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**THE RISK OF DISPERSAL OF THE HIGHLY
PATHOGENIC AVIAN INFLUENZA VIRUS H5N1
BY *ANSER ALBIFRONS ALBIFRONS* IN EUROPE**

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The risk of dispersal of the highly pathogenic avian influenza virus H5N1 by *Anser albifrons albifrons* in Europe

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Abstract

Three different kinds of influenza viruses can be distinguished: A, B and C. Only viruses of the former kind have the potential to develop into a pandemic through point mutations and reassortment. Since 1997 the highly pathogenic avian influenza A H5N1 virus has been spreading across the world, not only causing numerous fatalities amongst poultry and wild birds, but also some amongst domestic and wild felids and humans. At present the virus can be found in Asia, Europe and Africa. Though the virus primarily remained in Asia till the end of 2005, most outbreaks in 2006 have occurred in Europe. The role of wild birds in the possible dispersal of the H5N1 virus is still under debate, though (illegal) poultry transportation is definitely responsible for some spread of the virus. In this preliminary study the chance of dispersal of the H5N1 virus by a migratory goose species, the White-fronted Goose (*Anser albifrons albifrons*), in Europe is determined through spatial and probabilistic analyses. The White-fronted Goose breeds in the arctic tundra of Siberia and winters in Europe and west Asia, though the further eastwards breeding population winters in east and southeast Asia. Using a GIS model and Bayesian Networks it was determined that there is a considerable risk of White-fronted Geese contracting an infection and consequently spreading it along their migratory route and even passing it on to chickens, the latter probably through other H5N1 high risk wild bird species. The main risk factors for White-fronted Geese are the infection already being present in a country along the migratory route due to a previous outbreak or the geese being infected by other H5N1 high risk wild bird species, which occur in the staging and wintering sites together with the White-fronted Goose. Studies on the exact values of infection chances and transmissibility of the virus still need to be performed though and a higher spatiotemporal resolution of this study would be desirable as well.

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1. Introduction

1.1 Influenza viruses

Influenza viruses are distinguished in three different kinds: A, B and C. Though infection with the latter two will not result in more than a minor illness, the former has the potential of causing a pandemic (Allwinn & Doerr 2005, Nicholls 2006). Influenza A viruses contain an RNA strand composed of eight segments, with one gene per segment. Two of these genes encode for two surface antigens, namely hemagglutinin (HA) and neuraminidase (NA). There are 16 known subtypes of the former (H1 to H16), with H1, H2 and H3 being found in human influenza viruses; the latter has nine known subtypes (N1 to N9). All of these subtypes can be found in wild bird populations. Antigenic drift (point mutations) or antigenic shift (reassortment, where two different influenza strains are combined) create variation, enabling the virus to stay ahead of the host's immune system.

1.2 Background on highly pathogenic avian influenza A H5N1 virus

At present the highly pathogenic avian influenza (HPAI) A virus H5N1 is spreading across the world, causing fatalities amongst poultry, wild birds, domestic and wild felids (Kuiken *et al.* 2004, respectively Keawcharoen *et al.* 2006) and humans. It first caused an outbreak among geese in Guangdong Province, China, in 1996 (Xu *et al.* 1999). Through reassortment with other avian viruses it mutated into the strain that caused an outbreak amongst poultry in Hong Kong in 1997 and 18 human infections, six of which ended fatally (Hoffmann *et al.* 2000, Nguyen *et al.* 2005, Webster *et al.* 2002, Xu *et al.* 1999). Though the outbreak was stopped by slaughtering all poultry in Hong Kong, the virus continued to circulate.

In 1999 the H5 gene of the 1997 H5N1 virus was found in geese from Guangdong province, China (Cauthen *et al.* 2000). In 2000, ducks and geese from farms in Guangdong province, which were being exported to Hong Kong, were found to have three different subtypes of H5N1: a direct descendant of the 1996 goose virus, a subtype isolated from domestic ducks and a subtype formed through reassortment with other aquatic avian influenza viruses (Guan *et al.* 2002b). Webster *et al.* (2002) also found H5N1 in asymptomatic geese that were being exported from southeastern China to Hong Kong in 1999 and 2000. From 1999 through 2002 HPAI H5N1 was also found in asymptomatic ducks in the coastal provinces of China, between Guangdong and Shanghai (Chen *et al.* 2004).

The virus was even found to be circulating outside of Hong Kong and the adjacent coastal provinces of mainland China. In Hanoi, Vietnam, multiple subtypes of H5N1 were found to be circulating in asymptomatic ducks and geese late 2001, which were 98% similar to those present in Hong Kong waterfowl in 2000 and 2001 (Nguyen *et al.* 2005). Additionally Okazaki *et al.* (2000) found that duck populations were maintaining various influenza viruses in their nesting areas close to the arctic Circle in Siberia, enabling reassortment and creation of precursors of possible future pandemic influenza viruses.

In May 2001 a reassortant subtype of HPAI H5N1 caused another outbreak amongst chickens from live bird markets in Hong Kong, again leading to the slaughter of all poultry in Hong Kong (Guan *et al.* 2002a, Laver & Garman 2001, Webster *et al.* 2002). Late 2002 the third outbreak of HPAI H5N1 occurred amongst wild birds and waterfowl in parks in Hong Kong (Ellis *et al.* 2004, Normile 2004). It was not until February 2003 though, that H5N1 caused two human infections, including one fatality, again. This time it concerned a father and son in southern China (Guan *et al.* 2004). After these incidents the virus emerged more frequently, manifesting itself in three waves of outbreaks throughout various countries (WHO 2006).

During the first wave, that lasted from mid-2003 till mid-March 2004, the virus caused outbreaks amongst poultry in the Republic of Korea, Vietnam, Japan, Thailand, Cambodia, Lao PDR, Indonesia and China, appeared to be able to infect and kill wild felids (Keawcharoen *et al.* 2006)

and resulted in 12 cases of human infection in Thailand (8 of which fatal) and 23 cases in Vietnam (16 of which fatal) (WHO 2006). Among the Vietnam cases there were two family clusters in which it was not possible to rule out human-to-human transmission (Hien *et al.* 2004).

The second wave of outbreaks started in June 2004 and lasted till November 2004. During this wave there were outbreaks amongst poultry in China, Indonesia, Thailand and Vietnam again. New outbreaks amongst poultry were reported by Malaysia. The H5N1 virus was found to have become endemic in poultry (Li *et al.* 2004) and increasingly lethal to mammals (Chen *et al.* 2004). It seems to be the first influenza A virus capable of causing severe disease in domestic cats (Kuiken *et al.* 2006). H5N1 viruses were also isolated from dead migratory birds, indicating that they might be involved in the spread of the virus (Li *et al.* 2004). During this wave the WHO confirmed 5 human cases (4 fatal) in Thailand and 4 cases (all fatal) in Vietnam.

The third wave started in December 2004 and is still continuing at present. Besides recurring poultry, wild bird and human outbreaks in the previously mentioned countries, new outbreaks of H5N1 were reported for poultry and migratory birds in Russia and Kazakhstan mid-2005. New outbreaks in migratory and wild birds were reported by Mongolia (mid-2005), Croatia (October '05), Kuwait (December '05), Azerbaijan (February '06), Denmark (March '06) and from February 2006 till present many cases of H5N1 in dead swans (Bulgaria, Greece, Italy, Iran, Austria, Germany, Hungary, Slovakia, Bosnia-Herzegovina, Georgia, Serbia-Montenegro, Poland, Czech Republic and UK) and ducks (France, Sweden and Switzerland) were reported. New outbreaks amongst poultry were reported by Turkey and Romania in October 2005, by Ukraine in December 2005, in February 2006 by Nigeria (being the first African country to get hit by H5N1), Egypt, India, France (being the first European Union's country with infected poultry) and Niger and in March 2006 by Albania, Cameroon, Myanmar, Afghanistan, Israel, Pakistan, Jordan, Burkina Faso and Germany. Germany found H5N1 in 3 deceased domestic cats, Austria found it in 3 healthy cats and Sweden found it in a mink. New human cases were reported by Cambodia, Indonesia, China, Turkey, Iraq, Azerbaijan and most recently by Egypt, raising the total number of confirmed human cases reported to the WHO since the onset in 2003 to 192 (109 fatal) on April 6th 2006.

1.3 H5N1 at present - possible consequences for humans and poultry

At present the state of H5N1 is classified as phase 3 of pandemic alert in the WHO global influenza preparedness plan. This phase is characterized by the presence of a new animal virus, that is causing human cases as well, but which still has not achieved any, or merely very limited, human-to-human transmission. People have already been fearing the mutation of H5N1 into a virus of pandemic proportions for some time (amongst others Ferguson *et al.* 2004, Laver & Garman 2001, Li *et al.* 2004, Okazaki *et al.* 2000), especially since this is the first avian influenza virus to directly infect humans, without infecting pigs first for instance (Allwinn & Doerr 2005, Kaiser 2004). Though the Asian 1957 and Hong Kong 1968 pandemics (caused by the reassortant H2N2 and H3N2 subtypes respectively) were relatively mild, with the latter killing about 1 million people, the "Spanish flu" pandemic of 1918 (caused by the H1N1 subtype) infected half of the world's population (1.9 billion at the time) and killed between 20 and 100 million people (Allwinn & Doerr 2005, Enserink 2004a, Laver & Garman 2001, Nicholls 2006). The risk of human-to-human transmission seems to be lower than previously suspected, though. Recent research has shown that, unlike human influenza viruses, the H5N1 virus attaches itself to receptors in the lower respiratory tract, thus making spread of the virus through coughing and sneezing less likely (Riel *et al.* 2006, Shinya *et al.* 2006).

The risk for poultry and even wild birds is still great though. By October 2005 already over 150 million birds had died or been slaughtered since the onset of the H5N1 avian influenza outbreaks (Allwinn & Doerr 2005), and, considering the additional amount of outbreaks since then, this is likely to have become much more in the meantime. Though it has been suggested that the spread of the H5N1 virus seems to be following migratory routes (Chen *et al.* 2005, Ellis *et al.* 2004, Li *et al.* 2004, Liu *et al.* 2005, Normile 2005b), the role of migratory birds in the spread of the virus is still under heavy debate. Especially the role of (il)legal transport of poultry and poultry

products should not be ignored, when examining factors that could contribute to the spread of the H5N1 virus.

1.4 Possible candidates for the spread of H5N1

There are numerous examples of the role human activities could play in the spread of the highly pathogenic avian influenza (HPAI) H5N1 virus over seemingly improbable distances (Melville in Normile 2005b). For instance, the HPAI H5N1 virus has been found in duck meat that was being exported to Japan from the Chinese Shandong Province in 2003 (Mase *et al.* 2005) and in duck meat exported from Shanghai Province to South-Korea in 2001 (Lu *et al.* 2003, Tumpey *et al.* 2002). Poultry movement from Guangxi seems to be the cause of the introduction of the H5N1 virus in Vietnam (Chen *et al.* 2006) and an outbreak amongst poultry in Tibet in January 2004 was caused by transportation of infected chickens from Lanzhou, China, 1500 kilometers away (Normile 2005a). Examples of illegal transportation of infected birds include smuggling of infected fighting cocks and doves into Malaysia (Sims *et al.* 2005, respectively Anon 2005 in Sims *et al.* 2005), smuggling of infected mountain hawk eagles from Bangkok into Belgium (Enserink 2004b) and ducks into Taiwan (Li *et al.* 2004).

There are also indications that poultry could have played a greater role in the outbreaks of HPAI H5N1 than wild birds. Shortridge (1999) found that, in Hong Kong from December 23rd till 29th 1997, the percentage of H5N1 infection was 19.5% in chickens and only 2.4 and 2.5% in ducks and geese respectively. Combined with the finding by Seo & Webster (2001), that prior infection with H9N2 avian influenza can make chickens asymptomatic carriers of H5N1 capable of shedding the virus, this makes it likely that poultry were responsible for the outbreak amongst humans in 1997 (Shortridge *et al.* 1998). This notion is also supported by Perkins & Swayne (2002). Even though they found high morbidity of the 1997 HPAI H5N1 in geese, it is not likely that these birds played a major role in the transmission to the live bird markets, as some signs of disease would have been expected in infected geese prior to the outbreaks. It has also been established that H5N1 viruses have become endemic in domestic poultry in southeast Asia and have even evolved into distinct regional sublineages. This suggests transmission through poultry and poultry products as the major mechanism through which the H5N1 virus manages to spread and persist in this region. If continued reintroductions by wild birds would have been responsible, there would not have been so many regional differences (Chen *et al.* 2006).

Even with outbreaks of HPAI H5N1 in remote locations, migratory waterfowl need not necessarily be responsible. On April 30th 2005 there was an outbreak amongst wild birds at Qinghai Lake, a remote, protected nature reserve in western China, resulting in the death of 6.345 wild birds (WHO 2006), 90 percent of which were bar-headed geese (*Anser indicus*). Chen *et al.* (2005) believe this outbreak was caused by a single introduction, presumably from poultry in southern China, and did not find any transmission of the virus between the migratory birds at the lake. Later the virus also turned up at a poultry farm in the same province (Normile 2005a). Others believe migratory wild birds can be blamed for this outbreak, stating that the H5N1 strain of Qinghai can be traced back to the H5N1 that was present in migratory ducks at Poyang Lake (Chen *et al.* 2006). This would indicate that H5N1 is circulating in migratory bird species (Normile 2006). Chen *et al.* (2006) even found HPAI H5N1 in asymptomatic migratory birds just before their migration.

Other indications for involvement of wild migratory bird species include the fact that, though various H5N1 subtypes exhibit a differing pathogenicity in ducks (Kishida *et al.* 2005), surviving asymptomatic ducks can shed the virus for a prolonged period of time (Hulse-Post *et al.* 2005, Sturm-Ramirez *et al.* 2004). Asymptomatic geese exhibiting rather long periods of viral shedding could also contribute to the dispersal of HPAI H5N1 (Webster *et al.* 2002). Outbreaks amongst chickens during the first wave in the beginning of 2004 occurred in those parts of the country that had lots of free-grazing ducks. This was also the case for the second wave of outbreaks in the second half of 2004, though subsequent outbreaks also occurred in areas with high chicken densities (Sturm-Ramirez *et al.* 2005). Additionally, Li *et al.* (2004) note that the timing and distribution of the outbreaks in China seemed to coincide with the winter migration to southern

China, though they add that it is not clear if H5N1 has become established in wild birds, contrary to the endemicity in poultry. Ornithologists, on the other hand, have shown that the outbreaks did not neatly follow any known migratory patterns and add that, had migration been responsible, the virus should also have turned up in Taiwan and the Philippines at the time (Normile 2005a).

In 2001 the H5N1 virus was also found in healthy geese and mostly ducks in Hanoi, Vietnam, but this strain was more related to the one that had caused the 1997 outbreak, than to the later ones responsible for the 2004 outbreak in Vietnam (Nguyen *et al.* 2005). Other arguments against involvement of migratory waterfowl include the fact that the Guangdong virus caused 40% mortality amongst geese (Xu *et al.* 1999) and that a high proportion of the H5N1 viruses is lethal to ducks (Sturm-Ramirez *et al.* 2005). Furthermore, HPAI H5N1 virus has only been found in migratory birds in areas where HPAI outbreaks had occurred amongst poultry and not outside of those areas (Lee *et al.* 2005). Sampling of tens of thousands of birds entering Hong Kong and crossing the Bering Strait has not found a single healthy wild bird carrying HPAI H5N1 and evidence has shown that migratory birds are killed nearly as efficiently by the virus (Normile 2005a).

It has been suggested that an as of yet unidentified species may be responsible for the spread of the virus. An outbreak at the remote Erkhel Lake in Mongolia in April 2005 seems to rule out human and poultry involvement. Samples taken from living and dead birds turned up HPAI in the dead birds, but not in the living ducks, gulls, geese or swans. This suggests that an unknown species had introduced the virus at Erkhel Lake and had been responsible for infecting the birds that had died (Suarez, respectively Sims in Normile 2005a). This notion is strengthened by the fact that swans have been dying of H5N1 in Europe in the beginning of 2006. Obviously the swans are not spreading the virus, as they are succumbing to it. They could have been infected by another aquatic species, though surveillance has failed to turn up any H5N1 in healthy birds in Europe (Normile 2006). The fact that the virus, which was continuously changing in the first couple of years, seems to have remained almost identical for nearly a year during its spread to Qinghai Lake, Mongolia, Turkey and even Nigeria, suggest that the virus has adapted to a host species in its highly pathogenic form (Enserink 2006, Normile 2006).

As of yet it is thus not clear which species is or are responsible for the spread of the HPAI H5N1 virus. Transportation of poultry and poultry products has at least played a role in the spread of the virus. Chen *et al.* (2005) fear the current H5N1 virus will establish itself in bar-headed geese (*Anser indicus*), like the 1996 Guangdong subtype had done at the time, enabling the virus to be carried along the migratory routes and spread even further. As geese have been found to be asymptomatic carriers of the virus in some of the previously mentioned studies, this study will focus on the chances that a migratory goose species, the White-fronted Goose (*Anser albifrons albifrons*), can contribute to the spread of H5N1 in Europe. This species is on the provisional list of the Standing Committee on the Food Chain and Animal Health (2005) of wild bird species that could present a higher risk for dispersion of avian influenza.

1.5 The White-fronted Goose

The White-fronted Goose has its breeding grounds in the arctic tundra pools and marshes of northern Siberia and western Russia (Ogilvie & Young 1998, Speek & Speek 1984). During the winters the species can be found in the open farmlands and steppes of western Europe, southeastern Europe, on the Black Sea coasts and in the Caspian Sea area (Bijlsma *et al.* 2001, Ogilvie & Young 1998). The total population size was estimated at 1.4 million during the 1990s, half of which occur in western Europe (Mooij *et al.* 1999, Ogilvie & Young 1998). Of the approximately 600,000 individuals that spend their winters in the North Sea and Baltic Sea area, 80% (or in severe winters even more than 90%) will spend them in the Netherlands (Bijlsma *et al.* 2001). White-fronted Geese can be found in the Netherlands from October till March, though the majority is found from December till February with a peak in January (Koffijberg *et al.* 1997).

2. Research objective and research questions

The research objective of this study is to determine the chance of the spread of highly pathogenic avian influenza H5N1 by the migratory White-fronted Goose *Anser albifrons albifrons* in Europe.

In order to be able to fulfill this research objective the following research questions will be addressed:

1. Which countries have exhibited H5N1 outbreaks?
2. What is the migratory route of the White-fronted Goose?
3. Which factors could influence the chances of White-fronted Geese contracting an H5N1 infection (e.g. habitat, behavior, other waterfowl present)?
4. What are the chances of the virus being sustained and passed along within the goose population and subsequently spread along their migratory routes?
5. What are the chances of the virus being spread to poultry?

3. Methodology

For the first three research questions, the locations of H5N1 outbreaks amongst wild birds, the migratory route of White-fronted Geese and the factors that could influence the infection of White-fronted Geese with the H5N1 virus were derived from literature. In order to be able to answer the last two research questions (4 and 5) concerning the chances of the virus being spread by White-fronted Geese along their migratory routes and the chances of the geese passing the virus on to poultry, the information gathered in the previous research questions was used in spatial and probabilistic analyses.

GIS models are very suitable for the prediction and analysis of the spread of phenomena, like infectious diseases, over space and time (Haggett 1994 in E.M.C.D.D.A., Cromley 2003). Thomas *et al.* (2004) used ESRI-model builder to compose monthly spatial risk maps of various infectious diseases lacking any specific occurrence data. Another example of an infectious disease of which the spatial and temporal dispersal and consequently outbreaks have been determined using GIS is bilharzia (schistosomiasis; Crump 2006, Math Ecology 2006). Various other epidemiological examples, like modeling and simulation of smallpox, West Nile virus, chronic wasting disease and even pandemic influenza can be found at Math Ecology's website.

Bayesian networks, which are probabilistic models, are also suitable for predicting and analyzing the spatial and temporal dispersal of infectious diseases like influenza, especially if occurrence data are not abundant or the mechanism is not yet fully understood (Abbas *et al.* 2005). West Nile virus is an example of an infectious disease for which both GIS- and Bayesian Network spatiotemporal models have been constructed in order to determine high risk areas (Wallis 2005, Forbes 2006 resp. Orme-Zavaleta 2006). Abbas *et al.* (2005) have also used Bayesian networks to model the spatial and temporal flow of diseases like pneumonia and influenza.

Thus both a GIS model and a Bayesian Network seem appropriate for determining the spatiotemporal risk of highly pathogenic avian influenza H5N1 dispersal by *Anser albifrons albifrons* in this study, especially since both have already been used to model the high risk areas of human influenza dispersal and both are suitable in cases where incidence data are lacking or not very abundant.

Besides the buffer distance of 10 kilometers around outbreak points, which was derived from the Animal Health and Welfare Department of the European Commission (2006b), and the buffer distance of 10 kilometers around the wetlands and inland waters (after Cramp & Simmons 1997, Niethammer *et al.* 1968, Mooij *et al.* 1999 in Madsen *et al.*), all values used in these spatial and probabilistic analyses are estimated guesses.

3.1 GIS model for determining the H5N1 risk of geese and poultry

In this model the extent and location of the H5N1 risk areas for White-fronted Geese were determined in Europe. This was done by determining where the outbreaks had occurred, assessing whether the geese passed through these locations and increasing the risk if other H5N1 high risk wild bird species happened to occur in the same sites. The result is a distribution throughout Europe of the risk of H5N1 infection for the White-fronted Goose. With this result the risk of the chickens at these locations was also determined. Thus both research questions 4 and 5 are dealt with.

ArcMap (ESRI ArcGIS 9.1) was used for the design and execution of the GIS model.

The input, process and output of the GIS model are given in Figure 1.

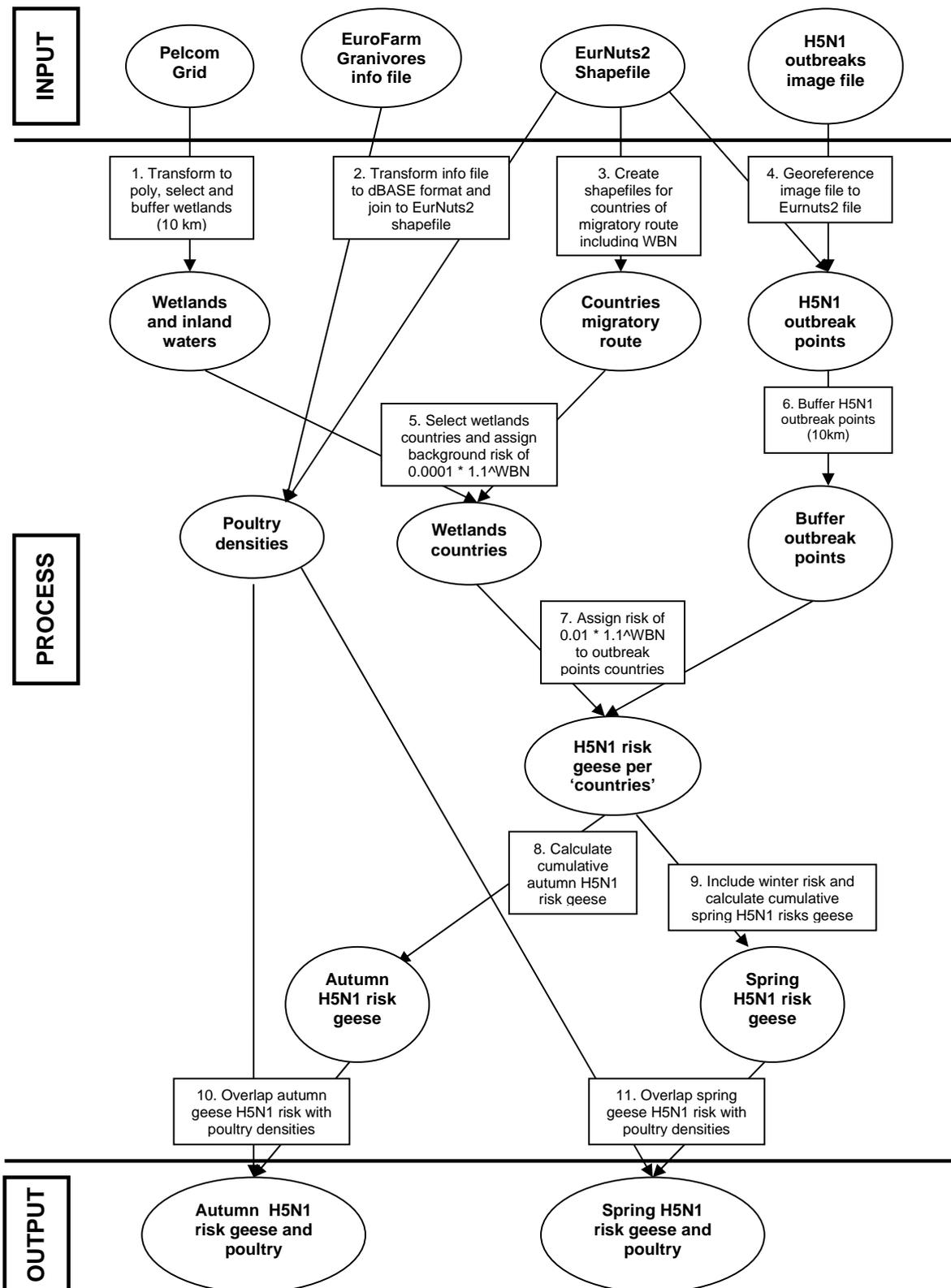


Figure 1. Overview of the input, process and output of the GIS model for determining the autumn and spring H5N1 risk for geese and poultry

3.1.1. Input files of the GIS model

The following input files were used in the ArcGIS model:

- Pelcom grid
- Eurostat NewCronos 2000 Eurofarm Granivores selection info file, containing information on granivores (pigs and poultry) in Livestock Size Units (LSU) for the European Nuts2 regions.
- EurNuts2 shapefile. This is a map of Europe which is divided into various administrative units of the European Union based on a hierarchical structure, with two letters denoting the country and two numbers denoting certain regions or provinces within this country (with the amount of numbers increasing with an increasing Nuts level, for example Nuts2 level data (two numbers) have a more specific subdivision than Nuts1 level data (1 number)).
- Image file containing the locations of the H5N1 outbreak points amongst wild birds, obtained from the Animal Health and Welfare department of the European Commission (2006a).

3.1.2 Process executed in the GIS model

The following steps were executed in process of the GIS model (see Figure 1):

1. The Pelcom grid is transformed from grid to poly and from the Albers conical equal area projection (WGS72 spheroid) to the 1927 North American Datum projection (Clarke 1866 ellipsoid) of the EurNuts2 file. In this step the wetlands and inland waters are also selected and a 10 km buffer is created around these.
2. The Eurofarm file Granivores_selectie_eu2000.xls is transformed to the dBASE IV file format using Microsoft Excel 2003 SP2. This file with information on the number of granivores (pigs and poultry) is consequently joined to the various European Nuts1 and Nuts2 regions of the EurNuts2 file. As the Eurofarm Granivores selection file was given per Nuts2 region for some countries, but for Nuts1 regions for the other countries, the EurNuts2 file was modified in ArcView GIS 3.3 (ESRI) to match this distinction. For the Nuts2 regions that were combined in order to form Nuts1 regions, the average number of livestock was calculated and assigned to the encompassing Nuts1 regions. As the livestock file is comprised of both pigs and poultry data, it is assumed that these are distributed proportionally among the various Nuts regions. As it is not certain how great a proportion of this total consists of poultry, the numbers were not used for calculations.
3. Creating shapefiles for the countries of the migratory route of the White-fronted Goose (*Anser albifrons albifrons*). The data on the migratory route were obtained from the website of BirdLife International (2006) by searching for those sites in the countries of the EurNuts2 file that contained passing or wintering White-fronted Geese. If the term 'passage' was used, the species was assumed to pass through these countries during their autumn and spring migration. If the term 'non-breeding' was used, it was assumed that the species wintered at these sites.

For the order in which the geese passed through these various regions and countries, Mooij *et al.* (1999; figure 5.3, page 97 in Madsen *et al.*) was referred to. This resulted in the geese entering Europe in Estonia, Latvia and Lithuania (countries 1), continuing towards various regions in Poland (countries 2) and then splitting up into 2 groups, namely the Baltic-North Sea group heading towards the Netherlands and Belgium (countries 3a) as wintering grounds and the Pannonic group heading towards the wintering grounds of the Czech Republic, Hungary, Slovakia and Slovenia (countries 4) after passing through various regions of Austria, Hungary and Slovakia (countries 3b)

(see Figure 2). The BirdLife International White-fronted Goose's migratory and wintering sites were selected from the EurNuts2 file, grouped for these 'countries' and saved as separate shapefiles. A list of the names and locations of these sites and their consecutive grouping is given in Appendix I.

A field was added to the countries' shapfiles using ArcView, in which the number of other wild bird species posing a high risk to the spread of H5N1 through their migration was noted (WBN; wild bird number). The species were derived from the Standing Committee on the Food Chain and Animal Health (2005) and the White-fronted Goose's BirdLife International sites were checked for the presence of these wild birds. Thus the total number of wild birds was obtained by adding the number of these high risk bird species present. The WBN for the various sites, with a specification of the species present, is given in Appendix II.

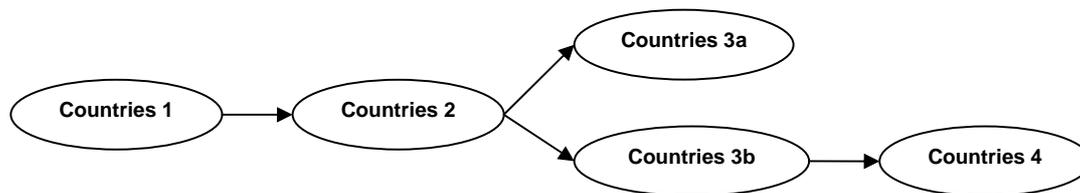


Figure 2. Autumn migratory route of the White-fronted Goose; the geese enter Europe at countries 1 (Estonia, Latvia and Lithuania), continue towards countries 2 (Poland), from there 91% continues towards countries 3a (the Netherlands and Belgium) to winter there and 9% migrates through countries 3b (Austria, Hungary and Slovakia) to winter in countries 4 (the Czech Republic, Hungary, Slovakia and Slovenia)

4. The H5N1 outbreak locations image file was georeferenced to the EurNuts2 shapefile using ArcMap, after which the outbreak points were traced to a point-shapefile in ArcView.
5. The background risk (0.0001) of the of the geese contracting an H5N1 contamination is added to the countries and corrected for the number of other H5N1 high risk wild bird species present (by multiplying with $1.1^{(\text{number of high risk wild bird species present})}$).
6. A 10 kilometer buffer is created around the H5N1 outbreak points.
7. In this step the buffered wetlands are selected for the various countries along the migratory route. Where these overlap with the 10 km buffer around the H5N1 outbreak points, a risk factor of 0.01 is assigned and corrected for the number of other H5N1 high risk wild bird species present (see above under 3). Combined with the background risk an average risk for these countries is obtained, which is transferred to the consecutive country along the migratory route by joining and consequently adding it to the background and outbreak risk of that country.
8. The various cumulative autumn risks of the spread of H5N1 by the White-fronted Goose are calculated per group of 'countries' of the migratory route, as it is assumed the White-fronted Geese take this risk along to the next country along the migratory route.

As the majority of the birds migrating from countries 2 heads towards countries 3a as opposed to countries 3b (91% and 9% respectively, based on Mooij *et al.* (figure 5.6 page 102 in Madsen *et al.* 1999) and BirdLife International 2006), the risks of H5N1 spread from countries 2 to countries 3a and 3b were corrected by multiplying them with this ratio.

9. The winter risk is calculated for the geese in countries 3a and 4 by multiplying the autumn risk by 1.5, as they will have an increased risk during this period due to their prolonged stay in these countries and their different behavior. The process for calculating the risk of H5N1 spread by migrating White-fronted Geese in spring is similar to that of the autumn process described above. The main differences are the fact that the order of the

countries is now reversed and that the spring risk is also added to the autumn or winter risk in order to obtain the total risk of the whole migratory period. The risks of countries 3a and 3b are corrected again, like in step 8, before incorporating them in the risk of countries 2.

10. The autumn H5N1 risks of the White-fronted Geese are combined with the poultry densities.
11. The spring H5N1 risks of the White-fronted Geese are combined with the poultry densities.

Due to a lack of countries from the EuroFarm granivores selection file, the final poultry H5N1 risk was obtained by multiplying the H5N1 risk of the White-fronted Goose by 5% (the chance of the geese transmitting the virus to poultry). Consequently a second final poultry risk was calculated by multiplying this White-fronted Goose's poultry risk by 1.1, 1.3 and 1.5 to the power of the number of wild bird species that occurred in the migratory sites with the White-fronted Goose and respectively posed a low, medium or high risk of passing the H5N1 virus on to poultry.

3.1.3 Output of the GIS model

The output of the GIS model is a file in which the autumn and spring H5N1 risk of the White-fronted Geese is displayed together with the poultry densities.

3.2 Bayesian Network for determining H5N1 risk of geese and poultry

Due to the different possibilities with Bayesian Networks, a Bayesian Network was designed for the migration of the White-fronted Geese in order to be able to answer research questions 4 and 5 as well. A basic model (Model 1) was designed of the autumn migration of the White-fronted Geese in which they have the chance to become infected with the H5N1 virus through the infection already being present in the country itself (due to a previous outbreak), other H5N1 high risk wild bird species (occurring together with the White-fronted Geese) being infected or because the geese themselves had already become infected in the previous country along their migratory route. In each country the geese also have the chance to pass the virus on to the local poultry population. This model was made more realistic by including influences of the other factors on each other, due to travel of people, poultry transportation, migration or dispersal of the other H5N1 high risk wild bird species and such (Model 2). The basic model was also run with the results of the GIS model as input values (Model 3) and this model was extended to include the wintering and spring migration as well (Model 4). In the last model (Model 5) only the geese and poultry were observed, but including the wintering and spring migration. Specific descriptions of these models and their different input values can be found below.

The first three models were constructed and run using Hugin Lite 6.7 and the default values of this program (Number of cases: 10000, Percent missing values: 5, Rule size: MCAR (as opposed to MAR)). As Model 4 and 5 both exceeded Hugin's limits concerning the number of variables used, Bayesian Network tools in Java (BNJ) 3.1 was used to construct and run these last two models. A disadvantage of BNJ is that chances smaller than 0.1% are noted as being 0.0% and thus no distinction can be made between the smaller chances. All chances calculated in BNJ are also given with a precision of merely one decimal place. This is why Hugin, which gives results with up to six decimal places, was used to run the first three models. BNJ seems to give the same results for these first three models though.

All models were run with the theoretically assigned values and rerun using the fact that outbreaks have indeed occurred in countries 2, 3b and 4 of the geese's migratory route, thus making the state of the variables of the chance of an infection being present in the wetlands of these countries 100% true.

3.2.1 Model 1 – A basic model for the H5N1 risk of geese and poultry

In this model (Figure) the process of H5N1 dispersal is modeled for the autumn migration as described in Figure 2. The chance of an H5N1 infection of geese is modeled as being dependent on the chance of an H5N1 infection already being present in the country (due to a previous outbreak), the chance of an H5N1 infection occurring in other high risk wild birds species and where applicable, the chance of the geese migrating into the country already having been infected in the previous country along the migratory route. For each country the geese are modeled to be able to pass the H5N1 infection on to the local poultry population or to the geese of the following country.

The same theoretical values were used for the Bayesian Networks as in the GIS model, namely of the geese having a background risk of 0.0001 (0.01%) of contracting the virus in the absence of direct risks and 0.01 (1%) when these are present.

Thus the following chances are used in this model:

- Chance of an H5N1 outbreak having occurred in the country 0.5%
- Chance of an H5N1 infection being present in the high risk wild bird population 0.5%
- Chance of chickens contracting an H5N1 infection:

through infected geese	5%
through background risk	0.01%
- Chance of geese contracting the H5N1 virus by infection in the previous country, the infection being present in the current country (due to an outbreak) or the virus being present in other high risk wild birds:

if all three are true	3%
if two are true	2%
if one is true	1%
if none are true	0.01%

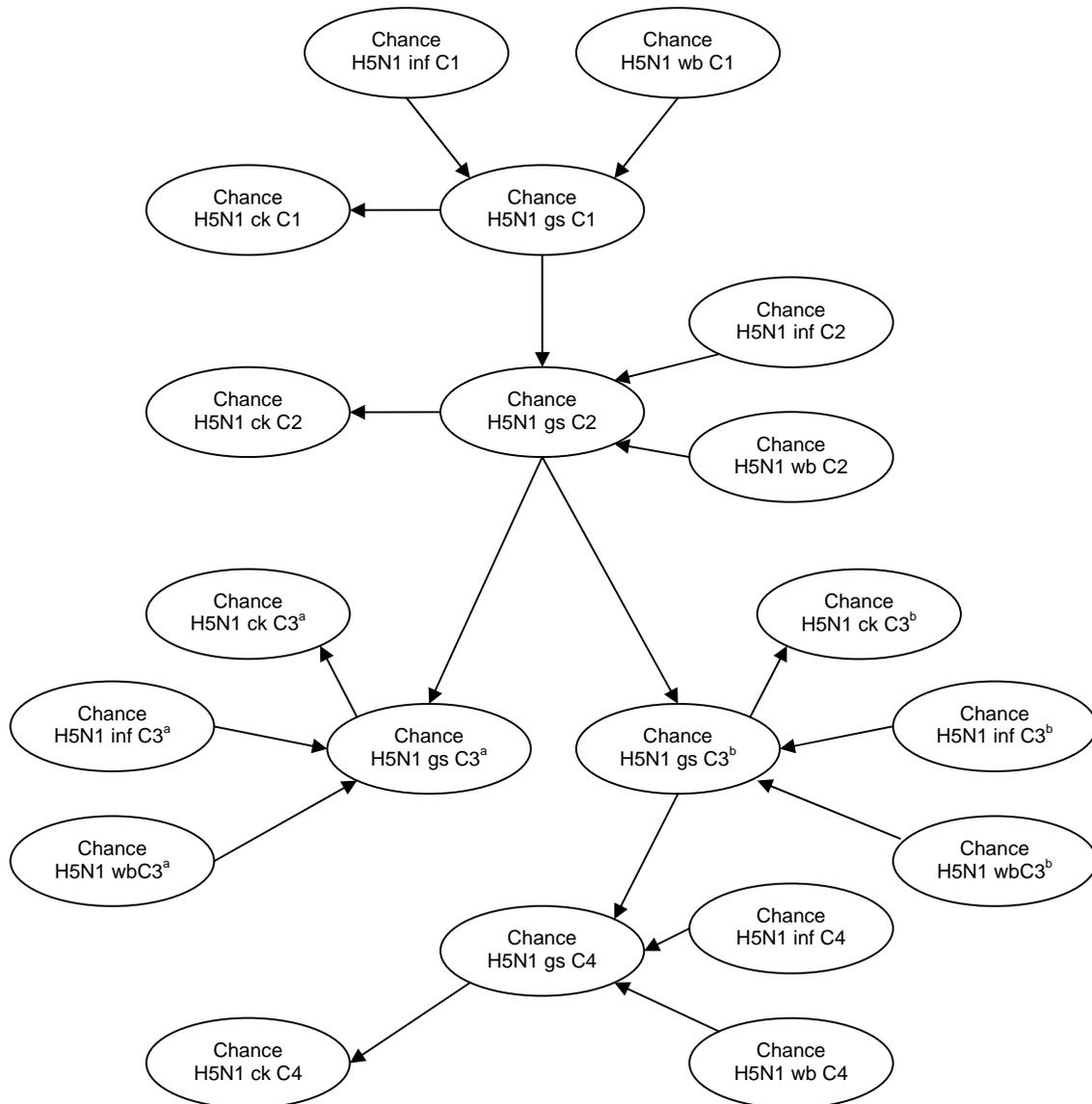


Figure 3. Layout Bayesian Network Model 1. C = countries, inf = infection being present in countries themselves (outbreak), wb = high risk wild birds, ck = chickens

Model 1 was also used to test the effect on the poultry and the input factors if an outbreak were to occur amongst the geese of one, more or all of these countries. This resulted in 31 different scenarios of outbreaks occurring amongst the geese of these various countries. This model will be referred to as Model 1g.

3.2.2 Model 2 – A more realistic model for the H5N1 risk of geese and poultry

In this model the factors other than the geese population are also considered to be influenced by the risks of those factors in the previous country. In this model it is thus assumed that chickens can pass on the virus to chickens of another country (through transportation of infected poultry or

poultry products), wild birds to other wild birds (through migration) and even countries to other countries (through for example human movements).

The following variations were made of the model:

- The basic variant, where only the aforementioned factors of the immediately previous countries influence these factors of the next countries, thus in a manner identical to the modeled migratory route of the White-fronted Geese (see Figure 2). In this variant chances were increased proportionally when the state of a factor of the previous country was found to be true. For example, the chance of an infection being present in countries 2 would be 1% for the chance of an infection in countries 1 being true and 0.5% (as in Model 1) for it being false.
- a. A variant where all the previous countries influence all the next countries (so with countries 1 influencing all other countries and countries 4 being influenced by all countries), though Bayesian Networks are thusly limited that a factor (node) can not be influenced by a factor it is influencing itself. In this variant chances of a certain factor were increased proportionally in accordance with the number of previous states found to be true. For example, the chance of H5N1 occurring in wild birds in countries 3b is 0.5% as a basic state (all others being false), but is 1% for either the chance of H5N1 occurring in wild birds in countries 1 or in countries 2 being true and 1.5% for both of them being true.
- b. A variant similar to the basic variant of Model 2, with the only difference being that the chances of all factors, including those of the geese, were doubled for an additional factor being true, instead of merely being increased proportionally. Due to the limited amount of factors influencing other factors, this merely resulted in the chance of infection of some geese increasing to 4% instead of being 3%.
- c. A variant similar to variant a, which also exhibits doubling of chances for each additional previous factor being true, like Model 2b.

3.2.3 Model 3 – The basic model (Model 1) for the H5N1 risk of geese and poultry, using the outputs of the GIS model as input values

This model resembles Model 1. Instead of the theoretically assigned input chances (the wild bird number and the chance of an infection already being present in the country), the mean values as calculated by the GIS model were used. For the wild bird number, the background risk of 0.0001 was multiplied by 1.1 to the power of the the number of high risk wild bird species, like in the GIS model. For the chances of an infection already being present in the country, the risks as calculated for the geese in the GIS model were used.

3.2.4 Model 4 – Model 3 including wintering and spring migration

This model resembles Model 3, but the wintering and consequent spring migration is also included in the model. For the wintering it is assumed that a contracted infection in autumn will result in a 99.99% probability of the infection still being present in the geese population in the winter and 0.0001% of them contracting it if they had not already done so.

3.2.5 Model 5 – Model 4 with only geese and poultry

This model resembles Model 4, but it does not include the wild bird number and country infection factors. The mean chances of the geese contracting an infection, as calculated in the ArcGis model, were used for the chances of an H5N1 infection occurring in the geese. When joining the risks of countries 3a and 3b in countries 2, these risks are corrected for their ratios as mentioned under the GIS model. If merely one of the countries was found to be true, the spring geese risk for countries 2 was calculated as the mean plus the risk of the concerned country multiplied by its

accompanying correction ratio. If both were found to be true, both corrected risks were added to the spring mean of countries 2.

The input values of all of the chances used in these eight different versions of the basic model are given in Appendices IV.A-IV.H.

3.2.6 Additional model runs

Models 1, 2, 3, 4 and 5 (all basic models) were also run with the risk of an H5N1 infection being 95% for geese of a certain country, if an infection had been contracted in the previous country. For each additional factor being true (infection already present in country or wild bird number) an additional 1% was added and for an additional geese factor of another previous country being true (only for countries 2 during spring migration in Model 4) an additional 2% was added. This was done, as the risk of the geese passing the virus on (or actually taking it along) to the next country is basically 100% in the GIS model. The models were named 1a, a2 (as opposed to Model 2a, see above), 3a, 4a and 5a. An example of the resulting input values is given in Appendix IV.J for Model 1a.

4. Results & Discussion

The research objective of this study was to determine the chance of the spread of highly pathogenic avian influenza H5N1 by the migratory White-fronted Goose *Anser albifrons albifrons* in Europe by answering the following five research questions:

4.1 H5N1 outbreak locations

In June 2006 H5N1 outbreaks had occurred amongst wild birds in the following European countries: Denmark, Germany, Sweden, France, Czech Republic, Slovakia, Austria, Italy, Slovenia, Hungary, Greece, Romania and Bulgaria (Animal Health and Welfare department of the European Commission 2006). The locations of the outbreaks in these countries are given in Figure 4. These outbreak locations were used in the GIS model.

By July 2006 the virus had spread even further in these countries and to Scotland, Spain, Croatia, Bosnia and Herzegovina, Serbia and Montenegro, Albania and Turkey as well, with outbreaks amongst poultry in Sweden, Denmark, Germany, France, Romania, Serbia and Montenegro, Albania, Bulgaria and Turkey (WHO 2006). In the Netherlands, a possible infection with the H5N1 avian influenza virus has occurred in Northern Hawk Owls (*Surnia ulula*) in the Blijdorp zoo of Rotterdam during the first half of August 2006 (Meerhof 2006).

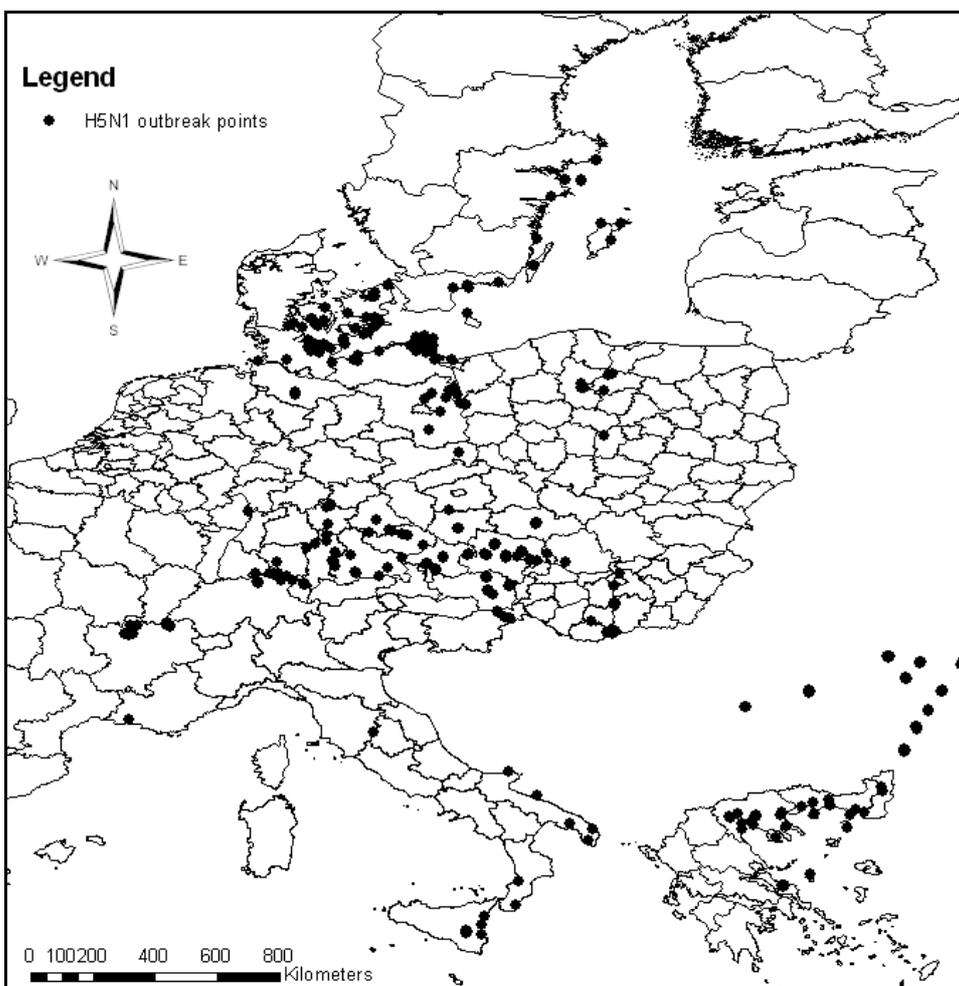


Figure 4. H5N1 outbreaks amongst wild birds in Europe till June 2006

The outbreak points (till June 2006) seem mainly restricted to coastal areas, with those occasional inland outbreaks seemingly occurring near rivers (for instance along the Elbe, Danube and Odra) and inland waters. This would suggest the involvement of waterfowl in the spread of the avian influenza virus. The countries in which outbreaks of the virus had already occurred in June are all countries in which the White-fronted Goose has migratory and wintering sites. The consequent spread in July, also to poultry, cannot be attributed to the White-fronted Goose though, as they still remain at their breeding grounds at this time of the year. This is not to say that another high risk wild bird species cannot be responsible for the spread or even humans directly or indirectly through transportation of infected poultry and such. The infection of the owls in the Blijdorp zoo also seems to have been caused by wild birds though, as no animals from Asia are allowed to be imported and all of the adult birds had been vaccinated (Meerhof 2006).

As can be seen in Figure 4, there are also H5N1 outbreaks that have occurred beyond the extent of the study area based on the Nuts 2 level data (mainly in Romania and Bulgaria). Due to the fact that these and other Balkan countries, besides Greece, are missing from the file, an important part of the Pannonic and Pontic population is missing, as Romania is an important staging and wintering site for these populations. Especially since numerous outbreaks have occurred in this country (168 amongst poultry from the end of 2003 to August 2nd 2006, making it the European country with the greatest number of outbreaks amongst poultry and ranking it as the fifth country worldwide; OIE World Organization for Animal Health 2005a), of which at least two were in the vicinity of small populations of approximately 530 and 2300 individuals of White-fronted Geese (OIE World Organization for Animal Health 2005b respectively 2005c), this could have had great influences on the calculated chances of dispersal of H5N1 by White-fronted Geese in Europe. Thus a study with a complete detailed map of Europe would be recommended.

4.2 The migratory route of the White-fronted Goose

The White-fronted Goose breeds in the arctic tundra from the Kanin Peninsula in the west (44° E) to the Kolyma river in the east (155° E) between the 4° C and 10° C July isotherms, which is roughly between 66 or 67° N and 74 or 77° N (Owen 1980, Mooij *et al.* 1999 in Madsen *et al.*, Rutschke 1987, Leuret *et al.* 1976, Mineyev & Van Impe in Hagemeyer *et al.* 1997). The Whitefronts breeding in this area can be distinguished in two populations. The western Palearctic population of White-fronted Geese breeds west of the Yenisey (83° E) or Chatanga (102° E) River (Rutschke 1987 resp. Mooij *et al.* 1999 in Madsen *et al.*) and migrates in a western and southwestern direction to winter in Europe and southwest Asia. The adjacent eastern Palearctic population of geese, whose breeding area reaches till the Kolyma River, migrates in southeastern direction to winter in east and southeast Asia (Owen 1980, Niethammer *et al.* 1968, Mineyev & Van Impe in Hagemeyer *et al.* 1997, Mooij *et al.* 1999 in Madsen *et al.*). In the following descriptions, only the western Palearctic population of White-fronted Geese will be considered.

Though the Eurasian White-fronted Geese breed as a single population, they split up in different populations during their migration and the ensuing wintering. The breeding sites cover a stretch of about 3000 kilometers, which is similar to the distance between the most western and most eastern wintering sites of the western Palearctic White-fronted Goose population. Thus most of the geese travel a similar distance when migrating from their breeding to their wintering sites, assuming the migratory routes do not contain any detours (Rutschke 1987). All White-fronted Geese generally fly 3000-5000 kilometers in two months during their migration (Mooij *et al.* 1999 in Madsen *et al.*)

In mid-August most geese leave the breeding sites in the north and head for small local assembly points, but some geese will remain at the breeding sites until October (Rutschke 1987, Leuret *et al.* 1976). From these small local assembly points they continue together through intermediate assembly points to the great assembly points. By the beginning of September all the White-fronted Geese have gathered in groups of tens of thousands at these great migratory assembly points, which are usually hundreds of kilometers apart, where they will roost for a few weeks in anticipation of their departure at the onset of the arctic winter.

In spring a similar process of gathering in assembly points is followed, with the migration starting immediately after the improvement of the weather conditions, usually during the second half of February or the beginning of March. In March intermediate staging areas can shortly harbor up to 50,000 geese and at the end of May most geese have reached the breeding grounds (Rutschke 1987).

The following wintering populations of geese are distinguished and are traditionally said to follow the accompanying migratory routes to and from their wintering sites (Rutschke 1987, Cramp & Simmons 1977):

- The Baltic-North Sea population winters mainly in the Netherlands, besides England, Wales, Belgium and, in severe winters, France. This population is said to originate from the western part of the geese's breeding grounds (northeast Europe and west Siberia). From its breeding grounds at the White Sea it heads southwest for the Baltic Sea, reaching it at the Gulf of Finland. From here most geese continue along the Baltic Sea shores until they reach the coasts of Germany at the beginning of October, where they may stage for some time, most even till December, before continuing towards the Netherlands and possibly onwards. Some geese will cross southern Sweden though and continue over Denmark towards the German coasts. In spring the geese start leaving England in March and most have left the Netherlands by the beginning of April, with some geese staging in Estonia at the end of April before they continue their migration in May. Though part of the population may follow the same migratory route as in autumn, others have been found to head towards Moscow first and consequently head up north from there, returning to their breeding grounds by the end of May (Bezzel 1985). A lot of the geese even fly a long way east and then turn around to head towards their breeding areas, with some turning only after arriving east of the Ural. These latter migratory routes, which have also been found in other water bird species, could be explained by the fact that the thaw sets in earlier in mid-Russia than in the northwestern part of the country (Lebret 1976). Mooij *et al.* (1999 in Madsen *et al.*) estimated the wintering population size as 400,000-600,000 for the period 1990-1993 and in 1996 Madsen *et al.* (in Scott & Rose 1996) estimated it at 600,000.
- The Pannonic population is said to originate from the breeding grounds east to those of the Baltic-North Sea population. It migrates through eastern Europe, and has some autumn staging sites in southeast Austria and southern former Czechoslovakia, but mainly in Pannonia (plains in Hungary and northern former Yugoslavia, bordering on Romania), where it will occur from the beginning of October till the end of November. The wintering sites of this population are located in Yugoslavia, north Italy, Albania and north Greece. In spring it returns through Pannonia from late February till early March. Mooij *et al.* estimated the wintering population at 10,000-40,000 individuals for the period 1990-1993, whereas Pirot *et al.* (in Scott & Rose 1996) made it 100,000 in 1989.
- The Pontic population is said to breed east of the Pannonic population. From their breeding grounds they head for southeast Europe at the Black Sea and continue along its west coast towards their autumn staging sites in east and southeast Romania. Their wintering sites are found on or near the Black Sea, including the Danube Delta, European Turkey, the west coast of Turkey, Bulgaria and northeast Greece (Thrace). The Pontic and Anatolian wintering populations were estimated at 350,000-700,000 geese altogether (including 330,000 unidentified geese) by Mooij *et al.* and at 650,000 by Madsen *et al.* (1996 in Scott & Rose).
- The Anatolian population presumably breeds even further east. The migratory routes are not known in detail, but certainly pass through southwest Russia. The population winters at several lakes on the Anatolian plateau in Turkey, though some geese may also continue towards Egypt and Israel in small numbers. Though it is usually considered to be a different population than the Pontic population, it probably also has flocks that winter in the Bay of Iskenderun. The Anatolian wintering population size was estimated together with the Pontic population and is mentioned above.

- The Caspian population occurs even further east than the Anatolian population. It migrates through Russia towards its wintering grounds around the south coasts of the Caspian Sea, in the north of Iran and probably also in the Tigris-Euphrates Basin in Iraq. Rose & Scott (in Scott & Rose 1996) estimated the extent of the wintering geese population at 15,000 individuals in 1994.

According to Mooij *et al.* (1999 in Madsen *et al.*), the recent views on the migratory routes of the White-fronted Geese are that the wintering populations do not travel separately from their breeding grounds to their wintering grounds. In their opinion there are five major flyways which have a number of common staging areas along them:

- A northern White Sea flyway, utilized by the Baltic-North Sea and Pannonic wintering populations and including the breeding areas at the Kara Sea, but otherwise similar to the one described for the Baltic-North Sea population above.
- A central Russian flyway, utilized by the Baltic-North Sea, Pannonic and Pontic wintering populations, which passes through central Russia and Belarus.
- A southern Caspian/Black Sea flyway, utilized by the Pontic, Anatolian and Caspian wintering populations, which follows the Ob River through Siberia to the Turgayskaya Region in Kazakhstan and consequently continuing through the Volga delta to the northern Black Sea coast.
- A western Ukrainian flyway, utilized by the Pontic and Anatolian wintering populations, which originates in the western breeding grounds and continues through the western parts of European Russia and the Ukraine to the wintering ground in southeastern Europe and Turkey.
- An eastern Volga flyway, utilized by the Pontic, Anatolian and Caspian wintering populations, which follows the Volga valley west of the Ural Mountains.

According to Mooij *et al.* no truly separate wintering populations exist either, due to the fact that geese from the same breeding grounds end up in different wintering sites, which is supported by ringing recoveries in different wintering populations in different years (Cramp & Simmons 1977, Bezzel 1985) and due to the fact that lots of mixing of the populations occurs at the common staging areas along the migratory routes, which is also mentioned by Scott & Rose (1996). Mooij *et al.* also note some exchange between the traditional five wintering populations during the winter, which has been mentioned by Bijlsma *et al.* (2001), Rutschke (1987) and Mineyev & Van Impe (in Hagemeijer *et al.* 1997) as well.

Detailed information on the distribution and abundance of migratory and wintering western Palearctic White-fronted Geese can be found in Mooij *et al.* (in Madsen *et al.* 1999). For the whole migratory route, locations and numbers can be found in Lebret *et al.* (1976) and Scott & Rose (1996). Global worldwide distributions and numbers, thus also including the migration of the eastern Palearctic White-fronted Goose population to Asia, are given by Delacour (1954) and Owen (1980). More local information is also available, for example for Middle-European countries (e.g. Niethammer *et al.* 1968), per country (e.g. Lebret *et al.* 1976, Bijlsma *et al.* 2001 or Roomen *et al.* 2005 for the Netherlands) or even per province or region (e.g. Dijk *et al.* 1982 for the province of Drenthe, Ganzevles *et al.* 1985 for the province Limburg, Avifauna Groningen *et al.* 1983 for Groningen or Gerritsen *et al.* 1986 for the IJsseldelta; all located in the Netherlands).

The migratory sites of the White-fronted Goose as used in this study (see Methodology) are given in Figure 5.

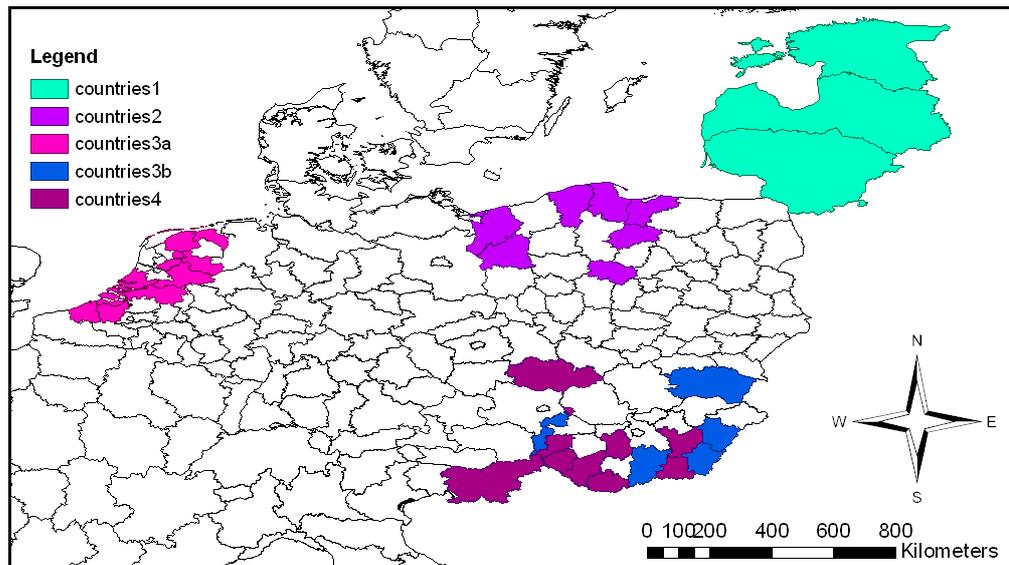


Figure 5. Sites of the migratory route of the White-fronted Goose, with geese wintering in countries 3a and 4

As the White-fronted Goose populations seem to have overlapping migratory routes, mingle at staging sites and assembly points and are even found in other wintering populations in later years, this could result in great risks of dispersal of contracted influenza viruses along their migratory routes. Due to the differences in population size and different numbers of Whitefronts passing through the various staging sites, it might be recommendable for future studies to include the number of individuals of White-fronted Geese in the calculations of the risk of the spread of the highly pathogenic H5N1 virus along the migratory route of these geese. Especially if the White-fronted Geese are indeed found to be asymptomatic carriers of the virus and a greater spatial and temporal distinction is achieved in the analyses, the results might become more precise by including these numbers. If asymptomatic geese occur at greater densities or in larger areas due to higher numbers of individuals, this could increase the risk of transmission.

As can be seen in Figure 5, the size of the regions of the Nuts2 file greatly varies, with there being no distinction in any regions in Estonia, Latvia and Lithuania. This will obviously influence the risk areas as calculated along the migratory routes, as the White-fronted Geese only occur in certain sites in these countries, instead of in the whole country (see Appendix I). Obviously it would be recommendable to use a more detailed data file for the migratory route of the White-fronted Geese, preferably even a map including all of the sites as mentioned by BirdLife International (2006).

The number of sites, where the White-fronted Goose is said to stage or winter according to BirdLife International, is limited as well. Though most geese migrating towards countries 3a will pass along the shores of Poland, some will also pass through southern Sweden and Denmark on their way to Germany. Though the number of White-fronts may be limited in the former two (with an autumn peak number of 2000 in Sweden and about 150 in Denmark in the 1990s (Mooij *et al.* 1999 in Madsen *et al.*)), the numbers in the latter are known to be much higher, as most of the White-fronted Geese using the Baltic-North Sea flyways stage in Germany (with circa 300,000 in the early 1990s; Mooij *et al.* 1999 in Madsen *et al.*). Other important staging and wintering sites are thus likely to be lacking from the BirdLife International data as well.

The BirdLife International data were used nevertheless, as these sites contained data on the presence of other H5N1 high risk wild birds species as well, a factor which could otherwise have not been incorporated in the spatial and probabilistic analyses of this study, as it would not have been available for all the migratory and wintering sites. Though a simplified migratory route is thus presented here, it can nevertheless give an indication of the process and the possible extent of the spread of the H5N1 virus along the geese's migratory route. The final risks as estimated in

this study, could have been much higher though, if Germany and the other countries were included, as outbreaks have occurred here as well (see Figure 4).

As the geese and other migratory species are leaving their breeding grounds again at present and preparing for their migration to Europe, it is important to remain cautious and alert concerning the dispersal of highly pathogenic avian influenza. A commission of avian influenza experts has advised the Dutch minister of Agriculture to keep unvaccinated poultry sheltered during the autumn migration, as they have no reason to assume that the risk of an infection is less this year than it was last year (Horst 2006).

4.3 Possible factors influencing the occurrence of an H5N1 infection in White-fronted Geese

4.3.1 *Habitat of the White-fronted Geese*

Whilst in their breeding areas, the White-fronted Geese occur in the wet moss, shrub and sometimes even forest arctic tundra. The breeding itself mainly occurs on raised dry areas or slopes in the vicinity of water sources, like the sea, rivers and lakes. During their breeding season, the geese mainly forage on mosses, grasses, sedges, cotton grass (Niethammer *et al.* 1968, Flint *et al.* 1984 and Lebret *et al.* 1976).

In general White-fronted Geese strongly prefer fresh water (Cramp & Simmons 1977) and during their migration they can be found in various low-lying habitats along the seashore and inland waters like floodplains, meadows, marshes, bogs, pastures, steppes and lakes, where they will feed on shoots of grasses, sedges or even on halophyte or arid vegetations, as well as on the grasses, cereals, clovers, peas and fallows of agricultural lands (Flint *et al.* 1984, Mooij *et al.* 1999 in Madsen *et al.*, Cramp & Simmons 1977). During their autumn migration the geese gradually switch from natural to more agricultural habitats as they close in on their wintering grounds, whereas during the spring migration the opposite can be observed (Mooij *et al.* 1999 in Madsen *et al.*).

During their wintering period the geese prefer cultivated habitats, provided there is enough water in the vicinity (Lebret *et al.* 1976). In the west European coastal areas they will occur in grasslands, and especially in partially flooded or swampy large meadows and cattle pastures and often even halophyte lawns. In the interior of the countries the geese are also found mainly on moist pastures and meadows (Niethammer *et al.* 1968, Cramp & Simmons 1977). In southeast Europe the geese occur more frequently on arable lands though, due to the scarcity of grasslands there (Lebret *et al.* 1976). The geese prefer large open waters for roosting, though they will usually find a place where they can still stand. If this is difficult due to ice formation, they tend shift their roosting sites to deeper water (Niethammer *et al.* 1968).

The Whitefronts will usually feed in groups in the daytime, with mainly disturbances causing them to start feeding at night. The geese forage on greens of winter cereals, stubble fields with grass, clover or cereals, rape seeds and harvested fields with remains of potatoes or sugar beets (Cramp & Simmons 1977, Lebret *et al.* 1976).

The geese move freely between their roosting and feeding sites (Scott & Rose 1996), where the distance traveled between these two mostly depends on the availability of water. In England the geese generally feed very close to their roosting sites at 1 to 2 kilometers distance. In the Netherlands they travel 10 to 15 kilometers, in Hungary less than 10, but in the Pannonic region, where water is scarcer, distances of 30 and even up to 60 kilometers can be traveled. In Belgium feeding sites are also about 30 kilometers from the roosting site, but geese here will save energy by remaining on the feeding grounds during the night as well (Cramp & Simmons 1977, Niethammer *et al.* 1968, Mooij *et al.* 1999 in Madsen *et al.*). For other countries terms like within flight range, surrounding and more distant were used to note the relation between feeding and roosting sites (Mooij *et al.* 1999). During the short winter days, White-fronted Geese in England were found to forage for 90% of the day, which only increased slightly for longer days (Owen 1972a in Cramp & Simmons 1977).

Thus the main risks for the White-fronted Goose of contracting an infection with the H5N1 virus would be if it was already present in the habitats it prefers, which are generally the wetlands and inland waters (see Figure 6) and the cultivated lands within a 10 (though sometimes up to 60) kilometer radius from these sites, where they prefer to forage. At these roosting and foraging sites other wild birds are often also present and, if they have been infected with the virus, they might pass it on to the White-fronted Geese as well.

4.3.2 Contact of Whitefronts with other H5N1 high risk wild bird species

According to the Standing Committee on the Food Chain and Animal Health (2005), the fifteen species, as listed in Table 1, have a higher risk of contracting an H5N1 infection due to their (migratory) behavior.

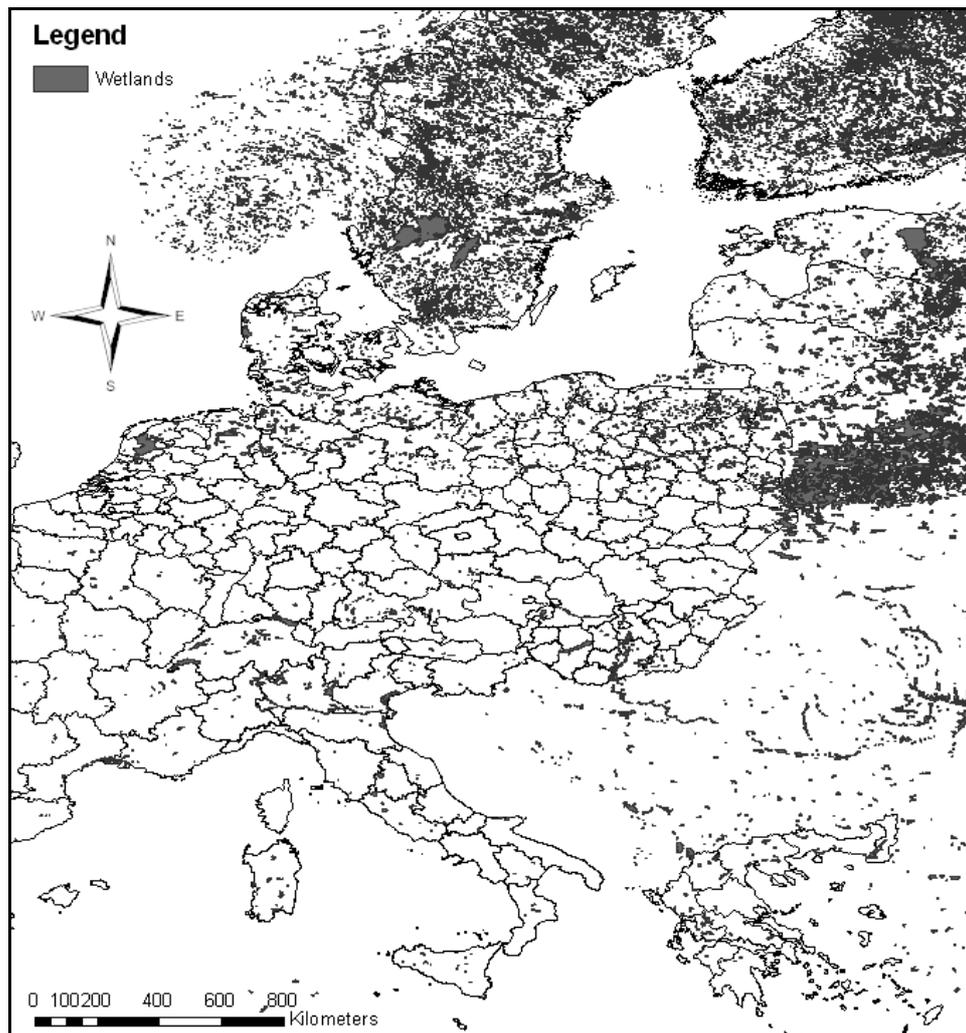


Figure 6. Wetlands and inland waters as taken from Pelcom

THE RISK OF DISPERSAL OF THE HIGHLY PATHOGENIC AVIAN INFLUENZA VIRUS H5N1 BY *ANSER ALBIFRONS ALBIFRONS* IN EUROPE

Table 1. H5N1 high risk wild bird species and the number of White-fronted Goose's migratory sites they occur in (#)

Species	#	Species	#
White-fronted Goose (<i>Anser albifrons</i>)	58	Garganey (<i>Anas querquedula</i>)	2
Bean Goose (<i>Anser fabalis</i>)	37	Common Pochard (<i>Aythya ferina</i>)	4
Mallard (<i>Anas platyrhynchos</i>)	7	Tufted Duck (<i>Aythya fuligula</i>)	5
Gadwall (<i>Anas strepera</i>)	10	Northern Lapwing (<i>Vanellus vanellus</i>)	0
Northern Pintail (<i>Anas acuta</i>)	7	Ruff (<i>Philomachus pugnax</i>)	4
Northern Shoveler (<i>Anas clypeata</i>)	7	Black-headed Gull (<i>Larus ridibundus</i>)	1
Eurasian Wigeon (<i>Anas penelope</i>)	5	Mew Gull (<i>Larus canus</i>)	1
Common Teal (<i>Anas crecca</i>)	6		

The Bean Goose is found most often in association with the White-fronted Goose, occurring together at most of the migratory or wintering sites. This is also often mentioned in literature (e.g. Mooij *et al.* 1999 in Madsen *et al.*). In certain regions the White-fronted Goose is also regularly found in association with Gadwall, Mallard, Northern Pintail or Northern Shoveler. Only sporadically are Garganey, Black-headed Gull and Mew Gull found in the migratory or wintering sites of the White-fronted Goose. Of these fifteen high risk species only the Northern Lapwing was never found in the migratory sites of the White-fronted Goose. There were even 11 migratory sites that did not contain any other high risk wild bird species besides the White-fronted Goose (see Appendix II). The total number of these high risk wild bird species, other than the White-fronted Goose itself, occurring in the White-fronted Geese's migratory and wintering sites is given in Figure 7.

All of these fifteen wild bird species are also mentioned by the European Food Safety Authority (2006) as posing a higher risk for the spread of H5N1 to the European Union due to their migration outside of the European Union, susceptibility, behavior and habitat use. They mention the following additional species as well though:

- Bewick's Swan (*Cygnus columbianus*)
- Mute Swan (*Cygnus olor*)
- Pink-footed Goose (*Anser brachyrhynchus*)
- Lesser White-fronted Goose (*Anser erythropus*)
- Greylag Goose (*Anser anser*)
- Barnacle Goose (*Branta leucopsis*)
- Brent Goose (*Branta bernicla*)
- Red-breasted Goose (*Branta ruficollis*)
- Canada Goose (*Branta Canadensis*)
- Marbled Teal (*Marmaronetta angustirostris*)
- Red-crested Pochard (*Netta rufina*)
- Eurasian Golden Plover (*Pluvialis apricaria*)
- Black-tailed Godwit (*Limosa limosa*)

As only the previously mentioned fifteen high risk wild bird species were noted by both sources, the additional species were not used for the calculation of the White-fronted Goose's wild bird number (WBN).

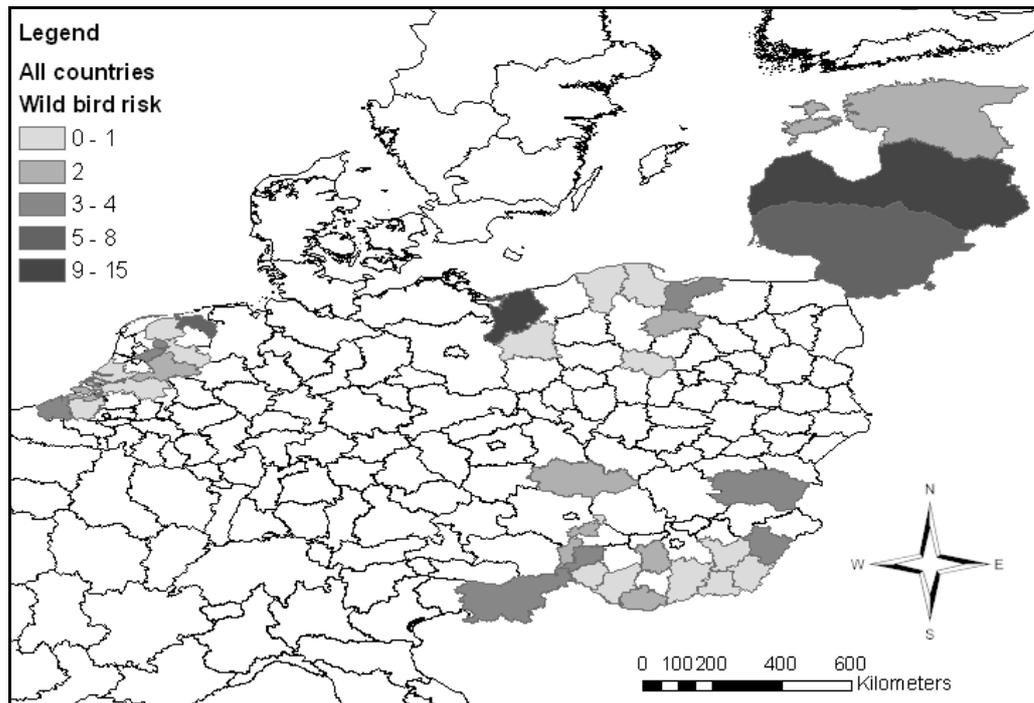


Figure 7. Wild bird number (number of other H5N1 high risk wild bird species) for the *Anser albifrons* migratory sites

The WBN is especially high in Latvia and the northwestern administrative unit of Poland (see Figure 7). It is relatively high in the northeast of the Netherlands and in Lithuania and quite low for most regions in countries 2, 3a and 3b. If the number of other H5N1 high risk wild bird species is high, the White-fronted Goose has an increased chance of contracting an H5N1 infection, even if no H5N1 outbreaks have occurred at that specific site. Likewise a high number of high risk wild bird species also increase the chances of infecting the White-fronted Goose, if an outbreak has occurred.

4.3.3 Discussion of model results of possible H5N1 risk factors for Whitefronts

The wetlands (Figure 6) of the European administrative units give a relatively good impression of the migratory and wintering sites of the White-fronted Goose, though, as previously mentioned, there is no distinction in regions in countries 1, so the actual extent of the occurrence of the White-fronted Geese will be overestimated here. There are also other countries for which the Pelcom grid file does not have a lot of wetlands and inland waters marked, resulting in the exclusion of these countries from the migratory and wintering sites of the White-fronted Goose, though they are known to occur there. Belgium is an example of one of these countries that is excluded from the performed analyses due to lack of classification of the wetlands and inland waters. A more detailed map of Europe, including specifications of land use would be strongly recommended for future studies. In summary the main risks of the geese contracting an H5N1 infection are if the infection is already present in the goose's habitat due to a previous outbreak or if other high risk wild bird species occurring in the geese's migratory sites have been infected.

4.5 Chances of dispersal of H5N1 by White-fronted Geese along their migratory routes

The chances of dispersal of H5N1 by White-fronted Geese along their migratory routes and consequently even the possible infection of poultry, based on the previously mentioned migratory

routes, habitats and other wild bird species present, have been determined using a GIS model and a Bayesian network. Both will be dealt with separately below.

4.5.1 The risk of H5N1 spread by White-fronted Geese using GIS

For the White-fronted Goose the results of the GIS model concerning the spread of the highly pathogenic avian influenza virus during its autumn and spring migration in Europe are given in Figure 8 and Figure 9 respectively. In these figures the 10 km buffers of the H5N1 outbreak points and wetlands are also shown, as well as the poultry density. The autumn and spring minimum, mean and maximum H5N1 risks of the White-fronted Goose are given for the various countries in Table 2.

Generally the H5N1 risk of the White-fronted Geese can be viewed to increase along its migratory route. This makes sense, as the geese are thought to take the virus along to the next country along their migratory route. Thus the minimum risk of a certain country is always equal to the background risk plus the mean risk of the previous country, with the risk in countries 3a and 4 increasing from autumn to spring due to the wintering risk in these countries. In autumn the risk increases from a minimum of 0.01% in countries 1 to a maximum of 5.37% in countries 4. In spring the risk increases from a minimum of 2.61% in countries 4 to a maximum of 14.83% in countries 2. Even though the mean spring risk is thus highest in countries 1, the spring maximum risk is found to be highest in countries 2, as this country has exhibited H5N1 outbreaks, whereas countries 1 itself has not.

As can be observed from Figure 8 and Table 2, the autumn H5N1 risks (minimum, mean and maximum) in countries 3b are all lower than in countries 3a, even though H5N1 outbreaks have previously occurred in the former and not in the latter. This can be explained by the fact that the geese split up into two different directions when migrating from countries 2 (see Figure 2). As merely 9% heads for countries 3b, the autumn minimum there is 9% of the autumn mean risk of countries 2 plus the background risk in those sites of countries 3b that have not exhibited previous H5N1 outbreaks. The remerging of these separate wintering populations during the spring migration in countries 2 also explains why the H5N1 risk increases markedly from countries 3a to countries 3b. The minimum risk of countries 2 is the sum of the means of the previous countries (3a and 3b), corrected for the ratio between their population sizes, and the background risk.

Table 2. The autumn and spring mean, minimum (min) and maximum (max) H5N1 risks (in %) for the White-fronted Goose in the various countries of its migratory route with the wild bird number (WBN) of these countries

Countries	Autumn mean	Autumn min	Autumn max	Spring mean	Spring min	Spring max	WBN
Countries 1	0.02	0.01	0.04	14.34	14.33	14.35	23
Countries 2	3.15	0.03	4.51	14.31	6.10	14.83	24
Countries 3a	2.88	2.88	2.89	4.34	4.33	4.36	20
Countries 3b	1.72	0.29	1.86	11.71	9.06	11.85	13
Countries 4	4.74	1.73	5.37	8.76	2.61	9.42	16

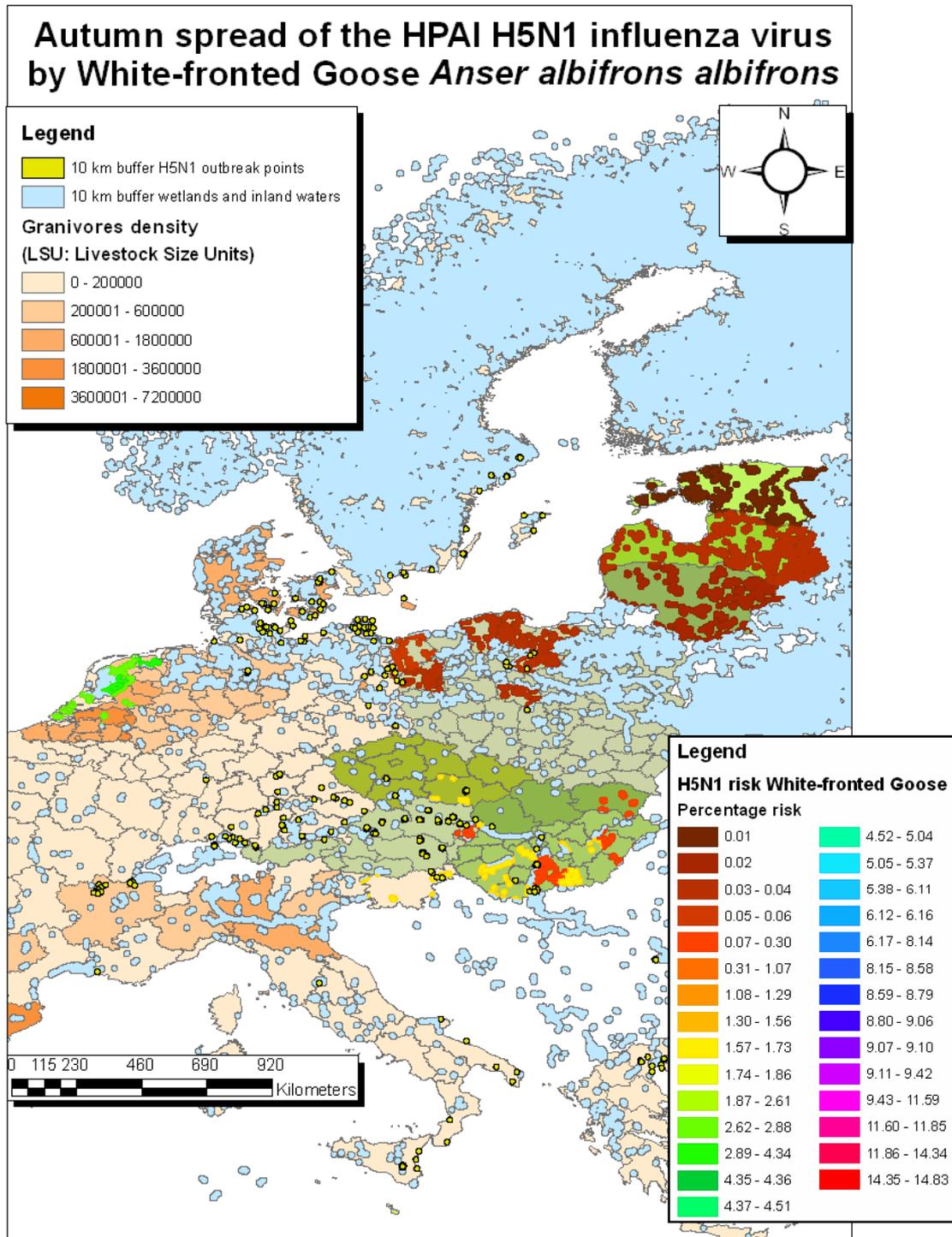


Figure 8. Autumn spread of the H5N1 influenza virus by the White-fronted Goose's migration through Europe, countries missing from the Livestock file are shown in greenish colors for orientation purposes

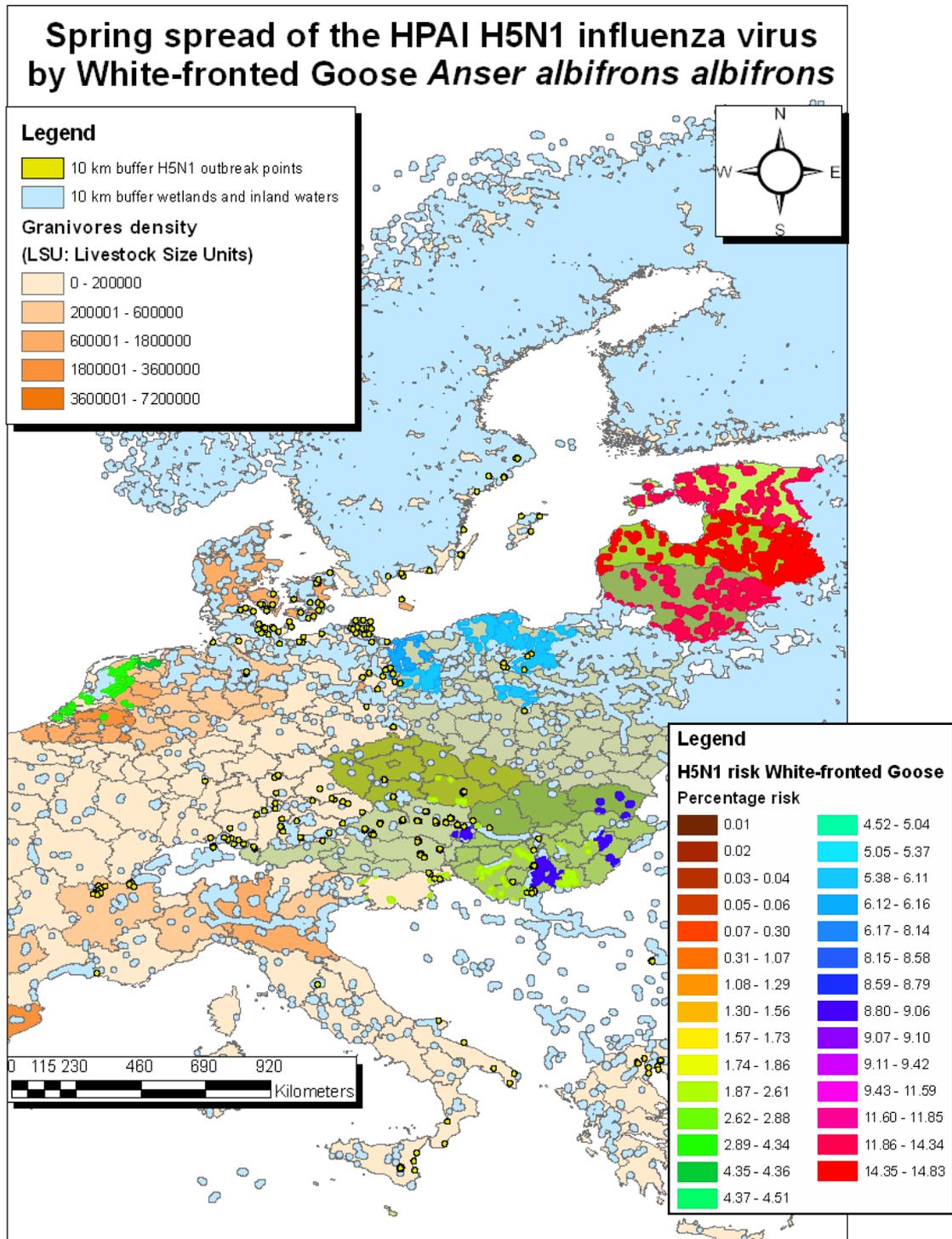


Figure 9. Spring spread of the H5N1 influenza virus by the White-fronted Goose's migration through Europe, countries missing from the Livestock file are shown in greenish colors for orientation purposes

The minimum and maximum risks in countries 1 and 3a do not differ markedly (less than 0.03%, whereas for the other countries these two differ at least 1%). This is due to the fact that no outbreaks have occurred in these countries previously. Thus the only differences between the different sites of these countries are caused by the differences in the background risks, due to different wild bird numbers of the different sites. Though the wild bird number does not cause great differences in the H5N1 risk for those countries that have not previously experienced an H5N1 outbreak, the difference does increase markedly if an outbreak has already occurred and the minimum risk is high (e.g. the spring maximum risk for countries 2).

The influence of the wild bird number is also illustrated in the individual countries' autumn and spring migratory risks in Figure 10 - Figure 14 (for countries 1-4). In these figures the individual countries' risks are depicted in order to be able to observe the regional differences better. The sites of the various countries are marked as in Figure 5, with the outlines of neighboring European administrative units displayed for reference. H5N1 outbreak locations are also included in the figures.

In countries 1 (Figure 10; for legend see Figure 8 & Figure 9 or Figure 14) the differences are only slight and caused by the different wild bird numbers (WBN) as mentioned above. In Estonia the risks is lowest (WBN = 2), increasing for Lithuania (WBN = 7) and being highest for Latvia, which has a WBN of 14 (see Appendix II). Though no previous outbreaks have occurred in countries 1, the H5N1 risk of the White-fronted Geese of these countries has managed to increase more than thousand fold for Estonia and even almost four hundred fold for Latvia during their migration and wintering periods, illustrating the potential risk of the migratory spread of H5N1.

In most sites of countries 2 (Figure 11), the autumn risk is very low, merely the background risk that varies slightly per region, due to differences in the wild bird number. The risk becomes much higher in the areas that lie within 10 kilometers of H5N1 outbreak points. This increased risk is higher in some regions (in the upper left corner for instance) than in others (in the region immediately below for instance). This is also due to the different wild bird numbers. In spring the difference between the minimum background risk and the maximum outbreak buffer risks is caused by the higher minimum risk, resulting in a greater increase when multiplying with the wild bird numbers.

In countries 3a (Figure 12) no H5N1 outbreaks have occurred as of yet, so the only regional differences in H5N1 risks are caused by the wild bird number. The only difference between the autumn and spring risk is caused by the wintering risk of the White-fronted Geese, so there is only a proportional increase.

In countries 3b (Figure 13) the autumn risk is very low for most sites, which is caused by the low percentage of birds migrating from countries 2 to countries 3b. Again the differences are mainly caused by the wild bird number and the H5N1 outbreak points. That the difference between the various regions that have not exhibited H5N1 outbreaks, is only slight and caused by the wild bird number, is clearly illustrated when comparing the autumn and spring risks. For the spring risks, the risk categories were thusly customized, that no differences can be observed for the different wild bird number regions during spring, though in autumn this distinction is visible. Incidentally there indeed seem to be less wetlands in countries 3b (and 4) than in countries 1, 2 and even 3a, as was mentioned above under the results of research question 3. This can also clearly be seen in Figure 8 and Figure 9.

In countries 4 (Figure 14), there are also different regions with different background and outbreak risks due to different wild bird numbers. The difference between autumn and spring is also formed by the wintering risk, as for countries 3a.

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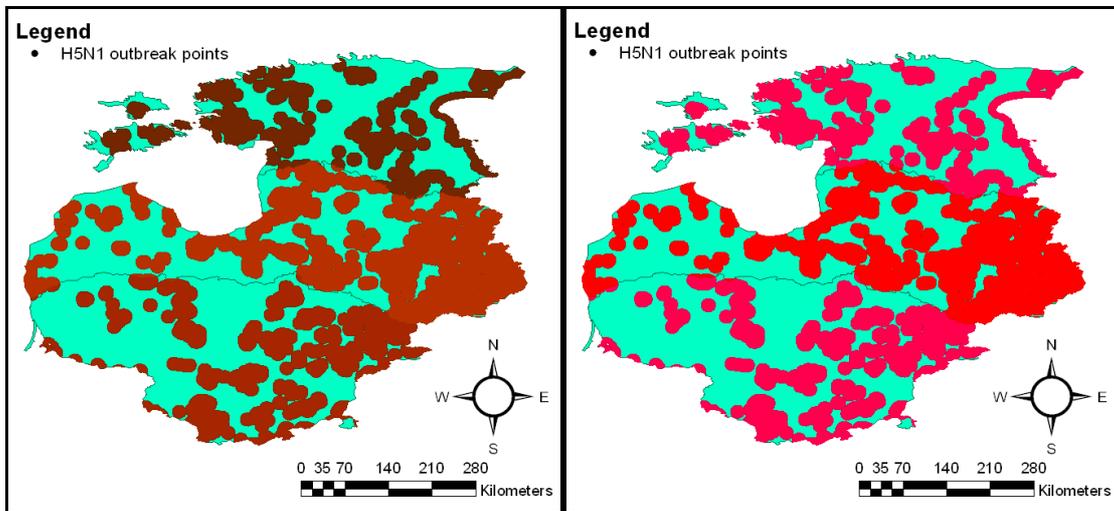


Figure 10. Autumn (left) and spring (right) H5N1 risk for White-fronted Geese in countries 1

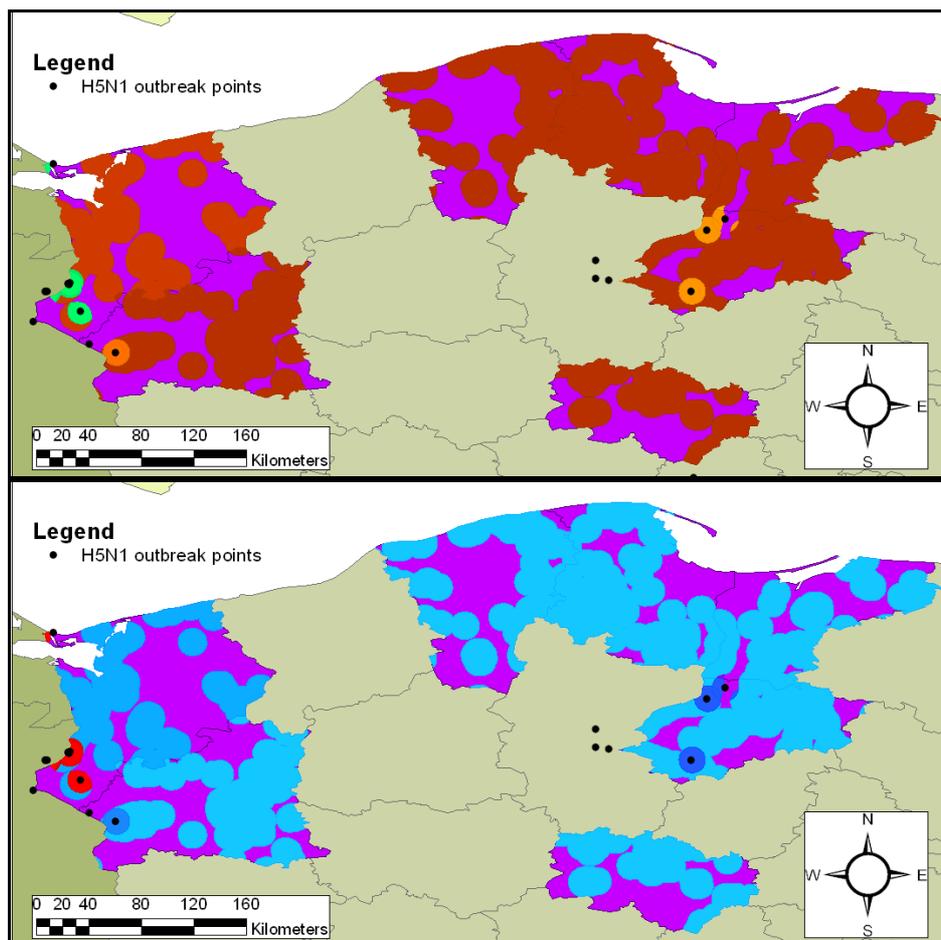


Figure 11. Spring (top) and autumn (bottom) H5N1 risks for White-fronted Geese in countries 2

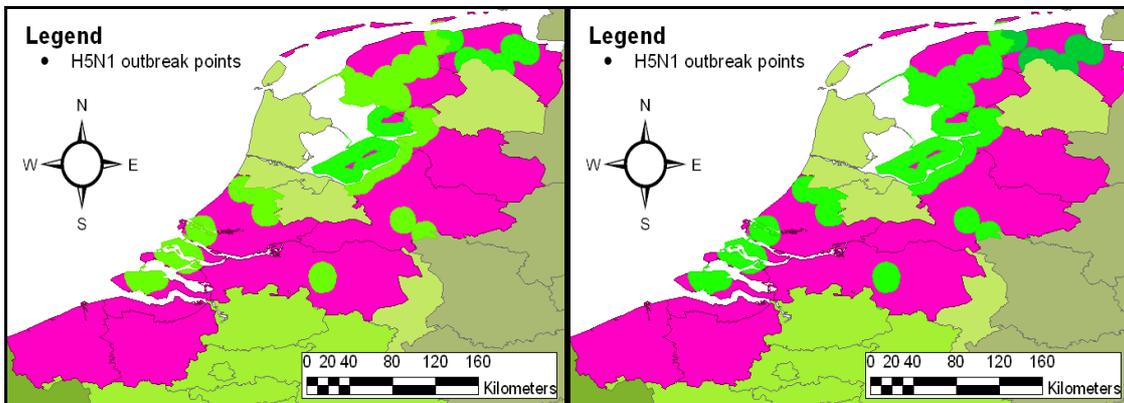


Figure 12. Autumn (left) and spring (right) H5N1 risks for White-fronted Geese in countries 3a

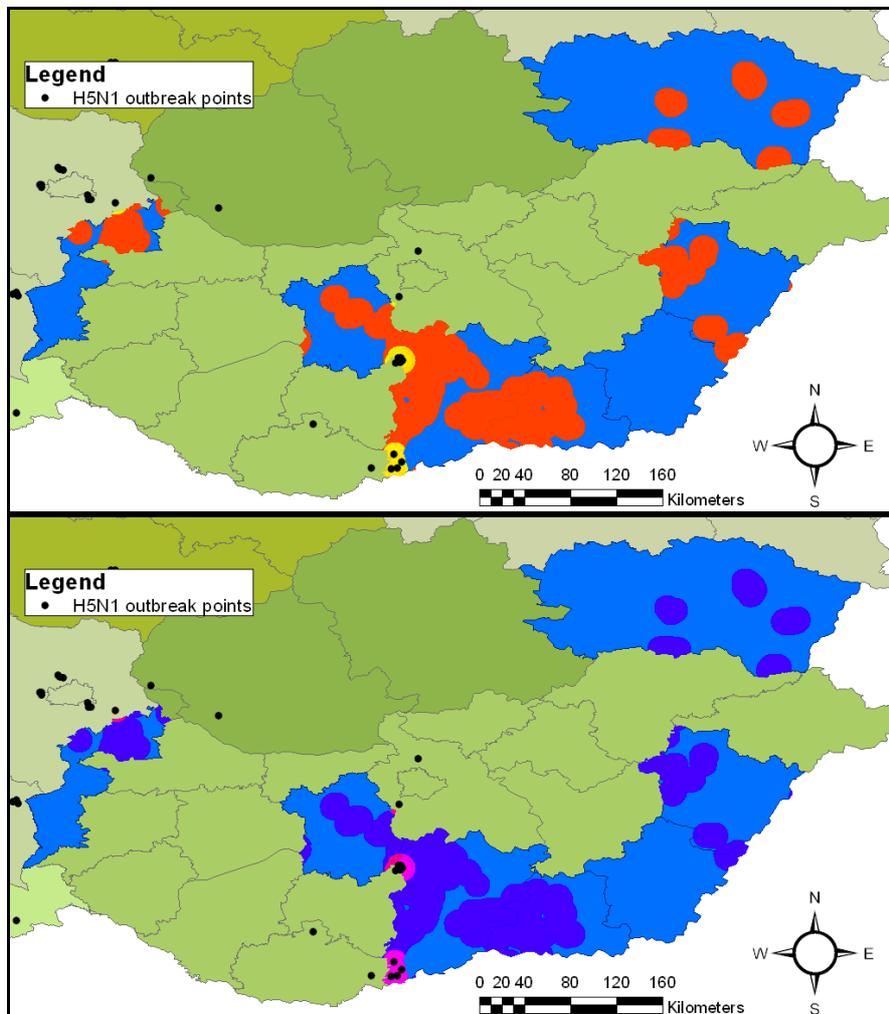


Figure 13. Autumn (top) and spring (bottom) H5N1 risk for White-fronted Geese in countries 3b

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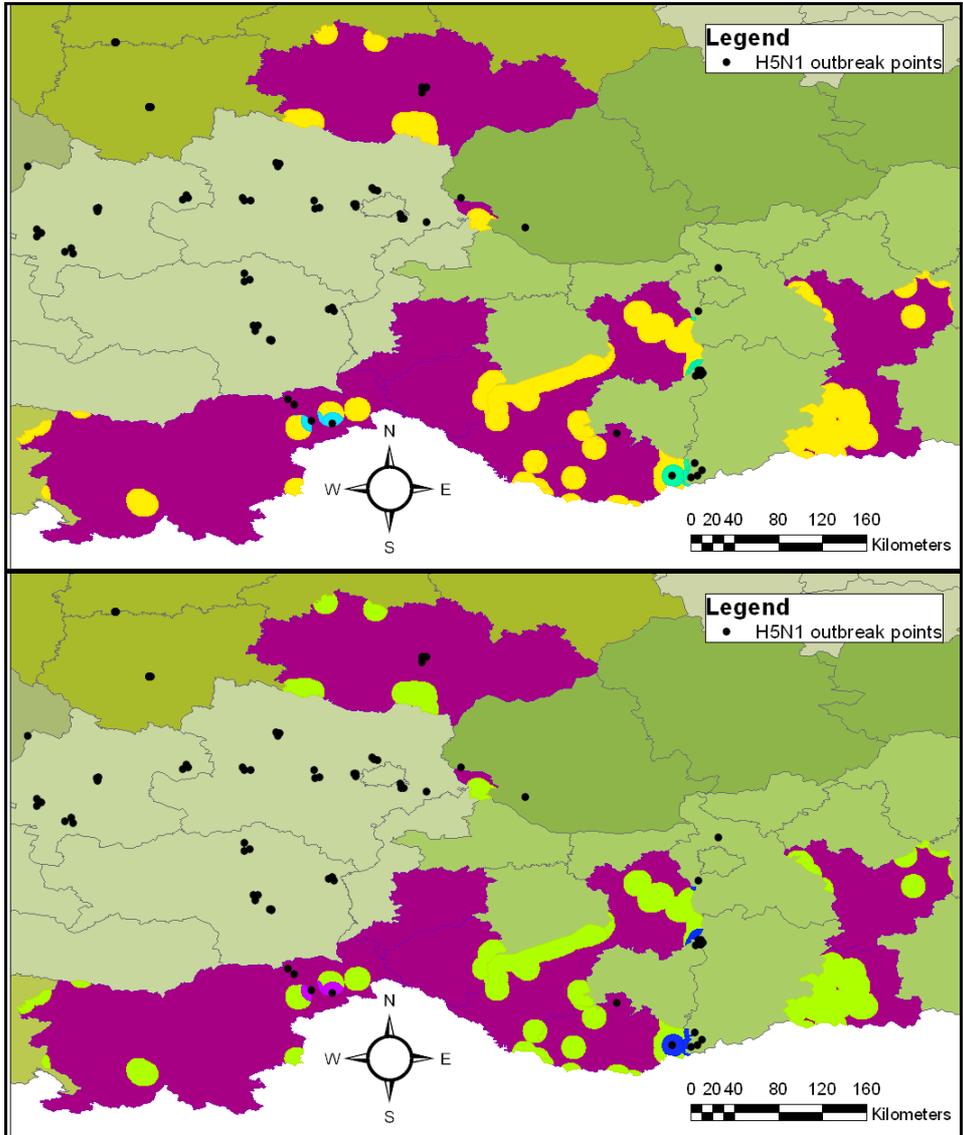
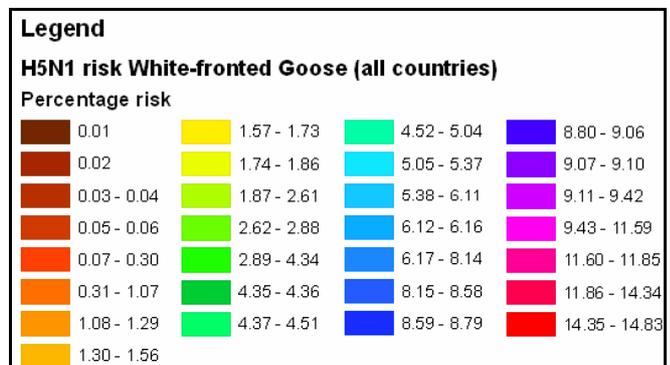


Figure 14. Autumn (left) and spring (right) H5N1 risks for White-fronted Geese in countries 4



4.5.2 The risk of H5N1 infection of poultry by White-fronted Geese using GIS

Concerning the risks of the H5N1 virus being spread to poultry, the following can be said, based on Figure 8 and Figure 9. For countries 1, 2, 3b and, besides Slovenia, also countries 4, no real data exist on the poultry densities in the Eurofarm Granivores selection file. This is why no calculations were performed with these data. Nevertheless, in countries 3a, especially in the Netherlands, the highest poultry densities are found, which, combined with its small size, would place this country at considerable risk. Lots of the H5N1 risk areas are also located in the second lowest poultry density category though, which is also the case for all risk areas in Slovenia.

Besides the spread of the H5N1 virus along the migratory routes of the White-fronted Goose, other H5N1 high risk wild bird species might increase the risk of poultry being infected with the virus. The European Food Safety Authority (2006) mentions the domestic Mallard (*Anas platyrhynchos*) as having a high risk of contact with poultry due to intimate association with the poultry production in Europe. The Common (*Larus canus*) and Black-headed Gull (*Larus ridibundus*) could pose a high threat, the Northern Lapwing a medium threat and the Eurasian Golden Plover (*Pluvialis apricaria*) a low risk of contact with poultry, due to the possibility of sharing farmland with domesticated poultry in north Europe. Wild waterbirds that could pose a threat to poultry due to sharing wetlands with domesticated waterbirds, include the Mute Swan (*Cygnus olor*) and the Greylag Goose (*Anser anser*), which pose a medium threat, and *Anas* and *Aythya* spp. of ducks, which pose a low threat.

The cumulative low, medium and high poultry risks for the various countries are given below in Table 3. The autumn and spring mean minimum and maximum H5N1 risks for poultry, including (see Table 4) and excluding (see Table 5) the risks posed by other wild birds than the White-fronted Goose, are given below as well.

Table 3. The number of H5N1 high risk wild bird species that pose a low, medium or high threat to poultry per country

	Low	Medium	High	Total
Countries1	12	1	0	13
Countries 2	15	2	2	19
Countries3a	14	4	0	18
Countries3b	4	6	4	14
Countries4	3	9	3	15

Table 4. The autumn and spring mean, minimum and maximum H5N1 risks (in %) of poultry in the various countries of the White-fronted Goose's migratory route, including the low, medium and high risks of other H5N1 high risk wild bird species

	Autumn mean	Autumn min	Autumn max	Spring mean	Spring min	Spring max
Countries 1	0.00	0.00	0.01	2.92	2.92	2.93
Countries 2	2.50	0.03	3.59	11.37	4.84	11.78
Countries 3a	1.56	1.56	1.57	2.35	2.35	2.36
Countries 3b	3.08	0.53	3.33	20.94	16.20	21.20
Countries 4	11.29	4.12	12.80	20.87	6.21	22.43

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Table 5. The autumn and spring mean, minimum and maximum H5N1 risks (in %) of poultry in the various countries of the White-fronted Goose's migratory route, excluding the low, medium and high risks of other H5N1 high risk wild bird species

	Autumn mean	Autumn min	Autumn max	Spring mean	Spring min	Spring max
Countries 1	0.00	0.00	0.00	0.72	0.72	0.72
Countries 2	0.16	0.00	0.23	0.72	0.30	0.74
Countries 3a	0.14	0.14	0.14	0.22	0.22	0.22
Countries 3b	0.09	0.01	0.09	0.59	0.45	0.59
Countries 4	0.24	0.09	0.27	0.44	0.13	0.47

All countries basically have the same total of high risk wild bird species posing a threat to poultry (see Table 3), though it is somewhat higher for countries 2 and 3a. The distribution differs greatly though, with especially countries 3b and 4 having lots of medium and high risk bird species. This is also the reason why both the autumn and spring risks of these countries are so much higher than those of the other countries (see Table 4), even despite the fact that the risk for countries 3b was relatively low due to the small percentage of geese migrating towards this country from countries 2.

The risk for countries 1 was already quite low in autumn and, as this country has the lowest total of high risk wild bird species posing a threat to poultry and only one medium risk species and no high risk species, it remains quite low (at a mean of approximately 0.005%). Even in spring the risk is only slightly higher than the risk in countries 3a (with a mean of approximately 3% versus 2.4%), even though this is the last stop on the goose's spring migratory route. For countries 2, 3a and 3b the autumn mean basically is between 1.5 and 3% and for countries 4 the autumn mean is a little over 11%. The spring mean poultry risks for countries 3b and 4 are almost 21%, whereas for countries 2 it is a little over 11%. These are considerable risks and comparable to those found for the White-fronted Geese themselves.

The method used to incorporate the threat of other H5N1 high risk wild bird species to poultry, has probably caused an overestimation of the extent of the risk though. The chance of the geese passing the virus on to these other H5N1 high risk wild bird species is also assumed to be 1 in these calculations, which is not likely. A correction for this transmission should also lead to a reduced risk. Nevertheless, the other H5N1 high risk wild bird species can pose a great threat to the poultry, especially if the White-fronted Goose passes the virus on to them.

When merely considering the White-fronted Goose's H5N1 poultry risks (Table 5), the distribution is the same as for the H5N1 risks of the White-fronted Geese themselves (Table 2). The risks are lowest in autumn in countries 1 and gradually increase along the migratory routes, till the mean risk is maximal in countries 1 in spring. Besides the autumn risks of countries 1 and the minimum autumn risk of countries 3b, all poultry risks are basically around 1 to 7 ‰, which is considerably lower than when taking the high risk wild bird species posing a threat to poultry into account.

Even though indications of the poultry risk have been given based on the White-fronted Goose's risk, including and excluding the additional wild bird number for poultry, it would be desirable to perform these calculations with specific information on the poultry farm locations and densities. With these data the exact locations of the poultry farms actually at risk could be indicated.

4.5.3 The risk of H5N1 spread by White-fronted Geese along their migratory routes and to chickens using Bayesian Networks

Several Bayesian Networks were designed, all of which calculated the risk of an H5N1 infection for both the White-fronted Goose and poultry. Thus both of these risks will be discussed in this sub-chapter together. The results of all models (1 through 5) and their reruns as calculated with Bayesian Network tools in Java (BNJ) are given in Appendix IV.A. The results of Models 1 till 3 and their reruns as calculated using Hugin Lite are given in Appendix IV.B. The results of Models 1a till 5a and their reruns are given in Appendix IV.C. The results of Model 1g are given in Appendix IV.D.

Generally the input chances do not change as these are the chances that are specified in the model for the factors that are not influenced by any other factors. In Model 1g and the reruns of Model 2 these chances can change though, as they may need to have a certain minimum value to be able to return a chance of 100% for the following variable. Chances of less than 0.1% are noted in BNJ as being 0%.

In general the following observations can be made, concerning the results of all of these models. Though the risk for the geese and chickens increases along the migratory route for all the regular runs of the models (with it being higher in countries 3a than in countries 3b in Models 3 and 3a due to higher input values from the GIS model as a larger proportion of the geese migrates towards countries 3a), the risk for the geese and chickens in countries 3a is slightly lower in the reruns, than for those of countries 2. This is due to the fact that the risk of an infection being present in countries 2 is set at 100% in the reruns. The same holds for the risks of countries 1 in spring in the reruns of Models 4, 4a, 5 and 5a, these are lower than those of countries 2 in spring, due to the risk of infection being set at 100% in countries 2.

For the geese and chickens in countries 1, the autumn chances stay the same during the regular runs of the models, irrespective of whether Model 1 or any variant of Model 2 is used. This is due to the fact that the input chances do not change in these models. For the reruns of the variants of Model 2, these autumn chances increase, in order to be able to achieve the increased chances of the linked variables for countries 2, but not as much as they increase for countries 3a, due to the fact that the geese bring the chance of infection with them from the preceding countries.

For the basic models, the final autumn risk in countries 4 is highest for Models 3 & 4. Though for countries 1 these are lower, due to lower input risks, the input risks of infections being present in the following countries are much higher (even though the wild bird numbers are lower), resulting in higher risks further down the migratory route. Though the results of Model 5 are the lowest of all models, the results of the reruns are the highest, due to the fact that the risks of the geese of the countries that have exhibited an infection had been set at 100%, resulting in an increase for the geese of the preceding and following countries and consequently also of the chickens.

The results of the Models 1a-5a are obviously also all higher than their basic counterparts, except for the risks of countries 1, as the input risks do not change. The increase, relative to the basic models, becomes greater further along the migratory route. Thus the autumn risks in countries 4 have increased more than two fold in all the reruns of the models, and this becomes an increase of more than twenty fold for the spring geese of countries 1 in the rerun of Model 4. For the reruns of Model 5, increases of more than 10 fold are observed.

In model 1g it was found that the risks are highest for those countries in which infections are present amongst geese of the immediately preceding and following countries, especially in countries 2 (irrespective of countries 4). It seems unlikely though that the risk of for example the geese in countries 3b is merely 34.12% for the risks of these geese in countries 2 and 4 being 100% (irrespective of countries 1 or 3a). This would insinuate that the geese somehow mostly got rid of the infection for only the duration of their migration through countries 3b, before fully acquiring it again in countries 4.

It would perhaps have been better to perform these analyses of Model 1g with Model 1a instead of Model 1, as the chance of transmission to the next countries would have been 95% then, resulting in more realistic values. This would also improve the results of the chance of infection being merely 1.01% for those countries in which the risk of the geese in the immediately preceding (but not in any of the following) countries was set at 100%. For an even more realistic result, the analyses should ideally be performed with a variant of Model a2.

All in all the results of the reruns of the Models 1a-4a are most similar to those found using the GIS model, though they cannot be compared thoroughly, as Model 3 is the only one that was extended to incorporate the spring migration of the geese (resulting in Model 4). Furthermore, in the GIS model, the wintering risk of the geese was incorporated by multiplying the autumn risks for those countries by a factor of 1.5, though it is not possible to do so in the Bayesian Network, which also partly explains why the risks of the latter are somewhat lower. Another reason why the chances are lower is due to the wild bird number. In the GIS model, the background or outbreak risk could be multiplied by the wild bird number. In the Bayesian Networks this is not possible; a higher chance can merely be assigned in case of a higher wild bird number.

4.6 Discussion of the modeling process

In this study two kinds of models have been developed in order to be able to determine the risk of H5N1 spread by White-fronted Geese along their migratory route and of the possible consequent spread to poultry. Due to the limited scope of the study, the limited parameters and other information available from literature and the small spatiotemporal resolution of most input files, the results of this study can merely be viewed as an indication of the possible extent of the spread of the virus. Below the reliability of the input files and parameters will be discussed and the limits in the present knowledge will be pointed out, giving an indication of the further experimental research that needs to be conducted in order to be able to give a more accurate representation of the aforementioned risks. As the model developed using Bayesian Networks did not have any input files, the first subchapter (4.6.1 The model's input files) only applies to the GIS model.

4.6.1 The model's input files

- Pelcom grid: As previously mentioned, the areas classified as wetlands were too limited in their extent. This causes an underestimation of the occurrence of the White-fronted Geese in certain areas. Ideally a map should be used in which these wetlands are denoted more precisely and in which other land use types are classified more specifically, so the foraging sites of the White-fronted Geese can be incorporated as well.
- EuroFarm Granivores info file: As previously mentioned, this file contains information on too few countries along the migratory route of the White-fronted Goose. Apart from that, it does not even contain information on poultry itself, but merely the combination of poultry and pigs. Also it is linked to the administrative Nuts1 and 2 regions for the European Union countries, which limits the spatial resolution of the data.

Ideally a file should be used in which the exact locations of poultry farms are given for all European countries together with the kind of poultry farm (for example farms containing free ranging poultry or caged poultry). With this information different kinds of risks could be assigned to the different kinds of poultry farms and an assessment could be made of the risk of the individual farms when incorporating the distance to potentially infected wild birds like the White-fronted Goose.

- EurNuts2 shapefile: As previously mentioned, not all European countries are included in this file, making it impossible to select all the migratory and staging sites of the White-fronted Goose. Also the spatial resolution of the administrative Nuts regions is not too high, especially for countries like Estonia, Latvia and Lithuania. Ideally a file should be

used in which the exact migratory and staging sites of the White-fronted Geese could be selected.

- H5N1 outbreak points image file: As previously mentioned, this file contains the H5N1 outbreak locations amongst wild birds. There is no distinction for species, number of individuals involved or even the time of the outbreak. Ideally these factors should be known as well. Though the former two would mostly contribute to the extent of the risk, the latter is especially important as it should be expected that the risk of other wild birds becoming infected at that outbreak location is highest in the first couple of days and will diminish as time passes and no further outbreaks occur at that location. In order to be able to relate the time of the outbreaks to the time of passage of wild birds like the White-fronted Goose, a greater temporal resolution is required for the migratory route of the White-fronted Goose than the one derived from literature at present. Thus an input file containing the migratory and staging sites of the White-fronted Goose with a great spatiotemporal resolution and preferably also the numbers of individuals at each site should ideally be included in this kind of study.

4.6.2 *The model's parameters*

As previously mentioned, all of the model's parameters are merely estimated guesses. The values of these parameters still need to be determined experimentally. Of all of these estimated variables, the risk parameter based on the number of other high risk wild bird species (the "wild bird number", WBN) is likely to be the most inaccurate. Other parameters that should be determined experimentally, so they can ideally be included in the model as well, include the risk of transmission of the H5N1 virus amongst geese, the risk of transmission of H5N1 to and from other H5N1 high risk wild bird species and the risk of transmission of H5N1 to poultry.

Factors that should also ideally be included as parameters in the model, but could not be included due to a lack of information on the exact numbers at the various staging and migratory sites and the low temporal resolution of the duration of the stays at these sites, are the parameters on the general populations dynamics of the White-fronted Goose, the mortality rate of infected individuals and the infectious period of the infected individuals. If input files with a greater spatiotemporal resolution would be used, especially through the inclusion of the time of an outbreak and the infectious period of the infected geese, a more limited but spatiotemporally more reliable extent of the spread of the virus could be given. It would be very elaborate though to try to achieve a greater spatiotemporal resolution for the model developed using Bayesian Networks, though the accuracy in the present state could definitely be improved through experimental determination of the used parameters.

4.6.3 *Summary of the model's discussion*

In conclusion the model in its present status can merely give a rough indication of the areas at risk of the potential migratory spread of the H5N1 virus through White-fronted Geese. A greater spatiotemporal resolution would be desirable though, which could be achieved through the use of more detailed input files and the experimental determination of the values of the aforementioned parameters which at present are still unknown. For this purpose the GIS model would be more suitable, due to the fact that Bayesian Networks are more suitable for theoretical approaches.

4.7 Overall Discussion

In general the following can be said about this preliminary study on the chance of the spread of highly pathogenic avian influenza H5N1 by the migratory White-fronted Goose *Anser albifrons albifrons* in Europe.

The White-fronted Goose itself has a considerable risk of contracting and spreading H5N1 infections, as it migrates through a lot of the outbreak areas and in most staging and wintering sites other H5N1 high risk wild bird species can be found as well. This can be seen in all of the spatial analyses, where the geese of countries 1 are found to have a considerable risk of being infected with the H5N1 virus in spring, even though no H5N1 outbreaks have occurred in these countries as of yet.

Consequently the virus infection can be passed onto chickens, though for most countries along the migratory route it is unknown whether great poultry densities actually occur there. The risk is also considerably lower if other H5N1 high risk wild bird species that pose a threat to poultry are not taken into account, as the White-fronted Goose itself is not mentioned by the European Food Safety Authority (2006) as posing a threat to poultry through intimate association with the poultry production, sharing farmland with domesticated poultry or sharing wetlands with domesticated waterbirds.

The GIS model and the Bayesian Network are two distinct approaches, both applicable for analyzing spatiotemporal problems. Whereas in the GIS model the actual outbreak locations can be entered and a greater spatial precision can be achieved for the calculated risks of the White-fronted Geese, this is hard to realize in the Bayesian Networks. The latter is more suitable for theoretical approaches, in which no great spatial resolution is desired. Even when setting the chances of outbreaks in the countries in which outbreaks had occurred to 100%, lower chances are obtained than with the GIS model. This is due to different calculation methods for the incorporation of the wild bird number in these models.

Given the fact that lots of data on infection rates and transmissibility of the virus to and from wild birds are still unknown, Bayesian Networks are a useful tool in determining how far the virus would spread under different scenarios and different values of these risks (like Model 1g, though higher inter-geese transmission risks are required for a more realistic outcome). A GIS model could consequently give more precise spatiotemporal information, should the exact risk values become known for this, or another, avian influenza virus. As different kinds of results can be obtained with both of these approaches, the combined application of these two seems insightful. Ideally goose mortality due to the virus, goose density and population size should be included in the analyses and a greater spatiotemporal precision should be realized through distinguishing smaller population movements and smaller time periods.

Though it has not yet been established whether wild birds really contribute to the spread of the highly pathogenic avian influenza H5N1 virus, this study has shown that, using the specified estimated values, the risk can be considerable should any high risk wild bird species indeed be found to be an asymptomatic carrier of the virus. When data on the specific values of the chances of infection and transmissibility of the virus between wild bird species, within a species and to poultry become available, a more detailed study on the actual chances could be undertaken. The results of this preliminary study can namely merely be viewed as indications, due to the use of estimated values, a small spatiotemporal resolution, the absence of certain staging and wintering sites from the BirdLife International White-fronted Goose sites and the EurNuts2 file and the limited extent of the poultry data. It also has to be noted that these results are based on an average winter, as the White-fronted Geese occur more south in severe winters, with for example most of the geese from the Netherlands heading towards France.

Though lots of outbreaks are likely to occur in the near future with the onset of the autumn migration, at least the potential threat of the H5N1 virus developing into pandemic proportions in humans seems to have passed for now, as Maines *et al.* (2006) found that, even through reassortment with the human H3N2 influenza virus, the H5N1 virus lacks the possibility of obtaining efficient human-to-human transmissibility at present using a ferret model.

5. Conclusions and recommendations

5.1 Conclusions based on the research questions

For the formulated research questions, the following conclusions can be drawn:

1. Which countries have exhibited H5N1 outbreaks?

In June 2006 H5N1 outbreaks had occurred amongst wild birds in the following European countries: Denmark, Germany, Sweden, France, Czech Republic, Slovakia, Austria, Italy, Slovenia, Hungary, Greece, Romania and Bulgaria. By July 2006 the virus had spread even further in these countries and to Scotland, Spain, Croatia, Bosnia and Herzegovina, Serbia and Montenegro, Albania and Turkey as well, with outbreaks amongst poultry in Sweden, Denmark, Germany, France, Romania, Serbia and Montenegro, Albania, Bulgaria and Turkey.

2. What is the migratory route of the White-fronted Goose?

The White-fronted Goose migrates 3000 to 5000 kilometers from its breeding grounds in the arctic tundra (from 44° E to 155° E, between the July 4° and 10° isotherms) to its Eurasian wintering grounds through different migratory routes. The western Palearctic population of geese migrates to Europe and southwest Asia, whereas the eastern population migrates to east and southeast Asia. Of the five wintering populations of the western Palearctic breeding population the following two were incorporated in this study with their traditionally distinguished accompanying migratory routes (though most populations will also use routes of neighboring populations):

- Baltic-North Sea population: this population winters mainly in the Netherlands, besides England, Wales, Belgium and in severe winters also France. It migrates from the western part of the breeding grounds at the White Sea southwest to the Gulf of Finland from where it either follows the Baltic Sea shores to Germany and then consequently to the wintering grounds, or it crosses southern Sweden to reach the German coasts through Denmark.
- Pannonic population: this population winters in Yugoslavia, north Italy, Albania and Greece. It migrates from its breeding grounds east of those of the Baltic-North Sea population through eastern Europe, southeast Austria, Czechoslovakia and Pannonia (plains in Hungary and northern former Yugoslavia).

3. Which factors could influence the chances of White-fronted Geese contracting an H5N1 infection (e.g. habitat, behavior, other waterfowl present)?

The White-fronted Geese could mainly contract an H5N1 infection if there was already an infection present in the habitat it mainly occurs in, namely the wetlands of the previously mentioned migratory or wintering countries, or if it got infected by another high risk wild bird species with which it could occur together in these migratory or wintering sites.

4. What are the chances of the virus being sustained and passed along within the goose population and subsequently spread along their migratory routes?

Using the specified estimated input values, the risk can increase rapidly along the migratory routes from a chance of 0.01% in autumn in countries 1 (Estonia, Latvia and Lithuania) to 15% in spring in countries 2 (Poland) according to the GIS model and from 0.01% in autumn in countries 1 (Model 3) to 4.7% in spring in countries 2 (rerun Model 4a) according to the Bayesian Network.

5. What are the chances of the virus being spread to poultry?

Using the specified estimated input values, the risk of the poultry, excluding the additional wild bird number, was found to range from 0.002% in autumn in countries 1 (Estonia, Latvia and Lithuania) to 0.74% in spring in countries 2 (Poland) in the GIS model and from 0.003% in autumn in countries 1 to 22% in spring in countries 4 (Czech Republic, Hungary, Slovakia and Slovenia),

when including the additional high risk wild bird species threat. The risks as calculated with the Bayesian Networks ranged from 0.06% in autumn for countries 1 (Model 3) to 0.2% in spring in countries 1 (rerun Model 4a).

5.2 General conclusions and recommendations

Generally it can be concluded that, even though outbreaks might not yet have occurred in a country, the risk for the wild birds and poultry can become considerable if a wild bird species has become infected with a highly pathogenic avian influenza virus previously along its migratory route. Sheltering the animals from any contact with wild birds (even in the form of dropping feces during flight), should prevent most instances of infection, though humans can also transport these infectious agents to the poultry if no precautions are taken.

With the currently circulating H5N1 avian influenza virus A humans themselves are not at a great risk though, especially not from merely passing wild birds or if the necessary precautions are taken when they regularly come into close contact with poultry or wild birds for professional or recreational purposes. Even if this is the case, the infection rate is quite low and it can not readily be passed on from human to human. It should be borne in mind though, that through reassortment another kind of avian influenza (with a different H and N subtypes) could be formed that could be even more infectious for birds and/or humans.

The results of this preliminary study are based on estimated guesses on the extent of the basic risks and the study has been conducted using spatiotemporally limited input files. Parameters like the chances of wild bird species contracting a highly pathogenic avian influenza infection (from either a previous outbreak or from asymptomatic carriers of the virus), of them sustaining it within the population and of them passing it on to other species (like poultry) need to be determined experimentally. With these risks and more detailed input files a more accurate study, both spatially and temporally, could be performed in order to determine the true extent of the risks of the spread of highly pathogenic avian influenza viruses by migratory wild bird species.

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Appendix I – *Anser albifrons albifrons* migratory sites

The names and locations of the sites of the countries of the EurNuts2 file where the White-fronted Goose is found to pass (countries 1, 2 and 3b) or winter (countries 3a and 4) during its migration.

Countries 1

Estonia

- Põhja-Liivimaa (25°41' East 59°22' North)
- Ropka-Ihaste (26°46' East 58°20' North)

Latvia

- Ziemelu bogs (24°54' East 57°58' North)
- Teici and Pelecare bogs (26°27' East 56°35' North)
- Cena bog (23°51' East 56°51' North)
- Lielais and Pemmas bogs (24°49' East 57°23' North)
- Dviete flood-plain (26°13' East 56°4' North)
- Irbe valley and Dizpurvs (22°3' East 57°35' North)
- Svete lower reaches (23°39' East 56°43' North)
- Berzpils bogs and flood-plains (27°0' East 56°52' North)
- Lubans and fish-ponds (26°52' East 56°44' North)
- Zabolotje bogs (28°0' East 56°37' North)

Lithuania

- Nemunas delta (21°15' East 55°18' North)

Countries 2

Poland

- Lower Odra river valley (14°21' East 53°7' North)
- Miedwie lake (14°52' East 53°16' North)
- Wisla river mouth (18°57' East 54°21' North)
- Wisla lagoon (19°29' East 54°19' North)
- Marshy valley of the Drweca river (19°34' East 53°17' North)
- Warta flood-plain-Slonsk (14°43' East 52°34' North)
- Druzno lake (19°27' East 54°4' North)
- Slowinski National Park (17°16' East 54°41' North)
- Goplo Millenium Park (18°25' East 52°36' North)
- Swidwie lake (14°22' East 53°33' North)

Countries 3a

The Netherlands

- Dollard (7°8' East 53°17' North)
- Gelderse Poort (6°2' East 51°53' North)
- Westerschelde and Saeftinghe (3°50' East 51°23' North)
- Donkse Laagten (4°48' East 51°54' North)
- Lauwersmeer (6°13' East 53°22' North)
- Biesbosch (4°50' East 51°46' North)
- Lake Witte and Zwarte Brekken (5°41' East 53°0' North)
- Yerseke and Kapelse Moer (4°2' East 51°29' North)
- Zwarte Water and Overijsselse Vecht (6°5' East 52°37' North)
- Lake Leekstermeer (6°26' East 53°11' North)

- Oostvaardersplassen (5°21' East 52°26' North)

Belgium

- Zwin (3°21' East 51°20' North)
- Polderkomplex (3°13' East 51°15' North)
- Krekengebied (3°40' East 51°15' North)

Countries 3b

Austria

- Southern Seewinkel and Zitzmannsdorfer Wiesen (16°50' East 47°45' North)

Hungary

- Hortobágy (21°4' East 47°37' North)
- Danube plain (19°15' East 46°49' North)
- Lake Fehér at Kardoskút (20°28' East 46°30' North)
- Sárvíz valley (18°33' East 47°0' North)
- Puszta at Pitvaros (20°43' East 46°19' North)
- Biharugra fish-ponds (21°34' East 46°58' North)

Slovakia

- Zemplínska Sírava (22°0' East 48°48' North)

Countries 4

Hungary

- Lake FertS (16°38' East 47°36' North)
- Lake Öreg at Tata (18°18' East 47°39' North)
- Lake Velence and Dinnyés marshes (18°31' East 47° 10' North)
- Kisköre reservoir (20°30' East 47°30' North)
- Béda-Karapancsa (18°46' East 45°56' North)
- Gemenc (18°45' East 46°7' North)
- Kis-balaton (17°13' East 46°40' North)
- Inner Somogy (17°18' East 46°13' North)
- Pusztaszer Landscape Protection Area (20°10' East 46°15' North)

Slovakia

- Syslovské fields (17°6' East 48°2' North)

Czech Republic

- Nove Mlyny middle reservoir (16°36' East 48°54' North)

Slovenia

- River Drava from Maribor to Sredisce (15°55' East 46°25' North)

Appendix II – WBN for the *Anser albifrons albifrons* sites

The wild bird number (WBN) for the *Anser albifrons albifrons* sites, with a specification of the H5N1 high risk wild bird species, other than *A.a.albifrons*, as defined by the Standing Committee on the Food Chain and Animal Health (2005).

Countries/regions	WBN	H5N1 high birds risk species
Countries 1	23	see individual countries
<i>Estonia</i>	2	<i>see individual regions</i>
- Põhja-Liivimaa	1	Bean goose (<i>Anser fabalis</i>)
- Ropka-Ihaste	1	Bean goose (<i>Anser fabalis</i>)
<i>Latvia</i>	14	<i>see individual regions</i>
- Ziemeļu bogs	2	Bean goose (<i>Anser fabalis</i>), Ruff (<i>Philomachus pugnax</i>)
- Teici and Pelecare bogs	2	Bean goose (<i>Anser fabalis</i>), Ruff (<i>Philomachus pugnax</i>)
- Cena bog	1	Bean goose (<i>Anser fabalis</i>)
- Lielais and Pemmas bogs	1	Bean goose (<i>Anser fabalis</i>)
- Dviete flood-plain	1	Bean goose (<i>Anser fabalis</i>)
- Irbe valley and Dizpurvs	1	Bean goose (<i>Anser fabalis</i>)
- Svete lower reaches	2	Bean goose (<i>Anser fabalis</i>), Northern Pintail (<i>Anas acuta</i>)
- Berzpils bogs and flood-plains	1	Bean goose (<i>Anser fabalis</i>)
- Lubans and fish-ponds	2	Bean goose (<i>Anser fabalis</i>), Northern Pintail (<i>Anas acuta</i>)
- Zabolotje bogs	1	Bean goose (<i>Anser fabalis</i>)
<i>Lithuania</i>	7	<i>see individual regions</i>
- Nemunas delta	7	Bean goose (<i>Anser fabalis</i>), Gadwall (<i>Anas strepera</i>), Eurasian Wigeon (<i>Anas penelope</i>), Northern Shoveler (<i>Anas clypeata</i>), Northern Pintail (<i>Anas acuta</i>), Common Pochard (<i>Aythya ferina</i>), Tufted Duck (<i>Aythya fuligula</i>)
Countries 2	24	see individual countries
<i>Poland</i>	24	<i>see individual regions</i>
- Lower Odra river valley	4	Bean goose (<i>Anser fabalis</i>), Gadwall (<i>Anas strepera</i>), Common Pochard (<i>Aythya ferina</i>), Tufted Duck (<i>Aythya fuligula</i>)
- Miedwie lake	1	Bean goose (<i>Anser fabalis</i>)
- Wisla river mouth	2	Tufted Duck (<i>Aythya fuligula</i>), Mew Gull (<i>Larus canus</i>)
- Wisla lagoon	2	Common Teal (<i>Anas crecca</i>), Common Pochard

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		(<i>Aythya ferina</i>)
- Marshy valley of the Drweca river	0	none
- Warta flood-plain-Slonsk	8	Bean goose (<i>Anser fabalis</i>), Gadwall (<i>Anas strepera</i>), Eurasian Wigeon (<i>Anas penelope</i>), Mallard (<i>Anas platyrhynchos</i>), Northern Shoveler (<i>Anas clypeata</i>), Garganey (<i>Anas querquedula</i>), Common Pochard (<i>Aythya ferina</i>), Tufted duck (<i>Aythya fuligula</i>)
- Druzno lake	2	Bean goose (<i>Anser fabalis</i>), Gadwall (<i>Anas strepera</i>)
- Slowinski National Park	1	Bean goose (<i>Anser fabalis</i>)
- Goplo Millenium Park	1	Bean goose (<i>Anser fabalis</i>)
- Swidwie lake	3	Bean goose (<i>Anser fabalis</i>), Gadwall (<i>Anas strepera</i>), Garganey (<i>Anas querquedula</i>)
Countries 3a	20	see individual countries
<i>The Netherlands</i>	17	<i>see individual regions</i>
- Dollard	2	Bean goose (<i>Anser fabalis</i>), Common Teal (<i>Anas crecca</i>)
- Gelderse Poort	2	Bean goose (<i>Anser fabalis</i>), Northern Shoveler (<i>Anas clypeata</i>)
- Westerschelde and Saeftinghe	2	Eurasian Wigeon (<i>Anas penelope</i>), Northern Pintail (<i>Anas acuta</i>)
- Donkse Laagten	0	None
- Lauwersmeer	6	Gadwall (<i>Anas strepera</i>), Eurasian Wigeon (<i>Anas penelope</i>), Northern Shoveler (<i>Anas clypeata</i>), Northern Pintail (<i>Anas acuta</i>), Common Teal (<i>Anas crecca</i>), Ruff (<i>Philomachus pugnax</i>)
- Biesbosch	1	Gadwall (<i>Anas strepera</i>)
- Lake Witte and Zwarte Brekken	0	None
- Yerseke and Kapelse Moer	0	None
- Zwarte Water and Overijsselse Vecht	0	None
- Lake Leekstermeer	0	None
- Oostvaardersplassen	4	Gadwall (<i>Anas strepera</i>), Northern Pintail (<i>Anas acuta</i>), Northern Shoveler (<i>Anas clypeata</i>), Common Teal (<i>Anas crecca</i>)
<i>Belgium</i>	3	<i>see individual regions</i>
- Zwin	0	none
- Polderkomplex	3	Bean goose (<i>Anser fabalis</i>), Eurasian Wigeon (<i>Anas penelope</i>), Northern Shoveler (<i>Anas clypeata</i>)
- Krekengebied	0	none
Countries 3b	13	see individual countries

<i>Austria</i>	2	<i>see individual regions</i>
- Southern Seewinkel and Zitzmannsdorfer Wiesen	2	Bean goose (<i>Anser fabalis</i>), Gadwall (<i>Anas strepera</i>)
<i>Hungary</i>	8	<i>see individual regions</i>
- Hortobágy	4	Bean goose (<i>Anser fabalis</i>), Northern Shoveler (<i>Anas clypeata</i>), Common Teal (<i>Anas crecca</i>), Ruff (<i>Philomachus pugnax</i>)
- Danube plain	1	Northern Pintail (<i>Anas acuta</i>)
- Lake Fehér at Kardoskút	0	none
- Sárvíz valley	2	Bean goose (<i>Anser fabalis</i>), Mallard (<i>Anas platyrhynchos</i>)
- Puszta at Pitvaros	0	none
- Biharugra fish-ponds	1	Mallard (<i>Anas platyrhynchos</i>)
<i>Slovakia</i>	3	<i>see individual regions</i>
- Zemplínska Sírava	3	Bean goose (<i>Anser fabalis</i>), Mallard (<i>Anas platyrhynchos</i>), Common Black-headed Gull (<i>Larus ridibundus</i>)
Countries 4	16	see individual countries
<i>Hungary</i>	10	<i>see individual regions</i>
- Lake FertS	3	Bean goose (<i>Anser fabalis</i>), Gadwall (<i>Anas strepera</i>), Common Teal (<i>Anas crecca</i>)
- Lake Öreg at Tata	1	Bean goose (<i>Anser fabalis</i>)
- Lake Velence and Dinnyés marshes	1	Bean goose (<i>Anser fabalis</i>)
- Kisköre reservoir	0	none
- Béda-Karapanca	1	Bean goose (<i>Anser fabalis</i>)
- Gemenc	1	Bean goose (<i>Anser fabalis</i>)
- Kis-balaton	1	Bean goose (<i>Anser fabalis</i>)
- Inner Somogy	1	Bean goose (<i>Anser fabalis</i>)
- Pusztaszer Landscape Protection Area	1	Mallard (<i>Anas platyrhynchos</i>)
<i>Slovakia</i>	2	<i>see individual regions</i>
- Syslovské fields	2	Bean goose (<i>Anser fabalis</i>), Mallard (<i>Anas platyrhynchos</i>)
<i>Czech Republic</i>	1	<i>see individual regions</i>
- Nove Mlyny middle reservoir	1	Bean goose (<i>Anser fabalis</i>)
<i>Slovenia</i>	3	<i>see individual regions</i>
- River Drava from Maribor to Sredisce	3	Bean goose (<i>Anser fabalis</i>), Mallard (<i>Anas platyrhynchos</i>), Tufted Duck (<i>Aythya fuligula</i>)

Appendix III.A – Input chances Model 1.

The input values of the chances as used in the Bayesian Network of Model 1 including an example of the application of these values in the Bayesian Network itself.

FOR	TABLE	GIVEN
ChanceH5N1infC1	0.0050 0.995	
ChanceH5N1wildBirdsC1	0.0050 0.995	
ChanceH5N1geeseC1	0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1infC1 ChanceH5N1wildBirdsC1
ChanceH5N1chickenC1	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC1
ChanceH5N1geeseC2	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC1 ChanceH5N1infC2 ChanceH5N1wildBirdsC2
ChanceH5N1infC2	0.0050 0.995	
ChanceH5N1wildBirdsC2	0.0050 0.995	
ChanceH5N1chickenC2	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC2
ChanceH5N1infC3a	0.0050 0.995	
ChanceH5N1infC3b	0.0050 0.995	
ChanceH5N1geeseC3a	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3a ChanceH5N1wildBirdsC3a
ChanceH5N1geeseC3b	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3b ChanceH5N1wildBirdsC3b
ChanceH5N1wildBirdsC3a	0.0050 0.995	
ChanceH5N1wildBirdsC3b	0.0050 0.995	
ChanceH5N1chickenC3a	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC3a
ChanceH5N1chickenC3b	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC3b
ChanceH5N1geeseC4	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC3b ChanceH5N1infC4 ChanceH5N1wildBirdsC4
ChanceH5N1infC4	0.0050 0.995	
ChanceH5N1wildBirdsC4	0.0050 0.995	
ChanceH5N1chickenC4	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC4

An example of the application of the shaded factor above (ChanceH5N1geeseC2) is given in the table below. When neither of the previous factors exhibits an infection, the chance of the geese in countries 2 of contracting an infection is 0.0001 (0.01%). If one of these factors is true, the geese have a chance of 0.01 (1%) of becoming infected. If two are true, this chance is 0.02 and for all it is 0.03.

GeeseC2

cWBc2	Inf				No inf			
	Inf		No inf		Inf		No inf	
cInfC2	Inf	No infect						
GeeseC1	Infection	No infect						
Infection	0.03	0.02	0.02	0.01	0.02	0.01	0.01	1.0E-4
No infection	0.97	0.98	0.98	0.99	0.98	0.99	0.99	0.9999

Thus depending on the chances of the variables under “Given” the variable mentioned under “For” has a chance mentioned under “Table” of becoming infected itself. If nothing is mentioned under “Given” the variable under “For” just has a single chance of being true and a chance of one minus that chance of being false. If the variable under “For” is influenced by a variable under “Given” it has a chance of being true when the variable under “Given” is true, a chance of being true when the chance under “Given” is false, a chance of being false for “Given” is true and a chance of being false for “Given” is false, thus resulting in these 4 figures under “Table”.

Appendix III.B – Input chances Model 2.

The input values of the chances as used in the Bayesian Network of Model 2.

FOR	TABLE	GIVEN
ChanceH5N1infC1	0.0050 0.995	
ChanceH5N1wildBirdsC1	0.0050 0.995	
ChanceH5N1geeseC1	0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1infC1 ChanceH5N1wildBirdsC1
ChanceH5N1chickenC1	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC1
ChanceH5N1geeseC2	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC1 ChanceH5N1infC2 ChanceH5N1wildBirdsC2
ChanceH5N1infC2	0.01 0.99 0.0050 0.995	ChanceH5N1infC1
ChanceH5N1wildBirdsC2	0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC1
ChanceH5N1chickenC2	0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC1 ChanceH5N1geeseC2
ChanceH5N1infC3a	0.01 0.99 0.0050 0.995	ChanceH5N1infC2
ChanceH5N1infC3b	0.01 0.99 0.0050 0.995	ChanceH5N1infC2
ChanceH5N1geeseC3a	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3a ChanceH5N1wildBirdsC3a
ChanceH5N1geeseC3b	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3b ChanceH5N1wildBirdsC3b
ChanceH5N1wildBirdsC3a	0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC2
ChanceH5N1wildBirdsC3b	0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC2
ChanceH5N1chickenC3a	0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC2 ChanceH5N1geeseC3a
ChanceH5N1chickenC3b	0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC2 ChanceH5N1geeseC3b
ChanceH5N1geeseC4	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC3b ChanceH5N1infC4 ChanceH5N1wildBirdsC4
ChanceH5N1infC4	0.01 0.99 0.0050 0.995	ChanceH5N1infC3b
ChanceH5N1wildBirdsC4	0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC3b
ChanceH5N1chickenC4	0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC3b ChanceH5N1geeseC4

Appendix III.C – Input chances Model 2a.

The input values of the chances as used in the Bayesian Network of Model 2a.

FOR	TABLE	GIVEN
ChanceH5N1infC1	0.0050 0.995	
ChanceH5N1wildBirdsC1	0.0050 0.995	
ChanceH5N1geeseC1	0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1infC1 ChanceH5N1wildBirdsC1
ChanceH5N1chickenC1	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC1
ChanceH5N1geeseC2	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC1 ChanceH5N1infC2 ChanceH5N1wildBirdsC2
ChanceH5N1infC2	0.01 0.99 0.0050 0.995	ChanceH5N1infC1
ChanceH5N1wildBirdsC2	0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC1
ChanceH5N1chickenC2	0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC1 ChanceH5N1geeseC2
ChanceH5N1infC3a	0.015 0.985 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1infC1 ChanceH5N1infC2
ChanceH5N1infC3b	0.015 0.985 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1infC1 ChanceH5N1infC2
ChanceH5N1geeseC3a	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3a ChanceH5N1wildBirdsC3a
ChanceH5N1geeseC3b	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3b ChanceH5N1wildBirdsC3b
ChanceH5N1wildBirdsC3a	0.015 0.985 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC1 ChanceH5N1wildBirdsC2
ChanceH5N1wildBirdsC3b	0.015 0.985 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC1 ChanceH5N1wildBirdsC2
ChanceH5N1chickenC3a	0.15 0.85 0.1 0.9 0.1 0.9 0.05 0.95 0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC1 ChanceH5N1chickenC2 ChanceH5N1geeseC3a
ChanceH5N1chickenC3b	0.15 0.85 0.1 0.9 0.1 0.9 0.05 0.95 0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC1 ChanceH5N1chickenC2 ChanceH5N1geeseC3b
ChanceH5N1geeseC4	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC3b ChanceH5N1infC4 ChanceH5N1wildBirdsC4
ChanceH5N1infC4	0.025 0.975 0.02 0.98 0.02 0.98 0.015 0.985 0.02 0.98 0.015 0.985 0.015 0.985 0.01 0.99 0.02 0.98 0.015 0.985 0.015 0.985 0.01 0.99 0.015 0.985 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1infC1 ChanceH5N1infC2 ChanceH5N1infC3a ChanceH5N1infC3b
ChanceH5N1wildBirdsC4	0.03 0.97 0.025 0.975 0.025 0.975 0.02 0.98 0.02 0.98 0.015 0.985 0.015 0.985 0.01 0.99 0.02 0.98 0.015 0.985 0.015 0.985 0.01 0.99 0.015 0.985 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC1 ChanceH5N1wildBirdsC2 ChanceH5N1wildBirdsC3a ChanceH5N1wildBirdsC3b
ChanceH5N1chickenC4	0.2 0.8 0.15 0.85 0.15 0.85 0.1 0.9 0.15 0.85 0.1 0.9 0.1 0.9 0.05 0.95 0.15 0.85 0.1 0.9 0.1 0.9 0.05 0.95 0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC1 ChanceH5N1chickenC2 ChanceH5N1chickenC3b ChanceH5N1geeseC4

Appendix III.D – Input chances Model 2b.

The input values of the chances as used in the Bayesian Network of Model 2b.

FOR	TABLE	GIVEN
ChanceH5N1infC1	0.0050 0.995	
ChanceH5N1wildBirdsC1	0.0050 0.995	
ChanceH5N1geeseC1	0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1infC1 ChanceH5N1wildBirdsC1
ChanceH5N1chickenC1	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC1
ChanceH5N1geeseC2	0.04 0.96 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC1 ChanceH5N1infC2 ChanceH5N1wildBirdsC2
ChanceH5N1infC2	0.01 0.99 0.0050 0.995	ChanceH5N1infC1
ChanceH5N1wildBirdsC2	0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC1
ChanceH5N1chickenC2	0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC1 ChanceH5N1geeseC2
ChanceH5N1infC3a	0.01 0.99 0.0050 0.995	ChanceH5N1infC2
ChanceH5N1infC3b	0.01 0.99 0.0050 0.995	ChanceH5N1infC2
ChanceH5N1geeseC3a	0.04 0.96 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3a ChanceH5N1wildBirdsC3a
ChanceH5N1geeseC3b	0.04 0.96 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3b ChanceH5N1wildBirdsC3b
ChanceH5N1wildBirdsC3a	0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC2
ChanceH5N1wildBirdsC3b	0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC2
ChanceH5N1chickenC3a	0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC2 ChanceH5N1geeseC3a
ChanceH5N1chickenC3b	0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC2 ChanceH5N1geeseC3b
ChanceH5N1geeseC4	0.04 0.96 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC3b ChanceH5N1infC4 ChanceH5N1wildBirdsC4
ChanceH5N1infC4	0.01 0.99 0.0050 0.995	ChanceH5N1infC3b
ChanceH5N1wildBirdsC4	0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC3b
ChanceH5N1chickenC4	0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC3b ChanceH5N1geeseC4

Appendix III.E – Input chances Model 2c.

The input values of the chances as used in the Bayesian Network of Model 2c.

FOR	TABLE	GIVEN
ChanceH5N1infC1	0.0050 0.995	
ChanceH5N1wildBirdsC1	0.0050 0.995	
ChanceH5N1geeseC1	0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1infC1 ChanceH5N1wildBirdsC1
ChanceH5N1chickenC1	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC1
ChanceH5N1geeseC2	0.04 0.96 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC1 ChanceH5N1infC2 ChanceH5N1wildBirdsC2
ChanceH5N1infC2	0.01 0.99 0.0050 0.995	ChanceH5N1infC1
ChanceH5N1wildBirdsC2	0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC1
ChanceH5N1chickenC2	0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC1 ChanceH5N1geeseC2
ChanceH5N1infC3a	0.02 0.98 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1infC1 ChanceH5N1infC2
ChanceH5N1infC3b	0.02 0.98 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1infC1 ChanceH5N1infC2
ChanceH5N1geeseC3a	0.04 0.96 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3a ChanceH5N1wildBirdsC3a
ChanceH5N1geeseC3b	0.04 0.96 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3b ChanceH5N1wildBirdsC3b
ChanceH5N1wildBirdsC3a	0.02 0.98 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC1 ChanceH5N1wildBirdsC2
ChanceH5N1wildBirdsC3b	0.02 0.98 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC1 ChanceH5N1wildBirdsC2
ChanceH5N1chickenC3a	0.2 0.8 0.1 0.9 0.1 0.9 0.05 0.95 0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC1 ChanceH5N1chickenC2 ChanceH5N1geeseC3a
ChanceH5N1chickenC3b	0.2 0.8 0.1 0.9 0.1 0.9 0.05 0.95 0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC1 ChanceH5N1chickenC2 ChanceH5N1geeseC3b
ChanceH5N1geeseC4	0.04 0.96 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC3b ChanceH5N1infC4 ChanceH5N1wildBirdsC4
ChanceH5N1infC4	0.08 0.92 0.04 0.96 0.04 0.96 0.02 0.98 0.04 0.96 0.02 0.98 0.02 0.98 0.01 0.99 0.04 0.96 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1infC1 ChanceH5N1infC2 ChanceH5N1infC3a ChanceH5N1infC3b
ChanceH5N1wildBirdsC4	0.08 0.92 0.04 0.96 0.04 0.96 0.02 0.98 0.04 0.96 0.02 0.98 0.02 0.98 0.01 0.99 0.04 0.96 0.02 0.398 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 0.0050 0.995	ChanceH5N1wildBirdsC1 ChanceH5N1wildBirdsC2 ChanceH5N1wildBirdsC3a ChanceH5N1wildBirdsC3b
ChanceH5N1chickenC4	0.8 0.2 0.4 0.6 0.4 0.6 0.2 0.8 0.4 0.6 0.2 0.8 0.2 0.8 0.1 0.9 0.4 0.6 0.2 0.8 0.2 0.8 0.1 0.9 0.2 0.8 0.1 0.9 0.1 0.9 0.05 0.95 0.4 0.6 0.2 0.8 0.2 0.8 0.1 0.9 0.2 0.8 0.1 0.9 0.1 0.9 0.05 0.95 0.2 0.8 0.1 0.9 0.1 0.9 0.05 0.95 0.1 0.9 0.05 0.95 0.05 0.95 1.0E-4 0.9999	ChanceH5N1chickenC1 ChanceH5N1chickenC2 ChanceH5N1chickenC3a ChanceH5N1chickenC3b ChanceH5N1geeseC4

Appendix III.F – Input chances Model 3.

The input values of the chances as used in the Bayesian Network of Model 3.

FOR	TABLE	GIVEN
ChanceH5N1infC1	2.32E-4 0.999768	
ChanceH5N1wildBirdsC1	8.95E-4 0.999105	
ChanceH5N1geeseC1	0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1infC1 ChanceH5N1wildBirdsC1
ChanceH5N1chickenC1	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC1
ChanceH5N1geeseC2	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC1 ChanceH5N1infC2 ChanceH5N1wildBirdsC2
ChanceH5N1infC2	0.031546 0.968454	
ChanceH5N1wildBirdsC2	9.84973267580763E-4 0.999015026732419	
ChanceH5N1chickenC2	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC2
ChanceH5N1infC3a	0.028833 0.971167	
ChanceH5N1infC3b	0.017202 0.982798	
ChanceH5N1geeseC3a	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3a ChanceH5N1wildBirdsC3a
ChanceH5N1geeseC3b	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3b ChanceH5N1wildBirdsC3b
ChanceH5N1wildBirdsC3a	6.7275E-4 0.99932725	
ChanceH5N1wildBirdsC3b	3.45227E-4 0.999654773	
ChanceH5N1chickenC3a	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC3a
ChanceH5N1chickenC3b	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC3b
ChanceH5N1geeseC4	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC3b ChanceH5N1infC4 ChanceH5N1wildBirdsC4
ChanceH5N1infC4	0.047428 0.952572	
ChanceH5N1wildBirdsC4	4.59497E-4 0.999540503	
ChanceH5N1chickenC4	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC4

Appendix III.G – Input chances Model 4.

The input values of the chances as used in the Bayesian Network of Model 4.

FOR	TABLE	GIVEN
ChanceH5N1infC1	2.32E-4 0.999768	
ChanceH5N1wildBirdsC1	8.95E-4 0.999105	
ChanceH5N1geeseC1	0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1infC1 ChanceH5N1wildBirdsC1
ChanceH5N1chickenC1	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC1
ChanceH5N1geeseC2	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC1 ChanceH5N1infC2 ChanceH5N1wildBirdsC2
ChanceH5N1infC2	0.031546 0.968454	
ChanceH5N1wildBirdsC2	9.84973267580763E-4 0.999015026732419	
ChanceH5N1chickenC2	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC2
ChanceH5N1infC3a	0.028833 0.971167	
ChanceH5N1infC3b	0.017202 0.982798	
ChanceH5N1geeseC3a	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3a ChanceH5N1wildBirdsC3a
ChanceH5N1geeseC3b	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3b ChanceH5N1wildBirdsC3b
ChanceH5N1wildBirdsC3a	6.7275E-4 0.99932725	
ChanceH5N1wildBirdsC3b	3.45227E-4 0.999654773	
ChanceH5N1chickenC3a	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC3a
ChanceH5N1chickenC3b	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC3b
ChanceH5N1geeseC4	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC3b ChanceH5N1infC4 ChanceH5N1wildBirdsC4
ChanceH5N1infC4	0.047428 0.952572	
ChanceH5N1wildBirdsC4	4.59497E-4 0.999540503	
ChanceH5N1chickenC4	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC4
SprCH5N1geeseC3b	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	SprCH5N1wildBirdsC3b SprCH5N1infC3b WinCH5N1geeseC4
SprCH5N1wildBirdsC3b	3.45227E-4 0.999654773	
SprCH5N1infC3b	0.117052 0.882948	
SprCH5N1chickenC3b	0.05 0.95 1.0E-4 0.9999	SprCH5N1geeseC3b
SprCH5N1geeseC2	0.04 0.96 0.03 0.97 0.03 0.97 0.02 0.98 0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	SprCH5N1geeseC3b SprCH5N1wildBirdsC2 SprCH5N1infC2 WinCH5N1geeseC3a
SprCH5N1chickenC2	0.05 0.95 1.0E-4 0.9999	SprCH5N1geeseC2
SprCH5N1wildBirdsC2	9.84973267580763E-4 0.999015026732419	
SprCH5N1infC2	0.143131 0.856869	
SprCH5N1geeseC1	0.03 0.97 0.02 0.98 0.02 0.98 0.01 0.99 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	SprCH5N1geeseC2 SprCH5N1wildBirdsC1 SprCH5N1infC1
SprCH5N1chickenC1	0.05 0.95 1.0E-4 0.9999	SprCH5N1geeseC1
SprCH5N1wildBirdsC1	8.95E-4 0.999105	
SprCH5N1infC1	0.143363 0.856637	
WinCH5N1geeseC3a	0.9999 1.0E-4 1.0E-4 0.9999	ChanceH5N1geeseC3a
WinCH5N1geeseC4	0.9999 1.0E-4 1.0E-4 0.9999	ChanceH5N1geeseC4
WinCH5N1ckC3a	0.05 0.95 1.0E-4 0.9999	WinCH5N1geeseC3a
WinCH5N1ckC4	0.05 0.95 1.0E-4 0.9999	WinCH5N1geeseC4

Appendix III.H – Input chances Model 5.

The input values of the chances as used in the Bayesian Network of Model 5.

FOR	TABLE	GIVEN
ChanceH5N1geeseC1	2.32E-4 0.999768	
ChanceH5N1chickenC1	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC1
ChanceH5N1geeseC2	0.031546 0.968454 1.0E-4 0.9999	ChanceH5N1geeseC1
ChanceH5N1chickenC2	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC2
ChanceH5N1geeseC3a	0.028833 0.971167 1.0E-4 0.9999	ChanceH5N1geeseC2
ChanceH5N1geeseC3b	0.017202 0.982798 1.0E-4 0.9999	ChanceH5N1geeseC2
ChanceH5N1chickenC3a	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC3a
ChanceH5N1chickenC3b	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC3b
ChanceH5N1geeseC4	0.047428 0.952572 1.0E-4 0.9999	ChanceH5N1geeseC3b
ChanceH5N1chickenC4	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC4
SprCH5N1geesec3b	0.058576 0.941424 0.058576 0.941424	WinCH5N1geeseC4
SprCH5N1chickenC3b	0.05 0.95 1.0E-4 0.9999	SprCH5N1geesec3b
SprCH5N1geeseC2	0.143131 0.856869 0.07101816 0.92898184 0.04208068 0.95791932 1.0E-4 0.9999	SprCH5N1geesec3b WinCH5N1geeseC3a
SprCH5N1chickenC2	0.05 0.95 1.0E-4 0.9999	SprCH5N1geeseC2
SprCH5N1geeseC1	0.087638 0.912362 1.0E-4 0.9999	SprCH5N1geeseC2
SprCH5N1chickenC1	0.05 0.95 1.0E-4 0.9999	SprCH5N1geeseC1
WinCH5N1geeseC4	0.9999 1.0E-4 1.0E-4 0.9999	ChanceH5N1geeseC4
WinCH5N1ckC3a	0.05 0.95 1.0E-4 0.9999	WinCH5N1geeseC3a
WinCH5N1ckC4	0.05 0.95 1.0E-4 0.9999	WinCH5N1geeseC4
WinCH5N1geeseC3a	0.9999 1.0E-4 1.0E-4 0.9999	ChanceH5N1geeseC3a

Appendix III.J – Input chances Model 1a.

The input values of the chances as used in the Bayesian Network of Model 1a.

FOR	TABLE	GIVEN
ChanceH5N1infC1	0.0050 0.995	
ChanceH5N1wildBirdsC1	0.0050 0.995	
ChanceH5N1geeseC1	0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1infC1 ChanceH5N1wildBirdsC1
ChanceH5N1chickenC1	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC1
ChanceH5N1geeseC2	0.97 0.03 0.96 0.04 0.96 0.04 0.95 0.05 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC1 ChanceH5N1infC2 ChanceH5N1wildBirdsC2
ChanceH5N1infC2	0.0050 0.995	
ChanceH5N1wildBirdsC2	0.0050 0.995	
ChanceH5N1chickenC2	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC2
ChanceH5N1infC3a	0.0050 0.995	
ChanceH5N1infC3b	0.0050 0.995	
ChanceH5N1geeseC3a	0.97 0.03 0.96 0.04 0.96 0.04 0.95 0.05 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3a ChanceH5N1wildBirdsC3a
ChanceH5N1geeseC3b	0.97 0.03 0.96 0.04 0.96 0.04 0.95 0.05 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC2 ChanceH5N1infC3b ChanceH5N1wildBirdsC3b
ChanceH5N1wildBirdsC3a	0.0050 0.995	
ChanceH5N1wildBirdsC3b	0.0050 0.995	
ChanceH5N1chickenC3a	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC3a
ChanceH5N1chickenC3b	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC3b
ChanceH5N1geeseC4	0.97 0.03 0.96 0.04 0.96 0.04 0.95 0.05 0.02 0.98 0.01 0.99 0.01 0.99 1.0E-4 0.9999	ChanceH5N1geeseC3b ChanceH5N1infC4 ChanceH5N1wildBirdsC4
ChanceH5N1infC4	0.0050 0.995	
ChanceH5N1wildBirdsC4	0.0050 0.995	
ChanceH5N1chickenC4	0.05 0.95 1.0E-4 0.9999	ChanceH5N1geeseC4

Appendix IV.A – Bayesian Network results using BNJ

The chances of infection with the H5N1 virus for various variables as determined with BNJ, using the specified models (Mx = Model x, r = rerun). For the variables an explanation of the abbreviations is given in Figure 3, with c = chance, w = winter and s = spring. If no season is specified, it concerns the autumn chance. Shaded values represent those values that had not been assigned to the model initially, with a lighter shading indicating values smaller than 0.1%.

Variable	M1	Mr1	M2	Mr2	M2a	Mr2a	M2b	Mr2b	M2c	Mr2c	M3	Mr3
cH5N1infC1	0.5%	0.5%	0.5%	1.0%	0.5%	2.0%	0.5%	1.0%	0.5%	3.9%	0.0%	0.0%
cH5N1wbC1	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.1%	0.1%
cH5N1gsC1	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.1%	0.0%	0.0%
cH5N1ckC1	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
cH5N1infC2	0.5%	100%	0.5%	100%	0.5%	100%	0.5%	100%	0.5%	100%	3.2%	100%
cH5N1wbC2	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.1%	0.1%
cH5N1gsC2	0.0%	1.0%	0.0%	1.0%	0.0%	1.0%	0.0%	1.0%	0.0%	1.0%	0.0%	1.0%
cH5N1ckC2	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%
cH5N1infC3 ^a	0.5%	0.5%	0.5%	1.0%	0.5%	1.3%	0.5%	1.0%	0.5%	2.1%	2.9%	2.9%
cH5N1wbC3 ^a	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.1%	0.1%
cH5N1gsC3 ^a	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
cH5N1ckC3 ^a	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%	0.0%
cH5N1infC3 ^b	0.5%	100%	0.5%	100%	0.5%	100%	0.5%	100%	0.5%	100%	1.7%	100%
cH5N1wbC3 ^b	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.0%	0.0%
cH5N1gsC3 ^b	0.0%	1.0%	0.0%	1.0%	0.0%	1.0%	0.0%	1.0%	0.0%	1.0%	0.0%	1.0%
cH5N1ckC3 ^b	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%
cH5N1infC4	0.5%	100%	0.5%	100%	0.5%	100%	0.5%	100%	0.5%	100%	4.7%	100%
cH5N1wbC4	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.0%	0.0%
cH5N1gsC4	0.0%	1.0%	0.0%	1.0%	0.0%	1.0%	0.0%	1.0%	0.0%	1.0%	0.1%	1.0%
cH5N1ckC4	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%	0.0%	0.1%

THE RISK OF DISPERSAL OF THE HIGHLY PATHOGENIC AVIAN INFLUENZA VIRUS H5N1 BY *ANSER ALBIFRONS ALBIFRONS* IN EUROPE

Variable	M4	Mr4	M5	Mr5
cH5N1infC1	0.0%	0.0%	-	-
cH5N1wbC1	0.1%	0.1%	-	-
cH5N1gsC1	0.0%	0.0%	0.0%	6.8%
cH5N1ckC1	0.0%	0.0%	0.0%	0.4%
cH5N1infC2	3.2%	100%	-	-
cH5N1wbC2	0.1%	0.1%	-	-
cH5N1gsC2	0.0%	1.0%	0.0%	100%
cH5N1ckC2	0.0%	0.1%	0.0%	5.0%
cH5N1infC3 ^a	2.9%	2.9%	-	-
cH5N1wbC3 ^a	0.1%	0.1%	-	-
cH5N1gsC3 ^a	0.0%	0.0%	0.0%	5.6%
cH5N1ckC3 ^a	0.0%	0.0%	0.0%	0.3%
cH5N1infC3 ^b	1.7%	100%	-	-
cH5N1wbC3 ^b	0.0%	0.0%	-	-
cH5N1gsC3 ^b	0.0%	1.0%	0.0%	100%
cH5N1ckC3 ^b	0.0%	0.1%	0.0%	5.0%
cH5N1infC4	4.7%	100%	-	-
cH5N1wbC4	0.0%	0.0%	-	-
cH5N1gsC4	0.1%	1.0%	0.0%	100%
cH5N1ckC4	0.0%	0.1%	0.0%	5.0%
wcH5N1gsC3 ^a	0.0%	0.1%	0.0%	5.7%
wcH5N1ckC3 ^a	0.0%	0.0%	0.0%	0.3%
wcH5N1gsC4	0.1%	1.0%	0.0%	100%
wcH5N1ckC4	0.0%	0.1%	0.0%	5.0%
scH5N1infC3 ^b	11.7%	100%	-	-
scH5N1wbC3 ^b	0.0%	0.0%	-	-
scH5N1gsC3 ^b	0.1%	1.0%	0.0%	100%
scH5N1ckC3 ^b	0.0%	0.1%	0.0%	5.0%
scH5N1infC2	14.3%	100%	-	-
scH5N1wbC2	0.1%	0.1%	-	-
scH5N1gsC2	0.2%	1.0%	0.0%	100%
scH5N1ckC2	0.0%	0.1%	0.0%	5.0%
scH5N1infC1	14.3%	14.3%	-	-
scH5N1wbC1	0.1%	0.1%	-	-
scH5N1gsC1	0.2%	0.2%	0.0%	8.8%
scH5N1ckC1	0.0%	0.0%	0.0%	0.4%

Appendix IV.B – Bayesian Network results using Hugin Lite

The chances of infection with the H5N1 virus for various variables as determined with Hugin Lite, using the specified models (Mx = Model x, r = rerun). For the variables an explanation of the abbreviations is given in Figure 3, with c = chance, w = winter and s = spring. If no season is specified, it concerns the autumn chance. Shaded values represent those values that had not been assigned to the model initially.

Variable	M1	Mr1	M2	Mr2	M2a	Mr2a	M2b	Mr2b	M2c	Mr2c	M3	Mr3
cH5N1infC1	0.5%	0.5%	0.5%	0.995025%	0.5%	2.931541%	0.5%	0.995025%	0.5%	3.901506%	0.023200%	0.023200%
cH5N1wbC1	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.5%	0.089500%	0.089500%
cH5N1gsC1	0.019900%	0.019900%	0.019900%	0.024801%	0.019900%	0.043974%	0.019900%	0.024801%	0.019900%	0.053577%	0.011116%	0.011116%
cH5N1ckC1	0.010993%	0.010993%	0.010993%	0.011238%	0.010993%	0.012194%	0.010993%	0.011238%	0.010993%	0.012673%	0.010555%	0.010555%
cH5N1infC2	0.5%	100%	0.502500%	100%	0.502500%	100%	0.502500%	100%	0.502500%	100%	3.154600%	100%
cH5N1wbC2	0.5%	0.5%	0.502500%	0.502500%	0.502500%	0.502500%	0.502500%	0.502500%	0.502500%	0.502500%	0.098497%	0.098497%
cH5N1gsC2	0.020097%	1.005199%	0.020147%	1.005273%	0.020147%	1.005465%	0.020147%	1.005275%	0.020147%	1.005564%	0.042316%	1.001096%
cH5N1ckC2	0.011003%	0.060159%	0.011554%	0.060724%	0.011554%	0.060780%	0.011554%	0.060724%	0.011554%	0.060809%	0.012112%	0.059955%
cH5N1infC3 ^a	0.5%	0.5%	0.502513%	1%	0.505038%	1.526440%	0.502513%	1%	0.505038%	2.055941%	2.883300%	2.883300%
cH5N1wbC3 ^a	0.5%	0.5%	0.502513%	0.502512%	0.505038%	0.505037%	0.502512%	0.502512%	0.505038%	0.505037%	0.067275%	0.067275%
cH5N1gsC3 ^a	0.020099%	0.029853%	0.020149%	0.034829%	0.020199%	0.040069%	0.020149%	0.034830%	0.020199%	0.045313%	0.039630%	0.049125%
cH5N1ckC3 ^a	0.011003%	0.011490%	0.011582%	0.014768%	0.012133%	0.015641%	0.011582%	0.014768%	0.012133%	0.015928%	0.011978%	0.012451%
cH5N1infC3 ^b	0.5%	100%	0.502513%	100%	0.505038%	100%	0.502512%	100%	0.505038%	100%	1.720200%	100%
cH5N1wbC3 ^b	0.5%	0.5%	0.502512%	0.502513%	0.505038%	0.5%	0.502512%	0.502512%	0.505038%	0.505037%	0.034523%	0.034523%
cH5N1gsC3 ^b	0.020099%	1.015052%	0.020149%	1.015078%	0.020199%	1.015105%	0.020149%	1.015129%	0.020199%	1.015157%	0.027791%	1.010356%
cH5N1ckC3 ^b	0.011003%	0.060651%	0.011582%	0.063683%	0.012133%	0.064295%	0.011582%	0.063685%	0.012133%	0.064324%	0.011387%	0.060417%
cH5N1infC4	0.5%	100%	0.502513%	100%	0.510201%	100%	0.502513%	100%	0.5%	100%	4.742800%	100%
cH5N1wbC4	0.5%	0.5%	0.502513%	0.502513%	0.510201%	0.510201%	0.502513%	0.50213%	0.5%	0.502525%	0.045950%	0.045950%
cH5N1gsC4	0.020099%	1.015151%	0.020150%	1.015176%	0.020302%	1.015255%	0.020150%	1.015228%	0.020302%	1.015228%	0.057684%	1.010563%
cH5N1ckC4	0.011003%	0.060656%	0.011583%	0.063835%	0.013349%	0.068292%	0.011583%	0.063838%	0.013358%	0.068353%	0.012878%	0.060427%

Appendix IV.C – Bayesian Network results for Models 1a, a2, 3a, 4a and 5a.

The chances of infection with the H5N1 virus for various variables as determined with BNJ, using the specified models. For the variables an explanation of the abbreviations is given in Figure 3, with c = chance, w = winter and s = spring. If no season is specified, it concerns the autumn chance. Shaded values represent those values that had not been assigned to the model initially, with lighter shading (for Models 4a and 5a, which were run with BNJ instead of Hugin Lite) indicating values smaller than 0.1%.

Variable	M1a	Mr1a	Ma2	Mra2	Mr3a	Mr3a
cH5N1infC1	0.5%	0.5%	0.5%	0.995025%	0.023200%	0.023200%
cH5N1wbC1	0.5%	0.5%	0.5%	0.5%	0.089500%	0.089500%
cH5N1gsC1	0.019900%	0.019900%	0.019900%	0.024801%	0.011116%	0.011116%
cH5N1ckC1	0.010993%	0.010993%	0.010993%	0.011238%	0.010555%	0.010555%
cH5N1infC2	0.5%	100%	0.502500%	100%	3.154600%	100%
cH5N1wbC2	0.5%	0.5%	0.502500%	0.502500%	0.098497%	0.098497%
cH5N1gsC2	0.038804%	1.023905%	0.038853%	1.028586%	0.052765%	1.011545%
cH5N1ckC2	0.011936%	0.061093%	0.012487%	0.061887%	0.012633%	0.060476%
cH5N1infC3 ^a	0.5%	0.5%	0.502512%	1%	2.883300%	2.883300%
cH5N1wbC3 ^a	0.5%	0.5%	0.502512%	0.502512%	0.067275%	0.067275%
cH5N1gsC3 ^a	0.056760%	0.992509%	0.056857%	1.001931%	0.089332%	1.000080%
cH5N1ckC3 ^a	0.012832%	0.059526%	0.013460%	0.063089%	0.014458%	0.059904%
cH5N1infC3 ^b	0.5%	100%	0.502512%	100%	1.720200%	100%
cH5N1wbC3 ^b	0.5%	0.5%	0.502512%	0.502513%	0.034523%	0.034523%
cH5N1gsC3 ^b	0.056760%	1.977710%	0.056863%	1.982182%	0.077493%	1.961313%
cH5N1ckC3 ^b	0.012832%	0.108688%	0.013461%	0.112004%	0.013867%	0.107870%
cH5N1infC4	0.5%	100%	0.502513%	100%	4.742800%	100%
cH5N1wbC4	0.5%	0.5%	0.502513%	0.502513%	0.045950%	0.045950%
cH5N1gsC4	0.073816%	2.883824%	0.073964%	2.888098%	0.131020%	2.863707%
cH5N1ckC4	0.013683%	0.153903%	0.014363%	0.159715%	0.016538%	0.152899%

Variable	M4a	Mr4a
cH5N1infC1	0.0%	0.0%
cH5N1wbC1	0.1%	0.1%
cH5N1gsC1	0.0%	0.0%
cH5N1ckC1	0.0%	0.0%
cH5N1infC2	3.2%	100%
cH5N1wbC2	0.1%	0.1%
cH5N1gsC2	0.1%	1.0%
cH5N1ckC2	0.0%	0.1%
cH5N1infC3 ^a	2.9%	2.9%
cH5N1wbC3 ^a	0.1%	0.1%
cH5N1gsC3 ^a	0.1%	1.0%
cH5N1ckC3 ^a	0.0%	0.1%
cH5N1infC3 ^b	1.7%	100%
cH5N1wbC3 ^b	0.0%	0.0%
cH5N1gsC3 ^b	0.1%	2.0%
cH5N1ckC3 ^b	0.0%	0.1%
cH5N1infC4	4.7%	100%
cH5N1wbC4	0.0%	0.0%
cH5N1gsC4	0.1%	2.9%
cH5N1ckC4	0.0%	0.2%
wcH5N1gsC3 ^a	0.1%	1.0%
wcH5N1ckC3 ^a	0.0%	0.1%
wcH5N1gsC4	0.1%	2.9%
wcH5N1ckC4	0.0%	0.2%
scH5N1infC3 ^b	11.7%	100%
scH5N1wbC3 ^b	0.0%	0.0%
scH5N1gsC3 ^b	0.3%	3.7%
scH5N1ckC3 ^b	0.0%	0.2%
scH5N1infC2	14.3%	100%
scH5N1wbC2	0.1%	0.1%
scH5N1gsC2	0.5%	4.7%
scH5N1ckC2	0.0%	0.2%
scH5N1infC1	14.3%	14.3%
scH5N1wbC1	0.1%	0.1%
scH5N1gsC1	0.6%	4.6%
scH5N1ckC1	0.0%	0.2%
Variable	M5a	Mr5a

cH5N1infC1	-	-
cH5N1wbC1	-	-
cH5N1gsC1	0.0%	68.8%
cH5N1ckC1	0.0%	3.4%
cH5N1infC2	-	-
cH5N1wbC2	-	-
cH5N1gsC2	0.0%	100%
cH5N1ckC2	0.0%	5.0%
cH5N1infC3 ^a	-	-
cH5N1wbC3 ^a	-	-
cH5N1gsC3 ^a	0.0%	95.1%
cH5N1ckC3 ^a	0.0%	4.8%
cH5N1infC3 ^b	-	-
cH5N1wbC3 ^b	-	-
cH5N1gsC3 ^b	0.0%	100%
cH5N1ckC3 ^b	0.0%	5.0%
cH5N1infC4	-	-
cH5N1wbC4	-	-
cH5N1gsC4	0.0%	100%
cH5N1ckC4	0.0%	5.0%
wcH5N1gsC3 ^a	0.1%	95.1%
wcH5N1ckC3 ^a	0.0%	4.8%
wcH5N1gsC4	0.1%	100%
wcH5N1ckC4	0.0%	5.0%
scH5N1infC3 ^b	-	-
scH5N1wbC3 ^b	-	-
scH5N1gsC3 ^b	0.1%	100%
scH5N1ckC3 ^b	0.0%	5.0%
scH5N1infC2	-	-
scH5N1wbC2	-	-
scH5N1gsC2	0.1%	100%
scH5N1ckC2	0.0%	5.0%
scH5N1infC1	-	-
scH5N1wbC1	-	-
scH5N1gsC1	0.1%	95.0%
scH5N1ckC1	0.0%	4.8%

Appendix IV.D – Results of Model 1g.

Listed below are the chances of H5N1 infection occurring in the various variables, if an outbreak were to occur in the goose population of one, more or all countries as determined for Model 1g. At the top of each column the goose populations manifesting an H5N1 outbreak are specified.

Variable	1	12	123a	123a4	123ab	123ab4	123b	123b4	124	13a	13ab
ch5N1infC1	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%
ch5N1wbC1	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%
ch5N1gsC1	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
ch5N1ckC1	5.0%	5.0%	5.0%	5.0%	5.0%	5.0%	5.0%	5.0%	5.0%	5.0%	5.0%
ch5N1infC2	0.5%	0.992574%	0.992574%	0.992574%	0.992574%	0.992574%	0.992574%	0.992574%	0.992574%	0.664739%	1.0%
ch5N1wbC2	0.5%	0.992574%	0.992574%	0.992574%	0.992574%	0.992574%	0.992574%	0.992574%	0.992574%	0.664739%	1.0%
ch5N1gsC2	1.01%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%	34.116763%	96.334558%
ch5N1ckC2	0.060399%	5.0%	5.0%	5.0%	5.0%	5.0%	5.0%	5.0%	5.0%	1.712426%	4.817094%
ch5N1infC3a	0.5%	0.5%	0.992574%	0.992574%	0.992574%	0.992574%	0.5%	0.5%	0.5%	16.974770%	1.881751%
ch5N1wbC3a	0.5%	0.5%	0.992574%	0.992574%	0.992574%	0.992574%	0.5%	0.5%	0.5%	16.974770%	1.881751%
ch5N1gsC3a	0.029900%	1.01%	100.0%	100.0%	100.0%	100.0%	1.01%	1.01%	1.01%	100.0%	100.0%
ch5N1ckC3a	0.011492%	0.060399%	5.0%	5.0%	5.0%	5.0%	0.060399%	0.060399%	0.060399%	5.0%	5.0%
ch5N1infC3b	0.5%	0.5%	0.5%	0.664739%	0.992574%	0.992574%	0.992574%	0.992574%	0.664739%	0.5%	1.881751%
ch5N1wbC3b	0.5%	0.5%	0.5%	0.664739%	0.992574%	0.992574%	0.992574%	0.992574%	0.664739%	0.5%	1.881751%
ch5N1gsC3b	0.029900%	1.01%	1.01%	34.116763%	100.0%	100.0%	100.0%	100.0%	34.116763%	0.357690%	100.0%
ch5N1ckC3b	0.011492%	0.060399%	0.060399%	1.712426%	5.0%	5.0%	5.0%	5.0%	1.712426%	0.027849%	5.0%
ch5N1infC4	0.5%	0.5%	0.5%	16.974770%	0.5%	0.992574%	0.5%	0.992574%	16.974770%	0.5%	0.5%
ch5N1wbC4	0.5%	0.5%	0.5%	16.974770%	0.5%	0.992574%	0.5%	0.992574%	16.974770%	0.5%	0.5%
ch5N1gsC4	0.020196%	0.029900%	0.029900%	100.0%	1.01%	100.0%	1.01%	100.0%	100.0%	0.023442%	1.01%
ch5N1ckC4	0.011008%	0.011492%	0.011492%	5.0%	0.060399%	5.0%	0.060399%	5.0%	5.0%	0.011170%	0.060399%

Variable	13ab4	13a4	13b	13b4	14	2	23a	23a4	23ab	23ab4	23b
ch5N1infC1	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	0.742656%	0.742656%	0.742656%	0.742656%	0.742656%	0.742656%
ch5N1wbC1	25.250939%	25.250939%	25.250939%	25.250939%	25.250939%	0.742656%	0.742656%	0.742656%	0.742656%	0.742656%	0.742656%
ch5N1gsC1	100.0%	100.0%	100.0%	100.0%	100.0%	1.000098%	1.000098%	1.000098%	1.000098%	1.000098%	1.000098%
ch5N1ckC1	5.0%	5.0%	5.0%	5.0%	5.0%	0.059905%	0.059905%	0.059905%	0.059905%	0.059905%	0.059905%
ch5N1infC2	1.0%	0.711512%	0.664739%	0.664739%	0.5%	25.008332%	25.008332%	25.008332%	25.008332%	25.008332%	25.008332%
ch5N1wbC2	1.0%	0.711512%	0.664739%	0.664739%	0.5%	25.008332%	25.008332%	25.008332%	25.008332%	25.008332%	25.008332%
ch5N1gsC2	96.334558%	43.516394%	34.116763%	34.116763%	1.495287%	100.0%	100.0%	100.0%	100.0%	100.0%	100.0%
ch5N1ckC2	4.817094%	2.181468%	1.712426%	1.712426%	0.084615%	5.0%	5.0%	5.0%	5.0%	5.0%	5.0%
ch5N1infC3a	1.881751%	14.694573%	0.5%	0.5%	0.5%	0.5%	0.992574%	0.992574%	0.992574%	0.992574%	0.5%
ch5N1wbC3a	1.881751%	14.694573%	0.5%	0.5%	0.5%	0.5%	0.992574%	0.992574%	0.992574%	0.992574%	0.5%
ch5N1gsC3a	100.0%	100.0%	0.357690%	0.357690%	0.034705%	1.01%	100.0%	100.0%	100.0%	100.0%	1.01%
ch5N1ckC3a	5.0%	5.0%	0.027849%	0.027849%	0.011732%	0.060399%	5.0%	5.0%	5.0%	5.0%	0.060399%
ch5N1infC3b	1.881751%	0.7%	16.974770%	16.974770%	0.741491%	0.5%	0.5%	0.664739%	0.992574%	0.992574%	0.992574%
ch5N1wbC3b	1.881751%	0.7%	16.974770%	16.974770%	0.741491%	0.5%	0.5%	0.664739%	0.992574%	0.992574%	0.992574%
ch5N1gsC3b	100.0%	15.411276%	100.0%	100.0%	1.495287%	1.01%	1.01%	34.116763%	100.0%	100.0%	100.0%
ch5N1ckC3b	5.0%	0.779023%	5.0%	5.0%	0.084615%	0.060399%	0.060399%	1.712426%	5.0%	5.0%	5.0%
ch5N1infC4	0.992574%	21.5%	0.5%	0.992574%	24.888207%	0.5%	0.5%	16.974770%	0.5%	0.992574%	0.5%
ch5N1wbC4	0.992574%	21.5%	0.5%	0.992574%	24.888207%	0.5%	0.5%	16.974770%	0.5%	0.992574%	0.5%
ch5N1gsC4	100.0%	100.0%	1.01%	100.0%	100.0%	0.029900%	0.029900%	100.0%	1.01%	100.0%	1.01%
ch5N1ckC4	5.0%	5.0%	0.060399%	5.0%	5.0%	0.011492%	0.011492%	5.0%	0.060399%	5.0%	0.060399%

Variable	23b4	24	3a	3ab	3a4	3ab4	3b	3b4	4
cH5N1infC1	0.742656%	0.742656%	0.502402%	0.582749%	0.503580%	0.582749%	0.502402%	0.502402%	0.502402%
cH5N1wbC1	0.742656%	0.742656%	0.502402%	0.582749%	0.503580%	0.582749%	0.502402%	0.502402%	0.502402%
cH5N1gsC1	1.000098%	1.000098%	0.029604%	0.354161%	0.034362%	0.354161%	0.029604%	0.029604%	0.019996%
cH5N1ckC1	0.059905%	0.059905%	0.011477%	0.027673%	0.0%	0.027673%	0.011477%	0.011477%	0.010998%
cH5N1infC2	25.008332%	25.008332%	0.742633%	8.857663%	0.861582%	8.857663%	0.742633%	0.742633%	0.502402%
cH5N1wbC2	25.008332%	25.008332%	0.742633%	8.857663%	0.861582%	8.857663%	0.742633%	0.742633%	0.502402%
cH5N1gsC2	100.0%	100.0%	1.009902%	34.114559%	1.495143%	34.114559%	1.009902%	1.009902%	0.029897%
cH5N1ckC2	5.0%	5.0%	0.060394%	1.712316%	0.084608%	1.712316%	0.060394%	0.060394%	0.011492%
cH5N1infC3a	0.5%	0.5%	25.005953%	16.975305%	24.888242%	16.975305%	0.5%	0.5%	0.5%
cH5N1wbC3a	0.5%	0.5%	25.005953%	16.975305%	24.888242%	16.975305%	0.5%	0.5%	0.5%
cH5N1gsC3a	1.01%	1.01%	100.0%	100.0%	100.0%	100.0%	0.029899%	0.029899%	0.020196%
cH5N1ckC3a	0.060399%	0.060399%	5.0%	5.0%	5.0%	5.0%	0.011492%	0.011492%	0.011008%
cH5N1infC3b	0.992574%	0.664739%	0.5%	16.975305%	0.741491%	16.975305%	25.005953%	25.005953%	0.742633%
cH5N1wbC3b	0.992574%	0.664739%	0.5%	16.975305%	0.741491%	16.975305%	25.005953%	25.005953%	0.742633%
cH5N1gsC3b	100.0%	34.116763%	0.029899%	100.0%	1.495240%	100.0%	100.0%	100.0%	1.009999%
cH5N1ckC3b	5.0%	1.712426%	0.011492%	5.0%	0.084612%	5.0%	5.0%	5.0%	0.060399%
cH5N1infC4	0.992574%	16.974770%	0.5%	0.5%	24.888218%	0.992574%	0.5%	0.992574%	25.005953%
cH5N1wbC4	0.992574%	16.974770%	0.5%	0.5%	24.888218%	0.992574%	0.5%	0.992574%	25.005953%
cH5N1gsC4	100.0%	100.0%	0.020196%	1.01%	100.0%	100.0%	1.01%	100.0%	100.0%
cH5N1ckC4	5.0%	5.0%	0.011008%	0.060399%	5.0%	5.0%	0.060399%	5.0%	5.0%