

## **Chapter 7: General Discussion**

### **7.1. Introduction**

The objective of this thesis has been to explore issues relevant to the development of a decision support system (DSS) that is capable of optimising decisions within beef cattle production systems. The successful application of any DSS is highly dependent on the base model used to represent the production system being optimised. Any inaccuracies contained within a model and thus its outputs, regardless of model complexity will be present in the outcomes evolved by the optimisation procedure, potentially reducing the viability of these outcomes when applied. However, using a model that has been shown to be highly representative of the production system removes these inaccuracies, increasing the information available for decision making and thus the quality of the decisions. The allocation of animals to market endpoints is one production decision that would be improved by using information obtained from accurate growth and composition models. This information would assist in allocating animals to markets whose requirements appropriately match the production potentials of the animals.

### **7.2. Available Models**

#### **7.2.1. Feeding and Growth Models**

Chapter 2 explored a number of growth models available in the scientific literature for predicting beef cattle growth. The concepts that form the basis of these models and the models themselves were developed to address specific issues associated with growth and perceived inadequacies of other modelling attempts. However, the predictive accuracy of these models is seldom tested outside their development context and thus they cannot be considered appropriate for predicting growth in a variety of production environments.

The purpose of chapter 3 was to test the predictive accuracy of some of these growth models in environments outside those in which they were developed. This testing used data taken from a serial slaughter trial conducted by NSW Agriculture at the Agricultural Research Centre, Trangie, New South Wales. Animals were grown from

weaning to a maximum of 3 years and 8 months and had their daily feed intakes recorded. This allowed the models to be tested across a number of degrees of maturity, which is important when whole beef enterprises (cows, bulls, etc) are being optimised rather than just the growth of slaughter animals.

Growth models from all the categories discussed in chapter 2 were represented in this testing, except those models whose predictions are based on DNA content of the body (Baldwin and Black 1979; Di Marco et al. 1989; Hoch and Agabriel 2004a). The complexity and operating costs of these types of models preclude their use in routine management applications as growth predictors, thus restricting their use to research purposes only (Oltjen et al. 1985). This approach has several other interlinked disadvantages. These models use a large number of parameters that are affected by sex and breed (e.g. 26 in the case of the model developed by Hoch and Agabriel (2004a)). The metabolic processes, such as rates of protein synthesis and degradation, that some of these parameters represent require that large quantities of metabolic and physiological data are available. Collecting such data in a production context would be impractical.

The issues discussed above preclude parameter estimates being obtained down to an individual animal level. This prevents these model types in their present form from being used as a means of predicting potential animal growth and dietary requirements. Predicting these animal attributes would be highly desirable as it would allow optimisation procedures to determine whether a given animal can achieve a desired production level (in terms of weight gain and composition) and if so, what form the production environment should take to support such an animal. Although these limitations restrict the use of these model types for predicting growth the concepts used to develop them should not be discounted. The possibility exists for future technologies (e.g. gene and protein expression arrays/microarray) to be used to estimate parameters that are difficult to obtain using conventional methods. However, the question exists as to whether information from such sources would be sufficiently representative of real driving factors to provide good transportability across environments and genotypes. In terms of beef cattle production, these driving factors relate primarily to the productive potential of an animal (e.g. mature size, growth

capacity, specific carcass characteristics such as marble score and efficiency) rather than specific metabolic processes (e.g. protein deposition and mobilisation).

The type of information used during the testing conducted in chapter 3 had important impacts on the results obtained. The Gompertz model only used age data. The polynomial, Kinghorn and Parks models used age data in conjunction with feed intake data while the Freer and Amer models used age and feed intake data along with different measures of diet quality (e.g. ME, CP). This gave these last two models a greater ability to predict growth in different nutritional environments. However, these two models ignored other types of information, primarily those concerning climate variables. This occurred primarily due to a lack of such information being recorded throughout the experiment. The potential impact environmental variables can have on animal growth was illustrated when an attempt was made to fit a 4 parameter sine function to the feed intake data to describe the impact that annual oscillations in temperatures have on feed intake.

The information used to test the robustness of parameter estimates was taken from a single dataset due to a shortage of other such suitable datasets. The results obtained using this dataset should be viewed with caution because other datasets may have led to different conclusions being drawn on model suitability. This is an inherent problem associated with beef cattle production in Australia where animals spend the vast majority, if not all, of their lives on pasture as opposed to being housed in carefully controlled conditions. Those that do spend time in the confines of a feedlot are there for relatively short periods of time (typically 100 days) and have only limited information recorded. This does not pose a concern for other enterprises such as pig and poultry production where animals spend their entire lives in intensive environments where larger quantities of information can be recorded.

### **7.2.2. Body Composition Models**

The carcass characteristics required by the markets targeted in the Australian beef cattle industry make it hard to comprehend the apparent lack of models available in the literature for predicting physical body composition. This lack of models and the form available models take (e.g. Soboleva et al. (1999) and Hoch and Agabriel

(2004a)) could be interpreted as being a reflection of the complexity that is associated with growth and development. In an effort to model the development of physical components, such as fat and lean deposits, these models have reverted back to one of the most basic units, DNA content or simplifications of this concept (Soboleva et al. 1999), on which to base predictions. In scientific surroundings these models are able to use all available information to predict growth. However, their use is considered to be limited in practical circumstances due to their complexity and operating costs (Oltjen et al. 1985).

The successful application of allometric equations for describing developmental patterns of body components (Butterfield et al. 1983a; Butterfield et al. 1984b; Emmans 1988; Emmans and Kyriazakis 1995; Thonney et al. 1987b) provided the inspiration for the body composition models developed and tested in chapter 4. The Actual EBW (ActEBW), Degree of Maturity (DOM) and Hierarchical Degree of Maturity (HDOM) models simply reflected how allometric equations had been previously applied in different developmental studies. The two Chemical Degree of Maturity (ChemDOM) models were an extension of how allometry is applied to describe growth of the chemical body by Amer and Emmans (1998). This approach uses allometric relationships to describe how ash, water and lipid contents of the body are related to mature protein content. This was extended to predict the ash, water and lipid contents of each body component based on their mature protein contents.

The consistent performance of the HDOM model was shown to be due to the accuracy of estimating the  $Z_i$  parameter in equation (4.4) in comparison to estimating the  $Z_i$  parameter of the DOM model in equation (4.3). Figure 4.8 illustrated that this increase in accuracy was not attributable to the allometric coefficients ( $b$ ) being estimated more accurately because the development pathways predicted for each body component were identical for both models. This result indicated that the manner in which models partition the whole body has important influences on the accuracy of predictions. Partitioning the body into higher order functional components (CHTF and BSV) and subsequently partitioning these components in a hierarchical manner was proven to be an appropriate means of obtaining physical body composition. When deeper datasets exist (i.e. datasets containing more detailed composition information) then models could be developed and tested for predicting lower level body

components. An intuitive next step, using the HDOM model as the base, would be to either obtain or produce data that would allow a model to be developed that partitioned flesh into lean and fat deposits. These components could be further partitioned into muscle, subcutaneous, intermuscular and intramuscular fat groups. The viscera could also be further partitioned into non-carcass fat and visceral organs. Partitioning lean and viscera into these additional groupings would also require appropriately rich datasets to be developed to allow model development.

The poor performance of the ChemDOM2 model in comparison to the ActEBW, DOM and HDOM models, was possibly the result of chemical components in the empty body not being partitioned appropriately between body components because diet characteristics were not considered. The form of the model itself could also be a contributing factor in this poor performance. Perhaps a more desirable form for the ChemDOM2 model would be to partition the chemical body components in a hierarchical manner. The possibility exists for the HDOM model to form the basis of a more comprehensive body composition model that uses the rationale behind the ChemDOM models for partitioning chemical components between physical body components. Such an approach could potentially have draw-backs, including an increase in model complexity, number of estimable parameters and data required for development.

Although, these models are some-what basic in their description of body composition, they can be considered as a starting point from which more precise models could be developed. These models could potentially incorporate concepts taken from the models developed by Soboleva et al. (1999) and Hoch and Agabriel (2004a), which would then enable important influences on body composition, such as compensatory growth, to be taken into consideration. Models capable of predicting physical body composition would provide large quantities of information (e.g. carcass components) that would increase the quality of decisions made following optimisation procedures.

### **7.3. Estimating Input Parameters**

Incorporating between-animal variation into growth simulation models is an important area of research. This allows growth models to move from simply

representing a perceived ‘average’ animal to reflecting the diversity that is present in animal growth potentials. Such an outcome is particularly important when these models are used to simulate production systems, predict nutrient requirements or for economic optimisation (Knap 1995; Pomar et al. 2003).

Achieving an outcome of this nature is not an easy task given the difficulty associated with repeatedly measuring the traits required by such models. This difficulty was addressed in chapter 5 by using “inverted modelling”, where, as the name suggests, growth model input parameters become the subject of the evaluation while model outputs become the inputs. This approach provided a means of estimating input parameters that used small quantities of live weight data and did not require large quantities of metabolic or physiological data. It also allowed variation in model input parameters to be estimated given the variation seen in live weight within a cohort.

The sampling method used by this procedure is important because it impacts on the accuracy of the parameters estimated. Using stochastic random sampling has a number of problems associated with it, including sampling error of parameter estimates that is a function of the number of samples taken. Another potential problem is the selection of parameter values that are systematically “lucky” under an optimisation algorithm because of their more variable impact. Deterministic sampling offered an alternative method free of these problems that produced parameter estimates with greater accuracy and lower standard errors in comparison to random sampling. This superiority was attributed to the location of sampling points within the parameter space taken by each method. Random sampling provided poor coverage to some areas of the parameter space while others were highly covered in a pattern that differed between replicates. In contrast, deterministic sampling covered the parameter space evenly in a pattern that was identical between replicates.

The computational resources required by deterministic sampling were shown to be a major benefit of using it to obtain parameter estimates, requiring just over a third of the time required by random sampling. This is a direct reflection of the number of sample points taken by deterministic sampling. However, an important property of deterministic sampling is that computation time increases substantially with the number of parameters being estimated. In cases where the number of parameters

estimated exceeds ~12 then the efficiency of deterministic sampling is lost and an alternative is required.

Quasi-random numbers are sequences of numbers that have had their serial independence removed in order to eliminate the clumping that is characteristic of fully stochastic random numbers. These numbers would need to be used in conjunction with the weighting system used by deterministic sampling to provide an unbiased representation of the sample distribution. Combining these would allow parameter estimates to be obtained when the number of parameters prohibits the use of deterministic sampling. These parameter estimates would be obtained without the standard errors of random sampling and using the same computational resources. Potentially, the uniformity offered by quasi-random numbers could reduce the total number of sample points required thus reducing the overall computational resources required. However, the potential of this method in comparison to deterministic sampling needs to be tested, particularly when intermediate numbers of parameters are being estimated (e.g. 8-12).

The predictive accuracy of the parameters estimated by deterministic and random sampling (EPP) was tested in comparison to the parameters estimated by the method used in chapter 3 (EIP). The inferior predictive ability of the parameters estimated by EPP when tested with the full Trangie dataset could be considered unfair because of the amount and type of information available to EIP. EIP used feed intake, age and live weight data while EPP only used live weight averages and standard deviations. EIP also used between 15 and 165 data points per animal while only four data points were used by EPP.

Using such quantities of data in the manner EIP used them could also be questioned when the test results using the Beef CRC dataset are examined. The parameters estimated by EIP were directly influenced by daily variation in the feed intake data which is a result of the production circumstances of the animals. EPP used population estimates of live weights at defined ages which removed the daily fluctuations in the feed intake data and only allowed these fluctuations to influence parameter estimates through the live weight data. This reduces the influence daily intake fluctuations that

vary between production environments have on parameter estimates and thus makes them more robust when moving between different nutritional environments.

#### **7.4. Optimising Market Allocation**

The diversity of the markets serviced by the Australian beef industry offers the potential to exploit the diversity seen in growth potential of beef cattle. This provides an alternative means for improving efficiency and reducing the environmental impact of production. A problem of this nature can be viewed as an allocation problem where animals need to be placed in a cohort that is destined for a market appropriate to their production potential. The Random Key Representation (RK) has recently been proposed as a method for solving the well known allocation problem, the Travelling Salesman Problem. RK uses a sequence of random numbers and the concept that any sequence can be sorted into an order. This method offers a viable option for allocating animals to different market endpoints, using optimisation of RK to arrive at an optimal allocation.

The simulated production system used to test the RK for allocating animals to market cohorts was based on an enterprise producing Angus steers only to reduce the level of complication associated with whole beef enterprises whilst remaining representative of Australian systems. The system was developed by assimilating information concerning markets targeted in Australia and price structures associated with these, the costs of production and annual pasture production cycles. The feeding and growth model presented by Amer and Emmans (1998) and tested in chapter 3 along with the HDOM body composition model developed and tested in chapter 4 formed the basis of the modelling system used to predict animal growth and development. Extensions were made to these models to allow them to function in production circumstances other than when consuming feedlot rations and included milk composition, milk energy utilisation and feed intake. Linear regression analyses were also used to develop functions for predicting P8 fat depth and IMF percent.

Testing the ability of DE to allocate animals to market cohorts using RK involved four different production scenarios. The first was the base scenario which simply used the simulated production system. The second involved a reduction in the value of the



Japanese B3 market due to a disease outbreak. The third simulated a reduction in pasture production due to drought and the fourth dealt with increased production costs associated with the Japanese B3 market. All four scenarios represent circumstances that are realistic in the Australian production environment. The drafting system was able to find optimal drafting proportions and ages that maximised the profitability of the whole enterprise while appropriately sacrificing the profitability of some individual animals.

Comparison of the market allocation pattern and the growth model input parameters of each animal revealed that interactions between the parameters ( $P_m$ ,  $Q$  and  $B^*$ ) had important impacts on market allocations. Two particular examples were used to illustrate these interactions. The allocation of animal 3 to the B3 market in scenario 4 was found to be primarily due to its  $Q$  value which increased the energy required to attain any given weight and thus increased feeding costs. In the EU market the carcass produced by animal 3 was not of sufficient value to overcome this inflated feeding cost, where as the carcass produced for the B3 market was able to overcome these costs. The impact the  $B^*$  parameter has on animal growth was illustrated when comparing animals 7 and 9. These animals had similar  $P_m$  parameters (48.82 vs 47.78) but animal 7 had a lower  $B^*$  value compared to animal 9 (0.017 vs 0.022). In scenario 2 the lower  $B^*$  value of animal 7 prevented it from attaining the carcass characteristics required by the EU market at 590 days of age. However, in scenario 3 the later slaughter age of 740 days reduced the impact of the  $B^*$  value of this animal and allowed it to achieve a carcass weight that was acceptable and of high value to the EU market. In contrast, the higher  $B^*$  value of animal 9 allowed it to meet the carcass characteristics required by the EU market in scenario 2. In scenario 3 the drought conditions decreased the carcass weight achieved and increased the costs of growing this animal for the EU market making the HS market more attractive.

An important outcome from this testing was that the drafting system behaved sensibly in response to changing production circumstances. The different optimal drafting ages identified for each scenario is an example of this behaviour. In the scenarios when the B3 market was available the optimal slaughter age for the EU market was found to be 740 days. This was to allow animals with lower  $P_m$ ,  $Q$  and  $B^*$  parameter values to be included in this cohort. In circumstances when the B3 market became unattractive the

optimal slaughter age was reduced to 590 days to compensate for animals with higher  $P_m$  and  $B^*$  values being included in the EU market. This reduction in slaughter age also resulted in the reallocation of animals with lower  $P_m$ , and  $B^*$  values to the HS market because they were unable to achieve the carcass characteristics required by the EU market when slaughtered at 590 days.

The sensible behaviour of the drafting system described above is a result of the information and modelling systems used to describe the production system. The production cost structures (e.g. selling, drenching and pasture) and market prices are specific to September 2006 and January 2007, respectively for the Glen Innes area. These costs and prices will change across time and differ for different production environments both in Australia and in other countries. Therefore, an important outcome of this study is the results obtained are the consequence of these cost, price structures and thus are specific to this system and can not be applied to any other system. Using a system such as that presented in chapter 6 requires that the optimisation procedure is firstly, run repeatedly for a single enterprise and secondly, run independently for each different enterprise that is to undergo optimisation. However, this should not be considered a limitation as the system has sufficient flexibility to operate in any animal production system when presented with the appropriate information relating to price and cost structures.

The flexibility of the system described in chapter 6 would be increased if its limitations were addressed. Refinements to the system would increase the accuracy of model predictions, increase the transportability between production environments and increase the confidence that could be placed in animal allocations. These refinements range from model development to animal representation (input parameter values) to the optimisation criterion.

One possible refinement that could be made to the modelling system is associated with further development of the linear regression models used to predict P8 fat depth and IMF percentage. The regressions currently only explain just over 50% of the phenotypic variation seen in the developmental patterns of these traits and do not consider other variables such as nutrition, disease, environment, breed or sex. Other refinements could involve using the water holding capacity of forage to predict feed

intake and using the equations presented by Coffey et al. (2001) to predict the effective energy requirements for milk production.

Full knowledge of the input parameters for each animal, as used during chapter 6, could be considered unrealistic. One possibility, that is perhaps more practically relevant, would be to partition animals between markets based on where their measured production traits are located in the distribution of observed production traits. This approach would require the input parameters of the cohort, as estimated in chapter 5 using measured production information (e.g. live weight), which would be incorporated into the drafting procedures to allow distributions of model outputs to be produced and then partitioned in order to meet target market requirements. This system would use information about production traits that is readily available rather than difficult to measure information required to estimate the growth model input parameters.

The allocation of animals to target markets could have occurred at birth given there was full knowledge of the growth model input parameters available however this is not a realistic possibility in production systems. The purpose of this study was therefore to test the ability of RK to allocate animals to target markets. The sensible behaviour of RK during this study supports its suitability for allocating animals to target markets based on the location of measured production traits relative to the remainder of a cohort, as discussed above, and the prevailing market requirements. The criterion used in chapter 6 could also be extended to allow the future inclusion of non-monetary factors to be optimised when animals are allocated to markets. The appropriate use of mineral nutrients is one example that has been explored across a whole dairy herd (Wang et al. 2000a, 2000b).

### **7.5. Future Directions**

Flexibility is a desirable property of a DSS used for optimising decisions in a beef production enterprise. This flexibility can potentially take two forms. These include the ability to incorporate new information into the base modelling system and using innovative approaches to develop DSS so as to give them true value in deriving optimal decisions when targeting single or multiple product endpoints. The modelling

system used as the basis of the DSS will benefit from continual development to maintain and increase how representative it is of beef production enterprises as well as allow more production scenarios to be explored. The optimisation problems that could potentially be addressed by a DSS of this nature are large and varied. These applications could range from manipulating feeding, breeding and logistic characteristics of beef production to incorporating the requirements of different production systems within a single farm enterprise.

### **7.5.1. Potential Model Developments**

The ability to incorporate new innovative outcomes from research is and will remain vital to the successful application of any DSS. This is because our power to predict phenotype is only beginning to be sufficiently accurate to be useful for decision making. A large number of potential improvements are possible and range from developing the models used to predict growth and body composition in chapters 3, 4 and 6, particularly those relating to P8 fat depth and IMF percentage, to incorporating other factors that have very important influences on production, including genetics, management methods (e.g. growth hormone) and disease.

Chapters 3, 4 and 6 have each described a number of possibilities for improving the predictive abilities of the growth and composition models that form the basis of the drafting system developed in chapter 6. Improvements to the feeding and growth model pertain primarily to the digestion of feed protein and efficiency of use for growth. It was proposed that using a method similar to that used in pigs (Kyriazakis and Emmans 1992a, 1992b) could be an alternative to the system that is currently applied. However, the shortcomings in the body composition models identified in chapters 3 (relating to the Song and Dinkel models) and 6 are of perhaps greater concern. In both cases, two factors have detrimental effects on the predictive ability of both models, which include their functional form and ignoring the effect external influences have on animal development, the most obvious of which is nutrition.

The different allometric models developed in chapter 4 represent an attempt at using mechanistic approaches to predict body composition. The success of these methods was illustrated in comparison to the regression models developed by Song and Dinkel

(1978b). However, their predictive ability is limited as they do not consider the direct impact of nutritional inputs; rather they indirectly use the impact nutrition has on live weight. The regressions used in chapter 6 to predict P8 fat depth and IMF percent also lack the mechanistic structure and fail to consider the effects of nutrition. This occurs even though the discussion in chapter 2 highlighted the importance of nutrition. The effect environmental factors have on growth and development has been highlighted in chapters 3 and 5 as well as by Harper and Pethick (2001) and Pethick et al. (2006). Incorporating a mechanistic structure similar to that used by Amer and Emmans (1998) for the whole body and even some attributes used by Soboleva et al. (1999) (e.g. lag effect) would allow the conversion from chemical to anatomical to be made by modelling the effects that varying nutrition has on metabolic pathways. Developments such as these would increase the predictive accuracy and the transportability of the composition models between populations. In addition to these improvements including the effects of sex and breed would increase both the predictive ability and accuracy of these models and the confidence that could be placed in any optimisation outcomes. Improvements of this nature are a continual process and require DSS to be flexible to allow their future incorporation.

Although only briefly mentioned above, the impact genetics has on animal growth can never be over-looked. Differences between breeds and sexes can be dramatic and thus are important when describing whole production systems. However, genetic information from within breeds is also extremely important because it helps describe differences between lineages of animals and the variation present within cohorts. The exercise conducted in chapter 5 merely focused on the estimation of phenotypic variation. Wellock et al. (2004b) and Dzama (1993) have illustrated how genetic variation can be included in growth simulation models to describe the variation seen in animal populations. Development of the “inverted modelling” technique used in chapter 5 can also be used to capture this type of genetic information (Doeschl-Wilson et al. 2007). However, what would perhaps be of greater benefit is the development of a method for estimating growth model parameter EBV's that uses information from both animals and their relatives. Although EBVs only explain a proportion of the variation seen in animal phenotypes (e.g. perhaps up to 40%) achieving an outcome such as this would facilitate the drafting of cohorts by providing more information to help predict if animals are capable of meeting the

demands of desired market endpoints. However, two obvious challenges associated with developing such a system are the non-linearity of many growth simulation models and how this would be overcome along with obtaining the quantity of data required to achieve such an outcome.

The expansion of DNA technologies has led to the discovery of quantitative trait loci (QTL) and in some cases single mutations that have significant impacts on production traits. In an effort to fully utilise such discoveries diagnostic tests have been developed to identify animals that have favourable QTL alleles. One of the first examples in Beef production in Australia was a single nucleotide polymorphism (SNP) in the 5' leader sequence of the Thyroglobulin gene (TG5) that was found to be associated with marbling (Barendse 1997). This SNP was commercialised by Genetic Solutions Pty Ltd as the first of four GeneSTAR® marbling 4 diagnostic tests. Information provided by these diagnostic tests could be used to develop and increase the accuracy of the linear regression used in chapter 6 for predicting IMF percent and marble score. Diagnostic tests have also been released for evaluating feed efficiency (GeneSTAR® feed efficiency 4) that could be used to help improve the prediction of feed requirements of individual animals and cohorts. The use of microarrays/gene and protein expression arrays to help develop the understanding of functional genomics is a more recent genetic technology that could potentially provide information that would aid further development of predictive models.

Predictions of animal growth made by simulation models can be assisted by factors other than genetics. Management practices can be used to manipulate the development of animals to achieve certain goals. Although vitamin A injections are routinely given prior to feedlot entry in Australia, an association has been discovered between vitamin A deficiency and elevated intramuscular fat content (Harper and Pethick 2004). Oka et al. (1998) have illustrated that low vitamin A supplementation of young Waygu steers resulted in an increase in mean marble score compared to animals that were supplemented to a higher level. Incorporating the effects of vitamin A supplementation into growth models would not only increase the accuracy of predicting marbling scores but also help determine the most appropriate time(s) to administer vitamin A to obtain the desired results. Although controversial, the administration of exogenous growth hormone (GH) is another management practice

that has been used in Australia to alter growth patterns. Research has shown that exogenous GH increases average daily gain and dramatically decreases fat deposition, resulting in an increase in feed efficiency (Enright 1989). Accurately predicting growth outcomes with a growth simulation model following the administration of GH would assist in determining the most appropriate time and application for GH.

Animal health and welfare are issues that are receiving increasing attention in the general community (Colditz et al. 2006) but have received little attention throughout this thesis. A central component of animal welfare that has important impacts on production is the presence or absence of disease. The \$40 million per year problem Bovine Respiratory Disease (BRD) represents to the Australian feedlot sector (Sackett et al. 2006) is one example of the impact disease can have on production. The impact of diseases such as BRD are not confined simply to medical treatment and animal losses, economic losses also occur as a result of the development of subclinical symptoms that can suppress feed intake, reduce growth performance and carcass quality. As a result interest has been heightened in relation to the partitioning of nutritional resources when dealing with disease challenges (Coop and Kyriazakis 2001). In pig production the general partitioning rule tested by Sandberg et al. (2005b) has been further developed to predict the feed intake of animals that have been exposed to infectious diseases (Sandberg et al. 2006). The development of modelling systems analogous to this for extensive grazing systems, such as that presented by Louie et al. (2007), would be particularly useful in determining the effect not only disease challenges have on production but the impact of management strategies designed to counteract them. An example that is pertinent to Australian agriculture is the impact grazing and nutritional supplementation strategies designed to counter the development of anthelmintic resistance in sheep nematodes (Besier and Love 2003), have on animal growth and development.

The development of diseases such as BRD, and final meat quality attained by animals, have both been related to social stressors (Colditz et al. 2006). The mixing of unfamiliar cattle is a management strategy that is often used to meet logistical constraints of production systems. For this reason modelling key aspects of animal performance, including nutrient partitioning, during periods of social stress is an area of research interest that would prove to be beneficial for predicting production

outcomes of different management strategies, and one that has been explored for pig production (Wellock et al. 2003c).

All the issues discussed above are of direct relevance to beef cattle production in Australia. This thesis has clearly identified areas where current information sources are limited (chapters 3, 4 and 5) thus reducing the accuracy of model predictions. In some cases, developing models to address these issues and recording the information required to run such models in beef cattle production systems is a difficult task. The possibility exists for the concepts explored in this thesis to be explored and applied initially in more intensive industries (e.g. pig and poultry). However, this should not prevent the development of such systems for extensive industries given the increasing advancement of technology could allow the information required for development and functioning of appropriate models to be collected. Any developments to incorporate the above issues into modelling systems would increase the potential number of applications a DSS based on growth models could be used to solve. The inclusion of disease and molecular genetic effects are issues of particular interest in the future, due to increasing pressure from consumers to produce food that could be considered “clean and green”. The inclusion of molecular genetic effects would also offer the potential to more directly exploit the specific biological impact of key mutations identified.

### **7.5.2. Recommendations**

The recommendations made above would all contribute to increasing the power of predicting phenotype on which managerial decisions could be based. However, currently the most urgent improvements revolve around the prediction of body composition and the limited amount of information that is used to make these predictions. The “Keep it Simple” approach to prediction (linear regressions) was shown to be ineffective in chapter 4 and had questions raised about it in chapter 6. Ideally, a mechanistic approach is required that incorporates, most importantly, the effects nutrition has on metabolic pathways that influence body composition. The form this mechanistic approach takes could be based on the models developed in chapter 4 similar to the system used by Amer and Emmans (1998) to predict whole body chemical composition. A composition model could also include the effects that



other environmental factors have on body composition, such as the effect of temperature on fat deposition patterns. The improvements suggested above should not be limited by the quantity of information that is currently available from production systems as the advent of new technologies will provide greater quantities of information. DSS should remain flexible so as to apply this information in the form of new innovative outcomes from research. One possibility that could accelerate the development of optimisation systems for extensive industries such as beef cattle is their prior application to more intensive industries such as pigs and poultry. Possible lessons could be learnt quickly in these industries and thus applied more appropriately in the extensive industries.

### **7.5.3. Potential Applications**

The drafting of animals using RK to appropriately match animal potential to market requirements, conducted in chapter 6, is only one potential application of growth simulation models for optimising logistical operations in beef cattle production systems. A particularly appealing extension of this application would be to incorporate the possibility of drafting and recombining cohorts when production circumstances make this an attractive option. A mechanism such as this would increase the flexibility of a production system allowing it to adapt to changing market, feeding and logistical conditions. The recombining of cohorts would not have to be confined to reconstituting a group that had previously been split; it could also be capable of creating new cohorts from those present when prevailing conditions change. Figure 7.1a represents a system where initially two markets are being targeted and two cohorts targeted at these markets have been established. Figure 7.1b illustrates a desirable drafting outcome when the emergence of a new target market results in animals from the two original cohorts being reallocated to constitute a third cohort destined for this market.

are not under direct selection, are difficult or expensive to measure and thus have little genetic information available. However, due to the large number of assumptions made by this approach it is suggested that this method would only be the preferable method if reliable genetic estimates associated with food intake were not available.

Growth models not only provide a means of determining the effect genetic changes have on production, they also offer the potential to determine what genetic changes would be optimal within a given production system. A mate selection aid such as Total Genetic Resource Management could be driven by a dynamic production model, based around a growth simulation model, rather than by static breeding objectives (Kinghorn and Shepherd 1999). This would result in breeding decisions being made based on production and processing pathways considered optimal for future progeny. Given appropriate extensions the system would have the ability to not only make *ad hoc* tactical optimisation decisions concerning drafting, feeding levels, logistic, price and cost constraints (Kinghorn 2000) but also to identify the type and quantity of data required to make these decisions. An example relates to the use of DNA technologies to identify animals that have specific gene sequences e.g. GeneSTAR® Marbling 4. These decisions would relate to what is the optimal number and which animals to select for testing as well as when would be the optimal time during an animal's life to decide on such a test.

This discussion has focused on beef cattle production in isolation, but the reality of Australian agriculture is that many operations are the result of coexistence between multiple enterprises (e.g. cropping, sheep and beef cattle). Many of these enterprises are also interdependent e.g. feedlots are dependent on grain production while feedlot waste can be used as a nutrient supply for cropping. This level of interaction means the ultimate would be to develop DSSs that could be used for optimising the level and method of production in each enterprise to efficiently utilise available land and water resources.