Porcine reproductive and respiratory syndrome (PRRS) in metapopulations: A mathematical model of persistence and control

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"It always seems impossible until it's done"
- Nelson Mandela

Declaration

All work presented in this thesis is the result of original work conducted by Daniel Franklin. This thesis or any part of it has not been presented previously for any other degree.

Summary

This thesis presents research on the dynamics and control of porcine reproductive and respiratory syndrome (PRRS) caused by the PRRS virus (PRRSV) in the pig population of Great Britain (GB). The roles of the metapopulation of pig herds (metaherd) and individual herd characteristics are examined, and different control and intervention strategies assessed.

A novel stochastic model of a metaherd was created, incorporating the births, deaths, slaughter, culls and movement of pigs within and between herds. The metaherd was structured to have characteristics representative of the GB metaherd: the distribution of herd sizes, 'source' herds per herd, and numbers of pigs moved per movement. The metaherd was arranged into a typical pyramidal structure. A stochastic infectious process of PRRSV was included. Herd size was found to be key to within herd persistence of PRRSV, with infection failing to persist in smaller (~250 sow) herds. Fadeout did not occur in larger herds once infection established in the rearing herd.

PRRSV reduces productivity of herds and the metaherd. There was variability in productivity both between herds and within herds over time. The number of source herds did not influence the dynamics, persistence or prevalence of infection within a herd. Breeding herd production was further decreased by PRRSV when the herd also had a rearing herd (breeder finisher).

The model was extended to test the effects of control and intervention strategies. Vaccination effect increased with herd size, and reduced variability in production. Vaccination in small herds was ineffective in increasing production due to PRRSV failing to persist regardless of vaccination. Vaccination of the breeding herd produced higher gains per vaccine dose than vaccination of the rearing herd only. Vaccination of the rearing herd only resulted in higher total herd and metaherd gains, with less variability. Partial de-population combined with vaccination increased the probability of increasing herd performance unless the herd was small (<100 sows) or very large (>1000 sows).

Results highlighted the value of modelling to support the decisions of individual farmers to vaccinate and partially depopulate, showing that the optimal decision is influenced by the herd size. Results also demonstrated that the decision to introduce interventions is different for individual farmers.

1 Introduction

Porcine reproductive and respiratory syndrome virus (PRRSV) causes morbidity and mortality in the respiratory and reproductive systems of pigs: porcine reproductive and respiratory syndrome (PRRS). PRRS leads to reduced numbers of live born piglets and reduced daily weight gain in growing pigs and so affected herds are typically less productive and profitable than unaffected herds. In this chapter the context of the thesis is outlined, and the disease and methods introduced.

1.1 Commercial pig production in Great Britain

In 2009 the number of breeding sows in the UK was 426,000 and the total number of pigs was 4,540,000 (BPEX 2012). Pigs are clustered in herds and herds are geographically clustered: 59% of all breeding sows are in Yorkshire and Humberside and Eastern regions (DEFRA 2010). Within three assurance schemes (Genesis Quality Assurance (GQA); Assured British Pigs (ABP); Quality Meat Scotland (QMS)) 51% of herds are owned by a medium (5-50 farms) or large (>50 farms) company (Smith et al., 2013) and approximately 20% of the entire GB pig herd belong to four large companies (BPEX communication 2013).

Commercial gilts (young females before their first pregnancy) are mated for the first time when approximately 33 weeks of age. Sows have a mean of 2.25 litters per year (BPEX 2012). In the UK, 51% of breeding sows are replaced each year (BPEX 2012). Replacement gilts are either homebred or purchased from other herds. The

flow of pigs between herds is described in a pyramid structure. At the apex of the pyramid there are a small number of nucleus herds that provide grandparent breeding stock to a larger number of multiplier herds that in turn provide parent breeding stock for a much larger number of breeding herds. This parent stock produces pigs for meat that leave the farm either at weaning (4 weeks of age), 10 weeks of age or slaughter age (24 weeks of age). Farms that breed and rear pigs to slaughter are known as breeder-finisher farms and those that breed and sell pigs at 4 or 10 weeks are known as breeder-weaner farms. Farms that buy pigs at weaning or 10 weeks of age are known as finisher farms.

1.1.1 Structure of a commercial pig herd

Pigs are grouped by age and stage of management. Sows are typically separated into replacement gilts, a service group (non-pregnant, non-lactating) where pigs are mated, a 'dry' group, where sows / gilts are pregnant and a farrowing group, where sows are in farrowing accommodation (arcs or single pens) from one week before farrowing until piglets are weaned. Weaned piglets are usually grouped by age and mixing is avoided (although occurs) and thinning of a group may occur as pigs are selected for slaughter. Pigs within a group have more contact with each other than pigs between groups and adults have more contact with adults in other groups than with growing pigs, similarly growing pigs have more contact with other groups of growing pigs than with sows. This structure mostly assumes continuous farrowing, although some breeding herds do breed in batches, farrowing every three weeks, and some finisher herds are all-in all-out systems, taking in large batches and not bringing in a new batch before the previous has gone to slaughter. This thesis and the model developed assume continuous farrowing.

1.1.2 The structure of networks of herds

There has been little research on the real networks between pig herds in GB. Smith et al., (2013) reported a high level of clustering in geographical areas; however these clusters are not completely isolated from herds outside the area. Farms belonging to large or medium sized companies were reported to have 61.5% of their movement connections between farms of the same company (Smith et al., 2013). The herds and movements analysed (Smith et al., 2013) all belonged to one assurance scheme suggesting that all herds are guaranteed to comply to particular basic standards, reducing the probability of behaviour that did not conform to accepted knowledge and standards. In studies of one pig farm network in Germany (Büttner et al., 2013b, Büttner et al., 2013c) breeding herds had more outgoing contacts than incoming, whilst the reverse was true for finisher herds. Also highlighted was that to capture the true dynamics of a network of pig herds, indirect trade contacts must be considered. As well as direct movement of pigs between herds, herds are also connected by indirect contacts through people (e.g. veterinarians) and equipment (e.g. feed lorries), and are often close together (Woodbine et al., 2007).

The British pig industry considers that it operates with a pyramidal structure of farms (British Pig Association), like that displayed in Figure 1.1.Figure 1.1 The top of the pyramid being made up of a small number of nucleus farms selectively breeding particularly for commercial success. The next step of the pyramid is made up of multiplier farms that cross breed pigs from nucleus farms. This progeny then goes to commercial breeding farms to be the parent animals of the pigs that go into the food chain. There are other intermediate steps between the commercial breeders and slaughter of pigs. Commercial breeding farms can be breeder weaner farms where by the weaned piglets leave the farm to go to a finisher farm. Some breeding farms rear

their weaners to 10 weeks old before they are sent to a finisher farm, whilst other

breeder finish farms rear their pigs to slaughter.
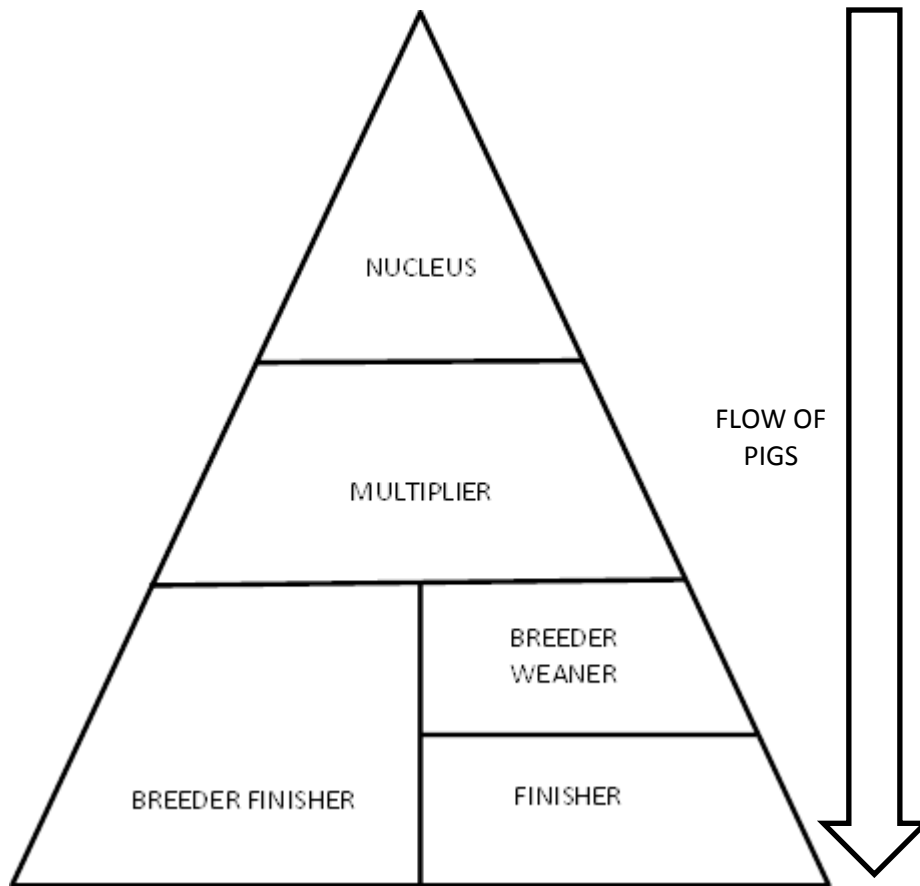
Figure 1.1. Pyramid of pig farms in the GB pig industry.

1.2 GB pig movement data

As part of this project, three years' worth of GB pig movement data was obtained

from DEFRA. It is a legal requirement to register as a pig keeper, and to register

movements of pigs on and off of registered properties with a movement licence. This

data was recorded by means of a paper based form which was submitted to Trading

Standards. The data obtained contained the county parish holding (CPH) number of

each holding (from and to), the holding types, the date of the movement and the

number of pigs moved (but not the age of pigs). Other information was collected on

the movement licences, but not included in the recording of the data. In three years there were over 570,000 recorded movements.

This movement data was intended to be used directly in a model of pig herds connected by movements of pigs, and to reconstruct the demography and size of herds. The data were used to try and infer the age of pigs moved in each movement. The principal assumption was that every pig slaughtered (movements to slaughter houses were recorded) was born ~24 weeks previously in a litter of 12 piglets, and the only "movement" unrecorded was birth. The logic of the analysis was that the births on different farms could be inferred (back-calculated) so that movements into a herd (including inferred births) were matched with movements out, and the age of pigs could then be inferred. After extensive descriptive analysis a simulated annealing algorithm was developed to use the reported movement data to reconstruct demography and movement. However the data were not complete or accurate enough to make this work within a reasonable time period. In an attempt to understand the completeness and accuracy, movement records were obtained directly from a herd, and these compared with the national data. The comparison revealed that a large proportion of the herd's movements were missing from the national data. Miss-classification of holdings was also shown by obtaining a list of slaughterhouses from Animal Health and Veterinary Laboratories Agency (AHVLA). CPH numbers classified as agricultural holdings (farms) in the national data were recorded by AHVLA as slaughterhouses, which accounted for the flow of pigs into the holdings, and limited out-flow. The errors and missing data made the movement data unsuitable for use as originally intended without considerable further work and imputation / inference (which would have reduced the accuracy of the results). However observations from the data were possible. Herds were identifiable as

breeding herds if they had far greater numbers of pigs out than pigs in. Herds were identifiable as rearing herds if the number of pigs in and out were similar. There were many more breeding herds than rearing only herds. Herds were arranged in networks that sometimes appeared pyramidal (fewer herds at the top). However there was evidence of 'lateral' movements, where pigs are moved between herds at the same level. Perhaps more surprisingly there was evidence of 'cycles' of pig movements, whereby two herds sent pigs to each other. This was most alarming when the cycle included pigs moving back up the pyramid. In the GB pig industry the higher in the pyramid, the stricter the biosecurity and the higher the herd health.

Consequently, the demographics and movement patterns of pigs and herds presented in the thesis are not based directly on observed data. This aspect is considered further in the discussion.

1.3   Porcine Reproductive and Respiratory Syndrome Virus

PRRSV is an enveloped positive single stranded RNA virus in the genus arterivirus (Mettenleiter and Sobrino, 2008). PRRSV invades and kills macrophages, particularly in the lungs (Wensvoort et al., 1992). Up to 40% of the macrophages can be destroyed which leads to enhanced susceptibility to other infections, which can proliferate and cause further disease.

PRRSV was first recognised in North America in 1987 and in Europe in 1990 with the European strain detected in the UK in 1991 (Wensvoort et al., 1992). PRRS is now endemic in many countries. The estimates of herd level prevalence of PRRS range from 33.6% (National Animal Disease Information Service, UK, 2010) (UK data) to 39.8% (Evans et al., 2008) (GB data).

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1.3.1 Disease and productivity

PRRS presents with many clinical signs that vary by age and sex of pigs (Hopper et al., 1992). PRRSV is an important cause of reproductive disease in sows (Hopper et al., 1992). If infection occurs in late gestation, PRRSV can cause stillbirths, mummified piglets, late pregnancy abortions and premature farrowing. Infection early in pregnancy can cause abortion that is detected as return to service and also respiratory signs. PRRSV can cause pre-weaning mortality in piglets infected *in utero* (Kranker et al., 1998): the piglets are born weak, affecting their ability to get to the teat leading to hypoglycaemia and starvation coupled with respiratory disease, all of which increase pre-weaning mortality. Respiratory disease is the main clinical sign in weaned growing and finishing pigs (Drew, 2000).

PRRSV infects pigs in herds of all health states, densities and sizes (Mortensen et al., 2002, Wu et al., 2008). The results of infection in non-pregnant pigs vary greatly between herds from no detectable disease to severe disease: generally the higher the health status of the herd the less severe the disease (Feng et al., 2001, Xu et al., 2010, Li and Yang, 2003). In herds with <250 sows natural fadeout of virus can occur (Evans et al., 2008, Evans et al., 2010).

Because PRRSV is immunosuppressive it results in more severe clinical signs when other pathogens are present. This has been described for *Streptococcus suis* (Feng et al., 2001, Xu et al., 2010), porcine respiratory coronavirus and swine influenza virus (Van Reeth et al., 1996) and classical swine fever (Li and Yang, 2003).

1.3.2 Transmission of PRRSV

PRRSV is spread via saliva and nasal secretion (Wills et al., 1997b, Ruiz et al., 2009), most commonly by nose to nose contact. PRRSV has also been infrequently

found in urine (Wills et al., 1997b, Rossow et al., 1994) although it is not clear whether transmission is possible via this route. Virus has previously been isolated in urine from other arteriviruses (Notkins and Scheele, 1963, Neu et al., 1988). The most common explanation for spread between farms is movement of infected pigs, in particular breeding gilts and boars in breeding herds and weaner pigs in finisher herds. The transmission of PRRSV via semen used in artificial insemination has been reported, but there is conflicting research on duration of infection in semen (Christopher-Hennings et al., 1995, Shin et al., 1997). Studies suggest that PRRSV is also transmissible by aerosol; it can be airborne for up to 2 miles (Wills et al., 1997a, Kristensen et al., 2004). Experimental studies have shown that PRRSV can also be spread by a number of mechanical vectors (Otake et al., 2002, Otake et al., 2004), and birds (Zimmerman et al., 1997). Re-introduction of PRRSV has been demonstrated on previously PRRS negative farms (Holtkamp et al., 2010), where external risks including introduction of replacement pigs from other herds were shown to be significant in re-introduction.

1.3.3   International strategies to eliminate or control PRRSV

Various control and intervention strategies have been reported for PRRS. In populations with large numbers of susceptible individuals, either because of population structure or the stage of outbreak, test and removal of infected pigs have been shown to eliminate infection (Dee et al., 2000, Yang et al., 2008) as has depopulation (Dee et al., 1993) or deliberately exposing pigs to virus to create herd immunity (Fano et al., 2005). Intervening to prevent mechanical spread of PRRSV via personnel and fomites has also been utilised (Pitkin et al., 2011).

In Sweden, there is a national sero-surveillance programme for PRRSV; in 2007 PRRSV was detected in only 7 herds and was eliminated by de-population and

disinfection (Carlsson et al., 2009). The Swedish system appeared to detect an outbreak in its early stages. Chile eliminated PRRSV after it was endemic in 30% of herds (Torremorell et al., 2008). This was achieved through depopulation and herd closures, aided by limited movement of pigs between herds. Sweden and Chile are both recognised by the World Organisation for Animal Health (OIE) as being PRRS free as of 2013.

1.3.4   Vaccines

There are several vaccines against PRRSV, both dead and live attenuated. The dead vaccine does not induce protective immunity (Zuckermann et al., 2007, Scortti et al., 2007). Live attenuated vaccines do not prevent shedding and transmission of virus, but result in shedding for a shorter period than in non-vaccinated pigs (Cano et al., 2007a, Linhares et al., 2012). Vaccination can reduce but not eliminate clinical disease and reduction in performance (Martelli et al., 2009, Linhares et al., 2012, Mavromatis et al., 1999). There are conflicting reports on whether vaccination reduces viral load (Zuckermann et al., 2007, Cano et al., 2007a). PRRSV has the fastest evolutionary rate reported for any RNA virus (Hanada et al., 2005). This has clear implications for vaccination. Pigs vaccinated with a range of PRRSV strain vaccines and then challenged with multiple PRRS strains, including the vaccination strain were found to be infected with heterologous strains (Mengeling et al., 2003), suggesting that a pig's immune response to PRRSV is strain specific. Pigs have a high level of protection against reinfection with a homologous strain (Shibata et al., 2000, Lager et al., 1997), therefore it seems reasonable to suggest a vaccine matching a field strain would offer high levels of protection against that field strain. After vaccination and subsequent inoculation with either a 98% matching virus strain or an 84% matching virus strain, the highly matching virus inoculated pigs remained

virus free, whilst the lower matching virus inoculated pigs all were positive for virus (Labarque et al., 2004). Vaccination has been shown to have varying impact on disease and prevalence (Martelli et al., 2009, Cano et al., 2007b, Cano et al., 2007a, Linhares et al., 2012, Zuckermann et al., 2007). The studies in which vaccine and virus strains were matched were controlled experiments. The evolution rate and number of strains in a geographical region (Wang et al., 2014) suggest that vaccine development to match prevalent wild types would be very problematic.

1.3.5 Prevalence of PRRSV

In GB, 39.8% of pig herds were seropositive for PRRSV antibody with a further 26% of herds vaccinated (Evans et al., 2008). Seronegativity was more likely if the herd had less than 250 sows and if the nearest pig herd was located at a distance of at least 2 miles. Prevalence of infected herds in the UK was also reported as approximately 32%, with a further 26% vaccinating (National Animal Disease Information Service, UK, 2009).

The basic reproduction number, R_0, for PRRSV has been estimated as 3 in a herd of 115 sows (Nodelijk et al., 2000) and 2.6 (Charpin et al., 2012) in an experimental infection study of piglets. Both of these studies were small and thus may not provide ideal estimates of R_0 but are the only published estimates. However reports of PRRSV outbreaks (Hopper et al., 1992, Stevenson et al., 1993, Gordon, 1992, Pejsak and Markowska-Daniel, 1997) suggest that regardless of herd size, the outbreak tends to happen at the same rate, indicating the same or similar value of R_0, therefore density independent transmission is deemed suitable. Of these outbreaks, that which happened in the largest herd (Pejsak and Markowska-Daniel, 1997), suffered a greater impact on production suggesting that R_0 may have been higher. However the

pattern of the outbreak and severity suggest that the outbreak was not of PRRSV, or of not only PRRSV.

1.4   Mathematical modelling

Mathematical modelling of infectious disease dynamics has been used for many decades as a means to better understand the population patterns in infection (e.g. persistence) that are generated from individual host processes (e.g. contact and immunity) (Anderson and May, 1991). In many circumstances, mathematical models provide the only route to designing population intervention strategies, because the appropriate trials are logistically or ethically impossible to perform.

1.4.1   Mathematical models of PRRSV in single herds

(Nodelijk et al., 2000) published a within herd model of PRRSV transmission, but this did not include the contact structure of the sub-groups within the herd. A detailed within-herd model of PRRSV including sub-group structure has been published (Evans et al., 2010). This model concluded that fadeout and persistence of PRRSV is herd size dependant, fadeout being more likely in smaller herds, and persistence more likely in larger herds. The study also reported that persistence of PRRSV was more likely once infection was present in the rearing herd.

1.4.2   Network analysis of pig networks

Models of infection transmission in individual herds have to make assumptions regarding the introduction of infection. For example, Evans et al., (2010) included a continuous inward flow of infectious gilts as a fixed proportion of the new gilts introduced, i.e. the context of the herd is fixed. This model demonstrates the importance of movements of pigs between herds by demonstrating the dependence on rate of reinfection. For any individual herd its status in terms of inward challenge

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of PRRSV is dependent on other herds with which it has contact. In turn these other herds' status is dependent on all other herds. Consequently, to be able to understand the transmission dynamics within the total pig population, a metapopulation model is required, i.e. populations of pigs within a population of connected herds. We use the term metaherd to describe this structure.

Network analysis has been produced for herds in Ontario Canada (Dorjee et al., 2013) and France (Rautureau et al., 2012). These, however, do not investigate the effect of the network on the spread of pathogens and only discuss the implications of the network composition on the spread of an infectious agent. The network parameters of both Danish and German networks of pig herds are right skewed (Noremark et al., 2011, Büttner et al., 2013b, Büttner et al., 2013c), i.e. herds making up a small proportion of the network are highly connected to the rest of the network. The most efficient way of interrupting the infection chain within a network is the targeted removal of those herds with the highest number of destination herds (herds pigs are moved to) (Büttner et al., 2013a), splitting the network into smaller clusters or fragments (Büttner et al., 2013b). High levels of clustering of herd networks have also been reported in GB (Smith et al., 2013) and Spain (Martinez-Lopez et al., 2009).

In GB, it is assumed that movements of pigs occur down the production pyramid. When simulating disease where herd types are not considered in the movement of pigs between herds, the final epidemic size is increased, as is the rate at which herds in a network become infected, whilst variability of outbreaks is decreased (Lindstrom et al., 2012). The assumption of pyramid structure in Britain is not entirely true, although it is the intended strategy.

In Scotland, pig movements have been reported as not likely to spread disease (Tildesley et al., 2011), this seems unlikely. However the authors acknowledge that the herds in Scotland are predominantly finisher herds, therefore their outward movements are to slaughter only. That the Scottish pig industry is dominated by one large company may be a factor in the dynamics of the pig movements in Scotland.

Methicillin-resistant *Staphylococcus aureus* becomes endemic, sustained by pig movements alone in a real heterogeneous contact network (Ciccolini et al., 2012) despite extremely low predicted prevalence, demonstrating the role movement of pigs can have in transmission and persistence of infection.

1.4.3   Modelling of infection dynamics in metapopulations

Whilst applied metapopulation research does exist (Lopez et al., 2005), metapopulation research is mostly theoretical in both ecology (Keeling, 2000) and disease transmission (Jesse and Heesterbeek, 2011, Jesse et al., 2008, Keeling, 2000, Rowthorn et al., 2009) and has not been applied to a specific host and/or pathogen species very often. Some metapopulation research simply states basic epidemiological theory that is axiomatic for homogeneously mixing populations and extends it to metapopulations. For example (Cross et al., 2007) states that the effect of the duration of infectiousness, group size and recruitment of new susceptible individuals is important in predicting spread of pathogens in a metapopulation.

The structure of a metapopulation can increase the probability of persistence of infection. One of the first applied metapopulation models for infectious disease research modelled the persistence of measles (Bolker and Grenfell, 1995), finding that the metapopulation structure allowed persistence. A model of Feline leukaemia virus in a case of two subpopulations plus the presence of feral cats also showed that

spatial heterogeneity promoted disease persistence (Fromont et al., 2003). Metapopulation models have also been used to investigate the importance of a sub-divided population for control interventions (Glass and Barnes, 2013, Keeling et al., 2001). However, the great majority of metapopulation models have not included both within and between herd transmission dynamics explicitly, although some come close to this detail (Ezanno and Lesnoff, 2009). Inclusion of within herd dynamics alongside between herd dynamics is necessary in anything but very rapidly spreading pathogens (Courcoul and Ezanno, 2010).

An applied metapopulation model incorporating many applied parameters modelled Phocine distemper virus in harbour seals (Swinton et al., 1998). The model was parameterised for the pathogen species and partially for the host species. The subpopulations within the metapopulation had no internal structure, which was thought accurate given the contact structure between individuals in the same location. In this model the subpopulation sizes and mixing between subpopulations was hypothetical and uniform across the subpopulations, thus the metapopulation lacked an accurate demographic structure. A metapopulation model of *Mycobacterium bovis* in possums has been developed (Fulford et al., 2002). The model explored a hypothetical metapopulation with hypothetical numbers of subpopulations and links between subpopulations, it also did not account for variation in subpopulation size.

The contacts and structure of a metapopulation can determine whether infection can or cannot persist within it, and thus there are key metapopulation characteristics (nodes or links) that can be targeted to disrupt that persistence. The size of an epidemic of influenza in a metapopulation of horse yards is heavily dependent on the index yard (yard in which infection is first seeded); furthermore the impact of

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vaccination within a yard is determined not only by its infection and vaccination status, but that of the other yards in the metapopulation (Baguelin et al., 2010). Removal or downsizing of large subpopulations within a metapopulation can help eradicate disease, as shown in a model of feline enteric coronavirus (Foley et al., 1999). A model of a fragmented trade network has suggested that such fragmentation can reduce the probability of sustained transmission of avian influenza (Hosseini et al., 2013). However such a result is highly dependent not only on network demography but also on the key pathogen specific parameters.

Lurette et al., (2011) modelled salmonella in a metapopulation of French pig herds in which movement restrictions between herds was found to reduce prevalence of disease. This study is the most similar to the model presented in this thesis. In the (Lurette et al., 2011) study a metapopulation was created using movement and demographic data of a single large producer in France and infection through the metaherd was simulated. Control and intervention strategies were also modelled. These strategies took the form of hypothesised biosecurity improvements, and the restriction of pig movements. These strategies were implemented both when infection was endemic within the metaherd and in a newly infected structure. Restriction of movements alone was not found to reduce the number of infected herds when infection was endemic. However movement restrictions were effective when applied to prevent a new infection invading. Increased biosecurity was found to reduce prevalence of infection.

The metapopulation model presented in this thesis outputs results on three levels, that of the metaherd, the herd and groups within the metaherd. The model is structured and parameterised for the host demographics both within and between subpopulations and is also parameterised for the pathogen species. Where applied,

control strategies are also parameterised to represent physical actions that could be taken rather than suggesting a proportional change in a factor such as biosecurity (Lurette et al., 2011).

1.5 Aims and structure of thesis

In this thesis, PRRSV in a metapopulation of pig herds (metaherd) framework is modelled. The framework is parameterised for the demography both within and between the herds. Although the between herd parameterisation represents a simplification of the real life scenario, real movement data is used to inform the metaherd structure. The model is also parameterised for the infectious process of PRRSV and the PRRSV vaccine. The framework is used to develop understanding of transmission in a metaherd scenario, and to inform on the usefulness of control and intervention strategies.

The aims of this thesis were to investigate the role of the metaherd on the transmission and persistence of PRRSV in pigs, and also on the effectiveness of vaccination based control strategies.

- Chapter 2: The materials and methods of creating the demography within a metaherd, and within herds are presented. As are the details of the infectious process within the model.

- Chapter 3. The results of PRRSV transmission and persistence in a range of metaherd structures on both a herd and metaherd level are presented.

- Chapter 4. The materials and methods and results of implementing control strategies for PRRSV are detailed on a herd and metaherd level.

Finally there is a discussion of what this research presents and how it impacts the understanding of PRRSV transmission and persistence in the GB pig herd.

2 Modelling the demographic processes and transmission of PRRSV in a metaherd

2.1 Introduction

The simulation model presented in this chapter has been designed to include relevant aspects of the complexity of pig production and pig demography as well as states associated with infection, disease and immunity to PRRSV. There were six demographic groups within the herd structure, modelled by weekly time steps. The sum of the number of these weekly time steps was 54, which leads to 54 different pig sub-groups in a herd, although not all herd types have all groups. There are five different states (classes) of infection and immunity associated with PRRSV epidemiology. Thus the maximal model had 270 different groups per herd. Each herd was linked to other herds by movement of pigs. This chapter includes the details of the assumptions and implementation of the model and preliminary results used to validate the model implementation.

2.2 Within herd model structure and demography

The pig population within each herd was structured into 6 groups within the model:

1. Gilts – replacement breeding females before they have been mated; gilts enter the farm at 24 weeks old. Gilts go to their first service at 33 weeks old. The gilts are further divided into 9 weekly subgroups (pens).

2. Dry sows – pregnant sows and sows awaiting insemination. Sows are culled at a constant rate and replaced by new gilts. The dry sows are further divided into 16 weekly subgroups.

3. Lactating sows – sows with litters of piglets. The lactating sows are further divided into 5 weekly subgroups.

4. Piglets – piglets are suckling and housed with their dam; piglets are weaned by removing them from their dam at 4 weeks of age; no distinction was made on gender. Piglets are sold from the farm at weaning on some farms. The piglets are further divided into 4 weekly subgroups.

5. Growers - post weaning pigs aged 4-10 weeks; no gender distinction was made. Growers enter some farms at the start of the post-weaning phase (finishing farms). The growers are further divided into 6 weekly subgroups.

6. Finishers - pigs aged 11-24 weeks; no gender distinction was made. Growing and finishing pigs are collectively the rearing pigs. The finishers are further divided into 14 weekly subgroups.

Management cycles for the groups on each farm are as those used by (Evans et al., 2010) depicted in Figure 2.1. The arrows represent the movement of pigs between groups. Pigs are moved at the end of each week, which is both realistic and convenient for modelling. Demographic parameter rates are given in Table 2.2.

There was a background mortality of all pig groups in the model (Table 2.2); dead

pigs were removed at the end of each week. Pigs infected with PRRSV had a higher

mortality (Table 2.2).
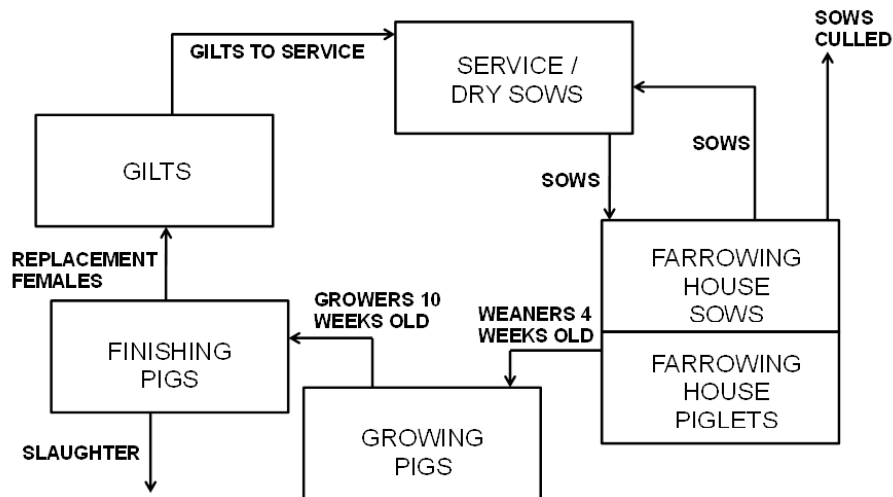
Figure 2.1. The within-farm demographic structure of pig population assumed in the model (from Evans et al., 2010).
Gilts have 9 subgroups (pens). Service/dry sows have 16 pens. Farrowing house sows have 5 pens. Farrowing house piglets have 4 pens. Growing pigs have 6 pens. Finishing pigs have 14 pens.

2.2.1 Gilt and sow cycle

Gilts were moved into the herd from another herd in the metaherd. Gilts were

sourced from the batch of finisher pigs at 24 weeks of age on the farm they

originated from. After nine weeks in the gilt house, and at 33 weeks of age, gilts

joined the sow group at service, replacing sows that had been culled.

The sow cycle was 21 weeks long. Sows spent 16 weeks in the dry sow house, with

the first week assumed to be in service. Sows then moved to the farrowing house 1

week before farrowing and stayed there for 4 weeks with their litters after farrowing.

After weaning a random sample of sows were culled, and the rest returned to service.

Approximately 50% of breeding sows were culled each year (BPEX, 2012). Unlike

pigs in the other demographic groups, sows could not be aged exactly as they were

modelled as a mixed age group. Random culling of sows means that they had an exponentially distributed life expectancy. Whilst it would have been possible to include information on parity and keep track of separate sow groups within the model, the additional complexity was not considered consummate with the potential effects on PRSSV persistence and transmission and there is no known epidemiological distinction.

2.2.2 Piglets and rearing pigs

An average of 11.2 piglets were born to sows not infected with PRRSV (BPEX, 2012). The piglets stayed in the farrowing house with the dams until they were 4 weeks of age, and then moved to the growing group (5-10 weeks of age) and finally the finisher group (11-24 weeks of age) and were sent to slaughter at 24 weeks of age.

2.3 Metaherd structure(s)

The farms in the metaherd were linked by pigs moving between them. This was either as replacement gilts, or 4 week old weaner pigs.

The numbers of pigs and herds increased down the pyramid of pig herds. However after the commercial breeding farms, there are fewer rearing farms. This was due to the presence of breeder finish farms, which do not send rearers to a separate rearing farm, and also due to the fact that the rearing farms are often very large, taking in pigs from several breeding farms.

The results presented here are those using a metaherd made up of 1 nucleus farm supplying 6 multiplier farms with replacement gilts, which in turn supplied 54 breeding farms with replacement gilts, 8 of which were breeder weaner farms, the rest breeder finisher. The breeder weaner farms sent their weaners to finishing farms

(Figure 2.2). This network was an example of a very well structured network, with a clear flow of pigs, and clear branching. The infection dynamics of a farm could only affect the infection dynamics of another farm if it sent pigs to it.

In the model the movement of pigs between farms occurred at exactly the same time, at the end of each week and the number moved was based on the number of pigs already on the receiving farm. This was necessary to keep the numbers of pigs on a farm constant. In the metaherd presented here, the multipliers received replacement gilts from the nucleus every 6 weeks. The breeding farms received replacement gilts from an individual multiplier every 9 weeks. Whilst the finishing farms received weaner pigs from the 3 breed-wean herds every 5 weeks, pooling the 3 deliveries into large batches.
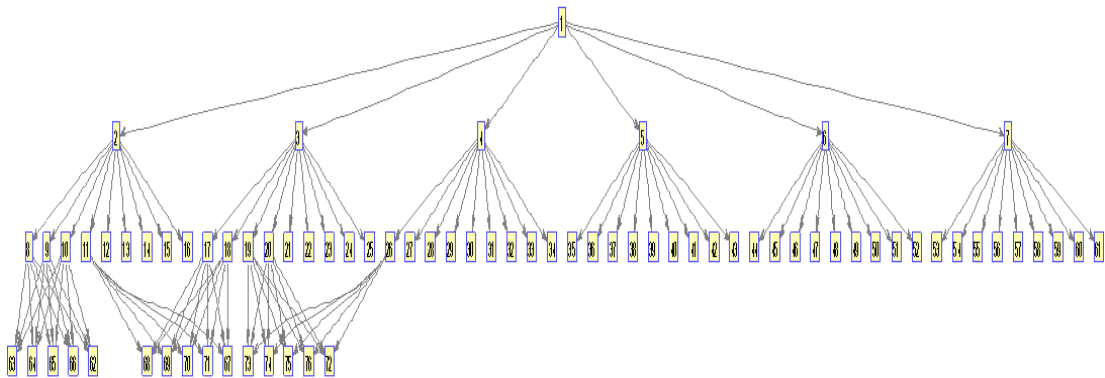
Figure 2.2. Metaherd pyramidal structure used in the model

2.4   Epidemiological states and rate parameters

To simulate the transmission dynamics of PRRSV within the pig population, a stochastic model with infectious states maternally immune (M), susceptible (S), infected and infectious (I), recovered - immune (R), and recovered - susceptible (RS) was used as in previous PRRSV models (Evans et al., 2010, Nodelijk et al., 2000). Transition between states occurs sequentially and at the rates given in Table 2.2.

2.4.1 Rate of loss of maternal immunity (π)

Piglets born to seropositive sows are born with maternal immunity which they had until 4-10 weeks of age (Houben et al., 1995, Nodelijk et al., 1997). In the model, sows that were infected or recovered-immune were considered seropositive. The rate of loss of maternal immunity (π) was 1/42 days (Evans et al., 2010).

2.4.2 Rate of recovery (γ)

The rate of recovery was the rate at which infected pigs become recovered and immune. Transmission has been shown to occur from infected pigs up to 56 days after inoculation (Terpstra et al., 1992), and previous single herd models have used 56 days as the average duration of infectiousness (Nodelijk et al., 2000, Evans et al., 2010). A more recent paper (Charpin et al., 2012) showed that inoculated pigs were no longer infectious from at least 42 days post infection, and that the average duration of infectiousness was approximately 20 days. The rate of recovery used in the model was 1/20 days.

2.4.3 Rate of loss of protective immunity (ω)

Immediately after recovery from PRRSV, pigs are assumed to be immune to further PRRSV infection. It has been shown that pigs can seroconvert becoming seronegative after recovery after approximately 4.5 months (Yoon et al., 1995) but can take more than 20 months (Desrosiers and Boutin, 2002). In the model the pigs became re-susceptible to infection with a constant rate $\omega = 1/252$ days (Evans et al., 2010). These pigs were susceptible to reinfection at the same rate as previously uninfected pigs.

2.5 Transmission

2.5.1 Horizontal transmission

The pig herd was divided into batches determined by week and grouping (Figure 2.1). The force of infection to susceptible individuals in batch i was calculated as in equation 1.

$$\Lambda(i) = \beta \sum_j \frac{\big(D(i,j) + \alpha \times \phi(i,j)\big)I(j)}{N(j)} \tag{1}$$

Where I(j) was the number of infected pigs in batch j, N(j) was the total number of pigs in batch j; β was the overall transmission coefficient and $\alpha \times \phi(i,j)$ was the relative rate of transmission from infectious pigs in batch j to susceptible pigs in batch i. D was a diagonal matrix specifying the mixing within pens. The ϕ matrix was the matrix given in Table 2.1but with diagonal elements equal to zero. The D matrix was a diagonal matrix using the diagonal values of Table 2.1 with zero otherwise. This formulation assumed density independent transmission.

		GILTS	DRY SOWS			FARROWING HOUSE SOWS		PIGLETS		GROWERS		FINISHERS	
			SERVICE	SAME BATCH	DIFFERENT BATCH	SAME BATCH	DIFFERENT BATCH	SAME BATCH	DIFFERENT BATCH	SAME BATCH	DIFFERENT BATCH	SAME BATCH	DIFFERENT BATCH
GILTS		1											
DRY SOWS	SERVICE		1										
	SAME BATCH			1									
	DIFFERENT BATCH	0.001	0.1		0.5								
FARROWING HOUSE SOWS	SAME BATCH					0.5							
	DIFFERENT BATCH	0.001		0.01			0.1						
PIGLETS	SAME BATCH							0.5					
	DIFFERENT BATCH	0.001		0.01			0.1		0.1				
GROWERS	SAME BATCH									1			
	DIFFERENT BATCH	0.001		0.01			0.01		0.01		0.5		
FINISHERS	SAME BATCH											1	
	DIFFERENT BATCH	0.001		0.01			0.01		0.01		0.1		0.5

Table 2.1. Matrix of relative rates of transmission between batches of pigs in the model.
Note that the matrix was symmetrical, and only the lower triangle is shown.

2.5.2 Transmission coefficient

The basic reproductive ratio (R_0) of PRRS has been reported as 2.6 (Charpin et al., 2012). The methods of this study imply that this is representative of a within pen R_0. Nodelijk et al., (2000) reported an R_0 of 3. The methods of this study imply that this is representative of a within herd R_0. Both of these R_0 values were incorporated in the model transmission calculations.

Beta (β) was the overall transmission coefficient. The value of β was derived from the simple relationship between R_0 and the rate of recovery (γ), $R_0 = \beta/\gamma$. Therefore calculating within a single pen (assuming homogeneous mixing) gives $\beta = 0.13$.

The relative rates (RR) of transmission (Table 2.1) are devised as such: groups of pigs that are isolated from each other are assigned an RR of 0.001. Within the model this existed between the gilt group and the rest of the herd. A value of 0.01 was assigned where the groups of pigs were likely to be in different buildings, e.g. all sows from rearing pigs. Values of 0.1 were assigned where the groups were in the same building but separate pens/rooms and were likely to have the same stockman. For example this was the relative rate of transmission between the grower and finisher groups. A value of 0.5 was assigned where the groups were likely to have the same stockman, be in the same building and be in connecting pens (so some nose to nose contact was possible). A value of 1 was assigned where free mixing was assumed, i.e. pigs in the same pen. Within the gilt house the relative rate of transmission was 1, as the gilt group was assumed to be freely mixing and a form of 'all in all out' group, which exists as a form of quarantine from the rest of the herd as well growing to the appropriate age for service. Apart from all pigs in the farrowing

house (sows and piglets) and the gilt group, pigs within the same weekly demographic group had a relative rate of transmission of 1. Susceptibility was not age dependent.

The relative rates of transmission within the farrowing house had a slightly different pattern to other groups in the herd due to the nature of the housing, as some pigs in the same week and demographic group are separate. The sows in the farrowing house were assumed to be in farrowing crates, thus have no contact with any other sows. Therefore the relative rate of transmission between farrowing sows in the same batch was assumed to be 0.5 (rather than 1). The relative rate of transmission between sows in the farrowing house but in different batches was 0.1 as the sows at different stages/batches (pre farrowing, 1, 2, 3 or 4 weeks post farrowing) are considered to be in separate rooms. The rate between piglets in the same week was 0.5 instead of 1, as although they are kept together in litters the litters are separate from each other with no possible direct contact.

The alpha (α) value was necessary to obtain the within pen $R_0 = 2.6$, and the overall herd $R_0 = 3$, i.e. without including $\alpha \ll 1$ the force of infection from other pens into a single pen was too great relative to the force within the pen as there are a large number of other groups in a herd. The value assigned to α was calculated using an eigenvalue approach (Keeling and Rohani, 2007). The herd R_0 and within group R_0, is defined in the following equations, where n is the number of groups in the herd (n=54) and $\underline{e_i}$ are the eigenvector values of the eigenvector associated with the dominant eigenvalue:

$$R_0 = \sum_{i=1}^{n} \left(R_{0,i} \underline{e}_i \right) \tag{2}$$

$$R_{0,i} = \sum_{j=1}^{n} \left(\frac{\beta}{\gamma} \left(D_{i,j} + \alpha \phi_{i,j} \right) \right) \tag{3}$$

Assuming $\alpha = 1$, then $D + \alpha\phi = D + \phi$ which was denoted χ.

First the model was considered as a system of differential equations describing the rate of change of infectious individuals in farm subpopulation i.

$$\frac{dI_i}{dt} = \sum_{j=1}^{54} \left(\frac{\beta \chi_{ij} S_i I_j}{N_j} \right) - (\gamma + \delta_i) I_i \tag{4}$$

Where j denotes the other subpopulations on the farm, S_i was the number of susceptible pigs in subpopulation i, I_j was the number of infected pigs in subpopulation j, N_j was the total number of pigs in subpopulation j, γ was the recovery rate, and δ_i was the infection induced mortality rate for subpopulation i.

The Jacobian matrix of the system of 54 differential equations was formed as the partial differential of each equation to each variable, and has the form given in equation 5. The eigenvector of the dominant eigenvalue of the Jacobian matrix provides the $\underline{e}_i$.

$$J = \begin{bmatrix} \beta \dfrac{\chi_{1,1} S_1}{N_1} - (\gamma + \delta_1) & \beta \dfrac{\chi_{1,2} S_1}{N_2} & \cdots & \beta \dfrac{\chi_{1,54} S_1}{N_{54}} \\ \beta \dfrac{\chi_{2,1} S_2}{N_2} & \beta \dfrac{\chi_{2,2} S_2}{N_2} - (\gamma + \delta_2) & \cdots & \vdots \\ \vdots & \vdots & \ddots & \vdots \\ \beta \dfrac{\chi_{54,1} S_{54}}{N_{54}} & \beta \dfrac{\chi_{54,2} S_{54}}{N_{54}} & \cdots & \beta \dfrac{\chi_{54,54} S_{54}}{N_{54}} - (\gamma + \delta_{54}) \end{bmatrix} \tag{5}$$

The elements of the eigenvector corresponding to the dominant eigenvalue are normalised so that the elements sum to 1. Equations 2 and 3 were rearranged:

$$\alpha = \frac{\frac{R_0 \gamma}{\beta} - \left(\sum_{i=1}^{54}\left(D_{i,i}\underline{e}_i\right)\right)}{\sum_{i=1}^{54}\left(\sum_{j=1}^{54}\phi_{i,j}\right)\underline{e}_i} \tag{6}$$

For $\beta = 0.13$ and $R_0 = 3$ the α value was 0.0193. This direct method of calculation results in using the eigenvector appropriate for $\alpha = 1$ to determine the true value of α. However as the elements of the eigenvector scale linearly with α and the eigenvector is normalized the correct result is obtained. This was checked by calculating the herd R_0 with the new α value, which resulted in the correct R_0. This was to be expected as R_0 scaled linearly with α (Figure 2.3). To further verify that the calculations are robust the dominant eigenvalue of the next generation matrix matches the calculated R_0 when α is 1 and 0.0193 (Diekmann et al., 2009, Keeling and Rohani, 2007). The more detailed calculation was required to calculate α.
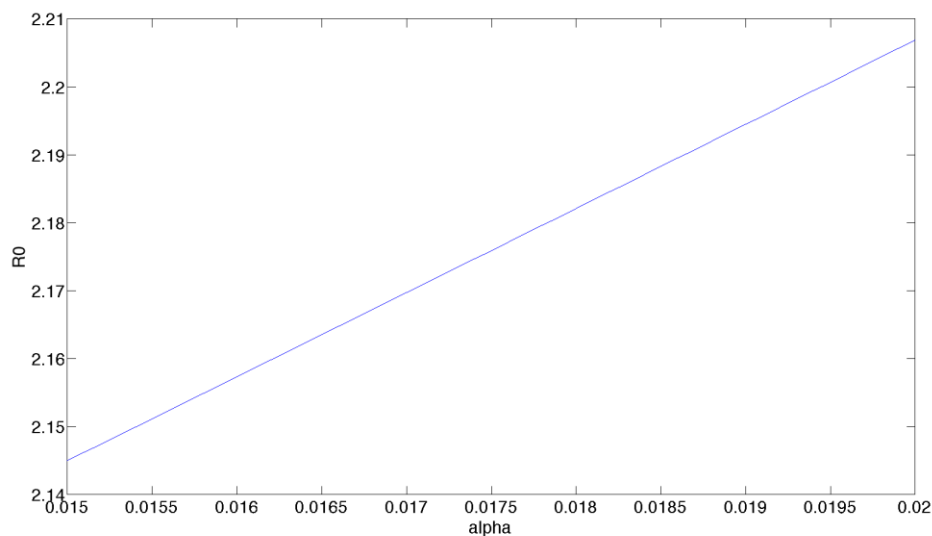
Figure 2.3. Plot of the change in R_0 with α.

2.5.3 *In utero* transmission

Experimental infection of gestating sows causes abnormal returns, abortions, premature farrowing, stillborn and mummified piglets (Kranker et al., 1998, Cano et al., 2009). Infection early in gestation has led to conflicting reports on the probability of *in utero* infection (Christianson et al., 1993, Kranker et al., 1998), and in the field the probability that infected sows return to service (i.e. do not become pregnant) or abort, and the probability that infection crosses the placenta and at what point during gestation are largely unknown.

In the model it was assumed that if sows are infected on or after week 12 of gestation that 10% would abort, as in previous a model (Evans et al., 2010). The number of sows aborting was modelled as a random number from a binomial distribution. Abortion was assumed to be detected at the expected time of farrowing, and sows that have aborted are moved back to service.

In the model, 15% of sows return to service by week 6 after service (Whittemore, 1993). The number of sows returning to service on infection was a random number

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drawn from a binomial distribution with probability 0.15 at 3 weeks after service.

Sows infected with PRRSV early in gestation or infected at service have an

increased probability of returning. In the model, of the sows infected during their

third week of gestation an average of 50% of them return.

Whilst PRRSV has been isolated from live piglets at birth (Botner et al., 1994), these

piglets also have a maternal immunity. Houben et al., (1995) suggests that PRRSV

spreads slowly among piglets with maternal immunity, and thus piglets do not play a

large role in transmission. In the model maternally immune piglets could not

transmit infection (Houben et al., 1995, Evans et al., 2010).

2.6   PRRSV induced mortality and morbidity

2.6.1   Pre-weaning

Kranker et al., (1998) inoculated sows at different stages of gestation with a Danish

isolate of PRRSV, reporting on the impact of numbers of piglets born dead, born

alive and those dying pre-weaning. Of those inoculated at 79-89 days gestation, a

mean of 75% of piglets were born alive, with 42% of those born alive dying pre-

weaning, so that 44% of all piglets born survived to weaning. In sows inoculated at

72 days gestation, a mean of 86% of piglets were born alive, with 19% of those

dying pre-weaning, so that 70% of those born survived to weaning. In the sows

inoculated at 42 days gestation, again 86% of piglets were born alive, 11% of those

died pre-weaning, meaning 77% of all piglets born survived to weaning.

Christianson et al., (1992) also inoculated sows at 93 days of gestation, where 49%

were born alive, although pre-weaning mortality was not reported.

As there was no evidence of a different outcome between sows inoculated at 72 and

42 days gestation, it was assumed that piglets born to sows infected up to 11 weeks

gestation proceeded to farrowing having an average litter of 8.3 live piglets that survived to weaning. Sows infected after 11 weeks of gestation had an average of 4.9 live piglets that survived to weaning (i.e. 4.9 multiplied by the number of sows infected in late gestation rounded to the nearest integer). Most weak-born piglets die in the first week of life (Gordon, 1992, Cano et al., 2009), so piglets dying pre-weaning never entered the model; the mean number of piglets that entered the herd from early and late gestation infected sows (8.3 and 4.9 respectively) took into account the number of piglets that died pre-weaning due to infection.

There are many reports of PRRSV causing early farrowing (Gordon, 1992, Hopper et al., 1992, Stevenson et al., 1993, Pejsak and Markowska-Daniel, 1997, Kranker et al., 1998, Cano et al., 2009, Christianson et al., 1992), particularly in sows infected late in gestation. The piglets of such sows tend to experience high mortality, and the low surviving number of piglets from sows inoculated late in infection in (Kranker et al., 1998) encapsulate this effect. In the model this was accounted for by the number of piglets entering the model from late gestation infected sows (4.9). Because of the difficulties in ensuring demographic integrity of the model, it was assumed that all sows farrowed at full term.

2.6.2 Post-weaning

The presence of PRRSV has been shown to increase post-weaning mortality. Stevenson et al., (1993) reported a mortality rise to 15%, and (Neumann et al., 2005) report mortality averaging 9-12%. Pejsak and Markowska-Daniel, (1997) however report mortality rising to almost 30% during the epidemic phase in post-weaning pigs on a PRRSV infected farm. These data were collected from a farm of far greater size than those seen in Great Britain, and the sudden rise, short duration of peak and sharp fall in mortality levels, and a similar pattern in other production values raises

the question of whether PRRSV was actually the causal pathogen, as this does not seem conclusive. In the model, at the end of each week an infected grower pig has a 23.53% chance of dying. An infected finisher pig has a 10.86% chance of dying at the end of a week. If a growing pig was infected for its entire 6 week period in the growing stage, this gives an 80% chance of dying during that growing stage. The probability of a finishing pig dying due to infection was 30%.

2.6.3 Slowed rearing pig growth

Infection with PRRSV leads to slowed growth in rearing pigs. In the model, pigs at slaughter age that had not been infected with PRRSV were assumed to be the same mass. The average daily gain has been reported as reduced by 0.091kg (Neumann et al., 2005) relative to non PRRSV infected pigs. In the model those pigs that had been infected were assumed to be underweight, calculated as 0.091kg multiplied by 20, as 20 days was the average infected period. Those infected at slaughter were assumed to be 0.091kg multiplied by 10 underweight. The amount underweight per pig was summed and averaged across the batch of pigs being slaughtered, providing an average amount underweight for every pig in the slaughtered batch.

Event	Demographic parameters	Source
Mean number of piglets born to healthy sow	11.2	BPEX (2012)
Baseline sow mortality (weekly)	3.6%	BPEX (2012)
Baseline piglet mortality (weekly)	12.7%	BPEX (2012)
Baseline grower mortality (weekly)	2.7%	BPEX (2012)
Baseline finisher mortality (weekly)	3.2%	BPEX (2012)
Mortality of PRRSV infected grower (weekly)	23.53%	See text
Mortality of PRRSV infected finisher (weekly)	10.86%	See text
Baseline sow abortions	0%	
Late gestation PRRSV infected sows abortions (weekly)	10%	Evans et al., (2010)
Baseline sow returns (at 3 weeks gestation)(weekly)	15%	Whittemore, (1993)
Early gestation PRRSV infected sows returns (at 3 weeks gestation)(weekly)	50%	
Weight not gained when infected with PRRSV relative to healthy rearing pig (daily)	0.091kg	Neumann et al., (2005)

Table 2.2. Within farm demographic parameters

Event	Rate	Transition	Value
Transmission of infection to susceptible pig in batch i	$\Lambda(i)S(i)$	$S = S - 1$ $I = I + 1$	$R_{0(herd)} = 3$ $R_{0(pen)} = 2.6$ $\beta = 0.13$ $\alpha = 0.0193$
Recovery	γI	$I = I - 1$ $R = R + 1$	$\gamma = 1/20$ days
Loss of maternal immunity	πM	$M = M - 1$ $S = S + 1$	$\pi = 1/42$ days
Loss of protective immunity	ωR	$R = R - 1$ $RS = RS + 1$	$\omega = 1/252$ days
Reinfection of recovered seronegative pigs in batch i	$\Lambda(i)RS(i)$	$RS = RS - 1$ $I = I + 1$	$R_{0(herd)} = 3$ $R_{0(pen)} = 2.6$ $\beta = 0.13$ $\alpha = 0.0193$

Table 2.3. Rates of transitions between infection states in the model of PRRSV in a metaherd

2.7   Programming

The code was written in MatLab R2011b. The model code and its calling function are included in Appendix 1. Model calling The model uses the tau-leap method (Keeling and Rohani, 2007) with a leap size of 1 day due to the size of the populations in the model. Early attempts using Gillespie's direct algorithm (Gillespie, 1977) proved computationally too expensive. The epidemiological states and transitions are modelled as shown in Table 2.3. The demography was updated weekly, i.e. all batches moved up, and all movements were completed. In practice, ensuring a consistent demography (i.e. so that the herd size did not shrink or grow exponentially) was a particular problem. The simulation is particularly demanding of random number generation, and binomial, multinomial and Poisson functions for generating distribution derived random numbers were recoded for speed, mostly eliminating multiple layers of checks and code that outputs details of input error. The code was validated at each step of development. As an indication of computing requirements, a metaherd of 250 sow herds with introduced PRRSV takes 4.3 hours to run 100 times for 10000 days on a single 2.8GHz CPU.

2.8   Validation Results

2.8.1   Demography results

Figure 2.4 shows that the demography of individual herds all of 250 sows worked as it should, in that it kept the herd sizes and the subgroups within the herd sizes stable. In less than 50 weeks the overall herd size of each herd within the metaherd reached a stable point (Figure 2.4A). This time to stabilisation was required as the initial

population sizes did not account for all the demographic processes involved within each herd, for example the various levels of mortality at each rearing stage. The rearing herd population was determined by the breeding herd population (Figure 2.4 B, C) and the baseline mortality levels.
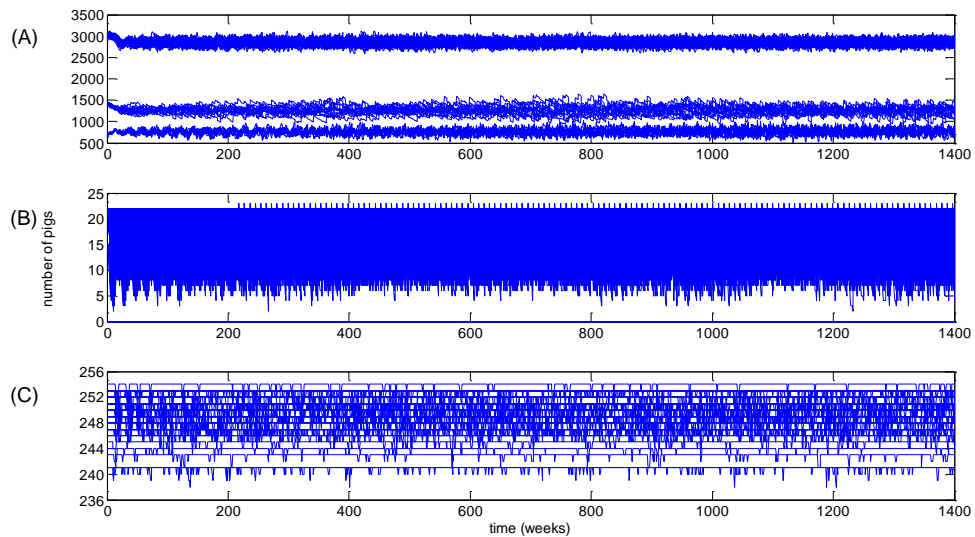
Figure 2.4. Pig numbers per herd in a metaherd of herds with 250 sows.
A. Total number of pigs per herd. B. Total number of gilts per herd. C. Total number of sows per herd. Populations remain stable when simulated with no infection.

2.8.2 Single herd results

The results of the transmission and persistence of PRRSV within a single completely susceptible herd of 250 sows are shown in Figure 2.5 given the introduction of one infectious gilt (result of one simulation only). Whilst the infection quickly faded out in the gilt group, the virus had already been transmitted to the dry sow group, and from there into the farrowing house sows and piglets. The sow herd experienced continual outbreaks followed by fadeout of infection averaging 2 outbreaks every 200 weeks. These outbreaks were driven by the endemic presence of virus in the grower and finisher herd. These subgroups were larger and thus allowed infection to persist. They were also continually supplied with new susceptible individuals from

the piglet group whilst the sow herd was replaced much more slowly, and thus were mostly in the recovered immune state. Infection was not sustained in the piglet group. There was a delay in the growing and finishing herds becoming infected, demonstrating the relatively low probability of transmission from the breeding to the rearing herd. The introduction of infection to the rearing herd may be due to transmission from the breeding herd, or an infected piglet being weaned into the rearing herd. The dry sows and finishers are two of the largest subgroups within the herd and show an epidemic peak upon first introduction of the virus.
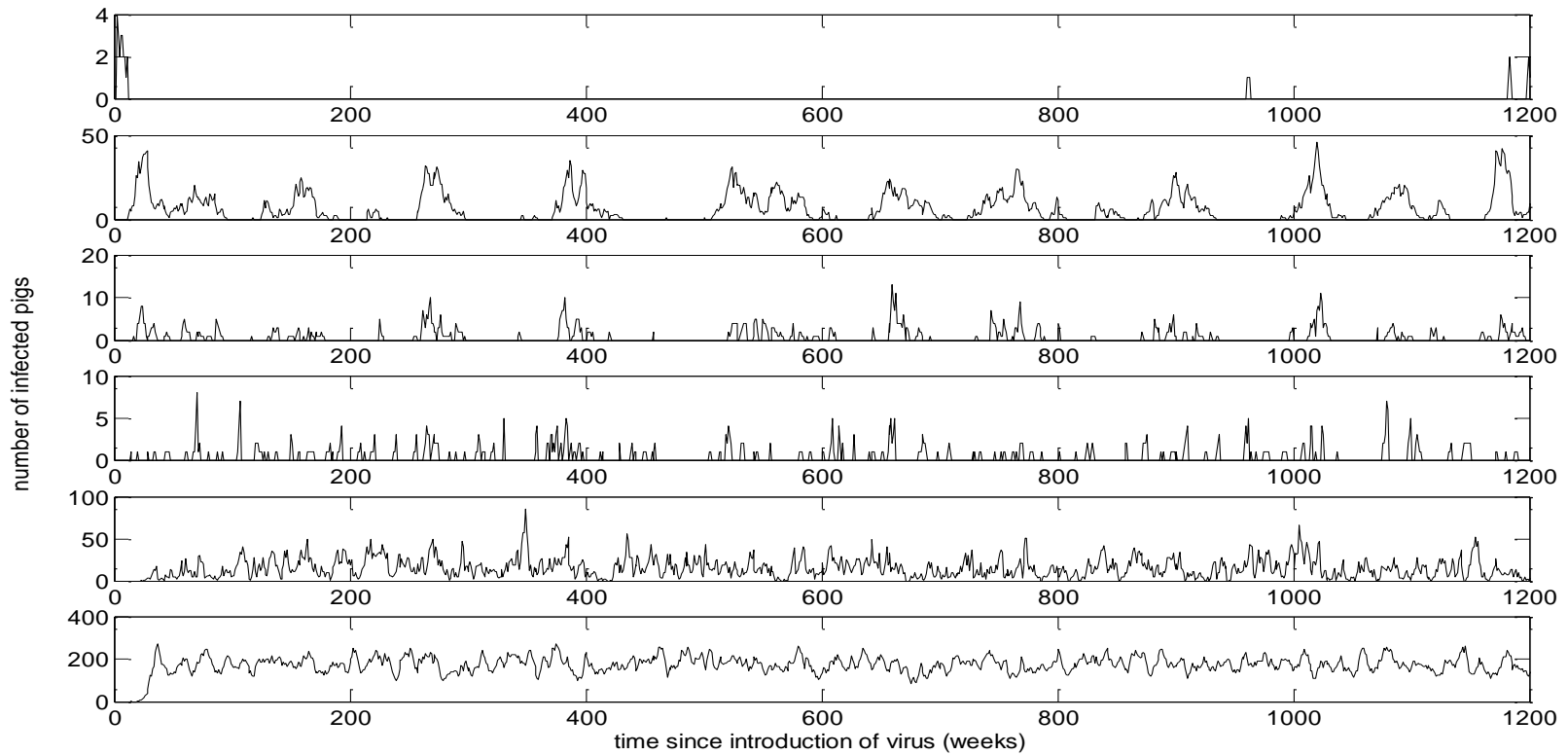
Figure 2.5. Number of infected pigs in each subgroup a herd of 250 sows.
Result of one model simulation. From top to bottom: Gilts, dry sows, farrowing house sows, piglets, growers and finishers.

As all the herds in the metaherd have 250 sows and experience no lateral infection pressure from other herds within the metaherd, similar infection dynamics are experienced by all herds (Figure 2.6). Infection moved down through the metaherd pyramid and outbreaks of infection occurred at different times within different herds (Figure 2.7). All multiplier herds had their first infectious pig present between 29 and 69 weeks, breeding herds between 93 and 653 weeks. The finishing herds had their first infectious pig present between 405 and 932 weeks after the introduction of infection to the metaherd. This first introduction of infection does not always equate to an outbreak of infection.
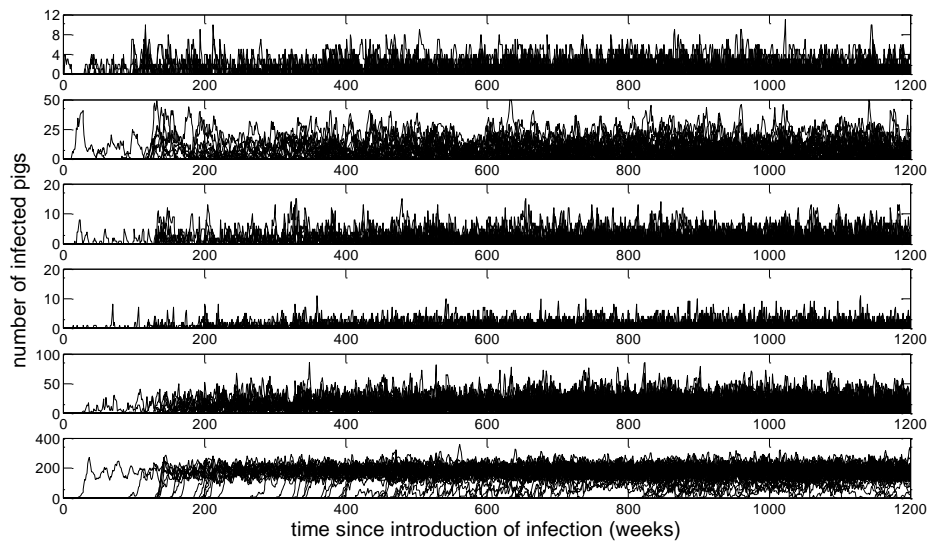
Figure 2.6. Number of infected pigs in each herd subpopulation.
Each line represents a single herd. From top to bottom: Gilts, dry sows, farrowing house sows, piglets, growers and finishers. Results of one simulation.
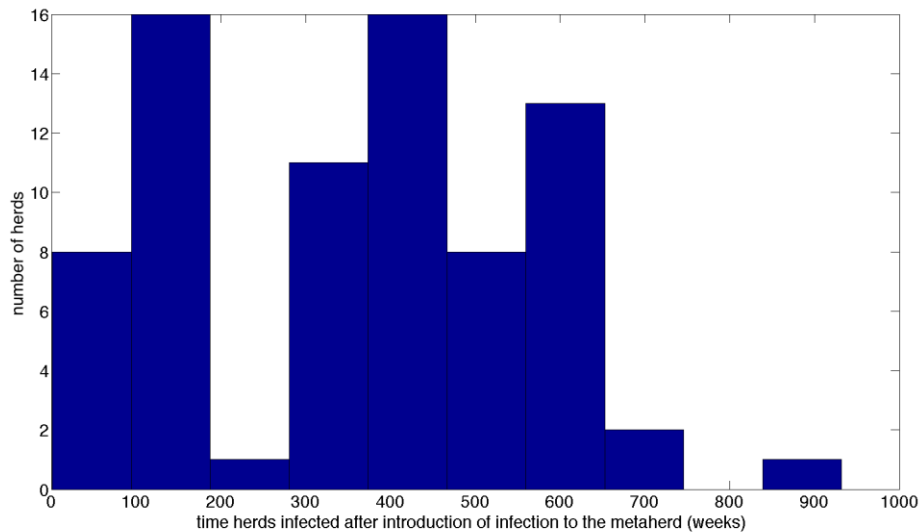
Figure 2.7. Distribution of time (after introduction of infection to the metaherd) at which infection is first present in all of the herds.
Result of one simulation.

A useful production parameter with which to measure herd performance was the number of pigs slaughtered per litter. Before infection was present the herds in the metaherd slaughtered between 7.3 and 9.6 pigs per litter with 75% of those herds slaughtering between 8 and 9 pigs per litter, the mean number slaughtered per litter was 8.4 (Figure 2.8). When infection was endemic in the metaherd production fell. The variance in the number of pigs slaughtered per litter increased, but there was an overall decrease to between 4.3 and 8.8 pigs per litter, with the mean 6.5. Those herds with higher production despite endemic infection in the metaherd had little or no infection present. The mean mass of pig produced per sow per year closely matched that of the figure the GB industry currently achieves, assuming a mean slaughter mass of 79.1kg per pig (BPEX, 2012), in the model the sows achieved 1,645kg per year (assuming no infection with PRRSV). The mean mass slaughtered per sow per year in GB was 1,671kg in 2011 (BPEX 2012).
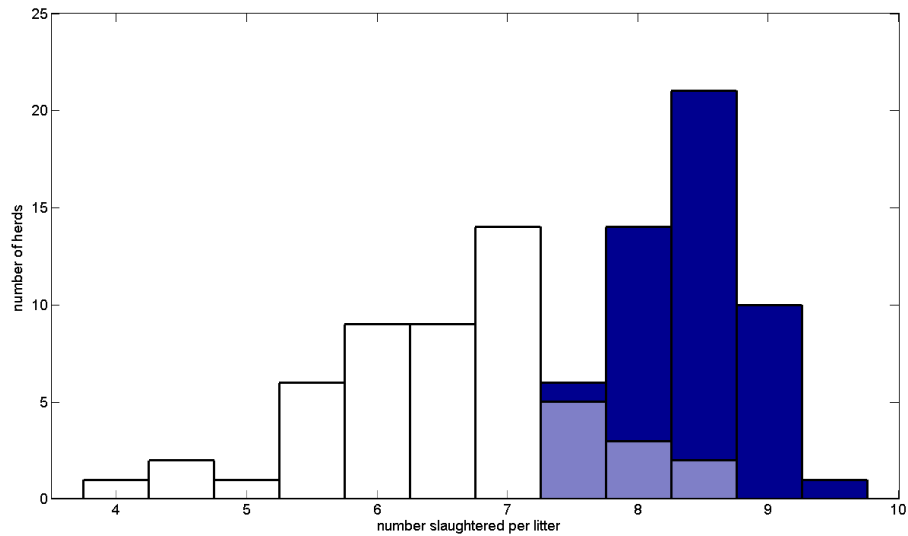
Figure 2.8. Mean number of pigs slaughtered per litter.
Breeder finisher herds only (including nucleus and multiplier herds). Blue bars are
the results from a single week before the introduction of infection. White bars are
results from a week once infection was endemic within the metaherd. Light blue
colour indicates overlap between the two distributions.

2.8.3 Metaherd level results

Of 100 simulations, infection faded out from the metaherd in 63. In the simulations
in which infection faded out, no herd other than the seeded herd had any infectious
pigs at any time. Once the finishing group of the seeded nucleus herd was infected
this herd remained endemically infected (there were always infected pigs in the
herd). Infected pigs would then be included in movements to the multiplier herds.
This explains the lack of fadeout in such simulations.

The impact of PRRSV infection on the metaherd was easily observed (Figure 2.9). It
reduced the number of pigs slaughtered per litter by approximately 24%. Before the
presence of infection within the metaherd, the metaherd mean number of pigs
slaughtered per litter ranged from 8.26 to 8.57 pigs with a mean of 8.43 across the 37
model simulations in which infection became endemic. Once infection was endemic
within the metaherd (infection was present or had been present on all herds, and the

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dynamics had reached equilibrium) the metaherd average performance decreased.

Again the variance in production increased, ranging from 6.00 to 6.87, with a mean

of 6.40 across the 37 model simulations. The averaging across herds within the

metaherd created a clear distinction between healthy metaherd production and

endemically infected metaherd production.
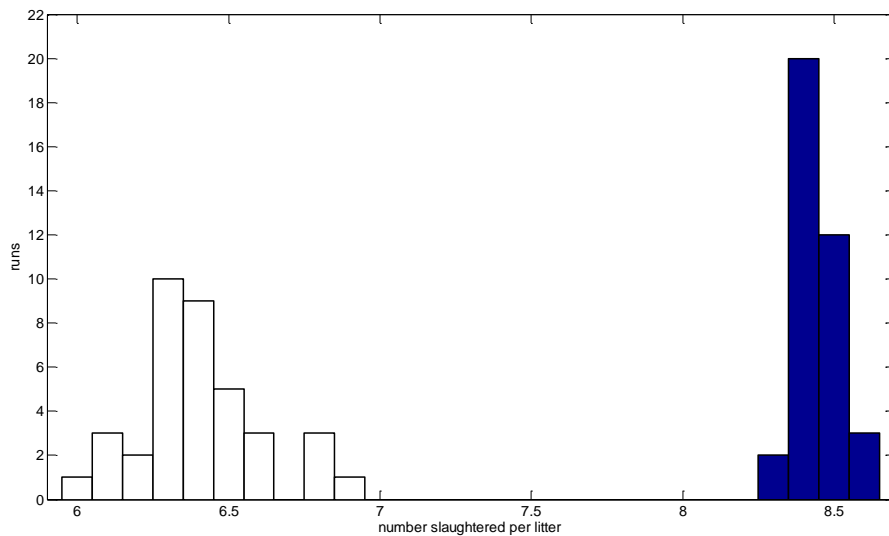
Figure 2.9. Metaherd mean number of pigs slaughtered per litter.
Breeder finisher herds only (including nucleus and multiplier herds). Blue bars are
the results from a single week before the introduction of infection. White bars are
results from a week once infection was endemic within the metaherd. Results of
model simulations which became endemically infected (37/100).

2.9   Discussion and Conclusions

In this chapter the modelling framework for PRRSV was described. This framework

was used to study the transmission dynamics of PRRSV in metaherds in later

chapters. In this chapter the model was shown to function as expected. Transmission

between groups on a farm was low according to the relative rates of transmission,

and the rate at which disease both invades and declines was in line with the

parameter values. The expected stochasticity was observed, leading to variation in

model simulations. This stochasticity captures some of the probabilistic nature of the spread of disease.

It was assumed that there was only one strain of PRRSV, or that strains are homologous, whereby pigs are immune to further infection whilst seropositive as in previous PRRSV models (Evans et al., 2010, Nodelijk et al., 2000).

The model includes the detailed age-structure of a pig herd and movements of pigs each week. Breeding farms are likely to have boars either for breeding or only using to detect oestrus in sows. For the purpose of simplicity the model does not include these boars. Nor does it allow for rearing pigs to stay beyond 24 weeks, as can occur with underweight slaughter age pigs. The pattern of infection was not expected to change given these assumptions, as they represent a small number of pigs in a large herd.

The metaherd mean number of pigs slaughtered per sow matches that of the herd level mean. However the metaherd level results fail to convey the variance in herd level production that can be seen within a metaherd without endemic PRRSV infection. Such results are important in that they show metaherd production levels may not be suitable for herd level decision making.

(Keeling and Rohani, 2007) reported that the inclusion of an 'exposed' state (between susceptible and infectious) acts to slow transmission dynamics, but that the dynamic properties are quantitatively similar to a system with an exposed state. Reports of the time after infection of the onset of clinical signs vary (Cano et al., 2009, Nielsen et al., 2002, Botner et al., 1994, Christianson et al., 1993). An exposed state was not included in the model, as the results are not based on the timing of individual epidemics.

The parameters of transmission β and α are calculated using R_0 estimates from the literature (Nodelijk et al., 2000, Charpin et al., 2012). The Nodelijk study however assumed an infectious period of 56 days. Both studies also used small samples/herds for their calculations. The R_0 calculation of 3 (Nodelijk et al., 2000) was derived using data from a herd of 115 sows, and it is not clear whether R_0 changes with herd size. In the current model, R_0 does not change with herd size.

Whilst the cross infection matrix (Table 2.1) was justifiable it was not based on data. The measurement of such relative rates in an empirical scenario would be logistically very difficult as it would require observation of many epidemics. The implication of the relative rates of transmission being inaccurate may affect the between group transmission and also influence the probability of persistence of PRRSV. That some authors have demonstrated conflicting results on PRRSV elimination (Fano et al., 2005, Dee et al., 1993) based on which herd group was controlled indicates that between group transmission might be highly variable between herds depending, for example, on the housing and staffing arrangements of individual farms.

3 Effects of herd size and metaherd structure on the spread of PRRS

3.1 Introduction

In the previous chapter, a model of PRRSV transmission was introduced. In this chapter, the model is explored in terms of different metaherd structures, the structures differ in number of source herds per herd, and herd size.. The results for homogeneous metaherds are presented initially, in respect of herd size and numbers of connections. Then results from increasingly heterogeneous metaherds are presented and the implications for PRRSV persistence and prevalence are discussed.

A metaherd analysis is necessary as it is the only way to capture the impact of each herd on another, and to observe different outcomes in each herd given its position in the metaherd compared to simulating one herd multiple times.

3.2 Materials and Methods

The infection dynamics and parameters are as described in chapter 2 as is the within herd model structure and demography. A number of different metaherd structures are used and described below.

The impact of infection of PRRSV is determined by observing the effect on the production measures. These measures outlined in chapter 2 are the mortality of

growing (4-10 weeks old) and finishing pigs (10-24 weeks old), the number of pigs weaned and then slaughtered per litter, abortions, returns to oestrus and the failure to gain weight of the rearing pigs (growers and finishers) measured at slaughter. A herd with both sows and rearing (grower and finisher) pigs will output all of these production measures. Only a herd with both sows and rearing pigs will output the number of pigs slaughtered per litter. A finishing herd will not output the number of pigs weaned and slaughtered per litter, as in a real finishing herd, the herd would not have the data on how many litters the pigs came from.

There is a difference between the metaherd outcome and the individual herd outcome. The metaherd outcome is representative of an industry perspective and does not address herd-level performance. However the results for the individual herds may highlight that different herds have different experiences and suffer different losses. In order to understand what occurs throughout the industry the difference between the metaherd results and the individual herd results is critical. This difference is the focus of this chapter.

3.2.1   Homogeneous metaherds

The metaherd structure was described in chapter 2 (Figure 2.2). The nucleus herd provided replacement gilts to six multiplier herds, each of which provided gilts to nine commercial breeding herds, a total of 54 commercial breeding herds, each of which received gilts from only one multiplier. Of these commercial breeding herds, 9 sent weaners onto 15 finisher herds. Each of the finishing herds received weaners from 3 commercial breeding herds. All of the herds in the network are the same size by virtue of having the same number of sows apart from the finisher herds whose size was determined by that of the source herd in the pyramidal structure. The spread of PRRSV and the associated production losses are compared when the number of

sows per herd was approximately 50, 100, 250 and 500, although as the model is stochastic population sizes fluctuate.

3.2.2 Metaherds of mixed herd sizes

In this experiment the structure of the metaherd remains the same, but the sizes of herds were randomly selected from a uniform distribution between 50 and 1000 sows. 54 herd sizes were randomly drawn from this distribution and used as the number of sows in the commercial breeding herds of the metaherd. The number of sows on the multiplier herds was determined by their largest destination herd to ensure adequate supply of replacement gilts to this destination. The nucleus herd is sized in the same way. Whilst the sizes of the nucleus and multiplier herds were not taken from the distribution, their size did not adversely skew the distribution of herd sizes. The size of the finishing herds within the metaherd was determined by their source herds.

3.2.3 Heterogeneously structured and sized metaherds

In this experiment a metaherd most representative of the British pig network was created by using representative herd sizes and number of source herds per herd. The metaherd was again made up of 76 herds. With the same number of each herd type as previously described.

The distribution of number of source herds per herd in Britain is taken from the pig movement data of 2007, i.e. the number of herds a single herd received pigs from directly. The metaherd is composed using the same numbers of herds as the structures in the previous experiments, therefore when sampling from the distribution to determine the number of sources per herd in the model, the distribution had to have limits that allowed this structure to work. As there is 1

nucleus herd and 6 multiplier herds the nucleus remained the sole source to the 6 multiplier herds. The number of sources to each of the commercial breeder herds however was taken from the distribution of sources from the data, except this was limited to the data between 1 and 6 sources, as these are the only possibilities in the model. The distribution of the number of sources in the pig movement data could be characterised by a lognormal distribution with parameters from the underlying normal distribution of mean 0.7663, and standard deviation 0.6338 (Figure 3.1).

The size of the herds is derived from the distribution given by (Defra, 2004), but as this output is only graphical some estimation is made. The probabilities of a herd being sized 50-99 sows, 100-199, 200-499 and 500-999 was assumed equal. The herd size probability within these boundaries was assumed to be uniform. A sample of 10000 numbers was taken from this distribution. These numbers form a lognormal distribution with parameters from the underlying normal distribution of mean 5.4653 and standard deviation 0.8883 (Figure 3.2), and a sample of 54 was taken from this distribution. These 54 numbers were rounded and used as the number of sows per herd for the 54 commercial breeding herds in the metaherd (pyramidal step below the multipliers). As the six multiplier herds need to be large enough to supply the breeding herds, the size of the multipliers is calculated given the size of the breeding herds they had to supply with replacement gilts. The same procedure was followed for determining the number of sows in the nucleus herd. The distribution of the number of sows on these 61 herds is shown in Figure 3.2.

Continuous distributions were fitted to the data in order to capture the underlying distributions from the grouped data. A fitted discrete distribution would have had the same effect, and sampling directly from the data would not have provided the small-scale variation. An alternative to the lognormal could have been used, but this is a

general distribution with well-known properties that provided a good fit to the

observations.
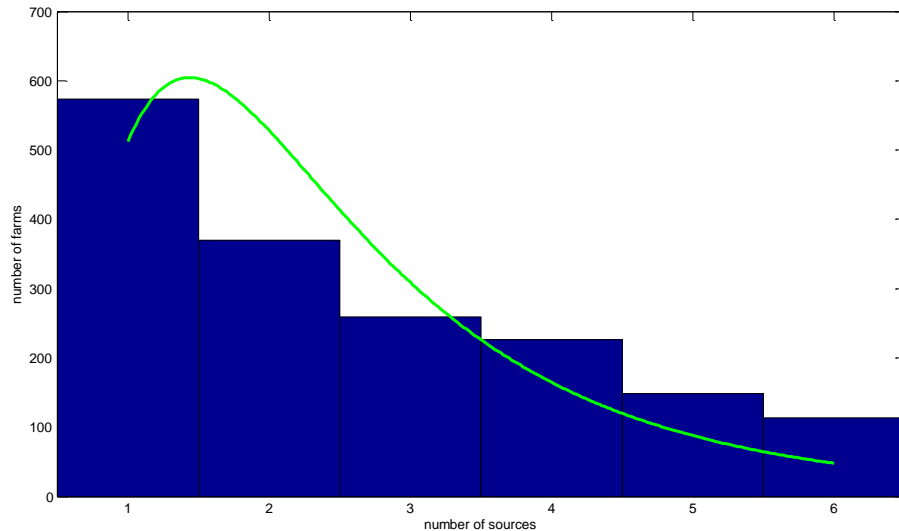
Figure 3.1. Distribution of number of sources per herd in 2007 between 1 and 6.
Blue – Number of sources taken from the movement data. Green - lognormal
probability density function with parameters from the underlying normal distribution
of mean 0.7663, and standard deviation 0.6338 fitted to the data.
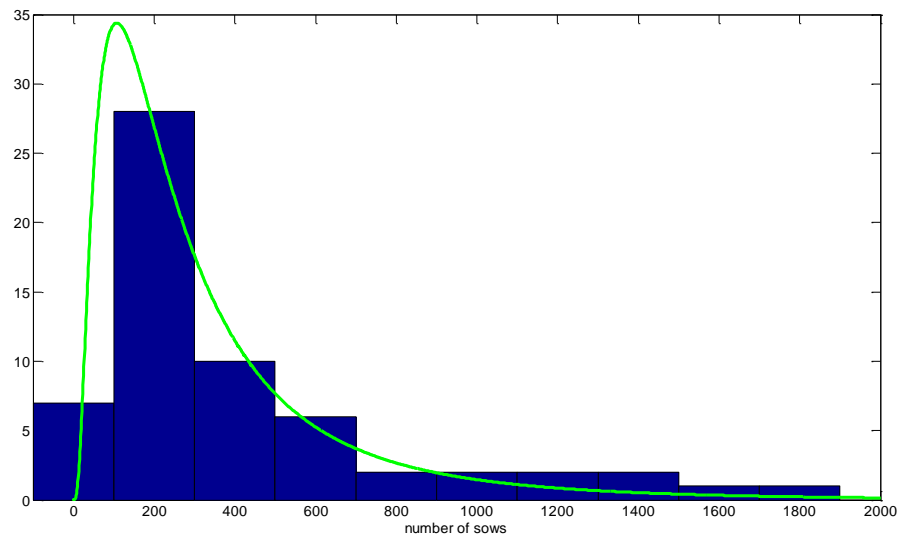
Figure 3.2. Distribution of herd sizes.
Blue – herd sizes in the model. Green - lognormal probability density function with
parameters from the underlying normal distribution of mean 5.4653 and standard
deviation 0.8883.

The number of sources per finisher herd is determined in the same way except the boundaries on the data are 1 and 9, as there is only 9 breed-wean herds in the metaherd. The samples are again taken from a lognormal distribution with parameters mean 0.9068, and standard deviation 0.7220. Breeder weaner herds are assigned at random to be the finisher sources. This links the herds into a metaherd as in Figure 3.3.
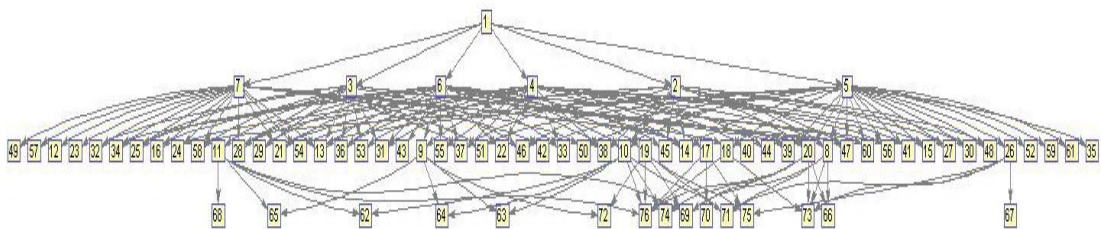
Figure 3.3. A metaherd with parameters drawn from pig movement data 2007.
Herd 1 (top) is the nucleus. Herds 2-7 (next layer) are the multipliers. Herds 8-61 are the commercial breeding herds and herds 62-76 (bottom layer) are the finish only herds. Mean breeding herd size is 420 sows.

By way of testing whether the metaherd was representative, the distribution of movement sizes (number of pigs moved) in the model were compared with the data. The distribution of herd size and number of sources dictates the size of the movements of pigs. The distribution of the size of movements of pigs in the model was a good fit to the real data (Figure 3.4).
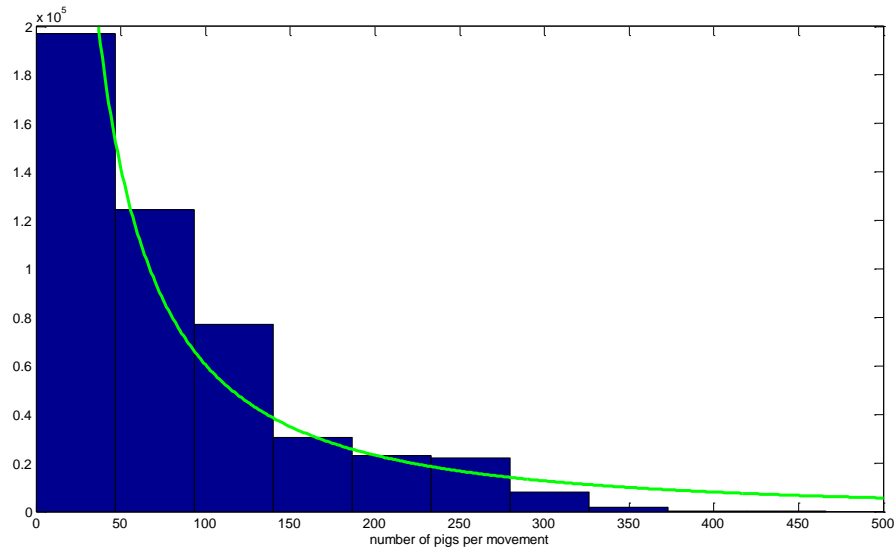
Figure 3.4. Frequency distribution of number of pigs per movement.
From the model over 8 years – Blue. The green line is the lognormal distribution
taken from the movement data of 2007 (rescaled to 8 years).

3.2.4 Seeding infection into the metaherd

Infection was seeded by adding an infectious gilt to the batch of susceptible gilts the

nucleus herd receives. All simulations were run for 10000 days, with infection

introduced after 1513 days, after demographic equilibrium had been reached. There

was no further introduction of infection. The model was simulated 100 times.

3.2.5 Combination of production measures

Analysis of a combination of production measures allows for increased

understanding of how PRRSV infection reduces herd and metaherd productivity.

However given this understanding a further measure is required to encapsulate the

previously defined production measures and output a total 'productivity'. This is

accomplished by reporting on the total mass of pig slaughtered in a fixed time frame.

This takes into account the number of failed pregnancies, and thus the number of

pigs never born into the herd, the mortality of the rearing pigs, pre and post weaning

and the failure to gain weight by rearing pigs causing them to go to slaughter

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underweight. A slaughter pig at optimum weight (not slowed by presence of infection) was assumed to be 79.1kg (BPEX, 2012). The mass of each pig slaughtered at each slaughter is simply 79.1 minus the mean underweight amount of the slaughtered batch of pigs. The total mass slaughtered is the mass of each pig slaughtered multiplied by the number slaughtered. This summed over a fixed time period gave an indication of the productivity during that time period. It is also a measure by which productivity of individual sows is used in the GB pig industry.

3.3   Results

3.3.1   Experiment 1 - Homogeneous metaherds

3.3.1.1   Metaherd level results

In 100 repetitions, when each metaherd was made up of herds of either 500, 250, 100 or 50 sows the disease faded out 47, 63, 91 and 100 times respectively. When the metaherd was made up of herds of 500 sows, 20% of the simulations that faded-out were within 7 days of introduction of virus, with the longest simulation fading out only 75 days post infection (PI). In no simulation with fadeout did infection spread from the gilt group to any other groups in the infected herd or to any other herds. When the metaherd was made up of herds of 250 sows, 54% of the simulations that faded-out were within 14 days PI, with the longest simulation fading out 102 days PI. In 5% of simulations virus was present in other subgroups of the herd (not gilts) before fading out of the herd and thus the metaherd completely. When the metaherd was made up of herds of 100 sows, 50% of the simulations that fadeout do so within 21 PI. The longest simulation faded out 5678 days PI. In this simulation infection spread to all 6 multiplier herds. This event was unlikely as when virus spread to other groups within the nucleus herd and to other herds fadeout was not seen in any

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other simulations. The second longest simulation faded-out after only 226 days, with infection never having spread from the nucleus herd. When the metaherd was made up of 50 sow herds, 100% of simulations faded out, and 53% were within 14 days of introduction of virus, with the longest simulation fading out 671 days PI. In 6% of these simulations, the infection spread to other groups of pigs in the inoculated herd.

Metaherd level results of 100 simulations per metaherd showed little variability. Figure 3.5 shows mean finisher mortality across the metaherd for all 100 simulations. Finisher mortality is a key production measure. The finisher mortality as a percentage of the finisher population increased with the size of herds in the metaherd. The non-infection mortality baseline was 3.2%. In a metaherd of herds with 500 sows average finisher mortality rose to approximately 8% when infection was endemic, whilst metaherds of herds with 250 and 100 sows rose to approximately 7 - 8% and 3.5% respectively. There was a slight decrease in variability between simulations as the herd sizes increased. All production measures at the metaherd level had similar low variability between simulations. This indicates that a single simulation in which infection becomes established is representative of all other simulations in which infection becomes established.
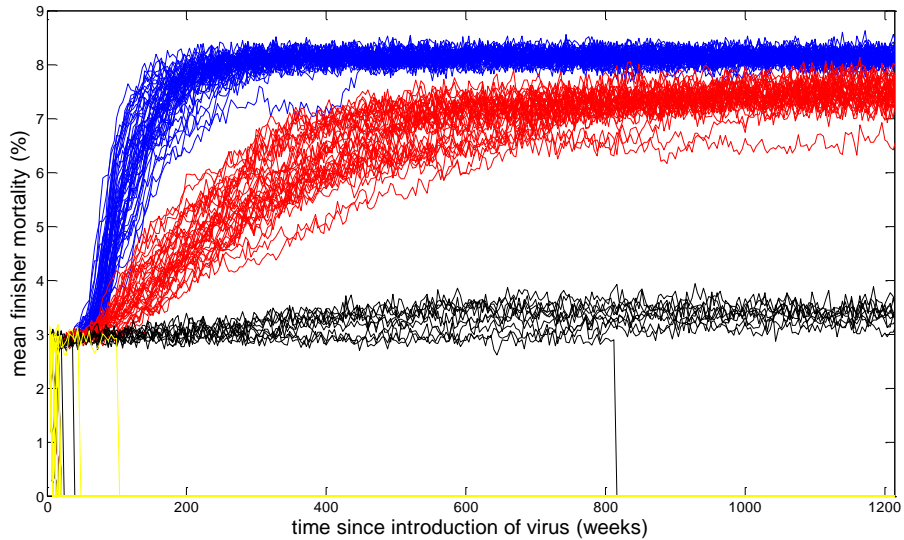
Figure 3.5. Mean finisher mortality across the metaherd from 100 simulations.
Blue herds with 500 sows. Red herds with 250 sows. Black herds with 100 sows.
Yellow herds 50 sows (showing 0% mortality due to simulations ending when
infection faded out). Fade out occurred soon after introduction of virus. Therefore
the simulations in which fadeout occurred are seen only as lines dropping to zero on
the far left of the graph.

When infection was endemic the mean amount underweight was approximately

1.4kg per pig in a metaherd of herds with 500 sows (Figure 3.6A). When the

metaherd was of herds with 250 and 100 sows, and infection was endemic the mean

underweight at slaughter was approximately 1.3kg and 0.08kg respectively.

The mean number of pigs slaughtered per litter without infection in the model was

7.4. In metaherds of herds with 500, 250 and 100 sows the mean number of pigs

slaughtered per litter was 5.7, 5.7, and 7.2 respectively (Figure 3.6B). The metaherd

with herds of 500 sows took approximately 200 weeks to reach this endemic level,

however the metaherd with herds of 250 sows took approximately 900 weeks to

reach endemicity.

The grower mortality without infection in the model was 2.7%. The mean mortality

in growing pigs when the metaherd was of herds with 500, 250 and 100 sows when

PRRSV infection was endemic was 4.3, 4.3 and 2.8% respectively of the grower population (Figure 3.6C).

The mean abortion rate when infection was endemic in the metaherds of herds with 500 and 250 sows was 0.5 and 0.32% respectively. When the metaherd was made up of herds with 100 sows, abortions occurred as infrequent one off events (Figure 3.6D).

The mean returns to oestrus rate when infection was endemic in the metaherds of herds with 500, 250 and 100 sows was 16.6, 16 and 14.5% respectively (Figure 3.6E). The rate of returns to oestrus without infection in the model was 15%, therefore the mean value in the metaherd with herds of 100 sows was not discernably lower, and this could simply be stochastic variation. Also a herd of 100 sows was small for the model's herd structure, given that only 4 or 5 sows were farrowing per week.

The mean number of pigs weaned per litter when the metaherd was of 500 sow herds decreased to 8 when PRRSV was endemic. When the metaherd was made up of 250 sow herds, it decreased to 8.2. When the metaherd was made up of 100 sow herds, the number weaned per litter did not to decrease from a baseline mean of 8.5 (Figure 3.6F).
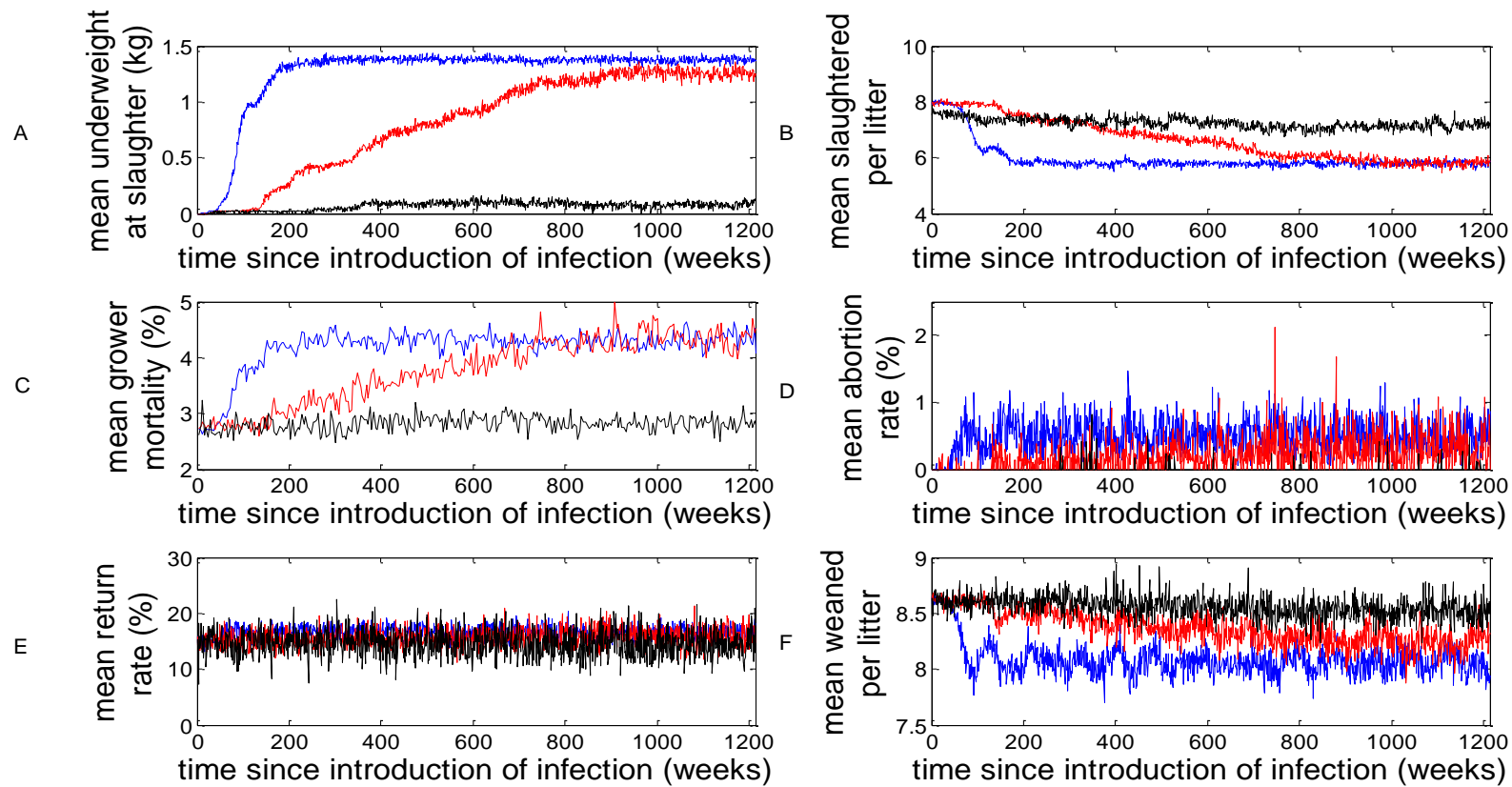
Figure 3.6. 6 Production measures shown at the metaherd level.
Each line represents a single simulation. Blue is metaherd of herds with approximately 500 sows. Red is metaherd of herds with approximately 250 sows. Black is metaherd of herds with approximately 100 sows.

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3.3.1.2 Production measures herd level results – herds of 500 sows

Here the results of the impact on production by endemic PRRSV infection are presented at the herd level in herds with 500 sows. These results differ from the metaherd level results in showing the effects that individual herds can experience within the metaherd.

As infection moves down the metaherd pyramid, outbreaks occurred at different times in different herds, thus the effects of the presence of infection began at different times. In one simulation, the outbreak started in different herds between 28 and 404 weeks after introduction of virus (using an increase in finisher mortality as a signal of the outbreak). The outbreak beginning at 404 weeks was in a breeding herd, but infection was first present in the herd 56 weeks after introduction of virus to the metaherd. The infection did not spread from the isolated gilts on the herd and faded out. Infected pigs were then continually introduced and infection continued to die out until week 382 when infected gilts moved into the sow house. From there the infection spread throughout the herd until increased losses in the finishers were seen after 404 weeks. This highlights that it is possible that the relative isolation of incoming gilts can prevent the spread of infection to the rest of the herd, but that continual introduction of infected gilts increases the probability of infection.

Figure 3.7 shows the frequency distribution of herd outcomes in a single simulation at one time point when the metaherd was endemically infected. The mean metaherd level of failure to gain weight was 1.4kg. At an individual herd level, there was modal result of 1.6kg, whilst 79% of breeder finish herds had loss between 1.4 and 1.6kg per pig (Figure 3.7A). This distribution had a left skew, with the one breeder finisher herd experiencing only 0.9kg loss per pig at slaughter. The finisher only herds suffered less loss of mass per pig at slaughter. With losses between 0 and

1.5kg, 60% of results falling between 0.9 and 1.3kg underweight per pig at slaughter. When the metaherd was endemically infected, the breeding herds maintained a mean of 1.4kg underweight per pig at slaughter through time (Figure 3.8A), whilst a single breeding herd oscillated frequently between 1.1 and 1.7 kg. The mean of the finishing only herds oscillated between 0.3 – 1.3kg, a single herd oscillated between losses of zero and 1.5kg underweight per pig at slaughter.

The number of pigs slaughtered per litter ranged from 4.2 to 7 when the metaherd was endemically infected with a modal value of 6.2 (Figure 3.7B). Only 4% of breeder finisher herds had less than 4.8 slaughtered per litter. During the epidemic period, one herd drops to only 3.8 pigs slaughtered per litter for a single week. During the endemic period a single herd's results mostly oscillated between a 4.3 and 8.5 pigs slaughtered per litter (Figure 3.8B).

The modal growing pig mortality was 4% in the breeder finisher herds, with a distribution between 2 and 7% (Figure 3.7C); 85% of breeder finisher herds had grower mortality of 3.25% or higher. The finisher only herds had a distribution of grower mortality between 2 and 4.5% Given that some distribution about the mean baseline is to be expected, metaherd infection with PRRSV may have little or no impact on the mortality levels in the finisher only herds. Through time when PRRSV infection was endemic within the metaherd a single breeder finisher herd experienced grower mortality between 3.4 and 6.4% (Figure 3.8C). One finisher only herd experienced grower mortality between 1.6 and 6.2% through time when the metaherd was endemically infected.

When PRRSV infection was endemic in the metaherd, finisher mortality increased. Finisher mortality was 3.2% in the model without PRRSV infection. Figure 3.7D

shows that breeder finisher herds had finisher mortality between 8 and 11%, with a modal value of 9.5%, whilst finisher only herds had finisher mortality between 4 and 8%, with one herd also experiencing mortality at 10.5%. Only 2 finisher only herds had mortality equal to or more than the lowest finisher mortality in the breeder finisher herds. Through metaherd PRRSV endemically infected time a single breeder finisher herd had finisher mortality that ranged from 7.5 to 11.5% (Figure 3.8D), whilst the finisher mortality in a finisher only herd was much more variable, ranging from 2.8% (baseline levels) to 10.8%. An obvious epidemic peak was observed in the finisher mortality of a single finisher only herd, followed by a period of time in which finisher mortality was mostly at the baseline level before then rising to epidemic like levels of mortality (Figure 3.8D).

Only 5 breeder finisher herds experienced PRRSV related abortions (up to 6%) (Figure 3.7E). The other herds show that no abortions occurred during the observed week. At this time point, no breeder weaner herds experienced any abortions. However abortions did occur in the other breeding herds, but they occurred sporadically (Figure 3.8E). The metaherd level results show that abortions remain present at a low level. The mean over time for breeding herds is 0.5%. However a single herd experiences sporadic outbreaks of abortion up to 15.8% interspersed with periods of no abortion. The averaging across all herds disguises this in the metaherd level results.

Returns in the breeder finisher herds ranged from 0% to 35% (Figure 3.7F). The modal value appeared to be at the baseline non infection level of 15%. The same pattern of results was seen in the breeder weaner herds. Suggesting that once infection is endemic, herds do not experience many returns to oestrus caused by infection. Metaherd level returns oscillated between approximately 10 and 19%.

However the returns for a single herd over time oscillate between 0 and 50% when infection is endemic within the metaherd (Figure 3.8F).

The distribution of pigs weaned per litter in breeder finisher herds was left skewed with a modal value of 10 (Figure 3.7G). The distribution ranged from 7 to 11, however only 6% of breeder finisher herds had less than 8.5 weaned per litter in the observed week when infection was endemic within the metaherd. The fewer breeder weaner herds had a similar distribution (Figure 3.7G). The modal value was the figure weaned per litter without PRRSV infection in the model, suggesting that the presence of endemic PRRSV infection does not have a negative effect on this measure in some herds. However over time (Figure 3.8G) a single herd mostly weans between 7.3 and 10.5 pigs per litter. However during the epidemic phase the herd weaned only 6.3 pigs per litter. Production decreased to this value infrequently during the endemically infected period too.

Figure 3.7. Frequency distributions of production measures per herd at 1000 weeks PI for 1 simulation of a metaherd of herds with 500 sows.
The y axis is number of herds in the metaherd. The blue bars represent breeder finisher herds, the white bars represent breeder weaner herds, and the red bars represent finisher only herds. Bars appear lighter blue where blue and white overlap, and purple where blue and red overlap.
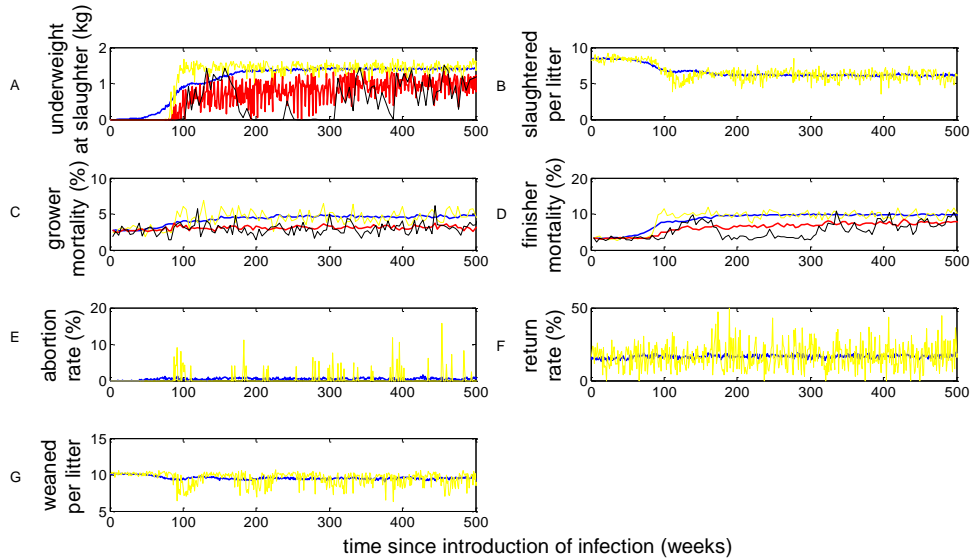
Figure 3.8. Production measures over time from the same simulation as Figure 3.7.
The x axis is time since introduction of virus to the metaherd in weeks. The thick blue line is the mean of all breeding herds. The thin yellow line is 1 breed finish herd. The thick red line is the mean of all finish only herds. The thin black line is 1 finish only herd.

3.3.1.3 Production measures herd level results – herds of 250 and 100 sows

Figure 3.9 shows the frequency distribution of production measures for a single simulation of herds with 250 sows and 100 sows in one week during which infection was endemic in the metaherd.

The metaherd mean underweight at slaughter for a metaherd of herds with 250 sows was 1.3kg. However at an individual herd level, herds were between 0 and 1.8kg underweight per pig at slaughter (Figure 3.9A). The modal value was 1.5kg. The lower metaherd mean can be attributed to the herds whose pigs at slaughter were not underweight at all. 87% of the herds had between 0.75 and 1.8kg loss. One herd over time once infected ranged between 0.7 and 1.8kg underweight at slaughter (Figure 3.10A). This contrasts with the results for a metaherd of herds of 100 sows. Here all but 5 herds had no underweight pigs at slaughter in the frequency distribution (Figure 3.9A). Two herds' pigs recorded pigs underweight by more than 1kg in the analysed week. However once a herd with 100 sows became infected, pigs went to slaughter between 0 and 1.7kg underweight (Figure 3.10A).

The number of pigs slaughtered per litter for a metaherd of herds with 250 sows ranged from 5 to 9 with a modal value of 6 (Figure 3.9B). Only 4% of herds slaughtered 8 or more per litter in the assessed week. Figure 3.10b shows that once PRRSV is endemic a single herd slaughters between 2.9 and 8.4 pigs per sow. This suggests that the herds with low numbers of slaughters per litter seen in Figure 3.9B were likely experiencing an infrequent dip in production rather than consistently low output. The number of pigs slaughtered per sow for a metaherd of herds with 100 sows ranged from 3 to 9.5 (Figure 3.9B). 77% of the herds however slaughtered 8 or more per litter, this level of production is the same as if no infection is present. Over time in an endemic metaherd a herd of 100 sows slaughters between 0 and 10.7 pigs

per litter. The zeros are caused by 100 sows not fitting the herd structure well. The stochastic nature of the model means that it is possible that only one sow could be farrowing in a week. Should that sow have poor reproductive performance followed by high mortality in the surviving litter, then the herd can appear to slaughter zero pigs per litter based on only one litter.

The distribution of grower mortality levels in a metaherd of herds with 250 sows is spread between 2 and 8% (Figure 3.9C). 2.7% is the baseline level of mortality and those herds around and below this level are experiencing normal levels of mortality. 64% of herds had grower mortality of 4% or less. The modal level is between 2.5 and 4.5%. This is a slight rise above the baseline however some of these herds may not have been suffering infection induced mortality and the increase is attributed to the probabilistic nature of mortality. Over time, one infected breeder finish herd experienced grower mortality as low as 2.3% and as high as 9.6% (Figure 3.10C). The distribution of grower mortality levels in a metaherd of herds with 100 sows is between 1 and 5.8%. 85% of all herds have mortality less than 4%. Over time a breeder finisher herd had grower mortality ranging from 1.3% to 10.2% (Figure 3.10C) whilst the metaherd was endemically infected with PRRSV.

When PRRSV was endemic in the metaherd finisher mortality within the herds of 250 sows in a metaherd was between 2 and 13% with a modal value of 9% (Figure 3.9D). Baseline mortality without infection was 3.2%. 86% of herds had mortality more than 4%. Finisher mortality over time in a breeder finish herd oscillated between 6.5 and 13% (Figure 3.10D). Finisher mortality in a metaherd of herds with 100 sows ranged from 1 to 7%, though one herd recorded 12% in the analysed week (Figure 3.9D), the modal value was 3%, signifying no deviation from the baseline uninfected mortality values. Over the time a breeder finisher herd of 100 sows

experienced finisher mortality between 5 and 13% once endemically infected with PRRSV (Figure 3.10D). The outbreak and subsequent fadeout after 424 weeks endemically infected in the breeder finisher herd with 100 sows is apparent in Figure 3.10D.

When PRRSV infection was endemic in a metaherd of herds with 250 sows, one herd experienced abortion of approximately 6% (Figure 3.9E). All other herds were free from abortion in the analysed week. Figure 3.10E however shows that over time an individual herd was likely to experience outbreaks of abortion. During these outbreaks abortion rose to approximately 7-8% on most occasions, sometimes reaching as high as 18%. In these small outbreaks, abortion did not appear to occur in consecutive weeks, often with a week or more of zero abortion before abortion was recorded again. All the herds in a metaherd of herds with 100 sows experienced zero abortion (Figure 3.9E, Figure 3.10E).

The distribution of returns to oestrus in a metaherd of herds with 250 sows per herd was spread between 0 and 40% (Figure 3.9F). However only 1 herd had returns above 35%. The non-infection baseline level of returns was 15%, only 48% of breeding herds had returns over 15%, and only 16% of herds had higher than 25% returns. Due to the probabilistic nature of the event, those herds with up to 25% returns could be experiencing normal production without PRRSV infection. A single breeder finisher herd through time had returns which oscillated about 15%, suggesting increased returns due to infection with PRRSV occurred rarely (Figure 3.10F), however returns did rise as high as 55% for single weeks, on one occasion reaching 66%. The distribution of returns to oestrus in a metaherd of herds with 100 sows per herd was spread between 0 and 70% (Figure 3.9F). However the distribution had a right skew and the modal value was 0% with 46% of herds having

zero returns. Only one herd had returns higher than 55%. The returns for a single herd oscillated frequently between 0 and 50%, occasionally reaching 100% (Figure 3.10F).

For a metaherd with herds of 250 sows, the number of pigs weaned per litter ranged from 7 to 10.5 (Figure 3.9G) across the breeder finisher herds. Figure 3.10G shows that once PRRSV infection was endemic within the herd, production fell to approximately 5.9 pigs weaned per litter, and continued to show increased variability. The decreases occurred in outbreaks, with normal numbers weaned per litter between, showing that even once PRRSV is endemic within a herd, the herd could still have high output, in some weeks weaning 11 pigs per litter. Herds in a metaherd of herds with 100 sows weaned between 8.5 and 11 pigs per litter, although one herd weaned only 7 (Figure 3.9G). When a breeder finisher herd of 100 sows was endemically infected, the number of pigs weaned per litter increased in variability through time (Figure 3.10G). The number weaned per litter frequently decreased to 5, and slightly less frequently to 0.

The number weaned and slaughtered per litter and the rate of returns took extreme values when the herd had only 100 sows due to the small subgroups (pens) of sows farrowing per week in the herd. Returns were determined by randomly sampling from a distribution with a small sample, and expressing the results as a percentage. Returns and mortality meant that pens could become empty, and therefore there were no births in that pen's week to farrow, and subsequently no pigs weaned or slaughtered in the respective weeks.
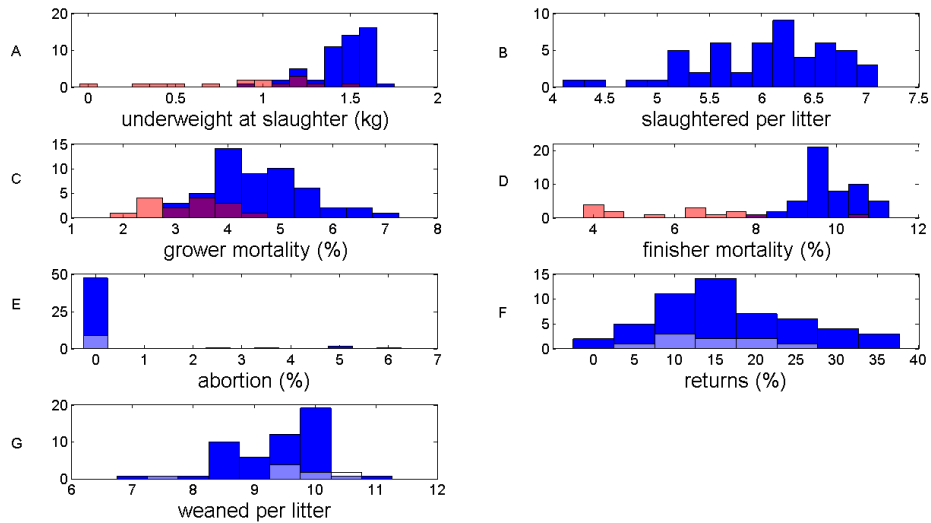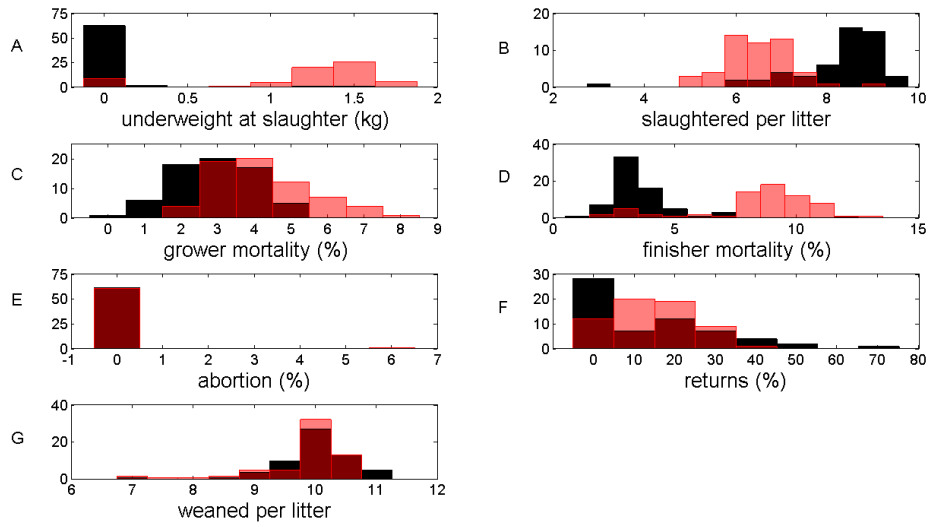
Figure 3.9. Frequency distribution of production measures per herd.
At 1000 weeks PI for single simulations of metaherds of herds with 250 sows (Red), and 100 sows (black). Overlap of the distributions is shown as a much darker, burgundy colour.
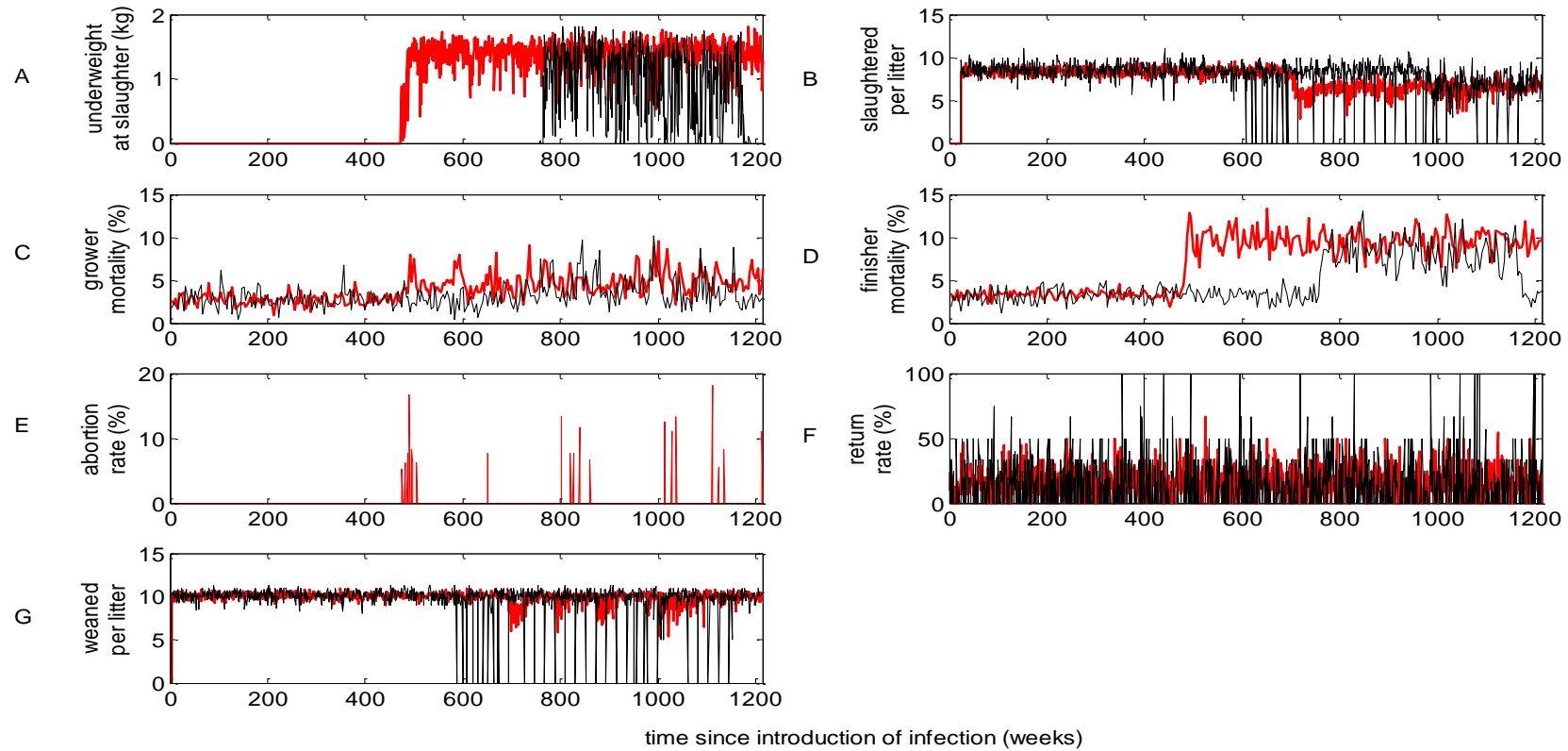
Figure 3.10. Production measures over time.
The x axis is time since introduction of virus to the metaherd. The red line is the result of one breeder finisher herd with 250 sows. The black line is the result of one breeder finisher herd with 100 sows.

3.3.2 Experiment 2 - Metaherds of mixed herd sizes

In a metaherd of herds with a mean of approximately 300 sows per herd, of 100 simulations the infection faded out 44 times.

As the metaherd is made up of differing size herds, there existed smaller herds that received pigs from larger herds. Larger herds were able to sustain infection, and therefore it is possible that small herds had continual introduction of infected pigs.

When the metaherd was endemically infected, PRRSV infection did not persist in all herds. Figure 3.11 shows the number of weeks each herd had an infectious pig present over a 5 year period (260 weeks) during which PRRSV was endemic within the metaherd. The number of weeks with at least one infectious pig present was calculated by adding the number of weeks each of the six subgroups had an infectious pig present and dividing that total by 6 (For breeder weaner herds, this total was divided by 4). The number of infected weeks increased with herd size. The variance across simulations decreased with herd size. Herds with less than 200 sows experienced differing outcomes in each simulation. A herd with 189 sows shows bimodal results. The higher points representing that PRRSV infection was likely endemic within some groups in the herd for a period of time within the analysed five years. The lower points representing simulations in which infection never persisted, but faded out after each re-introduction of infection. The herd with 231 sows showed slightly different dynamics than those with less than 200 sows in that in a greater proportion of simulations the herd became endemically infected. However in a small number of simulations, recurrent fadeout did occur. In one simulation only 20% of the time was there infected pigs in the herd. Herds with less than 100 sows had less than 5% of the time period with infected pigs. PRRSV could not persist in herds of this size. Breeder weaner herds experienced less time infected with PRRSV. A herd

of 336 sows had only 'partial' PRRSV persistence. In the worst simulation the herd

was infected only 52% of the time infected, and in the best simulation only 15% of

the time infected. A breeder weaner herd with 630 sows ranged from 31 – 71% of

the time infected, whilst a similarly sized (651 sows) breeder finisher herd was

infected 68 – 86% of the time.
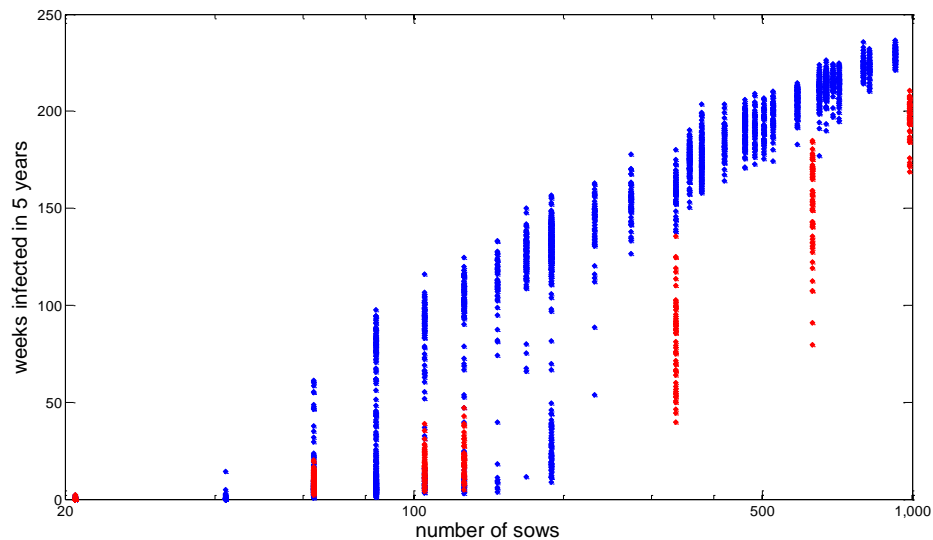
Figure 3.11. The number of weeks herds were infected in a 5 year period of metaherd PRRSV endemicity.
Blue are breeder finisher herds. Red are breeder weaner herds. All simulations in which infection did not fadeout from the metaherd (56/100) are shown.

Given the apparent change in dynamics of infection when a herd has more than 250

sows, the results were analysed grouping herds into groups with more or less than

250 sows. Herds with >250 sows are referred to as 'large'; those with ≤250 are

referred to as 'small'. When PRRSV infection was endemic, the mean amount of

weight not gained was 1.35kg per pig in the large herds and between 0.45 and 0.65kg

per pig in the small herds (Figure 3.12 A). The mean amount underweight in the

finisher herds ranged from 0.03 to 1.15kg, oscillating about a mean of 0.49kg.

The mean number of pigs slaughtered per litter was approximately 6 in the large herds and 7.5 in smaller herds (Figure 3.12 B). Even with averaging across herds, the larger herds suffered an epidemic peak, where the mean number slaughtered per sow fell to 5.8, whilst the smaller herds did not show an epidemic peak when averaging across the herds. Baseline grower mortality (with no PRRSV infection) was 2.8%. Mean grower mortality ranged between 4.4 and 5% with a mean over (endemic) time of 4.7% in the larger herds, and 2.8 – 4% with a mean of 3.4% in the smaller herds (Figure 3.12 C). Mean grower mortality in finisher herds was 3% but ranged from 2.5% to 4.1%. Baseline finisher mortality (with no PRRSV infection) was 3.2%. Mean finisher mortality was 9.9% in the larger herds, 5.9% in the smaller herds and 5.6% in the finisher herds. Mean finisher mortality was stable over time when endemically infected with PRRSV (Figure 3.12 D).

Mean abortion levels were between 0.1 and 1.9% in the large herds, oscillating frequently about a mean of 0.5% (Figure 3.12 E). Larger herds experienced an epidemic peak of abortion, rising to 2.7% 72 weeks after introduction of infection to the metaherd. For smaller herds the mean was 0.07%, whilst ranging from 0 to 1.5%.

Mean level of returns to oestrus were 13.6 to 19.9% with a mean over time of 16.8% for large herds (Figure 3.12 F). Results ranged between 4.9 and 25.9% with a mean of 12.7% for small herds.

The mean number of pigs weaned per litter was 9.5 in large herds and 10 in small herds (Figure 3.12 G). Mean number slaughtered per litter was stable over time when endemically infected with PRRSV.

As with the homogeneous metaherds the results over 100 simulations at the metaherd level showed little variability.
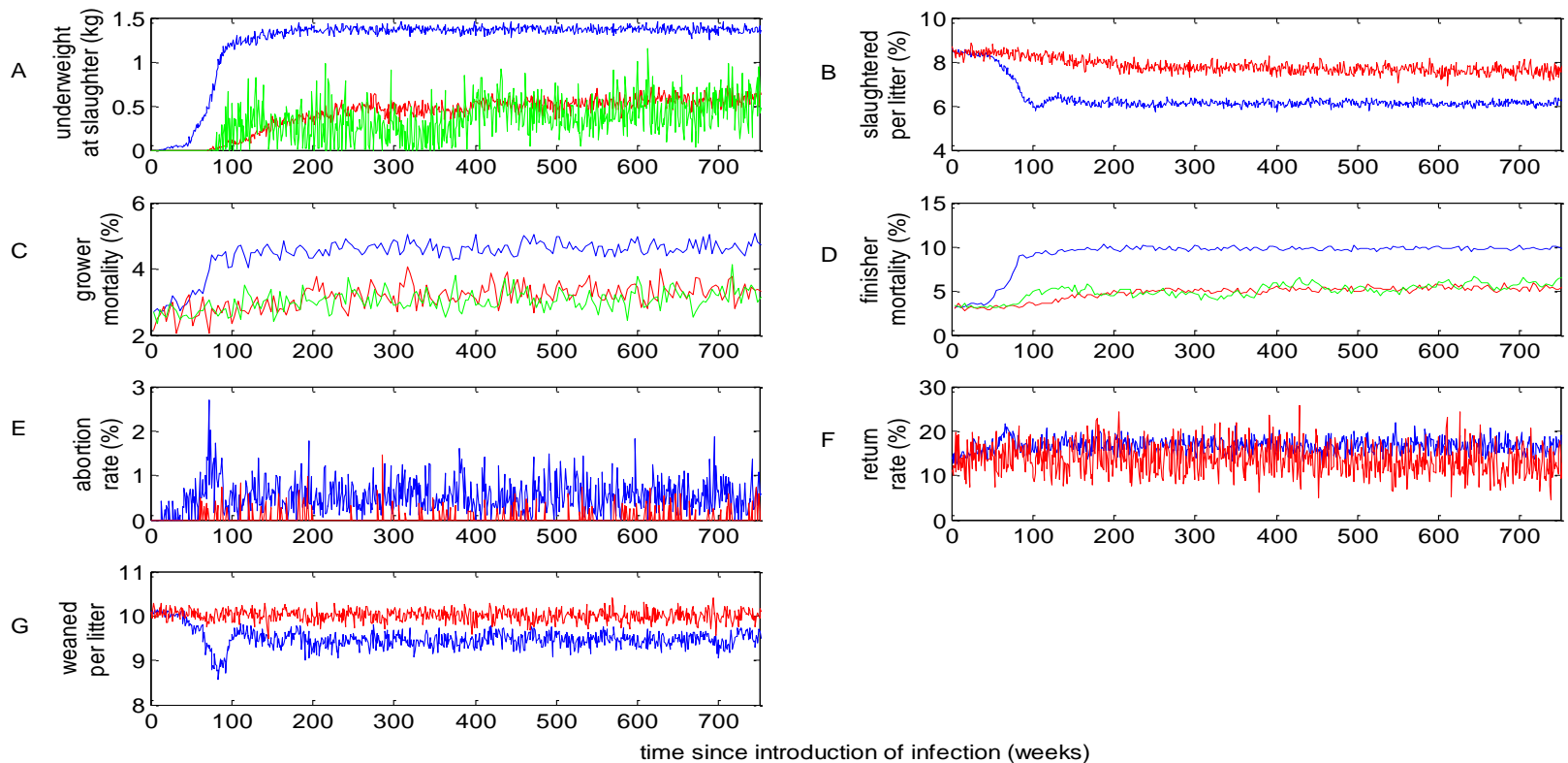
Figure 3.12. Mean of production measures across differently sized herds after metaherd infection with PRRSV.
Blue: Mean of herds with 250 sows or more. Red: Mean of herds with less than 250 sows. Green: Mean of finish herds. Results of one simulation in which the metaherd was endemically infected with PRRSV.

3.3.3 Experiment 3 - Heterogeneously structured and sized metaherds

3.3.3.1 Comparison of different metaherds with same parameter values

Model simulations of different metaherds generated with the same number of herds and from the parameter values described demonstrated whether the exact structure of a metaherd is important to the dynamics of PRRSV or whether the general characteristics of the metaherd (the given parameter values) alone define the dynamics of PRRSV in the metaherd.

Figure 3.13 shows the frequency distribution of the seven production measures previously described at the herd level across three metaherds generated from the same parameter values. The distributions from the three metaherds can be seen to be indistinguishable from each other, with the same variance and distribution shapes. As results at the herd level are indistinguishable, it follows that metaherd level results are similarly indistinguishable as the metaherd results are the result of the herd level results. Figure 3.13 shows one simulation result of each metaherd only, however results have already shown that multiple simulations produce similar results.

As results did not differ between the representative metaherds generated, exact metaherd structure was not important in the dynamics of PRRSV within the metaherd. Metaherds with the same distribution of herd sizes, source herds and size of movements produced the same effects when infected with PRRSV.
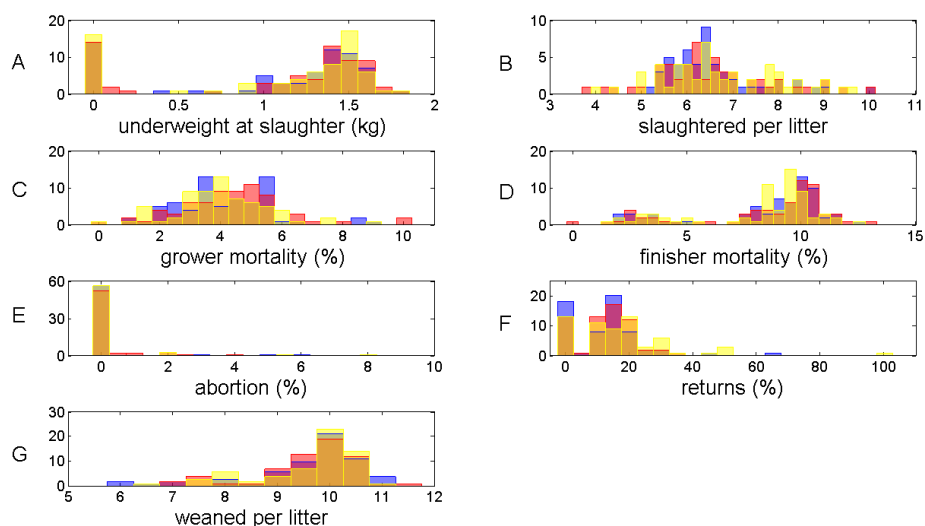
Figure 3.13. Distribution of herd level outcome at 1000 weeks PI.
Blue, red and green distributions represent the 3 different representative metaherds.

3.3.3.2 Results of a single representative metaherd

When PRRSV infection was endemic in the metaherd, the mean underweight at slaughter across the metaherd was between 1 and 1.2kg per pig. The mean number of pigs slaughtered per sow was between 5.4 and 6.3. The mean grower mortality was between 3.9 and 4.9%. Mean finisher mortality was between 8.9 and 9%. Mean abortion levels were between 0.04 and 1.3%. Mean level of returns to oestrus were between 10 and 21.2%. The mean number of pigs weaned per sow was between 7.9 and 8.7.

Figure 3.14 shows the frequency distribution for a single simulation of the representative metaherd. Herds with 250 sows or less in the metaherd are defined as small; herds with more sows are defined as large. Large breeder finisher herds sent pigs to slaughter between 0.5 and 1.75kg underweight with a modal value of 1.5kg (Figure 3.14A). Only 6% of these herds were less than 1kg underweight in the analysed week. The slaughtered pigs of small breeder finisher herds were less

underweight than the larger herds, having a distribution between 0 and 1.6kg per pig slaughtered, and a mode of 1.35kg. 29% of these herds were not underweight at all in the analysed week. The finisher herds sent pigs to slaughter 0 to 1.45kg underweight, where the modal value was 0. 53% of herds sent pigs to slaughter zero underweight in the analysed week, but 33% of finisher herds were between 1.2 and 1.45kg underweight at slaughter.

The number of pigs slaughtered per litter in the large breeder finisher herds was between 5 and 8 (Figure 3.14B) with a modal result of 6 - 6.5. The results of the small breeder finisher herds were more varied, distributed between 5.6 and 10.1 with a mode of 7. This captured herds which were slaughtering as many pigs as they would if there was no infection present. Despite PRRSV infection being endemic in the metaherd, these herds likely were not infected in the analysed week.

Grower mortality in the large breeder finisher herds ranged from 3 to 6% (Figure 3.14C). The mortality was less overall but more varied in the small breeder finisher herds, with a distribution between 1 and 9%, with a mode of 2-3% which matches the uninfected baseline grower mortality. Only 14% of herds have grower mortality higher than 6%. Finisher herd grower mortality was distributed reasonably symmetrically between 1 and 5%, around a modal value of 3%. This suggests that these herds were not experiencing PRRSV infection based grower mortality in the analysed week.

Finisher mortality in the large herds ranged from 8 to 12% with all herds therefore exhibiting increased finisher mortality when the metaherd was endemically infected with PRRSV (Figure 3.14D). Finisher mortality was approximately 2 to 10% in the small herds and in the finish only herds.

As in other metaherds the levels of abortion in a single week were very low, and the modal level was 0% for all herd types (Figure 3.14E), only 14% of large breeder herds had above zero abortions which were a maximum of 6%. No small breeder herds suffered any abortions in the analysed week.

The distribution of returns to oestrus in large breeding herds was from 0 to 30% (Figure 3.14F). However 3% of these herds had returns as high as 70% in the analysed week. The modal level was 20%, showing a slight increase from the baseline abortions when not infected with PRRSV. The small breeder herds had abortions between 0 and 40%. 42% of these herds recorded returns less than 5%.

The number of pigs weaned per litter in large breeder herds was between 6 and 10.5 (Figure 3.14G), only 11% of these herds weaned less than 8 pigs per litter in the analysed week. The small breeder herds' number of pigs weaned per litter distribution was higher than that of the larger herds, between 9 and 11 pigs per litter; however one herd weaned only 7 in the analysed week.
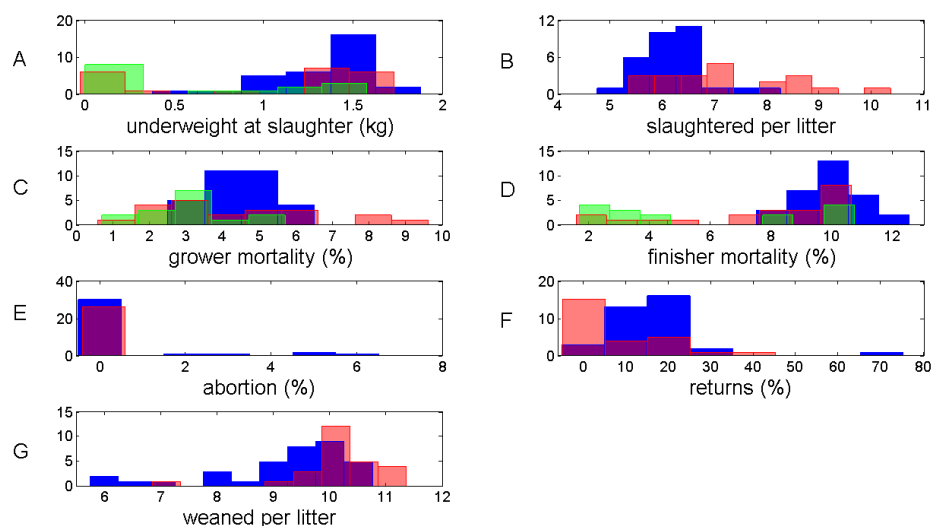
Figure 3.14. Frequency distribution of outcomes at 1000 weeks PI for 1 simulation of heterogeneous metaherd.
The y axis shows number of herds in the metaherd in each category. The blue bars represent breeding herds with more than 250 sows. The red bars represent breeding herds 250 sows or less. The green bars represent finish only herds.

3.3.3.3 The effect of the number of source herds on infection with PRRSV

The structure of the representative metaherd means that the herds had a range of

source herds. Figure 3.15 shows the effect the number of source herds had on the

dynamics of PRRSV within the metaherd. The number of sources appeared to have

no causal effect on the dynamics of PRRSV within the individual herds.
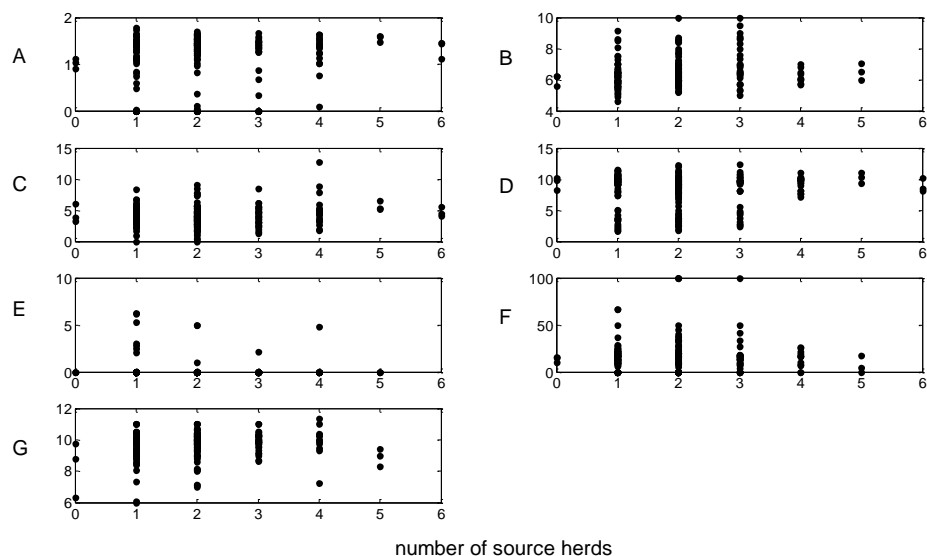
Figure 3.15. Distribution of outputs for all herds across 3 simulations according to number of source herds per herd.
A. Underweight at slaughter. B. Slaughtered per litter. C. Grower mortality. D. Finisher mortality. E. Abortion rate. F. Return rate. G. Weaned per litter.

3.3.3.4 Sensitivity of metaherd size results

Further representative metaherds were constructed in the same way as that expressed in 3.2.3 with 151 and 38 herds instead of 76. The metaherd with 151 herds had double the number of multipliers, breed wean herds, breed finish herds and finish only herds all of which descended from one nucleus herd. The metaherd of 38 herds had half the number of multipliers, breeding herds and finishing herds as the metaherd expressed in 3.2.3. The metaherd of 151 herds made it possible for herds to have more source herds.

The results of these experiments followed the results of the representative metaherd with 76 herds. Production measures at the metaherd level followed the same pattern through the epidemic phase, and then settled at the same endemic values. The same was true at the herd level, with the same dynamics over time, and the same distribution of outputs observed.

The larger metaherd with a larger sample of herds again showed no relationship between number of sources and productivity.

3.3.4 Combining of production measures

Figure 3.16 highlights the difference in production over five years with and without endemic PRRSV in herds of three sizes. The production of the nucleus herd of 902 sows was reduced by approximately 41% over 5 years. The production of a multiplier herd of 441 sows was reduced by approximately 32% over 5 years. The production of a breeder finisher herd of 166 sows was reduced by approximately 23% over 5 years. However given the small herd size, in some model simulations (5%) infection did not persist when infection was endemic in the metaherd and production matched that as when the metaherd was not endemically infected. Fadeout and reintroduction of PRRSV throughout the five year period meant that the distribution of production was right skewed. In some simulations PRRSV infection was present for differing proportions of the five years creating the tail in the distribution of results. This method of presenting and analysing results was used in chapter 4.
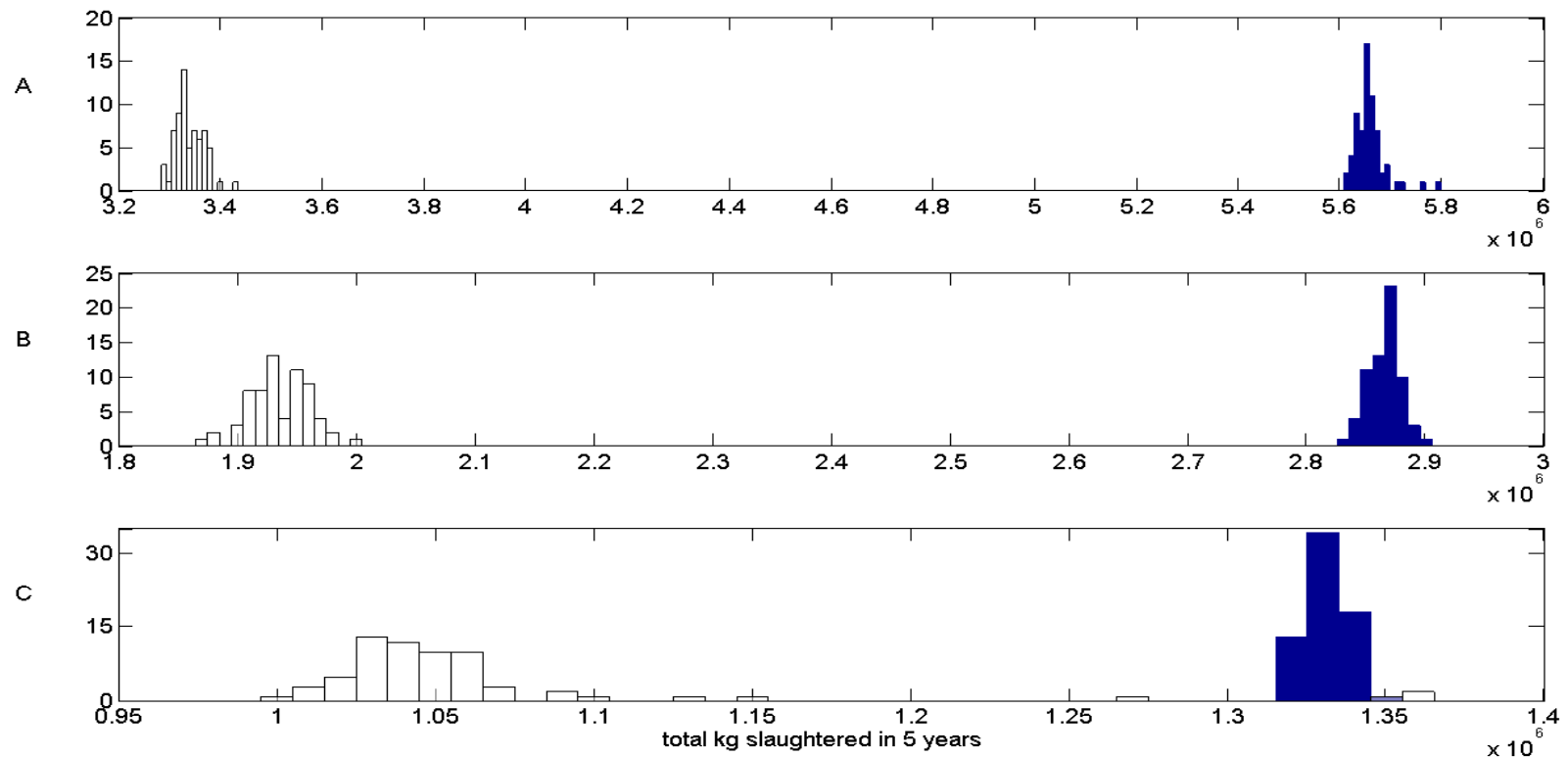
Figure 3.16. Mass of pig slaughtered in 5 years.
A. Nucleus herd – 902 sows. B. Multiplier herd – 441 sows. C. Breeder finisher herd – 166 sows. Blue distributions show the total slaughtered across multiple simulations when PRRSV not present in the metaherd. White distributions show the total slaughtered across multiple simulations when PRRSV was endemic in the metaherd.

3.4 Discussion

This chapter presented a model of the transmission of PRRSV in multiple metaherd scenarios following the single introduction of an infectious gilt and investigates the impact on production at both a metaherd and herd level. Longitudinal data of pig movements in Great Britain were used to estimate the demographic parameters of the metaherd. The aim was to determine the role of the metaherd on the transmission, persistence and impact of PRRSV. A full sensitivity analysis of the demographic parameters was not conducted as this was not necessary for this purpose.

It was assumed that herds of all types had the same distribution of number of source herds. As the movement data did not contain details on what type of herd each holding was, there was no way to split them. Thus sampling from the distribution may not be representative for all herd types. The distributions that the representative metaherds were drawn from were limited to the number of herds available in the metaherd.

The data was not complete enough to determine the pattern of movements of pigs between herds. Therefore each source herd supplies its destination herds on rotation one week after another. If this means a destination is due to receive pigs from more than one source herd in a single week, pigs are only taken from one source herd. This pattern of movements is unlikely to impact upon the transmission of disease.

The model assumes that all breeding herds breed and thus farrow continuously. That is farrowing occurs every week. For a herd to be managed this way, the sow population is divided into 21 subgroups representing the 21 week sow cycle. In herds with a low number of sows, this caused there to be very few farrowings per week. In reality a herd with a low number of sows would not farrow in such a system. Having

a low number of sows per subgroup resulted in extreme looking production outputs when expressed as percentages as seen in the results. Infectious and demographic processes occurred at probabilistic rates. When sows were removed from their subgroup either because of death or returning to oestrus, that sow was replaced at the end of the week from the gilt group but not into the same subgroup. In small herds this resulted in 'empty' weeks with no sows where zero production was recorded. In herds of less than 250 sows infection was found to be less likely persist, whilst it may be argued that this is influenced by the structure of the herd, it is unlikely as previous results have also found that PRRSV is not sustained in herds with less than 250 sows (Nodelijk et al., 2000, Evans et al., 2008, Evans et al., 2010).

To ensure demographic equilibrium in the representative metaherd with the variance in number of sources and destination herds, the all in all out nature of the gilt group was not maintained, as the metaherd structure meant that gilt deliveries were not as consistently spaced as in the previous metaherd scenarios.

The model assumes no spatial structure or edge effects. Although Figure 3.3 displays the herds in such a way that they have 'neighbours' there is no effect on disease spread by these neighbours size or proximity. Although PRRSV has been reported as transmitting via aerosol (Pitkin et al., 2009) , this is a low probability transmission route and its role in transmission is largely irrelevant relative to the role of contact engendered by the movement of pigs between herds. Aerosol transmission would play a more important role in the infection of a previously uninfected herd, rather than on persistence of and the disease profile of a herd in which PRRSV is endemic.

There exists a threshold herd size below which PRRSV cannot persist in the herd. This herd size is approximately 250 sows. Evans et al., (2008) determined that there

is an increased probability of a herd being seronegative to PRRSV if the herd had less than 250 sows. Evans et al., (2010) also modelled PRRSV in a single herd and found an inverse relationship between fadeout and herd size. PRRSV cannot persist in herds with only 50 sows.

The fadeout or persistence of PRRSV within a herd is determined by whether infection moves out of the gilt herd. The gilt herd is relatively isolated from the rest of the herd. In all simulations fadeout did not occur in herds above the threshold herd size once infection had reached other groups of the herd. Fadeout did occur in herds below the threshold size after infection had reached the rest of the herd. Therefore fadeout in the metaherd either occurs soon after infection or does not fadeout before the end of the simulation. This result has been documented previously (Evans et al., 2010). The dependency on infection reaching other groups of the herd other than the gilt group is due to the transmission probabilities between non gilt groups in the herd being relatively high (more than one hundredth). Whereas the relative transmission rate between the gilt group and all non-gilt groups is one thousandth.

The effect of the threshold on herd size can also be seen in the production measures. When viewed separately the production measures on small breeding herds (250 sows or less) are less affected by the presence of PRRSV in the metaherd than large breeding herds, with many small herds maintaining normal production levels. These herds are likely free from infection, despite repeated introduction of infected pigs.

Metaherd mean results do not accurately represent the experience of individual herds. Categorising the herds into 250 sows or more, less than 250 sows, and finisher herds more accurately represents individual herds.

The distribution of production measures across herds in the metaherd at one time point reflects the variance seen through time in one herd, even when herd sizes are not all the same. The results presented here focused mostly on the impact of endemic PRRSV infection. However some production measures showed epidemic peaks upon the introduction of infection to a herd. These were more distinct from the endemic stage in larger herds. Averaging across herds disguises the epidemic dynamics and the variability in production though time by smoothing the results.

The finish herds in the representative metaherd all had populations fitting into rough categories of approximately 2000, 3000 or 4000 pigs. Populations oscillate about these levels as batches of pigs come and go. Despite these being rather large herds, the impact of PRRSV infection on the number of pigs going to slaughter underweight is low relative to the small and particularly the large herds. Of the 3 categories of herd they also have the lowest mean grower and finisher mortality.

The key differences between finisher herds and breeder finisher herds are the presence of sows, and the grouping and housing of the rearing pigs. Sows remained in the herd for consecutive farrowing cycles, and were randomly culled at a low rate. This provided a mechanism for infected pigs to remain in the herd. In a breed finish herd, the rearing pigs were subdivided into 20 equal groups (as the same number of sows farrows every week). In a finish only herd the pigs arrive and are housed in 3 or 4 batches at any time. Due to the batching in the finisher herds, these herds were more susceptible to reintroduction of PRRSV as seen in Figure 3.8D.

A common theme among the results from all the metaherds is that of low sow related impact and high rearing pig related impact once infection is endemic. Mean levels of abortion, returns to oestrus and the number of pigs weaned per litter remained at or

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close to baseline levels when PRRSV was endemic within the metaherd. These production measures were subject to heavy fluctuations from these levels for short periods (often one week) before returning to baseline levels. This was due to large proportions of the sow herd having been previously infected with PRRSV and thus being recovered immune and not suffering further effects of the virus which would cause abortions, returns and small live litters. The fluctuation in production measures where high impact on production was recorded was caused by newly infected sows. These occur as fluctuations away from the baseline as each subgroup of the sow herd was likely to have the same infectious status.

The high impact on the rearing herd was due to the lack of resistance to PRRSV. The number of infected piglets' remained low, as once infection within the metaherd was endemic; many sows impart a maternal immunity to their piglets. This maternal immunity offers a high 'herd immunity' within the piglet group. No pig has maternal immunity lasting past 10 weeks old. Every week a subgroup of growing pigs by then mostly susceptible joined the finishing pigs, allowing infection to persist. Thus higher mortality and failure to gain weight occurs.

Results are presented from single weeks rather than averaging across weeks as this provides an informative snapshot of what a metaherd is experiencing at any one time. The distribution of herd performance within a metaherd in a single week closely matches the distribution of a single herd's performance across time. Averaging the herd's results over multiple weeks would remove the variability seen in the results, the distributions would narrow and as a result every herd appear to be have the same or similar performance with little variability around a mean.

3.5 Conclusion

PRRSV reduces productivity of a metaherd, but metaherd results are not highly dependent on the underlying structure of the metaherd.

The variability of the impact of infection with PRRSV is both between herds and within herds over time. That is herds in an endemically infected metaherd show variance in productivity. When herds are the same size, the variability in production between herds at one time point matches the distribution of production in one herd over time.

4 The impact of control and intervention strategies PRRSV in a metaherd

4.1 Introduction

The results of a model of PRRSV transmission dynamics in a metaherd were presented in Chapter 3. In this chapter, the model is developed and used to explore intervention and vaccination strategies in single herds and the metaherd with respect to the persistence of infection and the impact of PRRS on productivity.

The development of the model is described, emphasising the assumptions surrounding the vaccine and other control strategies, including the parameterisation of vaccination. The model is then explored in terms of the basic reproduction number, R_0, to investigate the changes in contact structure and impact of vaccination. Multiple vaccination strategies and combinations of vaccination and physical intervention are modelled. These results are then explored in the full metaherd model. Results are presented on the impact of interventions on the productivity of individual herds, and the influence of herd size. These are compared to the impact of interventions on the productivity of the whole metaherd.

4.2   Materials and Methods

The model structure and parameters are as described in Chapter 2 and Chapter 3 as is the within-herd model structure and demography. The metaherd used for all results in this chapter was the idealised representation of the metaherds within the British pig industry and was as described in section 3.2.3.

4.2.1   The PRRSV Vaccine

PRRSV vaccines are commonly live vaccines. Whilst there exists evidence that vaccinated pigs can shed PRRSV vaccine strain after vaccination (Cano et al., 2007a, Martelli et al., 2009, Linhares et al., 2012) this was not incorporated into the model, because the shedding is for a very short period. Furthermore vaccine is used on groups of pigs, not single pigs, so that shedding of vaccine virus will be primarily to other vaccinated pigs.

The vaccine was assumed to be 100% efficacious. What this means here is that all vaccinated pigs mount a response to the vaccine, which has a homogeneous effect among all vaccinated pigs. This effect is explained below. An implicit assumption in the model was that there was no differentiation between vaccine efficacies among different viral strains. In the model vaccine-generated immune protection lasted for 16 weeks (Porcilis PRRS advises vaccine should be administered every 4 months to give full coverage), after which protection waned at a constant rate of 1/56 days meaning that each day each vaccinated pig, vaccinated more than 16 weeks previously had a 1/56 chance of losing their vaccine protection, meaning that vaccine protection waned on average 24 weeks post vaccination. Vaccine-protected pigs were assumed to be as susceptible to infection as non-vaccinated pigs (Martelli et al., 2009). When vaccine-protected pigs became infected their survival, reproductive and growth performance was unaffected, as for uninfected pigs. Rearing pigs had normal

growth and mortality levels, whilst sows experienced no disease induced pregnancy losses and they did not have clinical disease (Linhares et al., 2012, Martelli et al., 2009, Martelli et al., 2007). Vaccinated-protected infected pigs shed PRRSV for a shorter period than non-vaccinated infected pigs (Cano et al., 2007a, Linhares et al., 2012), and the duration of shedding was assumed to be half the period of unprotected pigs, i.e. 10 days. Previously vaccinated-infected pigs upon recovery had the same protection as pigs having recovered from infection not having been vaccinated.

4.2.2 Productivity

To measure the effect of vaccination on herd productivity, the mass of pig slaughtered in any given time frame was analysed. Here results are presented for the impact over 5 years. The number of pigs slaughtered was impacted by pregnancy related losses (returns, abortions, still births and mummified piglets), as well as the increased mortality with infection of PRRSV pre and post weaning. The amount underweight per pig at slaughter was calculated as in Chapter 2 & 3, which averaged the amount underweight across all pigs in each slaughter batch. This meant that all pigs slaughtered were underweight by the same amount. These two measures combined to calculate the mass of pig slaughtered. A slaughter pig at optimum weight (weight gain not impeded by presence of PRRSV infection) was assumed to be 79.1kg (BPEX, 2012). The mass of each pig slaughtered was simply 79.1 minus the mean amount underweight. The total mass slaughtered was the mass of each pig slaughtered multiplied by the number slaughtered. This measure then incorporated both the reduced number of pigs being slaughtered and the amount those slaughtered were underweight.

The number of doses of vaccine administered was recorded as a surrogate measure of the cost of the relevant vaccination strategy. One dose was one vaccination of one pig, regardless of pig size, age and vaccination history.

4.2.3 Vaccination and control strategy scenarios modelled

The impact of the control strategies on productivity was considered over a time horizon of 5 years from the beginning of the strategy implementation. At the beginning of a breeding herd vaccination strategy, all the gilts were vaccinated, and vaccination of the sows after farrowing was implemented. Vaccination of the rearing herd was implemented by vaccinating batches of pigs as they were weaned. All scenarios were simulated 100 times.

Generally, it is assumed that the GB pig industry vaccinates the breeding herd, although there are no data collected on vaccine use. That is both the gilts before service and breeding sows. They are then vaccinated at regular intervals. The associated recommendation with the Porcilis PRRS™ vaccine is that breeding pigs should be "revaccinated at regular intervals…either before each next gestation or at random at 4 month intervals" (Porcilis PRRS fact sheet 2013). All vaccination strategies were implemented 3487 days after infection was first introduced to the metaherd to ensure disease was at endemic equilibrium in the metaherd.

- **Vaccination of the breeding herd**

In the model, the effect of vaccination was considered when all gilts were vaccinated on arrival into the herd and sows were vaccinated after each farrowing. This strategy was implemented once infection was endemic within the metaherd. Once the strategy was implemented, it was continued through the entire simulated time. The impact of herd size was investigated.

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- **Vaccination of the breeding herd and altered mixing within the herd**

There are split site 'single herds' in the industry where the pigs are moved onto another site at weaning. This is to try and remove the potential for infection transmission between the breeding and rearing herds. This was modelled by setting the cross infection between the two groups to 0. This scenario was simulated in the model once infection was endemic within the metaherd. Again, once the strategy was implemented, it was continued through the remaining simulated time.

Also simulated were scenarios where the gilt group were completely isolated from the rest of the herd (setting the cross infection potential to zero). Isolation of the gilts began before the introduction of infection. This was compared to simulations in which no control strategy was implemented. Simulations with isolation of the gilts before the introduction of infection and vaccination of the breeding herd when the metaherd was endemically infected with PRRSV were compared against simulations in which the breeding herd was vaccinated, but there was no change in mixing within the herd.

- **Vaccination of the breeding herd with partial depopulation**

De-population of an off-site all in-all out nursery herd for 14 days has been shown to eliminate PRRSV (Dee et al., 1993). To address the presence of infection in the rearing herd and the breeding herd simultaneously the rearing herd was depopulated (herd partially de-populated) for 14 days or 60 days together with vaccination of the breeding herd. In each case, the breeding and farrowing cycle was maintained, with pigs leaving the herd at weaning instead of moving into the rearing herd. Pigs leaving the herd were removed from the model. This control strategy was implemented only when PRRSV was endemic in the metaherd. The vaccination

aspect of the control strategy was continued through the simulated time. The 5 year period of production observed began after repopulation and the resumption of sending pigs to slaughter.

- **Vaccination of the rearing herd**

At the beginning of the control strategy, pigs were vaccinated at weaning. This was continued through the simulated time.

- **Vaccination implementation before introduction of infection**

Vaccination of the breeding herds was implemented and continued from the beginning of the simulations to compare preventative vaccination with vaccination in an endemically infected metaherd. The 5 year period of production observed started 15 years after the first introduction of PRRSV into the metaherd.

4.2.4   Introduction of PRRSV

All simulations were run with a single infectious gilt introduced to the nucleus herd every 6 months to analyse the effect of intervention when infection is endemic within the metaherd, as opposed to measuring the probability of infection becoming endemic within the metaherd. The introduction of infectious gilts periodically into the nucleus herd did not alter the endemic infection dynamic within the herd as the nucleus herd was of a size that meant infection reached endemic equilibrium and this was unaffected by the addition of one infectious gilt.

4.3   Results

4.3.1   Infection rates change with vaccination

A decrease in R_0 results in an increase in the threshold herd size for persistence of PRRSV infection as seen in Chapter 3. As outlined in Chapter 2, the herd basic

reproduction number (R_0) is chosen as 3 (Nodelijk et al., 2000), scaled so that the within pen R_0 is 2.6 (Charpin et al., 2012). If all pigs are protected by vaccination, then the duration of infectiousness is halved to 10 days, and the herd R_0 becomes 1.5, still above the threshold for persistence, although the fade-out threshold in terms of herd size increases. Similarly a shedding period of 5 days gives a herd R_0 of 0.75. Although mortality is included in the calculation of R_0, the effect is minimal because the mortality rates are so low. Thus the response to changes in recovery time is very nearly linear. The results of vaccination on the herd R_0 are seen in Table 4.1.

Group(s) vaccinated	R_0
None	3
Gilts	2.94
Sows	3
Gilts & sows	2.20
Piglets	3
Rearing herd	3
Gilts & rearing herd	2.95
All	1.5

Table 4.1. Table of herd R_0 values given PRRSV vaccination (halving infectious period) of pig herd subgroups

Altering the shedding times in only particular sub-groups has a minimal effect. For example, reducing the rearing herd shedding time by a half gives an R_0 of 3. However if shedding in the gilt herd alone is halved, R_0 becomes 2.94, due to the large effect of the assumed free mixing within the gilt herd.

Vaccinating the gilts and sows causes the herd R_0 to decrease to less than the within pen R_0. This is due to the averaging of the very low pen R_0 values of the breeding herd with the rest of the pen R_0 values. As the rate of recovery is not uniform across the herd, the dominant eigenvalue of the next generation matrix does not determine the herd R_0 as it would if recovery was uniform (Keeling and Rohani, 2007).

4.3.2 Infection rate change with changes in herd mixing

When the entire herd has the same mean shedding duration of 20 days, separating the breeding and rearing herds from each other resulted in a herd R_0 of 3.00. This is because of the disease associated mortality of the growing and finishing pigs, which results in a slightly shorter average duration of infection in this group, which in return means that the group-specific R_0 in growing and finishing pigs is slightly smaller than in the breeding herd (which does not have disease associated mortality). When the herd is fully integrated (i.e. there is transmission between breeding and rearing herd), this has the effect of reducing the overall average R_0. Separating the herd uncouples the components of R_0 (defined by the mixing matrix) so that the overall average is determined by the larger R_0 in the breeding herd. Whilst of no practical significance, given the numerical values involved, it is interesting theoretically that reducing mixing results in the same R_0, as determined by the initial growth rate of an epidemic.

4.3.3 Vaccination of the breeding herd

The total output per herd for 7 herds in the 5 years following implementation of vaccination is given in Figure 4.1, the larger the herd the greater the mass of pig slaughtered in the time period. The effect of vaccination was larger in larger herds. When the herd size was small (~210 sows or less) the distributions of mass slaughtered with and without vaccination overlapped, meaning that it is possible that

output might be lower when vaccinating. This is because despite infection being endemic in the metaherd, infection might not persist in smaller herds, and so production remains high in some unvaccinated herds or for some period of time in these herds. In the smallest herds (for example 62 breeding sows) the production total had the same distribution with and without vaccination (Figure 4.1 A1). Thus the expected (average) gain per dose is zero (Figure 4.1 A2). Herds with 105 and 126 sows exhibited a tri-modal distribution of mass gained per vaccine dose (Figure 4.1 B2, B3). This was due to the herd size being near a loose threshold around which infection may or may not persist within the herd. Therefore simulations in which infection persisted regardless of the presence of vaccination occurred as well as simulations in which infection did not persist and vaccination did not occur. These results demonstrate that vaccination does not lead to a herd that is as productive as a non-infected herd, because vaccination does not prevent transmission of PRRSV. Vaccination does however increase the threshold herd size for persistence of PRRSV. In the herds with 167 and 210 sows, the distributions of production showed far less overlap (Figure 4.1 D1, E1). As a result there is almost always a gain per dose of vaccine (Figure 4.1D2, E2), with the distribution of gains peaking between 20 and 40kg per dose in the herd, but with gains of up to approximately 300kg per dose. These high gains are due to infection failing to persist in the herd in the associated vaccinated simulation as vaccination has increased the threshold herd size at which PRRSV infection persists, whereas infection persisting in the face of vaccination leads to gains around the modal point of the distribution.

In larger herds of 546 and 1134 sows, the distributions of pig mass slaughtered in 5 years with and without vaccination were distinct from each other (Figure 4.1 F1, G1). An extra 70,000 - 320,000 kilogrammes of pig and 300,000 – 680,000

kilogrammes of pig respectively were slaughtered in 5 years with vaccination of the breeding herd, which is the equivalent of 177 - 809 and 758 – 1719 extra pigs slaughtered per year (assuming a slaughter pig weighs 79.1kg (BPEX 2012)) (Figure 4.1 F1, G1). The per dose gain distribution ranged from 23 to 82kg with modal values between 50 and 60kg for the 546 sow herd (Figure 4.1 F2) and from 43 to 83 kg with modal values between 60 and 70kg for the 1134 sow herd (Figure 4.1 G2). In these herds no extreme 'gains' were seen as in the smaller herds, as infection persisted even in the presence of vaccination.
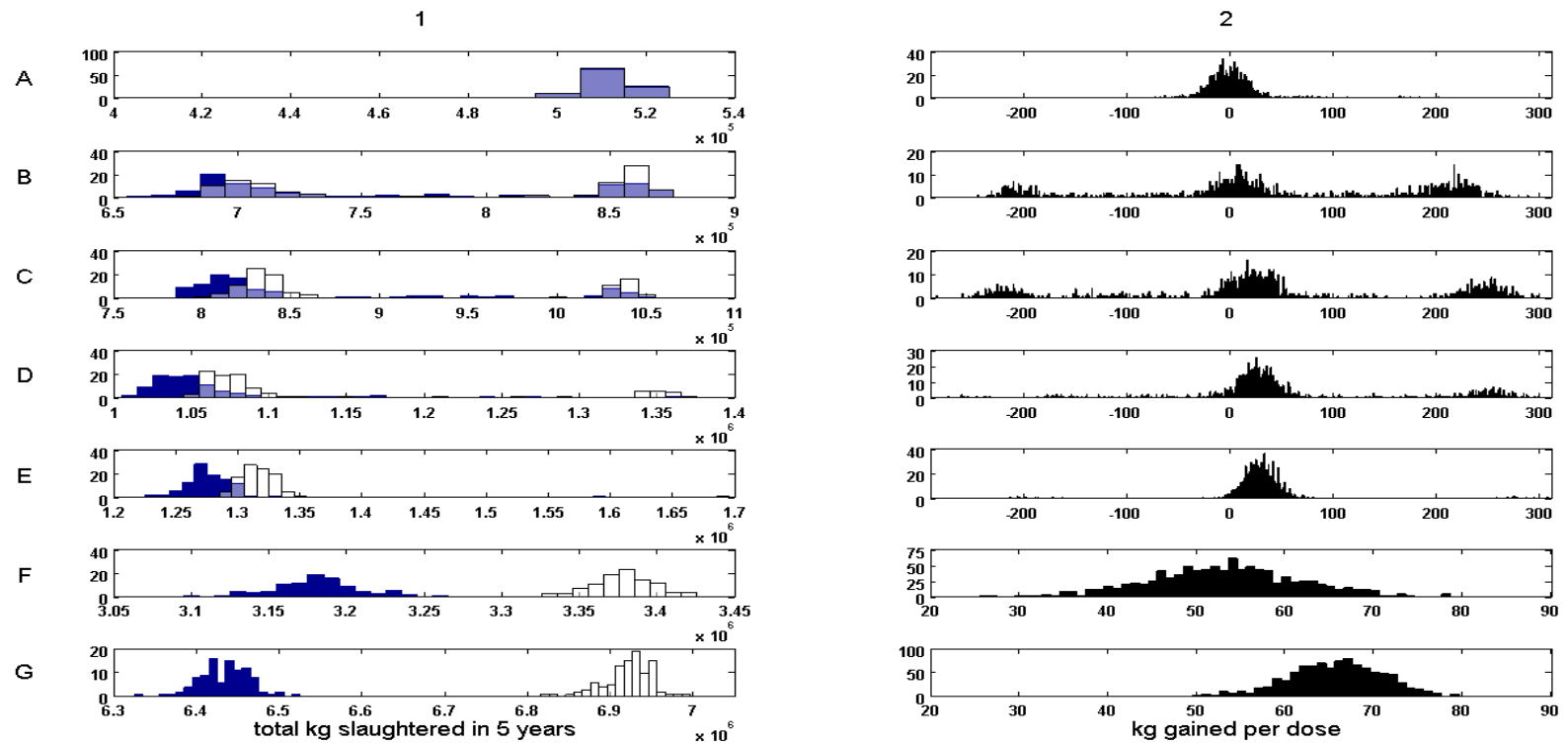
Figure 4.1. Impact of vaccination of the breeding herd on multiple herd sizes.
Graphs in column 1 display the total mass of slaughtered pig in a 5 year period for herds of different sizes when infection is endemic within the metaherd. The blue bars show 100 model simulations with no control or intervention of infection. The white bars show 100 model simulations with continual vaccination of the breeding herd. (Where the blue and white distributions overlap a lighter blue is present). Graphs in column 2 show the difference in mass slaughtered between randomly chosen non vaccinated and vaccinated model simulations, divided by the number of vaccine doses administered in a 5 year time period immediately following vaccination. Note the horizontal axis are not all aligned. Herd sizes: A 62 sows. B) 105 sows. C) 126 sows. D) 167 sows. E) 210 sows. F) 546 sows. G) 1134 sows.

4.3.4 Vaccination of the breeding herd with separation of the rearing herd

Figure 4.2 shows the total mass of slaughtered pig for 7 herd sizes over five years immediately following the implementation of vaccination of the breeding herd and separation of the rearing herd from the breeding herd, it is compared with the production output for the same herds when vaccination of the breeding herd occurred but the herd was not separated. For herds with up to 546 sows, the distribution of outputs was almost identical for the two control strategies (Figure 4.2 A, B, C, D, E, F). The herd with 546 sows seemed to show a distribution of production output indicating a small increase in performance over vaccination alone (Figure 4.2 F), however the distribution of added gain per dose for vaccinating the breeding herd with separation of the rearing herd centred around zero (not shown), indicating that including separation of the herd did not improve the performance of the herd when vaccinating the breeding herd. The herd with 1134 sows did show some improvement in performance (Figure 4.2 G). The distribution of added gain per dose for vaccinating the breeding herd with separation of the rearing herd over vaccination only ranged from 10-22 kg per dose, peaking at 4 kg per dose.
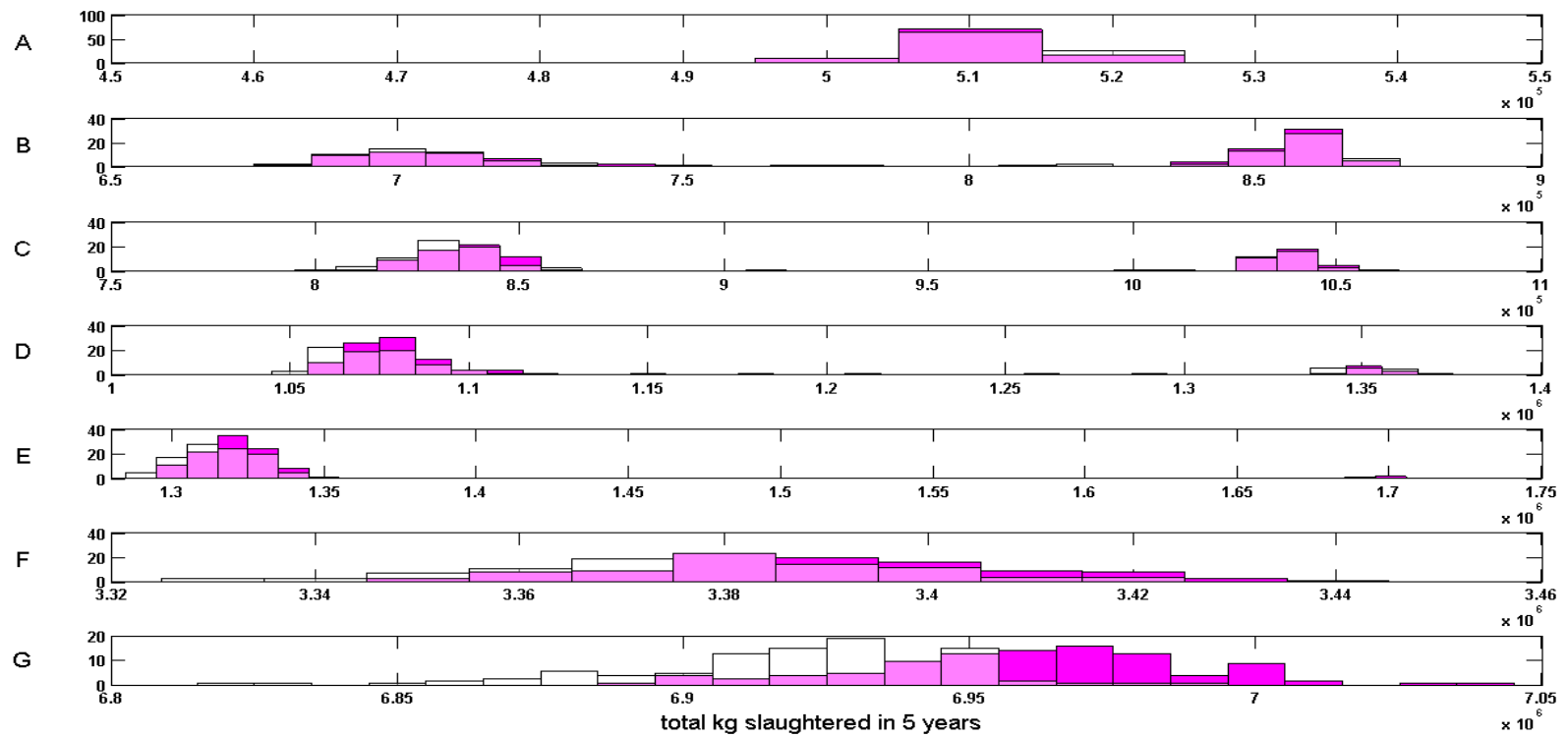
Figure 4.2. Impact of vaccination of the breeding herd with herd separation on multiple herd sizes.
Graphs display the distribution of the total mass of slaughtered pig in a 5 year period for herds of different sizes when PRRSV infection is endemic within the metaherd. The white bars show 100 model simulations with continual vaccination of the breeding herd. The magenta bars show model simulations of continual vaccination of the breeding herd plus separation of the rearing herd. (Where the distributions overlap a lighter magenta is present). Mass slaughtered is calculated as five years from when the intervention strategy began. Note the horizontal axis are not all aligned. Herd sizes: A 62 sows. B) 105 sows. C) 126 sows. D) 167 sows. E) 210 sows. F) 546 sows. G) 1134 sows.

4.3.5 Separation of gilts as a control strategy

Isolation of the gilt group from the rest of the herd before introduction of infection resulted in no difference in the mass of pig produced over 5 years when compared with taking no action. Isolation of the gilt group from the rest of the herd before introduction of infection with vaccination of the breeding herd when the metaherd was endemically infected resulted in the same production over 5 years as when vaccinating the breeding herd only.

4.3.6 Vaccination of the breeding herd with partial depopulation

The larger the herd the more likely it was that the finisher herd became reinfected after repopulation (Figure 4.3A), measured as the percentage of 100 total model simulations over a period of 713 weeks. In herds with 168 or fewer sows, the finisher herd became reinfected in less than half the simulations. All of the finisher herds of herds with more than 300 sows became reinfected in at least 60% of the simulations. The finisher herd of the three largest herds (all over 900 sows) became reinfected in every simulation after only 14 days partially depopulated. The finisher herd of the two largest herds and one other herd of 650 sows became reinfected in every simulation after 60 days partially depopulated.

Figure 4.3B shows the mean time to finisher herd reinfection following partial depopulation and later repopulation, including the time spent with an empty rearing herd. The time to reinfection of the rearing herd decreased with herd size. Herds with 168 or fewer sows had a mean of more than 500 weeks (more than 9.5 years) until reinfection of the finisher herd. Herds with more than 400 sows became reinfected with a mean time less than 300 weeks, and herds with more than 700 sows became reinfected in less than 100 weeks. The largest herd with 1491 sows became

reinfected after 11 weeks when partially depopulated for 14 days, and 26 weeks when partially depopulated for 60 days.

Depopulation of the rearing herd for 60 days offered small benefits over the depopulation for 14 days. The number of simulations in which the finisher herd became reinfected was slightly reduced, and the mean time to reinfection was slightly increased. This is attributed to two factors, firstly the longer the depopulated period, the more of the sow herd were vaccinated when repopulation occurred, as the sows were vaccinated after farrowing, therefore it would take 21 weeks to vaccinate the whole sow herd. The more of the sow herd vaccinated, the lower the prevalence of PRRSV within the sow herd due to the reduced infectious period. Secondly the extended period that the rearing herd was empty reduced the infectious pressure on the breeding herd. This in turn reduced the prevalence of PRRSV infection within the breeding herd, meaning that when the rearing herd was repopulated the infectious pressure from the breeding herd was reduced.

Figure 4.4 shows the total mass of pig slaughtered (kg) in five years when vaccinating the breeding herd and depopulating the rearing herd in comparison to only vaccinating the rearing herd.

The herd with 62 sows showed the same output with both strategies (Figure 4.4A) as infection does not persist in such a small herd, the control strategy makes no difference.

Herds with 105, 126 and 167 sows showed bi-modal results when vaccinating only (Figure 4.4 B, C, D). The higher peak represented 20-30% higher production than the lower peak but was the less likely outcome. The uni-modal output when vaccinating and partially de-populating matched the higher peak of the results of

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only vaccinating the breeding herd; therefore the depopulation of the rearing herd increased the success of vaccination of the breeding herd. Vaccination and partial depopulation resulted in output at worst equal to that of vaccinating the breeding herd only, on most occasions representing output 20-30% higher than vaccinating the breeding herd only. In a herd with 210 sows, vaccination and partial depopulation resulted in approximately 30% increased output over 5 years than vaccination alone in 87% of simulations (Figure 4.4E). In 6% of simulations vaccination and partial depopulation resulted in the same output as vaccination alone. In this 6%, the finisher herd becomes infected shortly after repopulation, negating the effect of originally depopulating.

In a herd with 546 sows, the probability of added production benefit of partially depopulating was reduced. The distribution of output for vaccination only and vaccination and depopulation again overlapped (Figure 4.4F). As the vaccination and depopulation was bi-modal there still existed a peak of results in which this strategy offered approximately 30% higher output over 5 years. The overlapping distributions were due to the simulation outcome when the finisher herd become reinfected upon repopulation. In these simulations reinfection of the finisher herd occurred shortly after repopulation (Figure 4.3B). Due to the size of the finisher herd, the presence of infection led to an epidemic peak of infected individuals. After this peak the endemic state reached was that of a higher prevalence of PRRSV than before depopulation. The mean number of infected finisher pigs in the 300 weeks after repopulation in comparison to the 300 weeks before depopulation was 8% higher (measured in one simulation). This outbreak upon reintroduction of PRRSV infection and higher prevalence negates the original benefit of partial depopulation.

The same patterns of results were seen in the herd with 1134 sows; however the

production output has a uni-modal distribution with a right skew. Only 14% of the

vaccination plus depopulation simulations have output more than 3% higher than

that of the highest outputting vaccination only simulation (Figure 4.4G). This

overlap in herd production with each strategy is due to the increased likeliness of

reinfection soon after repopulation of the finishing herd (Figure 4.3). The mean

number of infected finisher pigs in the 300 weeks after repopulation in comparison

to the 300 weeks before depopulation was 10% higher (measured in one simulation).
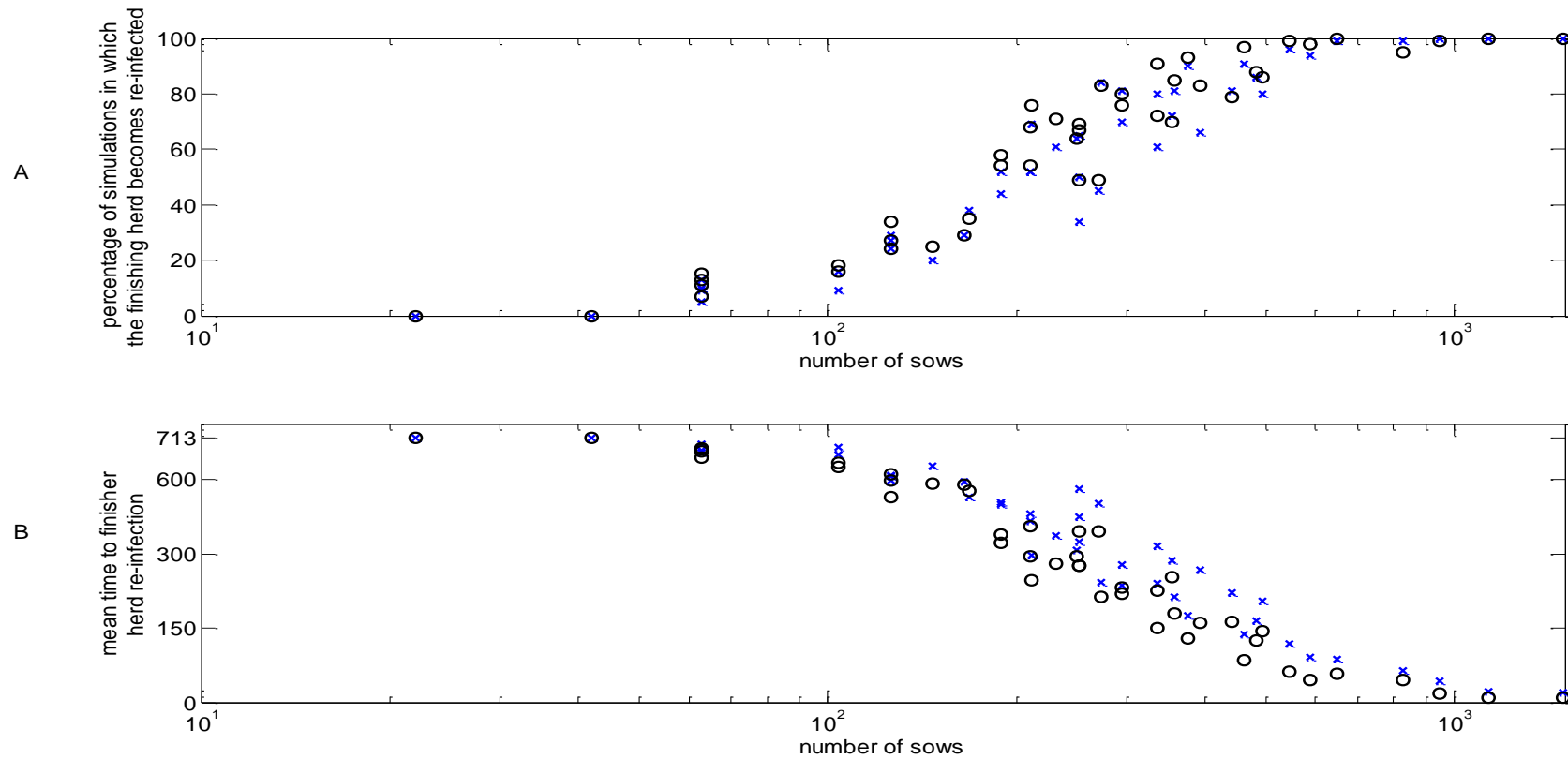
Figure 4.3. Pattern of reinfection after repopulation of the rearing herd.
A. Percentage of simulations in which finisher herds became reinfected in 713 weeks after repopulation. B. Mean time in weeks to reinfection of the finisher herd after repopulation. All herds are commercial breeder finisher. Herds remaining uninfected until the end of the simulation where empty for 713 weeks, these simulations are included in the mean. Blue crosses represent simulations where the finisher herd was empty for 14 days post de-population. Black circles represent simulations where the finisher herd was empty for 60 days post de-population.
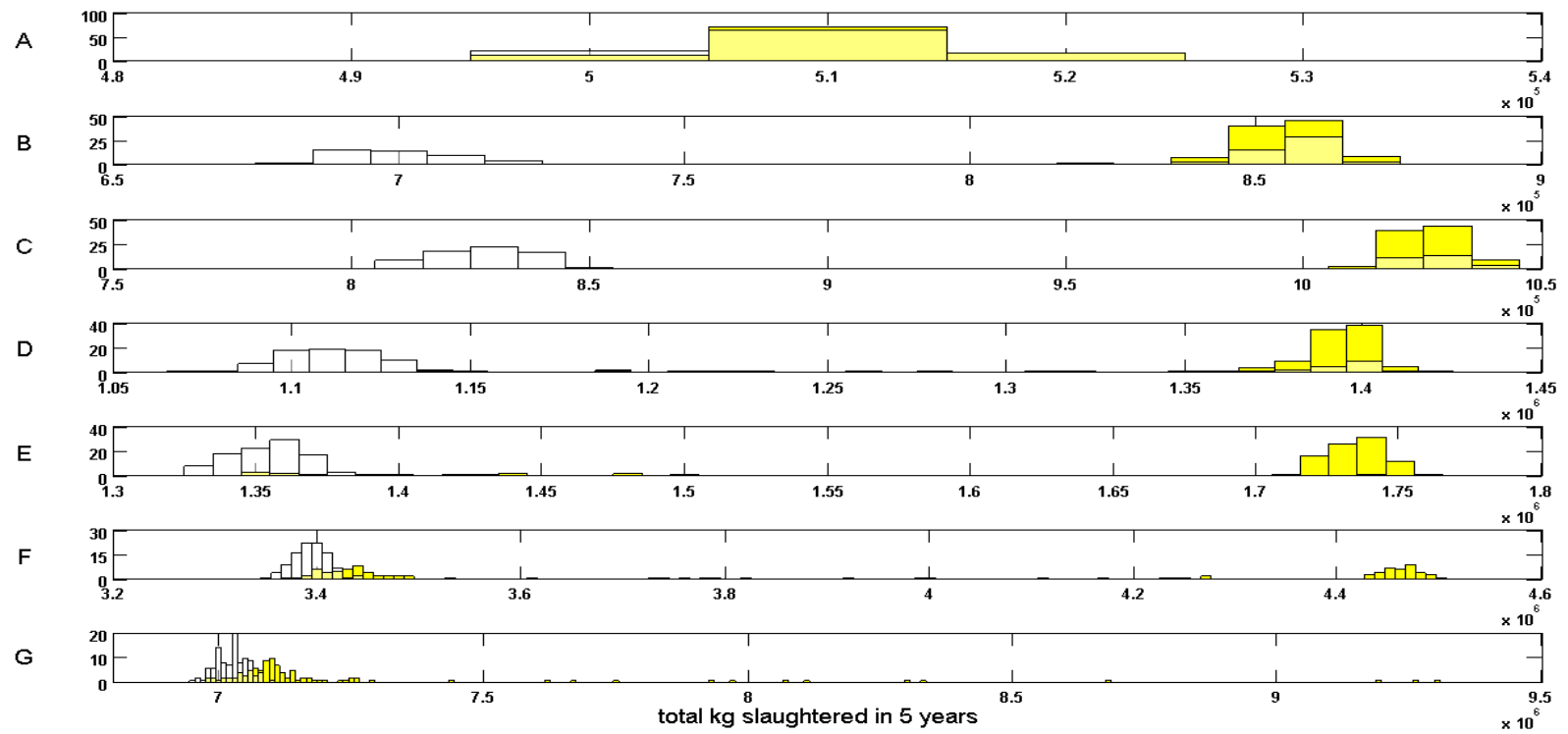
Figure 4.4. Impact of vaccination of the breeding herd with depopulation of the rearing herd on multiple herd sizes.
Graphs display the distribution of the total mass of slaughtered pig in a 5 year period for herds of different sizes when infection is endemic within the metaherd. The white bars show 100 model simulations with continual vaccination of the breeding herd. The yellow bars show model simulations of continual vaccination of the breeding herd plus depopulation of the rearing herd for 60 days (where distributions overlap, there is a lighter yellow). Mass slaughtered is calculated as five years from when the partially depopulated herds begin slaughtering again after repopulation. Note the horizontal axis are not all aligned. Herd sizes: A 62 sows. B) 105 sows. C) 126 sows. D) 167 sows. E) 210 sows. F) 546 sows. G) 1134 sows.

4.3.7   Vaccination of the rearing herd

The total output per herd for 7 herds in the 5 years following implementation of PRRSV vaccination is given in Figure 4.5, the effect of vaccination was greater in larger herds. When the herd size was small (167 sows or less) the distributions of mass slaughtered with and without vaccination overlapped, meaning that it is possible that when not vaccinating there is a possibility of output being at the same level as if vaccination were to occur. In the smallest herds (for example 62 sows) the production total displayed the same distribution with and without vaccination (Figure 4.5 A1). Thus the gain per dose is zero (Figure 4.5 A2), as with the other vaccination strategies. Again this results occur where infection did not persist in the simulations where no vaccination was used.

Herds with 105 sows again exhibited a bi-modal distribution of mass gained per vaccine dose (Figure 4.5 B2), as in 4.3.3 4.3.4 and 4.3.5. A similar pattern is seen in the results of a herd with 126 sows (Figure 4.5 C1, C2). However the first peak at zero gain per dose is smaller, thus on more occasions a vaccination of weaner pigs programme results in a gain of pig slaughtered per dose.

In herds with 167 and 210 sows, the distributions of production showed almost no overlap (Figure 4.5 D1, E1). As a result there is almost always a gain per dose of vaccine (Figure 4.5 D2, E2), with the distribution of gains peaking between 15 and17kg per dose.

In larger herds of 546 and 1134 sows, the distributions of pig mass slaughtered in 5 years with and without vaccination were distinct from each other (Figure 4.5 F1, G1). An extra 590,000 - 970,000 kilogrammes of pig and 1,290,000 – 1,770,000 kilogrammes of pig respectively were slaughtered in 5 years with vaccination of the

weaner pigs, which is the equivalent of 1491.8 -2452.6 and 3261.7 – 4475.3 extra

pigs slaughtered per year (assuming a slaughter pig weighs 79.1kg (BPEX 2012))

(Figure 4.5 F1, G1). The per dose gain distribution ranged from 15 to 19kg for both

herd sizes (Figure 4.5 F2).
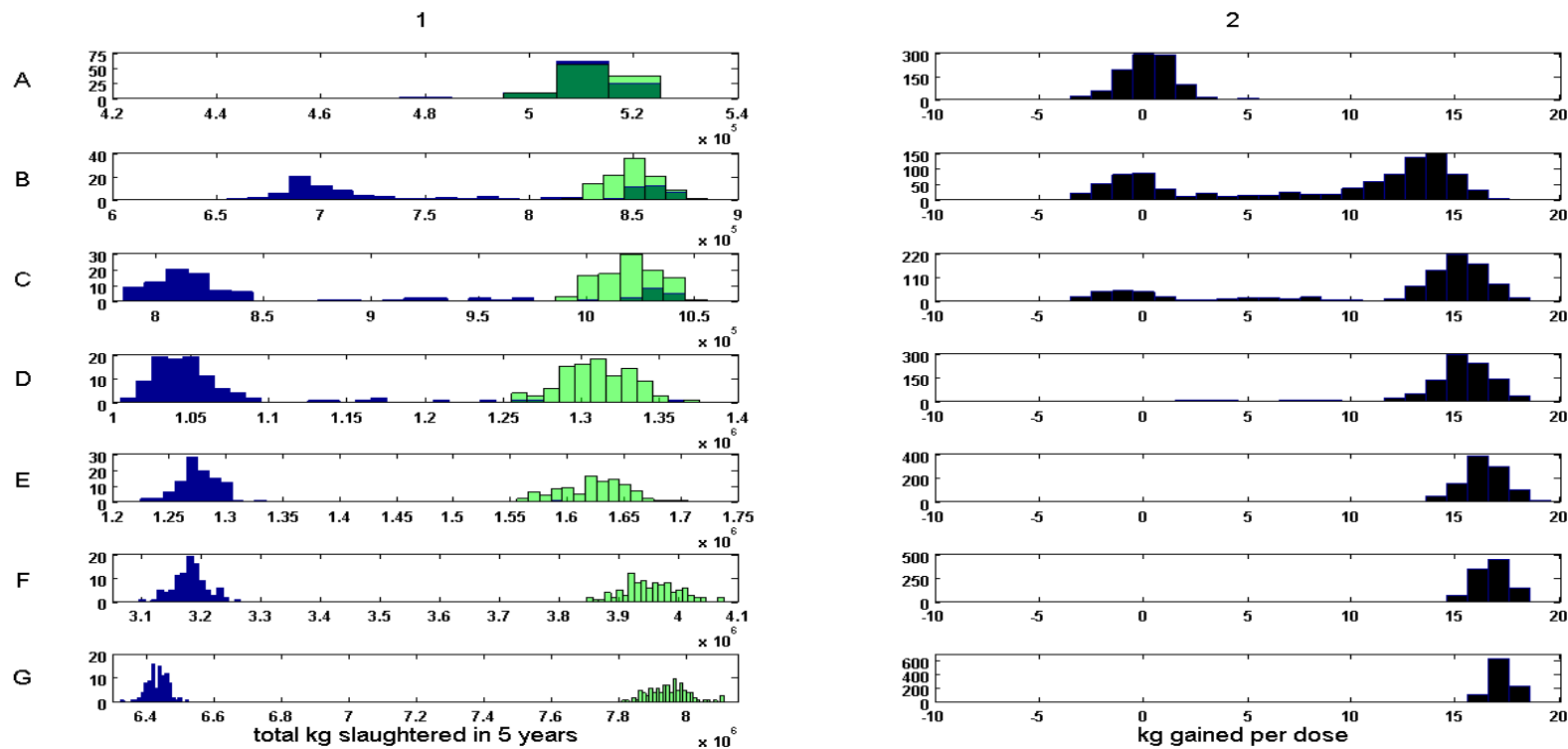
Figure 4.5. Impact of vaccination of the weaning herd on multiple herd sizes.
Graphs in column 1 display the total mass of slaughtered pig in a 5 year period for herds of different sizes when infection is endemic within the metaherd. The blue bars show 100 model simulations with no control or intervention of infection. The green bars show 100 model simulations with continual vaccination of weaning pigs. (Where the green and blue distributions overlap a darker green is present). Graphs is column 2 show the difference in mass slaughtered between randomly chosen non vaccinated and vaccinated model simulations, divided by the number of vaccine doses administered in a 5 year time period immediately following vaccination. Note the horizontal axis are not all aligned. Herd sizes: A 62 sows. B) 105 sows. C) 126 sows. D) 167 sows. E) 210 sows. F) 546 sows. G) 1134 sows.

4.3.8 Vaccination of the breeding herd before the introduction of infection

Figure 4.6 shows the difference in outcomes when vaccinating the rearing herd before the introduction of infection and once infection is endemic within the metaherd. Results display the total mass of pigs slaughtered over a five year period, 15 years after the first introduction of infection to the metaherd. In a herd of 62 sows, vaccination before the introduction of infection showed no benefit over vaccinating once infection had become endemic (within the metaherd) (Figure 4.6A).

For herds with between 105 and 210 sows, beginning vaccination before the introduction of infection led to more simulations in which infection did not become endemic within the herd, or at least not endemic within the rearing herd (Figure 4.6 B, C, D, E). Results for these herd sizes were bi-modal for both vaccination strategies. The percentage of simulations in the peak representing the higher output when vaccinating only when infection was endemic was 55%, 30%, 20% and 1% (100 simulations) respectively. When beginning vaccination before the introduction of infection, these rose to 91%, 85%, 88% and 44%. This peak in the distribution of output relates to simulations in which the herds do not experience persistent infection, either within the whole herd or just the rearing herd.

The herd with 546 sows had uni-modal distributions of production that were similar with both vaccination strategies (vaccinating when infection was endemic, and beginning vaccination before infection was present) (Figure 4.6F). However the distribution of production when vaccination began before the introduction of infection to the metaherd showed a right skew. In 21% of simulations production output was 2.6% - 30.3% higher over five years than the highest outputting simulation when vaccination began when infection was endemic.

In the herd with 1134 sows distributions of production over 5 years were almost identical (Figure 4.6G). However in two simulations in which vaccination was implemented before the introduction of infection, production over 5 years was 26% and 31% higher. In these simulations infection only reached the rearing herd towards the end of the 5 years observed. Thus the rearing herds in these simulations only became persistently infected nearly 20 years after introduction of the virus to the metaherd.

Where infection was endemic throughout the 5 year time period, or the persistence of infection was the same in both vaccination scenarios, the herd output was the same regardless of herd size.
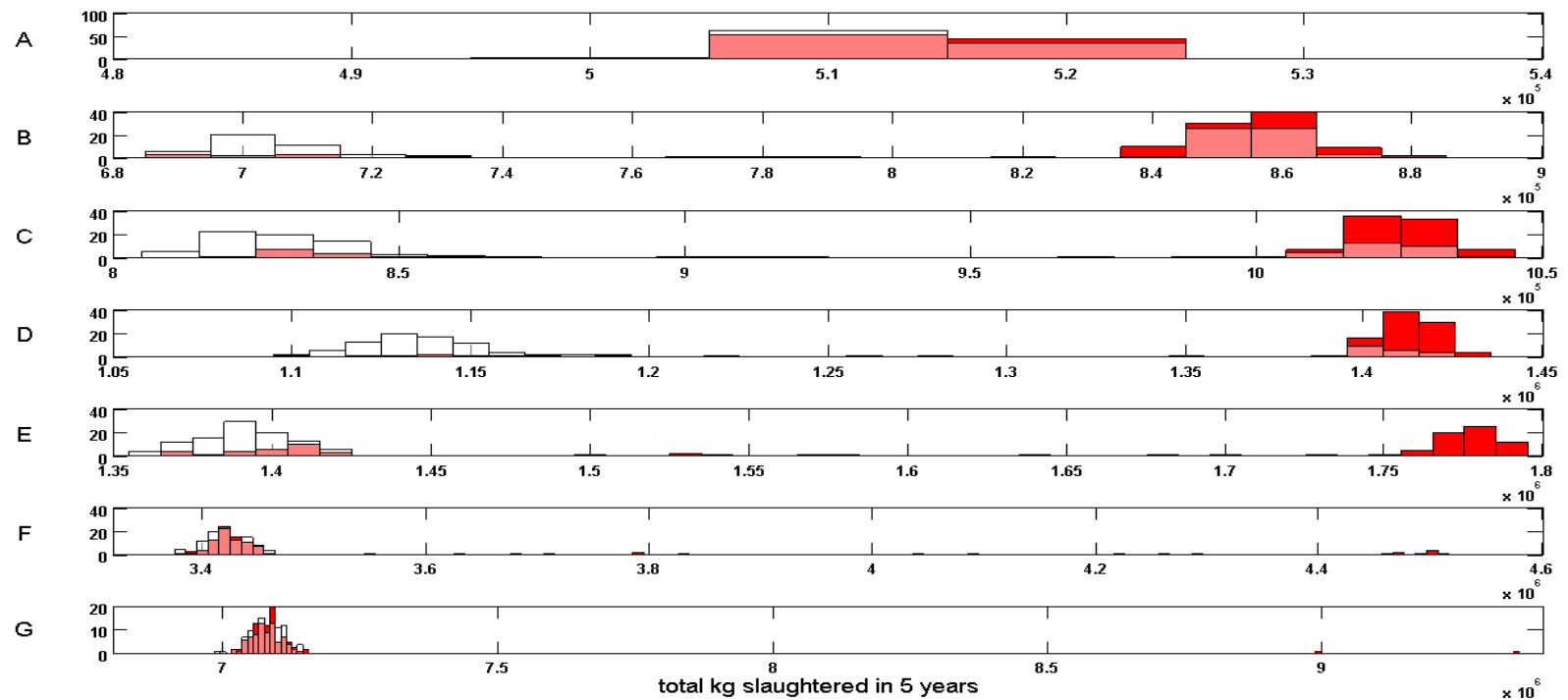
Figure 4.6. Impact of vaccination of the breeding herd before introduction of infection to the metaherd on multiple herd sizes. Graphs display the distribution of the total mass of slaughtered pig in a 5 year period for herds of different sizes. The white bars show 100 model simulations with continual vaccination of the breeding herd, vaccination having been implemented when infection is endemic within the metaherd. The red bars show model simulations of continual vaccination of the breeding herd which began before the introduction of infection to the metaherd (where the distributions overlap, a lighter red is seen). Total mass slaughtered is calculated over 5 years beginning 15 years after the first introduction of infection to the metaherd. Note the horizontal axis are not all aligned. Herd sizes: A 62 sows. B) 105 sows. C) 126 sows. D) 167 sows. E) 210 sows. F) 546 sows. G) 1134 sows.

4.3.9   Metaherd level results of control strategies

Results presented thus far are from single herds. The combined control and intervention strategies of these herds determined the metaherd level results. Vaccinating pigs at weaning, or vaccinating the breeding herds plus depopulating the rearing herd for 60 days of all the breeding herds resulted in the highest output of pig over five years (Figure 4.7A). The strategy of vaccinating the breeding sows and gilts alone in all breeding herds resulted in an overall gain of 3.3 - 5.2% in mass of pig slaughtered over 5 years (Figure 4.7A). Vaccinating the pigs at weaning in all breeding herds in the metaherd resulted in ~13% higher output with a narrow variance than the outcome when no control strategy was implemented. Vaccinating the breeding herd and depopulating the rearing herd resulted in 10-16% higher output over five years. The variation was due to the time of reinfection of the rearing herds after repopulation: early reinfection resulted in lower production. Vaccinating the breeding herd and separating the rearing herd from the breeding herd resulted in 3.9 -5.2% more pig slaughtered compared with when no control strategy was implemented. The modal value was slightly higher when separating the rearing herd from the breeding herd as well as vaccinating the breeding sows and gilts. Vaccination of the breeding sows and gilts in herds with 250 sows or more resulted in an overall gain over 5 years of 3.3 – 4.6%.

All of these strategies however showed different results when considering gains per vaccine dose (Figure 4.7B). The strategy of vaccinating all pigs at weaning required many doses more than vaccinating breeding herds, which led to a low gain per dose between 15 and 17 kg. In contrast, the gains per dose for breeding herd vaccination plus partial depopulation were 140-237kg, although with this strategy, vaccination is not the only element to the applied strategy, therefore the gain per dose is not a

completely 'honest' picture as there are other overheads (in terms of money and work) in implementing the strategy. Vaccination of only herds with 250 or more sows led to a metaherd pig slaughtered lower than when vaccinating all breeding herds, however the gains per dose of vaccine were higher (Figure 4.7B). The distribution of gains per dose for the full vaccination of breeding herds was 34 - 63kg, with a modal value of 51kg. An almost identical distribution of gains per dose resulted when including separation of the rearing to vaccination of the breeding herd. The distribution of gains per dose for only partial vaccination of the commercial breeders (>250 sows) was 40-75kg with a modal value of 58kg.
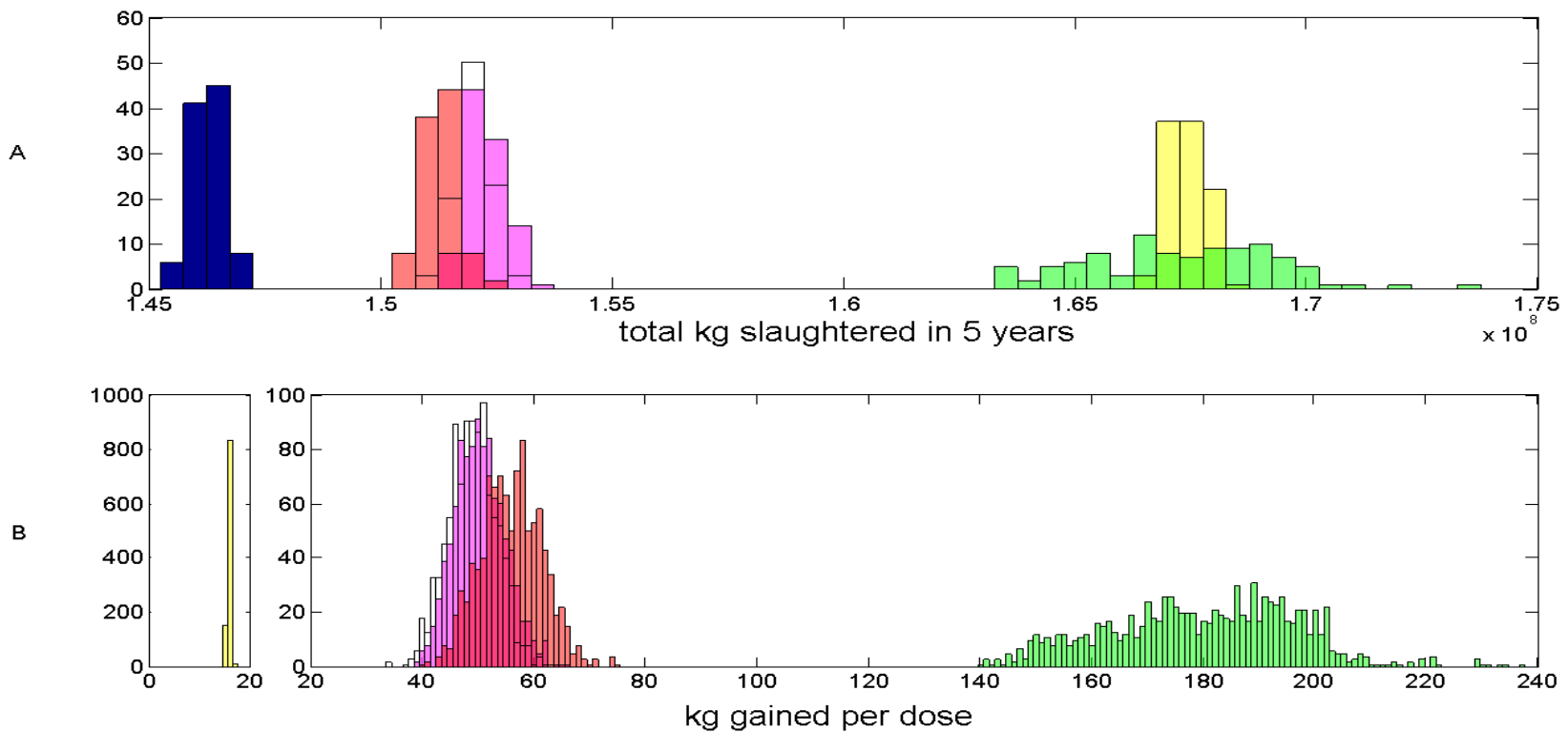
Figure 4.7. Metaherd level results of control strategies.
A. Total mass of pig slaughtered in metaherd over 5 years. B. Mass gained per dose of vaccine over non vaccinated simulations. Blue bars are simulations with no control strategy. White bars are simulations with all breeding herds vaccinating the gilts and sows. Magenta bars are simulations with all breeding herds vaccinating the gilts and sows plus separating the rearing herd from the breeding herd. Yellow bars are simulations with all breeding herds vaccinating the gilts and sows, plus depopulating the rearing herd for 60 days. Green bars are simulations with all breeding herds vaccinating pigs at weaning. Red bars are simulations with breeding herds with 250 or more sows vaccinating the gilts and sows. 5 year period began when intervention strategy was introduced, apart from depopulation strategy, where 5 year period began when slaughterings began again. Note different vertical axis on B plots.

4.3.10 Vaccine cost and pig meat price

Given that vaccine cost is approximately £1.20 per dose according to the manufacturer (Merck, personal communication 2014), and carcase price is approximately £1.64 per kilogram (as of February 2014 – this can vary greatly) then it can be concluded that on a metaherd level, all of the tested strategies represent an economically advantageous process. Given these figures, a gain of just 0.73kg would represent an economic gain. However a veterinary surgery reported (personal communication, 2014) that the cost per dose of the same vaccine was £1.48 to the surgery, and to the farmer would be approximately £2.22. Therefore a gain of 1.35kg per dose would be the minimum required to ensure that the vaccine was a cost effective option.

4.3.11 Comparison of strategies

Figure 4.8 presents the probabilities of achieving a range of kg gains per dose across multiple herd sizes for four control strategies. When the herd had only 62 sows, vaccination strategies that include vaccination of the breeding herd had equal probability of resulting in a gain per dose as a loss per dose (Figure 4.8 A). This is due to the strategy being ineffectual, and represents a range of outcomes regardless of vaccination. Vaccination of the rearing herd caused all simulations to have consistent output, although not representing any gain for the vaccination. For herds with ~210 or more sows, all of the vaccination strategies had zero probability of resulting in any loss per dose (Figure 4.8 E, F, G). In herds with ~105 sows or more, separating the rearing herd from the breeding herd when vaccinating the breeding herd did not increase the probability of higher gains per vaccine dosage than vaccination alone (Figure 4.8 B - G). Also in herds with ~105 sows or more, vaccination with depopulation of the rearing herd for 60 days had the highest

probability of high gains per vaccine dose (Figure 4.8 B-G). In a herd with 105 sows, the probability of gaining 100kg per vaccine dose or more and 200kg per dose or more was 64.7% and 47.3% respectively, whilst the probability of the same gains when vaccinating alone were only 34.8% and 23.2%. In a herd with 126 sows, the probability of gaining 100kg per vaccine dose or more and 200kg per dose or more was 80.0% and 68.3% respectively, whilst the probability of the same gains when vaccinating alone were only 24.4% and 22.2%. In a herd with 167 sows, the probability of gaining 100kg per vaccine dose or more and 200kg per dose or more was 97.3% and 90.5% respectively, whilst the probability of the same gains when vaccinating alone were only 18.7% and 15.8%. In a herd with 210 sows, the probability of gaining 100kg per vaccine dose or more and 200kg per dose or more was 91.9% and 86.9% respectively, whilst the probability of the same gains when vaccinating alone were only 1.1% and 1.1%. Partial depopulation of the herd with vaccination of the breeding herd even resulted in a 64.2% probability of gaining 300kg or more per vaccine dose. In a herd with 546 sows, the probability of gaining 100kg per vaccine dose or more and 200kg per dose or more was 56.4% and 49.0% respectively, whilst the probability of the same gain when vaccinating alone was only 0%. Partial depopulation of the herd with vaccination of the breeding herd even resulted in a 39.1% probability of gaining 300kg or more per vaccine dose. In a herd with 1134 sows, the probability of gaining 100kg per vaccine dose or more and 200kg per dose or more was 19.5% and 7.9% respectively, whilst the probability of the same gain when vaccinating alone was only 0%.
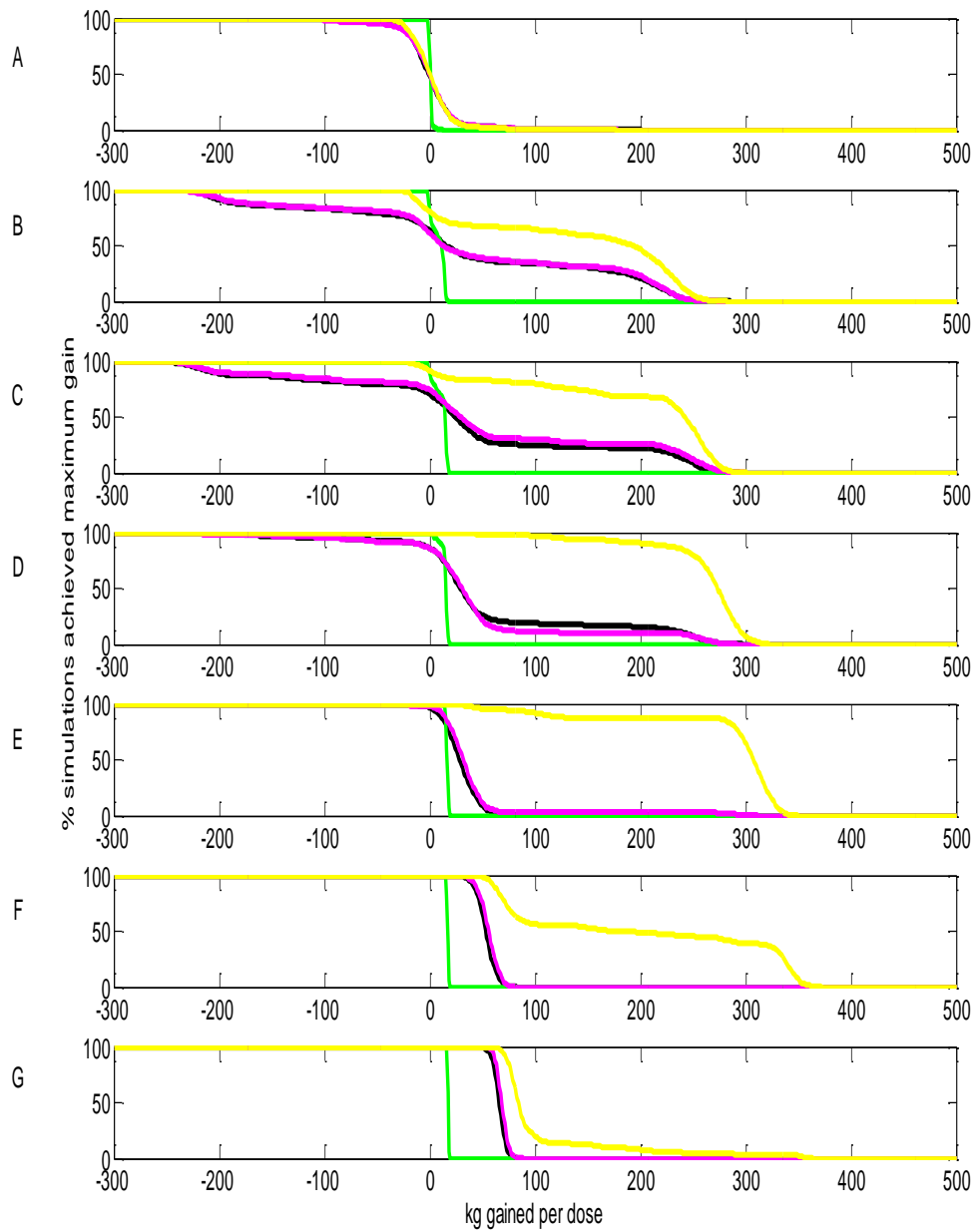
Figure 4.8. Probability distribution of achieving production gains per vaccine dosage.
The vertical axis represents the probability of achieving the associated gain or more shown on the horizontal axis. Black line represents the vaccination of the breeding herd only. The magenta line represents the vaccination of the breeding herd and the separation of the rearing herd from the breeding herd. The yellow line represents the vaccination of the breeding herd plus depopulation of the rearing herd for 60 days. The green line represents the vaccination of the rearing herd only. Herd sizes: A 62 sows. B) 105 sows. C) 126 sows. D) 167 sows. E) 210 sows. F) 546 sows. G) 1134 sows.

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4.4 Discussion

This is the first study to model control and intervention strategies of PRRSV in a metaherd of pigs.

Vaccination cannot be used to protect herds or metaherds from infection, but can have a significant impact on productivity. This is due to the vaccine properties. The vaccine does not prevent pigs from becoming infected or from shedding the virus. Therefore the virus can persist in a vaccinated population. Vaccination does reduce the mean infectious period by half, theoretically halving the R_0 in a vaccinated population, however this does not reduce the R_0 value below 1 (the threshold for invasion and persistence). Vaccination prevents individual pigs from suffering disease, these pigs therefore having productivity equal to that of a non-infected pig.

The results of the R_0 calculations generate some interesting points. When vaccination was applied the recovery rates of the different groups were no longer the same. When this is the case, the dominant eigenvalue of the next generation matrix is no longer the value of the herd R_0 (Keeling and Rohani, 2007) and the herd R_0 is not constrained by this value at all. No relationship between this dominant eigenvalue and the overall R_0 value could be drawn, as R_0 was then calculated using the eigenvector of the dominant eigenvalue of the jacobian and the differing recovery rates. The R_0 values then become a weighted average of the R_0 values across the groups within the herd. The value of R_0 when vaccinating all of the gilts and sows is due to those groups then having an R_0 of 1.5 which brings the herd mean R_0 down. The gilts and sow groups represent a large proportion of the herd.

Vaccination of breeding herds led to a higher mass of pig slaughtered due to a combination of a decrease in abortions and returns, an increase in number of pigs

born alive, a decrease in mortality pre and post weaning plus a decrease in suppressed growth (i.e. pigs went to slaughter at their target weight), therefore there were more pigs, and they were heavier. There was less variation in the productivity gained as the herd became larger, and therefore the outcome of vaccination was clearer. The mean and modal gain per dose of vaccination also increased with herd size. A study found vaccinating a large sow herd (1200 sows) improved performance within the herd (Olanratmanee et al., 2013), although some of this effect was negated by vaccinating at the wrong time in the sow cycle. Vaccination of the rearing herd in a herd with more than 1000 sows has been shown to increase herd performance significantly over not vaccinating (Mavromatis et al., 1999).

Vaccinating pigs at weaning led to higher production than vaccinating the breeding herd, and made increased production more likely at smaller herd sizes, more often resulting in a positive gain per dose of vaccine, despite using approximately10 times the doses. At herd sizes in which both methods gave mean and modal positive gains, the gain per dose was greater when vaccinating the breeding herd only, due to the fewer doses required. The decision on whether vaccinating the weaned pigs is preferable depends on the 'cost' of vaccine dose, both in terms of time and money.

Although R_0 remained the same when separating the rearing herd from the breeding herd, the results showed that when the herd is large (~1000 sows) there was a very small production advantage in separating the rearing herd from the breeding herd in the largest herds. This difference appeared negligible in the metaherd level results. Theoretically separating the breeding herd (gilts, sows and piglets) from the rearing herd (growers and finishers) prevents transmission between the breeding and rearing herds. The rearing herd is larger than the breeding herd and is replaced at a higher rate (thus supplying susceptible pigs) therefore a rearing herd will have more

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infected individuals. In the results with separation of the rearing herd, the breeding herd was also vaccinated, and thus had an infectious period half that of the rearing herd. The separation of the rearing herd from the breeding herd removes transmission events between them. This lack of transmission between groups can reduce the prevalence of infection in both groups, but more likely the breeding herd as infection is self-sustaining in the rearing herd. This reduction in prevalence in the breeding herd reduces abortions and returns, and increases live births. Therefore more pigs reach the rearing herd, and so production is higher. The production gains of vaccination and herd separation over vaccination of the breeding herd only are very small for what would be a difficult and expensive measure. Implementing the separation in a herd previously on one site would require the use of another site, plus the cost and time of moving the weaned pigs to the new site, which may require completion of a pig movement licence depending on the registration of the two sites.

Vaccination of the breeding herd combined with depopulation of the rearing herd when endemically infected with PRRSV proved an advantageous strategy for herds with more than 100 but less than 1000 sows. Herds with less than 100 sows rarely sustained infection and herds with more than 1000 sows only suffer another outbreak of infection when re-populated. This is supported by reports that partial depopulation (depopulation of the nursery herd) of herds with 250, 350 and 600 sows has been shown to increase production after repopulation (Dee and Joo, 1994) and the nursery herd to remain virus free for at least six months.

All of the tested control strategies resulted in improved metaherd output in every simulation. Vaccination of every commercial breeding herd's breeding herd did appear to be to the benefit of the metaherd, however not vaccinating herds with less than 250 sows resulted in a higher gain per vaccine dose across the metaherd, which

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could be important if the decision of PRRSV control was being made at the metaherd (or industry) level. Infection in herds of less than 250 sows is not likely to persist, but vaccination may reduce the impact of infrequent and short outbreaks of infection within the herd.

The order in which control strategies increase overall metaherd performance is not replicated when considering the gains made per dosage of vaccine. The gain made per dose when vaccinating all weaned pigs had the least variance, but was the lowest of the strategies tested (Figure 4.7B). It is possible that vaccination of only a proportion of the weaners of each herd would provide a larger benefit per dose.

Assuming vaccination once infection was already endemic, (or the farmer was unaware of the infection status) the most advantageous control strategy is to depopulate the rearing herd, and begin a vaccination programme within the breeding herd. This represented the strategy with the highest gain per dose of vaccine in the metaherd and an overall increase in production in the metaherd comparable only with vaccination of all rearing pigs (Figure 4.7). Figure 4.4 shows that this strategy is also advantageous for all but the smallest herds (62 sows here). As this is only a partial depopulation, restocking from another herd is not required eliminating a potential cost. The benefits of depopulating the rearing herd are not so obvious for large herds, and consideration as to the cost in terms of money and effort should be given by large herds considering implementing this strategy. The selling/moving on of weaned pigs is a common practice within the industry therefore this step does not represent a difficult task. It is assumed no virus can remain in the environment after depopulation. At a metaherd level, the gains equate to £224 - £372 per dose of vaccine, a 186 to 310 fold return on vaccine cost.

The vaccination assumptions here include only a single strain of virus and vaccine. Given that the literature informing the parameterisation of the vaccine covers instances of multiple strains and different amounts of heterogeneity between wild and vaccine strain, those results amount to an averaging of effects assuming multiple strains. There has been shown the potential for breakdown of disease within a herd with the vaccine strain (Botner et al., 1997, Madsen et al., 1998, Oleksiewicz et al., 1998, Storgaard et al., 1999). The literature makes reference to the breakdown of a herd with disease after the administration of the American type vaccine, not used in the UK. Both for this reason, and the risk of disease from vaccination being almost impossible to quantify, an outbreak of disease due to vaccine was not incorporated into the model.

The measurement of production over five years began when the strategy was implemented apart from in the case when depopulating the rearing herd with vaccination of the breeding herd. Here the measurement began once the rearing herd began sending pigs to slaughter after repopulation. This therefore is not a true comparison against the other strategies as the time period used to measure the effectiveness of the other strategies includes the time taken to vaccinate the whole subpopulations to be vaccinated as the herd is not vaccinated at once, but as part of the management cycle. The gains per dose seen in the strategy with depopulation of the rearing herd are also not solely attributable to the vaccine despite the scaling and naming of the output. There is a cost involved in depopulating, whereby normal income from the herd is not achieved as pigs are not sent to slaughter, plus the cost in time and overheads of implementing the depopulation. This would be mitigated partially by the recovery of income from the sale of weaner pigs assuming the breeding cycle is maintained, as it is in this model.

In reality farmers may mitigate the impacts of PRRSV infection by having more sows to make up for the loss of piglets, or rear pigs for longer, feeding them more to make up for the lack of weight gain. However, these mitigations cost money and resources and make each individual pig less productive. Increasing the density of pigs is expected to increase transmission of PRRSV and other pathogens. However the measures of the impact of PRRSV shown in this chapter (and the previous) might not be those actually experienced depending on farmer response.

4.5   Conclusions

The impact of vaccination and therefore its cost-effectiveness depends on the individual herd. The herd size, contact pattern within the herd and the probability of incoming pigs being infected all influence the decision to vaccinate or not. The 'cost' of vaccination will determine whether the effects are economically worthwhile. Results here suggest that at current prices vaccination in a herd in which infection persists is a beneficial thing to do both in terms of production gain and economic gain. However, the costs of vaccine delivery have not been included.

From a herd perspective, small herds (<100 sows) should not implement any control or intervention strategy, but instead attempt to source PRRSV free replacement gilts to reduce the probability of small outbreaks on infection in the herd. Herds with less than approximately 1000 sows but more than 100 sows should continually vaccinate the breeding herd (gilts and sows) and depopulate the rearing herd for 60 days, maintaining the farrowing cycle. Larger herds should vaccinate the breeding herd, and only implement further strategies, such as splitting the breeding and rearing herds, or depopulating the rearing herd if those strategies can be implemented with minimal cost and effort.

From the perspective of a metaherd, implementation of a control strategy is

beneficial to overall production when endemically infected with PRRSV.

5 Discussions and conclusions

The aim of this thesis was to investigate the transmission, persistence and control of porcine reproductive and respiratory syndrome virus (PRRSV) in a metapopulation of pig herds (metaherd). The influence of the metaherd, herd characteristics and control and intervention strategies were considered. The work in this thesis represents the first attempt to model PRRSV in a metaherd, and the first to model control of PRRSV.

5.1 Summary of results

A novel stochastic model of a metapopulation of pig herds (metaherd) was created, incorporating the births, deaths, slaughter, culls and movement of pigs within and between herds. Fadeout is most likely in small herds, where fadeout of infection can happen even after individuals in the breeding sows and rearing herd have become infected. Fadeout is increasingly unlikely in herds with more than 100 - 150 sows once breeding sows or rearing herd pigs have become infected, but can occur when infection is in the gilt group only as the gilt group is relatively isolated from the rest of the herd. Evans et al., (2010) found the same fadeout patterns, but found 250 sows to be the threshold above which fadeout becomes very unlikely. In a herd with 250 sows the breeding herd experiences continual outbreaks of infection followed by fade out. The piglet group only experiences very low numbers of infected individuals

due to the contact structure within the farrowing house and the maternal immunity conveyed from seropositive dams.

Herds within the metaherd can become infected at different times, and thus the metaherd level effect of endemic infection may not become apparent until many years after infection first appears in the metaherd. Infection was seeded at the top of the metaherd pyramid, and infection could only move via infected pigs to another herd when the infection in the seeded herd reached the rearing herd. Once present in other herds, infection may not persist immediately, but herds experience continual introduction of infection increasing the likelihood of episodes of persistence.

PRRSV reduces productivity of a metaherd by reducing the productivity of the herds in which infection persists. Infection with PRRSV increases the number of returns to oestrus, abortions and decreases the number of piglets born alive. Therefore the number weaned per litter is reduced. This plus increased grower and finisher mortality further reduces the number slaughtered per litter. PRRSV reduces weight gain, thus pigs are also underweight at slaughter age. There was variability both between herds (of the same size) and within herds over time in the model simulations. Production levels on breeder weaner herds were not decreased as much as on breeder finisher herds. The higher losses were due to the presence of a rearing herd, and ultimately an infected rearing herd increasing the force of infection on the breeding herd. Finisher only herds also experienced less loss than breeding herds. This was again due to decreased force of infection from a breeding herd, and also due to the batching of pigs in a finisher only herd.

When modelling the representative metaherd the number of sources of each herd was found not to influence the dynamics or persistence. The threshold herd size for persistence of PRRSV was approximately 250 sows.

The model was used to test the effects of control and intervention strategies. The larger a herd, the greater the effect of vaccination and the less variability in production with vaccination. Vaccination in small herds was ineffective in increasing production due to PRRSV failing to persist regardless of vaccination. Vaccination of the breeding herd produced higher gains per vaccine dose than vaccination of the rearing herd only. Vaccination of the rearing herd only resulted in higher total herd and metaherd gains, with less variability. Partial de-population increased the probability of vaccination increasing herd performance unless the herd was small (<100 sows) or very large (>1000 sows) as there was a high probability of establishing a virus free rearing herd. The time to reinfection of the rearing herd decreased with herd size.

Results highlighted the value of modelling to support the decisions of individual farmers to vaccinate and partially depopulate, showing that the optimal decision is influenced by the herd size.

5.2 Strengths of the model

This study models infection in a metapopulation with heterogeneous subpopulations, has a clear structure within the metaherd and is parameterised for host demography, pathogen dynamics and for practical interventions which output not only herd results as the individual unit, but calculate numbers of pigs in each infectious state in each herd subgroup. To the author's knowledge, this is the first study to utilise such a model which reports not only prevalence, but the impact of that prevalence on

numerous production measures, for example mortality, pregnancy failures, and growth retardation. These measures allow identification of the causes of production loss when infected with PRRSV and can assist in the understanding of the full impact of a pathogen and indicate where it may be possible or most advantageous to implement strategies to combat the negative impact of infection. Previous studies have modelled PRRSV in single herds (Evans et al., 2010, Nodelijk et al., 2000), this is the first to analyse not only PRRSV dynamics in single herds of varying sizes, but how the connection between herds influences those dynamics, and what the metaherd impact of PRRSV infection is.

(Lurette et al., 2011) modelled *Salmonella* in a metaherd of pig herds in a similar way. Herd size was claimed to not be significant to the prevalence of shedding pigs at slaughter, so all herds were assumed the same size. Due to a scarcity of data with which to parameterise, interventions are accounted for in a hypothetical way and not parameterised to represent real intervention or control strategies, and thus provide an indication of what efficacy of intervention is required for significant reduction of prevalence. This model only reported on whether herds have infected pigs or not and the prevalence of shedding pigs in slaughter pigs, not indicating the impact on persistence, or the dynamics of infection within the herd despite having a within herd demographic structure.

Other studies using a model of infectious disease which incorporate the movement of animals between holdings report only on the number of infected animals (Brooks-Pollock and Keeling, 2009).

The development of the transmission term to incorporate two R_0 values allows the complexity of a pig herd structure to be accounted for in the dynamics of PRRSV within a herd.

There are no published models of PRRSV vaccination and due to the heterogeneity between wild virus and vaccine strains, case studies report varying results. Whilst this model does not account for different strains, the literature was used to determine the likely effect of vaccination assuming some heterogeneity (as homogeneity between wild and vaccine strains is unlikely to occur). This represents an appropriate approximation of vaccine impact on PRRSV in GB.

The model structure can easily be developed for different infections and herd structures. Ideally it could use real demographic data to locate herds in a geographical context and use movement data to reconstruct the metaherd.

The model framework and metaherd structure that has been presented here is generalisable to other infections.

5.3   Weaknesses in the model

The detailed cross infection matrix can be justified but not validated. There was a lack of information or data with which to parameterise the matrix. Potentially a sensitivity analysis would reveal to what extent within-herd prevalence and persistence are determined by the relative sizes of the elements within the mixing matrix. Simulations performed with an alternative matrix developed by (Evans et al., 2010), demonstrated less variation in simulation results due to free mixing in the sow herd. This also led to higher prevalence in the sow herd, and a faster spread of infection upon introduction of PRRSV to a susceptible herd. In simulations where the mixing was changed, no cross infection between the breeding and rearing herds,

did not stop infection reaching the rearing herd as infected piglets moved into the rearing herd. No cross infection did lower prevalence of infection in the breeding herd however, as the infectious pressure was reduced. Complete isolation of the gilts had no noticeable effect on production over 5 years. Infected gilts were still moved into the sow herd. This measure could delay the outbreak of infection, but in herds large enough for infection to persist, once infection was present in the sow and/or rearing herd, production would be the same as without full gilt isolation. To make gilt isolation an effective strategy, this 'quarantining' would need to be coupled with testing of the gilts for virus before moving them into the sow herd to ensure they are virus negative. This is the case where infection is assumed to be introduced to herds through the movement of gilts, as modelled here. Modelled here was a very low probability of cross infection to and from the gilt group which is assumed to be the case as long as the gilt herd is on the same premises as the rest of the herd. Gilts were moved into the sow herd regardless of their infection state: testing gilts for presence of virus before adding them to the sows would be an additional intervention.

The model used two values of R_0 to determine the rate of infection. A within pen R_0 of 2.6 was taken from (Charpin et al., 2012), from which an average infectious period of 20 days was also derived. However the within herd R_0 of 3 was taken from (Nodelijk et al., 2000) which assumed an infectious period of 56 days. Assuming a longer infectious period would result in a higher R_0, the same study estimates that an infectious period of only 10 days would result in an R_0 of 2. The confidence intervals of these R_0 values have a large overlap however, (1, 4) and (1.5, 6) respectively. The small size of the sample herd (115 sows) from which calculations were made may have also led to an underestimate of R_0. A herd R_0 of 3, and a pen R_0 of 2.6 with an

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average infectious period of 20 days was deemed appropriate for this model, but may still not represent true figures due to both the rigour of the methods with which these R_0 figures were derived and that in reality R_0 is likely to vary between herds in a metaherd. This could be caused by different within herd housing and management structures, which likely exist. Further herd heterogeneity (other than herd type and size) would improve the model but be difficult to parameterise, computationally expensive, and at the metaherd level would not be impact upon to the dynamics of PRRSV. Density independent transmission was deemed appropriate for the model as in previous published models of PRRSV (Evans et al., 2010, Nodelijk et al., 2000). Density dependent transmission would be suitable where R_0 was expected to increase with herd size. However an increase in herd size would also influence herd structure and in turn affect the cross infection matrix, which would change transmission within the herd. The results presented in this thesis show that the effects of increasing herd size are captured in the model using density independent transmission.

All pigs in the model when infected were assumed to shed virus in the same quantity/at the same rate, making them all equally infected (even infected vaccinated pigs which simply shed for a shorter period). The presence of 'super-shedders' has been found to significantly alter the dynamics of disease transmission in humans (Lloyd-Smith et al., 2005) and livestock (Matthews et al., 2006a, Matthews et al., 2006b, Woolhouse et al., 1997). Super-shedding is better understood in the role of bacterial pathogens than viral pathogens as shedding of bacteria is usually easier to measure. The presence of super-shedders in this model would have been partially negated by the complex structure of the herd. Separation into pens would partially inhibit the impact of any super-shedders, and the presence in an endemically infected

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herd would be negligible. The presence of super-shedders in a small herd would have had greater impact due to the increased probability of outbreaks after reintroduction of infection. To the author's knowledge there is no information on whether super-shedding of PRRSV exists. Although super-spreading isn't known at the individual pig level, it might be at the herd level (Gates and Woolhouse, 2014).

The representative metaherd modelled was based on parameters from the GB pig movement data. However the metaherd conforms to average behaviour rather than being a real collection of herds. All of the movements were regular in time and in size. We know that movements of pigs exist that appear to be random (Chapter 1), and do not fit the general pattern. Simple observation of the movement data also shows that movements of pigs exist whereby the pigs apparently move sideways in the metaherd pyramid, or even upwards. Such movements are inaccuracies in the data; represent idiosyncratic decisions of farmers, or both.

The herd demography presented here has continuous farrowing, and better represents indoor pig farms than outdoor. Some herds farrow in batches, particularly outdoor. This different structure would also affect the cross infection matrix, as batches are likely to be housed/kept differently than pigs in a continuous herd.

Ensuring demographic equilibrium in each herd was made difficult in the representative metaherd. Multiplier herds provided replacement gilts on rotation. For a breeding herd with multiple source multiplier herds, this could mean the length of time between receiving incoming gilts was not always consistent, which can lead to there not being enough gilts to replace the number of sows dying naturally or being culled whilst waiting for the next delivery of gilts. This problem as with all the other demographic challenges had to be managed at a population level. One approach

would be to develop an individual based model. However, the demography of the herds is essentially determined by farmers, and without better data or a model framework on which to model farmers' (actual) decisions regarding selling and purchasing their stock, a full individual based model would not itself improve the ability to model PRRSV in the UK pig population. Additionally, individual based models are more computationally expensive.

Introduction of infection into individual herds in this model is via the movement of pigs. For breeding herds this means the introduction of gilts, and for finisher herds this means the introduction of weaner pigs. Transmission via aerosol from neighbouring herds and transmission via semen was not considered. However these routes would represent a further route into the herd. It is a simplification to assume infection can be introduced only into a particular subpopulation of the herd. Airborne transmission and transmission in semen represent routes into the other subpopulations of a herd. This may lead to different outbreak dynamics, but when considering the impact of virus when a herd is already endemically infected, the impact of these less likely routes of introduction are negligible.

5.4 Future work

A natural extension to this work would be to further investigate the impact of the metaherd structure. Interestingly, the pig movement data displays 'one-off' movements, connections between herds that occur only once. As well as what can appear to be random movements that do not fit within the pyramid of herds connected by a pattern of movements. These random movements could be included into the metaherd model structure to determine their effect on disease propagation and persistence. As well as these random movements, another interesting extension to the metaherd modelling would be to include the movements of pigs 'sideways' in

the pyramid or even upwards. These movements can be seen in the GB movement data. This modelling would be even more relevant if the infection was seeded elsewhere in the metaherd. Whist seeding infection in the nucleus herd represents a potential worst case scenario it also simplifies the control measures, as the avenues of infection into each herd is known.

As already discussed the model is most representative of continuous farrowing herds, further work would involve modelling batch farrowing systems. A metaherd of which may be more representative of regions in which outdoor pig farming was more prevalent, such as East Anglia.

Finally as a means of studying the knock on effects of PRRSV, this should be modelled as a co-infection as PRRS has most impact in the presence of other pathogens, as PRRSV serves as an immunosuppressant.

Data for validation were not available at the time of this study to either accurately model real metaherds within the GB pig industry, or to validate the infection dynamics, which would require longitudinal PRRSV prevalence data. Pig movement data in GB is now being collected electronically (mandatory since April 2012), which should yield data with less flaws and omissions which would make it much easier to use directly in a simulation model. Key would be the collection of data on type of pig moved, which was not recorded previously. It is an available field on the electronic form, however options exist that would make the data just as unusable (e.g. 'standard'). Collecting longitudinal data on PRRSV prevalence is difficult as it is expensive and time consuming, and likely to be highly variable. As PRRS is difficult to detect, capturing this data (from the introduction of infection) from a wild virus infection event would be very difficult.

The model assumes there is only one strain of PPRSV. In reality there are many circulating strains and many new emerging strains as the virus mutates. As previously discussed the cross immunity effect of multiple strains is variable and difficult to record as the profile of circulating strains is ever changing. The model could be further developed to include multiple PRRSV strains which confer partial immunity upon recovery to heterogeneous strains.

Interventions considered were limited, and future work could consider the impact of interventions in one herd on all the herds 'downstream'. Future work could also model interventions of PRRSV not considered in this thesis like test and removal methods (Dee et al., 2000, Yang et al., 2008). A further interesting intervention of PRRSV is deliberately exposing pigs to virus to create herd immunity (Fano et al., 2005). This differs from a herd being endemically infected with PRRSV, in that at the endemic equilibrium, a proportion of the herd remains susceptible. Inoculating the entire herd theoretically (assuming all pigs become infected) results in there being no susceptible individuals left and thus PRRSV could fade out. This strategy may require closing of the herd to ensure that no new susceptible individuals are introduced. This strategy was implemented in a small breeder finisher herd (130 sows) in Slovenia (Stukelj et al., 2013). PRRSV was eliminated in the breeding herd, however continued to circulate in the weaner herd (as the serum inoculation had occurred only in the breeding herd). The experiment's impact was negated by the introduction of a different strain of PRRSV entering the herd, which the herd was not immune to. The study highlighted the difficulty in implementing the required biosecurity measures in field conditions. Given that the strategy proved unsuccessful in a small herd (with therefore a high probability of natural fadeout) then the effectiveness of the strategy in larger herds appears even less.

5.5   Implications for GB pig industry

Despite the shortcomings of the model, it currently provides the most rigorous basis on which to design interventions against PRRSV at the herd and metaherd levels.

A key result is that although vaccination does not protect herds or metaherds from infection, it does have a significant impact on productivity, especially at the metaherd level. Vaccination against PRRSV prevents individual pigs from suffering disease, these pigs therefore having productivity equal to that of a non-infected pig. Clearly, from the perspective of the national herd (i.e. BPEX), widespread use of the vaccine would increase productivity. If pig farmers were able to co-ordinate their actions, then concerted vaccination would reduce the impact on production within a metaherd.

However, our results also demonstrate potentially why pig farmers in the UK do not currently universally adopt vaccination. The optimum approach to control PRRSV is herd size dependant, and dependant on whether a source is infected. A threshold sized herd (approx. 250 sows) is expected to experience spells of persistence and fadeout (unvaccinated). Herds below the threshold herd size can still reap a benefit on the majority of occasions when vaccinating. Vaccination may reduce the occurrence and impact of infrequent and short outbreaks of infection within the herd. Removing the source of new infected pigs will create longer periods of time PRRSV-free, thus reducing the benefit of the vaccine. Figure 4.8 demonstrates the probability of improved production with the introduction of different intervention strategies in different herd sizes. Intervention in herds with less than 100 sows is always to no advantage. It is always advantageous to implement vaccination strategies in herds with more than 210 sows. The most advantageous strategy to the metaherd is the vaccination of the breeding herds, and depopulation of the rearing

herd. However this strategy offers little advantage over vaccination only to herds with 1000 sows or more, particularly considering the added effort and cost of depopulating.

All of the tested control strategies resulted in improved metaherd output in every simulation. The most advantageous control strategy at the metaherd level is for all the individual herds to depopulate the rearing herd, and begin a vaccination programme within the breeding herd. This represented the strategy with the highest gain per dose of vaccine in the metaherd and an overall increase in production in the metaherd comparable only with vaccination of all rearing pigs. This strategy is advantageous for all but the smallest herds (62 sows here). The benefits of depopulating the rearing herd are not so obvious for large herds, and consideration as to the cost in terms of money and effort should be given by large herds considering implementing this strategy. At a metaherd level, the gains equate to £231 - £384 per dose of vaccine, a 193 - 320 fold return on vaccine cost. Vaccination of all pigs at rearing is the vaccination strategy with the lowest gain per dose, however at the metaherd level this strategy yields £24.6 gain per dose, a 20.5 fold return on the vaccine cost.

In reality farmers may mitigate the impacts of PRRSV infection by having more sows to make up for the loss of piglets, or rear pigs for longer, feeding them more to make up for the lack of weight gain. These mitigations cost money and resources and make each individual pig less productive. However the measures of the impact of PRRSV shown in this thesis might not be those actually experienced depending on farmer response. We have not addressed mitigation in the current model. Data on the decision-making of farmers and their response to PRRSV would be highly informative.

From an industry view point PRRSV control is clearly very effective and very cost-effective. However, to individual farmers, the effectiveness and cost-effectiveness depends on their circumstance. There is a well-known "free-rider" problem in infectious disease control, such that if all herds are vaccinating against PRRSV, then each farmers' best option is to stop vaccinating (McEldowney et al., 2013). A goal would be to generate the cohesion amongst farmers for them to be able to design a vaccination programme at the metaherd level, to maximally impact on productivity as a whole.

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Appendix 1. Model calling script

The code below is written in MatLab 2011b, and is a script from which the function running the simulation model is called. The script sets up data structures and records simulation output in a temporary file structure which is combined once all simulations have completed.

```
tic

%data file defining the metaherd
load representativemetaherd1a

%define the data required to run the simulations
dataIn.INF = int16(zeros( size( SUS ) ));
dataIn.SUS = int16(SUS);
dataIn.farmtypes = farmtypes;
dataIn.runtime = 500;
dataIn.ots = 7; %output step
dataIn.disgrowMORT = 0.2353; % 20% chance of surviving 6 weeks
infected
dataIn.disfinMORT = 543/5000; % 20% chance of surviving 14 weeks
infected
dataIn.farmout = farmout; %list of farms (rows) that each farm sends
to (cols)
dataIn.vaccinate_Herds = 8:61; %herds with any vaccination
dataIn.vaccinate_Time = 5000; %time to begin vaccination strategies
dataIn.vaccinate_Sows = true; %vaccinate breeding herd?
dataIn.vaccinate_Gilts = true;
dataIn.vaccinate_Rears = false; %vaccinate rearing herd

runs = 1;

%directory & root filename to save intermediary and final results
rootFName = 'runX';

for i = 1 : runs
    [ results ] = newmodVacc4thesis( dataIn ); % runs vaccination
model
    fname = [ rootFName num2str(i) '.mat' ];
    save ( fname, 'results' );
end
```

```matlab
RESULTS( runs ) = struct ( 'underweight_Slaughter', double(0),
'slaughtered_Persow', double(0), 'N', int16(0), 'fadeout',
int16(0),...
    'farm_Findeaths', double(0), 'farm_Growdeaths', double(0),
'farm_Abortions', double(0),...
    'farm_Returns', double(0), 'pigs_Lost', int16(0), 'runtime',
int16(0), 'endtime', int16(0),...
    'weaned_Persow', int16(0), 'wean_Week', int8(0),
'slaughter_Week', int8(0), 'doses', double(0), 'culls', int32(0),
'inf_In', int32(0), 'inf_Out', int32(0) );
for i = 1 : runs
    load([ rootFName num2str(i) '.mat'])
    RESULTS( i ) = results;
end

fname = [ rootFName ];
save ( fname, 'RESULTS' );

for i = 1 : runs
    delete([rootFName num2str(i) '.mat'])
end

toc
```

Appendix 2. Model function

The code below is the function that runs the model simulation (one iteration per call). The calling script supplies the relevant data structure (infection parameters and metaherd structure). The code has been divided with subheadings.

```matlab
function [ resOut ] = newmodVacc4( runP )
%function newmodVacc4: simulates in given metaheard with infection
introduced every 6 months
%runP - structure containing run parameters
%resOut - the results from the simulation

resOut = struct ( 'underweight_Slaughter', double(0),
'slaughtered_Persow', double(0), 'N', int16(0), 'fadeout',
int16(0),...
    'farm_Findeaths', double(0), 'farm_Growdeaths', double(0),
'farm_Abortions', double(0),...
    'farm_Returns', double(0), 'pigs_Lost', int16(0), 'runtime',
int16(0), 'endtime', int16(0),...
    'weaned_Persow', int16(0), 'wean_Week', int8(0),
'slaughter_Week', int8(0), 'doses', double(0), 'culls', int32(0) );
```

SET UP SIMULATION

```matlab
REC = int16(zeros( size( runP.INF ) ));
RSUS = int16(zeros( size( runP.INF ) ));
MAT = int16(zeros( size( runP.INF ) ));
Num_Pop = numel(runP.SUS);
M=reshape(MAT,1,Num_Pop);
S=int16(reshape(runP.SUS,1,Num_Pop));
I=reshape(runP.INF,1,Num_Pop);
R=reshape(REC,1,Num_Pop);
RS=reshape(RSUS,1,Num_Pop);
VS=RS; % vaccinated susceptible. Same shape and size as RS. All
zeroes.
VI=RS; % vaccinated infected. Same shape and size as RS. All zeroes.
VR=RS; % vaccinated, infected, recovered. Same as R, needs to be
recorded so only R fail to gain weight
clear MAT SUS INF REC RSUS
P=M+S+I+R+RS+VS+VI+VR;
Num_Farms = length(P)/54;
MT = M; ST = S; IT = I; RT = R; RST = RS; VST = VS; VIT = VI; VRT =
VR;
```

PARAMETERS

```
beta = 0.13; % transmission
gamma = 1/20; % recovery
pi = 1/42; % maternal immunity waning rate
omega = 1/252; % immunity waning
rho = 1/56; % waning of VS to S
tau = 1; %0.1; % time step under tau method
nextoutput = runP.ots;
nouts = 1;
time = 0; % start time
```

CREATE INFECTION MATRIX

```
alpha = 0.0193; %factor for making herd R0 from within group mixing
(see Chapters 2, 4)
INFMAT = createINFMATthesis ( alpha, Num_Farms );

numRecPts = floor(runP.runtime/runP.ots)+1;
N = int16(zeros( numRecPts, 6*8*Num_Farms )); % PATTERN Farm1: M( G
S S P W F ) S( G S S P W F )... I() R() RS(). Farm2: M() S() I()...
pointN = [ M S I R RS VS VI VR ];
for j = 1 : Num_Farms % does each farm % PATTERN Farm1: M( G S S P W
F ) S( G S S P W F )... I() R() RS(). Farm2: M() S() I()...
    for i = 1 : 8; % just does one farm - EACH i RECORDS THE 8
INFECTION GROUPS
        N( nouts, (1+(i-1)*6)+48*(j-1) ) = sum(pointN( (1+(i-
1)*Num_Pop)+54*(j-1):(9+(i-1)*Num_Pop)+54*(j-1) )); % gilts
        N( nouts, (2+(i-1)*6)+48*(j-1) ) = sum(pointN( (10+(i-
1)*Num_Pop)+54*(j-1):(26+(i-1)*Num_Pop)+54*(j-1) )); % dry sows
        N( nouts, (3+(i-1)*6)+48*(j-1) ) = sum(pointN( (27+(i-
1)*Num_Pop)+54*(j-1):(30+(i-1)*Num_Pop)+54*(j-1) )); % Farrow sows
        N( nouts, (4+(i-1)*6)+48*(j-1) ) = sum(pointN( (31+(i-
1)*Num_Pop)+54*(j-1):(34+(i-1)*Num_Pop)+54*(j-1) )); % piglets
        N( nouts, (5+(i-1)*6)+48*(j-1) ) = sum(pointN( (35+(i-
1)*Num_Pop)+54*(j-1):(40+(i-1)*Num_Pop)+54*(j-1) )); %
weaners/growers
        N( nouts, (6+(i-1)*6)+48*(j-1) ) = sum(pointN( (41+(i-
1)*Num_Pop)+54*(j-1):(54+(i-1)*Num_Pop)+54*(j-1) )); % finishers
    end
end
movetime = 7;
birthtime = 3;
sendtoorder = ones( 1, Num_Farms );
culled = zeros( 1, Num_Farms );
lorry = zeros( Num_Farms, 8 );
cullsperweek = zeros( 1, Num_Farms );
newearlyInf = zeros( Num_Farms, 18 );
newlateInf = zeros( Num_Farms, 6 );
pigsLostweek = zeros( 1, Num_Farms);
post11WeekSowGroups = [];
pre11WeekSowGroups = [];
for x = 10:54:Num_Farms*54
    pre11WeekSowGroups = [ pre11WeekSowGroups x x+1 x+2 x+3 x+4 x+5
x+6 x+7 x+8 x+9 x+10 x+11 ];
end
for x = 22:54:Num_Farms*54
    post11WeekSowGroups = [ post11WeekSowGroups x x+1 x+2 x+3 x+4 ];
end
TOTSOWmort = zeros( 1, Num_Farms );
```

```
tallySOWmort = zeros( 1, Num_Farms );
NUCgiltTime = 63;
fadeout = zeros( 1, Num_Farms);
```

MISCELLANEOUS RECORDING VARIABLES

```
underweight_slaughter = zeros( Num_Farms, numRecPts );
weaned_Persow = zeros( Num_Farms, numRecPts );
slaughtered_Persow = zeros( Num_Farms, numRecPts );
pigsLost = zeros( Num_Farms, numRecPts );
farm_Growdeaths = zeros( floor((floor(runP.runtime/runP.ots) +
1)/4), Num_Farms );
farm_Findeaths = zeros( floor((floor(runP.runtime/runP.ots) + 1)/4),
Num_Farms );
farm_returns = zeros( numRecPts, Num_Farms);
farm_abortions = zeros( numRecPts, Num_Farms);
Growdeaths = zeros( 1, Num_Farms );
Findeaths = zeros( 1, Num_Farms );
cum_growertotal = zeros( 1, Num_Farms);
cum_fintotal = zeros( 1, Num_Farms );
sowsfarrowed = zeros( Num_Farms, 24 );
count = zeros( 1, Num_Farms );
inf_In = zeros( 1, Num_Farms );
inf_Out = zeros( 1, Num_Farms );
notenoughgilts = zeros( 1, Num_Farms );
timesince_Vacc = zeros( Num_Farms, 21 );
timesince_Vaccrear = zeros( Num_Farms, 20 );
wean_week = zeros( numRecPts, Num_Farms );
slaughter_week = zeros( numRecPts, Num_Farms );
doses = zeros( numRecPts, Num_Farms );
infintro = 1513;
cullcount = zeros( 1, Num_Farms );
carry_Cull = false( 1, Num_Farms );
```

RUN SIMULATION THROUGH TIME

```
while (time < runP.runtime)

    %record state if at next recording time
    if time+tau > nextoutput % comes before the time actually chages
to time+timestep, so before the step is made
        nouts = nouts + 1;
        pointN = [ M S I R RS VS VI VR ]; % N(nouts,:) = [ M S I R
RS ];
        for j = 1 : Num_Farms % does each farm % PATTERN Farm1: M( G
S S P W F ) S( G S S P W F )... I() R() RS(). Farm2: M() S() I()...
            for i = 1 : 8; % just does one farm - EACH i RECORDS THE
7 INFECTION GROUPS
                N( nouts, (1+(i-1)*6)+48*(j-1) ) = sum(pointN(
(1+(i-1)*Num_Pop)+54*(j-1):(9+(i-1)*Num_Pop)+54*(j-1) )); % gilts
                N( nouts, (2+(i-1)*6)+48*(j-1) ) = sum(pointN(
(10+(i-1)*Num_Pop)+54*(j-1):(25+(i-1)*Num_Pop)+54*(j-1) )); % dry
sows
                N( nouts, (3+(i-1)*6)+48*(j-1) ) = sum(pointN(
(26+(i-1)*Num_Pop)+54*(j-1):(30+(i-1)*Num_Pop)+54*(j-1) )); % Farrow
sows
                N( nouts, (4+(i-1)*6)+48*(j-1) ) = sum(pointN(
(31+(i-1)*Num_Pop)+54*(j-1):(34+(i-1)*Num_Pop)+54*(j-1) )); %
piglets
```

```matlab
                N( nouts, (5+(i-1)*6)+48*(j-1) ) = sum(pointN(
(35+(i-1)*Num_Pop)+54*(j-1):(40+(i-1)*Num_Pop)+54*(j-1) )); %
weaners/growers
                N( nouts, (6+(i-1)*6)+48*(j-1) ) = sum(pointN(
(41+(i-1)*Num_Pop)+54*(j-1):(54+(i-1)*Num_Pop)+54*(j-1) )); %
finishers
            end
        end
        nextoutput = nextoutput + runP.ots;
        for i = 1 : Num_Farms % calculates number of farms infected
& mass lost
            pigsLost( i, nouts ) = pigsLostweek( i );
            pigsLostweek( i ) = 0;
        end
    end

    %do births
    if time + tau > birthtime % births should always occur at
earlier date than moves as births here are weekly, and births are
scheduled to happen first!
        for farm = 1 : Num_Farms % births
            group = (farm-1)*54;
            if P( 27+group ) > 0
                earlySowInf = newearlyInf( farm, 18 )*0.85; % % only
85% as the other 15% returned to service so never reach the
farrowing house
                lateSowInf = newlateInf( farm, 6 ); % number of sows
infected post 11 weeks gestation
                if ( earlySowInf + lateSowInf ) > (I( 27 + group ) +
R( 27 + group ))
                    ratioearly = earlySowInf/(earlySowInf +
lateSowInf);
                    ratiolate = lateSowInf/(earlySowInf +
lateSowInf);
                    earlySowInf = round((I( 27 + group ) + R( 27 +
group )) * ratioearly);
                    lateSowInf = round((I( 27 + group ) + R( 27 +
group )) * ratiolate);
                end
                healthySows = P( 27 + group ) - ( earlySowInf +
lateSowInf );
                aborted = binorndX( lateSowInf, 0.1 ); % number of
those sows aborting - approx 10 % go with this as no literature to
suggest otherwise, and Evans 2010 uses 10%
                if aborted > ( I( 27 + group ) + R( 27 + group ) +
RS( 27 + group ) )
                    aborted = 0;
                end
                farm_abortions( nouts, farm ) =
(aborted*100)/double(P(27+group));
                earlyinfpiglets = round(earlySowInf * (11.2*0.74));
                lateinfpiglets = round((lateSowInf - aborted) *
(11.2*0.44));
                healthysowpiglets = round(healthySows * 11.2);
                piglets = earlyinfpiglets + lateinfpiglets +
healthysowpiglets;
                pigsLostweek( farm ) = round(P( 27 + group ) * 11.2)
- piglets; % tally of piglets lost to disease of pregnancy
                healthysowbirthrate = [ (single(S( 27 + group )) +
single(RS( 27 + group ))) ((single(I( 27 + group )) + single(R( 27 +
group ))...
```

```matlab
                    + single(VR( 27 + group ))) - single(earlySowInf
+ lateSowInf)) (single(VS( 27 + group )) +  single(VI( 27 + group
))) ]; % working out prop piglets born susceptible
                healthysowbirthrate = healthysowbirthrate /
sum(healthysowbirthrate);
                X = int16(mnrndX( healthysowpiglets ,
healthysowbirthrate ));

                if aborted > I( 27 + group ) % SOMETIMES sows have
recovered before reaching term, so it is actually R sows that are
seen to have aborted
                    IT( 10 + group ) = I( 10 + group ) + I( 27 +
group ); IT( 27 + group ) = 0;
                    if ( aborted - I( 27 + group ) ) < RT( 27 +
group )
                        RT( 10 + group ) = RT( 10 + group ) + (
aborted - I( 27 + group ) ); RT( 27 + group ) = R( 27 + group ) - (
aborted - I( 27 + group ) );
                    else % if there are not enough sows in I and R,
take from RS
                        RT( 10 + group ) = RT( 10 + group ) + RT( 27
+ group ); RT( 27 + group ) = 0;
                        RST( 10 + group ) = RS( 10 + group ) + (
aborted - I( 27 + group ) - R( 27 + group ) ); RST( 27 + group ) =
RST( 27 + group ) - ( aborted - I( 27 + group ) - R( 27 + group ) );
                    end
                else
                    IT( 27 + group ) = I( 27 + group ) - aborted;
IT( 10 + group ) = IT( 10 + group ) + aborted; % aborted sows return
to service
                end
                %check for consistency
                if IT( 27 + group ) < 0 || RT( 27 + group ) < 0 ||
RST( 27 + group ) < 0
                    disp ('pop < 0')
                    keyboard
                end

                ST( 31 + group ) = S( 31 + group ) + X(1); % piglets
born to seronegative pigs
                MT( 31 + group ) = M( 31 + group ) + X(2) +
earlyinfpiglets + lateinfpiglets + X(3); % X(3) is the pigs born to
vaccinated sows
                sowsfarrowed( farm , 1 ) = P( 27 + group ) -
aborted;
            end
        end
        time = birthtime;
        birthtime = birthtime + 7;
        M = MT; S = ST; I = IT; R = RT; RS = RST; VS = VST; VI =
VIT; VR = VRT;
    end

    % do deaths, movements and vaccinations
    if time + tau > movetime % day on which all movements occur
        for farm = 1 : Num_Farms % MORTALITY  -  percentages from
2010, BPEX technical report
            group = (farm-1)*54;

            [ deaths ] = mortality( 0.0007, [ M( 10+group:30+group )
S( 10+group:30+group ) I( 10+group:30+group ) R( 10+group:30+group )
```

```
RS( 10+group:30+group ) VS( 10+group:30+group ) VI(
10+group:30+group ) VR( 10+group:30+group ) ] );
        M( 10+group:30+group ) = M( 10+group:30+group ) -
deaths(1:21);
        S( 10+group:30+group ) = S( 10+group:30+group ) -
deaths(22:42);
        I( 10+group:30+group ) = I( 10+group:30+group ) -
deaths(43:63);
        R( 10+group:30+group ) = R( 10+group:30+group ) -
deaths(64:84);
        RS( 10+group:30+group ) = RS( 10+group:30+group ) -
deaths(85:105);
        VS( 10+group:30+group ) = VS( 10+group:30+group ) -
deaths(106:126);
        VI( 10+group:30+group ) = VI( 10+group:30+group ) -
deaths(127:147);
        VR( 10+group:30+group ) = VR( 10+group:30+group ) -
deaths(148:168);

        TOTSOWmort(farm) = sum(deaths); % recorded per farm for
later use when bringing in gilts
        tallySOWmort(farm) = tallySOWmort(farm) +
TOTSOWmort(farm);
        [ deaths ] = mortality( 0.033384931, [ M(
31+group:34+group ) S( 31+group:34+group ) I( 31+group:34+group ) R(
31+group:34+group ) RS( 31+group:34+group ) VS( 31+group:34+group )
VI( 31+group:34+group ) VR( 31+group:34+group ) ] );
        M( 31+group:34+group ) = M( 31+group:34+group ) -
deaths(1:4);
        S( 31+group:34+group ) = S( 31+group:34+group ) -
deaths(5:8);
        I( 31+group:34+group ) = I( 31+group:34+group ) -
deaths(9:12);
        R( 31+group:34+group ) = R( 31+group:34+group ) -
deaths(13:16);
        RS( 31+group:34+group ) = RS( 31+group:34+group ) -
deaths(17:20);
        VS( 31+group:34+group ) = VS( 31+group:34+group ) -
deaths(21:24);
        VI( 31+group:34+group ) = VI( 31+group:34+group ) -
deaths(25:28);
        VR( 31+group:34+group ) = VR( 31+group:34+group ) -
deaths(29:32);

        [ deaths ] = mortality( 0.00681944, [ M(
35+group:40+group ) S( 35+group:40+group ) I( 35+group:40+group ) R(
35+group:40+group ) RS( 35+group:40+group ) VS( 35+group:40+group )
VI( 35+group:40+group ) VR( 35+group:40+group ) ] );
        M( 35+group:40+group ) = M( 35+group:40+group ) -
deaths(1:6);
        S( 35+group:40+group ) = S( 35+group:40+group ) -
deaths(7:12);
        I( 35+group:40+group ) = I( 35+group:40+group ) -
deaths(13:18);
        R( 35+group:40+group ) = R( 35+group:40+group ) -
deaths(19:24);
        RS( 35+group:40+group ) = RS( 35+group:40+group ) -
deaths(25:30);
        VS( 35+group:40+group ) = VS( 35+group:40+group ) -
deaths(31:36);
```

```matlab
            VI( 35+group:40+group ) = VI( 35+group:40+group ) -
deaths(37:42);
            VR( 35+group:40+group ) = VR( 35+group:40+group ) -
deaths(43:48);
            TOTgrowmort = sum(deaths); % not recorded per farm as
used within the same loop,
            [ deaths ] = mortality( 0.008097832, [ M(
41+group:54+group ) S( 41+group:54+group ) I( 41+group:54+group ) R(
41+group:54+group ) RS( 41+group:54+group ) VS( 41+group:54+group )
VI( 41+group:54+group ) VR( 41+group:54+group ) ] );
            M( 41+group:54+group ) = M( 41+group:54+group ) -
deaths(1:14);
            S( 41+group:54+group ) = S( 41+group:54+group ) -
deaths(15:28);
            I( 41+group:54+group ) = I( 41+group:54+group ) -
deaths(29:42);
            R( 41+group:54+group ) = R( 41+group:54+group ) -
deaths(43:56);
            RS( 41+group:54+group ) = RS( 41+group:54+group ) -
deaths(57:70);
            VS( 41+group:54+group ) = VS( 41+group:54+group ) -
deaths(71:84);
            VI( 41+group:54+group ) = VI( 41+group:54+group ) -
deaths(85:98);
            VR( 41+group:54+group ) = VR( 41+group:54+group ) -
deaths(99:112);
            TOTfinmort = sum(deaths);

            % grower and finisher infection induced mortality
considered different and coded separately
            % grower disease deaths
            if runP.farmtypes( farm ) ~= 3
                disease_growdeaths = binorndX( sum(I(
35+group:40+group )), runP.disgrowMORT );
                Ideathrates = (double( I(35+group:40+group) )./ sum(
I(35+group:40+group) ));
                X = int16(mnrndX(disease_growdeaths,Ideathrates));
                while any(X > I( 35+group:40+group ) )
                    if sum( X ) >= sum( I(35+group:40+group) )
                        X = I(35+group:40+group);
                    else
                        X =
int16(mnrndX(disease_growdeaths,Ideathrates));
                    end
                end
                I(35+group:40+group) = I(35+group:40+group) - X;

                % finisher disease deaths
                disease_findeaths = binorndX( sum(I(
41+group:54+group )), runP.disfinMORT );
                Ideathrates = (double( I(41+group:54+group) )./ sum(
I(41+group:54+group) ));
                X = int16(mnrndX(disease_findeaths,Ideathrates));
                while any(X > I( 41+group:54+group ) )
                    if sum( X ) >= sum( I(41+group:54+group) )
                        X = I(41+group:54+group);
                    else
                        X =
int16(mnrndX(disease_findeaths,Ideathrates));
                    end
                end
```

```matlab
                    I(41+group:54+group) = I(41+group:54+group) - X;

                    Growdeaths( farm ) = Growdeaths( farm ) +
(disease_growdeaths + TOTgrowmort);
                    Findeaths( farm ) = Findeaths( farm ) +
(disease_findeaths + TOTfinmort);

                    cum_growertotal( farm ) = cum_growertotal( farm ) +
sum( P(35+group:40+group) );
                    cum_fintotal( farm ) = cum_fintotal( farm ) + sum(
P(41+group:54+group) );

                    count(farm) = count(farm) + 1;
                    if count(farm) == 4
                        farm_Growdeaths( (nouts-1)/4, farm ) = (
Growdeaths( farm ) / (cum_growertotal(farm)/4) ) *100;
                        if isnan(farm_Growdeaths( (nouts-1)/4, farm ))
                            farm_Growdeaths( (nouts-1)/4, farm ) = 0;
                        end
                        farm_Findeaths( (nouts-1)/4, farm ) = (
Findeaths( farm ) / (cum_fintotal(farm)/4) ) * 100;
                        if isnan(farm_Findeaths( (nouts-1)/4, farm ))
                            farm_Findeaths( (nouts-1)/4, farm ) = 0;
                        end
                        Growdeaths( farm ) = 0;
                        Findeaths( farm ) = 0;
                        cum_growertotal( farm ) = 0;
                        cum_fintotal( farm ) = 0;
                        count(farm) = 0;
                    end
                end
        end % mortality, deaths per week

        for farm = 1 : Num_Farms % sows returning - record every
week
            if runP.farmtypes(farm) ~= 5 && runP.farmtypes(farm) ~=
6
                group = (farm-1)*54;
                inf_return1 = binorndX( I( 13 + group ), 0.5 ); %
binorndX cannot pick more than exist
                I(13+group) = I(13+group) - inf_return1;
                I(10+group) = I(10+group) + inf_return1;
                norm_return1 = binorndX( S( 13 + group )+R( 13 +
group )+RS( 13 + group )+VS( 13 + group )+VI( 13 + group )+VR( 13 +
group ), 0.15 ); % 15% return at week 3 gestation
                rates = double([ S(13+group) R(13+group)
RS(13+group) VS( 13 + group ) VI( 13 + group ) VR( 13 + group )
])./double(S(13+group)+R(13+group)+RS(13+group)+VS(13+group)+VI(13+g
roup)+VR(13+group));
                if any(rates) == 1
                    X = zeros( 1, 6 );
                    X( rates==1 ) = norm_return1;
                else
                    X = int16(mnrndX( norm_return1, rates ));
                end
                while any(X > [S(13+group) R(13+group) RS(13+group)
VS( 13 + group ) VI( 13 + group ) VR( 13 + group )] )
                    if sum( X ) >= (S(13+group) + R(13+group) +
RS(13+group) + VS( 13 + group ) + VI( 13 + group ) + VR( 13 + group
))
```

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```matlab
                               X = [S(13+group) R(13+group) RS(13+group)
VS( 13 + group ) VI( 13 + group ) VR( 13 + group )];
                       else
                           if any(rates) == 1
                               X = zeros( 1, 6 );
                               X( rates==1 ) = norm_return1;
                           else
                               X = int16(mnrndX( norm_return1, rates
));
                           end
                       end
                   end
                   S(13+group) = S(13+group) - X(1);   S(10+group) =
S(10+group) + X(1);
                   R(13+group) = R(13+group) - X(2);   R(10+group) =
R(10+group) + X(2);
                   RS(13+group) = RS(13+group) - X(3); RS(10+group) =
RS(10+group) + X(3);
                   VS(13+group) = VS(13+group) - X(4); VS(10+group) =
VS(10+group) + X(4);
                   VI(13+group) = VI(13+group) - X(5); VI(10+group) =
VI(10+group) + X(5);
                   VR(13+group) = VR(13+group) - X(6); VR(10+group) =
VR(10+group) + X(6);

                   farm_returns( nouts, farm ) = ((inf_return1 +
norm_return1)/double(P(13+group)))*100;
                   if isnan(farm_returns( nouts, farm ))
                       farm_returns( nouts, farm ) = 0;
                   end
               end
           end
       end

       %do within-herd movements
       for farm = 1 : Num Farms % all farms do all WITHIN FARM
MOVEMENTS and send pigs out onto LORRIES, no arrivals
           group = (farm-1)*54;
           % moves all gilts and sows along
           MT( 11+group:30+group ) = M( 10+group:29+group );% moves
all groups 10-29 into 11-30 sows
           ST( 11+group:30+group ) = S( 10+group:29+group );
           IT( 11+group:30+group ) = I( 10+group:29+group );
           RT( 11+group:30+group ) = R( 10+group:29+group );
           RST( 11+group:30+group ) = RS( 10+group:29+group );
           VST( 11+group:30+group ) = VS( 10+group:29+group );
           VIT( 11+group:30+group ) = VI( 10+group:29+group );
           VRT( 11+group:30+group ) = VR( 10+group:29+group );
           MT( 2+group:8+group ) = M( 1+group:7+group );% moves all
groups 1-8 into 2-9 gilts only
           ST( 2+group:8+group ) = S( 1+group:7+group );
           IT( 2+group:8+group ) = I( 1+group:7+group );
           RT( 2+group:8+group ) = R( 1+group:7+group );
           RST( 2+group:8+group ) = RS( 1+group:7+group );
           VST( 2+group:8+group ) = VS( 1+group:7+group );
           VIT( 2+group:8+group ) = VI( 1+group:7+group );
           VRT( 2+group:8+group ) = VR( 1+group:7+group );
           MT( 1+group ) = 0; % makes group 1 empty
           ST( 1+group ) = 0;
           IT( 1+group ) = 0;
           RT( 1+group ) = 0;
           RST( 1+group ) = 0;
```

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```matlab
            VST( 1+group ) = 0;
            VIT( 1+group ) = 0;
            VRT( 1+group ) = 0;
            MT( 9+group ) = MT( 9+group ) + M( 8+group );% adds
group 8 to remaining 9 gilts
            ST( 9+group ) = ST( 9+group ) + S( 8+group );
            IT( 9+group ) = IT( 9+group ) + I( 8+group );
            RT( 9+group ) = RT( 9+group ) + R( 8+group );
            RST( 9+group ) = RST( 9+group ) + RS( 8+group );
            VST( 9+group ) = VST( 9+group ) + VS( 8+group );
            VIT( 9+group ) = VIT( 9+group ) + VI( 8+group );
            VRT( 9+group ) = VRT( 9+group ) + VR( 8+group );
            % gilts added to group 10, after weaning

            cullsperweek( farm ) =
round(sum(P(10+group:30+group))*0.5/52); % 50% of sows replaced in a
year, Charlotte used 45% BPEX figures vary between 45 - 55%
            if carry_Cull( farm )
                cullsperweek2 = cullsperweek*2;
            else
                cullsperweek2 = cullsperweek;
            end
            transferrates = [ single(M( 30 + group ))/single(P( 30 +
group )) single(S( 30 + group ))/single(P( 30 + group ))...
                single(I( 30 + group ))/single(P( 30 + group ))
single(R( 30 + group ))/single(P( 30 + group ))...
                single(RS( 30 + group ))/single(P( 30 + group ))
single(VS( 30 + group ))/single(P( 30 + group ))...
                single(VI( 30 + group ))/single(P( 30 + group ))
single(VR( 30 + group ))/single(P( 30 + group ))];
            if P( 9 + group ) > 0
                weeks_Cull =
int16(mnrndX(cullsperweek2(farm),transferrates));
            else
                weeks Cull = zeros( 1, 8 );
            end
            while any(weeks_Cull>[ M( 30 + group ) S( 30 + group )
I( 30 + group ) R( 30 + group ) RS( 30 + group ) VS( 30 + group )
VI( 30 + group )  VR( 30 + group ) ])
                if cullsperweek2( farm ) >= P( 30 + group )
                    weeks_Cull = [ M( 30 + group ) S( 30 + group )
I( 30 + group ) R( 30 + group ) RS( 30 + group ) VS( 30 + group )
VI( 30 + group )  VR( 30 + group ) ];
                else
                    weeks_Cull =
int16(mnrndX(cullsperweek2(farm),transferrates));
                end
            end % returns weaned sows back to service minus culls
            MT( 10+group ) = M( 30+group ) - weeks_Cull( 1 );
            ST( 10+group ) = S( 30+group ) - weeks_Cull( 2 );
            IT( 10+group ) = I( 30+group ) - weeks_Cull( 3 );
            RT( 10+group ) = R( 30+group ) - weeks_Cull( 4 );
            RST( 10+group ) = RS( 30+group ) - weeks_Cull( 5 );
            VST( 10+group ) = VS( 30+group ) - weeks_Cull( 6 );
            VIT( 10+group ) = VI( 30+group ) - weeks_Cull( 7 );
            VRT( 10+group ) = VR( 30+group ) - weeks_Cull( 8 );

            culled( farm ) = culled( farm ) + cullsperweek( farm );
            if time + tau > runP.vaccinate_Time
                cullcount( farm ) = cullcount( farm ) + sum(
weeks_Cull );
```

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```matlab
            end
            if sum(weeks_Cull) < cullsperweek( farm )
                carry_Cull( farm ) = true;
            end

            transferrates = [ single(M( 9 + group )) single(S( 9 +
group )) single(I( 9 + group )) single(R( 9 + group )) single(RS( 9
+ group )) single(VS( 9 + group )) single(VI( 9 + group ))
single(VR( 9 + group )) ]./single(P( 9 + group ));
            giltsto_add = sum( weeks_Cull ) + TOTSOWmort(farm);

            X = int16(mnrndX( giltsto_add, transferrates )); %
brings in set number of gilts regardless of number culled
            X2=zeros(1,8);
            while any(X>[ M( 9 + group ) S( 9 + group ) I( 9 + group
) R( 9 + group ) RS( 9 + group ) VS( 9 + group ) VI( 9 + group ) VR(
9 + group ) ])
                if giltsto_add > P(9+group)

                    X = [ M( 9 + group ) S( 9 + group ) I( 9 + group
) R( 9 + group ) RS( 9 + group ) VS( 9 + group ) VI( 9 + group ) VR(
9 + group ) ];
                    giltsstillneed = giltsto_add - sum(X);
                    others = find( P( 1+group : 8+group ) > 0 );
                    if ~isempty(others)
                        other = max(others);
                        transferrates2 = [ single(M( other + group
)) single(S( other + group )) single(I( other + group )) single(R(
other + group )) single(RS( other + group )) single(VS( other +
group )) single(VI( other + group )) single(VR( other + group ))
]./single(P( other + group ));
                        if giltsstillneed > P(other+group)
                            giltsstillneed = P(other+group);
                        end
                        X2 = int16(mnrndX( giltsstillneed,
transferrates2 ));
                        while any(X2>[ M( other + group ) S( other +
group ) I( other + group ) R( other + group ) RS( other + group )
VS( other + group ) VI( other + group ) VR( other + group ) ])
                            X2 = int16(mnrndX( giltsstillneed,
transferrates2 ));
                        end
                    else
                        X2=zeros(1,8);
                    end
                elseif giltsto_add == P(9+group)
                    X = [ M( 9 + group ) S( 9 + group ) I( 9 + group
) R( 9 + group ) RS( 9 + group ) VS( 9 + group ) VI( 9 + group ) VR(
9 + group ) ];
                    X2=zeros(1,8);
                else
                    X = int16(mnrndX( giltsto_add, transferrates ));
                    X2=zeros(1,8);
                 end
            end

            MT( 10+group ) = MT( 10+group ) + X( 1 ) + X2( 1 ); %
adds required amount of gilts to sows
            ST( 10+group ) = ST( 10+group ) + X( 2 ) + X2( 2 );
            IT( 10+group ) = IT( 10+group ) + X( 3 ) + X2( 3 );
            RT( 10+group ) = RT( 10+group ) + X( 4 ) + X2( 4 );
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            RST( 10+group ) = RST( 10+group ) + X( 5 ) + X2( 5 );
            VST( 10+group ) = VST( 10+group ) + X( 6 ) + X2( 6 );
            VIT( 10+group ) = VIT( 10+group ) + X( 7 ) + X2( 7 );
            VRT( 10+group ) = VRT( 10+group ) + X( 8 ) + X2( 8 );
            MT( 9+group ) = MT( 9+group ) - X( 1 ); % removes number
of needed gilts from gilt group
            ST( 9+group ) = ST( 9+group ) - X( 2 );
            IT( 9+group ) = IT( 9+group ) - X( 3 );
            RT( 9+group ) = RT( 9+group ) - X( 4 );
            RST( 9+group ) = RST( 9+group ) - X( 5 );
            VST( 9+group ) = VST( 9+group ) - X( 6 );
            VIT( 9+group ) = VIT( 9+group ) - X( 7 );
            VRT( 9+group ) = VRT( 9+group ) - X( 8 );

            if sum(X2) > 0
                MT( other+1+group ) = MT( other+1+group ) - X2( 1 );
% removes number of needed gilts from other gilt group when 9
doesn't have enough
                ST( other+1+group ) = ST( other+1+group ) - X2( 2 );
                IT( other+1+group ) = IT( other+1+group ) - X2( 3 );
                RT( other+1+group ) = RT( other+1+group ) - X2( 4 );
                RST( other+1+group ) = RST( other+1+group ) - X2( 5
);
                VST( other+1+group ) = VST( other+1+group ) - X2( 6
);
                VIT( other+1+group ) = VIT( other+1+group ) - X2( 7
);
                VRT( other+1+group ) = VRT( other+1+group ) - X2( 8
);
            end

            if sum(X)+sum(X2) < giltsto_add
                notenoughgilts(farm) = notenoughgilts(farm) +
(giltsto_add - (sum(X)+sum(X2))); % keeps track of occassions where
sow group size is not maintained
            end
            % THIS PIECE OF CODE WILL ADD EXTRA GILTS IF IN PREVIOUS
WEEK THERE WERE NOT ENOUGH GILTS TO ADD
            if sum( [ MT( 9+group ) ST( 9+group ) IT( 9+group ) RT(
9+group ) RST( 9+group ) VST( 9+group ) VIT( 9+group ) VRT( 9+group
) ] ) > 0 && notenoughgilts(farm) > 0
                transferrates = [ single(MT( 9 + group )) single(ST(
9 + group )) single(IT( 9 + group )) single(RT( 9 + group ))
single(RST( 9 + group )) single(VST( 9 + group )) single(VIT( 9 +
group )) single(VRT( 9 + group )) ]./(sum( [ MT( 9+group ) ST(
9+group ) IT( 9+group ) RT( 9+group ) RST( 9+group ) VST( 9+group )
VIT( 9+group ) VRT( 9+group ) ] ));
                if notenoughgilts(farm) < sum( [ MT( 9+group ) ST(
9+group ) IT( 9+group ) RT( 9+group ) RST( 9+group ) VST( 9+group )
VIT( 9+group ) VRT( 9+group ) ] )
                    X = int16(mnrndX( notenoughgilts(farm),
transferrates ));
                    while any(X > [ MT( 9+group ) ST( 9+group ) IT(
9+group ) RT( 9+group ) RST( 9+group ) VST( 9+group ) VIT( 9+group )
VRT( 9+group ) ])
                        X = int16(mnrndX( notenoughgilts(farm),
transferrates ));
                    end
                    notenoughgilts(farm) = 0;
```

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                elseif notenoughgilts(farm) == sum( [ MT( 9+group )
ST( 9+group ) IT( 9+group ) RT( 9+group ) RST( 9+group ) VST(
9+group ) VIT( 9+group ) VRT( 9+group ) ] )
                    X = [ MT( 9+group ) ST( 9+group ) IT( 9+group )
RT( 9+group ) RST( 9+group ) VST( 9+group ) VIT( 9+group ) VRT(
9+group ) ];
                elseif notenoughgilts(farm) > sum( [ MT( 9+group )
ST( 9+group ) IT( 9+group ) RT( 9+group ) RST( 9+group ) VST(
9+group ) VIT( 9+group ) VRT( 9+group ) ] )
                    X = [ MT( 9+group ) ST( 9+group ) IT( 9+group )
RT( 9+group ) RST( 9+group ) VST( 9+group ) VIT( 9+group ) VRT(
9+group ) ];
                    notenoughgilts(farm) = notenoughgilts(farm) -
sum(X);
                end
                MT( 10+group ) = MT( 10+group ) + X( 1 ); % adds
required amount of gilts to sows
                ST( 10+group ) = ST( 10+group ) + X( 2 );
                IT( 10+group ) = IT( 10+group ) + X( 3 );
                RT( 10+group ) = RT( 10+group ) + X( 4 );
                RST( 10+group ) = RST( 10+group ) + X( 5 );
                VST( 10+group ) = VST( 10+group ) + X( 6 );
                VIT( 10+group ) = VIT( 10+group ) + X( 7 );
                VRT( 10+group ) = VRT( 10+group ) + X( 8 );
                MT( 9+group ) = MT( 9+group ) - X( 1 ); % removes
number of needed gilts from gilt group
                ST( 9+group ) = ST( 9+group ) - X( 2 );
                IT( 9+group ) = IT( 9+group ) - X( 3 );
                RT( 9+group ) = RT( 9+group ) - X( 4 );
                RST( 9+group ) = RST( 9+group ) - X( 5 );
                VST( 9+group ) = VST( 9+group ) - X( 6 );
                VIT( 9+group ) = VIT( 9+group ) - X( 7 );
                VRT( 9+group ) = VRT( 9+group ) - X( 8 );
            end

            % SLAUGHTERS
            if runP.farmtypes( farm ) == 4 || runP.farmtypes( farm )
== 6 % farms sending to slaughter
                if P( 54 + group ) > 0
                    slaughter_week( nouts, farm ) = P( 54 + group );
                    underweight_slaughter( farm, nouts ) =
((double(I( 54 + group))*0.5*20*0.091) + double(R( 54 + group ) +RS(
54 + group ))*20*0.091) / double(P( 54 + group )); % average mass
lost per slaughtered pig, assuming infected pigs have experienced
half infected period
                    if runP.farmtypes( farm ) == 4
                        slaughtered_Persow( farm, nouts ) =
double(P( 54 + group )) / sowsfarrowed( farm, 24 );
                    end
                end
                MT( 54+group ) = 0; % sent to slaughter emptys last
group before moving them forward
                ST( 54+group ) = 0;
                IT( 54+group ) = 0;
                RT( 54+group ) = 0;
                RST( 54+group ) = 0;
                VST( 54+group ) = 0;
                VIT( 54+group ) = 0;
                VRT( 54+group ) = 0;
                if (runP.farmtypes(farm) == 3 ||
runP.farmtypes(farm) == 4) && time > 1852
```

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```matlab
                        inf_Out(farm) = inf_Out(farm) + I( 54 + group );
                    end
                end

                if runP.farmtypes( farm ) == 1 || runP.farmtypes( farm )
== 2 % farms producing replacement gilts
                    if P( 54 + group ) > 0 % gilts taken off of farm,
onto a lorry
                        lorry( farm, : ) = [ M( 54 + group ) S( 54 +
group ) I( 54 + group ) R( 54 + group ) RS( 54 + group ) VS( 54 +
group ) VI( 54 + group ) VR( 54 + group ) ];
                        MT( 54+group ) = 0; ST( 54+group ) = 0; IT(
54+group ) = 0; RT( 54+group ) = 0; RST( 54+group ) = 0; VST(
54+group ) = 0; VIT( 54+group ) = 0; VRT( 54+group ) = 0;
                        slaughtered_Persow( farm, nouts ) = double(P( 54
+ group )) / sowsfarrowed( farm, 24 );
                        %                    slaughter_week( nouts,
farm ) = 1; number slaughtered recorded after pigs delivered to
destination herd
                    end
                end

                if runP.farmtypes( farm ) == 3 % breedwean, sending
weaners out
                    if P( 34+group ) > 0
                        lorry( farm, : ) = [ M( 34+group ) S( 34+group )
I( 34+group ) R( 34+group ) RS( 34+group ) VS( 34+group ) VI(
34+group ) VR( 34+group ) ]; % putting all weaners on a lorry
                        MT( 34+group ) = 0; ST( 34+group ) = 0; IT(
34+group ) = 0; RT( 34+group ) = 0; RST( 34+group ) = 0; VST(
34+group ) = 0; VIT( 34+group ) = 0; VRT( 34+group ) = 0;
                        weaned_Persow( farm, nouts ) = double(P( 34 +
group ) ) / sowsfarrowed( farm, 4 );
                        if isnan(weaned_Persow( farm, nouts ))
                            weaned_Persow( farm, nouts ) = 0;
                        elseif isinf(weaned_Persow( farm, nouts ))
                            weaned_Persow( farm, nouts ) = 0;
                        end
                        wean_week( nouts, farm ) = 1;
                    end
                    MT( 32+group:34+group ) = M( 31+group:33+group ); %
moves along all groups 31-33 into 32-34 piglets growers and
finishers on breedwean farms
                    ST( 32+group:34+group ) = S( 31+group:33+group );
                    IT( 32+group:34+group ) = I( 31+group:33+group );
                    RT( 32+group:34+group ) = R( 31+group:33+group );
                    RST( 32+group:34+group ) = RS( 31+group:33+group );
                    VST( 32+group:34+group ) = VS( 31+group:33+group );
                    VIT( 32+group:34+group ) = VI( 31+group:33+group );
                    VRT( 32+group:34+group ) = VR( 31+group:33+group );
                    MT( 31+group ) = 0;
                    ST( 31+group ) = 0;
                    IT( 31+group ) = 0;
                    RT( 31+group ) = 0;
                    RST( 31+group ) = 0;
                    VST( 31+group ) = 0;
                    VIT( 31+group ) = 0;
                    VRT( 31+group ) = 0;
                    if (runP.farmtypes(farm) == 3 ||
runP.farmtypes(runP.farmout) == 4) && time > 1852
                        inf_Out(farm) = inf_Out(farm) + I( 31 + group );
```

```matlab
                    end
                else

                    MT( 32+group:40+group ) = M( 31+group:39+group ); %
moves along all groups 31-39 into 32-40 piglets growers
                    ST( 32+group:40+group ) = S( 31+group:39+group );
                    IT( 32+group:40+group ) = I( 31+group:39+group );
                    RT( 32+group:40+group ) = R( 31+group:39+group );
                    RST( 32+group:40+group ) = RS( 31+group:39+group );
                    VST( 32+group:40+group ) = VS( 31+group:39+group );
                    VIT( 32+group:40+group ) = VI( 31+group:39+group );
                    VRT( 32+group:40+group ) = VR( 31+group:39+group );
                    MT( 31+group ) = 0;
                    ST( 31+group ) = 0;
                    IT( 31+group ) = 0;
                    RT( 31+group ) = 0;
                    RST( 31+group ) = 0;
                    VST( 31+group ) = 0;
                    VIT( 31+group ) = 0;
                    VRT( 31+group ) = 0;
                    if P( 34 + group ) > 0
                        weaned_Persow( farm, nouts ) = double(P( 34 +
group ) ) / sowsfarrowed( farm, 4 );
                        if isnan(weaned_Persow( farm, nouts ))
                            weaned_Persow( farm, nouts ) = 0;
                        elseif isinf(weaned_Persow( farm, nouts ))
                            weaned_Persow( farm, nouts ) = 0;
                        end
                        wean_week(nouts, farm) = 1;
                    end

                    MT( 41+group:54+group ) = 0; % moves along all
groups 40-53 into 41-54 into finishing, all maternal immunity wanes
                    ST( 41+group:54+group ) = S( 40+group:53+group ) +
M( 40+group:53+group );
                    IT( 41+group:54+group ) = I( 40+group:53+group );
                    RT( 41+group:54+group ) = R( 40+group:53+group );
                    RST( 41+group:54+group ) = RS( 40+group:53+group );
                    VST( 41+group:54+group ) = VS( 40+group:53+group );
                    VIT( 41+group:54+group ) = VI( 40+group:53+group );
                    VRT( 41+group:54+group ) = VR( 40+group:53+group );
                end
            end

        %do between herd movements
        for farm = 1 : Num_Farms % all farms have LORRIES arrive -
push transfers here farm represents the from

            if sum( lorry( farm, : ) ) > 0
                lorrytotal = sum( lorry( farm, : ) );
                if runP.farmtypes( farm ) == 1 || runP.farmtypes(
farm ) == 2 % farms producing replacement gilts
                    transferrates = lorry( farm, : )./lorrytotal;
                    giltsREQ = (culled(
runP.farmout(farm,sendtoorder(farm))) +
tallySOWmort(runP.farmout(farm,sendtoorder(farm))));

                    [ row, ~ ] = ind2sub( [Num_Farms,Num_Farms-1],
find( runP.farmout == ( runP.farmout(farm,sendtoorder(farm)))) );
                    if length(row) > 1
                        next = zeros( 1, length(row) );
```

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```matlab
                        numdests = zeros( 1, length(row) );
                        for k = 1: length( row )
                            position = find( runP.farmout(row(k),:)
== runP.farmout(farm,sendtoorder(farm)) );
                            numdests(k) = nnz(
runP.farmout(row(k),:) );
                            x = position - sendtoorder(row(k));
                            if x == 0
                                next(k) = numdests(k);
                            elseif x < 0
                                next(k) = (numdests(k) -
sendtoorder(row(k))) + position;
                            else
                                next(k) = x;
                            end
                        end
                        nextdelivery = min( next );
                        if nextdelivery > 9
                            lossesperweek = (((0.5/52) +
0.0007)*double(N(1,8+((runP.farmout(farm,sendtoorder(farm)))-
1)*48)+N(1,9+((runP.farmout(farm,sendtoorder(farm)))-1)*48)));%/21;
                            giltsREQ = giltsREQ +
ceil(lossesperweek*nextdelivery);
                            if sum(P( 1 +
(runP.farmout(farm,sendtoorder(farm))-1)*54 : 9 +
(runP.farmout(farm,sendtoorder(farm))-1)*54 )) > 0.15*sum(P( 10 +
(runP.farmout(farm,sendtoorder(farm))-1)*54 : 30 +
(runP.farmout(farm,sendtoorder(farm))-1)*54 ))
                                giltsREQ = 0;
                            end
                        end
                        clear next
                    end

                    X = mnrndX( giltsREQ, transferrates );
                    while any( X> lorry( farm, : ) )
                        if sum(X) > sum( lorry( farm, : ) )
                            X = lorry( farm, : );
                        else
                            X = mnrndX( giltsREQ, transferrates );
                        end
                    end
                    MT( 1 + (runP.farmout(farm,sendtoorder(farm))-
1)*54 ) = X( 1 );
                    ST( 1 + (runP.farmout(farm,sendtoorder(farm))-
1)*54 ) = X( 2 );
                    IT( 1 + (runP.farmout(farm,sendtoorder(farm))-
1)*54 ) = X( 3 );
                    RT( 1 + (runP.farmout(farm,sendtoorder(farm))-
1)*54 ) = X( 4 );
                    RST( 1 + (runP.farmout(farm,sendtoorder(farm))-
1)*54 ) = X( 5 );
                    VST( 1 + (runP.farmout(farm,sendtoorder(farm))-
1)*54 ) = X( 6 );
                    VIT( 1 + (runP.farmout(farm,sendtoorder(farm))-
1)*54 ) = X( 7 );
                    VRT( 1 + (runP.farmout(farm,sendtoorder(farm))-
1)*54 ) = X( 8 );

                    if
(runP.farmtypes(runP.farmout(farm,sendtoorder(farm))) == 3 ||
```

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```matlab
runP.farmtypes(runP.farmout(farm,sendtoorder(farm))) == 4) && time >
1852
                        inf_In(runP.farmout(farm,sendtoorder(farm)))
= inf_In(runP.farmout(farm,sendtoorder(farm))) + X( 3 );
                    end

                    % underweight at slaughter calculated from those
that are not used as replacement gilts - no preference of health to
becoming replacement gilt
                    underweight_slaughter( farm, nouts ) =
((double(lorry(farm,3)-X(3))*0.5*(1/gamma)*0.091) +
(double(lorry(farm,4)-X(4)+lorry(farm,5)-X(5))*(1/gamma)*0.091)) /
double(sum(lorry(farm,:))); % average mass lost per slaughtered pig,
assuming infected pigs have experienced half infected period
                    slaughter_week( nouts, farm ) = sum(lorry( farm,
: )) - giltsREQ;
                    if slaughter_week( nouts, farm )<0
                        slaughter_week( nouts, farm )=0;
                    end
                    lorry( farm, : ) = 0; % the rest are sent to
slaughter - CALCULATE MASS LOST OF THESE PIGS!
                    culled(runP.farmout(farm,sendtoorder(farm))) =
0;

tallySOWmort(runP.farmout(farm,sendtoorder(farm))) = 0;
                    sendtoorder( farm ) = sendtoorder( farm ) + 1;
                    if sendtoorder( farm ) > nnz( runP.farmout(
farm, : ) )
                        sendtoorder( farm ) = 1;
                    end

                end
                if runP.farmtypes( farm ) == 3 % breedwean farms

                    ST( 35 + (runP.farmout(farm,sendtoorder( farm )
)-1)*54  ) = ST( 35 + (runP.farmout(farm,sendtoorder( farm ) )-1)*54
) + lorry( farm, 2 ) + lorry( farm, 1 );
                    IT( 35 + (runP.farmout(farm,sendtoorder( farm )
)-1)*54  ) = IT( 35 + (runP.farmout(farm,sendtoorder( farm ) )-1)*54
) + lorry( farm, 3 );
                    RT( 35 + (runP.farmout(farm,sendtoorder( farm )
)-1)*54  ) = RT( 35 + (runP.farmout(farm,sendtoorder( farm ) )-1)*54
) + lorry( farm, 4 );
                    RST( 35 + (runP.farmout(farm,sendtoorder( farm )
)-1)*54  ) = RST( 35 + (runP.farmout(farm,sendtoorder( farm ) )-
1)*54  ) + lorry( farm, 5 );
                    VST( 35 + (runP.farmout(farm,sendtoorder( farm )
)-1)*54  ) = VST( 35 + (runP.farmout(farm,sendtoorder( farm ) )-
1)*54  ) + lorry( farm, 6 );
                    VIT( 35 + (runP.farmout(farm,sendtoorder( farm )
)-1)*54  ) = VIT( 35 + (runP.farmout(farm,sendtoorder( farm ) )-
1)*54  ) + lorry( farm, 7 );
                    VRT( 35 + (runP.farmout(farm,sendtoorder( farm )
)-1)*54  ) = VRT( 35 + (runP.farmout(farm,sendtoorder( farm ) )-
1)*54  ) + lorry( farm, 8 );
                    if
(runP.farmtypes(runP.farmout(farm,sendtoorder(farm))) == 3 ||
runP.farmtypes(runP.farmout(farm,sendtoorder(farm))) == 4) && time >
1852
                        inf_In(runP.farmout(farm,sendtoorder(farm)))
= inf_In(runP.farmout(farm,sendtoorder(farm))) + lorry( farm, 3 );
```

```
                    end

                    lorry( farm, : ) = 0;
                    sendtoorder( farm ) = sendtoorder( farm ) + 1;
                    if sendtoorder( farm ) > nnz( runP.farmout(
farm, : ) )
                        sendtoorder( farm ) = 1;
                    end
                end
            end
        end
        if time + tau > NUCgiltTime % adding suscpetible gilts to
nucleus farm
            ST( 1 ) = culled(1) + tallySOWmort(1);
            tallySOWmort( 1 ) = 0;
            culled( 1 ) = 0;
            if time + tau >= infintro; %1513 %757
                IT( 1 ) = IT( 1 ) + 1; % introduction of infectious
animal
%                 proceed = 1;
                infintro = infintro + 182;
            end
            NUCgiltTime = NUCgiltTime + 63; % new gilts every 9
weeks
        end
        newearlyInf( :, 2:18 ) = newearlyInf( :, 1:17 );
        newearlyInf( :, 1 ) = 0;
        newlateInf( :, 2:6 ) = newlateInf( :, 1:5 );
        newlateInf( :, 1 ) = 0;
        sowsfarrowed( :, 2:24 ) = sowsfarrowed( :, 1:23 );
        sowsfarrowed( :, 1 ) = 0;
        % WILL NEED TO ONLY +7 TO THOSE THAT HAVE BEEN VACCINATED
        a = find(timesince_Vacc > 0);
        timesince_Vacc( a ) = timesince_Vacc( a ) + 7;
        holding = timesince Vacc( :, 21 );
        timesince_Vacc( :, 2:end ) = timesince_Vacc( :, 1:end-1 ); %
after moving sows record their new location and time since
vaccination
        timesince_Vacc( :, 1 ) = holding;
        a = find(timesince_Vaccrear > 0);
        timesince_Vaccrear( a ) = timesince_Vaccrear( a ) + 7;

        timesince_Vaccrear( :, 2:end ) = timesince_Vaccrear( :,
1:end-1 ); % after moving sows record their new location and time
since vaccination
        timesince_Vaccrear( :, 1 ) = 0;
        time = movetime;
        movetime = movetime + 7;
        M = MT; S = ST; I = IT; R = RT; RS = RST; VS = VST; VI =
VIT; VR = VRT;

        % vaccination
        if runP.vaccinate_Sows && time+tau > runP.vaccinate_Time
            for i = 1 : length(runP.vaccinate_Herds)
                group = (runP.vaccinate_Herds(i)-1)*54; % vaccinate
when time since vacc = 0, as they haven't had their first
vaccination yet. Will only apply to applicable farms due to line
above
                if timesince_Vacc(runP.vaccinate_Herds(i),28-9) >=
(21*7) || timesince_Vacc(runP.vaccinate_Herds(i),28-9) == 0 % group
28 is the week after farrowing, 21 weeks later(1 litter), will
```

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```
vaccinate sows every litter, gilts not vaccinated until after first
litter, but their immunity will wane at the rate of the sows they
have joined
                        doses( nouts, runP.vaccinate_Herds(i) ) = doses(
nouts, runP.vaccinate_Herds(i) ) + S( 28+group ) + RS( 28+group ) +
I( 28+group );
                        VST( 28+group ) = VS( 28+group ) + S( 28+group )
+ RS( 28+group );
                        VIT( 28+group ) = VI( 28+group ) + I( 28+group
);
                        ST( 28+group ) = 0;
                        RST( 28+group ) = 0;
                        IT( 28+group ) = 0;
                        timesince_Vacc(runP.vaccinate_Herds(i),28-9) =
0.1; % 0.1 to distinguish between those just vaccinated and those
not vaccinated at all
                    end
                end

        end
        if runP.vaccinate_Gilts && time+tau > runP.vaccinate_Time
            for i = 1 : length(runP.vaccinate_Herds)
                group = (runP.vaccinate_Herds(i)-1)*54;
                doses( nouts, runP.vaccinate_Herds(i) ) = doses(
nouts, runP.vaccinate_Herds(i) ) + S( 1+group ) + RS( 1+group ) + I(
1+group );
                VST( 1+group ) = VS( 1+group ) + S( 1+group ) + RS(
1+group );
                VIT( 1+group ) = VI( 1+group ) + I( 1+group );
                ST( 1+group ) = 0;
                RST( 1+group ) = 0;
                IT( 1+group ) = 0;
            end

        end
        if runP.vaccinate_Rears && time+tau > runP.vaccinate_Time
            for i = 1 : length(runP.vaccinate_Herds)
                group = (runP.vaccinate_Herds(i)-1)*54;
                doses( nouts, runP.vaccinate_Herds(i) ) = doses(
nouts, runP.vaccinate_Herds(i) ) + S( 35+group ) + RS( 35+group ) +
I( 35+group );
                VST( 35+group ) = VS( 35+group ) + S( 35+group ) +
RS( 35+group );
                VIT( 35+group ) = VI( 35+group ) + I( 35+group );
                ST( 35+group ) = 0;
                RST( 35+group ) = 0;
                IT( 35+group ) = 0;
                timesince_Vaccrear(runP.vaccinate_Herds(i),1) = 0.1;
% 0.1 to distinguish between those just vaccinated and those not
vaccinated at all
            end
        end
        M = MT; S = ST; I = IT; R = RT; RS = RST; VS = VST; VI =
VIT; VR = VRT;

    else % infection process

        P=M+S+I+R+RS+VS+VI+VR; %population of each group in each
herd summing across inf states
        propI = zeros ( 1, Num_Pop ); %proportion infectious
        xx=find(P);
```

```matlab
        propI(xx)=(double(I(xx))+double(VI(xx)))./double(P(xx));
        tran = beta * propI * INFMAT; %rate of infection
        %calculate the number of events for each group
        matevent = int16(poissrndX(tau*pi*double(M)));
        infeventS = int16(poissrndX(tau*tran.*double(S)));
        infeventRS = int16(poissrndX(tau*tran.*double(RS)));
        infeventVS = int16(poissrndX(tau*tran.*double(VS)));
        recevent = int16(poissrndX(tau*gamma*double(I)));
        wanevent = int16(poissrndX(tau*omega*double(R)));
        waneventVR = int16(poissrndX(tau*omega*double(VR)));
        vwanevent = int16(poissrndX(tau*rho*double(VS))); % waning
of vaccine from vaccinated susceptible pigs
        vrecevent = int16(poissrndX(tau*(gamma*2)*double(VI))); %
recovery of infected but vaccinated pigs. Twice as fast as non
vaccinated

        for infprocess = 1
            whichgroups = find( matevent > 0 ); % maternal immunty
waning events
            for i = 1 : length( whichgroups )
                pop = whichgroups( i );
                if matevent( pop ) > M( pop )
                    matevent( pop ) = M( pop );
                end
                MT( pop ) = MT( pop ) - int16(matevent( pop )); ST(
pop ) = ST( pop ) + int16(matevent( pop ));
            end

            whichgroups = find( infeventS > 0 ); % infection events
            for i = 1 : length( whichgroups )
                pop = whichgroups( i );
                if infeventS( pop ) > S( pop )
                    infeventS( pop ) = S( pop );
                end
                if any(pre11WeekSowGroups == pop )
                    newearlyInf( ceil(pop/54) ,pop-
((floor(pop/54))*54 + 9) ) = newearlyInf( ceil(pop/54), pop-
((floor(pop/54))*54 + 9) ) + infeventS( pop ); % counts number of
new infections before 11 weeks of gestation
                end
                if any(post11WeekSowGroups == pop )
                    newlateInf( ceil(pop/54) ,pop-
((floor(pop/54))*54 + 21) ) = newlateInf( ceil(pop/54), pop-
((floor(pop/54))*54 + 21) ) + infeventS( pop ); % counts number of
new infections after 11 weeks of gestation
                end
                ST(pop)=ST(pop)-infeventS(pop);
IT(pop)=IT(pop)+infeventS(pop);
            end

            whichgroups = find( infeventRS > 0 ); % infection events
            for i = 1 : length( whichgroups )
                pop = whichgroups( i );
                if infeventRS( pop ) > RS( pop )
                    infeventRS( pop ) = RS( pop );
                end
                if any(pre11WeekSowGroups == pop )
                    newearlyInf( ceil(pop/54) ,pop-
((floor(pop/54))*54 + 9) ) = newearlyInf( ceil(pop/54), pop-
((floor(pop/54))*54 + 9) ) + infeventRS( pop ); % counts number of
new infections before 11 weeks of gestation
```

```matlab
                    end
                    if any(post11WeekSowGroups == pop )
                        newlateInf( ceil(pop/54) ,pop-
((floor(pop/54))*54 + 21) ) = newlateInf( ceil(pop/54), pop-
((floor(pop/54))*54 + 21) ) + infeventRS( pop ); % counts number of
new infections after 11 weeks of gestation
                    end
                    RST(pop)=RST(pop)-infeventRS(pop);
IT(pop)=IT(pop)+infeventRS(pop);
                end

                whichgroups = find( infeventVS > 0 ); % infection events
                for i = 1 : length( whichgroups )
                    pop = whichgroups( i );
                    if infeventVS( pop ) > VST( pop )
                        infeventVS( pop ) = VST( pop );
                    end
                    VST(pop)=VST(pop)-infeventVS(pop);
VIT(pop)=VIT(pop)+infeventVS(pop);
                end

                whichgroups = find( recevent > 0 ); % recovery events
                for i = 1 : length( whichgroups )
                    pop = whichgroups( i );
                    if recevent( pop ) > I( pop )
                        recevent( pop ) = I( pop );
                    end
                    IT( pop ) = IT( pop ) - int16(recevent( pop )); RT(
pop ) = RT( pop ) + int16(recevent( pop ));
                    if (sum( I( 1 + 54*((ceil(pop/54))-1) : 54 +
54*((ceil(pop/54))-1) ) )) == 0
                        fadeout(ceil( pop/54 )) = fadeout(ceil( pop/54
)) + 1;
                    end
                end
                whichgroups = find( wanevent > 0 ); % waning immunity
events
                for i = 1 : length( whichgroups )
                    pop = whichgroups( i );
                    if wanevent( pop ) > R( pop )
                        wanevent( pop ) = R( pop );
                    end
                    RT( pop ) = RT( pop ) - int16(wanevent( pop )); RST(
pop ) = RST( pop ) + int16(wanevent( pop ));
                end
                whichgroups = find( waneventVR > 0 ); % waning immunity
events
                for i = 1 : length( whichgroups )
                    pop = whichgroups( i );
                    if waneventVR( pop ) > VR( pop )
                        waneventVR( pop ) = VR( pop );
                    end
                    VRT( pop ) = VRT( pop ) - int16(waneventVR( pop ));
ST( pop ) = ST( pop ) + int16(waneventVR( pop ));
                end
                whichgroups = find( vwanevent > 0 ); % vaccine waning
from vaccinated susceptible pigs
                for i = 1 : length( whichgroups )
                    pop = whichgroups( i );
                    if vwanevent( pop ) > VST( pop )
                        vwanevent( pop ) = VST( pop );
```

```
                    end
                    farm = floor(pop/54)+1;
                    group = pop - (floor(pop/54)*54);
                    if group > 9 && group <=30
                        if timesince_Vacc( farm, group-9 ) > 112
                            VST( pop ) = VST( pop ) - int16(vwanevent(
pop )); ST( pop ) = ST( pop ) + int16(vwanevent( pop )); % waning
only occurs if the group was vaccinated more than 16 weeks ago
                        end
                    elseif group >=35
                        if timesince_Vaccrear( farm, group-34 ) > 112
                            VST( pop ) = VST( pop ) - int16(vwanevent(
pop )); ST( pop ) = ST( pop ) + int16(vwanevent( pop )); % waning
only occurs if the group was vaccinated more than 16 weeks ago
                        end
                    end
                end
                whichgroups = find( vrecevent > 0 ); % recovery of
infected vaccinated pigs
                for i = 1 : length( whichgroups )
                    pop = whichgroups( i );
                    if vrecevent( pop ) > VI( pop )
                        vrecevent( pop ) = VI( pop );
                    end
                    %                      VI( pop ) = VI( pop ) -
int16(vrecevent( pop )); S( pop ) = S( pop ) + int16(vrecevent( pop
));
                    VIT( pop ) = VIT( pop ) - int16(vrecevent( pop ));
VRT( pop ) = VRT( pop ) + int16(vrecevent( pop ));
                end

        end
        time = time + tau;
        M = MT; S = ST; I = IT; R = RT; RS = RST; VS = VST; VI =
VIT; VR = VRT;

    end

end

slaughtered_Persow(:,1:24) = 0; % would be errors, as these pigs
were 'born before' the simulation started
```

TIDY

```
resOut.N = N;
resOut.pigs_Lost = pigsLost;
resOut.fadeout = fadeout;
resOut.underweight_Slaughter = underweight_slaughter;
resOut.slaughtered_Persow = slaughtered_Persow;
resOut.farm_Growdeaths = farm_Growdeaths;
resOut.farm_Findeaths = farm_Findeaths;
resOut.farm_Returns = farm_returns;
resOut.farm_Abortions = farm_abortions;
resOut.endtime = time;
resOut.runtime = runP.runtime;
resOut.inf_In = inf_In;
resOut.inf_Out = inf_Out;
resOut.weaned_Persow = weaned_Persow;
resOut.wean_Week = wean_week;
```

```
resOut.slaughter_Week = slaughter_week;
resOut.doses = doses;
resOut.culls = cullcount;
end
```