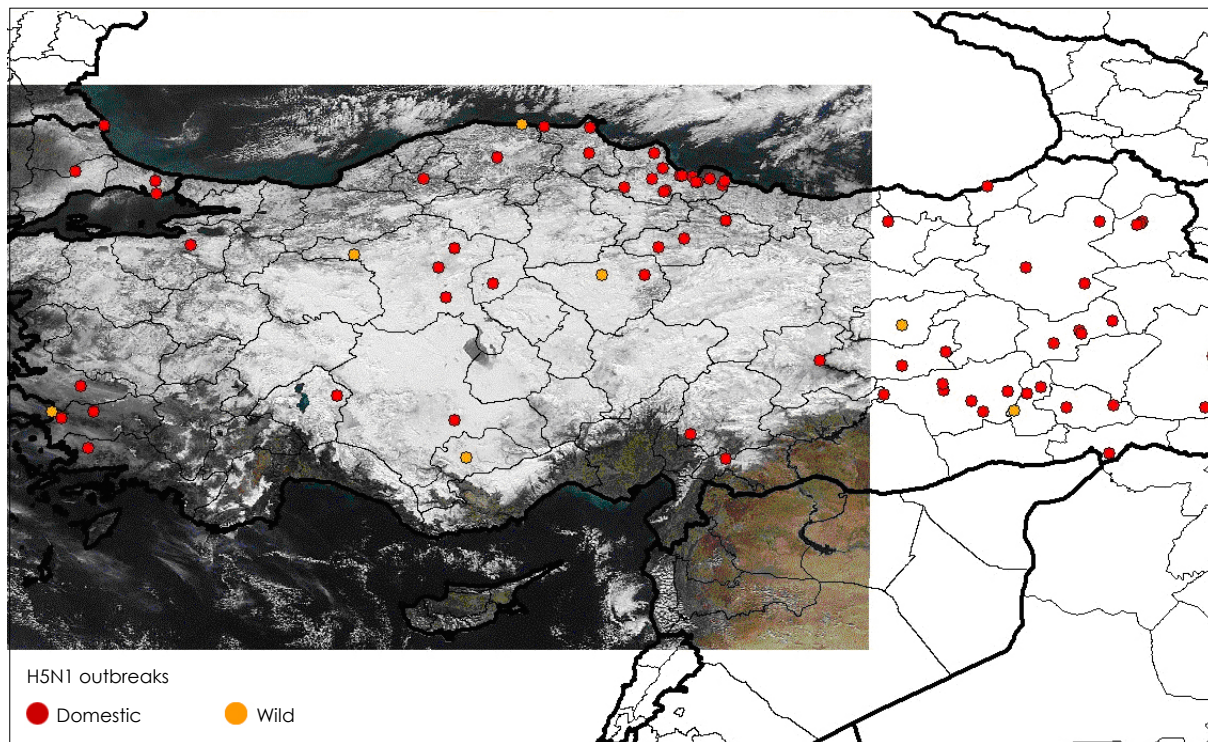Vincent Martin, Lorenzo De Simone & Juan Lubroth

Figure 2
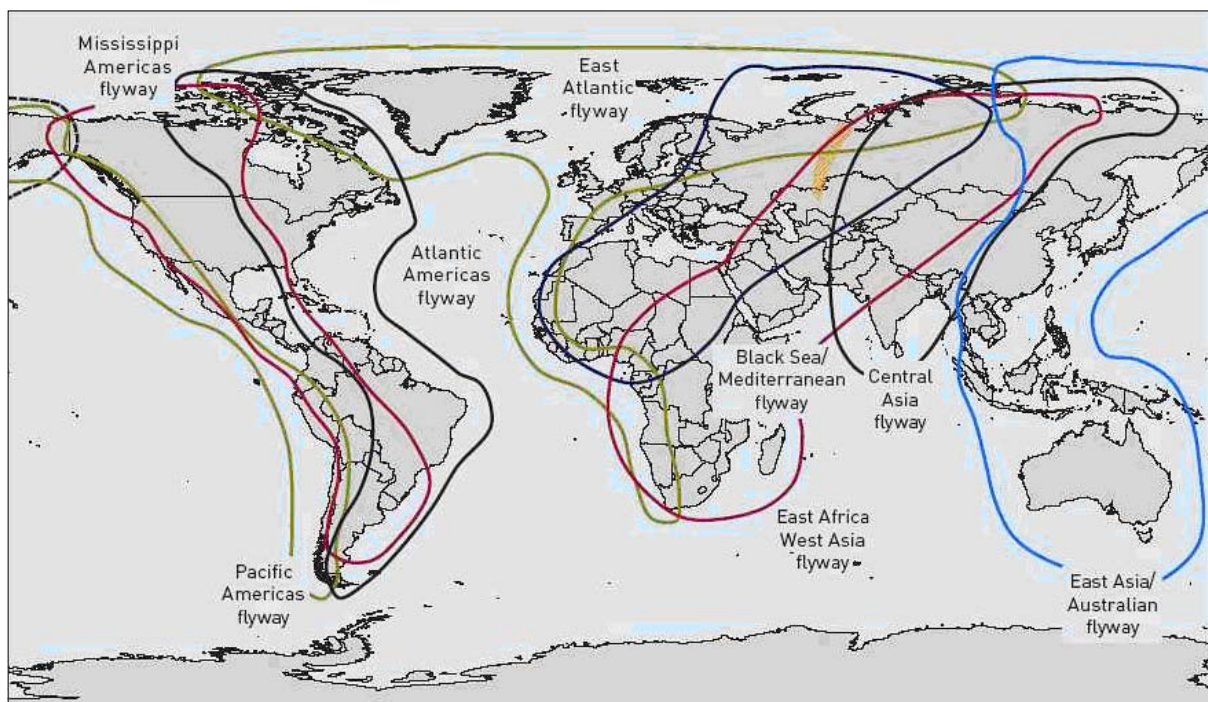Outbreak locations overlaid on remote-sensed imagery showing frozen areas of Turkey

Figure 3
Major fly paths of migratory shore birds (wader species)
Compiled by FAO AGAH, EMPRES Programme
Flyways: Wetlands International
© FAO, 2005

patterns considered to be indicative of clusters of cases, areas of elevated incidence, or to highlighting associations between the magnitude of disease and components of the environment or map series that imply shifts in spatial pattern over time.

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GIS supports ESDA through the calculation of various spatial explorative processes that may result in choropleth maps (Fig. 4) or smoothed surfaces (Fig. 5) derived from interpolation techniques applied to punctual variables over wide geographic areas. Measuring spatial trends is one ESDA quantification process commonly applied in GIS.

The most common way of measuring the trend for points or areas is to calculate the standard distance (Fig. 4) separately in the x and y directions. These two measures define the axes of an ellipse encompassing the distribution of features. The ellipse is referred to as the standard deviational ellipse, since the method calculates the standard deviation of the x coordinates and y coordinates from the mean centre to define the axes of the ellipse. The ellipse shows if the distribution of features is elongated, hence, it has a particular geographical orientation. While one can get a sense of the orientation by drawing the features on a map, calculating the standard

deviational ellipse makes the trend clearer. It is possible to calculate the standard deviational ellipse using either the locations of the features or using the locations influenced by an attribute value associated with the features. The latter is termed a weighted standard deviational ellipse.

Density of events over space and/or time is another useful ESDA measure which may contribute to providing insight into the most vulnerable areas of a certain disease and may assist in the understanding of the underlying spatial structures driving disease spread. Figure 5 shows an outbreak density map that is represented as a moving window (kernel) of a specified size passing through subsequent moves across the study area. At each location, a ratio is calculated between the area of the window and the number of outbreaks eventually falling within the window itself. This type of map helps to identify areas of maximum outbreak density and shows the shift of the animal epidemic, in 2006, from
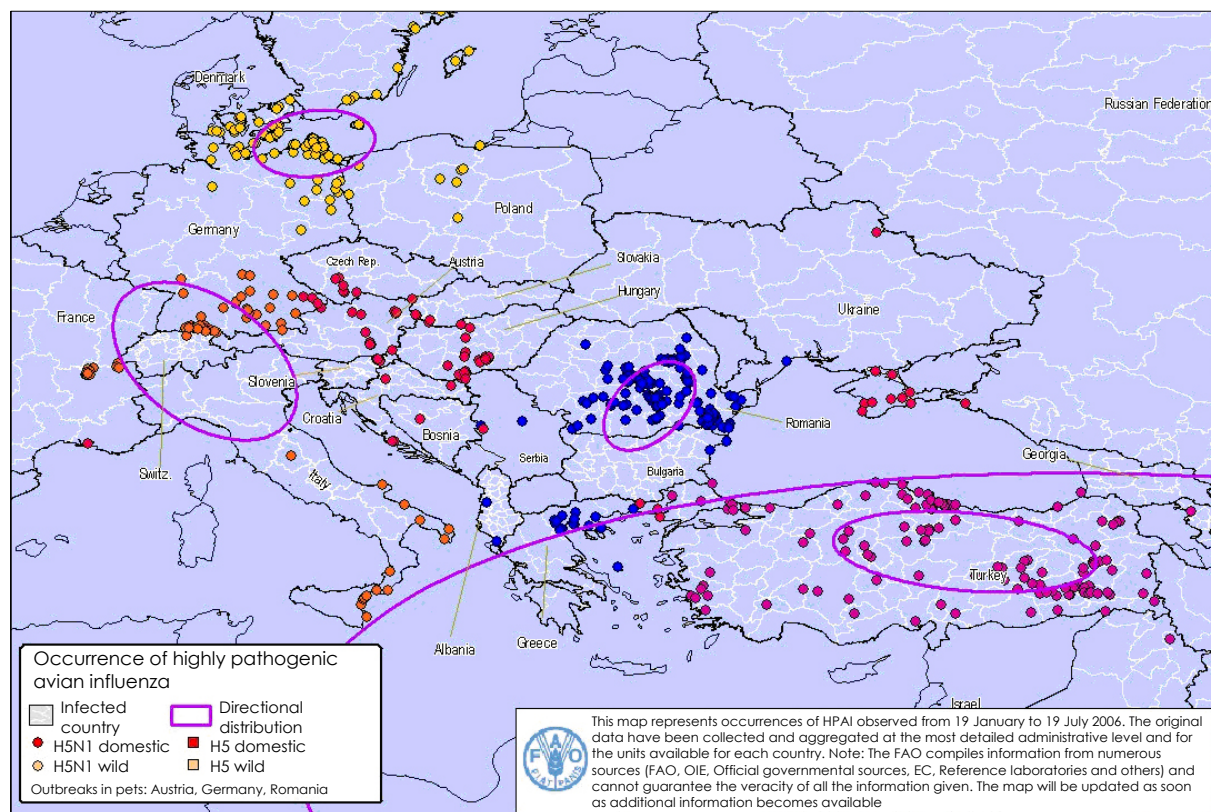

Figure 4
Directional distribution using standard deviational ellipses of outbreaks grouped by using different colours
Note the coloured dots that reflect data cluster cases independent of the species in which the disease is diagnosed

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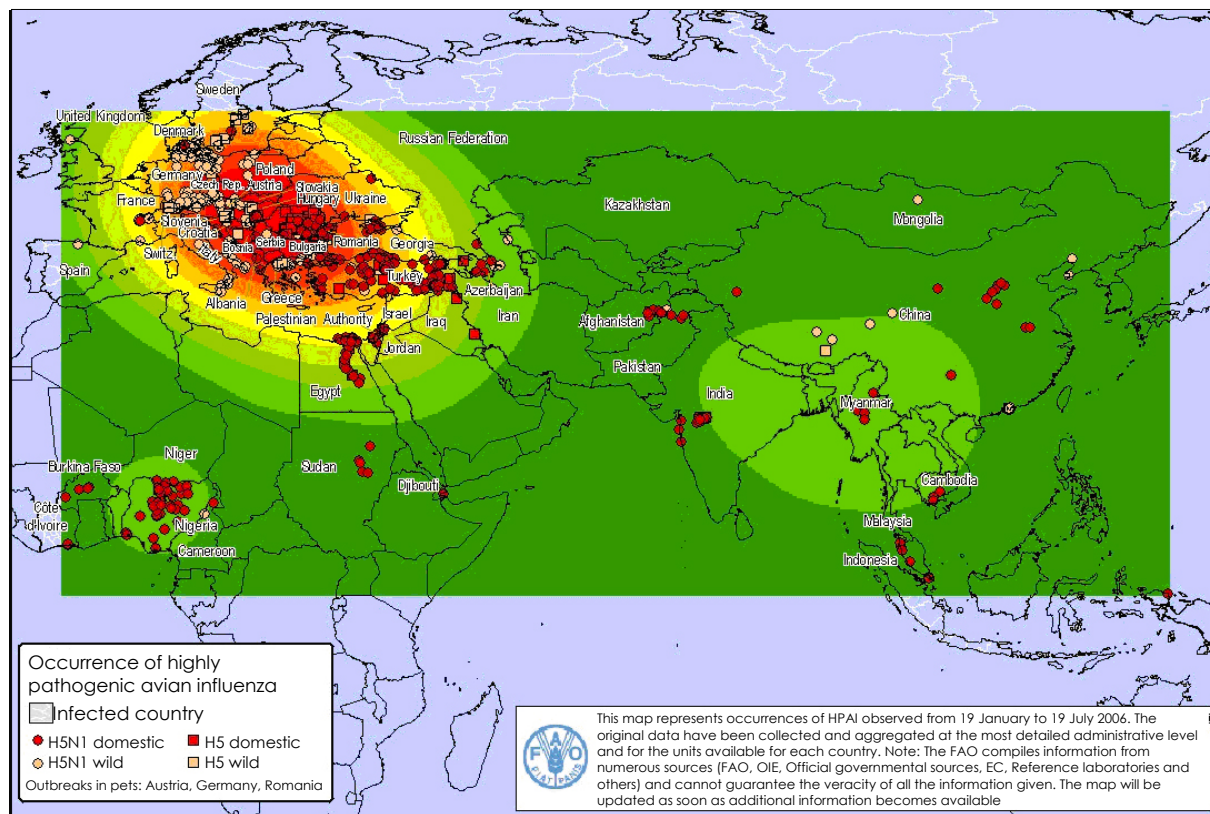Vincent Martin, Lorenzo De Simone & Juan Lubroth

Figure 5
Intensity of highly pathogenic avian influenza occurrence, January-July 2006

South-East Asia towards Central Europe and West Africa. However, the information provided by maps must be analysed with caution to avoid misleading interpretation. In this particular case, the apparent shift in the epidemic epicentre in Europe could be the consequence of better surveillance systems and increased case reporting.

Three-dimensional (3D) representations can also lead to a better understanding of the ecological and topographical features associated with the presence of disease and may help in the assessment of possible disease spread (Fig. 6).

Indeed, through a 3D display of natural features, such as topography, GIS may provide an insight into the spatial patterns of outbreak distribution and thus lead to rational intervention strategies. In the case of Pakistan and Afghanistan, it is clear that outbreaks extend along the valleys outlined by major topographic relieves (Fig. 7). It is commonly known that trade is conducted between the villages of the valleys, suggesting that HPAI
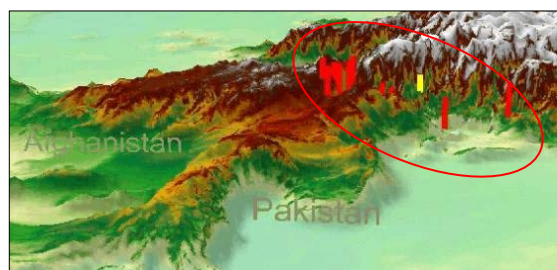

Figure 6
Three dimensional rendering of a digital elevation model and overlay of highly pathogenic avian influenza outbreaks in Afghanistan

outbreaks might be driven by the commerce in the area of interest. It also shows that outbreaks in both countries belong to the same ecosystem and that diseases do not recognise political or administrative borders. Finally, a map animation (Fig. 8) of temporal spread of an avian influenza outbreak can also have a strong visual impact, showing the rapid spread of the disease over wide geographic areas and distances.

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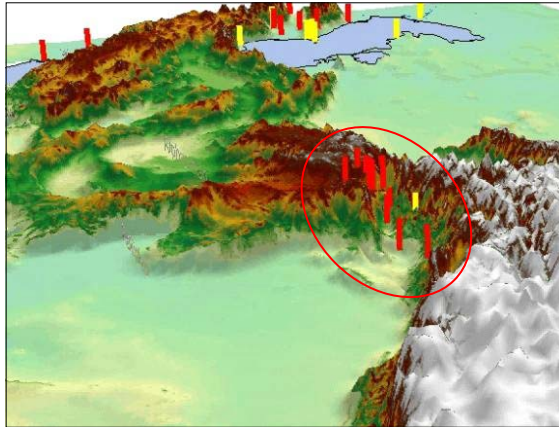a focus on highly pathogenic avian influenza

Figure 7
Three dimensional rendering of a digital
elevation model and overlay of highly
pathogenic avian influenza outbreaks in Iran

These examples show the importance of GIS in
revealing spatial or spatial-temporal patterns
that can subsequently be used in the
development of more rigorous causal
hypothesis tests. Among the most important
exploratory methods for epidemiology are
methods that identify space-time clusters or
'hot spots' of disease. Maps are used to display
the locations of significant clusters, showing
the proximity of clusters to hypothesised
environmental threats, such as the presence of
wetlands or rice fields as potential risk factors
for the emergence of avian influenza (4).
Furthermore, exploratory tools may be used to
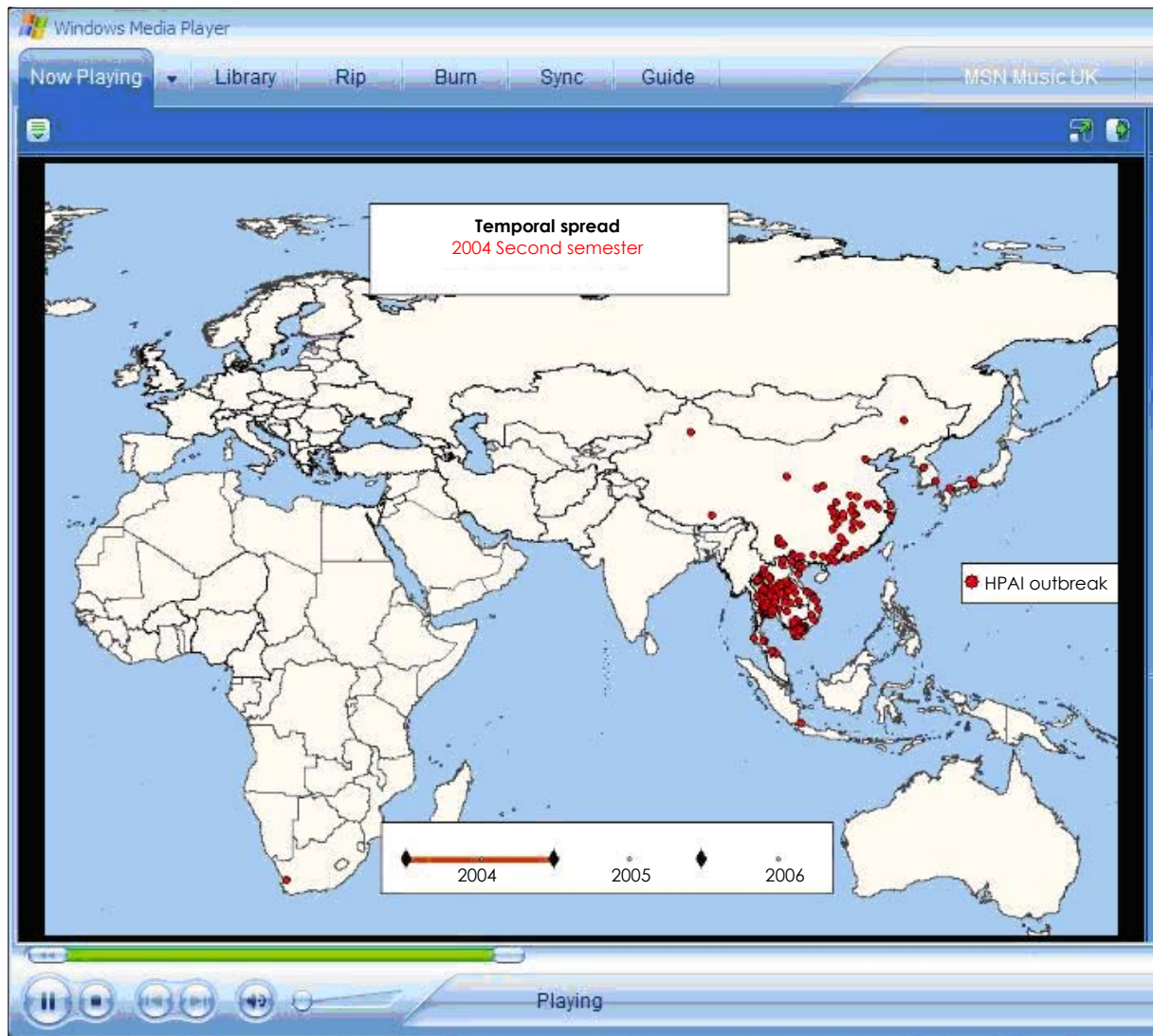identify areas (zones or districts) of high

Figure 8
Computer monitor running an animated map where disease occurrence in geographic space appears
over a time period (in this case, highly pathogenic avian influenza between 2004 and 2006)

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disease prevalence that can be mapped using a variety of methods which may rely on ratio measures between disease occurrence and the actual area of each district, or on probabilistic mapping to show the statistical significance of disease prevalence rates, using techniques such as the Bayes method that aims to smooth rates values towards regional average values.

Several of these analytical techniques have been applied to explore the emergence, spread and maintenance of HPAI in Asia. They contributed significantly to a better understanding of the disease epidemiology underlining the role of specific animal production systems and ecological conditions (6, 8).

Geographic information systems: a powerful tool applied to disease modelling and risk mapping

Once possible patterns or associations are detected or become apparent through ESDA, a scientific hypothesis can be developed to explain these spatial patterns. The significance of such a hypothesis may be tested by means of inferential statistics resulting in the assessment of how much the mechanism (variable under study) is explained by the hypothesis that can account for the space-time pattern observed. Once a hypothesis is validated, predictions can be made for probable disease occurrence or maintenance and for the specific conditions involving clustering, environmental proximity, or time-space spread forecasting. A single or a group of hypotheses may emerge that will lead to the design of a disease model of different complexities. There is a large spectrum of models that can be classified according to their conceptualisation, to the nature of input data, or to the type of output. However, the final goal of almost all prediction models is to support targeted actions, including those of outbreak control, risk mitigation or prevention.

When selecting an appropriate model, one must first consider the available knowledge of the phenomenon studied at the present time (a variable). Generally, the less the phenomenon is known scientifically speaking, the more flexible a model should be. A deterministic

model based on complex differential equation which may be applied to describe the movement of a solute in the vadose zone in hydraulics may not be at all suitable to describe the stochastic movement of wild birds that can become potential vectors of a given disease. Instead, a qualitative model that could be data-driven or knowledge-driven might be a more appropriate solution to the wild bird example, thus resulting in risk rankings or results in terms of probability or odds. The spatial extent to which a model can be applied should also be taken into account. Complex ecological systems, socio-economic regimes and microclimates may all represent constraints or promoters for the introduction, spread and maintenance of a particular virus. Modelling the behaviour of pathogens such as HPAI that cover wide geographic areas, encompassing very different environments may become very difficult if not meaningless; however, modelling subsets of smaller areas might provide a better insight and may not be applicable outside the study area to other parts of the world. Overlay index models, weight of evidence and spatial regression are some of the tools available that are often built-in GIS software and that can be used for predictive scope according to modelling needs, data availability and/or quality, extent of the study area.

Highly pathogenic avian influenza epidemiology in South-East Asia

Following the emergence and spread of the HPAI H5N1 strain from South-East Asia, the FAO coordinated several studies that included the use of GIS and remote-sensing techniques to identify the epidemiological features in specific ecosystems of Asia. The regional exploration of risk factors is recognised as having played an important role in providing a preliminary understanding of the ecology of the 2004 epidemic in poultry. Various exploratory analyses representing poultry density, water bodies, land cover and irrigated lands were used in a GIS, together with reported HPAI outbreaks, to identify

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hypothesised relationships with environmental risk factors. Due to limited data in 2003 and 2004 and the absence of a population census in risk areas, these relationships could not be explored using full and more accurate statistical methods. However, the methods used still gave an early indication of possible relationships that existed between outbreaks, irrigated lands and areas of low to medium poultry population densities. These relationships were further explored through national studies conducted in Thailand and Vietnam using logistic regression techniques and benefiting from the availability of national disease outbreak datasets which were much more accurate than the global dataset used for the above preliminary exploration. Both studies highlighted the importance of farming management practices and more particularly the role of free-ranging ducks in the occurrence and maintenance of viral infection.

In Thailand, a preliminary indication of the involvement of ducks raised in free-range systems was provided through the mapping of chicken outbreaks superimposed on the free-range duck populations, as well as the opposite (outbreaks in ducks in relation to chicken production areas). These relationships, including a broader range of risk factors, were further explored through regression logistic models. In Vietnam, two main clusters of infection were detected in the south and the north of the country and were related to the two main river systems, namely: the Mekong Delta in the south and the Red River Delta in the north. During the second wave of outbreaks in 2005, most outbreaks occurred in the south of the country where duck production is predominant. Logistic regression was used to investigate the role of various risk indicators, including waterfowl distribution, terrestrial poultry density, type of farming systems, degree of poverty and crop production. Interestingly, a strong correlation between outbreak locations and rice field production, as well as the increase in the percentage of irrigated lands was identified. In these studies, geospatial analyses demonstrated that free-grazing ducks played critical role in the epidemiology of the disease

in Thailand and Vietnam, both in terms of HPAI emergence and spread. In a subsequent study, the geographic association between free-grazing duck census counts and current statistics on the spatial distribution of rice crops in Thailand, in particular the crop calendar of rice production was explored. The analysis was conducted using both district level rice statistics and rice distribution data predicted with the aid of remote sensing, using a rice detection algorithm. Results indicated a strong association between the number of free-grazing ducks and the number of months during which second crop rice harvests take place (7), as well as the rice crop intensity as predicted by remote sensing. These results confirmed that free-grazing duck husbandry was strongly driven by agricultural land use and rice crop intensity and that this latter variable can be readily predicted using remote sensing. Analysis of rice cropping patterns in other countries may provide an indication of the location of populations of free-grazing ducks in other countries with similar mixed duck and rice production systems and less detailed duck census data (4).

Highly pathogenic avian influenza in Europe

When the disease first reached the European land area of the Eurasian land mass, explorative disease modelling was performed using the weight of evidence approach that produced a final H5N1 risk potential map (Fig. 9). The disease pattern was very different from that observed earlier in Asia and gave much more prominence to the role of wild birds, some species of which appeared to be severely affected by the disease. Several maps were combined using a weight of evidence model to predict H5N1 potential in a study area defined by countries bordering the Black Sea. The model used the spatial distribution of H5N1 outbreak occurrences to calculate a multi-map signature for a H5N1 outbreak, which was then employed to map areas at higher risk of experiencing H5N1 outbreaks. In the simulation outputs, H5N1 risk varies from very low in the majority of cases, medium in
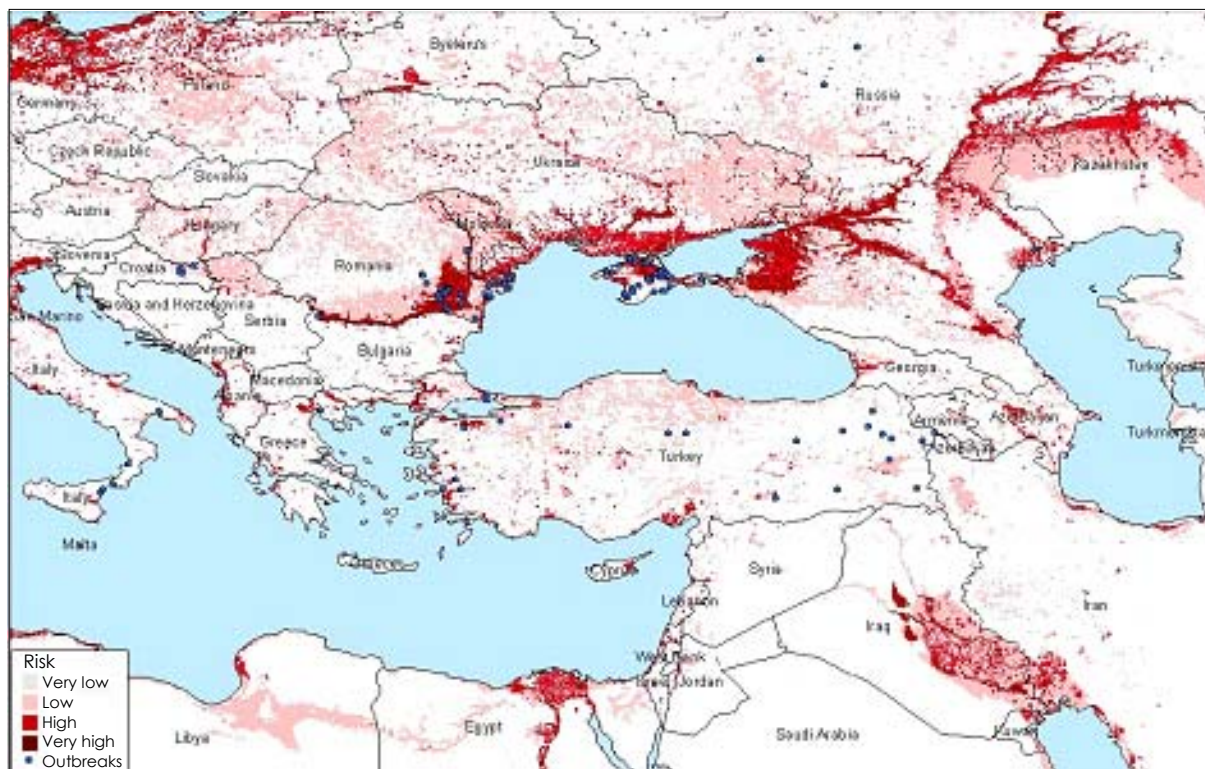
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Figure 9
Risk probability map for Central Europe based on poultry density, land use, distance to wetlands and
elevation above sea level, October 2005-10 February 2006

some areas and very high in a small number of cases.

The interpretation of the results should be made as follows: if an outbreak was to occur in the study area, then the probability would be less than one out of ten that it would occur in the low risk class, from one to two in the medium risk class, from five to eight in the high risk class. To achieve the final result in terms of a H5N1 potential map, statistical measures were conducted previously in an attempt to quantify the correlation between H5N1 outbreak location and single economic-environmental variables resulting in high correlation values for poultry density, proximity to perennial wetlands and land use.

In weight of evidence models, the log of the posterior odds of an outbreak occurrence lying within a unit area is determined by adding a weight for each input map to the log of the prior odds. The ultimate product is a map of posterior probability, or H5N1 potential. When the input maps are binary, the weight added is either W+ (binary pattern present) or W− (binary pattern absent). The variances of

weights enable the calculation of an uncertainty map, which is augmented further in areas where one or more of the input maps is missing. The strength of association between the input map and the H5N1 occurrence points is expressed as a contrast C = W+ –W–, and can be tested by estimating the variance $\sigma(C)$. The weights are calculated as log ratios of conditional probabilities. The model assumes that the input maps are conditionally independent of one another with respect to H5N1 outbreak points. This assumption is tested by pair wise tests and by an overall comparison of model predictions with observations, using all input maps. One of the principal advantages of such a method is the fact that it is objective, and avoids the subjective choice of weighting factors, as in the index overlay method, for example (2).

Conclusion

Understanding of the different ways in which soil, water, climate, plants, animals and people interact are at the heart of the FAO mandate to assist developing countries in their effort to

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increase food production and to provide nutritional security and safety. GIS technology provides the possibility of combining and integrating different sources of geographic information. An additional value of this technology lies in its capacity for modelling: constructing models of the real world from digital databases and using these models to simulate the effect of a specific process over time for a given scenario. Modelling is a powerful tool for the analysis of trends and identification of factors that affect them or for showing the possible consequences of planning decisions. This is why the FAO and more particularly its EMPRES programme has been using the technology for over 10 years, both at its headquarters in Rome and in many field projects in member countries. Since the beginning of the HPAI crisis in 2003, GIS have been critical to identify the role of specific risk factors in the evolution of the epidemic and to the implementation of corrective measures to curb the spread of the disease.

As part of the framework of global early warning systems for the control of TADs, there is an ever increasing scope for gathering and integrating information of predictive value through image analysis of remotely collected data of various types, such as vegetation mix and growth patterns, which can then be used to target ground information at sentinel sites which are most likely to yield representative (typical mix of herders) or indicator information (areas subject to flooding, those where particular feed types are cultivated). By using remote sensing to select sites at which to on-ground interviews and sampling can be conducted, a comprehensive data set can be accumulated and used to develop statistically valid indicator variables which can be measured in place of the variable of interest, and also provide a low-cost guide to disease developments. Through the appropriate use of these various techniques, it is becoming more practical to identify emerging patterns of disease early to enable the implementation of disease prevention and control measures, using economic methods to determine what mix of measures is most cost-effective.

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