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SPATIAL RISK ANALYSIS OF BLUETONGUE IN THE NETHERLANDS

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Spatial risk analysis of Bluetongue in the Netherlands

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“All animals are equal, but some animals are more equal than others.” George Orwell

Abstract

The past ten years an increase of zoonotic diseases (diseases caused by infectious agents that can be transmitted between animals and humans) occurred in Europe. Bluetongue disease is an infectious, non-contiguous, arthropod-borne viral disease, mostly of sheep, but also of other ruminants. An important factor in the distribution of BlueTongue Virus (BTV) worldwide is the availability of suitable vectors, usually biting midges of the species *Culicoides*. Wherever the required vectors are present, BTV can become endemic.
The objective of this thesis is to make a spatial risk analysis for Bluetongue in the Netherlands, determining which areas are susceptible for new epidemics. Literature research is used to identify vector species and host species occurring in the Netherlands. A spatial model, using vectorial capacity, is used to identify the areas in the Netherlands where sheep and other cattle live closely to populations of bluetongue vectors. Data on weather, the natural habitat of the bluetongue vectors, as well as data on different animal farms will be used.
Six species of Culicoides are identified as potential vectors. Ovine and bovine hosts are omnipresent in the Netherlands.
Temperature is a key factor in the process of Bluetongue development. A rise in temperature will lead to higher risks. During May till October temperature is high enough to cause a risk for Bluetongue outbreaks, with a peak in August.
Besides temperature few other factors can have a raising effect on the vectorial. The presence of peat vegetation and of pig farms can both heighten the risk of Bluetongue.

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1. Introduction

1.1 Context and background

1.1.1. Introduction

The past ten years an increase of zoonotic diseases (diseases caused by infectious agents that can be transmitted between animals and humans) occurred in Europe. Climate change is seen as the most important cause for this increase, but also international travelling and import are responsible. A number of these diseases is transferred by bloodsucking insects and ticks. In most cases the responsible vectors are known, however the geographic distribution and the effects of climate change are hardly researched (Takken et al. 2006).
Epidemiologists have traditionally used maps for analyzing the relationship between diseases, their location, and the surrounding environment. Geographic information systems (GIS) have been used in the surveillance and monitoring of vector-borne diseases, in relation to environmental health, disease policies and planning, the existing health situation in the area, generation and analysis of research hypotheses, identification of high-risk health groups, planning and programming of activities, and monitoring and evaluation of interventions. GIS has enabled researchers to determine locations of high prevalence areas and populations at risk. GIS has been an excellent tool for the monitoring of the spatial, temporal and environmental factors associated with diseases (Ulugtekin et al. 2006).
Spatial data have also become an essential component of the diseases information system. Spatial data, together with other thematic information has been used for the decision-making purposes for the control of epidemic and non-epidemic diseases (Ulugtekin et al. 2006).

In 2005 the Dutch Ministry of Agriculture, Nature and Food Quality assigned Wageningen University to start a research on the most important zoonotic disease vectors. Information on population dynamics, phenology and distribution of five genera of bloodsucking arthropods is gathered to develop effective measures against the diseases (Takken et al. 2006).
Culicidae is one of the genera studied. Midges of this genus are known to transmit the disease bluetongue. Formerly the only occurrences in Europe were located around the Mediterranean Sea. However in the summer of 2006 also the south of the Netherlands was struck by an outbreak (OIE 2006). Knowing the disease already can reach the Netherlands, the question arises which areas are susceptible for new epidemics.

1.1.2 Bluetongue disease

Bluetongue disease is an infectious, non-contiguous, arthropod-borne viral disease, mostly of sheep, but also of other ruminants. An important factor in the distribution of Blue Tongue Virus (BTV) worldwide is the availability of suitable vectors, usually biting midges of the species *Culicoides*. Wherever the required vectors are present, BTV can become endemic. Favourable winds can transport infected vectors towards areas, where if they come in contact with susceptible animals, they may infect them resulting in an epizootic (Parsonson 1990).

Bluetongue virus is the type species of the genus Orbivirus in the family Reoviridae. It causes an infectious, non-contagious, arthropod borne disease of ruminants, and there are 24 serotypes. The virus replicates in all ruminant species, but severe disease is mostly restricted to certain breeds of sheep and some species of deer (Purse et al. 2005). Mortality rate is normally low in sheep but can go up to 10% in some epizooties. Cattle, goats, dromedaries and wild ruminants generally show no clear signs of infection (OIE 2006).
Bluetongue is endemic in Sub-Saharan Africa, but outbreaks have also occurred periodically in de Mediterranean region (De Liberato et al. 2005). In the Mediterranean Basin the largest epidemic of bluetongue ever recorded occurred between 1998 and 2002 (Capela et al. 2003). In this region and other parts of the Old World, *Culicoides imicola* is considered to be the major bluetongue vector (De Liberato et al. 2005) Mellor et al., 2000).
The identification of BTV in areas such as Bulgaria, Turkey, and the Balkans, where *C. imicola* is known to be absent, however, has led to a re-evaluation of the Palaearctic *Culicoides* fauna as potential vectors (Carpenter et al. 2006). Also many of the areas recently affected by BTV, northern of the Mediterranean region, have been shown to be free of *C. imicola*, suggesting the involvement of alternative vector species (Tatem et al. 2003). These alternative vector species are likely to be members of the *C. obsoletus* and/or *C. pulicaris* groups, which are the commonest *Culicoides* species across northern Europe. It is also likely that climate change has, and will, extend the area at risk from BTV, as well as increasing the duration, severity and likelihood of BTV epizootics following the introduction of the virus (Tatem et al. 2003).

1.1.3 Geographic range of bluetongue

Many BTV serotypes have been circulating on the fringes of Europe, in sub-Saharan Africa, Turkey and the Middle East. For several decades BTV made only brief periodic incursions into southern Europe before 1998 (Purse et al. 2005).
The current BT epidemic in Europe began in October 1998, when BTV-9 was detected on four Greek islands close to the Turkish coast (Rhodes, Leros, Kos and Samos). In subsequent years up to 2004, BTV-9 spread northward (into western regions of Turkey, Bulgaria, Kosovo, Albania, Bosnia and Herzegovina, the former Yugoslav Republic of Macedonia, Serbia and Montenegro, and Croatia) and westward (into mainland Greece, Italy, Sicily, Sardinia and Corsica). A further three serotypes, BTV-1, BTV-4 and BTV-16, also entered Europe through Greece and then spread westwards. A separate incursion of BTV-2 also occurred in 2000, spreading from Tunisia and/or Algeria into Sardinia, Sicily, mainland Italy, Corsica and the Balearic islands. Late 2004, further incursions, this time of BTV-4, occurred from Morocco into south western Spain and southern Portugal (Purse et al. 2005).
A new serotype (BTV-8) entered Belgium, Netherlands, Germany, France, Algeria and Spain in 2006(OIE 2006).
Several features indicate a substantial change in the epidemiology of bluetongue in Europe: the expanded distribution of transmission, with outbreaks recorded more than 800 km further north than before; the increased persistence of transmission, with over-wintering of particular strains; the extension of the northern range limit of the traditional vector *C. imicola* into the Balearic Islands, mainland France, Switzerland, eastern Spain, mainland Greece, Sicily and mainland Italy; and the extension of transmission beyond the range of *C. imicola*, indicating a vector role for other *Culicoides* species (Purse et al. 2005).

Considering the responses of these biological processes to climate, it is likely that increases in temperature (particularly at night-time and in winter), as well as increases in precipitation (particularly in summer/autumn) will lead to an increased geographical and seasonal occurrence of BTV transmission. Also an increase in the number of *Culicoides* species able to transmit the virus is likely, by increasing the range, abundance and seasonal activity of vectors, increasing the proportion of a vector species that is competent and by increasing the development rates of the virus within vectors (Purse et al. 2005).

1.1.4 Blue tongue transmission cycle

Female *Culicoides* ingest a wide range of liquid foods including blood, sugars, water and nectar. Most of these liquids are deposited in a blind-ending sac, the mid-gut deverticulum. However, when feeding on blood, contraction of a sphincter muscle at the mouth of the mid-gut diverticulum ensures that most or all of the meal is directed to the hind part of the mid-gut. The midge can get infected with BTV by imbibing viraemic blood from an infected vertebrate host. As far as is known this is the only way in which wild *Culicoides* are able to acquire an infection with BTV (Mellor 1990).
Under natural conditions, the hind part of the mid-gut of female *Culicoides* receives most or all ingested viraemic blood, therefore it is logical to assume that the initial infection with virus occurs in cells in that area. Once infection of the mid-gut cells is achieved, replication ensues, prior to the release of progeny virus in the haemacoel. Secondary target cells, particularly fat body and salivary gland, may then become infected. Transmission to a vertebrate host becomes possible after replication in the salivary glands. After a latency period of a few days, the host can infect a new *Culicoides* vector (Mellor 1990). This process is summarised in figure 1.

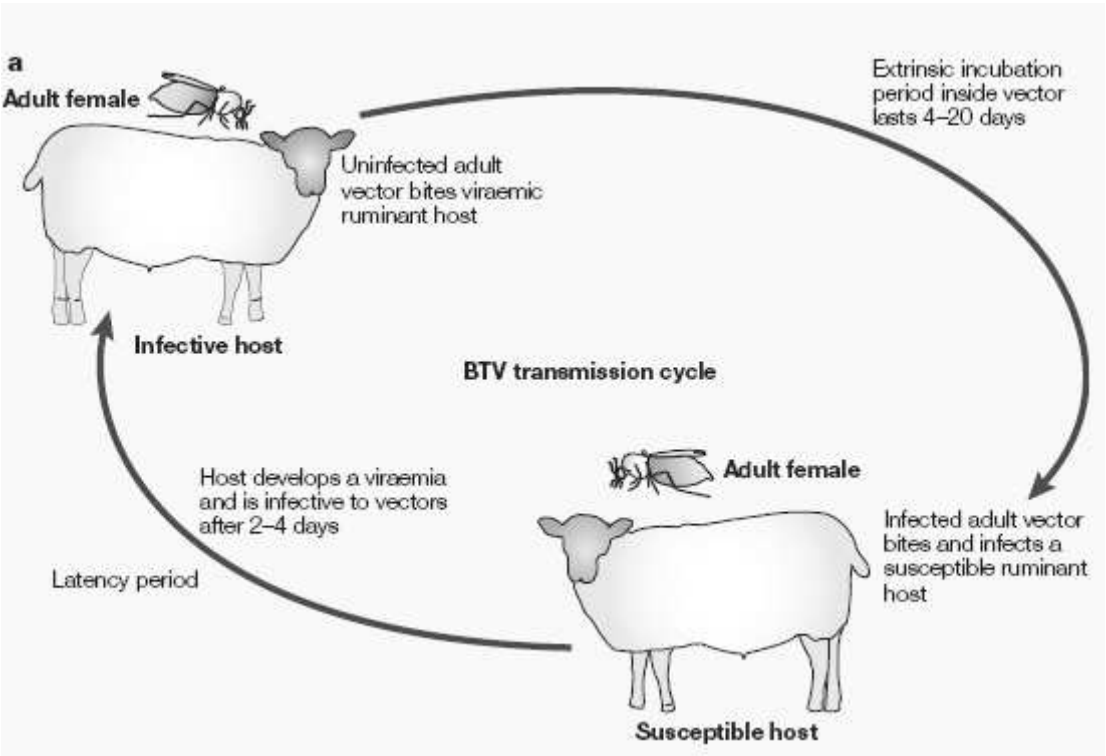

Figure 1 Transmission cycle of bluetongue virus (Purse et al. 2005)

1.2 The research

1.2.1 Research objective

The objective of this thesis is to make a spatial risk analysis for Bluetongue in the Netherlands, determining which areas are susceptible for new epidemics.
The model will identify the areas in the Netherlands where sheep and other cattle live closely to populations of bluetongue vectors. Data on weather, the natural habitat of the bluetongue vectors, as well as data on different animal farms will be used.

1.2.2 Research questions

The overall objective will be achieved by answering the following research questions.

1. Which potential bluetongue vectors are present in the Netherlands and what is their role in the bluetongue virus transmission cycle?
2. Which potential bluetongue hosts are present in the Netherlands and what is their role in the bluetongue virus transmission cycle?
3. Which are the spatial components of bluetongue transmission?
4. How to set up a model to predict areas which are susceptible for new epidemics using various scenarios?
5. How to evaluate the model results to identify areas at risk?

1.2.3 Research area

The Netherlands is located in north-western Europe. It is bordered by the North Sea to the north and west, Belgium to the south, and Germany to the east.
With an area of 41,526 km2 and 16,336,346 inhabitants it is densely populated. In 2005, 14,369 farms sheltered a total of 1,362,523 sheep. The number of cows was 3,798,804 distributed over 37,319 farms (CBS 2006).

1.2.4 Data collection

This is an explorative study trying to identify areas in the Netherlands where a risk exists of a bluetongue epizootic by using a spatial model. For identifying bluetongue vectors in the Netherlands and determining their role in the transmission, it is required to know which vector species are present. Two researches assigned by the Ministry of Agriculture, Nature and Food Quality can identify the vector species. The first research is conducted to identify bloodsucking insects as potential vectors for vector transmitted diseases in general. The second research is conducted after the outbreak of Bluetongue in 2006, to identify vectors especially for Bluetongue. Literature research will further clarify the susceptibly and rate of infection of the vector species responsible for BTV transmission.

Identifying bluetongue hosts in the Netherlands and determining their role in the transmission, will largely be done by means of literature research. Questions to be answered are which host species are present in the Netherlands and what is the rate of infection for each host species.

For establishing the spatial components of bluetongue transmission, partly literature research is needed as well as analysis of spatial data. To determine host location,

data on animal farming will be analysed. To determine vector location, vector habitats have to be identified. This can be achieved by looking at occurrence of plant species associated with *Culicoides* vectors. The dispersal of vectors is described in literature and can also be further analysed by looking at epidemiological data of current outbreaks. Dispersal of hosts can be clarified by looking at animal import and transport data.

Setting up a model to predict areas which are susceptible for new epidemics can only be done after identifying the relevant spatial factors. Various scenarios will be run, using various parameter values and different ways of management. Calibration and validation will be done using data on the recent outbreaks in the Netherlands as well as expert validation.

Evaluation of the model results is done after all previous questions are answered successfully. It should be possible to identify risk areas and quantify the chances of bluetongue epizootics.

2. Bluetongue in the Netherlands

2.1 Introduction

Many BTV serotypes have been circulating on the fringes of Europe, in sub-Saharan Africa, Turkey and the Middle East. For several decades BTV made only brief periodic incursions into southern Europe before 1998 (Purse et al. 2005). In 2004, 2005 and 2006 outbreaks occurred in Spain and in 2004 also in Portugal. On August 17, 2006 for the first time Bluetongue is identified in the Netherlands. Before this outbreak the serotype was occurring only in Africa in Sub-Saharan areas. How the virus could enter the Netherlands is still unknown (LNV 2006).

2.2 *Culicoides, a Bluetongue vector*

Approximately 30 of the 1 254 species of *Culicoides* across the world have been incriminated to varying degrees in the transmission of BT disease. These 30 species can be assigned to 8 of the 36 subgenera currently deemed to comprise the genus *Culicoides* and can be subdivided further amongst seven species complexes (Meiswinkel et al. 2004).
In the Old World, including the Mediterranean region, a single species, *Culicoides imicola*, has been implicated as the major vector of BTV. However, many of the areas recently affected by BTV have been shown to be free of *C. imicola*, suggesting the involvement of alternative vector species. These alternative vectors are likely to be members of the *C. obsoletus* and/or *C. pulicaris* groups, which are the most common Culicoides species across northern Europe (Tatem et al. 2003). It is likely that the vector species for bluetongue in the Netherlands belong to one or both of these complexes.

2.2.1 The Obsoletus Complex

In the Palaearctic region, the 30 or more described species of the subgenus *Avaritia* are usually referred to collectively as the *C. obsoletus* group (Meiswinkel et al. 2004). However, of the 20 species of *Avaritia* known to occur throughout the Holarctic, it is considered that only seven fall within the Obsoletus species complex *sensu stricto*. These are the *C. montanus*, *C.obsoletus*, *C.scotius* and a unidentified species, plus *C. sinanoensis*, *C. gornostaevae* and *C. sanguisuga*. Two related species are *C. chiopterus* and *C. dewulfi*, which Meiswinkel et al. (2004) prefer to keep separate from the above-mentioned Obsoletus Complex *sensu stricto*, and which they refer to as the Chiopterus Complex and the Dewulfi Complex.

2.2.2 The Pulicaris complex

The Pulicaris complex, as currently interpreted by most authors is polyphyletic and that the majority of the 50 species usually assigned to it belong to two other subgenera (Silvicola and Hoffmania) and to the hitherto unknown Fagineus species complex (subgenus unknown) (Gomulski et al. 2006).
The precise number of species that comprise the Pulicaris complex in the Palaearctic region is unknown, as various authors lump an agglomeration of some 50 disparately

related taxa into it. Also included by most authors is the notorious pest species *C. impunctatus* (Meiswinkel et al. 2004).
The Palaearctic sector of the Pulicaris complex sensu stricto now comprises at least 14 species (two undescribed). The twelve described species are: *C. deltus, C. halophilus, C. hulinensis, C. impunctatus, C. lupicaris, C. mcdonaldi, C. newsteadi, C. padusae, C. pelius, C. pulicaris, C. punctatus* (the subgenotype) and *C. subpunctatus*; the species new to science are 'dark *C. pulicaris*' and one – or both – of the two molecular forms of *C. newsteadi* (Gomulski et al. 2006).

2.2.3. Culicoides species in the Netherlands

In the Netherlands only two studies are performed investigating the presence of Culicoides species. In these studies six species are found. Only limited habitats are sampled in these studies. The first study conducted in 2005 and 2006, had sample locations in four types of habitat (wetland, peat land, biological farms and river plains). This study identified five species of Culicoides. *C. obsoletus* belonging to the Obsoletus complex. *C. impunctatus* and *C. pulicaris* belonging to the Pulicaris complex. These species coincides with the suggestion that members of the C*. obsoletus* and *C pulicaris* groups, are alternative vectors for BTV in areas where C. imicola does not occur (Tatem et al. 2003).

Table 1 *Culicoides* species caught in the Netherlands

	Wetland	Peat moor	River foreland	Biological farms	Total
C. impunctatus	1035	2599	1	5	3640
C. minutissimum				11	11
C. obsoletus	27	16	9	996	1058
C. odibilis	2				2
C. pulicaris	43			1	44
Culicoides sp.	20				20

The second study, perform in 2006 after the first outbreak in the Netherlands is only performed at farm sites in the province of Limburg. These catchings revealed a sixth species, *C. dewulfi,* also belonging to the Obsoletus complex *sensu lato* (LNV 2006).
Most individuals caught belong to *C. impunctatus* and *C. obsoletus* (table 1). It is likely that these two species are the most important vector species in a Bluetongue epizooc. However a more extensive research is needed to give a complete overview of all existing species in various habitats and farms types throughout the Netherlands.

2.2.4 Vector habitat

Habitat descriptions vary from general to more specific. According to Purse et al. (2005) *Culicoides* species breed in a range of moist microhabitats (such as irrigation channels, drainage pipes and dung heaps) that are omnipresent across many farmyard types. Willem Takken (pers. comm. 2006) states there are 200 biting vectors for every host animal (ovine and bovine). This implicates that every animal farm containing sheep or cows provides a suitable habitat for Culicoides.

Work examining the larval distribution of *C. impunctatus* suggests a more specific habitat. Associations are found with low soil pH, high organic and water content, and the presence of mosses (*Sphagnum* spp.), rushes (*Juncus* spp.) and bog myrtle (*Myrica gale*) (Carpenter et al. 2006). Testing showed a significantly higher proportion of eggs laid on upper layer *Sphagnum* spp. than any other substrate. *Juncus articulatus* was identified as having a significantly higher proportion of eggs laid than all other tested substrates, with the exception of upper layer *Sphagnum* spp. moss (Carpenter et al. 2006).
C. impunctatus is over wintering in damp acid soil with significant relationships between larval numbers and the distribution of *Juncus acutiflorus/J. articulatus*. Earlier studies associate moor land vegetation with breeding grounds (Blackwell et al. 1999). Breeding of *C. impunctatus* is largely restricted to bog land bearing *Sphagnum* spp. and *Polytrichum commune* (Kettle 1960).

Two different sorts of habitat seem to be suitable for Culicioides. A general habitat containing (animal) farm land and a more specific habitat formed by moor land with *Sphagnum* spp., J*uncus* spp., *Myrica gale* and *Polytrichum commune*.
When looking at the locations where most individuals of *C. impunctatus* are found in the LNV research, the relation with moor land is clearly seen. *C. obsoletus* seems to be found in varying wet habitats but mostly on biological farms, where *C. minutissimum* is also found. *C. dewulfi* is caught only in the sequential study performed near farms. *C. odibilis* and *C.pulicaris* are mostly found in small numbers in wetland, which might indicate other suitable habitats.

2.2.5 Vector dispersal range

Adult *Culicoides* are not strong fliers. Field observations by Kettle (Kettle 1951) on *C. impunctatus* in woodland shows a decrease in density of $1/10^{th}$ with every 65 yards distance from the breeding site and hence at 200 yards the adult density would be about $1/1000^{th}$ of the original value. In open field, over a distance of 1200 yards, there is an absence of a regression of density with distance. Earlier researches showed varying ranges for different species. *C. pelilouensis* may fly two miles and *C. tristriatulus* may fly five miles, both wind aided. For *C. grahamii* a decrease of $1/10^{th}$ every 370 yards was found. A range six times greater then results with *C. impunctatus*. Hill (Hill 1947) found a much smaller flight range for *C. impunctatus* of about 300 yards (Kettle 1960). However *Culicoides* midges can be passively dispersed by the wind, possibly up to several hundred kilometres in a single night, especially over the sea (Purse et al. 2005). In winds at speeds of 10–40 km/h, at heights up to 1.5 km and at temperatures between 12 and 35℃, Culicoides may be carried as aerial plankton for distances up to 700 km (Wittmann & Baylis 2000).

2.2.6 Vector infection

Individual Culicoides are infected with BTV in the wild by imbibing viraemic blood from an infected vertebrate host. As far as is known this is the only way in which wild Culicoides are able to acquire an infection with this virus (Mellor 1990).
Female Culicoides ingest a wide range of liquid foods including blood, sugars, water and nectar. Most of these liquids are deposited in a blind-ending sac, the mid-gut deverticulum. However, if the food source is blood, contraction of a sphincter muscle at the mouth of the mid-gut diverticulum ensures that most or all of the meal is directed to the hind part of the mid-gut (Mellor 1990).

Since, under natural conditions, the hind part of the mid-gut of female Culicoides receives most or all ingested viraemic blood, it is logical to assume that the initial infection with virus occurs in cells in that area. Once infection of the mid-gut cells is achieved, then replication ensues, prior to the release of progeny virus in the haemacoel. Secondary target cells, particularly fat body and salivary gland, may then become infected. Transmission to a vertebrate host becomes possible after replication in the salivary glands. The whole cycle from vector infection to transmission takes between 10-15 days at 25℃ (Mellor 1990).

Both *C. impunctatus* and *C. obsoletus* are susceptible to BTV, though infection rates were low. Despite the apparent very low susceptibility to BTV infection, the high associated biting rates could well pose a risk of transmission (Carpenter et al. 2006).

From the species caught in the Netherlands only *C. dewulfi* is found to be infected by the bluetongue virus. However the absence of infection of other Culicoides species does not signify these species do not play a role in the dispersal of bluetongue (LNV 2006).

In the Netherlands, Bluetongue Virus is only identified in *C. dewulfi*. Literature mentions other Culicoides as potential vector species. However often these species are infected under laboratory conditions. Further research is needed to determine if the other species of Culicoides caught, play a role in the transmission of BTV in the Netherlands.

2.2.7 Bluetongue hosts

Two groups of hosts are present in the Netherlands in big numbers, sheep and cows. Both groups are receptive to the Blue Tongue Virus. However not every breed is receptive in the same degree. Some breeds are more receptive than others and the symptoms and lethality can vary between breeds (Taylor 1987).
Some species of deer are mentioned as host for BTV, for example white-tailed deer and black-tailed deer (McLaughlin et al. 2003). In the Netherlands three species of deer do occur commonly, *Cervus elaphus, Capreolus capreolus* and *Dama dama* (Leutscher 1985). In what extent these species are receptive for the virus is not known. However it seems unlikely they are potential hosts (Niels Verhulst, pers. comm., 2007)
Finally there are various other hosts, occurring in the Netherlands in small numbers, like camels, gazelles, etc (Shimshony 1987). They can be found in zoos, circuses and private collections. When carrying the BTV during import, they may function as a potential source of an outbreak of bluetongue disease.

2.2.8 Climate and Culicoides

The duration of the life cycle depends on the species and climatic conditions, varying from 7 days in the tropics to 7 months in temperate regions, where most species diapause as fourth instar larvae during winter. The life-span of the adults is usually short and is dependent on ambient conditions. Most adults survive less than 20 days, although occasionally they live for up to 90 days (Wittmann & Baylis 2000). The daily survival rate of adult *C. sonorensis* decreased with increasing temperature and on average midges lived three times longer at 15℃ than at 30℃ (Wittmann et al. 2002).

The number of adults in a population is partly dependent on recruitment from developing immatures. Cooler conditions inhibit development and temperature is one of the major factors triggering diapause (Wittmann & Baylis 2000). The warmer the weather, the shorter the life cycle and the greater the number of generations and adults that can be produced in a season. Survivorship to adulthood is also influenced by temperature and there is usually an optimal range where survivorship is maximized (Wittmann & Baylis 2000).

Where temperature is suitable, precipitation can influence the distribution of Culicoides species, through its effect on the availability of breeding sites. For example, *C. imicola* breeds in wet, organically enriched, soil or mud, and in Africa it tends to occur in areas with rainfall of 300–700 mm per year. Areas with >700 mm rain/annum are probably unsuitable as *C. imicola* pupae drown when breeding sites are flooded (Wittmann & Baylis 2000). Precipitation can indirectly affect the development of immature Culicoides via the provision of more or better breeding sites, allowing the successful development of greater numbers of larvae (Wittmann & Baylis 2000).

The frequency of key adult activities such as mating, host-seeking, blood-feeding and oviposition can affect the population input. Warm conditions generally increase, while temperatures below 10℃ for *C. variipennis* and 18℃ for *C. brevitarsis* inhibit activity. Relative humidity can also positively affect the level of activity. However, wind negatively affects activity, which is suppressed at wind speeds greater than 3 m/s for C. imicola in Kenya and 2.2 m/s for *C. brevitarsis* in Australia (Wittmann & Baylis 2000).

The interval between virus ingestion and the subsequent ability to transmit virus is known as the extrinsic incubation period (EIP). The duration of the EIP is dependent on temperature and takes about 10 days at 25℃ (Wittmann & Baylis 2000). Since female Culicoides generally require a blood meal for every batch of eggs they mature, the biting rate is largely governed by the time required for the eggs to develop (gonotrophic cycle).

High temperatures adversely affect adult survival, but also decrease the duration of the viral EIP. In fact, transmission of BTV by *C. variipennis sonorensis* was favoured by high temperatures (e.g. 27–30℃), since the reduction in longevity was more than compensated for by the shorter EIP (Wittmann & Baylis 2000).

Temperature can also influence the vector competence of Culicoides vectors. For example, BTV and AHSV are unable to develop in *C. variipennis sonorensis* at temperatures below about 14–15℃ (Wittmann & Baylis 2000). The theoretical minimum temperature for virus development in *C. sonorensis* varied from 9.2℃ for BTV10 to 13.6℃ for BTV16 (Wittmann et al. 2002).

Thus, the theoretical minimum temperatures for development of these viruses were < 15℃ and adult survival trials at temperatures < 15 ℃ would therefore be required to improve the accuracy of the estimates. The optimum temperature for virus transmission varied between 27℃ and 28℃ (Wittmann et al. 2002).

3. Modelling Bluetongue Risk in the Netherlands

GIS models are very suitable for the prediction and analysis of the spread of phenomena like infectious diseases over space and time. With a model it is possible to compose monthly spatial risk maps of various infectious diseases without having any specific occurrence data (Groot 2006). Combining the data found in literature and of previous studies a model is created to predict the risk of Bluetongue in the Netherlands.

3.1 Vectorial capacity

The ability of a *Culicoides* population to transmit virus to a vertebrate population can be assessed by determining its vectorial capacity *(C)*, according to the following equation:

(1) $$C = \frac{m \cdot a^2 \cdot V \cdot p^n}{(-\ln p)}$$

where *C* = number of new infections arising per day from a currently infective case, *m* = the number of vectors per host, *a* = number of blood meals taken by a vector per host per day, *V* = vector competence, *p* = daily survival rate of the vector, and *n* = extrinsic incubation period in days (Mullens 1992). All of these parameters are affected by ambient conditions and it is in this way that climate change can affect the risk of Culicoides-borne disease occurring in the UK (Wittmann & Baylis 2000).

3.1.1 Number of vectors per host

To obtain the number of vectors per host it is necessary to know the numbers of vectors and the numbers of hosts.
Number of hosts can be found looking at spatial data on farming in the Netherlands.
Number of vectors is calculated from animal farm data in combination with vegetation data. *C. impunctatus* is associated with the following plant species: *Shagnum* spp., *Juncus acutiflorus/Juncus articulatus, Polytrichum commune*. and *Myrica gale*. According to Jacob Beeuwkes (pers. comm. 2007), per square kilometre of suitable vegetation an amount of 5000 Culicoides can be found. *C. obsoletus*, *C. minutissimum and C. dewulfi* are found near (biological) farms. According to Willem Takken (pers. comm. 2006) animal farms contain 200 midges per host animal.

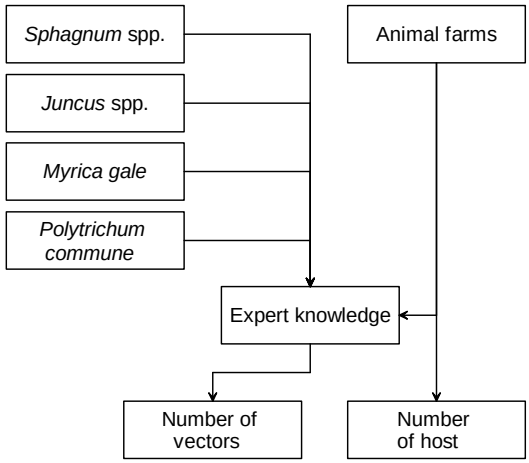

Figure 2 Calculation of number of vectors and hosts

3.1.2 Number of blood meals taken by a vector per host per day

Since female Culicoides generally require a blood meal for every batch of eggs they mature, the biting rate is largely governed by the time required for the eggs to develop (gonotrophic cycle). High temperatures reduce the duration of the gonotrophic cycle and thereby increase the biting rate. For example, female *C. variipennis sonorensis* blood-feed every three days at 30℃ and only every 14 days at 13℃ (Wittmann et al. 2002).

Table 2 Median extrinsic incubation period for two BTV serotypes in *C. soronensis* maintained at different temperatures (Wittmann et al. 2002).

	Median extrinsic incubation period (days)	
Temperature (℃)	BTV10	BTV16
15	26.0	19.9
20	13.0	20.2
25	15.0	7.2
30	7.0	4.8

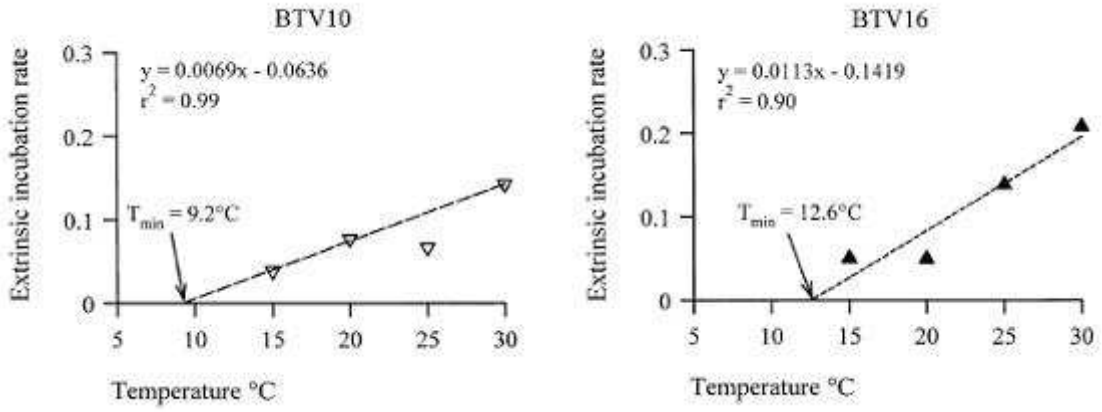

Figure 3 Relationship between temperature and extrinsic incubation rate of two BTV serotypes in *C. soronensis* (Wittmann et al. 2002)

The number of blood meals taken by a vector per host per day equals the inverse of the median extrinsic incubation period. Wittmann et al. (Wittmann et al. 2002)) calculated the extrinsic incubation rate for *C. sonorensis* looking at two strains of Blue Tongue Virus. The strain in the Netherlands is a different one (BTV8). In this model the average of these two functions is used to calculate the extrinsic incubation rate (formula 2)

(2) $a = 0.0091 \cdot T - 0.10275$

where a = number of blood meals taken by a vector per host per day, and T = temperature (℃).

3.1.3 Vector competence

Vector competence for bluetongue virus does not seem to be dependent on temperature (fig. 4). In the model the average value of the two values found by Wittmann et al. (2002) is used.

(3) $V = 19.43325$

where V = vector competence.

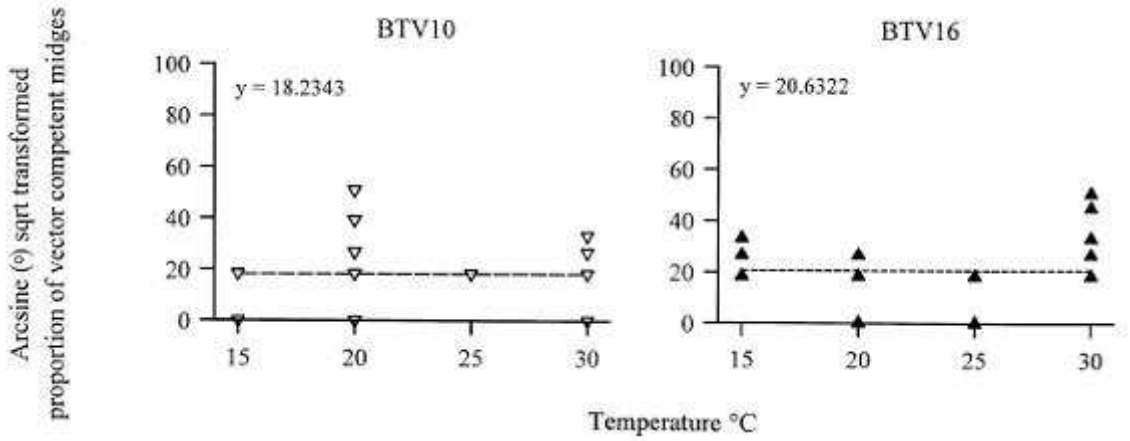

Figure 4 Relationship between temperature and the vector competence of *C. soronensis* for two BTV serotypes (Wittmann et al. 2002)

3.1.4 Daily survival rate of the vector

Longivity decreases significantly as the temperature increase from 15 to 30oC. However at low temperatures survival is greater at high relative humidity (85% r.h.) compared to lower humidities, but at high temperatures the impact of relative humidity is reversed.

Table 3 Survival of blood-fed female C. sonorensis at different temperatures and relative humidities (Wittmann et al. 2002).

Temperature (℃)	% Relative humidity	Saturation deficit (mbar)	Survival range (days)	Mean survival (days)	+SE	-SE	Survival rate/ day*
15	40	10.3	2-52	27.3	3.1	2.5	0.96
	75	4.3	1-46	27.5	1.4	1.3	0.96
	85	2.6	4-57	33.2	1.4	1.3	0.97
20	40	14.1	2-33	15.6	1.8	1.5	0.94
	75	5.9	2-31	18.8	0.8	0.7	0.95
	85	3.5	1-41	20.5	0.8	0.8	0.95
25	40	19.1	2-26	14.4	1.5	1.3	0.93
	75	8.0	2-23	13.4	0.6	0.6	0.93
	85	4.8	2-18	10.9	0.6	0.5	0.91
30	40	25.7	2-20	11.9	1.3	1.1	0.92
	75	10.7	2-15	10.2	0.5	0.5	0.91
	85	6.4	2-12	7.1	0.4	0.4	0.87

*Daily survival rate is $e^{-(1/meansurvival)}$

In the Netherlands the relative humidity varies between 75% and 90%. In spring and summer the humidity is lower. To calculate daily survival rate, daily survival rate values at a relative humidity of 75% are used. SPSS is used to calculate the logistic function for daily survival rate, with an upper bound of 1 (no mortality).

(4) $$p = \frac{1}{1+\left(0.0168 \cdot 1.0608^{T}\right)}$$ Sigf = 0.003

where p = daily survival rate of the vector and T = temperature (℃).

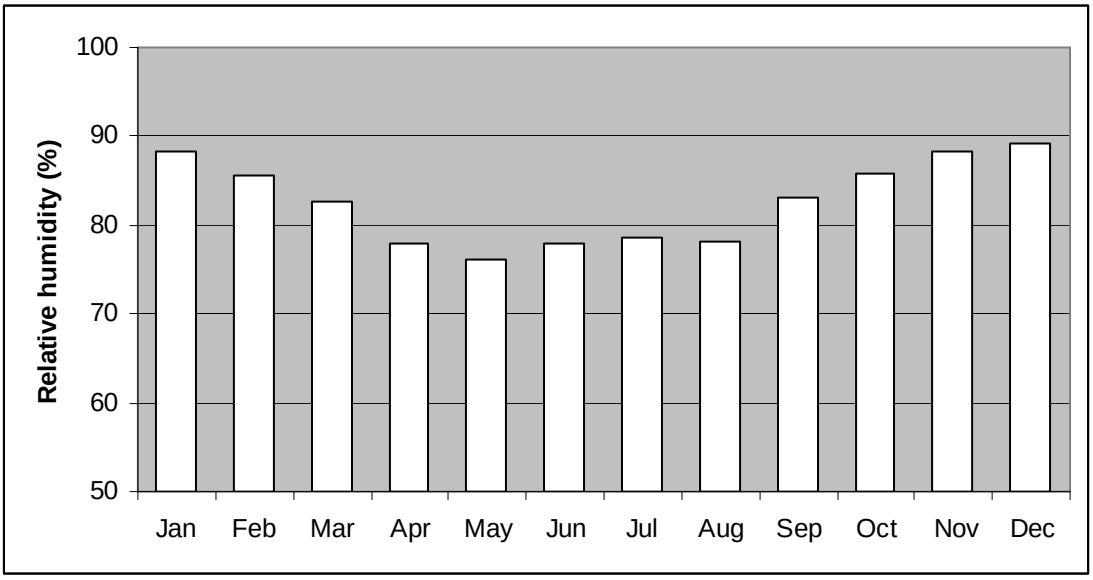

Figure 5 KNMI Multiannual averages (1971-2000)

3.1.5 Extrinsic incubation period in days

Extrinsic incubation period in days is closely related to the number of blood meals taken by a vector per host per day.

(5) $$n = \frac{1}{0.0091 \cdot T - 0.10275}$$

where n = extrinsic incubation period (days) and T = temperature (℃)

3.2 Spatial model for determining Vectorial Capacity

In this model the risk for a first outbreak of Bluetongue Virus is calculated in the Netherlands. This is done by determining the location of host species (ovine and bovine), identifying suitable habitats for BTV vectors and combining these with temperature data. The result will be a map showing the risk of a new outbreak in the form of vectorial capacity. Running various sensitivity analyses and scenarios, more understanding of the process can be gained. In figure 6 an outline of the model is presented.

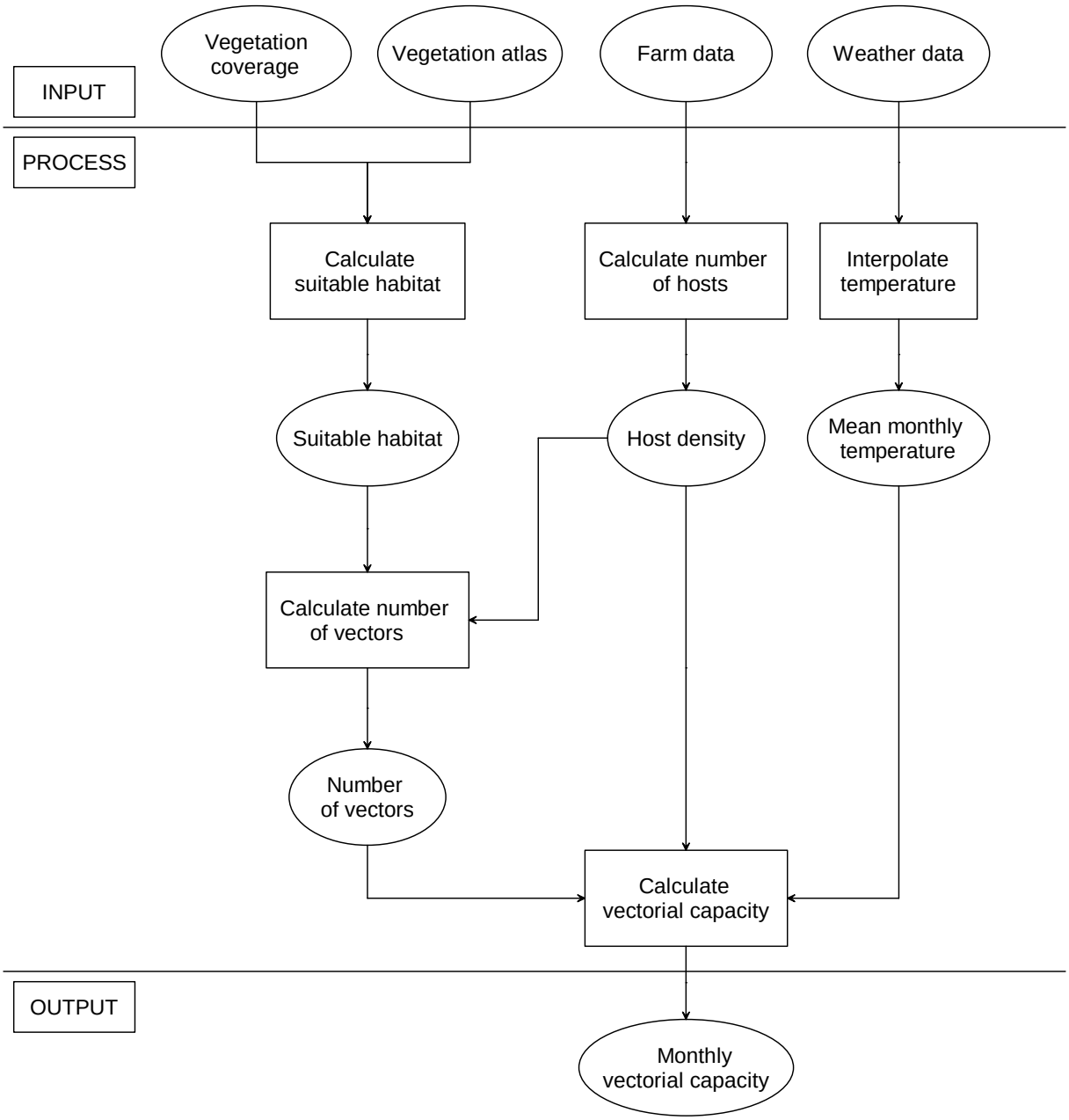

Figure 6 Overview of the input, process and output of the model

3.2.1 Model input

The following files are used as input for the model.

- Vegetation coverage Staatsbosbeheer – Website containing vegetation types with corresponding plant species. For every species a presence value (percentage of samples containing the plant species) is given.
- Vegetation Atlas (Vegatlas) – database containing distribution data on vegetation types. The Netherlands are divided in 5 x 5 km sample squares. For every sample square the occurring vegetation types are given.

- Farm data – Shape file provided by Geografische Informatie Agrarische Bedrijven (GIAB) describing all farms in the Netherlands containing sheep/goats, pigs or cows. For each farm the animal is given with the number of individuals on the farm
- Weather data – data containing the daily temperature (minimum, maximum and mean) for 52 weather stations in the Netherlands, Belgium and Germany.

3.2.2 Model processes executed in a GIS environment

The following steps were executed in process of the GIS model (see figure 6)

1 The vegetation typology website from Staatsbosbeheer (SBB) is used to select vegetation types containing one or more of the plant species corresponding with *Culicoides impunctatus* habitat. For *Sphagnum* the maximum presence value is calculated of all available *Sphagnum* species combined. The some is done with *Juncus*, where the maximum presence value of the two species, *Juncus acutiflorus and Juncus articulatus*, is used. *Myrica gale* and *Polytrichum commune* are used as a single criterion. All selected vegetation types are exported together with the presence value.

Vegetation codes from the SBB vegetation typology website do not correspond completely with the vegetation codes from Vegatlas. Corresponding codes are matched in a table (Appendix 1).

The coordinates of the sample squares in Vegatlas are situated at the left down corner of the sample square. A correction is made to locate the coordinates in the centre of the sample square.

A join is made between the table containing the vegetation codes of both Vegatlas as the SBB vegetation typology and the presence value of the plant species associated with *C. impunctatus* habitat.

Features are selected with a presence value of 50% or higher to comprise suitable habitat for *Culicoides impunctataus*. After the selection the selected features are transformed to raster with cell size of 5x5 kilometers (size of the original sample squares) and are then resampled to a cell size of 1x1 kilometer. One sample square is now presented by twenty five 1 km^2 squares.

2 The host density is calculated by a density function. All sheep/goats, cows and pigs are counted separately for every raster cell, sized 1x1 kilometer (appendix 2).

3. Data from all weather stations are analyzed before used in the model. Most of the stations are only lacking values at the end of December. Because in December the temperature is too low to get a positive value for the vectorial capacity these weather stations are used in the model. Some weather stations contain lacking values for various months. These weather stations are removed from the model (appendix 3).
The daily mean temperatures are used to get a monthly average for every used weather station. Temperature data is used from the years 2001 till 2005. These five years are averaged. The values gained in this way, are interpolated using a spline function. Spline interpolation is found to be best in the area where there is little change in physiography over a larger horizontal distance (Priyakant et al. 2002).

4. The number of vectors per square kilometer is calculated using both the data on habitat as on host density. Every square kilometer containing suitable habitat for *Culicoides impunctatus*, will provide for 5000 vectors (pers. comm. Jacob Beeuwkes 2007). Every host animal will be providing 200 vectors (pers. comm. Willem Takken 2006). Using host density, the total number of vectors is calculated per square kilometer.

5 Vectorial capacity is calculated combining data on vector density, host density and temperature.

3.2.3 Model limitations

The following limitations apply to the model or to the input files.

The Vectorial Capacity model calculates the number of new infections arising per day from a currently infective case. An infection already has to be present. By using the model for the whole of the Netherlands the assumption is made that an infection is present on every location. This assumption is valid because the first infection seems to be random. In the current outbreak the BTV-virus has found its way from Sub-Saharan areas in Africa to the Netherlands, traversing over hundreds of kilometres, meaning that the first outbreak can occur everywhere. The value of the Vectorial Capacity calculated this way gives a measure for the risk of outbreaks after infection. Locations with a high vectorial capacity value have a higher risk of secondary infections once BTV is present.

The Vectorial Capacity model is a model based on local functions. A value in one cell does not influence the value of the neighboring cell. Another limitation is the independence of the different time steps. Values calculated in one month do not influence values in the following month. As a result it is not possible to calculate the development of an outbreak. If a outbreak really occurs, it will have influence in neighboring cells and following times steps. These effects are not included in this model.

Only vector competence and incubation period within the vector is used in the Vectorial Capacity model. The period for viral development within the host species and the infection rate of the host is not included. In the case of Bluetongue the effect of this shortcoming will be limited. The period of viral development is short (fig. 1) and the infection rates from midge to host is highly efficient and is thought to be almost 100% (pers. comm. Bethan Purse, 2006)

As stated before the population size of Culicoides midges throughout the year is dependent on various external factors, like temperature. Because changes in the population size in the Netherlands are not known, a fixed number of 200 midges per host animal is used. This can cause an overestimation of the risk in spring and fall when temperatures are low, and an underestimation in summer when temperatures are high.

The number of vectors per host animal, as a result of farm habitat, is equal for all animals. It is likely that a difference exists between cows and sheep, but also within

one host species differences may exist. These differences can be caused by farm size, farm type, presence of other animals, storage of dung and surrounding habitats. However all these factors are not known.

The dataset from GIAB, containing farm locations, is based on postal address of the farms. The actual location of the farm and the animals it contains may deviate from this location. Also the size of the farm may be of influence on the amount of host animals and thus the amount of vectors present. If the stables and fields are dispersed over a bigger area, the amount of host animals per square kilometre will be lower.

The Vegatlas dataset is based on sampling cells of 5 by 5 kilometres. For every cell an inventory is made of the occurring vegetation type. If a certain vegetation type occurs for a small area within the cell, the whole cell is indicated as containing this vegetation type. This is likely to result in an overestimation of the area containing this type of vegetation. Also the exact location of the species is not known.
Vegatlas is using vegetation types in stead of separate species. The description of the vegetation type contains information on the likeliness to contain a certain species. If the vegetation type is assigned to an area, it may well be possible that a species described for this vegetation type is absent in the area. On the opposite, a species may be present, but is not listed in the description of the vegetation type.

3.3 Model analysis

3.3.1 Introduction

Analysis of a model can vary in nature, from very simple to very comprehensive and complex. Various methods exist to perform this analysis (Waveren et al. 1999). In this study a global analysis is performed, using standard input, and sensitivity analyses changing individual parameters in the model.

To analyze the characteristics of the model five sensitivity scenarios are run in ArcMap. As a basis (basic scenario) the method described above is used. In every next scenario one factor is changed to see the effect on the vectorial capacity (table 4, changed factor in grey). A total of five sensitivity scenarios are run.

Table 4 Properties of the sensitivity analysis

Factor	Temperature data	Habitat	Pig farms	Vectors
Standard input	2001-2005	Sphagnum + other plant species	-	Host dependent
Temperature	2006	Sphagnum + other plant species	-	Host dependent
Plant habitat	2001-2005	Sphagnum only	-	Host dependent
Farm habitat	2001-2005	Sphagnum + other plant species	+	Host dependent

Vector dependence	2001-2005	Sphagnum + other plant species	- Farm dependent

3.3.2 Basic scenario: standard input

In this basic scenario the model is run, using temperature values for the period 2001 to 2005. The number of vectors is determined only by the number of sheep and cows plus an extra amount created by suitable peat vegetation. This vegetation contains all plant species described before.
The amount of midges, determined only by farm habitat, is equal for each host. Therefore the range in vectorial capacity is solely dependent on differences in temperature (fig. 7). At about 11.3℃ the vectorial capacity reaches a value above 0, at 12.6℃ vectorial capacity is above 1, meaning new outbreaks are possible. With higher temperatures the value of the vectorial capacity rises quickly. At 19℃ (average temperature in august is 18.4℃) vectorial capacity approaches a value of 200.

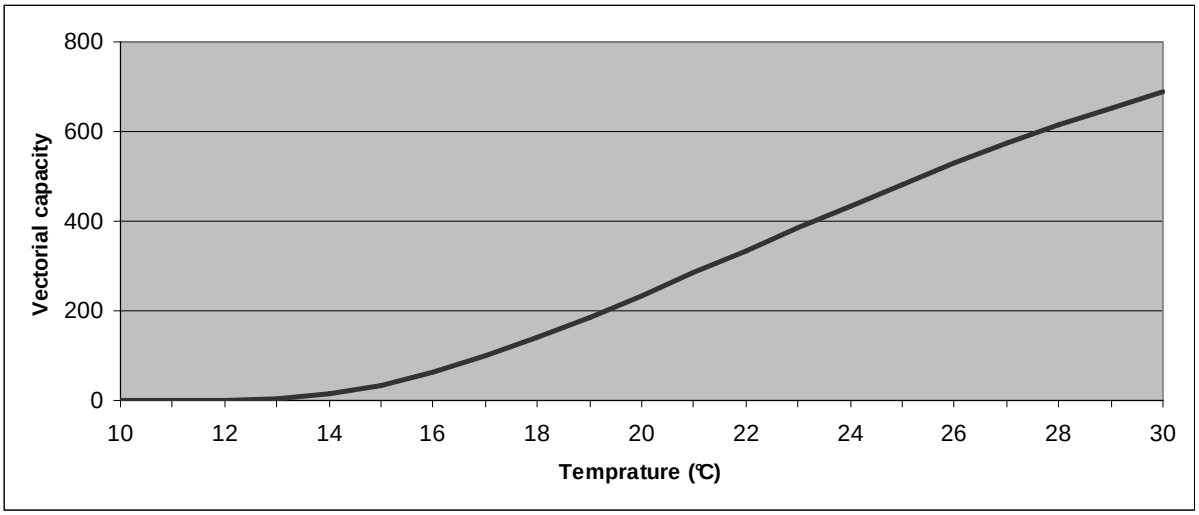

Figure 7 Relationship between temperature and Vectorial Capacity with 200 vectors per host

A clear seasonal change can be seen in the values of the vectorial capacity (appendix 4a). In May temperature reaches the level to get a positive value for the vectorial capacity. The south of the Netherlands has higher temperatures than the north, resulting in highest values in Limburg (22.5) In the north VC values are still below 1, meaning no outbreaks are possible (fig 8).

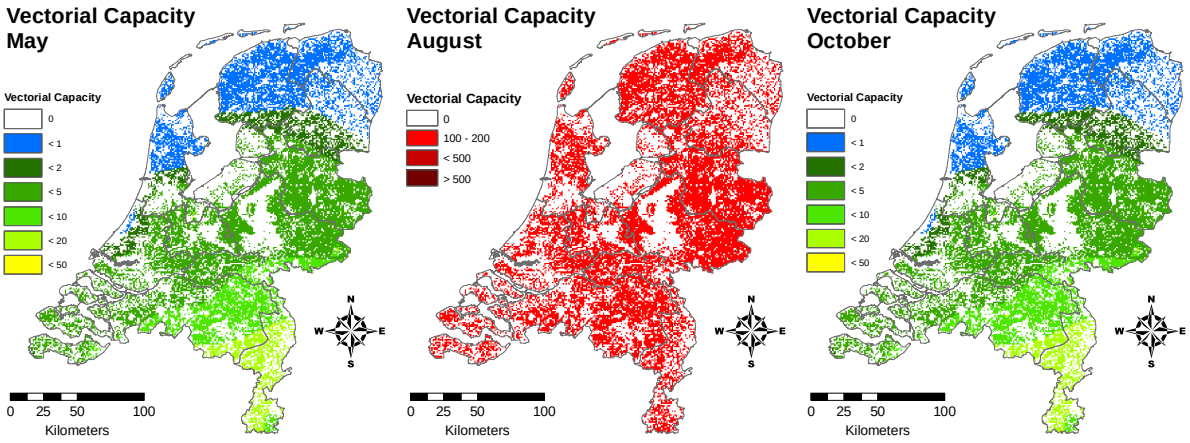

Figure 8 Vectorial capacity with standard input during May (left), August (middle) and October (right)

VC values are rising according to temperature. In June and July highest values are still found in the south. In august the vectorial capacity reaches the highest values, because of highest temperature that month. Besides high values in the south, also a rise in VC can be seen close to the coast, in comparison to the middle and east of the Netherlands, where the values are lowest.
In September and October VC decreases due to lower temperatures. Costal areas stay highest, at which Zeeland is the last province having values above one.

Locations containing *Sphagnum, Myrica gale, Polytrichum commune* and *Juncus acutiflorus/articulatus* have a higher VC, because of the extra amount of vectors. However only a limited number of locations coincide with the selected criterion of a presence value above 50% (figure 9).

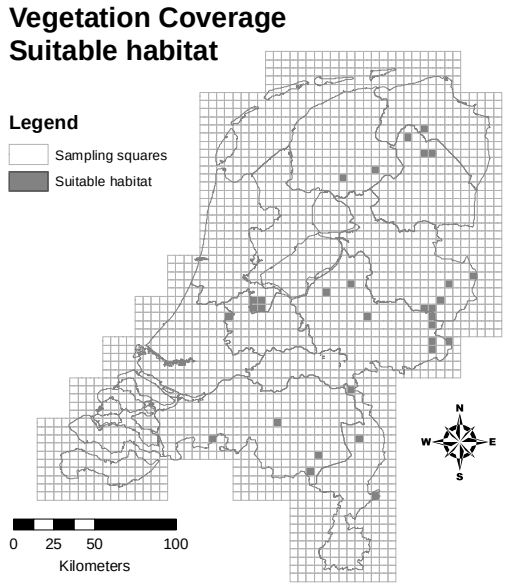

Figure 9 Locations containing a presence value above 50% for *Sphagnum* spp.. *Juncus acutiflorus/articulatus, Myrica gale* and *Polytrichum commune*

3.3.3 Sensitivity scenario 2006

This scenario is run with temperature data form the year 2006. Besides that this year is exceptional because of the high temperatures with many records, 2006 is also the first year in which an actual outbreak of Bluetongue occurred in the Netherlands.
In comparison to the years 2001 to 2005, the year 2006 has higher temperatures from May until December (figure 10). Except for august 2006, which has lower temperatures due to long rainy periods. June 2006 has parts of the Netherlands which are warmer (inland areas) and areas near the coast which are colder.
The higher temperature results in a higher vectorial capacity for 2006. In May a smaller part of the Netherlands show VC values below 1 (appendix 4b). In October the whole of the Netherlands has a value above 1, where in October 2001-2005 only a small part of the Netherlands has a chance of new outbreaks. Only August and part of the Netherlands in June show lower values in comparison to the period 2001 to 2005. This is caused by the lower temperature.

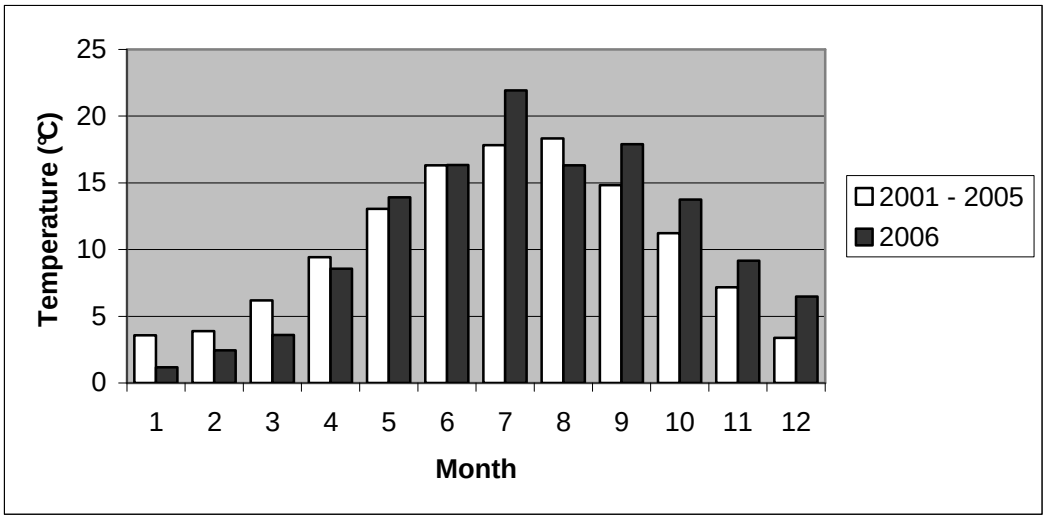

Figure 10 Mean monthly temperatures for 2001-2005 and 2006

3.3.4 Sensitivity scenario Sphagnum habitat

Polytrichum commune, *Myrica gale* and *Juncus acutiflorus/auriculatus* are listed in some, but not all articles dealing with *Culicoides impunctatus* habitat, like Sphagnum is. The use of these species, besides *Sphagnum*, has a limiting effect on the amount of suitable habitat. The combination of all species results in 775 km2 of suitable habitat, while only *Sphagnum* results in 12325 km2. The use of only Sphagnum may give a better estimation of the amount of suitable habitat for *Culicoides impunctatus*.
When using only *Sphagnum* spp. determining the habitat of *Culicoides impunctatus*, more locations have a suitable habitat. As a result more farms will have an extra amount of vectors resulting in an increase of the vectorial capacity value (appendix 4c).

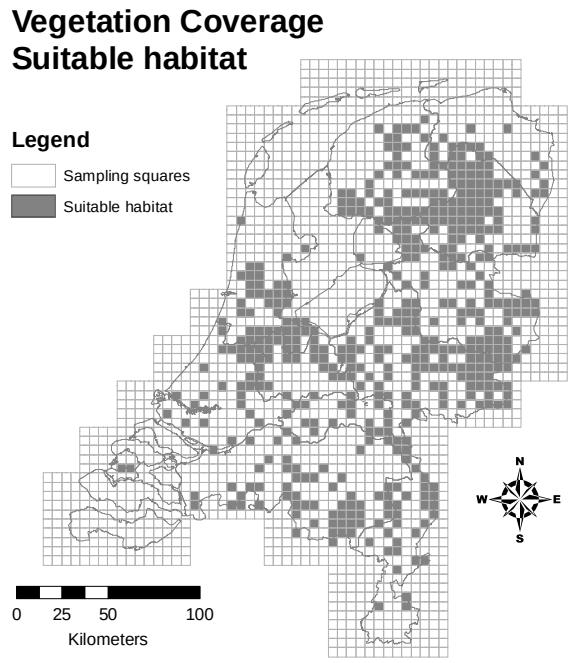

Figure 11 containing a presence value above 50% for *Sphagnum spp.*

3.3.5 Sensitivity scenario pigs

As stated before *Culicoides* species breed in a range of moist microhabitats (such as irrigation channels, drainage pipes and dung heaps) that are omnipresent across many farmyard types. It therefore is well possible that Culicoides midges not only occur on ovine and bovine farms, but also on other farms. The addition of pig farms as a potential habitat for *Culicoides*, results in a higher value for the VC, especially in Noord-Brabant and Limburg, where most pig farms are located (appendix 4d).
Raster cells with a low amount of sheep and/or cows have a high increase of the VC, while raster cells with a high amount of sheep and/or cows have a low increase. In the latter situation the extra number of midges is distributed over a higher number of hosts, resulting in a smaller increase of vectors per host.

3.3.6 Sensitivity scenario farm dependence

In all previous sensitivity scenarios the amount of vectors is determined by the number of host animals (*Sphagnum* not included). However it is not the animal itself which provides the habitat, but the farm it is located. Therefore it is interesting to use a fixed number of vectors for each farm. An error is made by assuming every farm is equally sized. Size is dependent on the amount of animals. However in this sensitivity scenario all farms produce the same amount of vectors. The amount is calculated by assigning equal amounts of host animals to each farm, with a total similar to the original dataset.
When the number of midges per farm is independent of the number of host, and therefore equal for every farm, the vectorial capacity becomes strongly dependent on the amount of hosts. Farms with few host animals show a high VC value, while farms with many animals show low VC. Farms with few animals are found throughout the

whole of the Netherlands, except the northern provinces seem to have a lower risk then the southern provinces (fig. 13, appendix 4e).

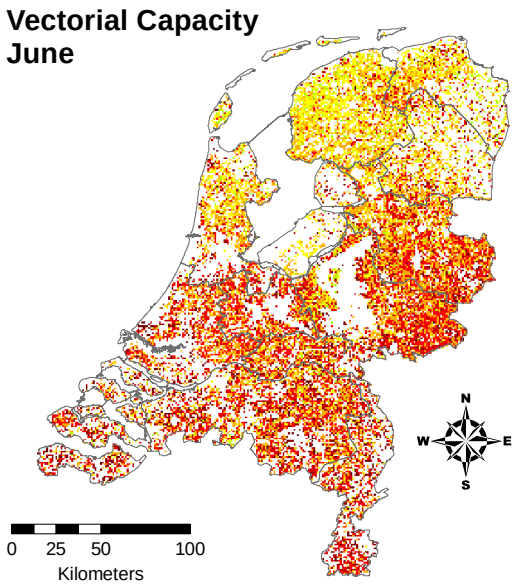

Figure 12 Vectorial capacity with farms determining the amount of vectors

3.3.7 Result sensitivity analysis

Combining the results of the sensitivity analysis it can be clearly seen that temperature is the most important factor as a cause of differences in vectorial capacity, both spatial and temporal. Besides temperature there are various other factors determining the value of vectorial capacity. All these factors will influence the amount of *Culicoides* midges present. The presence of suitable habitat for *Culicoides impunctatus* will lead to an increase of amount of midges. The use of different amount of habitat plant species will greatly involve the amount of suitable habitat and thus the amount of *Culicoides impunctatus* midges.
The presence of pigs in an area will have the same effect, but now on *Culicoides* species associated with animal farms. Another factor which might be of influence is the farm size in relation to the amount of farm animals.

3.4 Validation

In order to determine whether or not the model is a good predictor of the real situation, it must be validated. The model must be able to reproduce field observations from an independent data set (Waveren et al. 1999).
Although actual values for Vectorial Capacity are not known from the field, it is possible to compare the period of real outbreaks with the periods of risk calculated by the model.
The first outbreak occurred on August 17, in the south of Limburg. Although the values of vectorial capacity in August 2006 show a decrease, due to the rainy weather and lower temperatures, the values are all above 100 making outbreaks possible (appendix 4b).
In September and October the amount of outbreaks are rising (fig. 13) with a peak in October. This is remarkable because the vectorial capacity shows a decrease in

October, From November the vectorial capacity drop below zero, meaning outbreaks should not be possible, however throughout the winter new outbreaks, though in low numbers, keep occurring (appendix 5).
The real outbreaks seem to contradict the model prediction in a certain extent. The amount of outbreaks is rising while the vectorial capacity is already decreasing. Also when the model excludes new outbreaks they still occur.
This difference can be explained by the lack of temporal independence of the model. In this model the situation in one month does not affect the situation in the following month. In reality the presence of infected midges will increase the chance of new outbreaks. This will lead to new outbreaks as long as the environmental conditions allow the transmission of the virus. This can be seen in the data on actual outbreaks. As long as the value of vectorial capacity is above one the amount of new outbreaks keep rising. When the VC drops below one, the amount of outbreaks also drops to values close to zero.
The resulting outbreaks in November may be explained by a delay in appearance of symptoms and late identification of the disease. However also some outbreaks occur in the winter. It is possible that, although the temperature outside is too low, the indoor temperature in some stables may be high enough for development of the vectors and the virus. Outdoor dispersal will be limited, which results in a low amount of outbreaks in the winter. As a disturbing result Bluetongue Virus has a way to survive the winter, which inevitably will lead to numerous new outbreaks when the temperature will rise again.

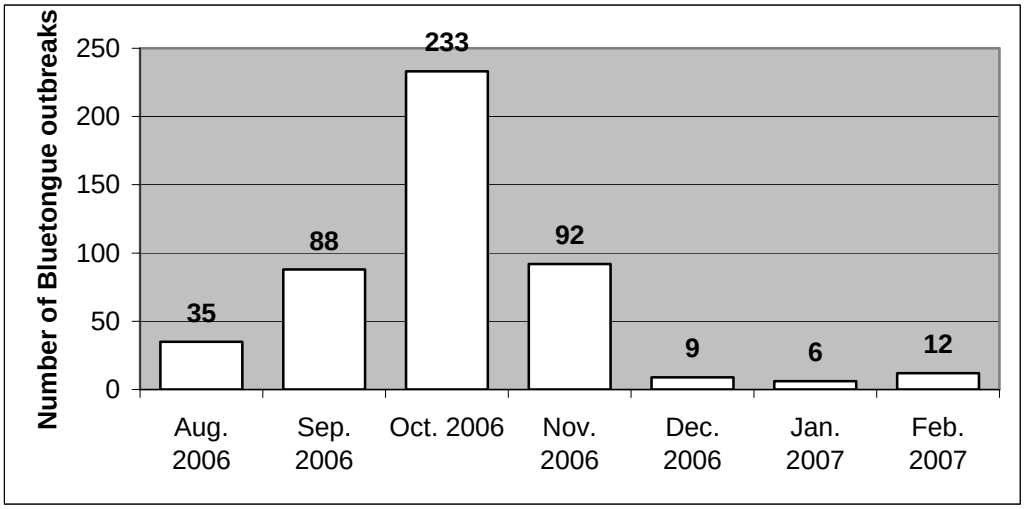

Figure 13 Number of Bluetongue outbreaks in the Netherlands in 2006 and early 2007

3.5 Model simulations

Once the model has been thoroughly tested the model may be used in all kinds of applications. With model simulations it is possible to imitate or estimate how events might occur in a real situation.

3.5.1 Climate simulation

The climate simulation is used to predict the risk after a climate change period of hundred years. Expected values for mean global warming for 2100, at a doubling of CO_2 concentrations, is between 2℃ and 4.5℃ with a be st estimation of 3℃ (IPCC 2007). In this simulation average monthly temperatures are derived from 2001 – 2005 and increased with 3℃ to calculate the temperature in 2100. Because it is hard to say if the temperature will rise equally over the whole of the Netherlands, possible spatial variation in temperature rise is neglected.

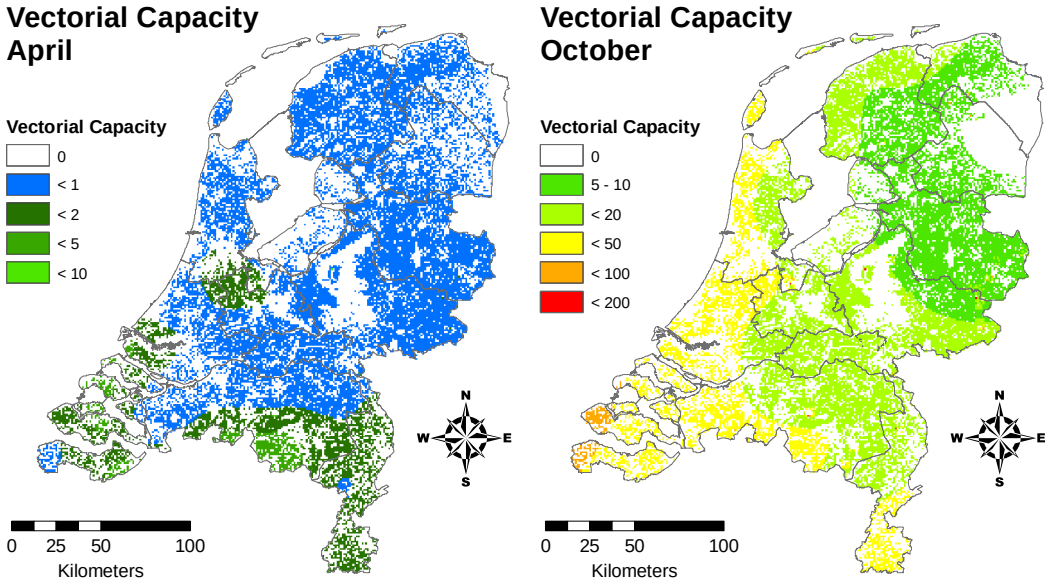

Figure 14 Vectorial capacity in 2100 for April (left) and October (right)

Because of the strong correlation between temperature and vectorial capacity, the vectorial capacity is higher in 2100 then it is at the present situation. Also the period in which an outbreak may occur is longer. Already in April the value for the vectorial capacity rises above one, where with the current temperature this is seen a month later. Also the period of risk ends later. Where at the current temperature vectorial capacity drops below one in most parts of the Netherlands, in 2100 the whole of the Netherlands will stay above this value where outbreaks still are theoretically possible.

3.5.2 Management simulation

To see what the effect is of different ways of management, various management scenarios are run (table 5). For easy computing every province is used to contain a different scenario. Two types of farming are simulated. Specialized farming with one species of animal, for sheep, cows and pigs in two densities. Secondly mixed farming where sheep, cows and pigs are held together in the same area.
Besides farming also three scenarios of nature conservation of peat land are simulates. First without any grazing, secondly with grazing by sheep and finally grazing combined with pig farming. Grazing can also be seen as farming of sheep, resulting both in a presence of host animals.

Table 5 Properties of the management scenarios

Scenario	Province	Number of animals
Specialized animal farming	Friesland	300 sheep
Specialized animal farming	Groningen	600 sheep
Specialized animal farming	Noord Holland	300 cows
Specialized animal farming	Utrecht	600 cows
Specialized animal farming	Drenthe	300 pigs
Specialized animal farming	Overijssel	600 pigs
Mixed animal farming	Flevoland	100 sheep
		100 cows
		100 pigs
Mixed animal farming	Gelderland	200 sheep
		200 cows
		200 pigs
Peat area	Zuid Holland	0
Peat area + grazing	Zeeland	300 sheep
Peat ares + grazing + pig farming	Noord Brabant	150 sheep 150 pigs
Peat ares + grazing + pig farming	Limburg	300 sheep 300 pigs

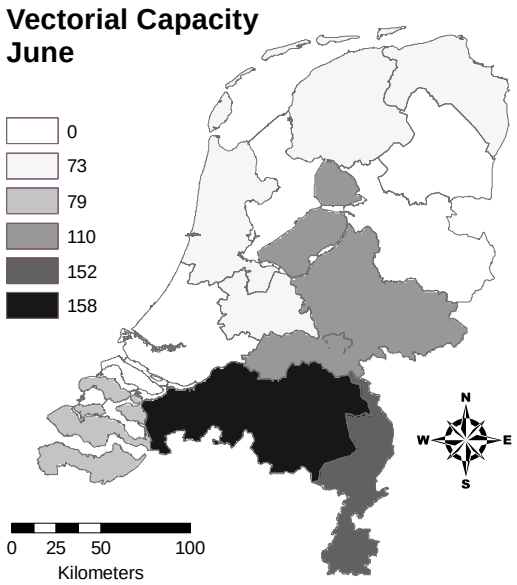

Figure 15 Vectorial capacity for different management scenarios

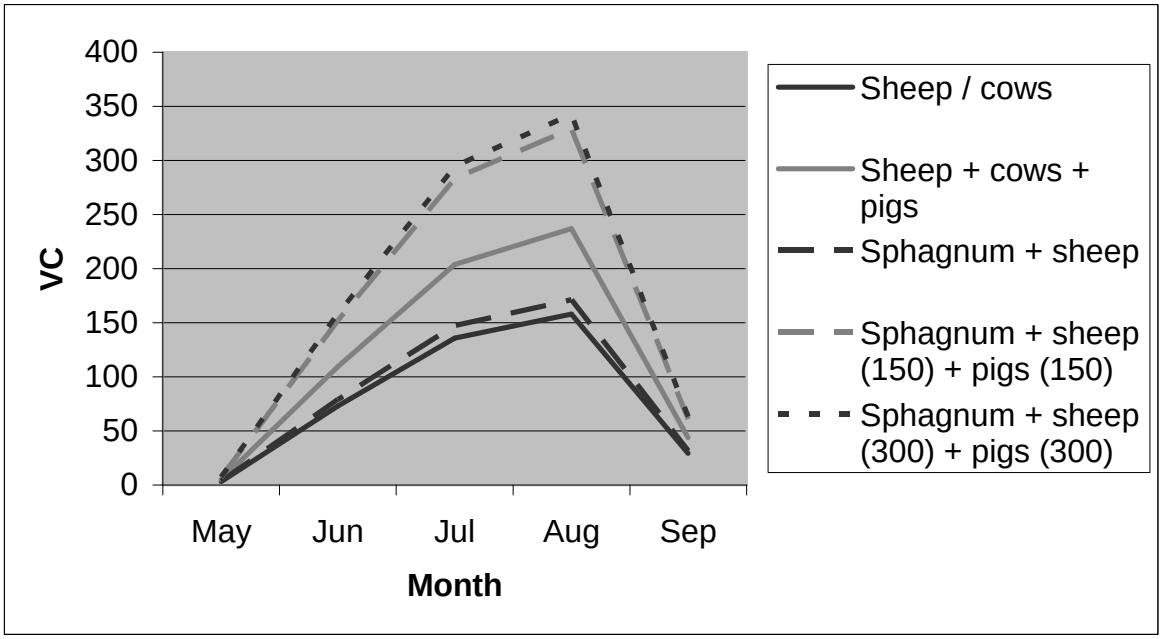

Figure 16 Vectorial capacity for different management scenarios from May till September

Logically, areas without host animals show a vectorial capacity of zero. Areas with specialized farming (sheep or cows) show all equal VC. This is caused by the amount of vectors per host animal, which is equal for both sheep and cows. Moreover because it is equal per animal, it is independent of the density of host animals.
The same effect seems to be true for the mixed farming. A higher VC capacity is found then without pigs, caused by the extra amount of vectors, but it is equal for both low density (Flevoland) as high density (Gelderland). However when changing the ratio, which stays the same in the performed model run, it will result in higher VC when the percentage of pigs will increase.
Looking at the areas with Sphagnum, the same increase described before of VC caused by pigs can be seen. However now there is a difference between low density (Noord Brabant) and high density (Limburg). In the area with a lower amount of host animals, the vectorial capacity is higher. The presence of Sphagnum results in a fixed number of bluetongue vectors per square kilometre. When the density of animals is low, the amount of vectors per host animal is high, resulting in high VC.
Finally, the addition of pigs seems to have a bigger effect on vectorial capacity than Sphagnum. This is easily explained by the amount of vectors they generate. Sphagnum generates 5000 midges/km2 while pigs generate 60,000 (300 * 200) midges/km2. When the amount of pigs is bigger than 25 the effect will exceed the effect of Sphagnum.

4. Conclusions

Ovine and bovine hosts are omnipresent in the Netherlands. Four species of deer occur in the Netherlands, but these species are not likely to be susceptible for Bluetongue virus.

In the Netherlands six species of *Culicoides* are found of which *C. impunctatus* and *C. obsoletus* are found in biggest amounts. *C. dewulfi* is the only species which is truly identified as infected with the Bluetongue virus.

Spatial distribution of *Culicoides obsoletus* is dependent on animal farms. *Culicoides impunctatus* is associated with peat vegetation and dependent on several plant species.

All plant species, *Sphagnum spp*., *Polytrichum commune*, *Myrica gale* and *Juncus acutiflorus/auriculatus,* associated with species preferring peat habitat, occur in the Netherlands. Farms close to these habitats have a higher risk of a bluetongue epizootic.

If *Sphagnum* spp is the only species required as habitat instead of a combination of the four species mentioned before, a bigger area of the Netherlands has a higher risk due to the midges present in this vegetation.

The whole of the Netherlands where sheep or cows are held has a chance of an epizootic of Bluetongue virus. The height of the vectorial capacity is dependent on temperature and not on host density. Therefore areas with high number of hosts have equal risk for an initial outbreak.

When pig farms are considered to be a suitable habitat for Culicoides species, these farms cause an increase of the risk of Bluetongue outbreaks.

In the case where the number of midges is determined by the farm in stead of the amount of hosts, farms with small amounts of host animals pose higher risk than farms with bog amounts of animals.

Temperature is a key factor in the process of Bluetongue development. A rise in temperature will lead to higher risks. Not only in exceptional warm years like 2006, but because of the global warming, the risk of Bluetongue epizootics will increase in the future.

Vectorial capacity can explain the actual amount of Bluetongue viruses partly. A more complex model is needed to predict the distribution of the disease in a better way.

5. Recommendations

5.1 Future research

Only little is known about the *Culicoides* species in the Netherlands. An extensive research is needed to quantify the factors involved with the transmission of Bluetongue in the Netherlands. More knowledge is needed on which species occur where, both looking at vegetation and different farm types. How does the population develop throughout the year and what is the incubation period in vector as well as in hosts.

The number for of vectors per host animal, as a result of farm habitat, is equal for all animals. It is likely that a difference exists between cows and sheep, but also within one host species differences may exist. These differences can be caused by farm size, farm type, presence of other animals and location. However all these factors are not known.

The vectorial capacity model only gives an indication of the risk after a randomly occurring first outbreak. However this model can not generate a risk prediction after an actual outbreak on one location. Also the dispersal of midges is not included within this model. To predict the development of an outbreak a more complex model is needed. Zonal functions have to be incorporated as well as temporal functions.

Indoor temperatures are likely to be different than outdoor temperatures. This may have an effect on the predicted outcome. Therefore it is useful to incorporate stable temperatures into the model for the periods that the host animals are located indoors.

5.2 Management

A combination of host animals with various Culicoides habitats, both pig farms and peat vegetation, gives the highest risk. To reduce the risk, these habitats have to be separated from the hosts. Ovine and bovine farms have to be avoided in areas containing vegetation with *Sphagnum spp., Polytrichum commune, Myrica gale* and *Juncus acutiflorus/auriculatus* and in areas with pig farms.

To prevent Bluetongue Virus from over wintering inside stables, temperature indoors should be kept below the value where survival of BTV or *Culicoides* species is not possible.

6. Acknowledgments

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I am also grateful for the people who provided me information on this reasonably unknown topic. Variables which were needed to create the model, but also background information on the process of Bluetongue transmission. These people are Jacob Beeuwkes, Niels Verhulst, Bethan Purse and Bradley Mullens.
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7. Literature

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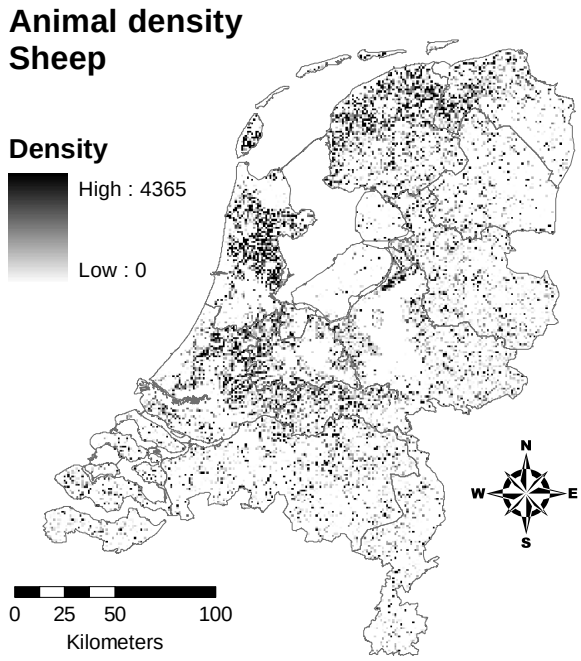
Verhulst N., PhD, Laboratory of Entomology, Wageningen University

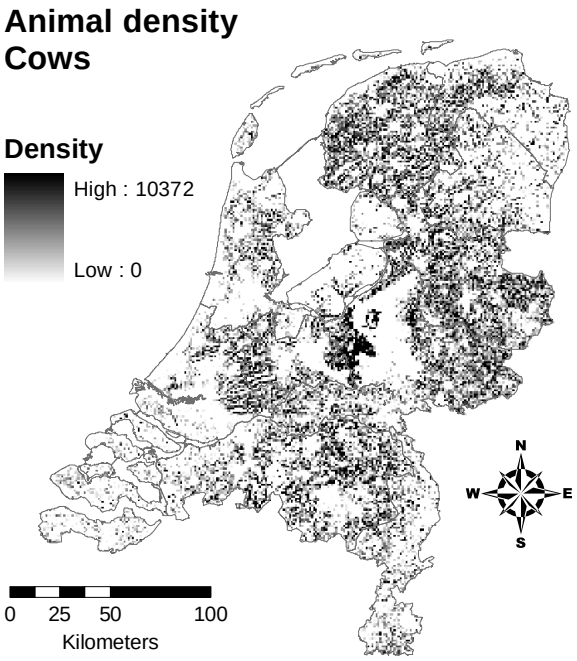
Appendices

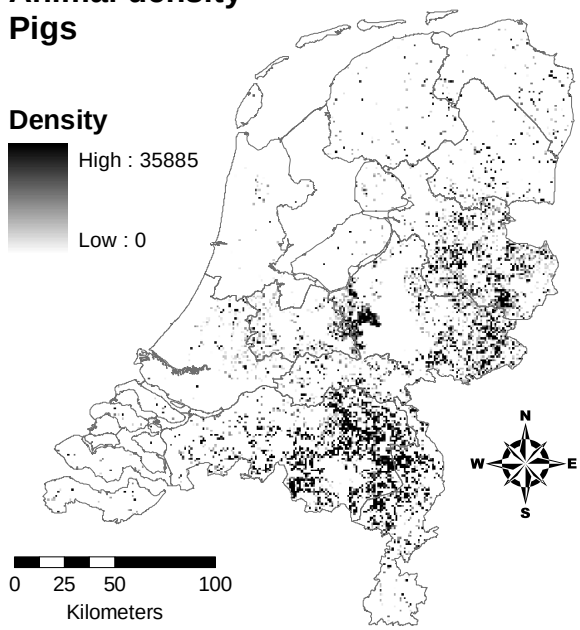
Appendix 1 Conversion table Vegetation typology StaatsBosBeheer to Vegatlas

Code SBB	Code Vegatlas
04A1	04AA01
04C1	04BB01
05E1	05CA01
05E2	05CA02
05E3	05CA03
05D1	05BC01
05D2	05BC02
05D5	05BC05
06/a	06RG01
06A1	06AA01
06-b	06RG02
06B1	06AB01
06B2	06AB02
06-c	06RG03
06C1	06AC01
06C2	06AC02
06C3	06AC03
06C4	06AC04
06D1	06AD01
07A1	07AA01
07A2	07AA02
08/a	08RG01
08A1	08AA01
08A2	08AA02
08B2	08BB03
08B3	08BB04
08C1	08BA02
08C2	08BC02
08C3	08BC03
08C4	08BC04
08C5	08BD01
08C6	08BD03
08-d	08RG03
08-e	08RG04
09A1	09AA01
09A2	09AA02
09A3	09AA03
09A-a	09RG02
09B3	09BA01
09C1	09BA02
09C3	09BA04
09-d	09RG01
09-h	09RG04
10/b	10DG02
10-a	10RG02
10A1	10AA01
10A2	10AA02
10A3	10AA03
10-b	10RG03
10-c	10RG01
10-e	10RG04
11/a	11RG03
11A1	11AA01
11A2	11AA02
11A3	11AA03
11B1	11BA01
11B2	11BA02
11-i	11RG02
12A1	12AA01
12A-a	12RG02
12B1	12BA01
12B2	12BA02
12B3	12BA03
12B4	12BA04
12B-f	12RG05
12B-i	12RG04
12B-j	12RG03
14C1	14BA01
16-a	16RG02
16A1	16AA01
16A2	16AB01
16B1	16AB04
16B2	16AB06
16B3	16AB02
16B4	16AB05
16B-e	16RG06
16C1	16BA01
16C4	16BC01
16C-d	16RG08
16C-e	16RG12
16-r	16RG04
19-a	19RG01
19A2	19AA02
19A3	19AA03
19-d	19RG02
20A1	20AA01
20A2	20AA02
20-c	20RG01
26C3	26AC04
27A2	27AA02
28A1	28AA01
28A2	28AA02
28A3	28AA04
29A1	29AA01
29A2	29AA02
29A4	29AA04
32-a	32RG01
32-g	32RG07
36A1	36AA01
36A2	36AA02
36A-b	36RG02
38A1	38AA01
38A2	38AA02
39A1	39AA01
39A2	39AA02
39A-c	39RG03
39A-d	39RG04
40A1	40AA01
40A2	40AA02
40A-a	40RG01
40A-b	40RG02
40A-c	40RG03
41A/a	41DG01
41A1	41AA01
41A2	41AA02
42A1	42AA01
42A2	42AA02
43B1	43AA01
43B2	43AA02
43C1	43AB01

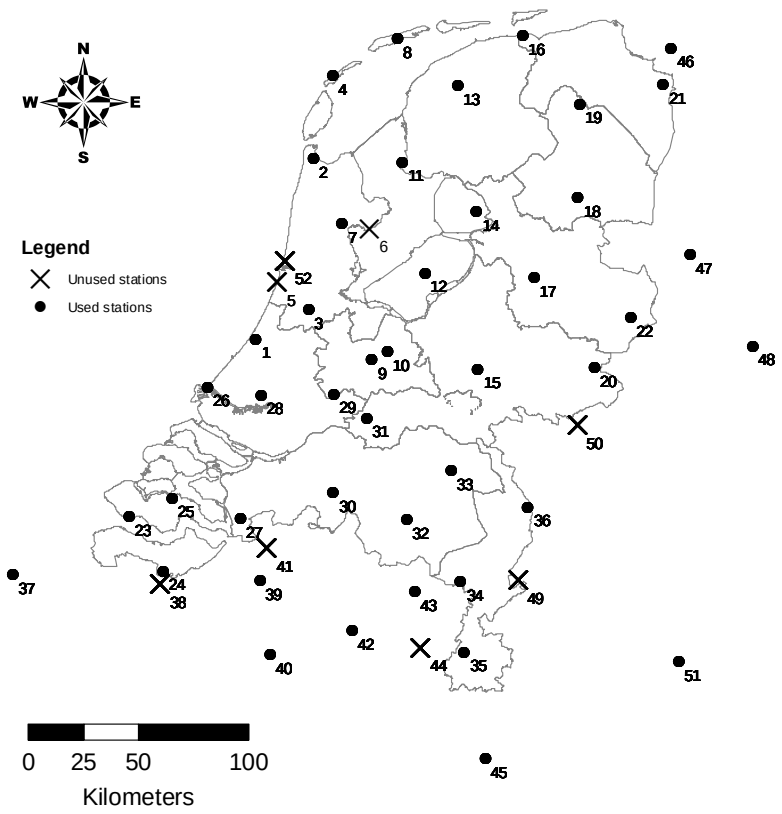
Appendix 2 Animal density





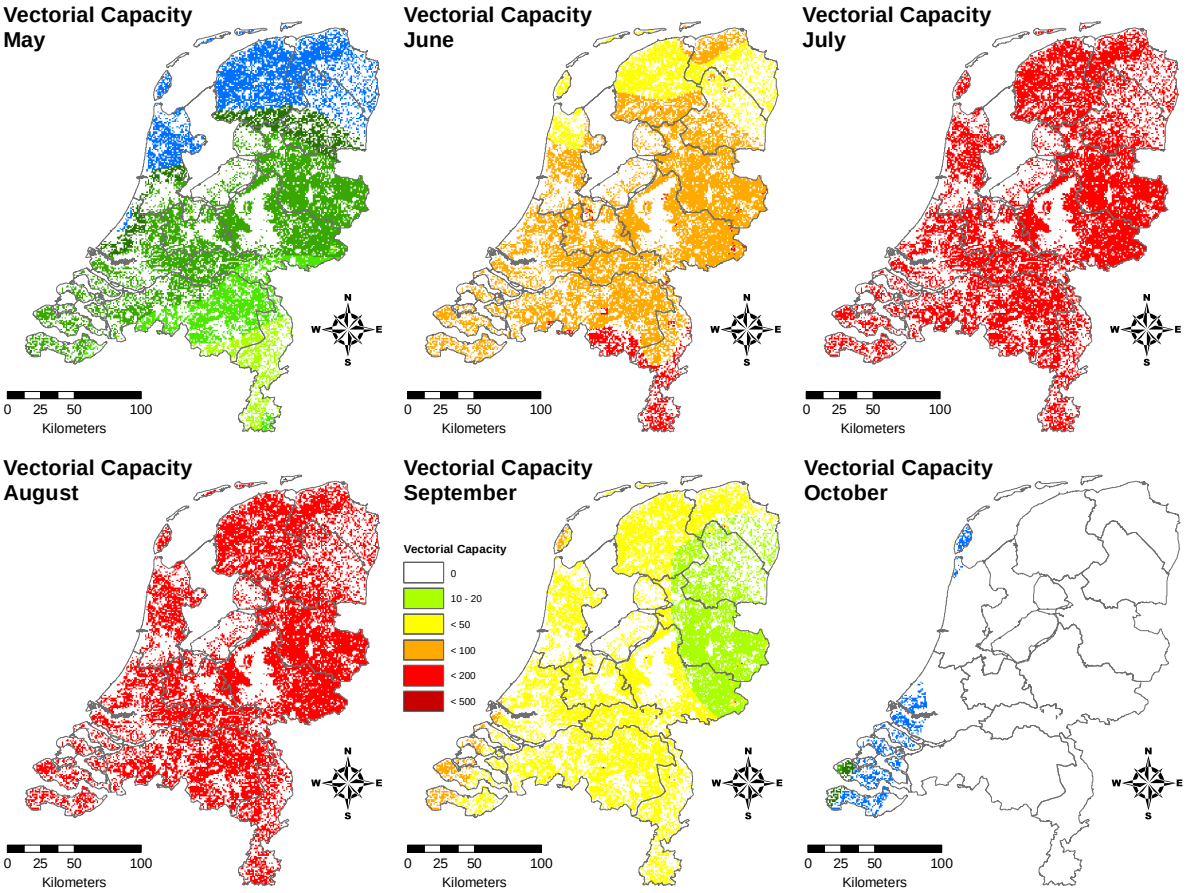


Appendix 3 Weather stations



ID	Name	ID	Name	ID	Name
1	Valkenburg	19	Eelde	37	Oostende Airport
2	De Kooy	20	Hupsel AWS	*38*	*Gent/Industrie Zone*
3	Amsterdam	21	Nieuw Beerta	39	Antwerpen/Deurne
4	Vlieland	22	Twenthe	40	Bruxelles National
5	*Bloemendaal a.Zee*	23	Vlissingen	*41*	*Brasschaat*
6	*Wijdenes*	24	Phillippine AWS	42	Schaffen
7	Berkhout	25	Wilhelminadorp	43	Kleine Brogel
8	Terschell./Hoorn	26	Hoek Van Holland	*44*	*Genk*
9	De Bilt	27	Woensdrecht	45	Spa/La Sauveniere
10	Soesterberg	28	Rotterdam	46	Emden
11	Stavoren AWS	29	Cabauw	47	Lingen
12	Lelystad	30	Gilze Rijen	48	Munster/Osnabruck
13	Leeuwarden	31	Herwijnen AWS	*49*	*Bruggen*
14	Marknesse AWS	32	Eindhoven	*50*	*Bocholt*
15	Deelen	33	Volkel	51	Koln/Bonn
16	Lauwersoog AWS	34	Ell	*52*	*Wijk aan Zee*
17	Heino AWS	35	Zuid Limburg		
18	Hoogeveen	36	Arcen		

Appendix 4a Vectorial Capacity Basic scenario

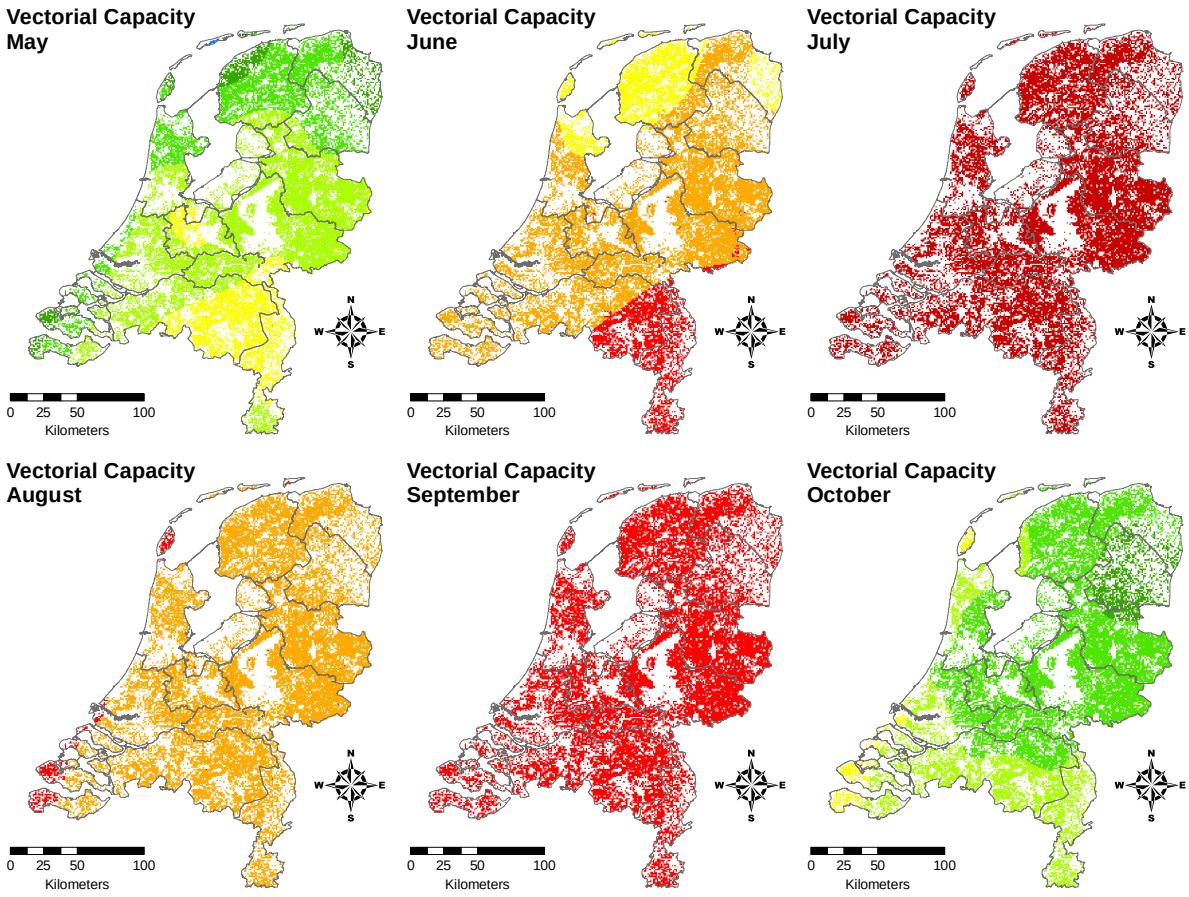


Legend

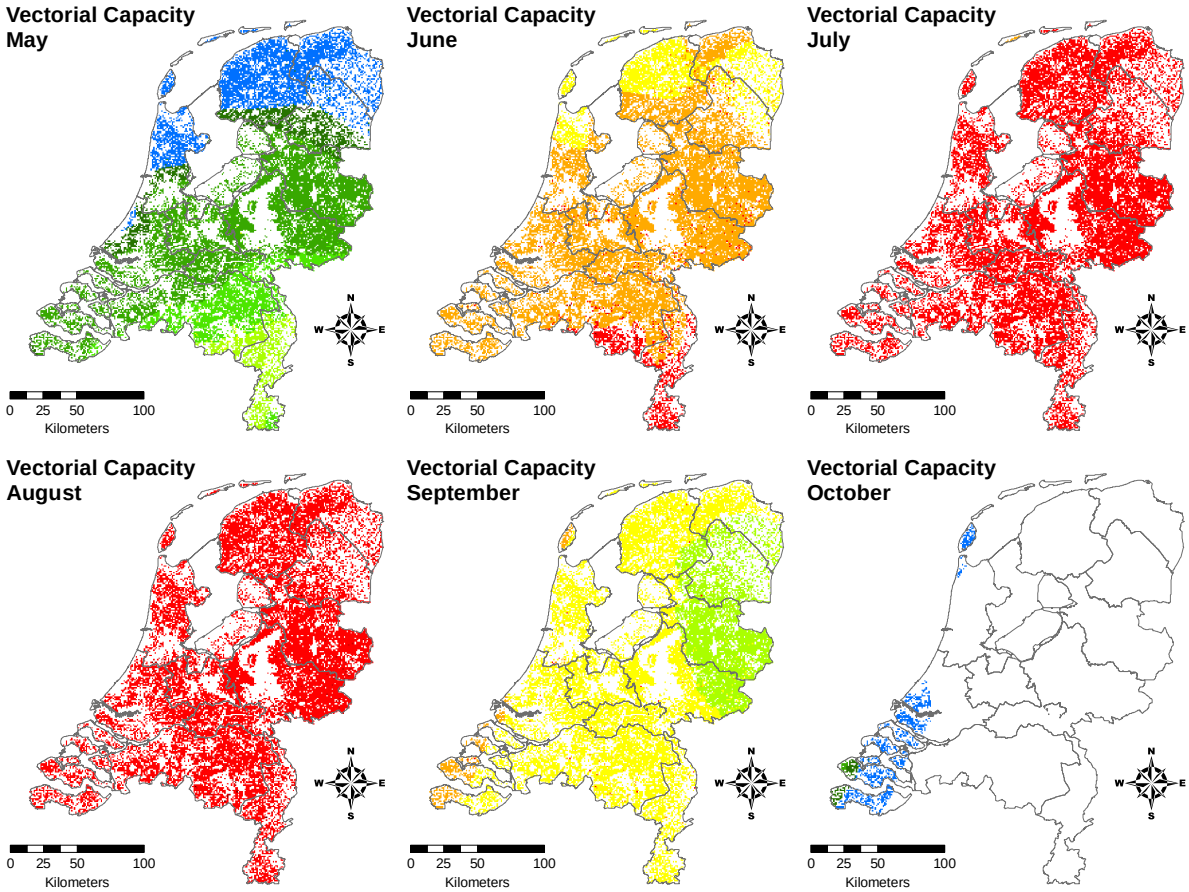
Vectorial Capacity

- 0
- < 1
- < 2
- < 5
- < 10
- < 20
- < 50
- < 100
- < 200
- < 500
- > 500

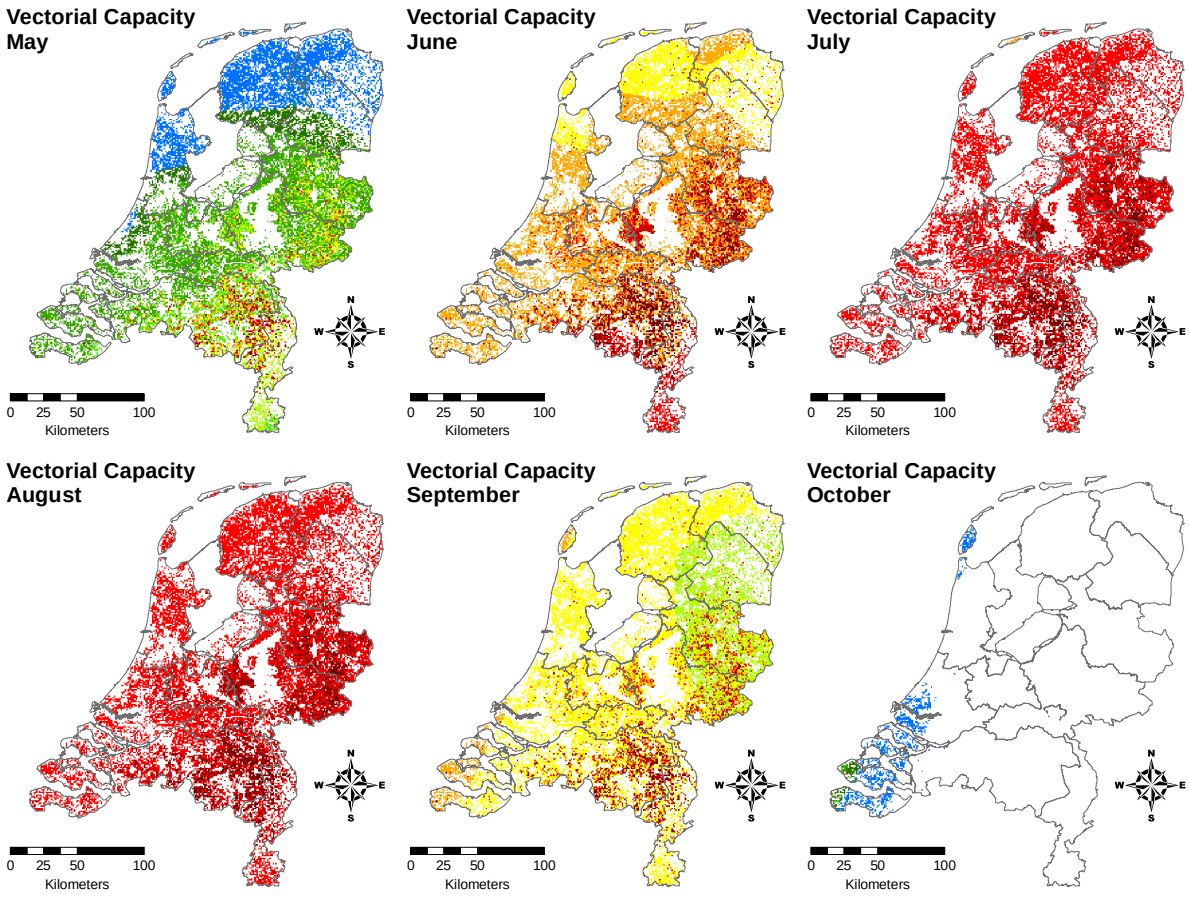
Appendix 4b Vectorial Capacity Sensitivity scenario 2006



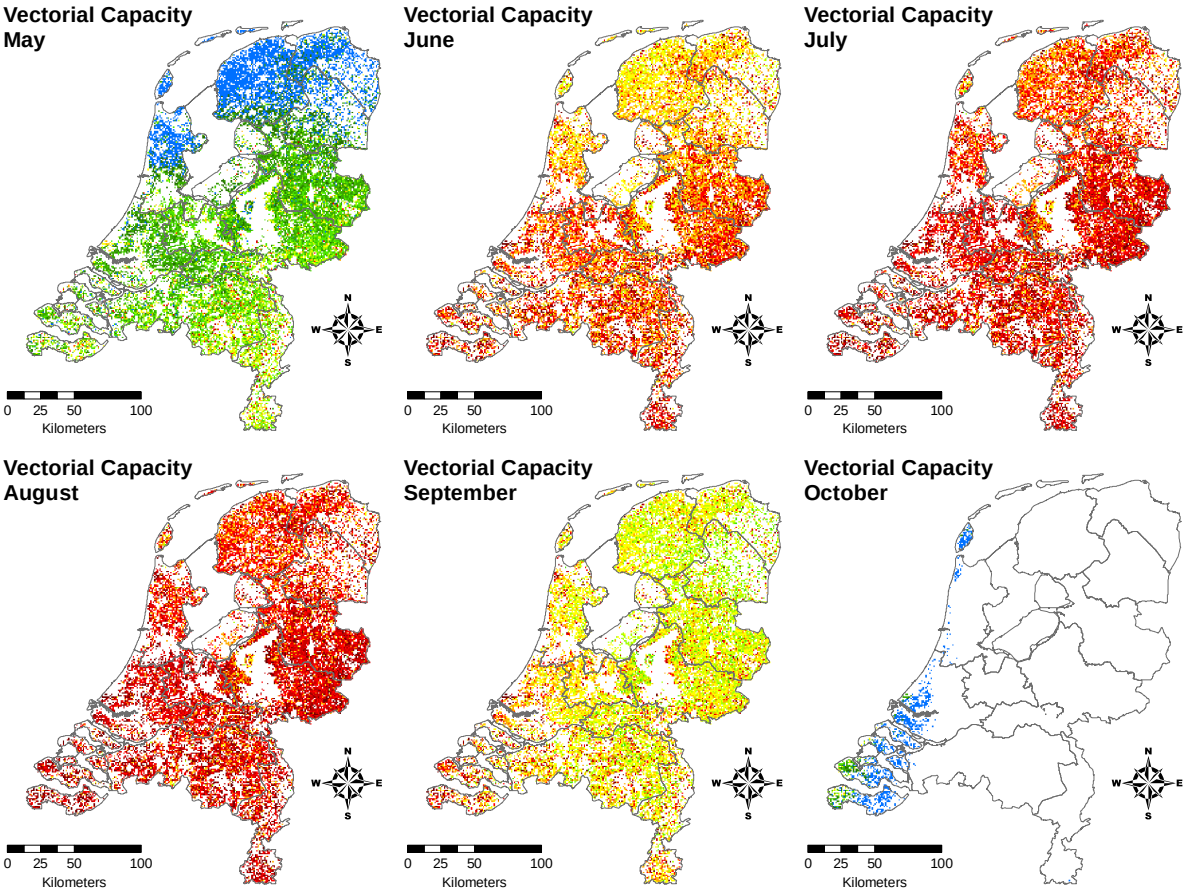
Appendix 4c Vectorial Capacity Sensitivity scenario Sphagnum habitat



Appendix 4d Vectorial Capacity Sensitivity scenario pigs

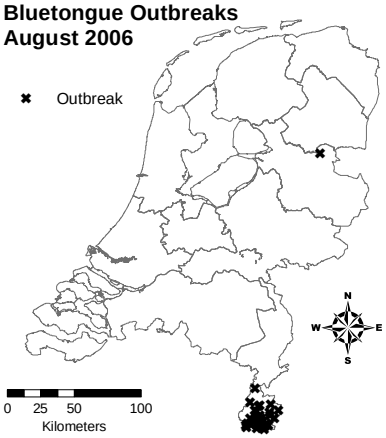


Appendix 4e Vectorial Capacity Sensitivity scenario farm dependence

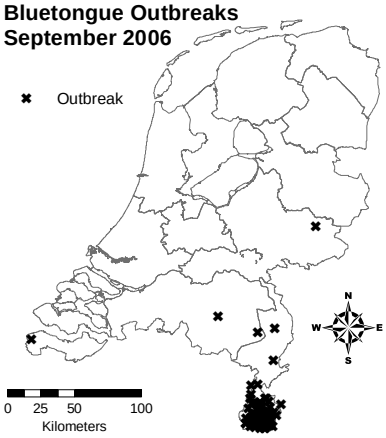


Appendix 5 Bluetongue Outbreaks in the Netherlands

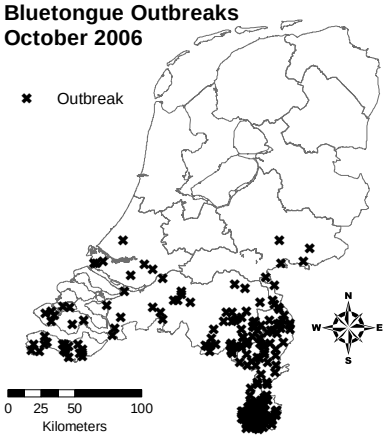
Bluetongue Outbreaks
August 2006



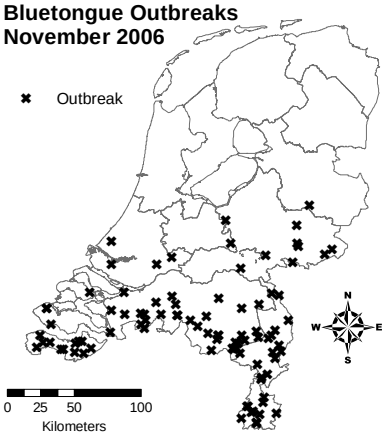
Bluetongue Outbreaks
September 2006



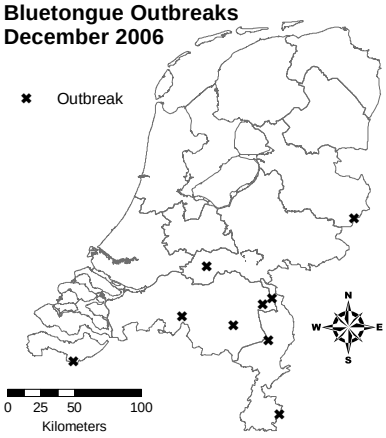
Bluetongue Outbreaks
October 2006



Bluetongue Outbreaks
November 2006



Bluetongue Outbreaks
December 2006



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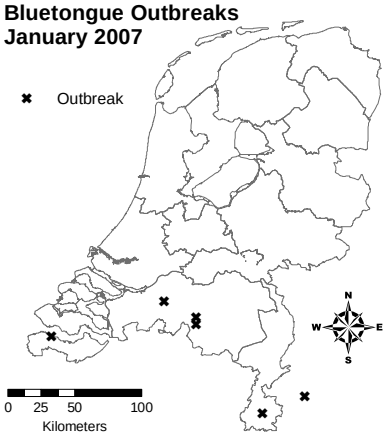
January 2007



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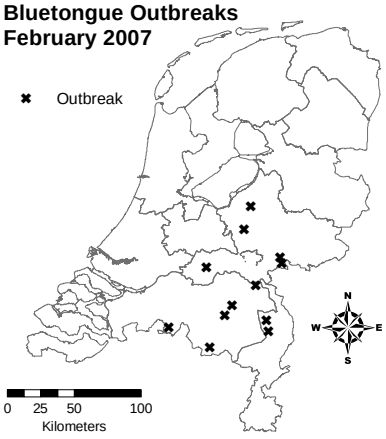
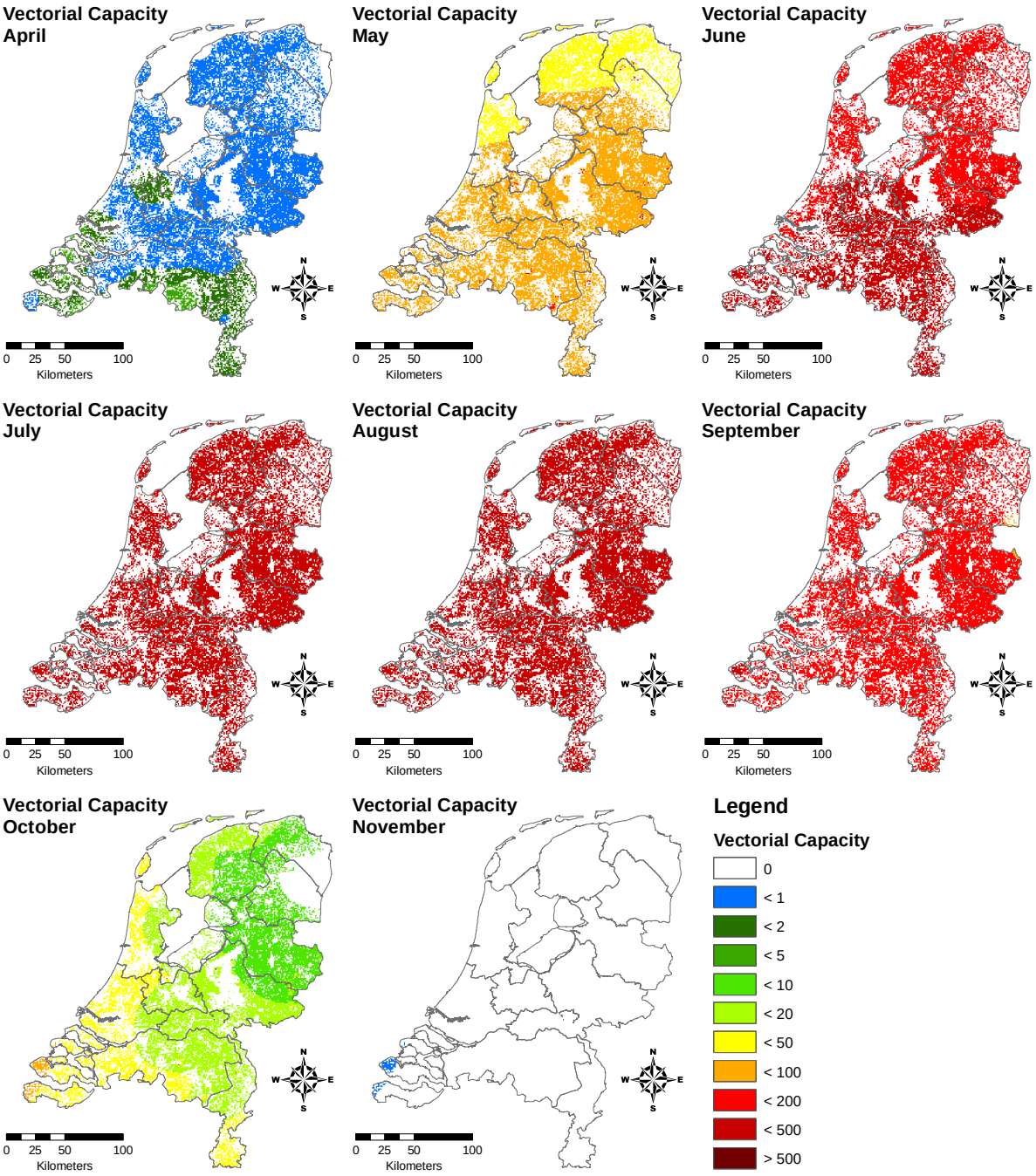
February 2007



Appendix 6a Vectorial Capacity Climate simulation



Appendix 6b Vectorial Capacity Management simulation