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Ph.D Thesis

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Nils Toft

February 28, 2001

Preface

This thesis is intended to fulfill the requirements for the Ph.D. degree at the Royal Veterinary and Agricultural University, Denmark. The research was carried out from 1996 to 2000, at the Department of Animal Science and Animal Health, The Royal Veterinary and Agricultural University and during 3 months in 1997 at Department of Dairy and Poultry Science, College of Agriculture, University of Florida, Gainesville, Florida.

Several people have inspired and supported me during the project. First, I would like to thank my supervisor Anders Ringgaard Kristensen for his qualified guidance and inspiration. Sincere thank is also offered to Erik Jørgensen for his inspiration, motivation and patience. Neither of you can be blamed if I still don't get it right.

Special thanks is also offered to: my fellow Ph.D students Thomas Nejsum Madsen and Micheal Höhle for their contribution to the daily life at the office.

In general I would like to thank the staff at the Department of Animal Science and Animal Health for a fruitful and pleasant time spent here.

A special thanks is offered to Anette and Gustav for keeping the project in its right perspective.

December 2000

Nils Toft

CONTENTS

CHAPTER 1

General Introduction

Decision support system is a term which covers a wide area of applications. Monitoring tools such as, e.g., Madsen and Ruby (2000); Madsen (2000) are examples of methods to produce and present information to the decision maker. Simulation tools such as Stärk et al. (2000) and Lloyd et al. (1994) are examples of tools that allow evaluation of different strategies or risk analysis. Despite the obvious differences in these applications they essentially do the same. Produce more information for the decision maker to include in her considerations when determining a course of actions. This is one perception of the term decision support.

Another way to perceive the concept of decision support is as a system that based on available relevant information present an *optimal policy* to the decision maker. Most applications of this type have addressed the *animal replacement problem* (see Kristensen (1994) for a survey). The traditional animal replacement problem regards a sow or a cow and her future successors. But problems such as delivery of slaughter pigs and fattening of bulls are essentially also animal replacement problems. Only the item considered for replacement is a group of animals. While monitoring tools have been widely adopted in livestock production, there has been some reluctance to accept the replacement models. Nonetheless, as the discussion and results of Kristensen (1993) emphasize, the value of such decision support systems for research purposes is equally important.

The framework of *Markov decision processes*(Bellman, 1957) has formed the theoretical foundation for the development of animal replacement problems. A Markov decision process is defined as a set of states (state space), a finite set of actions, a state transition function, and a reward function. A state is a description of the system (i.e., a sow, a cow or a batch of slaughter pigs) that captures all information relevant to the problem at hand. Early on it became clear that "all information relevant to the problem at hand" in the case of animal replacement problems is too much to handle efficiently in the original framework, hence the concept of hierarchic Markov processes was formulated in Kristensen (1988) to allow a decomposition of the state space to reduce the computational difficulties. The hierarchic Markov processes surfaced just as the computers started to get cheaper, bigger and faster. This combination resulted in a series of animal replacement models, which generally grew in terms of state space as the models were developed to include more information relevant to the decision problem.

Although the models grew, they still shared the same basic property inherited from the original Markov decision processes: Actions were chosen, carried out and rewarded within the time span between successive decision stages. The traits included in an animal replacement problem are affected by other management decisions, some of which not always fit this property. As an example, vaccination of a batch of slaughter pigs is usually done at the start of a new production period, but the effect remains throughout the entire production period. The optimal policy for the daily operation within the batch will(in general) differ between vaccinated and unvaccinated batches. Hence we require simultaneous optimization of decisions at multiple timescales. The concept of *multi-level hierarchic Markov processes*(Kristensen and Jørgensen, 2000) has been developed for modeling such decisions. It allows the modeling to progress from the original animal replacement problem towards a *decision complex*, in which the original replacement decision plays an important part, but other decisions are considered simultaneously.

When more decisions are included in the decision problem, solutions to the old problems of modeling and state space reduction become as urgent as ever. The Chapters 2 and 3 regards these problems. In Chapter 2 techniques for temporal abstraction and state space representation are reviewed. The ideas are assembled from different fields of research such as robot navigation and discussed within the context of herd management. Chapter 3 develops a decision support system for simultaneous optimization of decisions regarding delivery of slaughter pigs and control of a respiratory disease.

The works in the previous paragraph concerns the structural or qualitative elements of decision support. In Chapter 4 estimation of the herd specific parameters required by decision support systems, i.e., the quantitative aspect of modeling, is addressed. Exemplified by estimation of farm specific parameters for a model of the joint distribution of series of litter sizes for individual sows. While animal replacement models usually are well founded in terms structural representation, parameters are often chosen to reflect the behavior of a "typical" herd. However, for practical application of decision support system we need to consider whether these population estimates of a typical herd are adequate for modeling the individual herds. If not, then a robust method for obtaining herd specific estimates regardless the quality of data is needed. Deploying a decision support system for, e.g., culling of sows based on production history, is meaningless, unless the model underlying the decision process reflect the reality of the farm.

References

R. E. Bellman. *Dynamic Programming.* Princeton University Press, 1957.

A. R. Kristensen. Hierarchic markov processes and their applications in replacement models. *European Journal of Operational Research*, 35:207–215, 1988.

A. R. Kristensen. *Markov decision programming techniques applied to the animal replacement problem.* Dissertation, The Royal Veterinary & Agricultural University, 1993.

A. R. Kristensen. A survey of markov decision programming techniques applied to the animal replacement problem. *European Review of Agricultural Economics*, 21:73–93, 1994.

A. R. Kristensen and E. Jørgensen. Multi-level hierarchic markov processes as a framework for herd management support. *Annals of Operations Research.*, 94:69–89, 2000.

J. W. Lloyd, S. B. Harsh, J. B. Kaneene, G. D. Schwab, B. J. Thacker, and A. J. Thulin. Development of a computerized systems model for health management decision support in growing hogs. *Preventive Veterinary Medicine*, 19:249–265, 1994.

T. N. Madsen. A model for detection of changes in the drinking behaviour of young pigs. In *Proceedings of the International Symposium on Pig Herd Management Modeling and Information Technologies Related*, pages 61–70, 2000.

T. N. Madsen and V. Ruby. An application for early detection of growth rate changes in the slaughter pig production unit. *Computers and Electronics in Agriculture*, 25:261–270, 2000.

K. D. C. Stärk, D. U. Pfeiffer, and R. S. Morris. Within-farm spread of classical swine fewer virus - a blueprint for a stochastic simulation model. *Veterinary Quarterly*, 22:36–43, 2000.

CHAPTER 2

Recent developments in Markov Decision Processes and their application within livestock decision support systems.

(Submitted for journal publication)

Nils Toft and Anders R. Kristensen

Abstract: The development of animal replacement problems into livestock decision support systems which addresses the decision complex defined by the production system requires introduction of new techniques in the traditional Markov decision problem framework. The basic requirements are methods for handling temporal abstraction, i.e., the simultaneous optimization of decisions at multiple time scales, and techniques for state space decomposition. In this study we review some of the techniques developed for addressing these issues. We discuss the contributions with respect to their computational as well as modeling perspectives using examples of livestock decision support systems.

2.1 Introduction

The theory of Markov Decision Processes (MDP) originated in Bellman (1957) and has since then been applied to numerous applications within livestock management. The advent of the hierarchic Markov Process(HMP) (Kristensen, 1987) virtually exploded the size of the state space allowing the decisions to be based on more and more information. One of the largest models developed so far is the dairy cow replacement model by Houben et al. (1994) in which 6,821,724 unique states describes the conditions of a cow through her life. Models prior to the above are surveyed in Kristensen (1994). Since then applications such as optimal delivery of slaughter pigs (Kure, 1997), heifer rearing (Mourits et al., 1999), bull fattening (Makulska and Kristensen, 1999), experimental economics (Verstegen et al., 1998) and epidemic disease control (Toft et al., 2000b) have been developed within the MDP/HMP framework.

Previous studies have defined some features that render the animal replacement problem different from the industrial replacement problem (Kristensen, 1994). The essence of these considerations can be attributed to the difference between biological variation and mechanical precision as well as the repetitive nature of livestock production. The variation between presumably identical animals is substantially larger than the variation between machines of same brand. Hence the animal replacement problem needs to describe more traits in order to account for more features of the animals in question. This leads to models with very large state spaces as in the dairy cow replacement problem mentioned above.

For the traits of these very large state spaces one can make a number of observations. First, some traits evolve in a non-stochastic way, like, e.g., the age of an animal which tends to increase by the stage length until the animal is replaced and the age reset. Second, some traits remain constant for several decision periods, e.g., the milk yield of a cow in her previous lactation will remain constant throughout the entire duration of the current lactation. Third, not all traits are relevant to all decisions, i.e., the choice of boar for mating a sow might depend only on her genetic merit and previous litter size, while traits like age are ignored. Finally, we can observe that there are actions which have an impact that last for several decision periods, i.e., the choice of boar can be assumed to impact the value of the future litter, but all decisions made from mating to farrowing can also potentially influence the outcome.

In the previous paragraph we made an important, but hidden, assumption. By introducing actions which are not directly replacement decisions we progressed our context from the mere replacement problem towards the concept of a livestock decision support system. The replacement problem is still an important feature of any livestock decision support system. The decision complex regarding other actions than that of replacement, however, influence the traits which form the basis of the replacement problem, hence the need for simultaneous optimization of decisions on different aspects of production.

Thus, we can now identify two major issues to be addressed by a framework for decision support within livestock management: the complexity, hence size of the state space for the decision problem; and the simultaneous optimization of decisions on multiple time scales. In this paper we present some developments within the MDP framework which somehow address the questions raised here. The remainder of this paper progress as follows: First we summarize the concepts and basic theory of Markov decision problems. Then we present some examples typical to livestock decision support systems. Using these examples we introduce and discuss temporal abstraction and factored representations. Finally we briefly discuss an example of decision networks to represent and solve partially observable decision problems. The motivation for this example is to retract attention to possible benefits of modeling the state space independently of the decision problem. In the final discussion we try to devise a path for future research in the methodological elements of livestock management decision support systems.

2.2 The basics of Markov decision processes

A Markov decision process can be defined as a tuple $\{S, A_s, r(a,s), p(\cdot|a,s)\}$ where S is a finite set of states, A_s is a set of available actions at a given state s, $r()$ is a reward function and $p()$ is a transition function. A state is a description of the system which captures all the information available and relevant to the problem at hand. The set of states will be referred to as the *state space* of the decision problem. Observing a particular state s, the decision maker may chose among a set of available decisions A_s, which are carried out and rewarded (with reward $r(s,a)$) before the next stage to which transition occur with probability $p(\dot{|}s,a)$.

The term *Markov* indicates that the choice of action only depends on the present state of the system, i.e., all information relevant to the decision maker must be contained in the current state.

A *policy* π is a set of rules which determines the course of actions to be taken at each state. The consequence of adopting a certain policy is that the decision maker receives a reward at each stage. To determine the value of a policy we need to adopt some criteria of optimality. A criteria with a reasonable economic interpretation is the maximization of expected discounted future rewards where the current value of a reward received n stages into the future is discounted by a factor $\lambda^t (0 < \lambda < 1)$.

A *Markov decision problem*(MDP) is a Markov decision process plus a criteria of optimality. The *value* of a policy π under the above criteria is simply the sum of expected future discounted rewards obtained by following π. Since this value depends on the initial state, we denote the value of π at state s as $V_\pi(s)$. A policy π^* is optimal, if $V_{\pi^*}(s) \geq V_\pi(s)$, for all $s \in S$ and all policies π.

A particular useful method for determining the optimal policy and its value is the *policy iteration* algorithm (Howard, 1960). It proceeds as follows:

The policy iteration algorithm

1. Let π^* be any policy on S

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2. While $\pi \neq \pi^*$ do
    (a) $\pi = \pi^*$
    (b) (Policy evaluation) For all $s \in S$, calculate $V_\pi(s)$ by solving the set of $|S|$ linear equations:
        $$V_\pi(s) = R(s) + \lambda \sum_{s_j \in S} p(s_j|\pi(s), s)V_\pi(s_j), \quad \forall s \in S \qquad (2.1)$$
    (c) (Policy improvement) For all $s_i \in S$, if there is an action $a \in A_{s_i}$ such that
        $$R(s_i) + \lambda \sum_{s_j \in S} p(s_j|a, s_i)V_\pi(s_j) > V_\pi(s_j) \qquad (2.2)$$
        then $\pi^*(s_i) = a$; otherwise $\pi^*(s_i) = \pi(s_i)$
3. Return $\pi$
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This method is indeed very efficient and is guaranteed to produce an optimal policy, however, solving a set of $|S|$ equations will prove almost impossible for large state spaces. The *modified policy iteration* algorithm (Puterman, 1994) use partial evaluation to determine an approximate solution to the set of linear equations without actually solving the system.

The reason for discussing these results here is partly to establish a common foundation in terms of basic concepts and notation and partly to attribute the ideas underlying the policy and modified policy iteration algorithms, which have served as inspiration for most of the results presented in the next sections.

Please recall that the algorithms presented here apply to the concept of *semi-Markov decision problems* as well. If the choice of action and current state influence when the next decision point occur, the transition probabilities can be replaced by a discounted version. Consider the case where the effect of choosing action a in state $s \in S$ is that the system evolves to the new state $j \in S$ with probability $p(j|a, s)$, using $f(j|a, s)$ units of time. Applying the rate $\alpha > 0$ which relates to the discount factor λ as $\lambda = e^{-\alpha}$ we can write the discounted transition $q(j|a, s) = e^{-\alpha f(j|a,s)} p(j|a, s)$. Replacing the transition $p(j|a, s)$ by $q(j|a, s)$ everywhere in the above results and omitting explicit reference to λ render the results valid for this definition of semi-MDP, see, e.g., Puterman (1994) for elaboration.

2.3 Examples

In order to illustrate the shortcomings of traditional MDP theory and emphasize the potential of the proposed extensions we use examples from within the herd management community. Our primary examples will be those of Houben et al. (1994) and Toft et al. (2000b) which we shall discuss briefly below. However, to emphasize certain points we introduce further examples as our paper unfolds. Since our objective is to analyze the potential utilization of techniques for state space decomposition/reduction and temporal abstraction of actions our presentation of the examples will focus on these aspects, and ignore the more technical features emerging from the specific context.

2.3.1 Optimal replacement of mastitic dairy cows

The study presented in Houben et al. (1994) was initiated in order to include mastitis in the replacement decision in dairy cows. The study reports that the main reasons for culling cows are poor production and appearance (35%), poor fertility (20%), and mastitis (8%). The study concludes that a model which include these factors could successfully account for 63% of all replacement decisions. The analysis refrained from considering the scenario of untreated mastitic cows, hence a mastitic cow which is not replaced is implicitly assumed treated. The result is a model that optimizes three decisions, which can be made at each state and stage:

1. Keep the cow at least 1 more month and do not inseminate her when in estrus (keep).
2. Keep the cow at least 1 more month and inseminate her when in estrus (insm).
3. Replace the cow immediately by a replacement heifer (repl).

The foundation for these decisions are a total of 6,821,724 different states composed of the following factors: lactation number, production in current lactation, production in previous lactation, calving interval (and open cows), clinical mastitis in current month, accumulated number of mastitis quarters in current lactation up to and including current month, accumulated number of mastitis quarters in previous lactation.

We will ignore considerations regarding reward and estimation of the various parameters required by the model. Note that the formulation as a traditional MDP will result in model with a stage length of 1 month.

2.3.2 Optimal delivery and control strategies for slaughter pigs in presence of epidemic disease

The model in Toft et al. (2000b) addresses the issue of selecting the optimal control strategy for epidemic disease (in this case a flu-like condition) within the context of the production system. Thus the model simultaneously optimizes the delivery of slaughter pigs and the appropriate control measures available for disease reduction. Specifically the model seeks for an optimal policy involving the decisions:

1. Vaccination of the entire batch of pigs at insertion.
2. Reduce the stocking rate in the next batch of pigs
3. Use medicine after observing the onset of disease.
4. Empty the pen prematurely.
5. Deliver a certain fraction of pigs for slaughter.

These decisions are assumed to depend on the following factors: the disease pressure from outside sources, the number of pigs in the section, the number of healthy/sick pigs respectively and the fraction of pigs still left in the pen.

2.4 Temporal abstraction

When considering the two examples from the previous section especially the latter it seems that there is a problem with representing this decision problem in a traditional MDP setting. A key property of the MDP framework is that *actions* are selected, carried out and rewarded within the smallest increment of time, i.e. the distance between two successive decision epochs or stages. However, the two first decisions in the example of slaughter pigs are clearly decisions which are only considered at the onset of a new batch, but where the impact remain throughout the entire duration of that batch. Hence we must define these actions in a different manner to model the example as a traditional MDP. One obvious approach is to define such actions as mere states which remain constant for several stages.

In this section we will elaborate on methods for handling decisions where the time horizon goes beyond the next decision epoch. We shall report and discuss result from different fields of research including robot navigation, automated learning and management information systems. We shall try to clearly outline the difference in perception of temporal abstraction within the different fields. Ideas developed outside our own context might be better explained using the original examples, before applying the ideas within livestock production.

2.4.1 Macro-actions

Macro-actions, temporally extended actions, or options is a large collection of research emerging from the ideas presented in Sutton (1995). The nature of this work is somewhat philosophic, still it raises some important questions: Does a macro-action always take the same time? Should its duration be

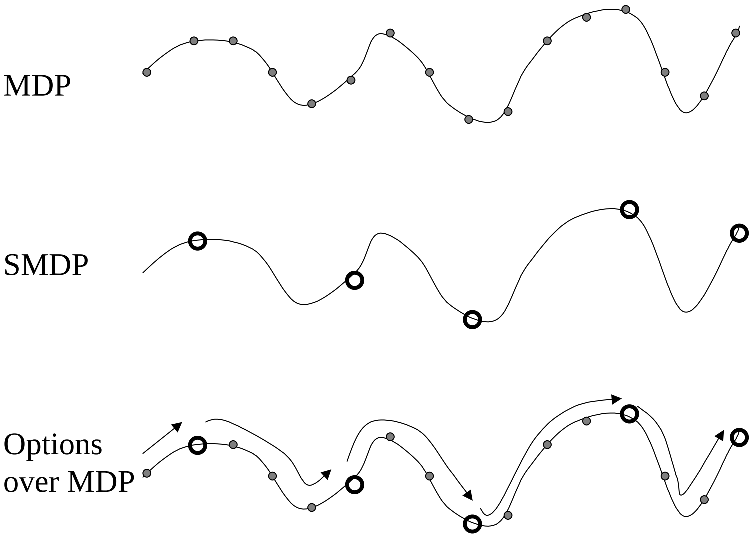


Figure 2.1: A possible state trajectory of an MDP, made up of small discrete-time transitions, whereas that of an SMDP comprises larger, continuous-time transitions. Macro-actions enable an MDP trajectory to be analyzed at either level. (Sutton et al., 1998, cf. Figure 1)

explicitly represented? Is it committed to once or redecided at each time step?

Precup et al. (1997) formally defines a macro-action as a triple (s, π, β), where s is the state in which the macro-action applies, π is the policy that specifies how the macro-action is executed, and β is a completion function specifying the probability of completing the macro-action on every time step. The policy does not have to be Markovian, i.e. it can depend on all available information obtained since t_0 the onset of the macro-action.

Adapting the macro-action concept render the MDP into a semi-Markov decision problem (semi-MDP). This implies that the algorithms developed for MDP's may still be applied to the model extended with a set of macro-actions. Figure 2.1 visualize the connection between MDP's, semi-MDP's and macro-actions.

To illustrate the idea of macro-actions consider a robot navigating through the rooms of a house in grid-world, where at each time step the robot may go up,down, right or left, given that no obstacle (e.g. walls) is in the way. A possible set of macro actions could then be methods for navigating through the different rooms of the house, i.e. for a certain macro-action s could be the state indicating that the robot is in a specific doorway, π a set of instructions like e.g. right, left, down, down etc, and β is 1 when the robot reaches another doorway and zero elsewhere.

Adding such a set of macro-actions to the original problem can speed up computation of optimal strategies for navigation dramatically, given that the macro-actions are optimal with respect to navigation within the individual rooms. Still, in more complex scenarios the cost of determining optimal macro-actions should be included. Furthermore, to solve our examples we need some sort of state space reduction or decomposition. Neither of which are attained within the original macro-action framework where one of two approaches was taken: use the full set of actions plus macro-actions to speed up computation while guaranteeing optimality, or use only a subset of original actions plus macro-actions to obtain near optimality (faster than the original problem).

Before we discuss the possible application of macro-actions to our examples, we will elaborate on the two issues of state space reduction and the actual generation of macro-actions.

Abstract decision processes

An observation which has been done independently by several authors is that in realistic problems the following applies: states are clustered together in regions with only a small number of states having transitions out of the region. Communication between regions is only carried out in a small number of states, and generally it is not possible to reach all states from the current, and not all state variables are of interest to the active set of actions.

Define *boundary* states as the states with transitions out of a region and the states to which transition is possible as *periphery*. Then a local finite MDP is defined on the region plus periphery states. A policy for this local MDP is termed an abstract action for the full problem. An *abstract decision process* is defined as an MDP on the regions, where the local policies define actions on the abstract states.

To illustrate the idea, consider once more a robot navigation problem as sketched in Figure 2.2, the doorways are periphery (and boundary) states for the rooms defining regions.

The approach taken here to decomposition can be seen as a *divide-and-conquer* method where the steps are:

1. Reformulate the problem in terms of smaller MDP's over the subspaces of the individual regions.
2. Solve each of these subproblems.
3. Combine the solution to obtain a solution to the original problem.

This is essentially the idea behind a number of different approaches (Kristensen, 1988; Dean and Lin, 1995; Hauskrecht et al., 1998) which differ somewhat in solution technique and result, but essentially use the above idea. Hauskrecht et al. (1998) generate all their local policies in advance which yields an algorithm only ensuring δ-optimality and might use substantial

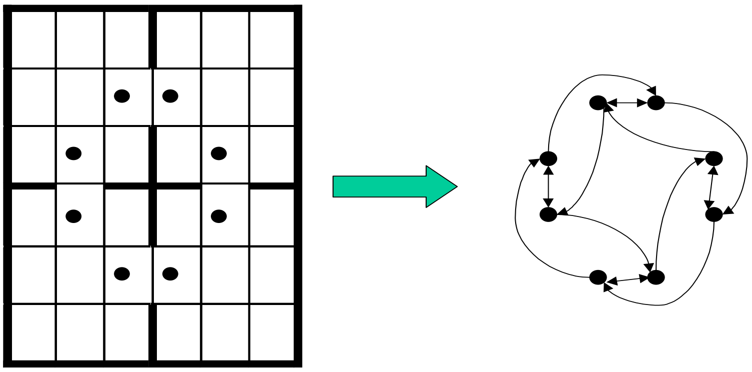


Figure 2.2: Abstract MDP for the 4 room example, black dots mark the peripheral states of the original MDP, i.e. states in the abstract MDP (Hauskrecht et al., 1998)

overhead compared to other approaches. Because a very large number of policies are needed for the subspaces by this approach. However, in special cases where, e.g. a large set of almost identical problems are solved, their idea might be efficient, see Hauskrecht et al. (1998) for details.

Both the approach in Kristensen (1988) and Dean and Lin (1995) are guaranteed to converge towards optimal solutions, since they are both special cases of a general class of methods that must converge. Any reasonable scheme that improves the policies in the regions and propagate the improvements through an abstract decision problem will produce an optimal policy as long as no regions "starve", i.e., never have their policies improved (Parr and Russell, 1998). To see why, observe that the abstract decision problem of assigning policies to regions, is really just a semi-MDP in which the set of permitted actions is the set of possible policies defined over regions. Hence, an optimal solution to high-level problem given the current set of local policies can be found using e.g., policy iteration. Once an optimal solution exists for the high-level problem, the local policies is improved if possible and the high-level problem is solved again.

Hierarchic abstract machines

The *Hierarchic abstract machine*(HAM)(Parr and Russell, 1998) is an attempt to develop a formal specification of macro-actions. The idea is to think of a policy as a program , i.e., a combination of small fragments applied in a possible stochastic way. In Parr (1998) the motivation for HAM's is given as:

> This approach is rooted in the observation that engineers and control theorists are generally quite good at designing controllers that will realize specific low-level behaviors. A worthy goal for

> artificial intelligence should not be the mere duplication of these efforts using different means, but should be the leveraging of these accomplishments to achieve more interesting higher-level tasks.

A HAM is based on a (sub)set of actions at the lowest level. An abstract machine, chooses among actions based on input of currents state. The hierarchic machine, includes a possibility to call another machine as a subroutine. A special case of machine is the *null* HAM, which at each state chooses among the entire set of available actions. A system with only the null HAM, would produce the original MDP.

Applying macro-action technique to the examples

It would not be to hard to imagine macro-actions applied to the herd management examples of this paper. The original formulation of the mastitic cow example rely on the hierarchic Markov processes (HMP) (Kristensen, 1988) to decompose the state space and render the model soluble. However, the approach towards macro-actions as a means of temporal abstraction did not come into play in the original formulation.

A macro-action is a plan to be carried out once a certain condition is observed until a new condition is met. This is very similar to the plans and guidelines already adopted in practical herd management. Historically these plans are developed in a trial-and-error manner or just established as rules-of-thumb. Still the objective is the same, to provide a policy for getting from one point in the production cycle to a new one, e.g., start of insemination to confirmed pregnancy.

The primary motivation for developing the large scale decision support systems in herd management is to find an *optimal* policy, i.e. determine whether or not the traditional guidelines and rules-of-thumb are optimal or some other policy should be adopted. Specifically, in the case of mastitic cows the study suggested that the optimal decision almost always was to treat and keep the mastitic cow rather than replace her. Whether or not this policy was already adopted is not important, but it is important to allow an unrestricted search through the entire space of policies in order to determine that the model suggest this as an optimal policy.

The idea of temporal abstraction was originally introduced to allow for easier modeling of complex high-level tasks, such as driving to work vs. taking the train, without worrying about low-level decisions involving operating the car or getting to the train station. However, the robot navigation community considers temporal abstraction as a sequence of low-level actions to be carried out according to some (predetermined) policy. For application within robot navigation this interpretation will probably suffice. But, as the example of slaughter pigs suggests there might be a need for a wider definition of temporal abstraction. In the slaughter pig example we introduced two kinds of disease control measures: preventive and proactive. The difference between these types of control measures is striking. The preventive measures are applied at the beginning of each batch and the effect remains until the last pigs in the batch have been delivered for slaughter. The proactive measures are applied only when disease is observed, and the decision to do so might be influenced by any previous preventive measures applied prior to this. Hence we can see that there apparently is a need for a framework for simultaneous optimization of decisions with different time horizons, i.e. the decision at the daily (operational) level depends on the policy chosen for the duration of the batch (tactical level). Conversely, the decisions at the tactical level cannot be optimized without considering the optimal policy for decisions to make during the duration of the tactical decision. A framework which allows modeling and optimization of such decision problems is defined in the *multi-level Hierarchic Markov processes* (ml-HMP) (Kristensen and Jørgensen, 2000).

Multi-level hierarchic Markov processes

The ml-HMP structure is defined as nested MDP's where the top level is an infinite stationary MDP. Each combination of state and action defined on the top level is expanded into a finite MDP with a time horizon equal to the length of a stage at the top level. This finite MDP may again be expanded into a set of lower-level MDP's using the same approach as above for each combination of stage, state and action. The time horizon of a lower-level (child) MDP is equal to the stage length of its parent. As an illustration see Figure 2.3, where dashed lines are transitions of a high level action at a high level state to the next high level decision epoch, and the full lines are the underlying low level decision problem. In the ml-HMP structure parameters are only specified at the lowest level. At higher levels the parameters are obtained by pruning parameters at lower levels. The idea is that the reward returned by a high level action depends on the underlying policy for the low level actions to be carried out during the time horizon of the high level action. Hence, the reward of a high level actions must be the net present value of the policy for the MDP expanding the high level stage for the given combination of state and action, i.e. given an optimal policy and associated transitions and rewards, the high level equivalents are just the product of the appropriate terms.

Solving ml-HMP's rely on essentially the same techniques as other methods for decomposition within the temporal abstraction framework, e.g., an abstract decision process (or *founder* process in ml-HMP nomenclature) is constructed with actions equal to policies of underlying MDP's. To give an impression of the structure of the algorithm recall the policy iteration algorithm. Essentially this algorithm is applied to the founder process except that in the *Policy improvement* step a more complex operation is carried

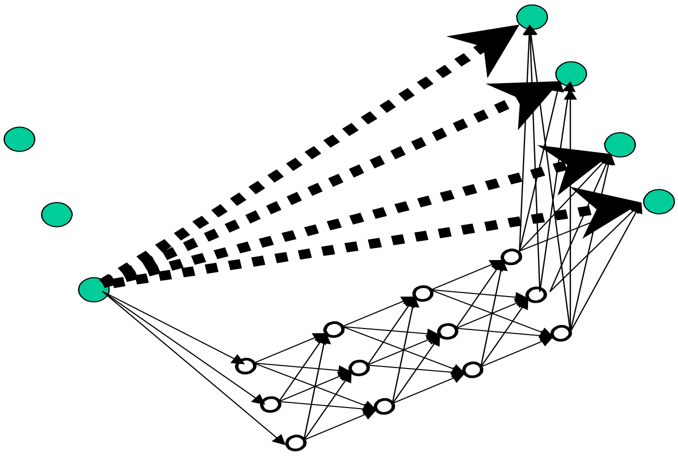


Figure 2.3: The expansion of a single stage of an HMP into a lower level full process

out. Starting as far down and back in the hierarchy as possible the optimal policies for the underlying processes are determined by working forwards and upwards solving the finite horizon MDP's while pruning parameters upwards in the process. Once back at the top level, the new set of values and transitions can be applied to determine the new optimal high level policy and corresponding value.

As mentioned in the previous section the ml-HMP framework is designed to handle temporal abstraction as in the slaughter pig example. Here the high level decisions are the preventive disease control measures, e.g., vaccination and reduced stocking rate. The optimal policy for applying these must be considered in conjunction with an optimal policy for daily operation, e.g., treatment of pigs and delivery (including early emptying of the section). It is obvious that the decision to initiate a treatment for disease given a number of sick pigs are observed must rely on whether we are operating under a vaccination policy or not, i.e., in an unvaccinated population observing sick pigs might result in initiation of treatment, whereas a few sick pigs in a vaccinated population might call for closer monitoring of the condition, but no treatment since the pigs supposedly are immune to disease.

As we pointed out earlier, the high-level decisions in the ml-HMP context can be considered states in the traditional perception of MDP's, however, from a modeling point of view we must emphasize the potential in the flexibility of modeling decisions at the same time scale as the state variables of which the decisions rely. An implementation of the ml-HMP algorithm and a GUI environment for easy specification and manipulation of models is available, see Kristensen (2000) for details.

2.4.2 Temporal abstraction revisited

We hope that it is clear at this point, that from a modeling point of view there is great potential in a formulation of actions of which the impact goes beyond the next decision epoch. Modeling high level actions without considering the full detail of the underlying policy for the duration of the abstract action gives the developer a powerful tool when constructing decision support models. From this point of view the ml-HMP framework seems most awarding, and the state space decomposition implicitly done by ml-HMP is crucial in the large scale models derived from problems taken from livestock management. Of course the approach of macro-actions and abstract decision problems render more or less the same decomposition, but the concept of temporal abstraction within this methodology is not as strong and flexible as the ml-HMP.

We propose that a reasonable path for future research in temporal abstraction for use in livestock decision support systems should focus on the ml-HMP technique, but try to incorporate some of the aspects from the macro-action and HAM techniques. The reason for this suggestion is that models in ml-HMP tends to grow very large because the researcher tries to embrace as many of the decisions involved in the livestock production as possible. Sometimes it is only specific elements of the production which are of interest. Still, we must aim at optimizing the full system in order to make inference about subsystems functioning within the context they are intended to. Instead of completely modeling the full system, macro-actions could be applied in the subsystems which are not directly under analysis, hence a set of reasonable policies for e.g., nursing of piglets could replace the full modeling of the nursing section of a sow model where the focus of the analysis is the mating operation.

2.5 Factored representation of Markov decision problems

The state space decomposition which emerged from the discussion of temporally extended actions in the previous section is the result of properties common to the state space of many decision problems including the two examples we use in this review. Should we chose ever to enumerate the states of either problem, we would not use a sequence of integers. Doing so would leave us with the problem of mapping state 23 to the corresponding values of lactation level, mastitic state etc. of the dairy cow example. Instead we would list the states of the decision problems by iteration through the possible values of the *factors* defining the state space for the decision problem. We have observed that states can be arranged in regions from which transition in and out only occur from a small subset of states. This assumption can be generalized into observing that not all factors depend on each other, e.g. transition from one state to another at the next decision epoch may depend on only a small subset of factors. This is also the case for the reward, where only a minor subset of the factors contribute to the cost/reward of the an action.

In the following subsections we focus on the idea of factored representations of MDP's using Dynamic Bayesian Networks (Darwiche and Goldszmidt, 1994) to represent the dependence between factors before and after an action. In addition we will briefly review an algorithm which benefit from the structure of a factored representation.

2.5.1 Bayesian network representations of MDP's

As discussed elsewhere the mastitic dairy cow problem can be described in terms of a set of state variables sufficient to characterize the state of the system. Unfortunately, state space grow exponentially in the number of variables of interest. The solution in the previous section was to decompose state space according to regions where local policies could be defined. However, another idea could be to utilize the natural decomposition inherited by the segmentation of the state space in relevant factors (or features). It is fair to assume that in general there might be (conditional) independence between several factors and that we can benefit from this in a compact representation of the state transitions and reward functions.

A *Bayesian Network* is a framework for compact representation of probability distributions in factored form. In Jensen (1996) a Bayesian Network (BN) is defined as:

- A set of *variables* and *directed edges* between variables.
- Each variable has a finite set of mutually exclusive states.
- The variables together with the directed edges form a *directed acyclic graph* (DAG)
- To each variable A with parents $B_1, \dots, B_n$ there is attached a conditional probability table $P(A|B_1, \dots, B_n)$.

If $U = \{A_1, \dots, A_n\}$ is the universe of variables then the joint probability $P(U) = P(A_1, \dots, A_n)$ can be calculated as

$$P(U) = \prod_i P(A_i|pa(A_i))$$

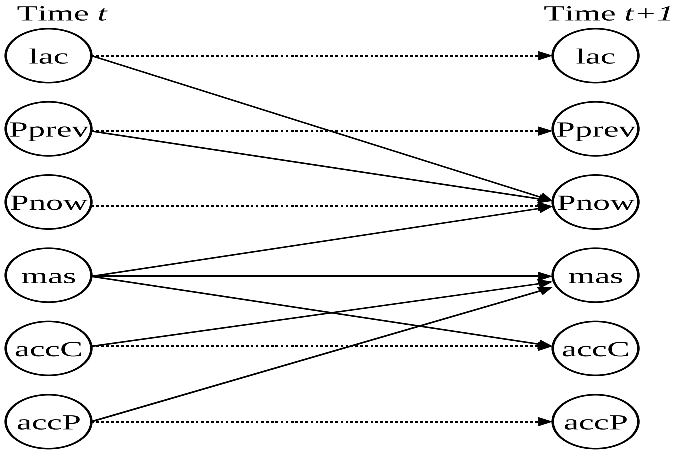
where $pa(A_i)$ is the the parent set of A_i. The above rule is known as the chain rule and is easily proved by induction. The representation of the joint distribution as the product of conditionals is called the factorization of U with respect to the DAG.

Typically BN's have been used for static problem domains, but it is also very efficient in capturing the (stationary) distribution and effect of stochastic actions associated by temporal decision problems. Specifically we use dynamic Bayesian networks or *action networks* as developed in Darwiche and Goldszmidt (1994). For the decisions keep and replace in the mastitic dairy cow example corresponding action network representations of the transitions are given in Figure 2.4, where circles represent variables, solid arrows are causal effects and dashed arrows are trivial transitions such as constant values or deterministic increments, e.g., age. The Markov and stationary assumptions allow the problem to be modeled as a two-stage dynamic Bayesian network. The reward functions can be represented in a similarly compact fashion. Rather than specifying a vector of rewards we can exploit the fact that only a subset of factors actually contribute to the cost/reward structure of the system. In the mastitic dairy cow problem only the current production level, the mastitic state of the cow and nature of the action contribute to the reward function. Using a diagram similar to the action network, with circles still being factors, the reward modeled as a diamond and the decision set as a square, the reward function for all three decisions are modeled in one diagram in Figure 2.5

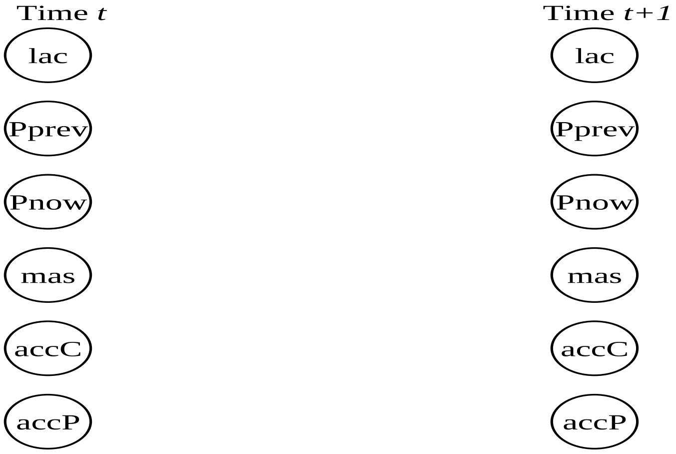
The benefit of this representation is dual: The potential saving in storage and the increased understanding of the qualitative structure of the transition and reward structure imposed by the graphical representation.

To make an approximate quantification of the storage reduction consider that the need for storage of reward values is reduced from three vectors of 6.821.724 elements to a table of $3 \times 2 \times 15 = 90$ elements. The same calculation for the transition suggest that a collection of tables of total size $12 \times 15 \times 15 \times 2 \times 18 + 2 \times 4 \times 4 = 97200 + 32 = 97232$ can replace a matrix of size $6.821.724 \times 6.821.724 \approx 4.6 \times 10^{13}$. The savings compared to the traditional MDP seems impressive, but remember that the dairy cow example was never actually implemented in this setting. Instead state space decomposition was done by adopting the hierarchic Markov decision processes.

The value function and actual policy of the MDP can also be represented in a compact way, see, e.g., Boutilier et al. (2000) for details. The savings in storage alone makes this approach promising, actual solution of the problem can be done using the original policy iteration or better still modified policy iteration. While the former always produce an optimal solution, the latter is much easier to implement, using the conditional probability and reward tables for look-up. However, there exists more clever ways of solving a factored representation of an MDP, one such method is the *Structured policy iteration* (SPI) (Boutilier et al., 1995) which is based on the modified policy iteration, but utilize the potential structure in value function and policy induced by the structure of reward and transition. In the next section we briefly outline the main ideas of the SPI algorithm.



(a) The action network for decision keep.



(b) The action network for the decision replace.

Figure 2.4: Action network representations of the state space for decisions keep and replace in the mastitic dairy cow example where the decision to keep or cull a sow is based on the variables: lactation(lac), production level now and in previous lactation (Pnow,Pprev), mastitic state(mas), and accumulated mastitis case in current and previous quarter (accC, accP). The absence of arrows in the replace network indicates complete independence between the state of the dairy cow and her replacement heifer. Dotted arrows indicate trivial or deterministic relationships not actually modeled. The associated conditional probabilities defined by the network structure are not shown.

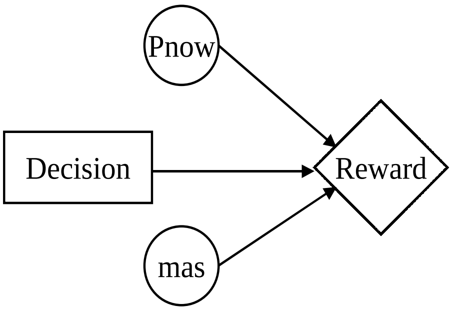


Figure 2.5: The reward function (diamond) for three decisions (square) of the mastitic dairy cow example. Although the state space contains all the variables in Figure 2.4 the reward only depends on the current production level, the mastitic state and the decision. The table of utility values associated with this graphical structure is not shown.

2.5.2 Structured policy iteration

We ignore how to actually represent value functions and policies in a compact way, but merely exploit the fact that at any stage in the computation: The current policy π might be structured as well as its value V_π or some estimate V^i thereof. According to Boutilier et al. (1995) two insights are crucial to the SPI algorithm:

1. Given a structured policy π and a structured estimate V^i for π, an improved estimate can often preserve much of this structure.

2. Given a structured value estimate V_π, it is possible to compute a structured improving policy π'

This suggests a structured form of successive approximation, combined with a way of improving policy that exploits structure. Recall that the modified policy iteration consists of a policy improving and partial policy evaluation phase. The SPI algorithm contain the same elements, however, using structured versions of the two phases. Hence, the algorithm progress as follows: choose a random *structured* policy, approximate the value function using *structured successive approximation*, produce an improved *structured* policy. The last two steps are then repeated until no improvement in policy is possible.

The structured successive approximation embodies the intuition that, given a structured value vector V^i, the conditions under which two states can have different values V^{i+1} can be determined from the action network representation. Especially, if the difference is only in variable(s) not relevant to the structured value vector V^i then these states must have identical values in V^{i+1}.

The structured policy improvement seek to exploit the structure in the network to avoid local comparison of policy in all states. The approach taken is essentially to calculate structured value vectors for possible candidate actions and compare them to the current policy. For further description and results the reader should consult Boutilier et al. (1995, 2000).

2.5.3 Factored representations revisited

The SPI algorithm is available for download, however, we have not tested its performance on any of the examples. The dairy cow example is too complicated to reproduce merely for reasons of comparison and the slaughter pig example exhibits some features which are not easily transferred to a general purpose algorithm.

Still the graphical representation of the dairy cow example in Figure 2.4 and 2.5 suggests that this is a powerful tool for future exploration. The ability to construct a graphical representation of the model is particularly useful in applications where several people are working together as a team. The conditional dependencies between factors are easily deduced from the Bayesian network. In general model construction, verification and validation using Bayesian networks has a reputation of causing less confusion between domain experts and computer scientist. Furthermore adopting this methodology for model specification allow the MDP researcher to utilize the numerous results regarding elicitation, visualization and verification of the conditional probabilities associated to the graphical structures, for inspiration see, e.g., Druzdel and van der Gaag (1995). Given enough data another approach might be to apply one of the many learning algorithms for learning the qualitative and/or quantitative structure of the network (Cowell et al., 1999).

One obstacle for immediate acceptance of factored representation and the SPI algorithm is the ability to model simultaneous optimization of decisions at multiple time scales, in the sense advocated by the ml-HMP technique. We shall refrain from proposing solutions to this problem here, but return to the issue in the discussion at the end of this paper.

2.6 Decision networks

The possibility of modeling the domain or state space of a decision problem using graphical representations, such as Bayesian networks has some obvious advantages. Still, to produce the equivalent of an MDP we are restricted to two-stage Bayesian networks where all factors represent elements which are known to the decision maker at the decision epoch. These restrictions can be a nuisance when modeling domains in cooperation with scientists from other fields of research.

The reward function network in Figure 2.5 contain all the elements required to define a *decision network*(Cowell et al., 1999). Circles are variables or chance nodes, squares are decision nodes and diamonds are utility nodes. The arcs in a decision network have different interpretation depending on the types of node they connect. Arcs into a decision node reflect knowledge available to the decision maker prior to choosing a policy for the decision. Arcs into variable nodes have the same meaning as in a Bayesian network. Finally, arcs into a utility node defines the domain for a utility node. Usually there is the requirement that there is a directed path through all decision nodes in the network, in order to ensure a unique sequence for evaluation of the decision nodes. Furthermore, in the best known special case of decision networks, the *Influence Diagrams* (Howard and Matheson, 1984) there is an assumption of no-forgetting, i.e., at the decision time all information known prior to this moment is remembered. Even though this assumption can be justified it is more or less a relic from the decision trees of which the Influence diagrams emerged. A recent addition to the decision networks is the *LImited Memory Influence Diagrams*(Lauritzen and Nilsson, 1999) in which all information arcs are explicitly drawn.

Using, e.g., LIMID for modeling decision problems we can model the state space independently of the decision problem. This implies that we can model the domain using hidden or unobserved variables to describe the causal effect of the decision problem's domain. To give an example consider a simplified version of the sow replacement problem described in Huirne (1990). We consider production results as the sole cause of voluntary culling, thus ignore the reproductive failure aspect of the original framework. Our decision problem is to decide upon weaning of the piglets, whether to keep the sow for one more production cycle, or to cull (replace) her immediately. To aide this decision we consider her previous production results, in Huirne (1990) it was assumed that the current and previous litter size would indicate the next (expected) litter size. Within the MDP framework this is a reasonable simplification, a tradeoff between accuracy and size of the state space. Still, there are models which are likely to give a more truthful image of the expected litter size of sow given her previous production record.

In a herd of sows, we can define a mean curve reflecting the expected litter size of sows at different ages. It is the variation around this mean that we seek to characterize. For longitudinal data such as production records for individual sows it is common to consider at least three different sources of variation: an additive or genetic effect, a serial correlation describing the within sow variation and a random noise effect. A model involving these elements is developed in Dethlefsen and Jørgensen (1996) and the corresponding decision problem is discussed in Toft et al. (2000a). The decision network for the sow replacement problem is given in Figure 2.6 where the model for litter size is defined by the unobserved nodes reflecting serial correlation and additive effect. In fact it can be seen that the litter size of

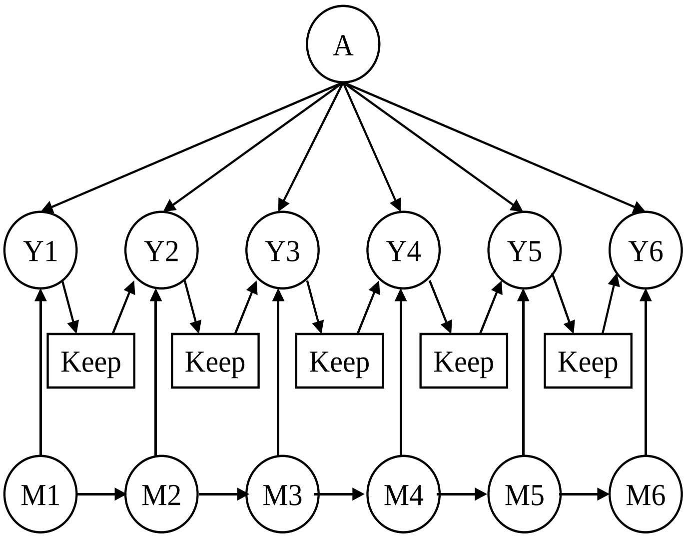


Figure 2.6: The sow replacement problem as a decision network where the model for litter size has been separated from the decision problem.The information arcs (arcs into decisions nodes) defines the decision problem and causal arcs (arcs into chance nodes) define the state space

individual parities are independent given we know the unobservable (hence unknown) quantities A and M_i. Modeling within the LIMID we can explore the effect of incorporating additional knowledge in our decision foundation, while maintaining the same model for expected litter size.

The potential problem with the formulation as a LIMID is that decision networks at the moment cannot handle infinite time horizon problems. The network of Figure 2.6 represents only the life time of one sow, the correct representation is an infinite sequence of the sow and her successors. At the moment work is carried out to remove this obstacle so the potential of LIMID's can be applied to the vast area of livestock management problems that are repetitive in nature and thus require a framework with an infinite time horizon.

2.7 Discussion

This survey of possible extensions of the traditional MDP framework is by no means exhaustive, still, we have introduced new elements of modeling, which can be useful to the livestock management community when developing the next generation of decision support models.

There has been reluctance among farmers and extension services to deploy the decision support models developed so far. Besides some obvious remaining obstacles regarding farm-specific parameters and other practical issues, the critique has always been that the models disregard some important synergy between certain elements, or that there are reasons for culling not explicitly defined in the model, etc. The essence of these complaints is that models should seek at embrace more of the decision *complex* defined in the specific production system.

The replacement decision will still be an important aspect of management in livestock production systems since it creates most of the dynamics of the system. However, the decision to replace a production animal is often based on its production parameters such as milk production or number of produced piglets and its health status, e.g., mastitic condition. Most of these factors are influenced by decisions made at some point in the production cycle, hence these decisions should be considered when addressing the replacement issue. This calls for deployment of ml-HMP or similar techniques.

As the models grow to cover more facets of the decision complex the apparent need for contributions from other fields of research grow. The ability to adapt to existing models may then become a valuable asset which calls for incorporating the use of Bayesian networks or derived techniques in the modeling phase. Thus a future challenge is how to connect the ml-HMP technique and the factored representation.

As the example in Figure 2.6 suggest there might even be a need for dropping the Markovian assumption and focus attention at the next level of modeling represented by decision networks, i.e., *Limited Memory Influence Diagrams*. The modeling issue has been addressed for years in the Bayesian network community, where developments such as *Object Oriented Bayesian Networks*(Koller and Pfeffer, 1997) has drawn some attention. The object oriented modeling approach has some obvious possibilities when modeling complex domains such as state spaces for livestock decision support systems. Since it allows for a sort of hierarchic modeling of the state space, where some can consider a factor like, e.g., feed as a unit, while others may divide the feedstuff in elements like carbohydrates, protein, etc. The object oriented approach has also been applied to LIMID's (Höhle et al., 2000), thus an object oriented modeling and design of decision problems is possible within the LIMID framework. The decomposition of the state space into objects has some promising features which should be examined in future research. The concept of temporal abstraction as defined by the ml-HMP technique is considered a crucial element in modeling, still the LIMID or its object oriented flavor cannot address this issue adequately. A logical extension of the LIMID idea is a multi-level hierarchic LIMID to handle the aspects of temporal abstraction in large realistic decision complexes.

2.8 Conclusion

In this study we have tried to devise a reasonable path for developing the theoretical and practical aspects of livestock decision support system. We find that the special properties of the livestock production system, i.e., the decision complex of interacting decisions and the large state space required by this decision complex, necessitate methods that allows for simultaneous optimization of decisions at multiple time scales and at the same time decompose the state space. We find that the multi-level hierarchic Markov processes is the framework which currently provides the most flexible tool for modeling livestock decision support system, however, techniques such as factored representations offer so many desirable features, i.e., the factored representation itself and a graphical framework for design and modeling. Merging these techniques is a worthy goal for future research. Still, perhaps even more promising is the application of decision networks in the form of limited memory influence diagrams. This tool allows for modeling of the state space independently of the decision problem, hence we can directly adopt existing theories in the development of the model, and define our decision problem afterwards in terms of observable traits.

References

R. E. Bellman. *Dynamic Programming.* Princeton University Press, 1957.

C. Boutilier, R. Dearden, and M. Goldszmidt. Exploiting structure in policy construction. In *Proceedings Fourtheenth International Joint Conference on Aritficial Intelligence (IJCAI-95)*, 1995.

C. Boutilier, R. Dearden, and M. Goldszmidt. Stochastic dynamic programming with factored representations. *Journal of Artificial Intelligence*, page To appear, 2000.

R. G. Cowell, A. Philip Dawid, S. L. Lauritzen, and D. J. Spiegelhalter. *Probabilistic Networks and Expert Systems.* Springer, 1999.

A. Darwiche and M. Goldszmidt. Action networks: A framework for reasoning about actions and change under uncertainty. In *Proceedings of the Tenth Annual Conference on Uncertainty in Artificial Intelligence (UAI-94)*, pages 136–144, 1994.

T. Dean and S.-H. Lin. Decomposition techniques for planning in stochastic domains. In *International Conference on Artificial Intelligence*, 1995.

C. Dethlefsen and E. Jørgensen. A longitudinal model for litter size with variance components and random dropouts. *Dina Research Report*, 50: 1–30, 1996.

M. J. Druzdel and L. C. van der Gaag. Elicitation of probabilities for belief networks: Combining qualitative and quantitative information. In *Proceedings of the Eleventh Annual Conference on Uncertainty in Artificial Intelligence (UAI-95)*, pages 141–148, 1995.

M. Hauskrecht, N. Meuleau, L. P. Kaelbling, T. Dean, and C. Boutilier. Hierarchical solution of markov decision processes using macro-actions. In *Proceedings of the Fourteenth Annual Conference on Uncertainty in Artificial intelligence*, 1998.

M. Höhle, E. Jørgensen, and D. Nilsson. Modeling with limids - examplified by disease treatment in slaughter pigs. In *Proceedings of the International Symposium on Pig Herd Management Modeling and Information Technologies Related*, pages 17–26, 2000.

E. H. P. Houben, R. B. M. Huirne, A. A. Dijkhuizen, and A. R. Kristensen. Optimal replacement of mastitic cows determined by a hierarchic markov process. *Journal of Dairy Science*, 77:2975–2993, 1994.

R. A. Howard. *Dynamic Programming and Markov Processes.* M.I.T Press, Cambridge, Massachutetts, 1960.

R. A. Howard and J. E. Matheson. Influence diagrams. In *Readings in the Principles and Applications of Decision Analysis*, 1984.

R. B. M. Huirne. *Computerized Management Support for Swine Breeding Farms.* PhD thesis, Department of Farm Management, Wageningen Agricultural University, Wageningen, The Netherlands, 1990.

F. V. Jensen. *An introduction to Bayesian Networks.* UCL Press, 1996.

D. Koller and A. Pfeffer. Object-oriented bayesian networks. In *Proceedings of the Thirteenth Annual Conference on Uncertainty in Artificial Intelligence*, pages 302–313, San Mateo, California, August 1997. Morgan Kaufman Publishers.

A. R. Kristensen. Optimal replacement and ranking of dairy cows determined by a hierarchic markov process. *Livestock Production Science*, 16:131–144, 1987.

A. R. Kristensen. Hierarchic markov processes and their applications in replacement models. *European Journal of Operational Research*, 35:207–215, 1988.

A. R. Kristensen. A survey of markov decision programming techniques applied to the animal replacement problem. *European Review of Agricultural Economics*, 21:73–93, 1994.

A. R. Kristensen. A software system for multi-level hierarchic markov processes. In *Proceedings of the International Symposium on Pig Herd Management Modeling and Information Technologies Related*, pages 37–46, 2000.

A. R. Kristensen and E. Jørgensen. Multi-level hierarchic markov processes as a framework for herd management support. *Annals of Operations Research.*, 94:69–89, 2000.

H. Kure. *Marketing Management Support in Slaughter Pig Production.* PhD thesis, The Royal Veterinary and Agricultural University, 1997.

S. L. Lauritzen and D. Nilsson. LIMIDs of decision problems. Technical Report R-99-2024, Department of Mathematical Sciences, Aalborg University, 1999.

J. Makulska and A. R. Kristensen. Economic optimization of bull fattening. In *Proceedings of the 2nd European Conference on Information Technology in Agriculture (EFITA/99)*, pages 443–449, 1999.

M. C. M. Mourits, R. B. M. Huirne, A. A. Dijkhuizen, and A. R. Kristensen. Economic optimization of dairy heifer management decisions. *Agricultural Systems*, 61:17–31, 1999.

R. Parr and S. Russell. Reinforcement learning with hierarchies of machines. In *Neural Information Processing Systems*, volume 11, 1998.

R. E. Parr. *Hierachical Control and Learning for Markov Decision Processes.* PhD thesis, University of California, Berkeley, 1998.

D. Precup, R. S. Sutton, and S. Singh. Planning with closed-loop macro actions. In *Proceedings of the AAAI Fall Symposion*, 1997.

M. L. Puterman. *Markov Decision Processes: discrete stochastic dynamic programming.* Wiley - Interscience, 1994.

R. S. Sutton. TD models: modelling the world at a mixture of time scales. In *Proceedings of the 12th International Conference on Machine Learning*, pages 531–539. Morgan Kaufmann, 1995.

R. S. Sutton, D. Precup, and S. Singh. Between MDPs and Semi-MDPs: Learning, planning and respresenting knowledge at multiple temporal scales. *Journal of Artificial Intelligence Research*, 1:1–39, 1998.

N. Toft, E. Jørgensen, and C. Dethlefsen. Estimation of farm specific parameters in a logitudinal model for litter size with variance components and random dropout. In *Proceedings of the International Symposium on Pig Herd Management Modeling and Information Technologies Related*, pages 127–136, 2000a.

N. Toft, A. Kristensen, and E. Jørgensen. A framework for decision support related to epidemic disease in slaughter pig production. In prep, 2000b.

J. A. A. M. Verstegen, J. Sonnemans, R. B. M. Huirne, A. A. Dijkhuizen, and J. C. Cox. Quatifying the effects of sow herd management information systems on farmers' decision making using experimental economics. *American Journal of Agricultural Economics*, 80(4):821–829, November 1998.

CHAPTER 3

A framework for decision support related to epidemic disease in slaughter pig production.

(Submitted for journal publication)[1]

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Abstract: Decision support in slaughter pig production exposed to epidemic disease requires simultaneous optimization of decisions regarding the delivery of pigs and the control of disease. This decision complex requires modeling and optimization of decisions at multiple time scales. We present the development and analysis of such a model using multi level hierarchic Markov processes as a framework. In an example of realistic proportions we demonstrate how the optimal policy at the daily operational level is affected by the state and action at the higher level of tactical control strategies.

3.1 Introduction

To be successful in modern pig production, the farmer must address a large number of problems. One particular problem is that pigs are exposed to various kinds of disease which may influence the return of the production system. It is important to distinguish between 2 different kinds of disease. The exotic diseases, e.g., classical swine fever, foot and mouth disease, etc.

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which require total eradication of the herd by law, and the more common diseases such as Swine Influenza which can be ignored by the pig producer if he or she sees fit. Decision support systems that address the former type of disease have been developed at national or regional decision levels (Saatkamp, 1995; Stärk et al., 2000). Modeling may have been applied to the within farm spread of disease, however, the farmer is never actually given a choice, since the eradication of the disease is a national concern.

Decision support systems for the more common kind of disease have also been developed, see, e.g., Lloyd et al. (1994); Cherry et al. (1998). However, these studies more or less assume that different control strategies are adopted and do merely evaluate the expected outcome. There is a number of diseases where this approach might be inadequate. Diseases of which the effect can be described in terms of mere weight loss or reduced growth, rather than animals dying by the numbers (i.e., Swine Influenza). The effect of such diseases might be serious enough, still, it will not be economically optimal to apply control measures at any cost.

To evaluate the possible benefit of control strategies of such diseases we feel that it is necessary to develop a decision support system which models the production system that the control strategies are intended to function in. The purpose of this study is to present the development and analysis of a system intended for optimization of the decision complex associated with growing pigs for slaughter when the pigs might be exposed to infectious disease. An example of realistic proportions follow the analysis.

3.2 Optimal slaughter pig marketing

The problem of optimal marketing of slaughter pigs has been addressed by several authors. However, according to Kure (1997) most studies tend not to

- clearly define the problem of marketing management and to separate and handle different aspects of the problem.
- discuss and handle the (in most situations) strong dependencies between the (internal) supply of weaners (from the farrowing operation) and the finishing operation.
- handle the stochastic variance and uncertainty of biological processes.

Kure (1997) proceeds to define slaughter pig marketing and the elements required to determine the optimal strategy for the decision scenario pertaining delivering pigs for slaughter. The essence of this analysis is: When marketing a batch of pigs for slaughter, the manager is in general faced with problems like:

- How to select and when to market individual pigs.

- How to manage the weaner supply and demand. In particular when to terminate a batch, i.e. when to insert a new batch of weaners, and how to market the remainder of a batch.

In addition to these problems, special kinds of production systems like continuous flow operations may allow for moving or re-grouping of pigs to increase space utilization and homogeneity among marketed pigs.

As one might expect, the answers to the above questions depend on the pricing system, and the type of operation on the individual farm.

The pricing system may vary among different packers, however, in Denmark the same system is used throughout the different slaughter houses. The carcass is priced on weight and leanness. It is not customary as far as the authors know, to market pigs based on their leanness. Hence we will ignore this aspect, but acknowledge that other options for pricing than weight exists. Furthermore, results based on simulated data in Kure (1997) leave little financial room for acquisition of equipment for measuring leanness.

As for the operation at the individual producer, several elements contribute to the definition of the problem and its possible solutions. It is customary to partition pig finishing operations into two subsets:

Batch operations, in which pigs are housed in physically separated units or sections. The expected effect is to reduce the transmission of infectious disease between sections and from pigs to weaners. Hence all pigs in a section must be marketed before inserting a new batch of weaners and replacement or reallocation of pigs is not possible.

Continuous flow operation, where no sectioning (except the pens) exists, thus no grouping of pigs into batches exists. Since pigs of different ages are housed together and mixing and regrouping is possible, this production form is generally more flexible and space efficient than batch operations. Pigs are normally sorted at insertion in order to increase the homogeneity of the pens.

Despite the differences between the two systems no conceptual distinction is needed. Pens can be regarded simply as small sections. However, no matter the obvious differences in production form some similarities exists as well. One such major concern when addressing the issue of marketing pigs for slaughter is the flexibility of supply. Given a surplus of weaners, one may always consider selling these at the weaner market. However, given that this batch was suppose to fill a section (which was suppose to be empty) then for the next production period this section will be empty unless another batch of weaners is available upon request. For a discussion of the different scenarios and their impact on delivery policies the reader should consult Kure (1997).

3.2.1 Defining the decisions and information pertaining optimal slaughter pig marketing.

Formally the problem of optimal slaughter pig marketing may be reduced to retrieving relevant information and acting upon this information in an optimal way.

Adopting the conventions of traditional decision theory some key issues are identifiable in this problem as well.

State-of-nature, the description of relevant traits of a system regarding the decision complex considered in the problem at hand. Here the relevant information is the weight of the animals and the number of animals (still) in the section. Thus for now we ignore information regarding the pricing system and cost of feed. Broekmans (1992) describes how the influence of price fluctuations may be included in the model.

Test decisions or non-intervening actions, some required information may not be freely available. A good example is the weight of the pigs, which may be established using different methods with varying cost and precision. In Jørgensen (1993) the influence of weighing precision on delivery decisions in different housing systems is explored.

Intervening actions, i.e. actions which directly influence the state-of-nature. Combined with the biological dynamics these actions evolves the system. The intervening actions defined in slaughter pig marketing are: Deliver the selected pigs for slaughter, and terminate the batch (i.e. deliver the remainder of the pigs regardless of their weight.

To summarize the discussion of optimal marketing management of slaughter pigs; the objective is to deliver pigs for slaughter based on observation of their live weight in a way which maximize the utility (or profit) of the entire operation in acknowledgement of the restrictions imposed by the operation itself, i.e. space, weaner supply etc.

3.3 A framework for decision support.

The system described above is adequately represented using the general framework of Markov decision processes (MDP) (Puterman, 1994), however, the concept of hierarchic Markov processes (HMP) (Kristensen, 1988) and its extension of multi-level HMP (ml-HMP) (Kristensen and Jørgensen, 2000) provides a more powerful tool for discussion and implementation of these ideas.

Adopting the ml-HMP technique each batch (or section) of pigs is modeled as a sub-process of finite length, thus the process consists of an infinite

Parameter	Description
λ_1	Energy consumption per kg metabolic weight, FU_p
λ_2	Energy consumption per kg gain, FU_p
λ_3	Logarithm of outgrown weight, ln(kg).
λ_4	Growth rate parameter

Table 3.1: Definition of parameters (λ_i) in Equation 3.2 model.

sequence of batches of pigs. Using this approach the peculiarities of the individual operations may be modeled, thus allowing the impact of different systems to be explored.

3.3.1 A stochastic growth model

A requirement of the MDP technique is an exact representation of the state space, i.e. all information regarding the state-of-nature must be included in (or easily derived from other variables of) the model. One such necessary information is the weight of the pigs in a given pen at a given time. Several models have been suggested through the years. Since our primary concern is short time prediction of the weight, i.e. the distribution of the weight tomorrow given today's distribution we will discard the more sophisticated approaches and use a (piecewise) linear approximation.

Assume that the initial weight W_0 of the individual pigs in a section is given as $W_0 \sim N(\mu_0, \sigma_0^2)$. Define $\zeta_t \sim N(\mu_{\zeta_t}, \sigma_{\zeta_t}^2)$ to be the daily gain of a pig from time $t-1$ to t, and assume that daily gain is independent of the current weight and the growth so far. Then the sum of these variables is a mixture of Gaussian distributions, however, we approximate by an appropriate Gaussian distributions. Hence, the weight of the individual pigs at day $t = 1, 2, \ldots$ may be defined as:

$$W_t = N(\mu_t, \sigma_t^2) \tag{3.1}$$

where $\mu_t = \mu_0 + \sum_{i=1}^{t} \mu_{\zeta_i}$ and $\sigma_t^2 = \sigma_0^2 + \sum_{i=0}^{t} \sigma_{\zeta_i}^2$. Using this representation of the weight the corresponding feed intake at day $t = 1, 2, \ldots$ may be calculated as in Jørgensen (1993):

$$F_t = \lambda_2 \lambda_4 [\lambda_3 - \ln(W_t)] W_t + \lambda_1 W_t^{0.75}, \tag{3.2}$$

where the parameters λ_i are described in Table 3.1. Hence, the total feed consumed until day t is just $\mathcal{F}_t = \sum F_t$.

At first this model may seem too simple. But assuming that daily gain is independent of the current, the piecewise linear growth curve suggested here can be adapted to virtually any growth curve, since we only require that it fits "once" a day. Hence, the distribution of the ζ_i's may be chosen to model a theoretic growth curve or simply estimated using an appropriate data set. The calculation of daily feed intake in Equation 3.2 is based on the traditional assumption that the total feed intake is dispensed on growth (the first term) and maintenance (the second term). It is implicitly assumed that the feed intake is big enough to allow for growth according to the Gompertz growth curve, see e.g. Jørgensen (1998) for a discussion of these issues.

It is questionable to assume independence between successive ζ_i's, however, our primary concern is the mean and variance of the weight at certain points in time, not how the weight of the pig evolves through time. Thus if we knew the distribution of the weight in a section at, say, day 70, then we would calculate the means and variance of the ζ_i's so that the initial (known) distribution plus the sum of the 70 ζ_i's would result in the desired distribution.

Modeling delivery of slaughter pigs

We will assume that the heaviest pigs in the population are the ones selected for slaughter at any given time. Hence our assumption of weight being Normal distributed will clearly become questionable after some subset of the population has been slaughtered. However, the hypothetical distribution of the entire population if no animals were slaughtered, may still be assumed Normal.

We have chosen to model delivery in terms of a certain fraction of the entire batch, hence we do not propose a threshold weight, but merely markets an appropriate fraction of the pigs. Hence, if ρ_p is the fraction of the original population still left and ρ_d is the fraction of pigs selected for marketing in the current week, then Figure 3.1 illustrates the idea of the selecting the heaviest pigs of the remaining population.

3.3.2 Adding disease to the problem of optimal marketing management

The elements of the decision support system described so far forms the necessary elements to explore the effect of different production systems on the profit returned by the production facility, i.e. the housing system. We can investigate the sensitivity of the proposed system with respect to different parameters like e.g. daily gain.

One factor known to affect the average daily gain of pigs is respiratory disease. If infected the pigs loose their appetite, hence reduce their feed intake which subsequently reduces growth. Fortunately a number of different control measures exists which can be applied at different times. Hence, to optimize the performance of the production system in an environment with presence of contagious disease it is necessary to simultaneously optimize the delivery and control strategies. To handle the situation, we now propose an extension of the system outlined so far. We expand the state space to allow

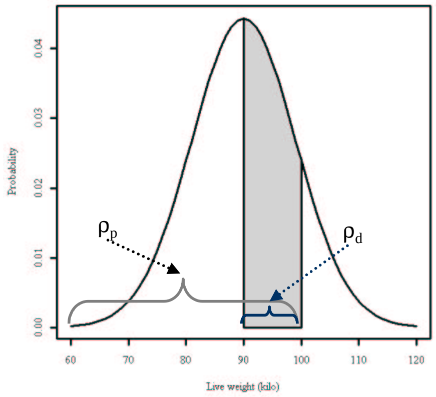

Figure 3.1: The hypothetical distribution of weight, with the remaining fraction of pigs (ρ_p) and the part of these selected for delivery (ρ_d) imposed in grey

modeling the spread of disease according to a widely accepted model, known as the *general epidemic* model. Within this state space we introduce the different control strategies which may be adopted. Some of these may not be available at the moment. Even so, the decision support system developed here may serve as a tool for exploring the cost-benefit of such controls.

3.3.3 The general epidemic model

In order to model the transmission of infectious disease between animals we will rely on the so-called General Epidemic model, introduced in its stochastic form by Bartlett (1949). The underlying assumptions are that all animals are initially susceptible for transmission of disease. Upon infection they become infectious for a period, after which they stop being infectious, recover and become immune. They are said to be removed. An animal who is infectious is called an infective. For convenience we will refer to models which assume that animals pass, in turn, through the *Susceptible, Infective* and *Removed* state, as SIR models.

Using the general epidemic model, the spread of a SIR infectious disease in a population of homogeneous individuals who mix uniformly, is modeled as a Markovian continuous-time model.

Let us here briefly introduce the model as defined in Daley and Gani (1999). Let $S(t)$, $I(t)$ and $R(t)$ denote the respective number of susceptible, infectious and removed individuals at time t. Consider a closed section of n animals, hence the relationship

$$S(t) + I(t) + R(t) = n, \qquad (\forall t \geq 0) \tag{3.3}$$

The initial conditions of an epidemic are specified by $S(0) = s_0, I(0) = i_0$ and $R(0) = r_0$. For now we will assume that these quantities are known. Assume that $\{(S,I)(t) : t \geq 0\}$ is a bivariate Markov process; Equation 3.3 ensure that $R(t) = n - S(t) - I(t)$ is known when $(S,I)(t)$ is known. The infinitesimal transition probabilities of the General Epidemic in the interval $(t, t + \delta t)$ is defined by

$$\begin{aligned}
&\Pr((S,I)(t+\delta t) = (i-1, j+1)|(S,I)(t) = (i,j)) \simeq \frac{\beta ij}{n}\delta t, \\
&\Pr((S,I)(t+\delta t) = (i, j-1)|(S,I)(t) = (i,j)) \simeq \gamma j \delta t, \\
&\Pr((S,I)(t+\delta t) = (i, j)|(S,I)(t) = (i,j)) \simeq 1 - \frac{\beta ij}{n}\delta t - \gamma j \delta t.
\end{aligned} \tag{3.4}$$

After some finite (random) time the are no infectious animals present in the section and the epidemic is over. The number of animals that are still susceptible and the number who have been removed are called the *final state* of the epidemic. The present formulation does not include exogeneous infectious agents, hence we implicitly assume that the first infectious animal is introduced either by a special event or at a rate which is negligible compared to the within herd infection rate.

There are several features of this model open to criticism. In slaughter pig production we can actually justify the assumption of homogeneity (contrary to most published applications) whereas that of uniform mixing may be questioned, since the pigs are usually grouped in pens.

The General epidemic model has two parameters β and γ. The parameter β is the rate at which an infectious animal has close contact with other animals in the section, hence $\beta S(t)I(t)/n$ is the aggregated rate at which infectious animals has close contacts with susceptibles. It is customary to reparametrize γ to γ^{-1}, the mean duration of the infectious period. The model implicitly assumes that the infectious period is exponentially distributed with parameter γ.

Most literature regarding epidemic models is concerned with estimation of these parameters, or determining the final state of the epidemic. A third often used property is the *basic reproduction ratio* $R_0 = \beta s_0/\gamma$ defined in DeJong et al. (1993) as:

> "..the expected number of new infections caused by a typical infected individual during its entire infectious period in a virgin(i.e. completely susceptible) population that is in a stable demographic state at the moment the infection is introduced."

For any eradication strategy to be effective, it has to reduce the basic reproduction ratio below 1, given that the epidemic behave in a deterministic way. In a stochastic framework, epidemics may fade out for R_0 slightly above 1, or they may fail do to so even if $R_0 < 1$. Still the bigger the value of R_0 the larger the expected final number of affected animals.

We will require the use of the model in a slightly different way. We are going to assume that at time t we have the *distribution* of $S(t), I(t)$ and $R(t)$. Given a specific set of β and γ we will determine the joint distribution of $\Pr(S(t+1), I(t+1), R(t+1) \mid S(t), I(t), R(t), \beta, \gamma)$.

One obvious approach is to apply Equation 3.4 directly. However, this method requires substantial computation and is increasing in complexity by the number of pigs in the section. We would prefer an updating procedure, which allowed for modeling of just about any number of pigs in a section without increasing the demand in computer capacity dramatically.

One method to efficiently handle the nonlinear Markov process describing the general stochastic epidemic is based on the assumption that the variates are normally distributed (Whittle, 1957). In Isham (1991) this method is applied to the SIR-model and compared to the traditional approach of stochastic simulation with encouraging results for parameters suitable for HIV epidemics in a population of 1000 individuals.

This approximation assumes that (S, I) has a bivariate normal distribution with mean $\boldsymbol{\mu} = (\mu_S, \mu_I)$ and covariance matrix

$$\Sigma = \begin{pmatrix} \sigma_{SS} & \sigma_{SI} \\ \sigma_{SI} & \sigma_{II} \end{pmatrix}$$

then the following five equations are obtained ($n = S + I + R$ as usual):

$$\begin{aligned}
\frac{d\mu_S}{dt} &= -\beta\frac{\mu_S\mu_I}{n} - \beta\frac{\sigma_{SI}}{n}, \\
\frac{d\mu_I}{dt} &= \beta\frac{\mu_S\mu_I}{n} + \beta\frac{\sigma_{SI}}{n} - \gamma\mu_I, \\
\frac{d\sigma_{SS}}{dt} &= -2\beta\frac{\mu_S\sigma_{SI} + \mu_I\sigma_{SS}}{n} + \beta\frac{\mu_S\mu_I + \sigma_{SI}}{n}, \\
\frac{d\sigma_{SI}}{dt} &= \beta\frac{\mu_S(\sigma_{SI} - \sigma_{II}) + \mu_I(\sigma_{SS} - \sigma_{SI}) - \mu_S\mu_I - \sigma_{SI}}{n} - \gamma\sigma_{SI}, \\
\frac{d\sigma_{II}}{dt} &= 2\beta\frac{\mu_S\sigma_{II} + \mu_I\sigma_{SI}}{n} + \beta\frac{\mu_S\mu_I + \sigma_{SI}}{n} - 2\gamma\sigma_{II} + \gamma\mu_I,
\end{aligned} \tag{3.5}$$

where explicit dependence on t has been dropped everywhere. This is just a set of ordinary differential equations which is easily solved using standard algorithms like Runge-Kutta (Press et al., 1992).

Starting the epidemic

So far we have ignored how to introduce the initial number of infectious animals (i_0), i.e. we need to determine the probability of animals contracting the disease from an outside source. For certain airborne diseases this risk might be substantial and should probably be modeled throughout the entire duration of the epidemic. Define ϕ as the transition intensity from S to I conditioned on no disease animals in the current batch. This can be interpreted as a measure of the prevalence of disease among herds. Using ϕ we will determine the corresponding probability p_{01} of introducing a sick animal between 2 decision epochs, e.g., from day to day. It seems reasonable to assume that the waiting time to introduction of disease is exponential, hence within a batch we have:

$$p_{01} = 1 - \exp(-\phi) \tag{3.6}$$

3.3.4 Decisions related to disease

Here we may again distinguish between intervening and non-intervening decisions.

Non-intervening or test decisions are necessary since we are facing decision making under uncertainty, and the precision of which we may obtain information depends on the method selected for information retrieval. As an example consider visual inspection of the frequency of coughing among a section of pigs compared to serologic analysis as an indicator of respiratory disease. These methods may both increase the certainty in the state-of-nature, however, at different costs and with different precision.

Intervening decisions or control measures may be divided into two different categories, operational and tactical decisions. This distinction reflects an important, however, often ignored property of control measures. Different control measures may react on different time scales. To elaborate on this statement, consider two completely different control measures for managing respiratory disease, e.g. move sick animals to an "emergency" unit or start a vaccination programme. The former decision is aimed at reducing the impact of the ongoing epidemic by reducing the number of infectives in the population (as well as the size of the population). Hence the main effect of this control strategy is on the current batch of pigs which is suppose to have a lesser epidemic, hence less reduction in daily gain. Any long term effect of this control strategy is only a desirable side effect of possible lower basic risk of introducing disease in the next batch. Initiating a complete vaccination programme on the other hand is a decision which has no impact on the current batch of pigs, since it is not customary to vaccinate pigs for a disease which they have already been infected with. Thus, the proposed effect of this control measure must be on the future batches of the current section (and present and future batches in the other sections of the production system).

Modeling the effect of different control measures.

We have chosen to model disease using only three parameters describing the evolution of disease plus a joint distribution of the three subsets of the population, hence we should be able to model the impact of the different control measures's effect of the outcome of the epidemic using these elements only. There is, nonetheless another important motivation for adopting some control strategies: the impact of disease on the affected animals is reduced.

In Table 3.2 some typical control measures are presented to illustrate the ideas of different time horizons and different mechanisms in the basic effect of disease related decisions. It is obvious that this short list is in no way exhaustive, but the different control measures represents the various mechanism that the modeling framework should allow for. Some additional comments to some of the control measures may be appropriate here.

Traditionally the effect of a vaccine is measured in terms of its *efficacy*(VE) defined in Becker and Britton (1997) as:

$$VE = 1 - \frac{\text{attack rate among vaccinated animals}}{\text{attack rate among unvaccinated animals}} \tag{3.7}$$

This is not a very satisfactory measure because it depends on both the housing system from which the data come and the time period over which the data are collected. Furthermore the protective efficacy may be interpreted differently dependent on the type of response it offers. It may be that a fully susceptible pig has a force of infection $\beta(t)I/n$ exerted upon it at time t, then a vaccinated pig has $\pi\beta(t)I/n$, where $\pi \in [0,1]$ is a measure of the protection that the vaccine offers. On the other hand, it might be that a fraction π of the vaccinated pigs are fully protected while the remainder have no protection at all. Again π is a measure of protective efficacy, however, the interpretation clearly differs in the two cases. In Figure 3.2, the difference between the expected development of disease in a fully susceptible population, a population with reduced susceptibility and a population in which some individuals are completely immune, is outlined. Note that within 15-18 days all individuals are infected in the unvaccinated population and the two vaccinated populations are indistinguishable. Hence at 15-18 days where the attack rates are the same for each of the vaccinated populations and 100% in the unvaccinated population, analysis would yield more or less the same efficacy for the two vaccines. But, at day 60 the efficacies of the two vaccines would differ.

Eradication or early delivery of the remaining pigs is supposed to lower the risk of transferring disease from the current batch to the next, hence we assume some sort of decay of infectious agents through time. It is not a topic widely studied in literature, although it is possible to find estimates of survivability of different bacteria or virus outside a host. We suggest the following model for transmission of basic risk through batches. Let Δl denote the number of time units the housing facility is empty, then we may assume that ϕ_t is given as:

$$\log(\phi_t) = \log(\phi_{t-1}) + \alpha I/n - \Delta l \epsilon + e_t, \quad e_t \sim N(0, V), \tag{3.8}$$

where α is a measure of generated disease pressure by a sick animal within the batch and ϵ is a measure of disease pressure decay per time unit. We

Time Horizon	Description	Effect in model
Operational	Move sick animals to a different location, e.g. an "emergency" unit, or simply cull them.	Reduce the expected mean of $I(t+1)$, hence reduce the expected effect of current epidemic.
Operational	Use medication to ease the effect of disease	The effect is modeled in two ways, the β is reduced to model the lower susceptibility, and the γ is reduced in order to reflect the expected faster recovery.
Tactical	Eradication, i.e. early delivery of the entire batch. That is to empty the section before the optimal slaughter weight is obtained. Eradication of the entire production facility is an action with the same effect, however, assumed much more thorough.	This action is suppose to lower the basic risk (ϕ) of transferring the disease to subsequent batches, i.e. the decision to empty a section early is probably accompanied by a decision to disinfect the entire section.
Tactical	Vaccination, i.e. vaccinate subsequent batches so the future populations will be less susceptible to the disease	Future batches will have reduced values of β, γ and ϕ to model that the disease is harder to introduce, does not spread as effectively and make the animals less sick.
Tactical	Reduce stocking rate, i.e. insert fewer pigs in the next batch	By reducing the number of pigs occupying the section, the pigs may be assumed less stressed, hence a dampening effect of the disease may be present, i.e. the disease will not effect the animals in the section as hard as if the stocking rate where at is maximum.

Table 3.2: Some typical operational and tactical control measures in respiratory disease

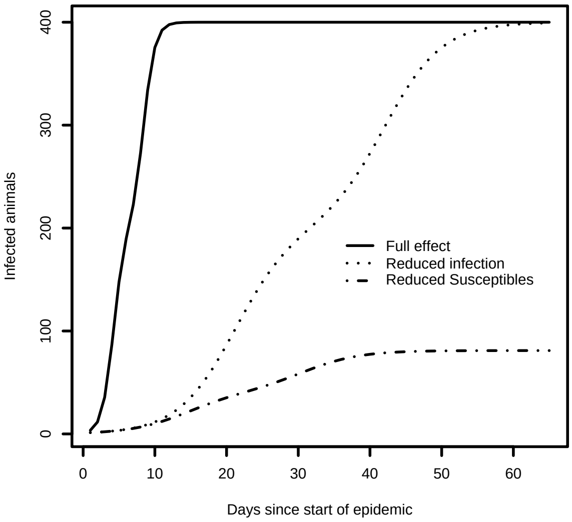

Figure 3.2: The effect of an epidemic with $\beta = 1.25$ among 400 susceptible pigs (solid lines) and the corresponding developments in vaccinated populations with different meaning of the same efficacy (VE $= 0.8$)

have chosen to model the intensity ϕ_t at the log scale to avoid problems with boundaries. I/n is the ratio of sick pigs at the termination of the batch. Equation 3.8 can be regarded as an auto regressive process, with added contribution from the batch and a constant decay per time unit empty. The choice of model may be questioned, however, in absence of a gold standard we note that this model allows for properties that can be justified as likely for decay/transition of the basic risk. Furthermore, we can explore the effect of different parameters in Equation 3.8 to quantify the influence on the overall results.

3.3.5 Linking disease and growth

So far we have described how to estimate the populations of susceptible, infectious and removed animals during an outbreak of an epidemic disease in a parsimonious way, using only three parameters to describe the evolution of the epidemic and three parameters to describe the joint distribution of the populations of S, I and R respectively.

We have only considered the effect of the different control measures on the outcome of the epidemic. It is time to explore how disease effect the growth of the animals. Two things must influence the impact of disease on the distribution of weights of the animals: The number of animals which acquire disease; and the severity by which they develop it.

Hence, we must introduce a parameter ψ to describe the *dampening* effect of a control measure on the growth reduction in slaughter pigs infected with the disease.

The most obvious explanation for a reduced growth caused by disease is that the animals consume less feed while sick, thus leaving less energy for growth (energy requirements for maintenance is assumed constant). However, we have chosen to model feed consumption as a result of growth and not the opposite. We will therefore have to assume that disease reduce the daily gain, hence implicitly the quantity of feed consumed.

It is likely that the period of time in which the daily gain is influenced differs from the time the animal is infectious. An example is the Swine Flu where the pigs are infectious for months but usually only sick for a couple of days. In general it is not feasible to keep track of the evolution of the disease due to the increase in state space such a procedure would require. Thus a different method to differentiate between being affected and infectious is required. Here we propose two different approaches which simplifies the problem without too much loss of generality.

The first idea is applicable to diseases like the Flu, where the relevant production traits are only affected in a short period of time when compared to the duration of the infectious period. Assume that all growth reduction occurs within the first day of disease. The number of newly infected animals is easily determined through the transition probabilities of the model. Define C_t as the expected number of new cases from day $t-1$ to day t. Then the expected daily gain of the entire population ζ was defined earlier as $\zeta_t \sim N(\mu_{\zeta_t}, \sigma^2_{\zeta_t})$. Now we assume that daily gain in a population exposed to epidemic disease (under a control strategy with dampening effect ψ) is $\tilde{\zeta}_t \sim N(\mu_{\tilde{\zeta}_t}, \sigma^2_{\tilde{\zeta}_t})$, with

$$\mu_{\tilde{\zeta}_t} = \frac{n - C_t}{n}\mu_{\zeta_t} - \frac{C_t}{n}(1-\psi)\mu_D; \quad \sigma^2_{\tilde{\zeta}_t} = \frac{n - C_t}{n}\sigma^2_{\zeta_t} + \frac{C_t}{n}\sigma^2_D \tag{3.9}$$

where the full effect of disease is assumed to be $N(\mu_D; \sigma^2_D)$.

Another approach suitable for diseases of which the impact is more or less permanent throughout the duration of the infectious period is to assume the growth rate constant for each of the subpopulations, i.e. define the daily gain of the population as the weighted sum of the daily gain of each subpopulation, using the expected proportion of animals in each category as weights. These numbers are also easily calculated from the transitions required by the model.

3.3.6 Summary of the generic framework

It is important to realize that while most of the discussion so far has been on representing state-of-nature and the effect of the respective control measures on the state-of-nature, the true nature of this problem should be regarded as a decision problem. That is to select the optimal strategy of choices among the presented control measures (and implicitly assumed available test decisions).

At this point it can be worthwhile to realize that the nature of the overall problem is unaffected by including the decision complex regarding disease. The main objective is still to maximize the total expected discounted reward of the current and subsequent batches of pigs occupying the section consider as the unit of interest here.

One major difference between the current problem and the original problem of optimal marketing management as outlined in Kure (1997) is that decisions are introduced at multiple time scales. Thus, the original assumption of Markov decision processes of actions being chosen, carried out and rewarded within the smallest considered increment of time is relaxed. We have operated with decisions on two time scales: The daily operational decisions with a time horizon of a couple of days, or at most until the end of the current batch, e.g. moving sick animals; and the tactical decision scenario where decisions have a time horizon measured in terms of batches, e.g. vaccination or eradication. Multi level hierarchic Markov processes (Kristensen and Jørgensen, 2000) are especially well suited to handle problems of decisions at multiple time scales with an infinite time horizon.

What is important to keep in mind is that the individual variables or parameters of the problem should be represented at the same level as the decisions which influence these. Hence, at the batch level where decisions aim at reducing disease pressure ϕ the state variable should be ϕ itself as well as other variables which remain constant throughout the duration of a batch. At the operational or daily level, the variables should be those describing the distribution of the populations of $S(t), I(t)$ and $R(t)$ respectively, as well as an appropriate description of the growth of the animals. Decisions represented here are the operational control measures, e.g. moving sick animals and use medication, but in addition to these, we must allow the original set of decisions, i.e. deliver some fraction of the heaviest pigs or terminate the current batch. Thus the state space of the multi level hierarchic Markov process is a discrete representation of the possible outcomes of ϕ, i.e. transition intensities of reasonable scale, at the founder level. Each child process have a stage for each ordinary day of the production and one for each delivery day. The states at each ordinary day are the possible configurations of susceptible and infectious pigs. The states for a delivery day are the configurations of susceptible and infectious pigs for the different number of pigs still left in the section.

3.4 An applied example — the case of Swine Flu

As an illustration of the framework presented here, we are going to implement an example using the Swine Flu as a model disease. In the implementation of this example we have made a series of simplifications, some due to the complexity of the problem while others are the result of inadequate information available to estimate possible effects.

3.4.1 Outline of the production facility and delivery policy

We are going to assume that the weaner supply is constant and inflexible, i.e. with a constant interval the section must be emptied so that the new batch can be inserted. Delivery of animals will occur in a fixed number of deliveries starting some predetermined number of weeks prior to termination. Appropriate initial weight and daily gain distributions are specified. Pigs are selected and delivered once a week in the last 4 weeks. The number pigs in each delivery is a multiple of some smallest quantity. Note that the Danish pricing system is using a basic price per kg. for carcasses within a certain weight interval (currently 67 - 79.9 kg) and a reduction of 0.1 dkr per deviating kilo. In addition there is a premium for increasing lean meat percentage above 59% (and a reduction below), however, we will ignore the premium for leanness. We have chosen not to model any cost other than food cost and the cost of applying e.g. vaccination or medicine. We implicitly assume that all other cost are constant regardless of strategies. The result is that output from the model should be compared in terms of relative effects, absolute values does not reflect the actual return by adopting an optimal scheme.

3.4.2 Modeling disease

The Swine Flu is characterized by certain properties which makes it an ideal disease from a modeling point of view. The two most important properties of the disease are: very few animals die from the flu and once sick, they remain infectious throughout the production period. Hence, we do not need to model animals dying and we only need to consider two types of animals, those susceptible and those infectious. The removal occur at delivery, hence the possible configurations of pigs is determined by the number of sick pigs alone. We have chosen to model this scenario by choosing $\gamma = 0$, although the pigs eventually would recover if they were not delivered for slaughter.

As previously discussed, there exists two levels of decision problem: the daily operation within each individual batch, and the tactical decision scenario of the sequence of batches. At each level some appropriate control measures may be applied, the nature of these is outlined in Table 3.2. Unfortunately neither vaccine nor medicine (if any available) is approved in

Denmark, still we include these as possible decisions in order to do cost-benefit analysis on these possibilities. We explicitly allow for a reduced stocking rate and model the possibility to terminate the batch at any of the given delivery times.

In Denmark, medication of animals requires successive retaining of pigs for some period. To simplify the model, we will assume that medication is prohibited once delivery has begun. Furthermore we assume that medication is a shoot-and-forget decision. Once medicine has been administered we do not observe the pigs until the onset of delivery. Usually it is not allowed to use medicine as a preventive measure, hence we assume that at least one animal is observed sick prior to start of medication. Hence for a large part of the transitions we can apply either the probability determined earlier as p_{01} or the distribution of sick animals at the next decision epoch, given the current number of sick pigs.

Only one special case needs attention; the transition from the state defined by zero sick pigs at a given time of delivery to the distribution of sick pigs at the next delivery. Define $SI(t)$ as the distribution of sick animals after t days given one animal is sick at time $t = 0$. The distribution of animals sick at, say, day l given no sick animals at day 1, can then be defined as the the mixture:

$$SI_l = \sum_{j=1}^{l} p_{01}(1 - p_{01})^{j-1} SI(l - j) \tag{3.10}$$

where $SI(t)$ is Gaussian as defined by Equation 3.5. Again we simply replace this mixture by a Gaussian approximation with mean and variance defined as the linear combinations suggested by Equation 3.10.

3.4.3 Scenario

When designing scenarios for application of the model the keyword should be simplicity. Still the analysis conducted so far has emphasized the complicated nature of the decision complex. It seem somewhat contradictory to illustrate the full complexity of the system by simple examples. We are nonetheless going to try, by focusing on only a small subset of the involved parameters. Specifically we are going to focus on one instance of a rather vicious flu-like disease (contact rate $\beta = 0.5$, weight reduction $N(\mu_D = 7, \sigma_D^2 = 3)$), for which there is a vaccine which reduce susceptibility for all animals (efficacy $= 0.95$) and a medication ($\beta_{med} = 0.3$) available.

The population exposed to this disease is a section of 200 animals with an average daily gain of 0.8 kg. New animals are introduced every 112 days, with 7 days allocated for cleaning the stables while empty.

Using this scenario we explore how the cost of vaccine and medicine may influence the optimal policy for different levels of disease pressure ϕ.

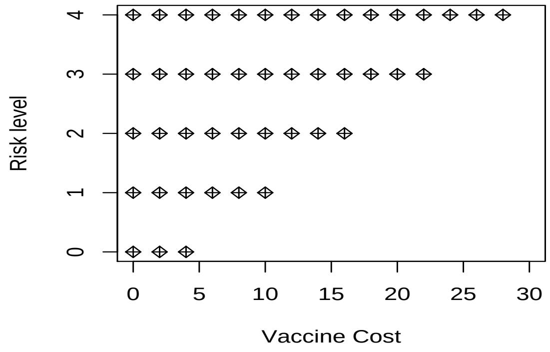

Figure 3.3: The optimal vaccination policy given a certain level of disease pressure for different cost (DKK) of the vaccine.

3.4.4 Scenario results and discussion

The scenario chosen for illustration left us with some possibilities for predicting the outcome, thus we can consider the results as more of a validation of the computer software than an example of practical importance. However, the major justification of a system such as this is probably knowledge acquisition (or more likely pinpointing where we know little, nothing or absolutely nothing about the mechanisms involved).

There seem to be three different elements of the results to report: The policy at the high level, the medication policy and the delivery policy. Partly due to specification and partly due to the nature of the problem, it is possible to present the results for different levels and aspects more or less independent of the others.

The policy for application of vaccine at different cost is shown in Figure 3.3. As expected the vaccine is suggested at any level of disease pressure for low cost and the policy is gradually changed towards recommendation of vaccine at high levels only as the cost increase. At 30 DKK there is no economic value in applying the vaccine.

The medication policy is of course dependent on the vaccine policy. Since the vaccine reduces the contact rate (β) below that of the medication, there is no point in applying the medicine in a vaccinated population. This is reflected in the optimal policy, hence medicine is only given in unvaccinated batches. Since the performance of the medicine is rather poor (a mere 40% reduction) the policy is rather conservative.

Since the disease pressure (ϕ) only influences the probability of the first sick animal our medication policy could be believed to be the same for all

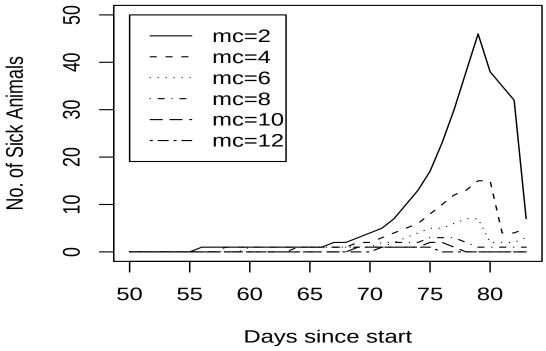

Figure 3.4: The threshold curves for applying the medicine at a given day for a given medicine cost (mc). Only when the number of sick pigs for a given day lies below the curve is medicine profitable at the specified cost.

levels of ϕ given no vaccine is applied. However, this is not the case for reasons which we will address shortly.

The actual policy for different medicine costs is given in Figure 3.4 below for a vaccine cost of 12 DKK, i.e., the medicine is given only at the 2 lowest levels of ϕ where the batch is not vaccinated (refer to Figure 3.3). The curves are upper boundaries for the number of sick animals to observe when initiating the medication treatment. Remember that medicine is assumed to work just as a vaccine but with much lower efficacy. A medicine that reduce the effect of disease would have a different optimal policy. It is noteworthy that even for low cost medicine, treatment is only profitable for late outbreaks that are determined fast. Hence the medicine treatment is much more sensitive to continuous monitoring of the herd. An outbreak that start in the evening might have evolved past the point of treatment before the morning. Automatic monitoring such as discussed in Madsen and Ruby (2000) will increase the value of available operational control measures, simply because early warning might be necessary for the strategy to be effective.

Returning to the issue of different policies for administering medicine at different levels of disease risk we will note that we have observed that for a very small set of states, i.e., the days from 70-75 and less than 2 sick animals, it is optimal to give medicine at the 2 states indicating highest disease states. The reason for this behavior is driven by slightly different motives than the medicine policy outlined in Figure 3.4. The reason for that behavior was to reduce the weight loss imposed by the disease. The high-disease-risk medicine policy aims at reducing the number of sick animals to reduce the probability of being at high disease risk state at the next batch as well. We shall see when discussing the delivery policy how the same is reflected there.

The complexity of the delivery policy makes it even harder to visualize this than the previous parts of the policy. Nonetheless, we are going to try to illustrate how the both the number of sick pigs and the disease pressure influence the delivery policy. As a first illustration consider Figure 3.5, where the delivery policy for the first delivery (of 4 with a week between each) for each level of ϕ is shown as well as the delivery policy for a vaccinated population. It is obvious that the delivery policy for high levels of disease risk attempts to adjust the transition towards a reduced disease risk at the next stage, i.e., cuts a loss now in anticipation of future rewards. However, there is also a different motivation for the termination of an entire batch of pigs at a lower weight than what would be expected in a healthy population. In Figure 3.6 the choice to deliver 120 pigs at the last delivery when all pigs are sick is a result of the required termination. Not a result of the remaining pigs reaching optimal slaughter weight at the same time. When only a few pigs are sick, we know that more will follow, and within a week most of the pigs will be sick. By terminating the batch we avoid the weight loss associated by the disease as well as gain an advantage at the next batch because of reduced disease risk.

In Figure 3.6 the ratio of pigs delivered at each delivery is visualized for 2 opposite cases, where the pigs are either healthy throughout the delivery or all pigs are sick prior to the first delivery. It is easily seen that while the scenario of no sick pigs result in an expected delivery pattern, the case of all sick pigs is clearly the result of forced delivery of pigs below the optimal delivery weight. This is imposed by the restraints in production system, where new pigs are awaiting to fill the section, thus forcing us to empty the section at last delivery.

The differences displayed in delivery policies affects the transition from a risk level at the current batch to the next, by means of increased probability of transition towards a lower level when cost of vaccine increase. The reason for this behavior lies in our (arbitrarily) chosen model which always reduce the expected level of ϕ in the next stage until the lowest level where it stays almost surely. If no vaccine is available it is important to reduce the risk of disease fast, hence deliver pigs early just to get rid the infectious animals. In presence of a vaccine as powerful as the one modeled here, we can disregard the benefit of early delivery as means of reducing disease transmission, simply because the disease develops slowly in a vaccinated population.

Hence it can be questioned whether pigs actually are better of without a vaccine, since that situation actually promotes an adjustment of the production towards a state with less risk of disease!

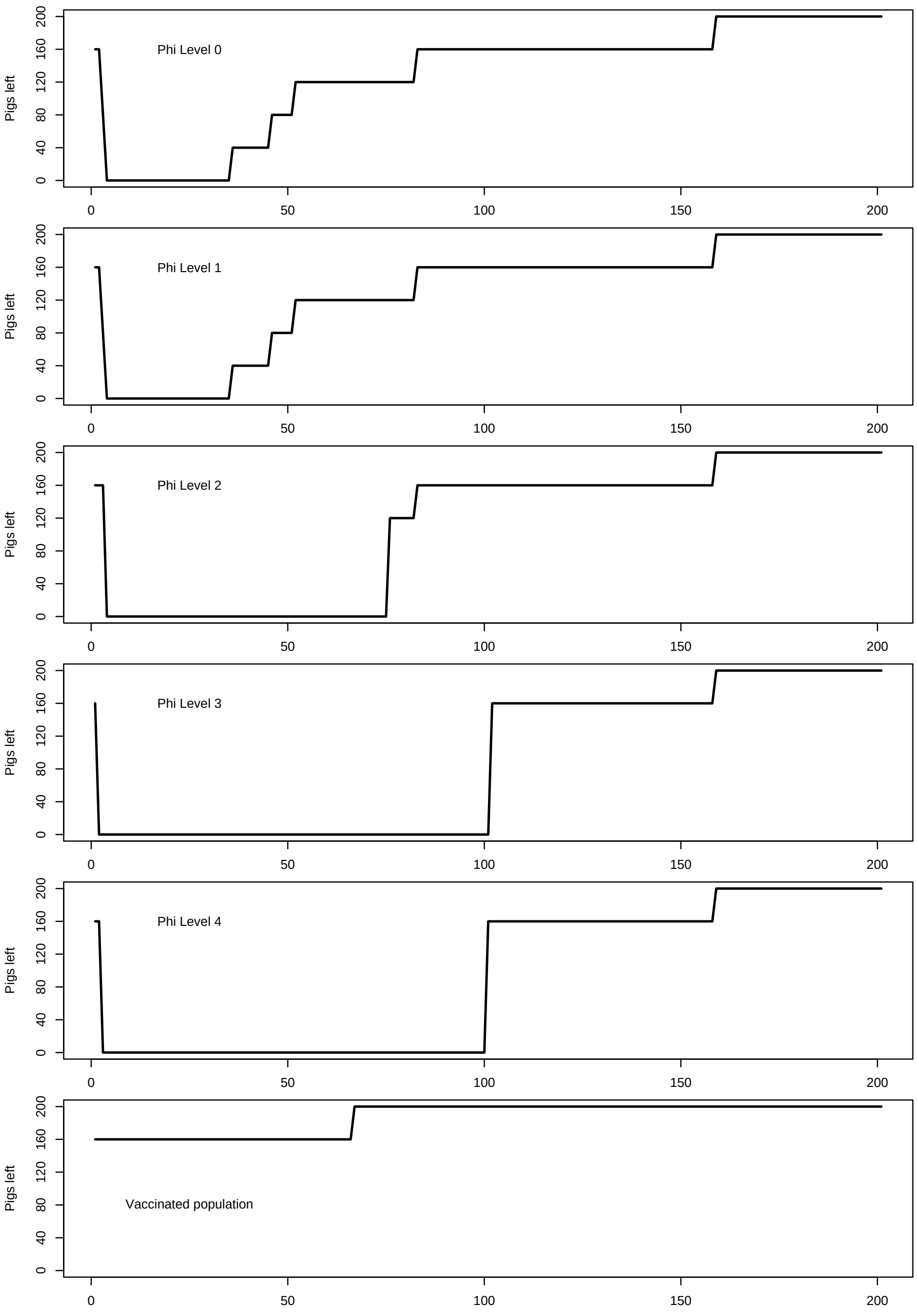

Figure 3.5: The delivery policy at first delivery (out of 4) expressed as the number of pigs left in the system given the number of sick pigs for each level of ϕ and for a vaccinated population.

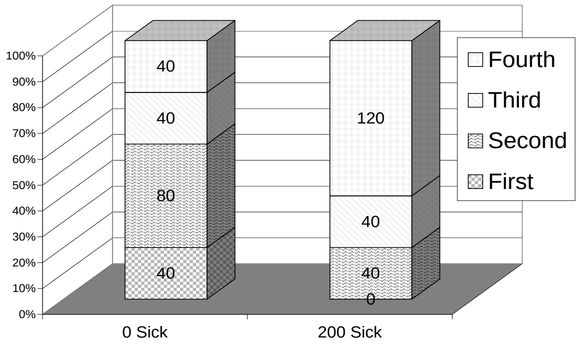

Figure 3.6: The optimal delivery policy as number of pigs delivered at each of 4 deliveries for the 2 cases of all pigs healthy throughout delivery and all pigs sick prior to delivery.

3.5 Concluding remarks

The decision complex faced by slaughter pig producers can of course be extended beyond the one outlined here, where we focus on delivery decisions and control strategies for epidemic diseases. However, we feel that we have raised an important point. The evaluation of elements such as disease control can be incorporated into the production system and decision complex already faced by the producer. By this approach it is possible to perform an economic evaluation of the suggested control strategies for a specific disease, thus allowing the pig producer to assess the value of, e.g., a vaccine within his own production system.

The section chosen here as modeling unit is typically one of many parallel sections operated by the pig producer. The usual system refills a section in a fortnight every 16 weeks, hence 8 sections are needed to allow for arrival of new pigs every week. This implies that we need to consider the risk of cross-section infection. Our model cannot directly address this issue, but can adjust by a suitable model disease pressure transition from batch to batch (Equation 3.8).

Our analysis included elements which have more or less been ignored by the example, e.g., the test decisions. The observations regarding disease have been modeled as visual inspection (of perfect performance) and the distribution of weight is assumed known implicit by knowing the days since start of the batch, start weight and number of sick animals. The reason we have ignored these in the specification of an example has to do with our choice of modeling framework as well as our attempt to focus on the linking of optimal control strategies and delivery policies.

We believe that the analysis of a framework for simultaneous optimization of delivery and control strategies and the resulting model will serve as a useful tool towards a better understanding of the mechanisms involved in this kind of decision complex and system.

References

M. S. Bartlett. Some evolutionary stochastic processes. *Journal of the Royal Statistical Society*, 11:211–229, 1949.

N. G. Becker and T. Britton. Statistical studies of disease transmission: An overview. In *Epidemics Workshop*. The Royal Statistical Society, 1997.

J. E. Broekmans. Influence of price fluctuations on delivery strategies for slaughter pigs. *Dina Notat*, 7:1–28, 1992.

B. R. Cherry, M. J. Reeves, and G. Smith. Evaluation of bovine viral diarrhea virus control using a mathematical model of infection dynamics. *Preventive Veterinary Medicine*, 33:91–108, 1998.

D. J. Daley and J. Gani. *Epidemic Modelling: An Introduction.* Cambridge Studies in Mathematical Biology. Cambridge, 1999.

M. C. M. DeJong, O. Diekman, and J. A. P. Heesterbeek. The computation of r_0 for discrete-time epidemic models with dynamic heterogeneity. *Mathematical Biosciences*, pages 1–18, 1993.

V. Isham. Assessing the variability of stochastic epidemics. *Mathematical Biosciences*, 107:209–224, 1991.

E. Jørgensen. The influence of weighing precision on delivery decisions in slaughter pig production. *Acta Agriculturæ Scandinavica, Section A*, 43 (3):181–189, August 1993.

E. Jørgensen. Stochastic modelling of pig production working paper: Growth models. Dina Notat 73, 1998.

A. R. Kristensen. Hierarchic markov processes and their applications in replacement models. *European Journal of Operational Research*, 35:207–215, 1988.

A. R. Kristensen and E. Jørgensen. Multi-level hierarchic markov processes as a framework for herd management support. *Annals of Operations Research.*, 94:69–89, 2000.

H. Kure. *Marketing Management Support in Slaughter Pig Production.* PhD thesis, The Royal Veterinary and Agricultural University, 1997.

J. W. Lloyd, S. B. Harsh, J. B. Kaneene, G. D. Schwab, B. J. Thacker, and A. J. Thulin. Development of a computerized systems model for health management decision support in growing hogs. *Preventive Veterinary Medicine*, 19:249–265, 1994.

T. N. Madsen and V. Ruby. An application for early detection of growth rate changes in the slaughter pig production unit. *Computers and Electronics in Agriculture*, 25:261–270, 2000.

W. H. Press, S. A. Tekolsky, W. T. Vettering, and B. P. Flannery. *Numerical Recipes in C. The Art of Scientific Computing.* Cambridge, second edition, 1992.

M. L. Puterman. *Markov Decision Processes: discrete stochastic dynamic programming.* Wiley - Interscience, 1994.

H. Saatkamp. *Simulation studies on the potential role of national indetification and recording systems in the control of Classiacl Swine Fever.* Ph.d. thesis, Department of Farm Management, Agricultural University, P.O. box 338, 6700 AH Wageningen. The Netherlands, Wageningen, 1995.

K. D. C. Stärk, D. U. Pfeiffer, and R. S. Morris. Within-farm spread of classical swine fewer virus - a blueprint for a stochastic simulation model. *Veterinary Quarterly*, 22:36–43, 2000.

P. Whittle. On the use of the normal approximation in the treatment of stochastic processes. *Journal of the Royal Statistical Society (Series B)*, 19(2):268–281, 1957.

CHAPTER 4

Estimation of farm specific parameters in a longitudinal model for litter size with variance components and random dropout

(Submitted for journal publication)

Nils Toft and Erik Jørgensen

Abstract: The estimation of farm specific parameters is often ignored in studies of decision support systems such as, e.g., sow replacement problems. This study concerns the specification and estimation of farm specific parameters in a model for litter size required by a replacement problem considering culling based on productive performance. This implies a joint distribution of the litter size at the parities under consideration. A non-linear parametric mean curve is used to model the expected litter size at different parities for sows within the same herd. The covariance matrix is modeled using variance components of random effects, serial correlation and measurement error. Data from a total of 43 herds are used to devise a likelihood based inference, using maximum likelihood to obtain initial estimates for maximum posterior estimation of farm specific parameters. The maximum posterior approach is required to obtain reasonable estimates in the cases where on-farm registrations are inadequate.

4.1 Introduction

Animal replacement problems is an area which has been developed through the last 30-40 years, see e.g. Kristensen (1994) for a survey. Usually an application is well founded in terms of qualitative modeling, e.g., definition of relevant decision variables and their structural transition through decision stages. The quantitative modeling of parameters, however, is rarely given the same attention. An example is the sow replacement model of Huirne (1990), where the model is well founded in terms of structure in state space, but use parameters obtained from literature to simulate a typical Dutch farm. As demonstrated in Jørgensen (1992) the variation among farms is too large to ignore: using parameters common to all herds will lead to erroneous results for some farms. Hence, it is necessary to use farm specific data to estimate the relevant parameters in a decision support system.

For a decision support system to aid replacement based on production results, i.e., piglets born per litter, a model for expected future production given the observed history of litter sizes is required. Thus a joint distribution of the expected litter size of the, say, first 15-20 litters is required. Of special interest is the covariance structure of the distribution, since culling based on production results rely on this dependence. Independence between subsequent litters would allow culling to be based solely on age: once the expected litter size for a given parity drops below a threshold value (which depend on the shape of the mean curve) replacement is optimal.

The purpose of this study is to describe a model for litter size and a method for estimation of the farm specific parameters required by this model. The choice of model must be a tradeoff between complexity and how well it describes data. The more parameters required to describe the model, the worse it is in terms of state space complexity of the associated decision problem. The estimation of the parameters must be able to address missing information at two levels. Records for the individual sows rarely contains registrations for all the parities of interest. Sows are culled at all parities for various reasons. Hence estimation within the herd must be done by methods that can handle missing values. In some herds the culling might be so hard that sows rarely grow old, hence estimation of the expected mean and covariance at the high parities is not possible using farm data only. To obtain useful estimates for such farms as well, the estimation procedure must include additional information, such as, e.g., an estimate of the distribution of the parameters within a population of herds. This implies that we should model the mean and covariance of the individual farms using the same parametric model.

4.2 Data

Data for this study has been extracted from the data base of the Danish Applied Pig Research Scheme (DAPR) run by the National Committee for Pig Production (Pedersen et al., 1995). The registrations are similar to the registrations used by the commercial nation-wide used Management Information

System, except they are performed in close scrutiny by a technician, who visits the farm on a weekly basis. Herds are numbered to ensure anonymity of the participating pig producers. Data are registrations of different sow events and include traits like: day of farrowing, sow number, parity number, number of piglets born alive, number of stillborn piglets, day of culling, herd number etc. The farms in DAPR usually participate for a couple of years, hence the data consists of many, short time series. For this study 43 herds with a total of 123227 registrations is used. We have chosen to model the total number of piglets born. It can be difficult to establish whether piglets are stillborn or died shortly after birth, hence additional variation might be introduced by using number of piglets born alive. We will ignore the difference in time between successive litters and treat parities as equidistant. In general it is assumed that the possible variation in time between farrowings does not contribute much to variation in litter size.

For modeling of litter size we transform data to series for individual sows, ideally these series would all be of the desired length. However, missing values occur for at least two reasons: censoring and drop-out. Censoring occurs as either left or right censoring when sows were present prior to the beginning of the study, or the study terminates before the sow is culled. The series can have either or both kinds of censoring. Dropout occur because the farmer is inclined to replace sows that perform at an unsatisfactory level. Hence the sows in a herd must be subject to a biased selection. The sample mean curve must be higher than the expected mean if no sows were culled. The mean curve in absence of culling can be regarded as the true mean. One objective of this study is to describe the evolution of the true mean as the parity increases.

For our study two properties of data for the individual herds are important: Long series for individual sows, and observations at high parities. In Figure 4.1 the combination of these two traits is plotted, the closer to the axes a herd lies, the less information can be anticipated from the data. The nature of a sow herd ensures that given a reasonable time span of observation in the herd, the parities below the maximum observed parity will all have observations as well, hence maximum observed parity can be considered a reasonable indicator of coverage through parities. The exceptions to this reflection must be the two leftmost dots, where max length of the series are 1 and 2 respectively, but max observed parity is 10 and 9. The herds underlying these combinations participated in the study for a very short time.

We will assume that observed litter sizes for sows at given parities in absence of culling (i.e. without biased selection) are realizations of normally distributed random variables. The normal plots for the observed values for the first 9 parities of a herd are shown in Figure 4.2, the other herds provides similar plots. Note that, as the parity increases the number of observations underlying each plot decreases. Obviously the assumption of Normality in

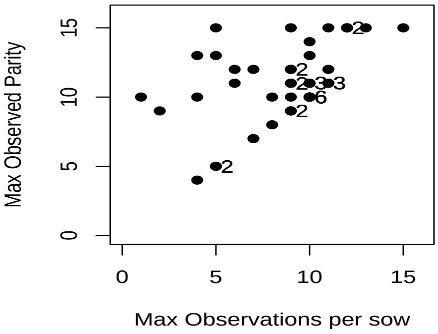

Figure 4.1: The combination of maximum observed parity and max series length for the herds in the study. A number to the right of a dot indicates more than one herd with this combination. The information in data decreases as the dots are placed closer the axes.

these plots (e.g., observed litters) can be questioned, apparently to few low litter sizes are produced, the result is a right-skewed distribution. Thus, the natural representation of the litter size using a Poison distribution would be even worse.

To get an idea of the variation among herds, the sample means and sample autocovariance has been calculated. The means are shown in Figure 4.3 individual means for the herds are joined by lines as visual aid. Observe how the curves seems to share the same pattern of increasing average until parity 4-5 followed by a steady decrease afterwards. Fluctuations towards the end of the curves is the due to the rapidly decreasing number of observations underlying these high parity means.

We will assume variance homogeneity across parities. The autocovariance between different lags is constructed as averages of covariance between lags of elements of the sample covariance matrix constructed using pairwise complete observations. Thus the uncertainty associated with the sample autocovariance increase dramatically as lag between parities grows. However, Figure 4.4 still gives an impression of a common covariance structure. The plots suggest that initial analysis should allow for a auto-regressive term as well as an additive effect.

We will assume that herds are independent and share the same mean and covariance structure with parameters from a common distribution. Within the herds we assume that sows are independent with common mean and covariance, i.e., that series of litter sizes from individual sows are realizations of the same multivariate Normal distribution.

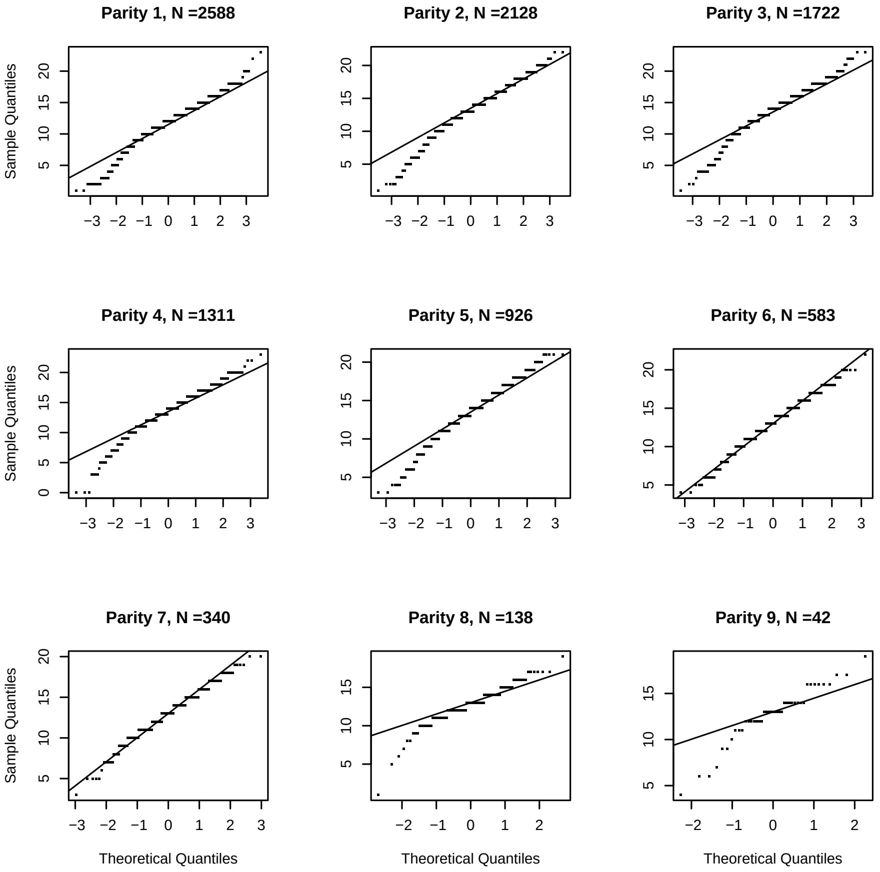

Figure 4.2: Normal plots for the first 9 parities of a typical herd, lines through data and distribution quartiles are added. N is the number of litters underlying each plot.

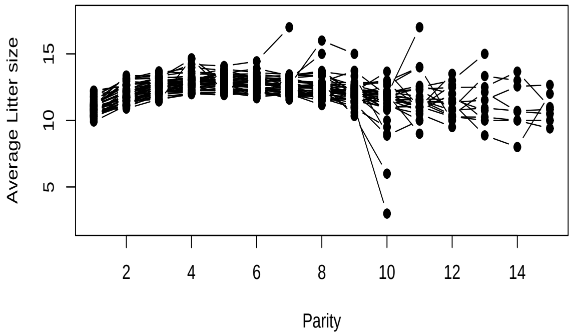

Figure 4.3: The sample mean curves for the individual herds. Fluctuations are increasing towards the end of the individual curves because these averages are based on fewer observations.

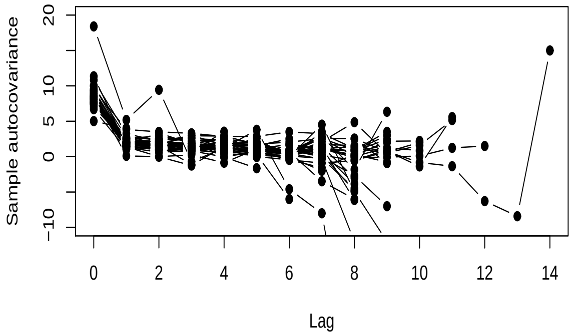

Figure 4.4: The sample autocovariances for the herds. Lag is the difference between parities of the pairs of observations used in the estimates. The wide fluctuations at the end of the curves is due to the extremely few pairs of observations underlying these estimates.

4.3 The model

To model the litter size of sows we need three elements: a part describing the common mean of a herd, a part describing the common covariance structure and a part describing the dropout process (culling) in a herd.

Assume the herd has m sows, with up to n litters per sow. In order to model the dropout process we introduce y^*_{ij} as the hypothetical litter size for sow i at litter j, which would have been observed in case of no missing values. Then $\mathbf{Y}^*_i$ is an n-dimensional vector of measurements for the ith sow and we assume that

$$\mathbf{Y}^*_i \sim \mathrm{N}_n(\boldsymbol{\mu}, \mathbf{V}), \tag{4.1}$$

i.e., a multivariate Normal distribution. Let $\mathbf{Y}_i$ define the corresponding actual observations with missing values because of culling (drop out) encoded as 0. Let d_i be the index of the first missing value due to culling in $\mathbf{Y}_i$. This implies that $2 \leq d_i \leq n$ indicates the dropout time, whereas $d_i = n + 1$ identifies no dropout. If we ignore censoring, the relationship between Y^*_{ij} and Y_{ij} can be expressed as $Y_{ij} = Y^*_{ij}$ for $j < d_i$ and $Y_{ij} = 0$ elsewhere.

4.3.1 The mean curve

The curve describing the mean should be non-linear in order to allow a structure where the expected litter sizes increase for the first 5-6 litters and then start to decrease. An obvious approach could be to fit a polynomial, however, we are especially interested in the prediction of litter sizes outside the region of observations. Thus we adopt the curve suggested originally by Jørgensen (1992) as a combination of a straight line and a Gaussian curve i.e.,

$$\mu_j = -\theta_1 \exp(-(j^2 - 1)\theta_2) + \theta_3 - \theta_4 j \tag{4.2}$$

For certain values of $\boldsymbol{\theta} = (\theta_1, \theta_2, \theta_3, \theta_4)$ the straight line dominates for large parities, while the Gaussian term causes the curve to bend downward for smaller parities. It is possible to reparametrize the model in terms of more easily interpretable parameters as suggested in Jørgensen (1992). A similar study on a smaller sample of herds (Dethlefsen and Jørgensen, 1996) indicates that this mean curve is a reasonable trade-off between complexity and available data. A complex model is used in the first parities, whereas a simpler linear model is applied at higher parities when observations become sparse.

4.3.2 The covariance structure

An unstructured multivariate approach to repeated measures leaves the variance matrix $\mathbf{V}$ entirely unspecified, i.e., a total of $n(n+1)/2$ parameters are required to specify the variance matrix (n is the max number of litters of a sow, hence $\mathbf{V}$ is a $n \times n$-dimensional matrix). It is a more or less straight forward approach to estimate these parameters as the sample covariance given we have enough data.

Here we use variance components in order to obtain a parsimonious parametrization of $\mathbf{V}$. In Diggle (1990) it is suggested that this can be achieved by incorporating time series structure into the variance matrix of the multivariate Normal distribution of (4.1).

Let y_{ij} be the number of piglets of the ith sow's jth litter. Assume that y_{ij} can be decomposed as $y_{ij} = \mu_j + \epsilon_{ij}$, where μ_j is the deterministic mean described in (4.2) and ϵ_{ij} is a random, zero-mean component. Adopting the notation in Diggle (1990) ϵ_{ij} can be decomposed into three components,

$$\epsilon_{ij} = A_i + M_i(j) + Z_{ij}. \tag{4.3}$$

In (4.3) the A_i are mutually independent $N(0, \nu^2)$ random variables, which represent the variation between sows. The Z_{ij} are mutually independent $N(0, \tau^2)$ random variables representing measurement error, or short term random influences. Finally the $\{M_i(j)\}$ are independent stationary random processes with common autocovariance function $\gamma(u) = \sigma^2\rho(u)$, where the correlation function $\rho(u)$ is such that $\rho(0) = 1$ and $\rho(u) \to 0$ as $u \to \infty$. Here we assume an exponential correlation function,

$$\rho(u) = \exp(-\alpha u), \tag{4.4}$$

i.e., a first order auto-regressive stationary process (AR(1)) under our assumption of equidistance between parities. The autocovariance function of ϵ_{ij} can be derived as,

$$\gamma(u) = \begin{cases} \nu^2 + \tau^2 + \sigma^2 & , u = 0 \\ \nu^2 + \sigma^2 \exp(-\alpha u) & , u > 0. \end{cases} \tag{4.5}$$

Hence, we have reduced the required set of parameters from $n(n+1)/2$ to just 4. Define $\boldsymbol{\phi}$ as the parameter vector describing the variance, i.e., $\boldsymbol{\phi} = (\nu^2, \tau^2, \sigma^2, \alpha)$. In general we cannot reduce this model when applying it to the full set of herds. However for some herds this covariance structure is over-parametrized which cause trouble in estimation of the parameters. This regards especially the additive effect, which for most herds decrease to nearly zero. As part of the initial analysis we will test for possible reductions of the model in terms of variance components. To compare the individual models we use Akaike's information criteria (AIC), which favor the model where

$$\text{AIC} = -2\text{log-likelihood} + 2n \tag{4.6}$$

is smallest (n is the number of parameters in the model).

4.3.3 The dropout structure

Let $H_k = (y_{i1}, \ldots, y_{ik})$ denote an observed sequence of litter sizes up to parity $k-1$, and define $p_d()$ as the probability of dropping out between parity $d-1$ and d. Diggle and Kenward (1994) distinguish between three different types of dropout: Completely random dropout where $p_d()$ depends neither on H_d nor Y_d^*, random dropout where $p_d()$ depends on H_d but not on Y_d^*, and informative dropout where $p_d()$ depends on Y_d^* (and possibly H_d). Informative dropout might be present in e.g. medical studies where the patient drops out of the study because she is too ill to attend the meeting (or dies). However, our dropout can be classified as random dropout, i.e., we expect culling to be based on previously observed litter sizes. This implies that the probability of dropout between parity $d-1$ and d can be modeled as:

$$P(d_i = d|\text{history}) = p_d(H_d, \boldsymbol{\beta}) \tag{4.7}$$

where $\boldsymbol{\beta}$ is a vector of parameters. The important feature of this dropout model is that dropout is modeled independently of the parameters describing mean curve and covariance structure. The modeling of dropout must admit the distinction between involuntary culling and culling based on production parameters. In our case we could consider any culling not related to litter size as involuntary culling, i.e., reproductive failure etc.

Diggle and Kenward (1994) suggest that a logistic linear model is used to model Equation 4.7. The true nature of the drop-out process is likely to be complex, and the logistic regression is a reasonable empirical model which permits investigation of the possible effect of including covariates, such as time.

For an initial dropout structure we will assume that dropout depends on the previous litter size only, but assume the following relationship:

$$\text{logit}(p_j) = \beta_{j,0} + \beta_{j,1} y_{j-1} + \beta_{j,2} y_{j-1}^2 \tag{4.8}$$

i.e. $p_j(H_j, \boldsymbol{\beta})$ where $\boldsymbol{\beta} = (\beta_{1,0}, \beta_{1,1}, \beta_{1,2} \ldots, \beta_{n,0}, \beta_{n,1}, \beta_{n,2})$. This implies that the dropout structure or culling rate depends on the parity number as well as the observed previous litter size. It seems reasonable to assume such dependence, primiparous sows are unlikely to be culled due to low litter size, or at least the threshold must be much lower than for older sows. In fact a standard advise in Denmark is to completely ignore the size of the first litter. This corresponds to assuming $\beta_{1,1} = \beta_{1,2} = 0$ in the above model.

The $\beta_{j,0}$ elements can be considered as the joint effect of all other causes than low production. Data does not provide much information about culling if explored on individual parities, hence we simplify the above model further and consider culling according to three different models: For first parity sows, for sows between second and fifth parity, and for sows at higher parities. We have tested the full model for possible reductions in each case. This suggest (using Akaike's information criteria) that the majority of herds fit the simple model (intercept only) for first parity sows, while the full model is preferred in the other two cases. The models suggested here only allow one-step back dependence of dropout. Logistic regression model can of course be extended to include the effect of earlier litter sizes. For future reference we list the models here, the dropout probabilities will henceforth be referred to as p_1, p_{2-5} and p_6+, i.e.,

$$\begin{aligned} \text{logit}(p_1) &= \beta_{1,0} && (4.9) \\ \text{logit}(p_{2-5}) &= \beta_{2-5,0} + \beta_{2-5,1} y_{j-1} + \beta_{2-5,2} y_{j-1}^2 && (4.10) \\ \text{logit}(p_{6+}) &= \beta_{6+,0} + \beta_{6+,1} y_{j-1} + \beta_{6+,2} y_{j-1}^2 && (4.11) \end{aligned}$$

where we have kept the original notion of y_{j-1} to represent the litter size of interest.

4.3.4 The joint distribution

We can now describe the joint distribution for $\mathbf{Y}_i$ using the sequence of conditional distributions of Y_{ik}. We can ignore the subscript i since all sows are assumed to share the same distribution. Let $f_j^*(y_j)$ denote the univariate Gaussian density of Y_j^* and $f_j^*(\mathbf{y}_k^j)$ the multivariate Gaussian density of the k to j elements of $\mathbf{Y}^*$. Define $f_j^*(y_j|H_j)$ as the conditional univariate Gaussian distribution of y_j given H_j. Similarly define $f_j(y_j)$, $f_j(\mathbf{y}_k^j)$, $f_j(y_j|H_j)$ as the distributions for the observed data.

We see that the relationship between $\mathbf{Y}^*$ and $\mathbf{Y}$ defined earlier and the dropout process (4.7) implies that

$$P(y_j = 0|H_j, y_{j-1} = 0) = 1 \qquad (4.12)$$

$$P(y_j = 0|H_j, y_{j-1} \neq 0) = p_j(H_j, \boldsymbol{\beta}) \qquad (4.13)$$

$$f_j(y_j|H_j) = \{1 - p_j(H_j, \boldsymbol{\beta})\} f_j^*(y_j|H_j, \boldsymbol{\theta}, \boldsymbol{\phi}), \text{for } y_j \neq 0 \qquad (4.14)$$

Using equations (4.13)-(4.14) we can determine the joint distribution of $\mathbf{Y}$. Suppressing dependence on the parameters $\boldsymbol{\theta}$,$\boldsymbol{\phi}$ and $\boldsymbol{\beta}$ and assuming no data missing because of censoring the PDF for a complete sequence is

$$f_n(\mathbf{y}_1^n) = f_1^*(y_1) \prod_{k=2}^{n} f_k(y_k|H_k) = f_n^*(\mathbf{y}_1^n) \prod_{k=2}^{n} \{1 - p_k(H_k)\} \qquad (4.15)$$

whereas for an incomplete sequence with dropout at time d, i.e.,
$\mathbf{Y} = (Y_1, \ldots, Y_{d-1}, 0, \ldots, 0)$, the PDF for the joint distribution is

$$\begin{aligned} f_n(\mathbf{y}_1^n) &= f_1^*(y_1) \left\{ \prod_{k=2}^{d-1} f_k(y_k|H_k) \right\} p_d(H_d) \\ &= f_{d-1}^*(\mathbf{y}_1^{d-1}) \left\{ \prod_{k=2}^{d-1} \{1 - p_k(H_k)\} \right\} p_d(H_d) \qquad (4.16) \end{aligned}$$

Censoring

Because of censoring the data seldomly consist of complete series, hence the expressions in (4.15) and (4.16) should be modified to allow for right or left censoring. This is simply done by only considering the part of the series which contain data, i.e., start at litter l instead of the first litter and likewise end at litter s rather than the nth litter.

4.4 Estimation

Estimation should be likelihood based to handle missing values and dropout structure. We propose the following procedure for estimation of parameters for individual herds. First derive the likelihood function and obtain maximum likelihood estimates for the herds where data is of a quality that permits credible estimates. Using these we estimate the population mean and between-herd variance of the parameters. This distribution of parameters among herds is taken as our prior belief of parameters in a herd. The combination of this prior and the likelihood function can be used to obtain maximum posterior estimates of the parameters of individual herds, i.e., the information from data adjusts the initial estimates to adapt the properties of the herd. This implies that absence of data force estimates to be based on the specified prior. Hence we can obtain estimates of, e.g., θ_4 even when no high parity litters are available from the herd.

4.4.1 Likelihood function

The joint distribution derived in Section 4.3.4 for the different scenarios (Equations (4.15)-(4.16)) and the similar derivations in the case of censoring all share the same property. The joint distribution can be written as the product of terms involving $\boldsymbol{\phi}$ and $\boldsymbol{\theta}$ describing the evolution of the true mean and $\boldsymbol{\beta}$ modeling the dropout structure. The consequence is that the log-likelihood for $\boldsymbol{\theta}$ and $\boldsymbol{\phi}$, and $\boldsymbol{\beta}$ can be written as the sum of independent terms:

$$L(\boldsymbol{\theta}, \boldsymbol{\phi}, \boldsymbol{\beta}) = L_1(\boldsymbol{\theta}, \boldsymbol{\phi}) + L_2(\boldsymbol{\beta}) \tag{4.17}$$

This is a special case of the general expression in Diggle and Kenward (1994) and implies that we can derive ML estimates for the mean curve independently of the dropout structure since $L_1()$ and $L_2()$ can be optimized independently. For m sows, let $(\mathbf{y_i})_{k_i}^{d_i} = \{y_{ij} : j = k_i, \ldots, d_i\}$ denote the observed litters of the ith sow. Recall that $f_j^*(\mathbf{y}_k^j)$ denotes the joint PDF of observed litters for a given sow. Let $(f_i)_{d_i}^*(\mathbf{y}_{k_i}^{d_i})$ denote the joint PDF for the ith sow, then

$$\log(f_i)^*_{d_i}(\mathbf{y}^{d_i}_{k_i}) = -\{(d_i - k_i - 1)/2\}\log(2\pi) - \frac{1}{2}\log|\mathbf{V}^{d_i}_{k}(\boldsymbol{\phi})| - \frac{1}{2}\left[(\mathbf{y_i})^{d_i}_{k} - \mu^{(i)}\right]^T \left[\mathbf{V}^{d_i}_{k}(\boldsymbol{\phi})\right]^{-1} \left[(\mathbf{y_i})^{d_i}_{k} - \mu^{(i)}\right] \quad (4.18)$$

where $\mu^{(i)} = (\mu_{k_i}(\boldsymbol{\theta}), \ldots, \mu_{d_i}(\boldsymbol{\theta}))$ and $\mathbf{V}^{d_i}_{k_i}(\boldsymbol{\phi})$ is the relevant part of the covariance matrix. $L_1()$ is just the sum of (4.18) for each sow, i.e.,

$$L_1(\boldsymbol{\theta}, \boldsymbol{\phi}) = \sum_{i=1}^{m} \log(f_i)^*_{d_i}((\mathbf{y}_i)^{d_i}_{k_i}) \quad (4.19)$$

This expression can be optimized using a non-linear optimization algorithm, like the Powell algorithm from Press et al. (1992). Care should be taken to avoid problems with negative values of parameter estimates. All parameters are assumed non-negative. This can be efficiently accomplished by a log-transformation of the parameters, or by adding a non-negativity constraint. The latter has been used here.

Since estimates for the parameters regarding drop-out structure can be obtained independently of the remaining parameters due to our assumption of random drop-out, analysis of drop-out is carried out by means of generalized linear models using the *glm* function in R (R D, 2000).

4.4.2 Maximum Posterior estimation

The ML estimates derived in the previous section are rather sensitive to the nature of available data. As explored in the initial data analysis the number of sows, the length of the series and the coverage of the entire set of parities vary considerably between herds. For some herds the quality data does not permit reasonable ML estimates, however, *penalized Maximum Likelihood*(Armitage and Colton, 1998) provides a suitable alternative for estimation in sparse herds. The best motivation for this approach is in the Bayesian interpretation, i.e., suppose we write the likelihood of the data $\mathbf{Y}$ given the unknown $(\boldsymbol{\theta}, \boldsymbol{\phi})$ as:

$$p(\mathbf{Y}|\boldsymbol{\theta}, \boldsymbol{\phi}) \propto \exp(L_1(\boldsymbol{\theta}, \boldsymbol{\phi})) \quad (4.20)$$

and place a prior distribution on $(\boldsymbol{\theta}, \boldsymbol{\phi})$ of the form

$$p(\boldsymbol{\theta}, \boldsymbol{\phi}) \propto \exp(\Phi(\boldsymbol{\theta}, \boldsymbol{\phi})) \quad (4.21)$$

then by Bayes' theorem

$$p(\boldsymbol{\theta}, \boldsymbol{\phi}|\mathbf{Y}) \propto \exp(L_1(\boldsymbol{\theta}, \boldsymbol{\phi}) + \Phi(\boldsymbol{\theta}, \boldsymbol{\phi})). \quad (4.22)$$

The $(\hat{\boldsymbol{\theta}}, \hat{\boldsymbol{\phi}})$ estimator maximizing Equation 4.22 is called the *maximum a posterior* estimator (MAP). Equation 4.20-4.22 implies the penalized log-likelihood function

$$L(\boldsymbol{\theta}, \boldsymbol{\phi}) = L_1(\boldsymbol{\theta}, \boldsymbol{\phi}) + \Phi(\boldsymbol{\theta}, \boldsymbol{\phi}) = \sum_{i=1}^{m} \log(f_i)^*_{d_i}((\mathbf{y}_i)^{d_i}_{k_i}) + \log(\pi(\boldsymbol{\theta}, \log(\boldsymbol{\phi})), \quad (4.23)$$

where $L_1()$ is log-likelihood function defined in Equation 4.19 and $\pi()$ is the multivariate Normal density of the joint distribution of $\boldsymbol{\theta}, \log(\boldsymbol{\phi})$ defined by the sample mean and covariance of the ML estimators for the herds with sufficient data. The log-transformation of the variance component parameters, $\log(\boldsymbol{\phi})$, is chosen to improve the approximation with the Normal distribution.

4.5 Results

Results can be divided in two parts since analysis of dropout and litter size can be carried out independently, hence reported independently. As mentioned earlier, the choice of dropout model can be questioned, still under the assumption of random dropout, the results regarding litter size model are not affected when inference is likelihood based. As we have previously pointed out our primary concern is the analysis of the litter size model, hence we do not investigate dropout in a maximum posterior setting, but merely present and discuss the dropout results from the herds where ML estimates of litter size parameters could be obtained. Thus we implicitly assume that these herds provides enough data to ensure sound estimates for dropout as well.

4.5.1 Litter size estimates

Initial analysis showed that ML estimates for some herds were questionable. That is, the optimization either failed to produce a maximum or the estimates were obviously far from any reasonable values. The problems occurred when no observations for higher parities were available (to estimate θ_4) or when the individual series were too short to produce a reasonable estimate of correlation structure. This suggested that all herds with no series longer than 7 was dropped from the initial study, in Figure 4.1 this implies that the herds representing the 13 leftmost combinations was dropped. The remaining 30 herds was analyzed using the full model with non-linear mean curve and variance components reflecting short-term variation (Z_{ij}), additive effect (A_i) and serial correlation ($M_i(j)$). We also analyzed the 30 herds with the reduced models of no additive effect and no serial correlation. Akaike's information criteria (Equation 4.6) implies that the log-likelihood of the full model (8 parameters) must be at least 1 greater than the log-likelihood of the model without additive effect (7 parameters) and 2 greater that the model without serial correlation (6 parameters). Out of 30 herds, 28 favor the model without additive effect, 1 favor the full model and 1 suggest the last model. Hence we proceed with the model reduced to short-term variation and serial correlation. The estimates for the 30 herds are given in Table 4.1 below.

Using the estimates in Table 4.1 the mean and covariance matrix needed for the penalized maximum likelihood estimation was calculated. Define $\boldsymbol{\psi} = (\theta_1, \theta_2, \theta_3, \theta_4, \log(\tau^2), \log(\sigma^2), \log(\alpha))^t$, then we assume that $\boldsymbol{\psi}$ is multivariate normal distributed with mean

$$\mu_{\boldsymbol{\psi}} = (2.849, 0.243, 13.999, 0.229, 1.824, 0.856, -2.109)^t, \tag{4.24}$$

and covariance

$$\Sigma_{\boldsymbol{\psi}} = \begin{pmatrix} 0.553 & -0.068 & 0.540 & 0.078 & 0.007 & 0.021 & 0.025 \\ -0.389 & 0.055 & -0.055 & -0.013 & 0.007 & 0.006 & -0.005 \\ 0.827 & -0.267 & 0.769 & 0.097 & -0.005 & 0.017 & 0.050 \\ 0.790 & -0.416 & 0.830 & 0.018 & -0.002 & 0.000 & 0.009 \\ 0.098 & 0.317 & -0.055 & -0.168 & 0.009 & 0.003 & -0.009 \\ 0.185 & 0.172 & 0.123 & -0.022 & 0.191 & 0.024 & -0.020 \\ 0.073 & -0.044 & 0.125 & 0.144 & -0.196 & -0.288 & 0.207 \end{pmatrix} \tag{4.25}$$

with correlations given below the diagonal. Note the high correlation between the individual parameters describing the mean curve (the first 4 rows and columns in (4.25)). To see if there was a difference between using the population mean in Equation 4.24 and the individual estimates of Table 4.1 we applied once more AIC. The model of individual estimates used 210 parameters as opposed to the 7 parameters of the model using the common mean. The difference in log-likelihood was so big in favor of the full model, however, that AIC as well as χ^2-test, using twice the difference between log-likelihood, with 203 degrees of freedom absolutely favored the full model. To see how well the assumption of Normal distribution of model residuals fit, we have produced normal plots for the residuals (difference between observed and predicted values, where the predicted values are $E(y_i|y_{i-1}, \ldots, y_1)$, e.g., the conditional distribution of the expected litter size given the observed history). The plots in Figure 4.5 use the same herd as in Figure 4.2, but only series without left censoring have been used. It seems that the assumption of normality in residuals is somewhat justified, although the first 3 parities are questionable.

The maximum posterior estimates of all 43 herds (and the prior mean for reference) are given in Table 4.2 below.

To see how the estimated mean curve and sample means corresponds plots have been constructed using herd 2 in Table 4.1 and herd 12 in Table 4.2. The ML estimate is used here for herd 2, to get an impression of the "pure" effect of dropout.

Herd	$\hat{\theta}_1$	$\hat{\theta}_2$	$\hat{\theta}_3$	$\hat{\theta}_4$	$\hat{\tau}^2$	$\hat{\sigma}^2$	$\hat{\alpha}$
1	2.624	0.189	13.323	0.224	7.288	2.504	0.109
2	2.742	0.545	14.176	0.180	6.718	2.639	0.086
4	2.485	0.091	14.829	0.320	5.600	2.527	0.094
5	2.334	0.359	13.815	0.217	6.089	2.630	0.156
6	3.805	0.256	15.184	0.306	6.443	2.989	0.130
7	2.678	0.246	14.005	0.212	6.090	2.743	0.122
8	1.890	0.295	13.506	0.189	6.704	1.937	0.126
9	2.994	0.154	13.995	0.139	6.833	2.729	0.184
11	1.778	0.505	13.643	0.068	6.035	2.374	0.148
13	1.968	1.334	13.011	0.014	7.410	2.595	0.102
14	3.021	0.253	14.771	0.406	5.635	1.799	0.167
15	2.974	0.159	14.459	0.259	5.664	1.686	0.170
17	2.620	0.328	14.566	0.235	5.416	2.289	0.163
18	2.887	0.193	13.092	0.205	6.315	2.089	0.126
19	2.432	0.187	12.889	0.116	5.483	2.197	0.110
20	3.118	0.152	13.921	0.299	5.714	2.467	0.128
23	2.477	0.132	13.493	0.063	5.707	2.136	0.097
24	2.815	0.239	13.633	0.202	5.787	3.006	0.045
25	2.508	0.083	13.391	0.200	5.684	2.339	0.108
26	2.671	0.121	13.839	0.238	6.427	2.203	0.051
28	3.917	0.159	14.518	0.366	6.870	2.776	0.170
29	2.920	0.158	13.475	0.048	6.837	2.054	0.141
30	2.142	0.182	12.851	0.181	5.777	2.039	0.084
31	4.302	0.087	15.589	0.300	7.043	2.412	0.104
32	3.364	0.086	14.464	0.345	6.503	2.491	0.140
33	2.045	0.206	13.342	0.090	5.869	2.648	0.117
34	2.806	0.197	13.241	0.136	6.549	2.733	0.071
35	3.547	0.161	14.643	0.396	5.127	2.266	0.553
36	2.361	0.164	13.458	0.226	6.801	1.679	0.208
37	5.248	0.082	16.837	0.684	6.253	2.395	0.078

Table 4.1: The ML estimates of the reduced model $\boldsymbol{\theta}$ and $\boldsymbol{\phi}^* = (\tau^2, \sigma^2, \alpha)$ for the 30 herds where data allows ML estimation.

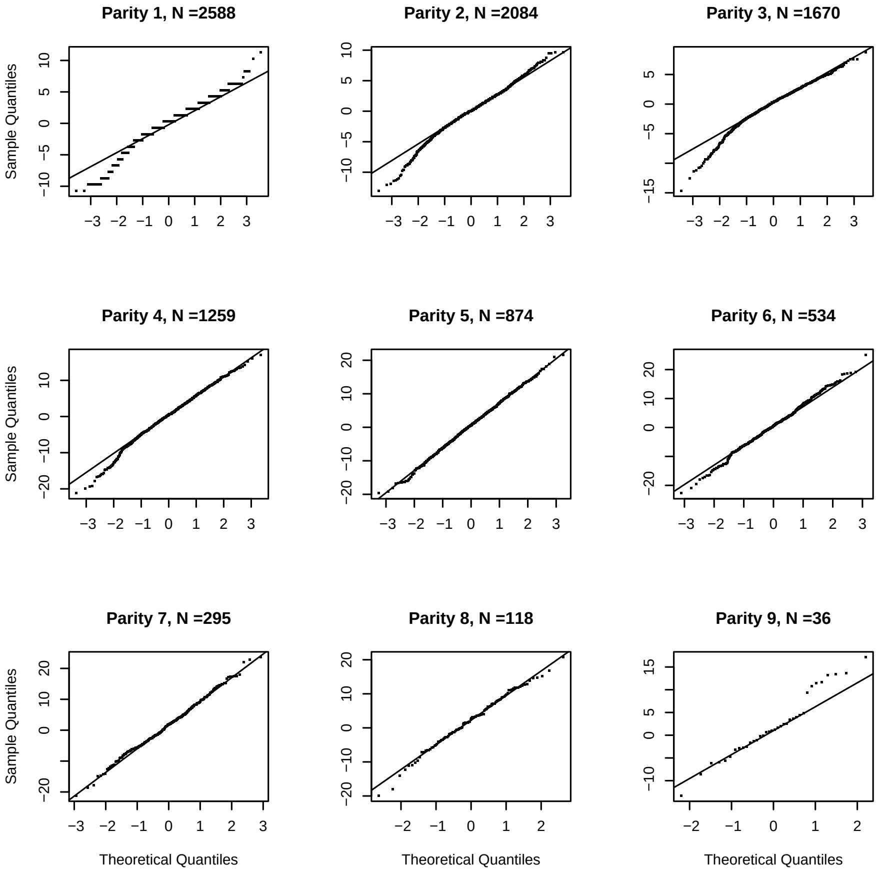

Figure 4.5: Normal plots for residuals of predicted versus observed value for the first 9 parities of a typical herd, lines through data and distribution quartiles are added. N is the number of litters underlying each plot.

Herd	$\hat{\theta_1}$	$\hat{\theta_2}$	$\hat{\theta_3}$	$\hat{\theta_4}$	$\hat{\tau}^2$	$\hat{\sigma}^2$	$\hat{\alpha}$
1	2.737	0.186	13.408	0.231	7.143	2.455	0.110
2	2.768	0.525	14.205	0.185	6.666	2.641	0.097
3*	2.439	0.495	14.038	0.189	6.229	2.264	0.115
4	2.571	0.094	14.816	0.317	5.597	2.413	0.103
5	2.398	0.352	13.842	0.219	6.189	2.453	0.132
6	3.632	0.271	14.996	0.282	6.534	2.745	0.116
7	2.703	0.247	14.015	0.213	6.161	2.579	0.110
8	1.924	0.301	13.495	0.185	6.541	2.055	0.144
9	3.100	0.153	14.119	0.164	6.887	2.535	0.143
10*	3.248	0.243	14.019	0.245	6.358	2.329	0.123
11	1.973	0.449	13.782	0.097	6.088	2.329	0.13
12*	0.758	0.687	12.960	0.000	9.196	2.09	0.087
13	2.082	0.799	13.154	0.039	7.375	2.599	0.104
14	2.943	0.261	14.662	0.385	5.578	1.907	0.178
15	2.885	0.165	14.364	0.250	5.580	1.908	0.188
16*	3.820	0.141	15.241	0.224	6.53	2.177	0.157
17	2.627	0.327	14.569	0.236	5.468	2.251	0.154
18	2.904	0.180	13.202	0.219	6.269	2.172	0.131
19	2.470	0.175	13.013	0.134	5.564	2.205	0.111
20	3.106	0.150	13.938	0.299	5.790	2.384	0.121
21*	3.889	0.119	14.841	0.386	6.337	2.053	0.175
22*	2.812	0.142	13.688	0.159	6.616	2.579	0.101
23	2.734	0.122	13.845	0.125	5.692	2.229	0.111
24	2.822	0.232	13.692	0.209	5.839	2.786	0.07
25	2.666	0.078	13.589	0.222	5.721	2.293	0.11
26	2.707	0.122	13.861	0.241	6.285	2.309	0.079
27*	3.037	0.126	14.304	0.237	5.507	2.335	0.132
28	3.572	0.170	14.154	0.301	6.907	2.548	0.134
29	3.373	0.143	14.126	0.181	6.661	2.295	0.143
30	2.276	0.158	13.045	0.201	5.742	2.110	0.101
31	3.504	0.110	14.671	0.204	6.784	2.536	0.118
32	3.311	0.087	14.377	0.331	6.480	2.405	0.129
33	2.295	0.188	13.622	0.137	5.964	2.460	0.108
34	2.930	0.180	13.443	0.166	6.514	2.674	0.082
35	3.133	0.173	14.199	0.319	5.692	1.906	0.274
36	2.529	0.158	13.616	0.247	6.505	1.942	0.199
37	3.529	0.103	14.761	0.375	6.147	2.437	0.109
38*	3.739	0.119	14.963	0.265	6.041	2.696	0.108
39*	2.213	0.360	12.934	0.045	5.491	2.278	0.113
40*	2.649	0.186	13.915	0.231	6.102	2.199	0.093
41*	2.032	0.277	12.981	0.164	5.461	2.078	0.116
42*	2.736	0.286	13.858	0.221	6.198	2.335	0.122
43*	2.833	0.244	14.014	0.230	6.168	2.343	0.122
Prior	2.849	0.243	13.999	0.229	6.222	2.379	0.136

Table 4.2: The maximum posterior estimates of the reduced model $\boldsymbol{\theta}$ and $\boldsymbol{\phi}^* = (\tau^2, \sigma^2, \alpha)$ for all 43 herds A star in Herd number indicates a herd excluded from prior analysis. At the last line the prior estimated from the ML samples in Table 4.1 is given.

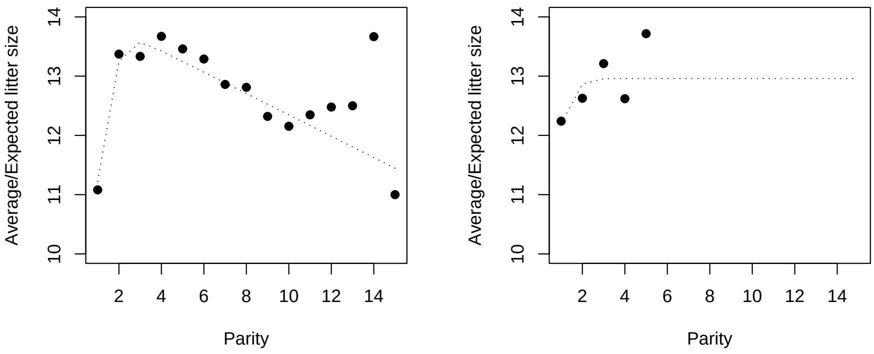

Figure 4.6: The estimated mean curves and the sample means for herd 2 (left), and herd 12 (right)

The sample autocovariance and the estimated curves have been plotted for the same two herds in Figure 4.7. By coincidence the serial correlation structure is almost identical in the two herds.

4.5.2 Dropout estimates

As discussed Section 4.3.3, the model for dropout has been reduced somewhat because data regarding dropout does not allow the full analysis. The logit model is essentially a function describing the probability of a positive outcome (culling) in a Binomial distribution. Data for this model is a matrix where one row contains the counts of sows culled at a certain litter size for the parity/parities under consideration (successes) and the other row contains counts of sows not culled (failures). For the 2 models including several parities, the counts are summed through parities for different litter sizes. Furthermore, litter sizes up to and including 8 are summed as one, just as litter sizes from 18 and up. The estimates for the parameters $\boldsymbol{\beta} = (\beta_{1,0}, \beta_{2-5,0}, \beta_{2-5,1}, \beta_{2-5,2}, \beta_{6+,0}, \beta_{6+,1}, \beta_{6+,2})$ used in Equations 4.9-4.11 are given in Table 4.3 The first parity model produces estimates between -0.988 and -2.665, which corresponds to dropout rates between 0.27 and 0.06 in the 2 herds, i.e., more than 4 times higher dropout rate in the first herd for first parity sows.

To compare the estimates with sample dropout rates, the estimated dropout curves for the 3 models has been plotted along the sample rates for herd 1,2 and 17 in Figure 4.8. The estimate of dropout rate at the higher litters can interpreted as an involuntary culling rate, since it is fair to assume that sows producing 16 to 18+ litters are likely to have been culled for other

Herd	$\hat{\beta}_{1,0}$	$\hat{\beta}_{2-5,0}$	$\hat{\beta}_{2-5,1}$	$\hat{\beta}_{2-5,2}$	$\hat{\beta}_{6+,0}$	$\hat{\beta}_{6+,1}$	$\hat{\beta}_{6+,2}$
1	-1.463	2.139	-0.524	0.017	3.060	-0.55	0.018
2	-1.786	3.597	-0.674	0.021	5.553	-0.688	0.018
4	-1.700	0.727	-0.281	0.006	2.588	-0.37	0.007
5	-1.348	4.092	-0.748	0.022	3.605	-0.421	0.006
6	-1.776	3.259	-0.765	0.028	5.796	-0.845	0.029
7	-0.988	-0.214	-0.120	0.002	2.646	-0.37	0.01
8	-1.745	4.088	-0.804	0.027	0.649	-0.045	-0.002
9	-2.660	3.792	-0.909	0.032	7.059	-1.02	0.033
11	-2.645	6.124	-1.041	0.031	3.114	-0.289	0.003
13	-2.665	6.046	-1.186	0.040	5.806	-0.819	0.024
14	-2.537	5.276	-1.068	0.037	6.702	-0.979	0.032
15	-1.703	0.511	-0.309	0.010	4.065	-0.640	0.021
17	-2.118	3.586	-0.761	0.025	7.331	-0.951	0.029
18	-1.420	1.961	-0.494	0.015	2.928	-0.489	0.015
19	-1.733	0.995	-0.368	0.011	5.350	-0.833	0.026
20	-2.168	5.185	-1.104	0.038	5.792	-1.006	0.031
23	-2.418	6.881	-1.199	0.038	6.569	-0.851	0.026
24	-1.794	2.386	-0.620	0.021	5.529	-0.876	0.031
25	-2.066	5.712	-1.152	0.041	2.347	-0.435	0.011
26	-1.397	2.136	-0.478	0.013	3.363	-0.439	0.008
28	-1.784	0.543	-0.266	0.006	7.955	-1.232	0.044
29	-2.128	3.250	-0.711	0.023	12.762	-1.759	0.052
30	-2.327	-0.010	-0.250	0.004	4.691	-1.022	0.036
31	-1.522	2.543	-0.633	0.023	3.258	-0.400	0.010
32	-1.938	2.579	-0.573	0.017	3.730	-0.634	0.019
33	-1.965	2.788	-0.751	0.026	-0.147	-0.007	-0.001
34	-2.243	5.621	-1.198	0.042	6.563	-0.947	0.028
35	-2.512	7.076	-1.422	0.054	8.629	-1.297	0.045
36	-2.338	5.169	-1.075	0.038	10.800	-1.662	0.057
37	-1.996	2.687	-0.598	0.019	2.324	-0.370	0.012

Table 4.3: The ML estimates of the 3 models for dropout, i.e., $\boldsymbol{\beta} = (\beta_{1,0}, \beta_{2-5,0}, \beta_{2-5,1}, \beta_{2-5,2}, \beta_{6+,0}, \beta_{6+,1}, \beta_{6+,2})$ from Equation 4.9-4.11.

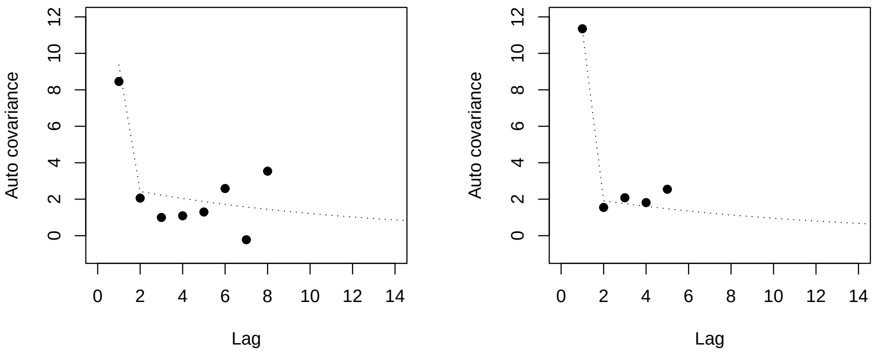

Figure 4.7: The estimated autocovariance curves and the sample autocovariance for herd 2 (left), and herd 12 (right)

reasons.

4.6 Discussion

Some initial comments regarding the results presented in the previous section might be appropriate.

The last two herds (42 and 43) in Table 4.2 have extremely few observations per sow (1.0 and 1.03). It can be seen, that the consequence is MAP estimates very close to the prior mean. In general the MAP estimates differ from the ML estimates in Table 4.1 in the cases where both estimates were obtained. In the analysis we have assumed that a sample size of 30 herds makes the influence of individual farms negligible in the prior, hence we have used the same prior in all MAP estimates. The MAP estimates reflects that inference is based on data as well as prior information, hence they lie closer to the prior mean than the ML estimates.

The left plot in Figure 4.6 shows, how the mean curve for herd 2 in general lies below the sample means at higher parities as a result of culling low producing sows. The paradox of illustrating this effect is that when high parity sample means are available, it implies that culling is moderate otherwise the sows would be culled earlier. Thus only the small deviations between sample means and mean curve in herd 2.

There seems to be apparent problems with estimation in herd 12 even using the MAP estimates (Table 4.2). This is somewhat explained in the sample means (Figure 4.6, right plot). It is obvious that the suggested mean curve cannot be fit to the sample means. Apparently the samples are based

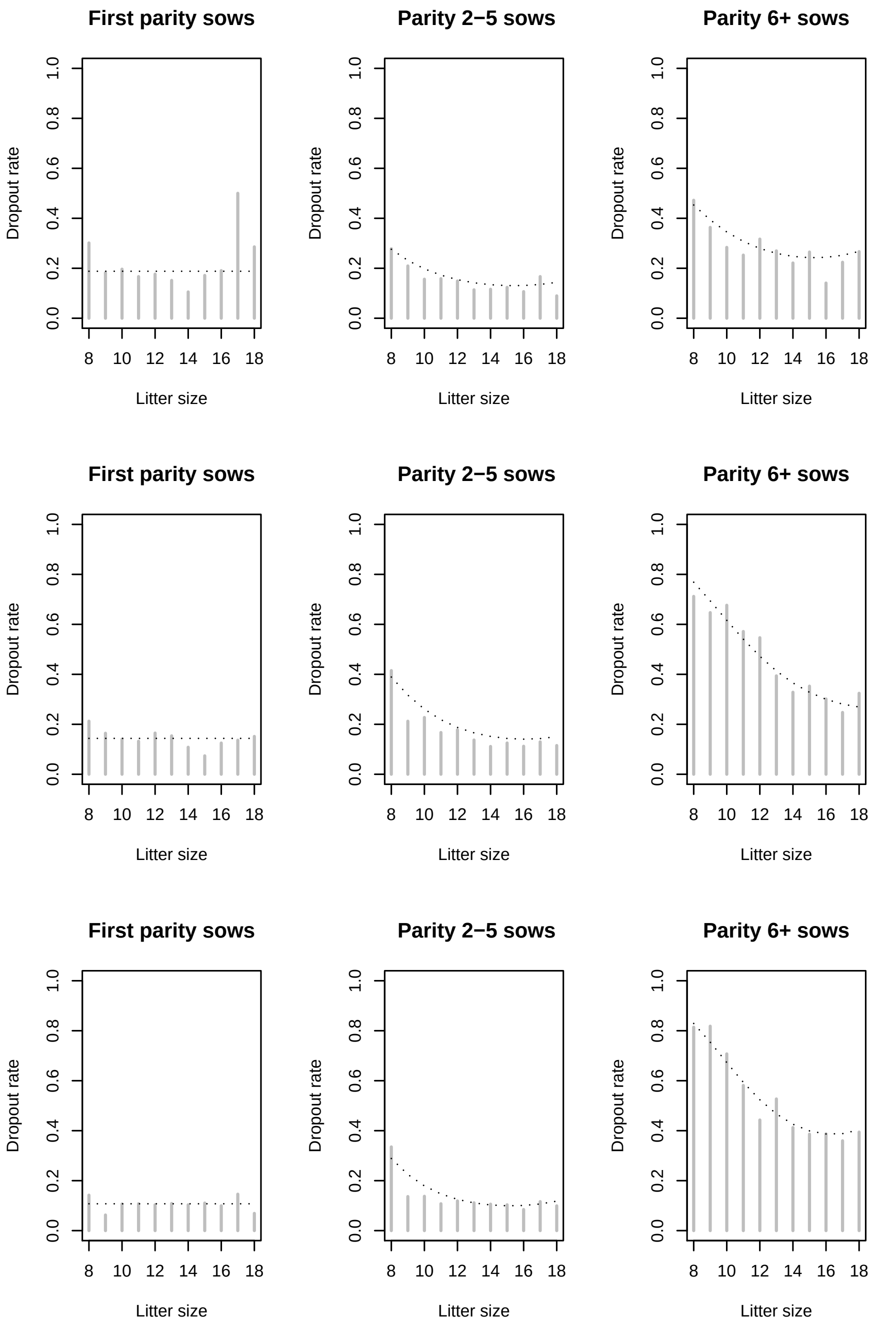

Figure 4.8: The estimated dropout curves and sample dropout rates (grey vertical lines) for herd 1 (top), 2 (middle) and 17 (bottom).

on so much data that they efficiently overrule the specified prior. The result is an extremely bad parametrization of the mean curve where there is no decline in litter size as the parity increase. This result could be due to hard consistent culling where no sows are allowed to grow old. Note how even for this obvious problematic herd, the choice of modeling the covariance structure using variance components enforce a reasonable autocovariance structure.

Although (and because) it is obvious that herd 12 is problematic to our estimation, it is an excellent example to elaborate on. Let us for a moment consider the effect of this farm adopting a new culling strategy based on production performance using the model described here. Since there is no decline in expected mean for higher parity litters, the sows are allowed to grow older, hence farm-specific information regarding the expected mean at these higher parities is received. Our system would have to include these new observations by re-estimating the parameters at a regular basis.

Our choice of model as well as some of the underlying assumptions in this study can be questioned. By assuming independence between sows we lose the information contained in knowledge of the pedigree of sows. Incorporating ancestral information could aid in estimating an additive effect as recognized in breeding models. Our choice of correlation function (Equation 4.4) can be substituted by other models, such as a Gaussian correlation structure, etc. The mean curve might be subject to further analysis. The residual plots for parity 1-3 in Figure 4.5 indicates potential problems with the shape of the curve at lower parities, the correlation between the θ's (the first four rows and columns of the covariance matrix (4.25)) suggest that a reparametrization might be appropriate. Regarding the dropout structure, it can be argued that when consider culling a sow the farmer observe her entire history by inspecting the sow's records. The model suggested here only includes the information from her previous litter, and it is left for future studies to test other models. Recall that the estimates of litter sizes parameters are independent of the dropout model, given random dropout. Thus the conclusions regarding the litter size model does not depend on the assumed dropout structure. Using the dropout models defined in Equation 4.9-4.11, Figure 4.8 illustrates the current culling policies in the three herds. The sample dropout rates for the first parity sows seems to justify the use of the simple model, i.e., in these herds first parity sows are not culled for low production. The constant dropout rate among first parity sows, must be regarded as involuntary culling, i.e., culling for other reasons. To obtain estimates from the herds excluded in Table 4.3 the maximum posterior estimation could be applied here as well, however, we have chosen to postpone this for future studies.

Despite any objections one might raise to the choice of model, the major concern here lies in the method for inference about farm specific parameters. There are several reasons to adopt an approach like maximum posterior estimation for inference of parameters. While the parametric advance to modeling covariance structure ensure that we can control the overall structure, we still require substantial amounts of data to achieve reasonable estimates. Even worse for the mean curve, where the shape at higher parities is determined primarily by θ_4, which can only be estimated when high parity litters are available. θ_4 can be interpreted as the decrease in litter size per parity. This is a rather important feature of the expected mean when considering culling based on productive performance. In Table 4.2 the value of θ_4 vary between 0 (herd 12) and 0.386 (herd 21). It is rather interesting that the maximum decrease from the ML-estimates in Table 4.1 was observed in herd 37 as 0.684. The MAP estimate for herd 37 is 0.375, which is a smaller decrease than, e.g. herd 14 (0.385). The ML estimate for herd 14 (0.406), however, is considerably smaller than the ML estimate for herd 37. This is yet another illustration of the effect of the prior in MAP estimation. Apparently the ML estimate of decrease in herd 14 had much stronger support in terms of data than the estimate in herd 37.

That the estimates differ significantly between herds was established by AIC and χ^2-test, however, by assuming that parameters for individual herds share a common distribution, the problem with absent high parity observations can be overcome. This problem is essentially the same for a newly started farm and a farm where heavy culling have prevented sows from getting old. Using only herd data, neither farmer can obtain reliable estimates of the expected mean at high parities. This observation raise an interesting point. Our primary interest in the parameters is for use in a decision support system to support culling decisions based on productive performance. It is straight forward to implement the litter size model suggested here as a sow replacement problem, see Jørgensen (1992) or Kristensen (1993). But if this model suggest that culling should be hard, no information of high parity sows is ever obtained, thus making it difficult to evaluate whether a less restrictive culling policy might be optimal in case some of the underlying model assumptions change.

These problems are essentially the same faced by breeders. Large data bases have been established in order to base inference on the entire population of animals rather than just on-farm records. For successful estimation of farm specific parameters there is a need for a similar setup. A central database of production records to exchange farm records for updated population distributions. In such a setup, it would be possible to pay farms to have sows producing beyond their economic optimal culling age, to obtain more records of very old sows.

To increase the precision in the prior density, cluster analysis etc., should be conducted to see if some traits or specific farm characteristics like, e.g., housing, could be used to stratify the herds. Because of the anonymity of the herds in this study, such information is unavailable, hence we have excluded such analysis from this study.

The perspectives of the work presented here is perhaps best seen in the context of a decision support system. Although other distinct reasons for explicit culling can be identified (In Huirne (1990) culling is based on productive and reproductive traits), we consider as system where the sole reason for voluntary culling is the expected future production. An appropriate definition of optimality, is to find the policy that maximize the expected discounted return of the sow and her future replacements. The implicit assumption underlying this model is that sows compete for some scarce resource, e.g., the pens in the farrowing section or some other constraint imposed by the production system. The model can also be used for dynamic ranking of the sows (Greve, 1995), when culling occur to introduce gilts purchased at regular intervals in the herd.

The sow replacement model is often modeled as a Markov decision process (Bellman, 1957), this implies that parameters are constant and that the assumption underlying the model remains unchanged through an infinite time-horizon. For a herd that adopt the culling policy devised as optimal using the farm specific estimates obtained by our method, the short term effect is a (perhaps) changed culling policy. However, in long run we would prefer the observations of litter sizes in this changed structure to be reflected in the farm estimates. Recall the discussion regarding herd 12 (with $\theta_4 = 0$), obviously the sows cannot produce high litters indefinitely, thus as the age structure in the herd change we will be able to produce a more realistic estimate of θ_4. In general the farm estimates should be revised frequently just as the population mean should be revised often. Even if the number of participating farms was increased to realistic proportions the estimation would be easy to conduct say, once, a week. In a larger population it would probably be possible to include only registrations of recent sows. Due to genetic progress by breeding programs, we generally expect older sows to have lower production performance, hence the information of current sows of other farms might be more informative for estimation of farm specific parameters than the registrations of past sows from the farm itself.

The nature and quality of decision support systems for sow replacement has evolved in recent years, taking further variables and other management decisions into account when devising an optimal policy, still the problem of farm specific parameter estimation have been ignored. As pointed out in the Introduction, this could lead to erroneous policies, because the variation among farms in general is too large to ignore. In this study we have initiated this aspect of on-farm decision support. We have restricted ourselves to analysis of litter size, but other parameters such as those regarding reproductive performance must eventually be given the same attention. In closing we propose that the parameter estimation should be given as much attention as the conceptual development of replacement models, and that a major difference in the two elements is that while the former can be achieved using existing theory, the latter necessitates an organization within the producing farms to handle the gathering and exchange of information.

4.7 Acknowledgments

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References

P. Armitage and T. Colton. *Encyclopedia of Biostatistics*, volume 4. John Wiley & Sons, 1998.

R. E. Bellman. *Dynamic Programming.* Princeton University Press, 1957.

C. Dethlefsen and E. Jørgensen. A longitudinal model for litter size with variance components and random dropouts. *Dina Research Report*, 50: 1–30, 1996.

P. J. Diggle. *Time Series. A Biostatistical Introduction.* Oxford Statistical Science Series. Oxford Science Publications, 1990.

P. J. Diggle and M. G. Kenward. Informative dropout in longitudinal data analysis. *Applied Statistics*, 43:49–93, 1994.

J. Greve. *The dynamic ranking approach and its application in piglet production.* Ph.d. thesis, Factulty of Technology and Science, Aalborg University., 1995.

R. B. M. Huirne. *Computerized Management Support for Swine Breeding Farms.* PhD thesis, Department of Farm Management, Wageningen Agricultural University, Wageningen, The Netherlands, 1990.

E. Jørgensen. Sow replacement: Reduction of state space in dynamic programming models and evaluation of benefit from using the model. *Dina Research Report*, 6:1–21, 1992.

E. Jørgensen. The utility value of information in pig production. In S. Martin Rillo, A. Aumaitre, L. den Hartog, G. Backus, P. Glodek, F. Saiz, and A. Salehar, editors, *European Association for Animal Production. Commision on Pig Production. Satellite Symposium on: Pig Management Information Systems. Madrid 12th september 1992, Spain*, pages 135–144. INIA Madrid, EAAP Roma, Madrid, Roma, 1992.

A. R. Kristensen. Bayesian updating in hierarchic markov processes applied to the animal replacement problem. *European Review of Agricultural Economics*, 20:223–239, 1993.

A. R. Kristensen. A survey of markov decision programming techniques applied to the animal replacement problem. *European Review of Agricultural Economics*, 21:73–93, 1994.

B. Pedersen, V. Ruby, and E. Jørgensen. Organization and application of research and development in commercial pig herds: The danish approach. In D. P. Hennessy and P. Cranwell, editors, *Manipulating Pig Production V. Proceedings of the Austalasian Pig Science Association (APSA)*, 1995.

W. H. Press, S. A. Tekolsky, W. T. Vettering, and B. P. Flannery. *Numerical Recipes in C. The Art of Scientific Computing.* Cambridge, second edition, 1992.

R Development Core Team. *An Introduction to R – Notes on R: A Programming Environment for Data Analysis and Graphics*, version 1.0.0 (2000 february 29) edition, 2000.

CHAPTER 5

General Discussion

The title of this thesis is "Elements of decision support systems in pig production". In the introduction (Chapter 1) three specific elements were outlined for analysis.

- An analysis of existing techniques for temporal abstraction and state space reduction/decomposition.
- Development of a decision support system for simultaneous optimization of delivery policies and strategies for control of epidemic disease in a slaughter pig production.
- Estimation of farm specific parameters in a litter size model required for culling based on production performance.

This chapter summarize the conclusions from these studies and discuss the perspectives for future work regarding the lines of research opened up by the contributions in this thesis.

The review of Chapter 2 focuses on three topics which seem promising in terms of future application to livestock decision support systems: Temporal abstraction, factored representations and decision networks.

Temporal abstraction seems to have been developed in two different contexts more or less simultaneously. The idea as formulated in the *macro action* definition allows for temporal abstraction in terms of sequential execution of series of actions, while the concept as defined in *multi-level hierarchic Markov processes*(ml-HMP) allows simultaneous optimization of decisions at multiple time scales. The difference between the two perceptions of temporal abstraction is mostly of modeling interest. The ml-HMP interpretation allows for a closer correspondence between modeling at the conceptual and computational level. The macro-action concept on the other hand has a close correspondence to the existing management techniques such as plans, rules-of-thumb, recommendations etc, i.e., predefined policies for carrying out certain tasks. An important reason for modeling the large scale decision support systems based on Markov decision process related techniques is to devise optimal policies, i.e., explore if the current recommendations or plans can be improved. This suggest that in general the macro-actions will be inadequate since the full set of original actions are needed as well to explore all possibilities.

Despite the differences both temporal abstraction methodologies decompose the underlying state space into regions in which most actions are local and transition to states outside the region only occur in a small subset of states. This provides an efficient method for decomposing the original problem into region based problems communicating through a high level (or abstract) decision problem.

Factored representations is a different concept for state space decomposition which utilize the underlying conditional independence of the state variables (or traits) describing the system. The savings by this approach can be considerable as outlined in Chapter 2. The structure in state space will often result in a structured policy, which can be improved to produce an optimal structured policy using substantial less computational effort in terms of time and storage. Another appealing property of the factored representations is the use of Bayesian network methodology, which includes a graphical formulation. Modeling of the state space can benefit from this framework since a graphical representation is easier to understand and provides a common basis for collaboration with domain experts.

The Bayesian network representation can be augmented by action and utility nodes to form a decision network. The major benefit of adopting one of the decision network techniques (e.g., *Limited memory influence diagrams* (LIMID)) is the possibility to separate the formulation of the state space and the decision problem. Currently this is at the cost of losing the infinite time horizon, which plays an essential part in the formulation of what is essentially still animal replacement problems.

The conclusion from this study is that the ml-HMP framework at the moment seems to possess the most features required in formulation and optimization of the decision complexes emerging from livestock production. However, as even the largest models are tradeoffs between complexity and computation, the ml-HMP technique needs refining. A reasonable path is to adopt first the factored representation in terms of Bayesian networks and later the decision networks, most likely in the shape of LIMID's.

The ml-HMP technique forms the framework for implementation of the decision support system developed in Chapter 3. The overall objective of the model is to optimize the decision complex of strategies for epidemic disease control and the delivery decisions. Analysis of the possible control measures revealed they were essentially divided in preventive measures applied prior to onset of disease, and active controls that can be considered once disease is observed in the batch. This suggested that an ml-HMP model, where the founder process modeled transition between batches and the child processes modeled the daily operations within the individual batches, was appropriate. The contributions from this study can be summarized in two parts. The analysis of the decision problem and an actual implementation of an example. The analysis focused on the conceptual development of the decision problem and did not consider the restrictions imposed by the ml-HMP framework. One of the major simplifications in the process from analysis to implementation is that the ml-HMP formulation requires full observability of the state space. In essence an epidemic is only partially observable, and furthermore there is a close correspondence between cost and precision when observing the disease state of a herd. These issues regard the so-called *test-decisions* that provides information of the *state-of-nature* while not affecting it. It is an obvious shortcoming of the current example that this aspect is ignored, but this had to be done in order to implement the model in the framework that regardless of this limitation allows for most of the other elements of the decision problem to be explored.

The implementation of the system and the somewhat preliminary results presented here show that there is interaction between the batch level of vaccination policies and the daily operations (of medication and delivery), however, further analysis is needed to describe and quantify these synergies. Still, the example has shown that the analysis of control strategies can be done within a model of the production system, i.e., within the slaughter pig production unit.

The studies of Chapter 2 and 3 both regards structural elements of decision support systems, i.e., methods for state space reduction and formulation of decision complexes involving decisions at multiple time scales. Such issues can be regarded as qualitative elements of decision support systems. The study in Chapter 4 address the quantitative aspect of decision support systems: Estimation of parameters, exemplified by estimation of herd specific parameters in a litter size model with variance component and random dropout. The study develops a parametric model which describes the mean and covariance structure using 7 parameters. Even this parsimonious model requires substantial amounts of data to produce reasonable estimates. Especially the slope of the mean curve at higher parities is problematic. In cases of heavy culling few sows get old, hence inference of the expected litter size at the high parities must be based on other information, e.g., estimates from other herds.

The study applied *penalized maximum likelihood* to obtain *maximum posterior* estimates of the herd specific parameters. The maximum posterior estimate can be regarded as a tradeoff between a common prior density for the parameters and the information obtained by the likelihood of the parameters given observed data. This allows estimation of all parameters even when data is sparse, however, as can be expected the less data the closer to the prior is the posterior estimate. The study concluded that the difference between herds was too large to ignore in the parameter estimation, and devised a method for estimation of the parameters even when data from the herd are sparse. The maximum posterior estimation imposes a prior which in this case was estimated using data from other farms, i.e., the prior is the distribution of the parameters among herds estimated as the population mean and between-herd variance. There is no reason why this prior could not be obtained by other methods, such as simulation studies, expert opinion, or using clinical trial results. Thus the maximum posterior approach is a promising candidate for estimation of other herd specific traits, when farm registrations are inadequate for estimation.

CHAPTER 6

Summary

During the last 2 decades a number of studies regarding optimization of livestock management decisions have been conducted. Most of these works have used the so-called animal replacement model, which optimizes the replacement of production animal(s) under uncertainty regarding its future production traits. Although the models have been applied to different areas, such as replacement of dairy cows, delivery of slaughter pigs and heifer rearing, the underlying assumptions have been the same: decisions are only effective until the next decision stage. This implies that decisions with other characteristics have been modeled as states of the system. To model more complex decision scenarios from livestock management it is necessary to extend the decision concept to include decisions with longer time horizons.

Decisions at multiple time scales and methods for handling these are introduced in this thesis by a review (Chapter 2) of existing methods for handling *temporal abstraction*. These ideas are assembled from different fields of decision problems, including livestock management. It is concluded that there is conceptual difference between the individual methods. From a modeling point of view, the idea as presented in the *multi-level hierarchic Markov processes* is preferred for livestock decision problems. Temporal abstraction is also an efficient method for state space reduction/decomposition. Despite minor differences all reviewed ideas essentially do the same as the *hierarchic Markov processes* applied by most studies of livestock replacement problems. Another approach to state space reduction is given in the *factored representations* also reviewed here. An appealing property of the factored representation is the modeling tool provided in terms of a graphical formulation using *Bayesian networks*. Finally *decision networks* are introduced to allow modeling in a graphical framework where state space and decision problem may be modelled independently. At the moment the price of this flexibility is a loss of the infinite time horizon, which is central in the formulation of replacement problems.

An example of a decision problem where temporal abstraction is needed, is defined in Chapter 3. The problem regards the simultaneous optimization of delivery policy and disease control in a section of slaughter pigs. The problem is defined as a delivery problem, where control of disease is added. The model operates with two different types of disease control: prevention and treatment. The latter is only initiated when disease is observed, while the former usually is applied at the beginning of a batch. Furthermore, preventive methods like, e.g., vaccine are assumed to be effective throughout the duration of the batch in question. The decision complex formed by this model has two decision horizons. A batch level where the vaccination policy is considered, and the daily operational level of delivery decisions. The results presented in Chapter 3 indicates the expected interaction between decisions at the two levels.

Another aspect of modeling is estimation of herd specific parameters for decision support systems. In Chapter 4 herd specific parameters in a litter size model are estimated for 43 herds. The specified parametric model using variance components and a non-linear mean curve, use only 8 parameters. Even for this parsimonious approach substantial amounts of data are needed. Thus *maximum posterior* estimation is applied using a prior based on *maximum likelihood* estimates from herds with sufficient data. The conclusions of this study are: that there is a documented difference between herds. Thus, herd specific parameter estimates are required. These cannot in general be estimated from farm data alone. But by applying additional information, as in this case a prior based on average parameter estimates and the between-herd variance, reasonable estimates are still possible to obtain.

CHAPTER 7

Sammendrag

Gennem de sidste 2 årtier er der lavet en række studier med henblik på at bestemme den optimale strategi for en given problemstilling indenfor husdyrbruget. De fleste af disse studier har taget udgangspunkt i de såkaldte udskiftningsmodeller, der optimerer udskiftning af et produktionsdyr (eller flok af sådanne) under hensyntagen til usikkerhed omkring dyrets egenskaber. Selvom disse modeller har beskæftiget sig med så forskellige ting som udsætning af malkekøer, levering af slagtesvin og opdræt af kvier, så har grundideen været den samme: beslutninger har kun effekt indtil det næste beslutningstidspunkt. Det har betydet at beslutninger med andre karakteristika er blevet behandlet som tilstande i systemet. For at kunne modellere mere komplekse problemstillinger fra husdyrbruget er det nødvendigt med en udvidelse af beslutningsbegrebet til også at omfatte beslutninger med længere varende tidshorisonter.

Beslutninger med forskellige tidshorisonter og metoder til håndtering af disse introduceres i denne afhandling i form af et review (Kapitel 2) over eksisterende metoder til håndtering af begrebet *temporal abstraktion*, hentet fra forskellige områder af beslutningstøtte verdenen. Det konkluderes, at der er væsentlige konceptuelle forskelle mellem de enkelte metoder. Fra et modellerings synspunkt er ideen som den fremstår i *multi-level hierarkiske Markov processer* umiddelbart at foretrække. Temporal abstraktion er udover en konceptuel modellerings ide også en effektiv metode til reducering/dekomponering af tilstandsrummet. På trods af mindre forskelle så er den gennemgående ide den samme i alle de reviewed metoder. Fundamentalt den samme ide, som danner grundlag for de hierarkiske Markov processer, der er anvendt i en del af de eksisterende arbejder inden for udskiftningsmodeller i husdyrbruget. En anden mulighed for reducering af tilstandsrummet er gennem de såkaldte *faktoriserede repræsentationer*, der også introduceres i bemeldte review. En væsentlig sidegevinst ved denne metode er et velfunderet tilhørende grafisk modellerings værktøj iform af *Bayesianske netværk*. Endelig præsenteres *beslutnings netværk*, der giver mulighed for at modellere tilstandsrum og beslutningsproblem uafhængigt af hinanden. I øjeblikket dog på bekostning af den uendelige tidshorisont, der er central i beslutningsproblemer.

Et eksempel på et beslutningsproblem, der tydeligt udnytter begrebet temporal abstraktion, er udviklet i Kapitel 3, hvor der fokuseres på simultan optimering af levering af slagtesvin, samt behandling af disse for en epidemisk sygdaom. Problemstillingen behandles som et leveringsproblem. der udvides med sygdomsbehandling. Der opereres med 2 slags sygdomsbehandlinger: forebyggende og behandlende. De sidstnævnte iværksættes først når sygdom er observeret, mens de forebyggende oftest iværksættes ved indsættelse af slagtesvinene i stalden. En forebyggelse som f.eks. vaccine må ydermere antages at være effektiv gennem hele forløbet. Dette giver et beslutnings kompleks, indeholdende 2 niveauer af beslutningshorisont, dvs med sygdomsforebyggende beslutninger på holdniveau, mens det daglige forløb inkluderer overvejelser omkring medicintildeling og levering af slagtesvin. De præsenterede resultater synes at indikere den forventede sammenhæng mellem beslutningerne på de 2 niveauer.

Et andet aspekt af modellering er estimation af besætningsspecifikke parametre til brug i beslutningsstøttesystemer. I Kapitel 4 bestemmes parametre i en kuldstørrelses model for 43 besætninger. Den specificerede parametrisk model med varianskomponenter, kræver ialt 8 parametre. Selv for denne model kræves der betydelige data mængder for at bestemme parametre for de enkelte besætninger. Derfor anvendes *maximum posterior* estimation med en prior baseret på *maximum likelihood* estimater for den del af besætningerne, hvor data var tilstrækkelige. Konklusionerne af dette studie er, at der er en dokumenteret forskel mellem besætninger. Dette kræver, at der anvendes besætningsspecifikke estimater til beskrivelse af kuld str. For at skaffe pålidelige estimater fra alle besætninger er det nødvendigt at basere disse på mere information end blot besætningsdata data, dette kan gøres som i dette tilfælde ved at basere estimaterne på en prior defineret som gennemsnitlige estimater og besætnings variatonen mellem disse.