

# **Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever**

**Stefan Widgren**

Handledare: Ivar Vågsholm  
Inst. för idisslarmedicin och epidemiologi.

Bitr.handledare: Marie Engel  
Inst. för idisslarmedicin och epidemiologi.

Bitr.handledare: Maria Nöremark  
Avdelningen för sjukdomskontroll och smittskydd, SVA.

Examensarbete 2004:13  
Veterinärprogrammet  
Veterinärmedicinska fakulteten  
SLU  
ISSN 1650-7045  
Uppsala 2004



## Summary

One objective of this study has been to demonstrate how graph theory can be a useful tool for intervention in the case of an outbreak of a contagious disease. By using graph theory algorithms on data from the Swedish surveillance network system (Grisregistret) and combining this with the power of graph layout engines for visualization of interherd movements, valuable information can rapidly be provided from data that is easily available. Thus a clear line of priority in the strategy of fighting the outbreak can be established from day 0. This can be invaluable during the first couple of days, before more thorough information concerning all different types of contacts has been collected by veterinarians during farm visits. Thus rapid control measures can be implemented and this should increase the likelihood that possible infectious holdings are found during an early stage of the outbreak. Combining the information of the geographical location of an infectious holding and the interherd movements during the relevant time period on the same map can improve the understanding of the spread of the outbreak. It would also be possible to add information concerning other types of contacts, when such information becomes available, to make the picture clearer.

Another objective has been to model a putative outbreak of classical swine fever without any interventions from authorities. The epidemiological model uses data from the Swedish surveillance network system of pig movements, Grisregistret, based on the reported flows of pigs between farms. The model includes all interherd pig movements that occurred within a community in southern Sweden during 6 months. Both a high virulent strain and a low virulent strain of classical swine fever virus have been modelled. The epidemiological model is based on a SEIRD model for each holding, which have been interconnected to each other through the reported movements of pigs.



## Sammanfattning

Ett syfte med den här studien har varit att visa hur grafteori skulle kunna vara ett användbart verktyg vid bekämpning av ett utbrott av en smittsam sjukdom. Genom att använda grafteori algoritmer på data från det svenska Grisregistret och kombinera detta med möjligheten att visualisera förflyttningar mellan gårdar kan man få fram värdefull information snabbt från data som är lätt tillgänglig. Därmed får man ett underlag för prioriteringar i bekämpningsstrategin redan dag 0. Detta är viktigt under de första dagarna, innan mer detaljerad information samlats in genom gårdsbesök av veterinär. På så sätt kan kontrollåtgärder snabbt sättas in och borde öka möjligheten att tidigt under utbrottet finna gårdar som kan vara smittade. Därutöver skulle det också vara användbart att markera gårdarnas läge och förflyttningar av djur mellan dem på samma karta för att ytterligare öka förståelsen för spridningen av sjukdomen. Det skulle också vara möjligt att komplettera med information avseende andra typer av kontakter, när sådan informationen finns tillgänglig, för att få en tydligare bild.

Ett annat syfte med studien har varit att modellera ett tänkt utbrott av klassisk svinpest utan att några insatser görs för att begränsa spridningen. Den epidemiologiska modellen använder data från det svenska Grisregistret, innehållande rapporterade förflyttningar av grisar mellan gårdar. Modellen inkluderar grisförflyttningar under 6 månader från en kommun i södra Sverige. Både en hög- och lågvirulent stam av klassiskt svinpestvirus har modellerats. Den epidemiologiska modellen bygger på en SEIRD modell för varje gård som kopplats samman genom de förflyttningar som är rapporterade till Grisregistret.



# Contents

Introduction .....	9
Material and methods .....	10
Classical swine fever .....	10
Etiology .....	10
Epidemiology .....	10
Clinical signs .....	11
Pathogenesis .....	12
Diagnosis .....	12
Surveillance network system .....	13
Graph theory .....	13
Terminology .....	14
Graph layout with the DOT language .....	15
Visualize movements from the surveillance network system .....	16
Epidemiological modelling .....	18
SEIRD model for one herd .....	18
Numerical example of the SEIRD model for one pig herd .....	21
SEIRD model in a population of herds with interherd movements .....	22
Results .....	24
Surveillance network system .....	24
Numerical example of the SEIRD model for one pig herd .....	28
SEIRD model in a population of herds with interherd movements .....	29
Discussion .....	32
Classical swine fever .....	32
Graph theory .....	32
Epidemiological modelling .....	33
Surveillance network system .....	34
Conclusions .....	34
Tack .....	34
References .....	35
Graph layout resources .....	36



## Introduction

Experience has illustrated that rapid control measures are crucial for the eradication and control of highly contagious disease outbreaks. However, these control measures are difficult or even impossible to test for highly contagious infections as for example foot- and mouth disease, avian influenza, and classical swine fever, under any other conditions than real life.

A model of an epidemic disease represents a simplification of the true state of nature that enables the modeller to assess relevant features of the disease and its impact. The purpose of models is often to gain insight into how an epidemic will behave under certain conditions and to assess the critical time limits before the epidemic explodes. A model of an epidemic can be constructed by using e.g. Reed-Frost models, SIR models or Markov chain models (Thrusfield, 1997; Noordhuizen *et al.*, 2001) all with their own particular assumptions that may render the type of model useful in a particular setting.

One of the more difficult epidemic diseases to control within the European Union (EU) has been classical swine fever (CSF) or hog cholera. There have been recurrent outbreaks within the EU during the last 10 years. The outbreaks are often associated with the movements of pigs within the herd, between herds in the neighbourhood area and to herds in another region (Taylor, 1999). CSF outbreaks are very expensive to eradicate and it is associated with high costs for the industry to have the disease endemic in the country. The last outbreak in U.S.A., 1976, cost a total of \$140 million and the cost of the control program in the Netherlands during the period 1983-85 amounted to \$93 million (Van Oirschot, 1999).

The main route of transmission of the CSF virus is the infected pig. The high virulent strains of the virus will soon lead to clinical symptoms enabling a rapid diagnosis and implementation of control measures. The low virulent strains of the virus can have a more insidious pattern, where a lot of herds might become exposed before any clinical suspicion is raised and thus control measures are delayed.

Under Swedish conditions the nature of a putative CSF outbreak has been difficult to predict, as the last outbreak was in 1944, and the structure of the industry has since then changed towards fewer and larger herds, the introduction of breeding pyramids and sow pools with entirely new patterns for pig movements.

There has recently been a study, STUDS, under the auspices of the Swedish Board of Agriculture (SBA) of how to control large outbreaks of epizootic diseases in Sweden. It was concluded that the use of computer-aided decision support systems would be a helpful tool during an outbreak. One possible aid could be to use Geographical information systems (GIS) to visualize the spread of the epizootic diseases, while another would be to model the transmission based on the flow of animals within a geographical area.

One objective of this study has been to model a putative outbreak of classical swine fever without any interventions from the authorities to control the outbreak.

The epidemiological model uses data from the Swedish surveillance network system of pig movements, Grisregistret, based on the reported flow of pigs between farms. The model includes all interherd pig movements during 6 months from a community in southern Sweden. Both a high virulent strain and a low virulent strain of classical swine fever virus have been modelled. Another objective of the study has been to use graph theory to visualize movements of pigs between holdings. This can be used as a tool to rapidly gain information about animal flow, thereby enabling that control measures are implemented early in an outbreak.

## Material and methods

### Classical swine fever

Classical swine fever (CSF) is a highly contagious disease among swine caused by a pestivirus. The disease can take very different courses in the herd, depending on the strains of the virus and the current immunological status of the pigs. For a population of several herds the interherd movements have an impact on the course of the outbreak. The clinical signs of the infection can vary from acute, subacute, and chronic to atypical or even inapparent (Taylor, 1999; Van Oirschot, 1999; Anonymous, 2002).

Classical swine fever virus (CSFV) originated in the United States, but has now an almost worldwide distribution (Radostis *et al.*, 2000). Outbreaks are reported to Office International des Epizooties, OIE, and the current epidemiological situation in the OIE member countries can be viewed at their homepage (<http://www.oie.int/>, 4-Sep-2003). Classical swine fever is an OIE List A disease. The last outbreak of CSF in Sweden was in 1944 (Anonymous, 2002).

### *Etiology*

Classical swine fever virus belongs to the family *Flaviviridae*, genus *Pestivirus*. Two other members of this genus are bovine viral diarrhoea virus (BVDV) and border disease virus (BDV), which can infect cattle, sheep and swine. CSFV is an enveloped single stranded RNA virus about 12.3 kb long with a diameter of 40-50 nm (Van Oirschot, 1999).

### *Epidemiology*

The only natural host for CSFV is the domestic pig and the wild boar (Van Oirschot, 1999; Anonymous, 2002). Virus is shed into the environment from oronasal and lacrimal secretions, from urine and faeces. The time that passes from infection to the distribution of CSFV throughout the pig is 5 to 6 days (Van Oirschot, 1988).

Classical swine fever virus has also been found in the male gonads and therefore semen can serve as a primary reservoir for the venereal spread of CSFV (Choi, Chae, 2002).

As other *Pestivirus* the virus can be vertically transmitted to the foetuses in utero. If sows are infected with low to moderately virulent strains of virus during pregnancy and then recover, there is a high risk that their offspring may be carriers of the virus (Van Oirschot, 1999; Anonymous, 2002; Radostis *et al.*, 2000; Dewulf *et al.*, 2001).

Virus transmission can occur by different routes, the most important being direct contacts between susceptible and infected animals. Direct contacts can occur after purchase of infected animals, during transports and at markets (Van Oirschot, 1999; Taylor, 1999; Stegeman, Elbers & de Jong, 2002).

Another route of virus transmission is airborne with infected aerosols that are generated by animals when they sneeze, cough and breath. Splashes of faeces and urine can also generate aerosols (Dewulf *et al.*, 2000; Laevens *et al.*, 1999). Airborne transmission is possible in the spread of disease from farm to farm, but the epidemiologic importance of this route during an outbreak is difficult to estimate (Dewulf *et al.*, 2000; Anonymous, 2003a).

Transmission of the CSFV between herds by mechanical vectors, such as trucks, farmers and veterinarians, are by many authors considered to be of great importance in an outbreak (Van Oirschot, 1999; Taylor, 1999). However, under experimental conditions it has been shown to be difficult to infect susceptible pigs by indirect transmission of CSFV by excretions of infected pigs (Dewulf *et al.*, 2002).

An important source of classical swine fever infection is swill feeding (Taylor, 1999).

### *Clinical signs*

The clinical signs caused by CSFV depend on several factors in the interaction between the virus and the host. Important factors are the virulence of the virus, age and nutritional status of the host as well as the immunological status of the host and the population (Van Oirschot, 1988; Radostis *et al.*, 2000). The CSF outbreaks can be classified according to the clinical signs as acute, chronic or mild.

Low virulent strains can be difficult to diagnose, the only expression may be reproductive signs such as abortion and the birth of mummified or stillborn piglets. The piglets born with congenital infection can shed virus for months. These carriers may appear as normal healthy piglets with no clinical signs of disease, but are persistently infected and immunotolerant. Therefore, it is particularly important to investigate, with regard to CSFV, herds with a high level of unexplained reproductive failure, such as abortion, mummification or birth of weak piglets (Van Oirschot, 1988, 1999; Radostis *et al.*, 2000).

Classical swine fever caused by high virulent strains on the other hand has an acute course where the affected animals show fever, 40.5-41.5 °C, are dull,

lethargic and anorectic. A typical sign is that the pigs huddle in piles and are cyanotic. Conjunctivitis and nervous signs, i.e. ataxia and convulsions, will follow. The acute form has a case fatality rate that may reach 100% and death is usually seen within 8-20 days after clinical signs are noted (Van Oirschot, 1988,1999; Radostis *et al.*, 2000; Taylor, 1999).

### *Pathogenesis*

After infection by oral or parenteral route, the primary site of virus replication is the tonsil. The replication starts within a few hours post-infection and 24 hours later there is a transient viraemia when the virus become localised in the endothelial cells of the blood vessels and lymphatics. At this time, CSFV virus can be found in the spleen, peripheral lymph nodes, bone marrow and Peyer's patches. The virus exerts its cytopathic effect on endothelial cells, lymphoreticular cells, macrophages and epithelial cells. The generalized damage to the vascular system results in widespread congestion, arteriolar thrombosis, haemorrhage and infarction, with the most severe lesions found in the lymph nodes, spleen, kidneys and gastrointestinal tract. A leukopenia is common in the early stages of the disease, followed by anaemia and thrombocytosis. In many cases secondary bacterial infections occurs and plays a role in the development of lesions and clinical signs (Van Oirschot, 1999; Radostis *et al.*, 2000; Taylor, 1999; Anonymous, 2003).

### *Diagnosis*

Virus isolation can be used to diagnose CSFV. The drawback of this method is that it is slow and the cytopathic effect may be low and some strains have low infectivity and limited growth in tissue culture.

A reliable method for the diagnosis of CSFV is animal inoculation. However this test is time-consuming and therefore not suitable in situations where rapid diagnosis is crucial.

Fluorescent antibody test from frozen tissue, immunoassay for antigen with ELISA and polymerase chain reaction (PCR) are some of the most frequently methods used (Taylor, 1999; Van Oirschot, 1999; Radostis *et al.*, 2000).

The demonstration of a specific antibody response in blood samples through virus neutralisation test or ELISA plays an important role in an outbreak when a large number of animals have to be examined.

## **Surveillance network system**

According to European Union Council Directive 97/12/EC of 17 March 1997 with amendments, each member state must introduce a surveillance network system for swine. This database is supposed to identify all relevant animals in a population and to record their movements and changes in inventory.

The purpose is to support the control of contagious diseases, such as classical swine fever, by monitoring all farms and movements of animals between them. This makes it possible to track any contact animals in the case of an epidemic.

The surveillance network system (Grisregistret) for pigs in Sweden was implemented 2002, according to SJVFS 2002:1, and is handled by the Swedish Board of Agriculture (SBA).

This study is based on an excerpt from the database of the Swedish surveillance network system from a community, with a 30 km radius, in southern Sweden. The excerpt consists of two sets of data where the first set contains information for each holding namely a unique identification number, the type of production and the number of sows and finishing pigs at the holding. The second set of data consists of movements of pigs between holdings, containing the identification of the source and destination holding, the date of the transport and the number of pigs moved.

The following information from the excerpt was used:

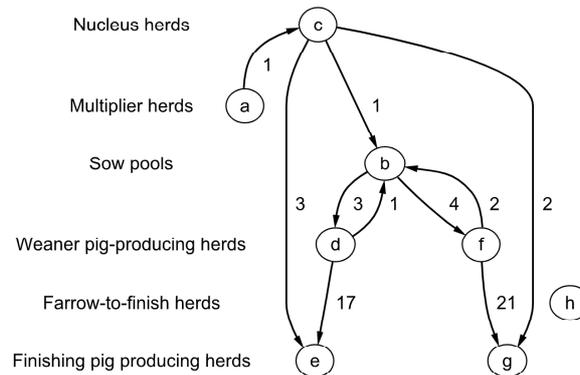
- Only movements between farms, that occurred between 2002-11-01 and 2003-04-30 are included.
- Only movements between holdings are included, i.e. movements to slaughterhouses were excluded.
- Only movements between holdings where both source and destination holdings are identified holdings, i.e. included in the first set of data, are included.
- A holding outside the 30 km radius is included if it is the destination holding of a transport and the source holding is inside the 30 km radius and included.

## **Graph theory**

Information can often be represented as a graph with vertices and edges. In a graph, we may think of a vertex as a point and an edge as a curve that connects two vertices. Thus a typical graph might be a family tree where vertices are persons and an edge connects to people as parent and child. Another graph might be a road map, where the vertices are towns or intersections and the edges are roads (Laufer H.B., 1984).

### Terminology

A graph model for a network of holdings (or herds) is shown in *Figure 1*. The ellipses, representing holdings, are labelled a through h, and the connections between them are labelled with the number of animals transported in one day.



*Figure 1.* An example with a network of holdings. The layout of the network mirrors the breeding pyramid. The connections are labelled with the number of animals transported in one day. Note, every holding does not have a transport, e.g. see h. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

In the terminology of graph theory, each holding in the example network is represented by a vertex and each transport by an edge. Since graph terminology is not completely standardized, another name for vertex is node, and another name for edge is arc. A graph  $G$  consists of a vertex set  $V$  and an edge set  $E$ . Thus we write  $G = (V, E)$ . The size of the vertex set (the number of vertices in the graph) is expressed as  $|V|$  and the size of the edge set as  $|E|$ . An edge is written as an ordered pair consisting of the vertices connected by the edge. The ordered pair  $(u, v)$  indicates the edge that connects vertex  $u$  to vertex  $v$  (Laufer H.B., 1984; Siek *et al.*, 2001). The holding network in *Figure 1* can be expressed using set notation as follows:

$$V = \{a, b, c, d, e, f, g, h\}$$

$$E = \{(a, c), (b, d), (b, f), (c, b), (c, e), (c, g), (d, b), (d, e), (f, b), (f, g)\}$$

$$G = (V, E)$$

If an edge  $(u, v)$  with  $u$  as the source vertex and  $v$  as the target vertex is distinct from the edge  $(v, u)$  the edge is directed. If the vertex ordering does not matter so that  $(u, v)$  and  $(v, u)$  are the same, the edge is undirected.

A graph could either be directed or undirected, meaning that the edge set in the graph consists of respectively directed or undirected edges.

If a group of vertices in an undirected graph are reachable from one another they are connected. Strongly connected vertices are a group of vertices in a directed graph that are mutually reachable. Maximum flow is the maximum quantity that

can flow through the network, e.g. the maximum number of pigs that can flow through the network of holdings.

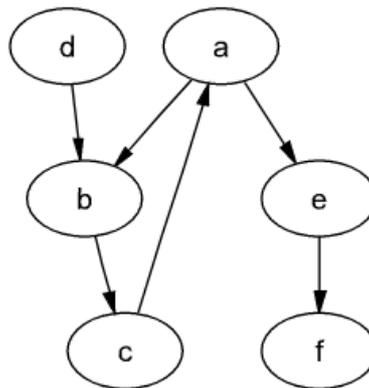
### *Graph layout with the DOT language*

To draw a graph it has to be defined in some way. The DOT language provides a language to describe the graph in simple words (Gansner E., Koutsofios E. & North S., 2002). The graph description can then be analysed by computer software that generates a digital image from the graph description. The graph layout software used in this work is GraphViz (Anonymous 2003b, <http://www.graphviz.org/>, 30-Nov-2003; Anonymous 2003c, <http://www.research.att.com/sw/tools/graphviz/>, 30-Nov-2003). An example of how it works, with 6 nodes and 6 edges in the graph can be described in the DOT language as shown in *Listing 1*.

```
digraph example {  
  a -> b  
  a -> e  
  b -> c  
  c -> a  
  d -> b  
  e -> f  
}
```

*Listing 1.* An example of a graph description in the DOT language with 6 nodes and 6 edges. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

The contents of *Listing 1* can now be used as input to GraphViz and a digital image is generated and the result of *Listing 1* is shown in *Figure 2*.



*Figure 2.* The result of *Listing 1* after graph layout with GraphViz. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

In this study *Figure 1, Figure 2, Figure 3, Figure 4, Figure 5* and *Figure 6* has been generated with the DOT language and converted to a digital image with Graphviz.

### *Visualize movements from the surveillance network system*

The movements in the surveillance network system contain data about the source and destination holding, the date of the movement and the number of pigs moved. This information can be grouped in a text file as follows.

```
source;destination;date;pigs
source;destination;date;pigs
      :
      :
source;destination;date;pigs
```

*Listing 2.* Grouping of the movements from the surveillance network system. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

By describing the interherd movements with the DOT language, it is possible to visualize the movements between herds, therefore the movements are converted from *Listing 2* to *Listing 3*.

```
digraph movements {
  source -> destination [label="date pigs"]
  source -> destination [label="date pigs"]
      :
      :
  source -> destination [label="date pigs"]
}
```

*Listing 3.* The movements of *Listing 2* in the DOT language. Each edge has been labelled with the date of the movement and the number of pigs moved. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

Assume that there are 8 holdings and 8 interherd movements, then this can be written as *Listing 4*.

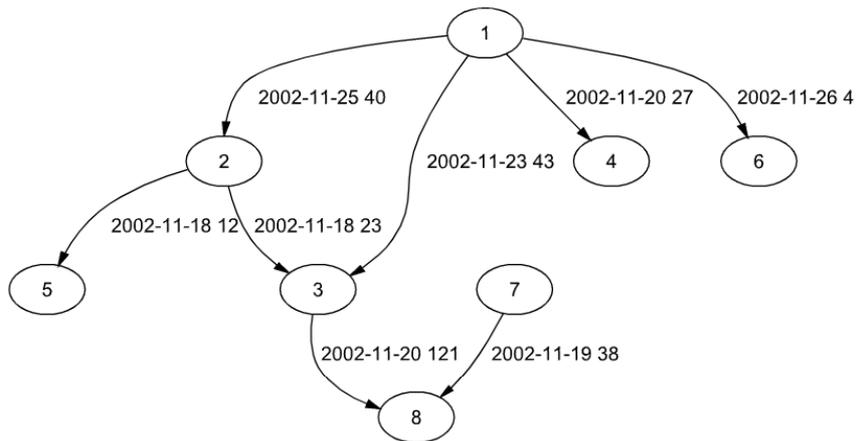
```
1;2;2002-11-25;40
1;3;2002-11-23;43
1;4;2002-11-20;27
2;3;2002-11-18;23
2;5;2002-11-18;12
1;6;2002-11-26;4
7;8;2002-11-19;38
3;8;2002-11-20;121
```

*Listing 4.* An example with 8 holdings and 8 interherd movements of pigs. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

Rewriting *Listing 4* to the DOT language gives the result shown in *Listing 5*.

```
digraph movements {
  1 -> 2 [label="2002-11-25 40"]
  1 -> 3 [label="2002-11-23 43"]
  1 -> 4 [label="2002-11-20 27"]
  2 -> 3 [label="2002-11-18 23"]
  2 -> 5 [label="2002-11-18 12"]
  1 -> 6 [label="2002-11-26 4"]
  7 -> 8 [label="2002-11-19 38"]
  3 -> 8 [label="2002-11-20 121"]
}
```

*Listing 5*. Shows the movements in *Listing 4* in the DOT language. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.



*Figure 3*. Shows the final layout of the movements in *Listing 4* after it has been rewritten to *Listing 5* and visualized with graphviz. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

To improve the layout of the graph there are several properties of the nodes and edges that can be used, e.g. see *Figure 5*.

## Epidemiological modelling

### *SEIRD model for one herd*

The epidemic in a herd can be described by using a compartment model, that divides the herd into certain classes (Thrusfield, 1997; Noordhuizen *et al.*, 2001). The SEIRD model consists of the susceptible, exposed, infectious, recovered and dead compartment. In the course of an epidemic a pig will then ‘flow’ from the susceptible compartment into the exposed, the infectious, and finally either to the recovered or dead compartment, depending on the case fatality rate of the infectious agent. Pigs are moved out of the herd with a rate that is proportional to the time they spend in the herd. To keep the size of the herd constant, there are introductions of new pigs to the susceptible compartment with the same rate as the pigs are moved out of the herd. The effect of moving pigs between herds will be discussed later in ‘*SEIRD model in a population of herds with interherd movements*’.

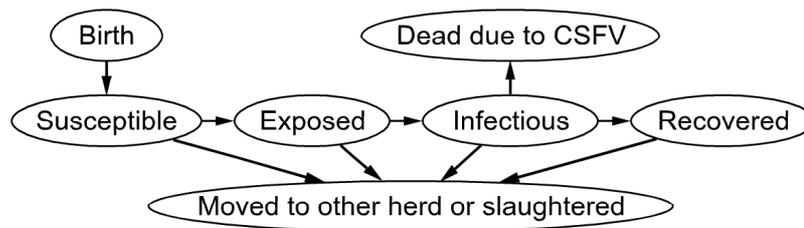


Figure 4. The compartment model for one herd. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

The compartment model can be translated into mathematical terms consisting of a system of coupled, nonlinear, first order ordinary differential equations. A differential equation is a relationship between a variable and its derivatives. The first-order ordinary differential equation shows how fast one variable changes when another is changed.

In this study the incubation time,  $T_{inc}$ , of the disease is from the infection till that the pig becomes infectious, and the case fatality rate,  $C_{cf}$ , is the proportion of the infected pigs that die of the disease. The case fatality rate can take values between 0 and 1, or 0 – 100%.

Table 1. *Definitions of parameters used in equations 1 – 12. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.*

<i>Parameter</i>	<i>Definition</i>
$S_s$	Number of susceptible sows in the herd
$S_f$	Number of susceptible finishing pigs in the herd
$S_p$	Number of susceptible piglets in the herd
$E_s$	Number of exposed sows in the herd
$E_f$	Number of exposed finishing pigs in the herd
$E_p$	Number of exposed piglets in the herd
$I_s$	Number of infectious sows in the herd
$I_f$	Number of infectious finishing pigs in the herd
$I_p$	Number of infectious piglets in the herd
$R_s$	Number of recovered sows in the herd
$R_f$	Number of recovered finishing pigs in the herd
$R_p$	Number of recovered piglets in the herd
$T_s$	Time that sows spend in the herd
$T_f$	Time that finishing pigs spend in the herd
$T_p$	Time that piglets spend in the herd
$T_{inc}$	Incubation time
$T_{inf}$	Infectious time
$N_{ps}$	Number of piglets born per sow and year
$C_{ir}$	Infection rate
$C_{cf}$	Case fatality rate

Equation 1, 2 and 3 describes the change of susceptible pigs  $\frac{dS}{dt}$  in the herd, where  $S_s$ ,  $S_f$  and  $S_p$  are the number of susceptible sows, finishing pigs and piglets respectively. The first term describes the introduction of new susceptible pigs into the herd. For sows and finishing pigs this is proportional to the number of pigs and how long time each pig stays in the herd. Sows stay in the herd for  $T_s$  days, which is proportional to the number of lactations and the length of the interval between two succeeding litters. Finishing pigs are in the herd for  $T_f$  days before they are sent to slaughter. For piglets the number of new susceptible individuals is dependent on the number of piglets born per sow,  $N_{ps}$ , and the total number of sows ( $S_s+E_s+I_s+R_s$ ). The second term describes the movement from the herd to either a new herd or the slaughterhouse. This transfer is proportional to the number of susceptible pigs divided with the number of days for the pig in the herd.  $T_p$  is the number of days a piglet stays in the herd. The final term describes the new cases and is proportional to the number of susceptible and infectious pigs and the infection rate  $C_{ir}$ .  $I_s$  is the number of infected sows,  $I_f$  is number of infected finishing pigs and finally  $I_p$  is the number of infected piglets.

$$Eq. 1. \quad \frac{dS_s}{dt} = \frac{S_s + E_s + I_s + R_s}{T_s} - \frac{S_s}{T_s} - C_{ir} \cdot S_s \cdot (I_s + I_f + I_p)$$

$$\text{Eq. 2. } \frac{dS_f}{dt} = \frac{S_f + E_f + I_f + R_f}{T_f} - \frac{S_f}{T_f} - C_{ir} \cdot S_f \cdot (I_s + I_f + I_p)$$

$$\text{Eq. 3. } \frac{dS_p}{dt} = \frac{N_{ps} \cdot (S_s + E_s + I_s + R_s)}{365} - \frac{S_p}{T_p} - C_{ir} \cdot S_p \cdot (I_s + I_f + I_p)$$

Equation 4, 5 and 6 describes the change of exposed pigs  $\frac{dE}{dt}$  in the herd, where  $E_s$ ,  $E_f$  and  $E_p$  are the number of exposed sows, finishing pigs and piglets respectively. These pigs are infected, but are not yet shedding the virus. The first term describes the new cases and equals the last term in equations 1,2 and 3. The second term describes those pigs that are moved to another herd or slaughtered. The final term describes those pigs that become infectious after the incubation time  $T_{inc}$ .

$$\text{Eq. 4. } \frac{dE_s}{dt} = C_{ir} \cdot S_s \cdot (I_s + I_f + I_p) - \frac{E_s}{T_s} - \frac{E_s}{T_{inc}}$$

$$\text{Eq. 5. } \frac{dE_f}{dt} = C_{ir} \cdot S_f \cdot (I_s + I_f + I_p) - \frac{E_f}{T_f} - \frac{E_f}{T_{inc}}$$

$$\text{Eq. 6. } \frac{dE_p}{dt} = C_{ir} \cdot S_p \cdot (I_s + I_f + I_p) - \frac{E_p}{T_p} - \frac{E_p}{T_{inc}}$$

Equation 7, 8 and 9 describes the change of infectious pigs  $\frac{dI}{dt}$  in the herd. The first term describes the new infectious pigs and equals the last term in equations 4, 5 and 6. The second term describes those pigs that are either moved to another herd or slaughtered. The third term describes those pigs that are no longer infectious after the infectious period  $T_{inf}$ .

$$\text{Eq. 7. } \frac{dI_s}{dt} = \frac{E_s}{T_{inc}} - \frac{I_s}{T_s} - \frac{I_s}{T_{inf}}$$

$$\text{Eq. 8. } \frac{dI_f}{dt} = \frac{E_f}{T_{inc}} - \frac{I_f}{T_f} - \frac{I_f}{T_{inf}}$$

$$\text{Eq. 9. } \frac{dI_p}{dt} = \frac{E_p}{T_{inc}} - \frac{I_p}{T_p} - \frac{I_p}{T_{inf}}$$

Equation 10, 11 and 12 describes the change of recovered pigs  $\frac{dR}{dt}$  in the herd, where  $R_s$ ,  $R_f$  and  $R_p$  are the number of recovered sows, finishing pigs and piglets respectively. The first term describes the number of infected pigs that become recovered after the infectious period  $T_{inf}$ . The flow from infectious to recovered is also affected by the case fatality rate  $C_{cf}$ . For low virulent strains of CSFV,  $C_{cf}$  equals 0 meaning that all infectious pigs will recover. Setting  $C_{cf}$  to 1 for high virulent strains makes all infectious pigs enter the ‘Dead due to CSFV’ compartment instead. The second term describes the number of recovered pigs that are moved or slaughtered.

$$Eq. 10. \quad \frac{dR_s}{dt} = \frac{(1 - C_{cf}) \cdot I_s}{T_{inf}} - \frac{R_s}{T_s}$$

$$Eq. 11. \quad \frac{dR_f}{dt} = \frac{(1 - C_{cf}) \cdot I_f}{T_{inf}} - \frac{R_f}{T_f}$$

$$Eq. 12. \quad \frac{dR_p}{dt} = \frac{(1 - C_{cf}) \cdot I_p}{T_{inf}} - \frac{R_p}{T_p}$$

This system of differential equations can be solved numerically with a fourth-order Runge-Kutta method (Andersson & Böiers, 1992; Råde & Westergren, 1990; Press *et al*, 1993).

#### *Numerical example of the SEIRD model for one pig herd*

To run the SEIRD model for one herd the parameters of *Table 1* have to be estimated. Assume that there are 200 sows,  $S_s$ , and 100 finishing pigs,  $S_f$ , at the start of the simulation and that the herd is a farrow-to-finish herd. To determine the number of piglets,  $S_p$ , the number of piglets born per sow and year,  $N_{ps}$ , and the time from birth to weaned,  $T_p$ , must be known. Let  $N_{ps}$  be equal to 21.0 and  $T_p$  equal to 35 days (Anonymous, 2002b).

$$Eq. 13. \quad S_p = \frac{S_s \cdot N_{ps} \cdot T_p}{365}$$

Using the above formula,  $S_p$  equals 403 piglets.  $N_{ps}$  and  $S_p$  are determined the same way for all other production types, with the exception of the central unit of the sow pools, for which they equal 0. To start the epidemic, one infectious sow is introduced making  $I_s$  equal to 1. The rest of the pigs,  $E_s$ ,  $E_f$ ,  $E_p$ ,  $I_f$ ,  $I_p$ ,  $R_s$ ,  $R_f$  and  $R_p$  all equal zero at the beginning of the simulation. The sow spends in average 494 days,  $T_s$ , in the herd and the finishing pig 110 days,  $T_f$  (Anonymous, 2002b). Assume that the incubation period,  $T_{inc}$ , is set to 5 days and the length of the infectious period,  $T_{inf}$ , is set to 20 days. The case fatality rate,  $C_{cf}$ , is set equal to 0 for the low virulent strain simulation and set equal to 1 for the high virulent strain

simulation. The infection rate,  $C_{ir}$ , is chosen so that the maximum of infectious animals is around 60 days, and equals 0.0005.

Table 2. *Definitions and values of parameters used in equations 1 – 12 at the start of the simulation of the numerical example. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.*

<i>Parameter</i>	<i>Definition</i>	<i>Value</i>
$S_s$	Number of susceptible sows in the herd	200
$S_f$	Number of susceptible finishing pigs in the herd	100
$S_p$	Number of susceptible piglets in the herd	403
$E_s$	Number of exposed sows in the herd	0
$E_f$	Number of exposed finishing pigs in the herd	0
$E_p$	Number of exposed piglets in the herd	0
$I_s$	Number of infectious sows in the herd	1
$I_f$	Number of infectious finishing pigs in the herd	0
$I_p$	Number of infectious piglets in the herd	0
$R_s$	Number of recovered sows in the herd	0
$R_f$	Number of recovered finishing pigs in the herd	0
$R_p$	Number of recovered piglets in the herd	0
$T_s$	Time that sows spend in the herd	494
$T_f$	Time that finishing pigs spend in the herd	110
$T_p$	Time that piglets spend in the herd	35
$T_{inc}$	Incubation time	5
$T_{inf}$	Infectious time	20
$N_{ps}$	Number of piglets born per sow and year	21
$C_{ir}$	Infection rate	0.0005
$C_{cf}$	Case fatality rate	0 and 1

### *SEIRD model in a population of herds with interherd movements*

The structure of the pig industry with specialized holdings for a certain type of production makes the breeding organised as a pyramid. In the top there are a few nucleus herds supplying multipliers with grandparent stock and these then produce the parents of the slaughter generation, which are sold to holdings. The need for movements between holdings and possible mixing of pigs can lead to a situation where disease can rapidly spread to a large number of holdings (Taylor, 1999).

The SEIRD models for all holdings are connected to each other through the reported movements of pigs to the surveillance system. The population of 156 holdings included in the study generates a population of 156 SEIRD models, one for each holding. During the epidemiological simulation, data from the graph of interherd movements is used to find interactions between holdings.

To study the impact of movements between holdings, the probability of transferring infectious pigs from the source to the destination holding has to be estimated. Here it is assumed that the destination holding will become infected if at least one exposed or infectious pig is among the moved pigs. Therefore, denote the group of susceptible and recovered pigs as group A and the exposed and infectious

as group B. Let  $N$ ,  $N_A$  and  $N_B$  be the total number of pigs, the number of pigs in group A and the number of pigs in group B, respectively at the source holding. Let  $k$  be the number of pigs to be moved. Rewrite the problem as finding the probability,  $P_A(k)$ , of transferring  $k$  pigs, all in group A. This follows a hypergeometric probability distribution. This distribution is used in connection with sampling without replacement from a finite population with elements of two kinds (Råde, Westergren, 1990; Blom, 1989).

$$\text{Eq. 14. } P_A(k) = \frac{\binom{N_A}{k} \binom{N_B}{0}}{\binom{N}{k}}$$

This can be approximated to a binomial distribution if the population size,  $N$ , is large in relationship to the number of pigs moved,  $k$  (Blom, 1989).

$$\text{Eq. 15. } P_A(k) \approx \binom{0}{k} \left(\frac{N_A}{N}\right)^k \left(\frac{N_B}{N}\right)^0 = \left(\frac{N_A}{N}\right)^k$$

Denote the probability of transferring at least one pig from the group B, as  $P_A^*(k)$ .

$$\text{Eq. 16. } P_A^*(k) = 1 - P_A(k) = 1 - \left(\frac{N_A}{N}\right)^k$$

During the simulation  $P_A^*(k)$  is calculated for each movement and then a random number between 0 and 1 is drawn from a random number generator. If this number is less than  $P_A^*(k)$  the destination holding becomes infected, i.e. one of the pigs in the susceptible compartment is moved to the infectious compartment thus making the destination holding infected.

One condition that has to be satisfied for a movement to occur is that the number of pigs at the source holding,  $N$ , is larger than the number of pigs to move,  $k$ . If this is not the case the movement is cancelled. This situation can occur for a simulation with a high case fatality rate,  $C_{cf}$ .

## Results

### Surveillance network system

In *Table 3* the holdings included in the study are summarized. Most of the holdings are outside the area of 30 km radius, meaning that many movements are out of the area. Movements into the area were not included in this study.

*Table 3. The number of holdings for each type of production inside the radius of 30 km and outside (receiving pigs from within the 30 km radius). Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.*

Production type	Number of holdings		Total
	Inside radius 30 km	Outside radius 30 km	
Nucleus herds	2	7	9
Multiplier herds	0	11	11
Sow pools	4	6	10
Weaner-pig producing herds	20	31	51
Farrow-to-finish herds	5	10	15
Finishing pig producing herds	6	54	60
Total	37	118	156

In *Table 4* all movements included in the study are shown. The columns with production type is the source holding for each movement of pigs, e.g. week 45 year 2002, 74 pigs left nucleus herds and 311 was moved from weaner pig producing herds making a total of 385 pig-movements reported. Movements to slaughterhouses were excluded in this study, yet there are interherd movements from finishing pig producing herds.

Table 4. *The number of pigs transported from holdings each week during the period from 2002-11-01 to 2003-04-30. The transports are ordered with respect to the source holding. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.*

Year	Week	Nucleus herds	Multiplier herds	Sow pool	Weaner pig producing herds	Farrow-to-finish herds	Finishing pig producing herds	Total	
2002	44	0	0	0	0	0	0	0	
	45	74	0	0	311	0	0	385	
	46	37	0	0	926	0	0	963	
	47	6	0	108	259	0	10	383	
	48	89	6	48	937	0	0	1080	
	49	84	0	147	192	275	0	698	
	50	12	0	0	339	0	0	351	
	51	87	0	0	476	0	0	563	
	52	17	0	0	489	0	0	506	
	2003	1	26	0	0	0	0	0	26
		2	19	0	0	227	0	0	246
		3	34	0	108	253	0	0	395
4		17	0	302	70	0	0	389	
5		50	2	129	175	44	0	400	
6		34	0	66	430	0	0	530	
7		114	2	6	580	17	0	719	
8		18	0	0	65	0	0	83	
9		0	0	0	569	0	0	569	
10		20	0	0	346	0	0	366	
11		67	0	248	505	60	0	880	
12		18	0	0	699	60	10	787	
13		4	0	174	276	78	0	532	
14		23	3	93	84	0	0	203	
15		57	0	0	525	0	0	582	
16		10	0	0	377	71	0	458	
17		26	0	0	558	40	0	624	
18		9	0	0	0	0	0	9	
Total		952	13	1429	9668	645	20	12727	

*Figure 5* shows the connections of the holdings included in the study. The holdings have been grouped to interconnected subpopulations, shown in different grayscales. These interconnected holdings are reachable from one another through interherd movements of pigs, i.e. it is possible to follow the connections and reach all holdings in the same grayscale. The movements include a period of 6 months. The holding with the highest number of movements leaving the holding, is marked with a large filled circle at level A in *Figure 5*.

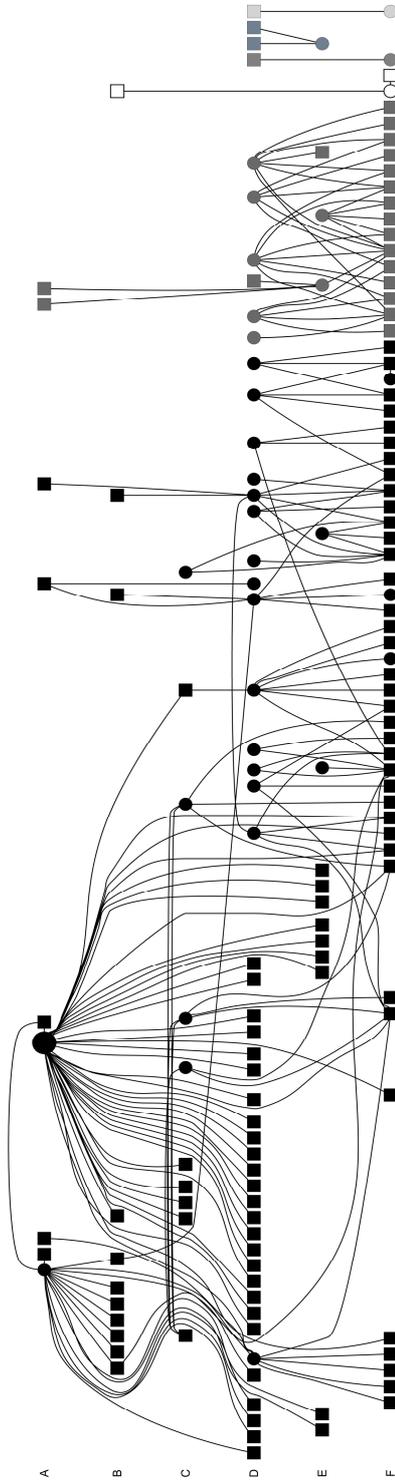
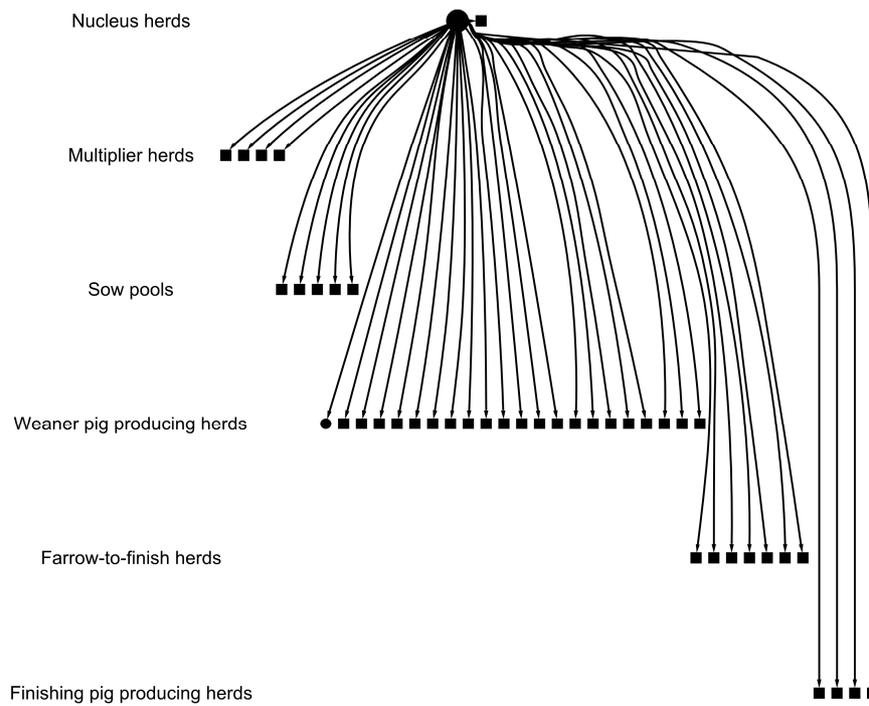


Figure 5. Undirected graph showing connections between holdings. Each connection represents at least one movement of pigs. There is one production type at each level, A = Nucleus herds, B = Multiplier herds, C = Sow pools, D = Weaner-pig producing herds, E = Farrow-to-finish herds and F = Finishing pig producing herds. Circles represent holdings inside the radius of 30 km and boxes represent holdings outside the radius of 30 km. The filling of the shapes groups the holdings to subpopulations within the population that are connected through interherd movements. The large filled point at level A is the holding with the largest set of connections. The interherd movements of pigs is over a period of 6 months and based on an excerpt from the Swedish surveillance system of pig movements in a community of southern Sweden. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

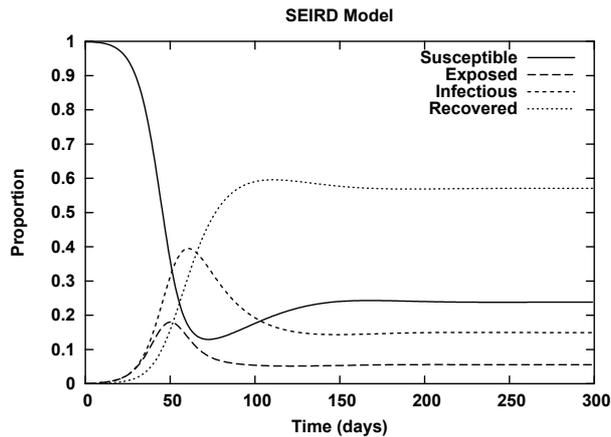
*Figure 6* is a directed graph with movements from the holding with the the highest number of movements leaving the holding. This holding is marked with a large filled circle at level A in *Figure 5*. *Figure 6* shows all target holdings, there are receivers of pigs at all types of production.



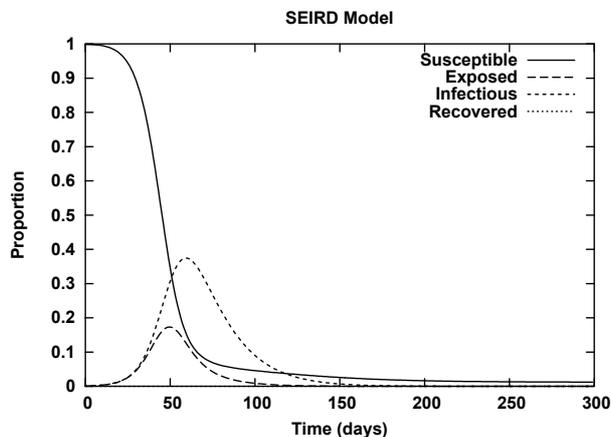
*Figure 6.* Directed graph showing movements from the holding with the highest number of movements leaving the holding. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

## Numerical example of the SEIRD model for one pig herd

In *Figure 7 & 8* the result from an outbreak derived from the parameters in *Table 2* is shown. The disease becomes endemic in the herd when the case fatality rate,  $C_{cf}$ , is 0. The outbreak dies out as the pigs die in the herd when the case fatality rate,  $C_{cf}$ , is 1. The proportion of each state is relative to the number of pigs in the herd. At day 0 there are 703 pigs in the herd.



*Figure 7.* A simulated outbreak of classical swine fever with parameters according to *Table 2* and a case fatality rate of 0. The proportion within the herd of susceptible, exposed, infectious and recovered pigs during the course of the disease. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.



*Figure 8.* A simulated outbreak of classical swine fever with parameters according to *Table 2* and a case fatality rate of 1. The proportion within the herd of susceptible, exposed, infectious and recovered pigs during the course of the disease. The proportion is relative to the number of pigs in the herd at day 0 of the outbreak. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

## SEIRD model in a population of herds with interherd movements

During the epidemiological simulation of the population one infectious pig has been introduced to one of the holdings in the population at day 0 of the outbreak. The disease is then introduced to the population and by using the known information from the surveillance network system (Grisregistret) about interherd movements of pigs in the population the epidemic can spread to new holdings if the source is infected at the time of the movement. In *Table 5, 6, 7 and 8* the result after 300 days of the outbreak is summarized. The result is grouped according to the production type of the holding where the infectious pig was introduced. The result is an average of 100 simulations.

In *Table 5* it is shown that an introduction of one infectious pig into a nucleus herd has the greatest spread of the disease in the population. There is no significant difference in the number of infected herds in the population with respect to the case fatality rate.

Table 5. Shows the number of infected herds in the population 300 days after introducing one infectious pig into a holding. Both a case fatality rate of 0 and 1 is shown. The result is an average of each production type and 100 simulations for each introduction. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

Introduction to production type	Number of infected herds in the population	
	Case fatality rate 0	Case fatality rate 1
Nucleus herds	6	7
Multiplier herds	1	2
Sow pools	2	2
Weaner pig producing herds	2	2
Farrow-to-finish herds	2	1
Finishing pig producing herds	1	1

In *Table 6* the survival of pigs in the population is shown. At day 0 there are 168570 pigs in the population. The survival is with respect to the number of pigs at day 0 of the outbreak. The herd size decreases when the case fatality rate is 1. As a result of the decreased size of a infected holding, it can no longer deliver pigs and the outbreak will die out, see *Table 8*.

Table 6. Shows the survival of pigs in the population 300 days after introducing one infectious pig into a holding. Both a case fatality rate of 0 and 1 is shown. The result is an average of each production type and 100 simulations for each introduction. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

Introduction to production type	Survival of pigs in the population	
	Case fatality rate 0	Case fatality rate 1
Nucleus herds	100%	95.24%
Multiplier herds	100%	99.11%
Sow pools	100%	96.99%
Weaner pig producing herds	100%	99.19%
Farrow-to-finish herds	100%	98.91%
Finishing pig producing herds	100%	99.12%

In *Table 7 & 8* the distribution of susceptible, exposed, infectious and recovered pigs in the population is shown. When the case fatality rate equals 0, the disease can be established in the population. With a case fatality rate of 1, the outbreak is self-limited since the pigs in an infected holding will die. As a result the infected holding can no longer deliver pigs.

*Table 7. Shows the distribution of pigs in the population 300 days after introducing one infectious pig into a holding. The case fatality rate is 0. The result is an average of each production type and 100 simulations for each introduction. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.*

<i>Introduction to production type</i>	<i>Distribution of pigs in the population</i>			
	<i>Susceptible</i>	<i>Exposed</i>	<i>Infectious</i>	<i>Recovered</i>
Nucleus herds	96,15%	0,24%	0,70%	2,91%
Multiplier herds	99,54%	0,02%	0,07%	0,36%
Sow pools	96,85%	0,21%	0,60%	2,33%
Weaner pig producing herds	99,18%	0,04%	0,13%	0,65%
Farrow-to-finish herds	98,60%	0,07%	0,22%	1,12%
Finishing pig producing herds	99,18%	0,04%	0,12%	0,67%

*Table 8. Shows the distribution of pigs in the population 300 days after introducing one infectious pig into a holding. The case fatality rate is 1. The result is an average of each production type and 100 simulations for each introduction. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.*

<i>Introduction to production type</i>	<i>Distribution of pigs in the population</i>			
	<i>Susceptible</i>	<i>Exposed</i>	<i>Infectious</i>	<i>Recovered</i>
Nucleus herds	99.99%	0.00%	0.01%	0.00%
Multiplier herds	100.00%	0.00%	0.00%	0.00%
Sow pools	100.00%	0.00%	0.00%	0.00%
Weaner pig producing herds	100.00%	0.00%	0.00%	0.00%
Farrow-to-finish herds	100.00%	0.00%	0.00%	0.00%
Finishing pig producing herds	100.00%	0.00%	0.00%	0.00%

Figure 9 & 10 shows the average of the distribution of the pigs for 100 simulations when the infectious pig is introduced to the holding with the the highest number of movements leaving the holding. This holding is marked with a large filled circle at level A in Figure 5. Figure 9 shows that the disease becomes endemic in the population when the case fatality rate,  $C_{cf}$ , is 0. Figure 10 shows that the outbreak dies out as the pigs die in the population when the case fatality rate,  $C_{cf}$ , is 1. The proportion of each state is relative to the number of pigs in the herd at day 0.

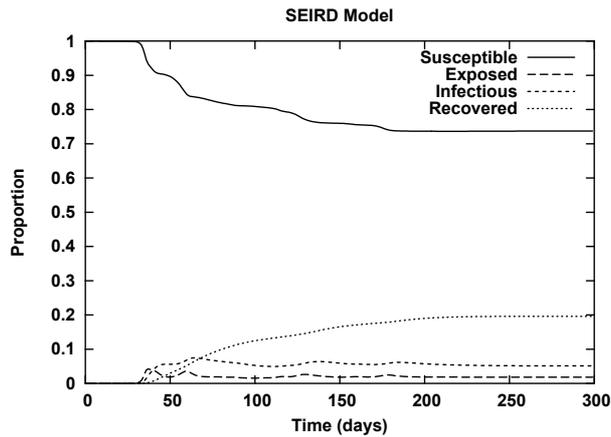


Figure 9. Shows the distribution of pigs in the population after introducing one infectious pig into the holding with the the highest number of movements leaving the holding. The proportion is with respect to the population size day 0. The result is an average of 100 simulations with a case fatality rate of 0. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

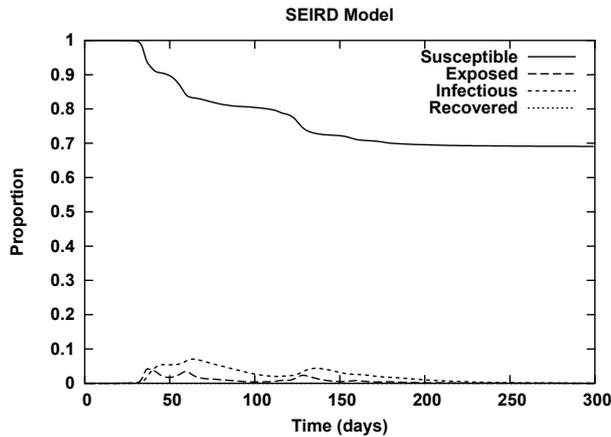


Figure 10. Shows the distribution of pigs in the population after introducing one infectious pig into the holding with the the highest number of movements leaving the holding. The proportion is with respect to the population size day 0. The result is an average of 100 simulations with a case fatality rate of 1. Graph theory in veterinary epidemiology - modelling an outbreak of classical swine fever, 2003.

## Discussion

### Classical swine fever

Classical swine fever is a serious and highly contagious viral disease. According to European Union Council Directive 2001/89 the authorities must implement interventions in case of an outbreak. These interventions are supposed to minimize the spread of the disease, and for classical swine fever it means stamping out infected herds and to hinder spread through animal movements in protection and surveillance zones. Emergency vaccination can also be considered under some circumstances. However a prolonged outbreak will be extremely costly and implementing good control measures are important to minimize the impact of the outbreak.

### Graph theory

Graph theory can be a useful tool for intervention in the case of an outbreak of a contagious disease. By using graph theory algorithms on data from the Swedish surveillance network system (Grisregistret) and combining this with the power of graph layout engines for visualization of interherd movements, valuable information can rapidly be provided from data that is easy available. Thus a clear line of priority in the strategy of fighting the outbreak can be established from day 0. This can be invaluable during the first couple of days, before more thorough information concerning all different types of contacts has been collected by veterinarians during farm visits, when rapid control measures are implemented and should increase the likelihood that possible infectious holdings are found during an early stage of the outbreak. Combining the information of the geographical location (GIS) of an infectious holding and the interherd movements during the relevant time period on the same map can improve the understanding of the spread of the outbreak. It would also be possible to add information concerning other types of contacts, when such information becomes available, to make the picture clearer.

Important for diseases such as classical swine fever, where the most significant route of transmission is through direct contacts between susceptible and infectious animals, is to rapidly answer the question of how holdings are connected to each other through movements of animals.

Another aspect of an outbreak that might be important is to determine where the maximum flow of animals is through the network of holdings. This information can be used to find the most likely path for the disease through the network, both backwards towards the source and forward to find possible infected holdings.

This study demonstrates that one “subpopulation” of interconnected herds with interherd movements can form a huge part of the total population, see for example *Figure 5*. The interconnected herds, in *Figure 5*, are likely to be more numerous in reality since only movements from the holdings inside the 30 km radius were included. It is probable that there are movements out of the area to holdings that

have connections with holdings inside the area. The interval between the start date and the end date of the included movements, affects the number of connected holdings.

## **Epidemiological modelling**

Epidemiological models are often constructed from statistical methods (stochastic) and/or differential calculus (deterministic). With the power of modern computational methods, it is possible to construct and model complex problems. One area in veterinary epidemiology where computer science is especially relevant is in the use of Geographic Information Systems (GIS) to allowing analytic approaches to spatial information.

The epidemiological model (SEIRD) used in this study is both deterministic and stochastic. The model is based on the idea that the pig can be susceptible, exposed, infectious, recovered or dead with respect to the classical swine fever virus. Assuming that contacts between susceptible and infectious pigs is the only transmission route for the CSFV, then virus can only spread to another herd through interherd movements in this model. To study the spatial spread of the infection through interherd movements, an excerpt from the Swedish surveillance network system (Grisregistret) is used. The outbreak is modelled without any interventions from the authorities to control the outbreak.

The SEIRD model shows that a low virulent strain of the virus could spread in the population and infect a large number of herds, this is due to the low case fatality rate. Furthermore, in the case of an outbreak with a low virulent strain of CSF it might be difficult to become aware of the disease in the herd since the clinical signs are mild.

Outbreaks with high virulent CSFV strains with a high case fatality rate will die out by itself when they are modelled with the SEIRD model. The reason for this is the assumption that contacts between susceptible and infectious is the only transmission route. Because of this assumption there will be no more infectious animals that can be moved to another holding when all pigs at an infected holding are dead.

An improvement of the epidemiologic model would be to include other possible ways of interherd virus transmission. Then the improved SEIRD model with interherd connections could be used as base for further research of different intervention measures and their impact on the outbreak. Another refinement of the epidemiological model would be to model each pig individually. By making this change one could easily introduce other aspects to the model, such as the age of the pig, other diseases in the population that make the individuals more susceptible or housing of the pigs to minimize spread of disease.

Validation of the epidemiological model with experimental studies is an important element of the modelling. There are several experimental studies of the transmission of classical swine fever virus within groups of pigs to find out the intraherd spread (Laevens *et al.* 1998; Laevens *et al.* 1998b; Laevens *et al.* 1999; Dewulf *et al.* 2000; Dewulf *et al.* 2001; Dewulf *et al.* 2002; Klinkenberg *et al.*

2002). They have studied different routes of transmission in different housing systems and different types of production.

### **Surveillance network system**

The surveillance network system (Grisregistret) was implemented 2002, according to SJVFS 2002:1, and is handled by the Swedish Board of Agriculture (SBA). The purpose is to support the control of contagious diseases, by monitoring holdings and movements of pigs between them.

It is clear that to fulfil the purpose of fighting an outbreak of a highly contagious disease the data must be both correct and complete. Therefore validation of this database is recommended to assess its usefulness for animal health purposes.

## **Conclusions**

The time that passes between the introduction of the infection and the detection of the disease is crucial for the consequences of an epidemic. Graph theory can be a useful tool for intervention in the case of an outbreak of a contagious disease by rapidly providing overview information, before more detailed information from the farmer is available. This makes it possible to establish risk-based priorities at day 0 of the detection of the outbreak.

To be able to use the Swedish surveillance network system of pig movements (Grisregistret) for its intended purpose, namely to support the control of contagious diseases, it is important that the information it contains is validated.

## **Tack**

Jag vill tacka mina handledare Marie Engel, Maria Nöremark och Ivar Vågsholm för all tid ni lagt ner på att hjälpa mig med att färdigställa denna rapport. Jag vill dessutom tacka Jordbruksverket för att jag fått tillgång till data ur Grisregistret.

## References

- Andersson, K. G., Böiers, L. C. 1992. Ordinära differentialekvationer. 2nd edition. Studentlitteratur, Lund. ISBN: 91-44-29952-4. 358 pp.
- Anonymous, 2002. Klassisk svinpest. I Epizootihandboken, Jordbruksverket, Jönköping, SVA, Uppsala, pp 66-8. [http://www.sva.se/pdf/epizhbok/Epizootihandbok\\_2002.pdf](http://www.sva.se/pdf/epizhbok/Epizootihandbok_2002.pdf)
- Anonymous, 2002b. Kompendium Svin. Institution för svinmedicin. Sveriges Lantbruks Universitet, Uppsala, Sverige. 152 pp.
- Anonymous, 2003. Generic Import Risk Analysis (IRA) for Pig Meat. Biosecurity Australia, Department of Agriculture, Fisheries and Forestry, Australian Government. <http://www.affa.gov.au/content/publications.cfm?ObjectID=EAA47406-D373-4205-AC85A3D6A8AA7046>
- Anonymous, 2003b. GraphViz, <http://www.graphviz.org>, 30-Nov-2003.
- Anonymous, 2003c. AT & T Labs Research, GraphViz. <http://www.research.att.com/sw/tools/graphviz/>, 30-Nov-2003.
- Blom, G. 1989. Sannolikhets teori och statistikteori med tillämpningar. Fjärde upplagan. Studentlitteratur, Lund. ISBN: 91-44-03594-2.
- Choi, C., Chae, C. 2002. Localization of classical swine fever virus in male gonads during subclinical infection. *Journal of General virology*. 83, 2717-2721.
- Dewulf, J., Laevens, H., Koenen, F., Mintiens, K., de Kruif, A. 2000. Airborne transmission of classical swine fever virus under experimental conditions. *Veterinary Record* 147, 735-738.
- Dewulf, J., Laevens, H., Koenen, F., Mintiens, K., de Kruif, A. 2001. An experimental infection with classical swine fever virus in pregnant sows: transmission of the virus, course of the disease, antibody response and effect on gestation. *Journal of veterinary medicine. Series B*. 48(8):583-91.
- Dewulf, J., Laevens, H., Koenen, F., Mintiens, K., de Kruif, A. 2002. An experimental infection to investigate the indirect transmission of classical swine fever virus by excretions of infected pigs. *J Vet Med B Infect Dis Vet Public Health*. 49(9):452-6.
- Gansner, E., Koutsofios, E., North, S. 2002. Drawing graphs with dot. AT & T Labs Research, <http://www.research.att.com/sw/tools/graphviz/dotguide.pdf>, 30-Nov-2003.
- Klinkenberg, D., de Bree, J., Laevens, H., de Jong, MC. 2002. Within- and between-pen transmission of Classical Swine Fever Virus: a new method to estimate the basic reproduction ratio from transmission experiments. *Epidemiology and infection*. (2002). 128, 293-299.
- Laufer, H. B. 1984. Discrete mathematics and applied modern algebra. Prindle, Weber & Schmidt, Boston. ISBN: 0-87150-702-2.
- Laevens, H., Koenen, F., Deluyker, H., Berkvens, D., de Kruif, A. 1998. An experimental infection with classical swine fever virus in weaner pigs. I. Transmission of the virus, course of the disease, and antibody response. *The veterinary quarterly*. Vol 20, No 2. April, 1998.
- Laevens, H., Deluyker, H., Koenen, F., Van Caenegem, G., Vermeersch, JP., de Kruif, A. 1998. An experimental infection with classical swine fever virus in weaner pigs. II. The use of serological data to estimate the day of virus introduction in natural outbreaks. *The veterinary quarterly*. Vol 20, No 2. April, 1998.
- Laevens, H., Koenen, F., Deluyker, H., de Kruif, A. 1999. An experimental infection of slaughter pigs with classical swine fever virus; transmission of the virus, course of the disease, and antibody response. *The veterinary record*. 145, 243-248.
- Noordhuizen, J.P.T.M., Frankena, K., Thrusfield, M.V., Graat, E.A.M. 2001. Application of quantitative methods in veterinary epidemiology. 2<sup>nd</sup> edition. Wageningen Pers, Wageningen. ISBN: 9074134890.
- Office International des Epizooties. 12, rue de Prony 75017 Paris, France. <http://www.oie.int/>, 4-Sep-2003.

- Press, W. H., Flannery, B. P., Teukolsky, S. A., Vetterling, W. T. 1993. Numerical recipes in C: The art of scientific computing. 2<sup>nd</sup> edition. Cambridge University Press. ISBN: 0521431085. 994 pp.
- Radostits, O. M., Gay, C. C., Blood, D. C., Hinchcliff, K. W. 2000. Veterinary Medicine, A Textbook of the Diseases of Cattle, Sheep, Pigs, Goats and Horses. Ninth edition. W. B. Saunders Company Ltd. ISBN: 0-7020-26042.
- Råde, L. & Westergren, B. 1990. BETA Mathematics Handbook. 2nd edition. Studentlitteratur, Lund. 494 pp.
- Siek, J. G., Lie-Quan L., Lumsdaine, A. 2001. The Boost graph library : user guide and reference manual. Addison – Wesley. 321 pp.
- Stegeman, J. A., Elbers, A. R., de Jong, M. C. 2002. Rate of inter-herd transmission of classical swine fever virus by different types of contact during the 1997-8 epidemic in The Netherlands. *Epidemiol Infect* 128, 285-291.
- Taylor, D. J. 1999. PIG DISEASES. 7th edition. St Edmundsbury Press Ltd. Bury St Edmunds, Suffolk. 412 pp.
- Thrusfield, M. 1997. Veterinary epidemiology. 2<sup>nd</sup> edition. Blackwell Science Ltd. ISBN: 0-632-04851-4.
- Van Oirschot, J. T. 1988. Classical swine fever and related viral infections. Martinus Nijhoff Publishing, Boston U.S.A. ISBN: 0-89838-969-0.
- Van Oirschot, J. T. 1999. DISEASES OF SWINE. 8th edition. Iowa state university press. Ames, Iowa U.S.A. p 159

## Graph layout resources

There are numerous WebPages with information about graph theory, and here I have listed a few that might be of interest.

- [http://directory.google.com/Top/Science/Math/Combinatorics/Software/Graph\\_Drawing/](http://directory.google.com/Top/Science/Math/Combinatorics/Software/Graph_Drawing/)
- <http://www.graphviz.org/>
- <http://www.cs.brown.edu/~rt/gd.html>
- <http://rw4.cs.uni-sb.de/users/sander/html/gstools.html>

Some specific pages devoted to the DOT language can be found at

- <http://www.research.att.com/~erg/graphviz/info/lang.html>
- <http://www.research.att.com/sw/tools/graphviz/dotguide.pdf>

A good source with information about graph theory and algorithms can be found at Boost Graph Library ([www.boost.org](http://www.boost.org), 30-Nov-2003; Siek, Lie-Quan & Lumsdaine, 2001). They provide a software package with implementation of graph theory algorithms that can be downloaded free of charge.