Mathematical modelling in agricultural systems: A case study of modelling fat deposition in beef cattle for research and industry

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Abstract: Agricultural production and marketing systems are rich in complexity and diversity. Understanding how such systems are structured and function requires the use of mathematical modelling frameworks that represent their key features. Disciplines that are required to develop and solve such models include: biology, computer programming, statistics, mathematics, economics, and social science. More recently models have been developed to investigate specific issues such as the effects of climate change, climate variability, and to assist third world countries improve their production at the farm gate.

This paper presents:

- An overview of mathematical modelling:
    - Past, present, and future
    - Modelling animal growth
    - Modelling body fat
- Process of model development:
    - Level of aggregation
    - Classification of models
- Case study of fat deposition in beef steers:
    - Biology of fat
    - Measurements of fat
    - Model development of the Davis Growth Model
    - Model development of BeefSpecs

The case study of fat deposition in beef cattle provides an illustration of:

1. The modelling process from the cell to the animal level for the research model (Davis growth model) and;

2. The modelling at the herd level for the industry model (BeefSpecs). BeefSpecs has been developed for producers and livestock officers and is available for use from the Meat & Livestock Australia (MLA) web site (http://www.mla.com.au).

Both the process of model development and the biology of fat were the building blocks to develop the research and industry models. A clear understanding of the 'how', 'why' and 'what' of any model is fundamental and it is imperative that models start out at a simple level and add complexity as required. At the very outset clear and concise objectives need to be stated.

Future modelling opportunities lie in the hands of large scale data sets generated from -omic (genomics, transcriptomics, proteomics, and metabolomics) technologies. Agricultural systems that make long-term and short-term predictions will continue to make significant contributions to the agricultural industries, but the number of data inputs that are required to drive the models are contrastingly different.

Keywords: Animal growth, BeefSpecs, body fat, model development, P8 fat

1. INTRODUCTION

Agricultural systems encompass both agricultural production and marketing systems. They are rich in complexity and diversity. Generally all systems include economic considerations (Spedding, 1975). Understanding how such systems are structured and function requires the use of mathematical modelling frameworks that represent their key features. Disciplines that are required to develop and solve such models include: biology, computer programming, statistics, mathematics, economics, and social science. Models have been developed to investigate specific issues such as weed infestation, soil health, nitrogen cycling, the effects of climate change, climate variability, and to assist third world countries improve their production at the farm gate.

Agricultural systems had their beginnings in the late 1950s. The concepts of system dynamics emerged in the 1960s and further developments emerged during the 1970 and 1980s with computer programming techniques (Barrett and Nearing, 1998). In the late 1980s the trend was beginning to appear of farmers purchasing computers to solve management problems (White, 1991). In the 1990s the portable computer (PC) revolution decreased the price of PCs increasing the access-ability of PCs into every household. The internet came into wide spread use in the late 1990s and has made information more readily available. The current decade has evaluated the uptake and use of Agricultural Systems (McCown et al., 2002; Carberry et al., 2002) and the techniques of evaluating systems have been discussed (Mitchell and Sheehy, 1997; Mitchell, 1997; Tedeschi, 2006). Agricultural systems have been developed for but, not limited to, the Beef, Dairy, and Sheep grazing industries, Pest Control, Irrigation, Environmental, and Rural Innovation. Specific systems have been developed to investigate weed infestation, soil health, and nitrogen cycling.

Agricultural systems have been used to address: the effects of climate change and assist third world countries improve their production at the farm gate. A range of diverse modelling tools (Table 1) are used in the development of agricultural systems.

Table 1. Modelling tools used in Agricultural Systems

Optimisation	Simulation	Other tools/systems
Linear Programming	Differential equations	Expert systems
Non-linear programming	Difference equations	Neural Networks
Dynamic programming	Matrix equation systems	
Quadratic programming		
Optimization routines[1]		

[1]Nelder-Mead, Direction Set, Conjugate Gradient, Quasi-Newton, Simulated Annealing, Particle Swarm, Levenberg-Marquardt, Generalized NL2S0L, Differential Evolution

Agricultural systems have been developed for research and industry applications. They aim to address and answer specific questions or problems. For example: GrassGro (Moore et al., 1997), a decision support tool that enables users to analyse grazing systems in terms of pasture and animal production for sheep and cattle, gross margins, and year-to-year variability is currently being used to assist the wool industry determine the impact of climate change in 2030 (Graham, NSW DPI. Project title: "Impact of climate change on wool production systems" pers.comm.). On the other hand, StockPlan (McPhee et al., 2009), a workshop and software package to assist cattle, sheep meat, and wool producers make management decisions before and during seasonal dry spells or in the early stages of drought is being used to address issues of climate variability within a year (Graham and Meaker, NSW DPI, pers.comm.). Both GrassGro (long-term agricultural systems) and StockPlan (short-term agricultural systems) make significant contributions to the agricultural industries, but the number of inputs and data that are required to drive the models are contrastingly different.

Each agricultural system that is developed can be used for specific tasks. It may be plausible that someone may need to use several packages to provide an answer to the question that they are addressing. Others may only need only 1 package. It will all depend on the complexity of the problem that is being addressed.

This paper presents:

- an overview of mathematical modelling;

- the process of model development; and

- a case study on fat deposition in beef cattle.

The paper focuses on mathematical modelling and the examples used in this study are based on animal studies with the view that the methodologies discussed are applicable to any agricultural system that is developed.

2.   MATHEMATICAL MODELLING

Mathematical modelling plays an integral role in the development of agricultural systems and they represent key functions of a system. For example, when modelling animal systems the quantitative values of: age, weight, scanning of fat measurements, estimating dry matter intake, and carcass evaluations are extremely important for developing body composition models. The numerical calculations and analysis range from simple to complex.

This section provides an overview of modelling animal nutrition: past, present, and future; modelling animal growth; and modelling body fat.

2.1.   Modelling animal nutrition

Past and present

An excellent review on mathematical modelling in animal nutrition was recently published by Dumas et al. (2008). The review defined mathematical modelling as "the use of equations to describe or simulate processes in a system which inherently applies knowledge and is indispensable for science and societies, especially agriculture". The review covered mathematical modelling and animal nutrition from 1925 onwards. Some of the principles discussed include: bioenergetics; growth functions of Gompertz and Verhulst; allometry $y = bx^c$; the development of growth functions and other time-related equations: e.g. Michaelis-Menton, von Bertalanffy and Richards equations; logistic and monomolecular growth functions; compartmental analysis common in physiological and pharmacokinetic studies; dynamic models that include differential equations based on principles of saturation kinetics and stoichiometry; and predicting the composition of biomass gain in animal nutrition and production [product quality (e.g. fatness, fatty acid composition and bioaccumulation of various constituents)].

Future

The Dumas et al. (2008) review looked forward anticipating that growth functions will continue to be used in models; applications of calculus for biological models describing the dynamic of a system would remain; animal models will address product quality, traceability of feed ingredients, environmental sustainability, and climate change; expression of mRNA (messenger ribonucleic acid), the coding for a particular protein, may replace the responses of weight gain and protein deposition; large scale data sets generated from -omic technology (genomics, transcriptomics, protomics, and metaboloimcs) will enhance the role of predicting cellular responses.

2.2.   Modelling animal growth

In developing animal growth models Tedeschi et al. (2004) cites a number of studies of theoretical models that have been developed to predict retained energy and growth rate (Lofgreen and Garrett 1968;, Garrett 1980;, Fox and Black 1984; Fox et al., 1992; NRC 1996; Williams and Jenkins, 1998). For example the study by Williams and Jenkins (1998) predicted composition of empty body weight changes as cattle grew from birth to maturity, under varying levels of nutrition, Some studies have used more detailed animal characteristics (i.e., lower level of aggregation) such as DNA accretion curves and protein to DNA ratio (Oltjen et al., 1986, 2000; Bywater et al., 1988; Di Marco and Baldwin, 1989). Some have developed more complex models based on metabolic processes (Gill, 1984, 1996; France et al., 1987 and Gill et al., 1989). "These complex models are based on the assumption that the distribution of nutrients in body tissues is controlled mainly by substrate availability, which follows the principles of saturation enzyme kinetics" (Baldwin, 1995). Baldwin and Smith (1971) were the first to introduce compartmental simulation models at the whole-animal level that were dynamic and included differential equations based on principles of saturation kinetics and stoichiometry (Dumas et al., 2008). Tedeschi et al. (2004) warns the reader that complex models have a number of short falls and in particular "the availability of suitable input data under feedlot and grazing conditions restrict their use." The availability of good data for any model that is developed is an issue and it is not always available either because the cost is prohibitive or the objectives of an experiment did not address the data requirements for the mathematical modelling.

2.3.   Modelling body fat

Over the past 3 decades, researchers have attempted to model body fat development in beef cattle. Simpfendorfer (1974) developed a relationship between empty body fat and weight for British breed beef steers. Oltjen and Garrett (1988) reported that the rate of fat gain also depends on rate of body gain and Fox and Black (1984) made adjustments to models for genetically different size cattle. A simple way to estimate

body composition is to add the estimated fat gain over a period to an initial estimate of body fat, however, this method fails when used to predict over short periods i.e., for animals nearing a compositional endpoint or for animals with moderate to severe feed restriction early in growth.

To precisely track changes in body composition, dynamic simulation models have been developed. Oltjen et al. (1986) proposed the use of a more general form, an energetics model based around NRC equations (NRC, 1976) that incorporate the concepts of hyperplasia (cell number) and hypertrophy (cell size) based on cell number and size mechanisms of growth to predict net protein synthesis. The model integrated the net energy system to estimate gain of fat and lean tissue. The model accounts for variations attributable to initial body composition and mature size, but does not always yield acceptable estimates of fat deposition, especially at high feed energy concentrations. This is not unexpected since fat accretion is computed after energy requirements for maintenance and protein gain are satisfied and therefore all errors are accumulated in the estimate of fat. Di Marco et al. (1989) continued developing growth models by extending the growth equations used by Oltjen et al. (1986) to two pools of protein, body and viscera, two associated DNA pools and a body fat pool. The model is useful for studies of complex interactions among diet, feed intake, age, physiological status, body composition, nutrient partitioning, and energy costs associated with maintenance and growth. Studies by Oddy et al. (1997; 2000) and Soboleva et al., (1999) have continued this work by implementing and evaluating some simple biochemistry pathways and physiological mechanisms that relate growth to body compartments.

3. PROCESS OF MODEL DEVELOPMENT

Descriptions of mathematical models are fundamental to a clear understanding of the 'how', 'why' and 'what' of any model. It is imperative that models start out at a simple level and add complexity as required. The old cliché "Keep it simple stupid" is applicable here. At the very outset clear and concise objectives need to be stated. These need to be simply stated, general over a range of situations and complex enough to represent the system (Baldwin, 1995). The objectives equate to the hypothesis statement made by biological, physical, and chemical scientists who generally take an empirical approach. As the objectives are being stated the inputs and outputs of a model need to be clearly stated and the level of aggregation (section 4.1) needs to be determined.

The next 2 important steps in the modelling process are assembly and evaluation. An assembly requires tracking assumptions related to the objectives, writing the equations and checking dimensions. After building a model it must be evaluated. The evaluation is a comparison of model predictions and observational behaviour of a system and a sensitivity analysis of parameters that have been estimated within the model. This evaluation addresses: "Is our understanding of the system adequate or is it not?" (Page 21, Baldwin, 1995). The comparative assessment process (Anderssen, 1992)

$$\text{build} \rightarrow \text{solve} \rightarrow \text{display} \rightarrow \text{amend} \rightarrow \text{compare}$$

is also applicable. It is a continuing process of exploration and comparison. Within the continuing process is the classification of a model (section 4.2).

3.1. Level of aggregation

All models are based on a number of assumptions, as mentioned above. The assumptions, purpose of the model, type of inputs, and the end use (i.e., is the model for scientists or for producers?) determine the level of aggregation of a model. The organizational hierarchy (Table 2) described by Thornley and France (1984) can be depicted as the level of aggregation (Baldwin, 1995). Baldwin (1995) uses Table 3 to distinguish the differences between the experimental and modelling approach. The experimental approach is from the top down which involves reduction and analysis. Alternatively, a modelling approach can play a unique role in taking science forward by building from the bottom up with the integration and synthesis of the biological principles.

Table 2. Organizational hierarchy of biological systems (Adapted from Thornley and France, 1984)

Levels of Aggregation	
Level	Description
$i+1$	Collection of organisms (herd, flock, crop)
i	Organism (animal, plant)
$i-1$	Organs
$i-2$	Tissues
$i-3$	Cells
$i-4$	Sub-cellular elements

3.2. Classification of models

Thornley and France (1984) described a scheme for classifying models (Table 3) that is widely recognized as a standard and used extensively by scientists modelling ecological, agricultural, hydrological, and environmental systems.

Table 3. Classification of models.

Classification
Dynamic or Static
Deterministic or Stochastic
Mechanistic or Empirical

In brief, Baldwin (1995) describes the clfassification as follows:

- *dynamic* - models based upon differential equations;
- *static* - models usually algebraic in form and solved for a specific set of conditions, which exist at a set point in time;
- *deterministic* - implies that all solutions of an equation or set of equations are exact;
- *stochastic* - refers to models defined by probability functions, which inherently seek to take account of the variance that is not fully understood;
- *mechanistic* - refers to equations derived from some theory or hypothesis about the fundamental nature of the system. A mechanistic model assumes that full knowledge of casual relationships within the system is implied and computed results should relate to a broad range of realities. Riggs (1963) originally used the term 'theoretical' and Thornley and France (1984) suggested the term 'mechanistic'; and
- *empirical* - refers to models that use existing data to describe the relationship of observations between one or two variables (Riggs, 1963). Empirical models are widely used in animal agriculture and care must be applied when extrapolating beyond the limitations of the data.

These definitions are of value but as Baldwin (1995) pointed out ambiguities do exist.

4. NOTATION AND UNITS

A number of symbols and special nomenclature are used in the case study of fat deposition (Sections 5.3 and 5.4). Table 4 outlines the notation with a description, units, and value where appropriate.

Table 4. Description of notation and units.

Item	Description	Units	Value
j	Increment for each fat depot: intermuscular, intramuscular, subcutaneous, visceral	-	1 2 3 4
t	Time	days	1 to DOF
$\beta(t)_j$	Proportion of total body fat gain in each fat depot j at time t in days	-	-
ADS_{MAXj}	Maximum adipocyte size for each fat depot adipose j	kg TG/g DNA	-
DMI	Dry matter intake	kg/day	-
DNA_j	Deoxyribonucleic acid	g DNA	-
DOF	Days on feed	days	-
EBW	Empty body weight	kg	-
FAT	Total body fat	kg	-
F_j	Fat in each fat depot j	kg TG	-
HSCW	Hot standard carcass weight	kg	-
$kFAT_j$	Fat parameter coefficient for each fat depot j	1/g DNA	-
KPH	Kidney, pelvic, and heart fat	%	-
MEC	Metabolisable energy concentrate	Mcal/kg DMI	-
P8 fat	fat measurement at the P8 rump site	mm	
PROT	Protein	kg	
TG	Triacylglycerol	-	-
TBF	Total body fat	kg	-

5. CASE STUDY OF FAT DEPOSITION IN BEEF STEERS

Fat deposition holds a great deal of interest for the beef industry because intramuscular fat (i.e., marbling) increases the value of the carcass while the other three fat depots: intermuscular, subcutaneous and visceral fat are potential waste products. The Australian meat processing sector is highly regulated where producers are penalized if they don't meet stringent market specifications related to both weight and subcutaneous fat (i.e., P8 fat (mm)). The number of animals failing to meet market specifications in Australia can be high which results in lower dollar returns. A study of 40,000 feedlot cattle (Andrew Slack–Smith, unpublished; 2008) reports that cattle not meeting market specifications impacts on the final quality, cost, and delivery of the product. The study reports that in short fed feeding situations (20,000 head) – 28% missed weight specifications with an estimated cost of $31,000 ($5.50/head); 16% missed P8 fat specifications costing $54,000 ($17.50/head). In the long fed situation (20,000 head studied) 29% missed weight specifications costing $62,000 ($11/head) and 70% missed the marbling specification of 3 marble score or better costing an estimated $1.5 million ($105/head). This case study discusses the biology of fat including the development of adipocytes, metabolic processes, and regulation; how fat measurements are made and lastly, the model development of a research tool called the Davis Growth Model and the application of the Davis Growth Model to develop an industry tool called BeefSpecs.

5.1. Biology of fat in cattle

The fundamental science of the growth of muscle, bone, and fat in cattle has been described by Berg and Butterfield (1976) and Allen et al. (1976), and substrate utilization in ruminant adipose tissue by Smith (1995). In brief, the main points and arguments put forward are as follows:

1. Normal growth of beef cattle follows a sigmoidal curve (Figure 1).
2. Rate of growth does not affect the muscle to bone ratio.
3. Fat is the most variable component.
4. Breed, sex and nutrition affects growth of muscle, bone, and fat.

A study by Smith and Crouse (1984), also suggests that different regulatory processes control de novo fatty acid synthesis in the intramuscular and subcutaneous adipose tissue. Vernon (2003) has also indicated that adipose tissue is subject to autonomic control by factors produced within the tissue which act either locally (e.g. modulation of insulin action) or outside the tissue (e.g. modulation of appetite) to adjust adiposity. The development of adipocytes, the metabolic processes, and regulation are discussed.
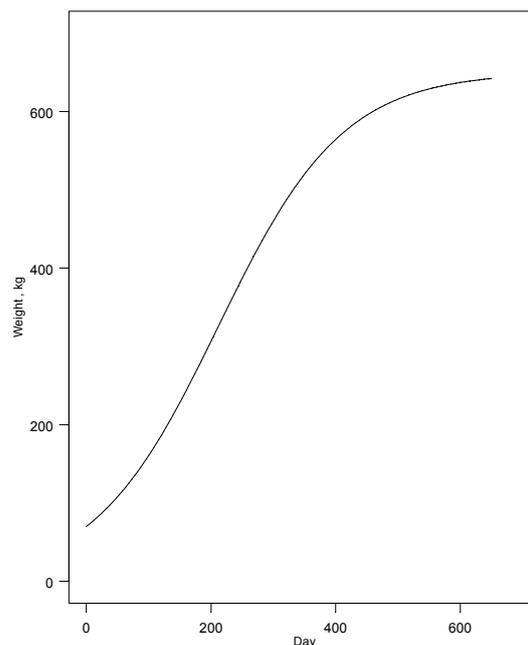

Figure 1. Sigmodial growth curve.

Fat is a collection of adipose cells (adipocytes) suspended in a matrix of connective tissue. . Adipose tissue is dynamic and found everywhere however, lipids, a major component of fat, get deposited in certain areas preferentially e.g. eyelids, nose, and ears seldom accumulate lipids whereas muscle does. The primary function of fat is to store and provide energy. Other functions of fat include: insulator against heat loss, padding between organs, protection against bruising, storage of fat soluble vitamins (A, D, E and K), structural membranes (e.g. phospholipids), and signalling (an interface between energy status and immune function). Anatomically, the main locations of fat are visceral (around kidneys, heart, pelvic (channel) and the intestinal tract), intermuscular (between muscle), subcutaneous (under the skin), and intramuscular (within muscle).

In ruminants, pre-adipocytes form into lobules that develop into brown fat (containing a high number of mitochondria) or directly into white fat. Brown fat is found in young (i.e., immature animals) and hibernating animals and functions in specific situations as the site of thermogenesis. The initial weight of animals in this case study start at 175 kg and therefore they no longer have brown fat. White adipose is characterized at one extreme as "fine evenly dispersed flecks or streaks of white fat (shimofori, or snow flake marbling) dispersed between the bundles of muscle fibers in bovine skeletal muscle" and to the other extreme as "thick, channels of fat that merge into the intermuscular fat depots" (Harper et al., 2001; Harper and Pethick, 2004). Mature marbling adipocytes range from 40-90 μm which are smaller than adipocytes from other fat depots (Cianzio et al., 1985; May et al., 1994; Lee et al., 2000). The cells are roughly spherical and cell volume varies disproportionately i.e., 80 is only twice as wide as 40 but it has 8 times the volume due to accumulation of intracellular lipid. Adipocytes cluster together as shown in the magnification 300x of intramuscular fat found in the rib eye area (Figure 2). Subcutaneous and intramuscular fat comprise 25-30% palmitic acid and 30-75% stearic and oleic acid. Differences in fat deposition are due to breed, sex, age, weight, and nutrition.
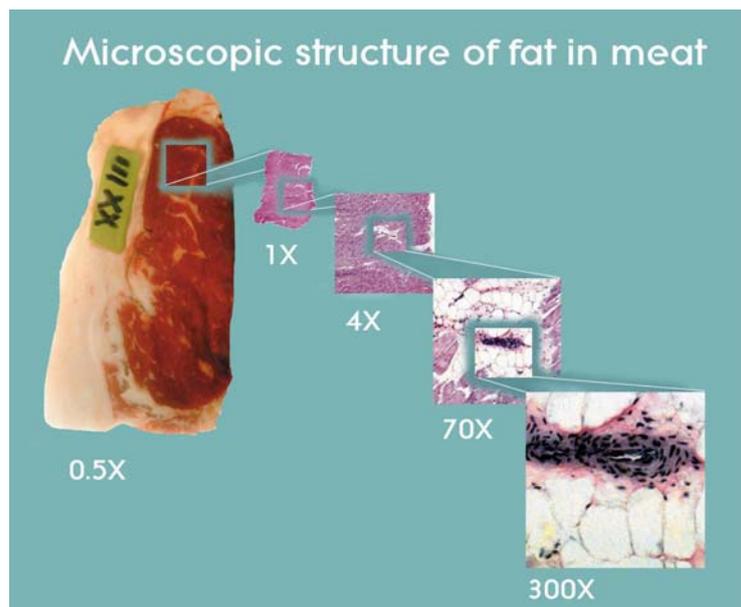
Figure 2. Histological images of marbling fat in muscle, showing the structure of marbling fat at magnifications of 0.5x, 1x, 4x, 70x and 300x. (Published by Harper and Pethick 2004; Acknowledgment for the source: P.G. Allingham, Beef CRC, CSIRO, Brisbane, Queensland, Australia.)

As fat adipose tissue develops cell differentiation and morphology may follow the following sequence given by Vance and Vance (2004).

mesenchymal cells → adipoblasts → pre-adipocytes → adipocytes.

There are different stages of adipose conversion (Table 5).

Table 5. Stages of adipose conversion (adapted from Bernlohr et al.*,* "Adipose tissue and lipid metabolism." Chapter 10, page 264-268, Vance and Vance, (2004))

Stages	Cell type	Characteristics
Stage 1	*Mesenchymal/pluripotent*	Multipotential – ability to differentiate into muscle, cartilage or fat
	Determination	
Stage 2	Adiploblasts	Unipotential – can only differentiate into adipocytes
	Commitment	
Stage 3	Pre-adipocyctes	No lipid accumulation, early transcription factors, e.g., C/EBPβ, and early markers of differentiation expressed, e.g. lipoprotein lipase

The main factor that varies among genetically-different animals is the number (hyperplasia) of adipocytes. Adipocyte size (hypertrophy) is the primary variable influenced by intake and nutrition. It has been proposed that new adipocytes may be recruited if needed (i.e., enough cells exceeded the size threshold) after hyperplasia ceases. Initial programming is critical i.e., body fatness and fat distribution are genetically controlled. In terms of composition, lipids contribute substantially, but there are other components. For example: enzymes responsible for lipogenesis and lipolysis, traces of certain minerals and minute quantities of glucose and glycogen and of glycerol. On a tissue basis, extractable lipids may represent 80 to 90% by volume in obese animals where 5 to 15% is water and the remainder is protein, minerals, and carbohydrates; however species, stage of growth, and state of nutrition do influence this.

Metabolic processes

Rate of fat deposition in adipose tissue is the function of the following metabolic processes: (1) absorption of preformed fatty acids from blood, (2) fatty acid synthesis (lipogenesis) and, subsequent esterification to triacylglycerols (TG), (3) lipolysis, re-esterification and mobilisation of free fatty acids to circulatory system and (4) *in situ* fatty acid oxidation to CO_2. Three key enzymes of importance in fat deposition are: (i) hormone sensitive lipase (HSL) a rate limiting step; (ii) lipoprotein lipase (LPL) a regulating factor in the uptake of TG of serum lipoproteins by adipose tissue. (LPL is produced and released from the adipocyte and

it is a diet adaptable enzyme.); and (iii) Acetyl-CoA Carboxylase (ACC) a key regulator of lipogenesis and the rate-controlling enzyme in adipose tissue of meat-producing animals. Of equal importance is NADPH (nicotinamide adenine dinucleotide phosphate) activity which is generated from two enzymes in the pentose phosphate pathway and from the malic and isocitrate dehydrogenase enzymes. NADPH is an indicator of fat storage potential and is positively correlated with lipogenesis.

In terms of substrate utilization acetate is the primary precursor for de novo fatty acid synthesis. Glucose also plays an important role to support lipid synthesis. Dietary regulation of fatty acid biosynthesis (level of food intake; high-energy diets) demonstrates an increase in ATP-citrate lyase. Therefore, diet has a role in changing the amplitude of the rate of lipogenesis. Age also influences the timing/onset of de novo lipogenesis.

Regulation

A recent study (Jacobi et al., 2006) suggested that adipocytes, act as active participants in the innate immune response which produce a number of metabolic regulators: leptin, adiponectin, and pro-inflammatory cytokines. The sole source of the anti-inflammatory adiponectin is found in the adipocyte which regulates the nuclear factor kappa-β transcription factor, locally, and in myofibers. "The production of such molecules strategically positions inter and intramuscular adipocytes to act as immunological sensors to regulate direct and indirect responses of myofibers to inflammatory signals" (Jacobi et al., 2006). Evidence from other studies in pigs (Ding et al., 2003) suggests that adiponectin is also in visceral and subcutaneous fat and hence not just isolated to inter and intramuscular adipocytes.

5.2.   How fat measurements are made

The research model is a net energy model that predicts total body fat (**TBF**; kg chemical fat) after taking account of protein and maintenance. Therefore to produce industry relevant outputs, 3 of the fat depots are converted to carcass characteristics: intramuscular (kg) to intramuscular (%); subcutaneous (kg) to 12th rib fat (mm) and subsequently from 12th rib fat (mm) to P8 fat (mm); and visceral fat (kg) to kidney, pelvic, and heart fat (**KPH**; %) (McPhee, 2008a). To model each of the 4 fat depots and to parameterize the fat depot logistic equations the size (hypertrophy) and number of cells (hyperplasia) are also required. A preliminary study on parameterizing the fat deposition models with data from the literature has already been conducted (McPhee, 2008b). Therefore this section outlines the industry relevant carcass measurements and the method of measuring hypertrophy and hyperplasia.

Carcass measurements of fat

The value of a carcass is principally determined by weight and fat. The fat measurements of interest are P8 fat (the standard carcass fat measurement for the Australian beef industry at the P8 rump site), and intramuscular fat. The P8 fat (mm) is directly related to the amount of subcutaneous fat in a carcass. Both P8 fat and marbling score (e.g. practically devoid or moderately abundant are the 2 extremes) are assessed by trained graders (Tume, 2004) on the cold carcass at the abattoir. Scanned subcutaneous fat at the P8 fat (mm) site during the life of an animal can also be recorded by ultrasound scanning (Upton, 2001).

Intramuscular fat samples in research trials are taken from the *M. longissimus* close to the 12/13th rib site. Measurements can be made either by solvent extraction using a Soxhlet apparatus or by a near infrared spectrophotometry (NIR) to estimate chemical fat content. These methods are described in more detail by Perry et al. (2001) and illustrate that the NIR results calibrated against Soxhlet extraction of fat in boiling chloroform for 24 hours explained 96% of the variation in measured intramuscular fat.

To convert marbling scores to intramuscular fat as a percentage Savell et al. (1986), developed a linear equation (intramuscular fat = 0.0127 * marbling score – 0.8043; R^2 = 0.78) to predict the percentage of ether extractable fat (intramuscular fat, %) based on the following marbling score conversions: Practically devoid, 100-199; Traces, 200-299; Slight, 300-399; Small, 400-499; Modest, 500-599; Moderate, 600-699; Slightly abundant, 700-799; Moderately abundant, 800-899.

Total body fat can be determined either by full dissections (Thompson et al. 1985; Perry and Arthur 2000); full chemical composition; carcass specific gravity (Garrett and Hinman, 1969); estimating TBF from the 9-11th rib fat section (Hankins and Howe, 1946) or X-ray scanning the carcasses and estimating TBF (Alston et al. 2004, 2005). Determining the amount of fat in the fat depots: intermuscular and subcutaneous can be determined by dissection which is extremely time consuming, and visceral fat (omental, mesenteric, kidney, heart, and channel fat) weighed at slaughter. Estimating the amount of fat in each depot using the scanned data to estimate TBF is currently under investigation.

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Cellular measurements of fat

Cell size (mean diameter) and the total number of cells/gram of tissue (relative frequency distribution of the size of the fat cells) in fat depots in cattle have been determined by using a Channel-analyzer attached to a Coulter counter with a 400 μm aperture (Cianzio et al., 1985). To free the fixed fat cells from any surrounding connective tissue matrix osmium tetroxide (Hirsch and Gallian, 1968) isolated in urea solution (Etherton et al., 1977) was used. More recently image analysis of histology sections of adipose tissue have been used to determine adipocyte size and number of cells (Chen and Farese, 2002; Yang et al., 2006).

5.3. Model Development of the Davis Growth Model

The Davis Growth Model is based on the Oltjen et al. (1986) dynamic animal growth model with the addition of 4 adipose depots: intramuscular, intermuscular, subcutaneous and visceral (Sainz and Hastings, 2000).
- *Objectives:*
  1. Parameterize the intermuscular, intramuscular, subcutaneous, and visceral fat depots for early and late maturing cattle for implanted and non-implanted steers to determine if there are metabolic differences between early and late maturity in the fat depot parameters.
  2. Determine if variation between phenotypic traits including growth of fat pools in different genotypes at different time points exist in beef cattle.
- *Users:* Researchers.
- *Inputs:* breed, sex, frame score (1 to 9), condition score (1, 2 or 3), initial live weight (kg), initial P8 fat (mm), **DMI** (dry matter intake; kg/day), metabolizable energy concentrate of (DMI) (Mcal/kg DMI), days on feed, implant status (yes or no).
- *Outputs:* live weight (kg), total body fat (%), P8 fat (mm), intramuscualr fat (%), KPH (%).
- *Level of aggregation:* animal. (Concepts of hypertrophy and hyperplasia are incorporated.)

Using the bottom up approach the cell, tissue, and animal level are described. The sub-cellular level (Table 2) is not used in the Davis Growth Model.

Cell level

At the cell level (1) calculates a proportion where $0 < \beta_j < 1$ and the $\Sigma\beta_j = 1$ is constrained.

$$\beta_j(t) = kFat_{j\times} DNA_j(t) \times \left[1 - \left(\frac{FSIZ_j}{ADS_{MAX\,j}} \right) \right] \qquad (1)$$

Tissue level

Each fat depot (2) at the tissue level is estimated by a first-order differential equation.

$$\frac{dFj}{dt} = \beta j(t-1) \times \frac{dFAT}{dt} \qquad (2)$$

Animal level

Each animal's EBW (3) is determined by a first-order differential equation.

$$\frac{dEBW}{dt} = \frac{1}{0.2201} \times \frac{dPROT}{dt} + \frac{dFAT}{dt} \qquad (3)$$

- *Classification of model:* dynamic, mechanistic, net energy based.

5.4. Model Development of BeefSpecs

The Davis Growth Model was used to develop a large matrix of inputs and outputs to develop a multiple regression equation (McPhee; unpublished).
- *Objective:* develop a tool to predict the mean P8 fat (mm) for a group of beef cattle.
- *Users:* Producers and livestock advisers for the beef industry.
- *Inputs:* initial weight (kg), initial P8 fat (mm), frame score, implant status (yes or no), feed type (grass or grain), production system (feedlot/strip grazing, easy, moderate, or hard grazing), growth rate (kg/day), days on feed, and dressing percentage (%).

- *Outputs:* prediction of final P8 fat (mm) and calculation of live weight (kg) and hot standard carcass weight (HSCW; kg).
- *Level of aggregation:* population.
- *Classification of model:* empirical.

This model does not have any bottom up approach and predicts the mean P8 fat (mm) of a group of cattle from an empirical relationship. The input of growth rate is a pseudo for DMI and metabolisable energy concentrate (**MEC**) because growth rate effectively represents the quantity and quality of feed available to animals and can be estimated by producers.
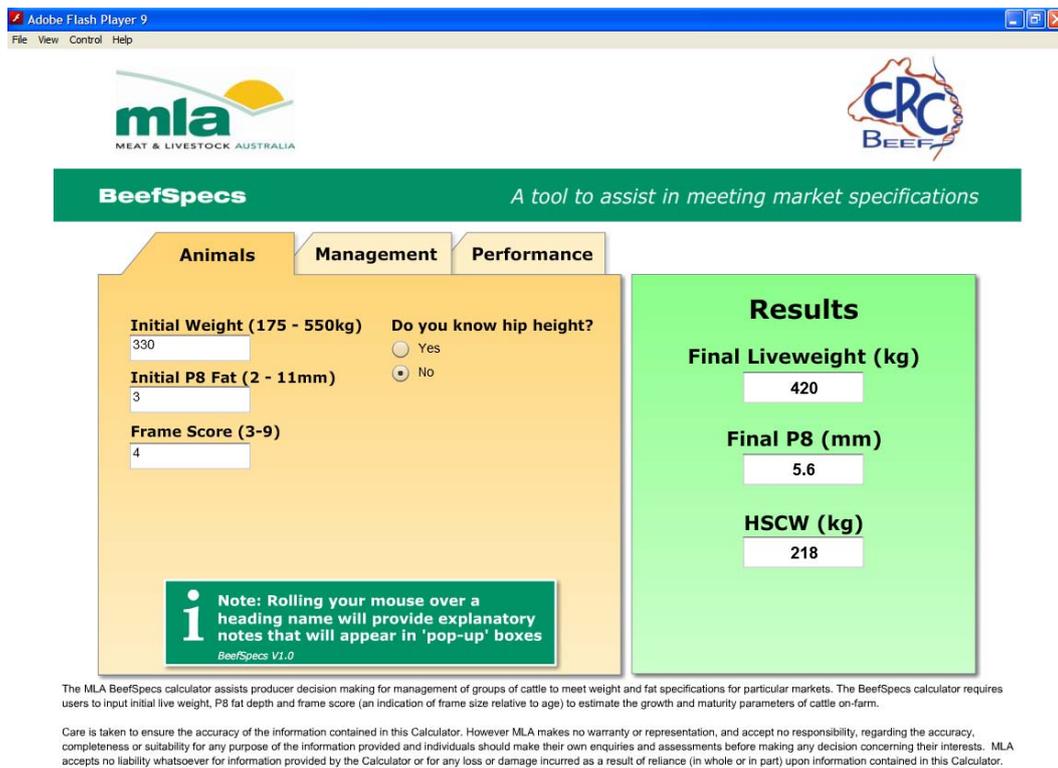
Figure 4. BeefSpecs fat calculator – Animals tab.

6. DISCUSSION AND CONCLUSIONS

This paper has provided an overview of mathematical modelling which is a functional component of agricultural systems. The future development of mathematical models could utilise data from -omic (genomics, transcriptomics, proteomics, and metabolomics) technologies e.g. the expression of mRNA (Dumas et al., 2008). The process of model development and the unending improvement to models is not too far distant from the Kaizen principles (Imai, 1986) of 'continuous improvement'.

The case study of modelling fat deposition in cattle illustrates the process of model development from research (i.e. Davis growth model) to industry tool (BeefSpecs). Modelling the biology of fat deposition in beef cattle has the potential to assist in the development of a human fat deposition model (Johnston, University of Davis, California, pers. comm.).

The Davis growth model and BeefSpecs were initially developed for *Bos taurus* cattle and the model is currently under evaluation for *Bos indicus* cattle. Future research will be conducted in the analysis of Angus, Hereford, and AngusxWagyu breeds in a serially slaughtered experiment (5 intervals). Additional data from Brahman cattle at slaughter will also assist in determining the differences in fat deposition for different breeds. Techniques in scanning carcasses and histological studies will assist in determining the size and number of cells in each of the fat depots. A future Davis growth model may include the modelling of NADPH activity or the regulation of adiponectin. Studies will also be conducted to phenotypically predict intramuscular fat (%) and assess if estimated breeding values (EBV) improve the phenotypic predictions of P8 fat and intramuscular fat.

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Agricultural systems that make long-term predictions (e.g. GrassGro) will continue to be used by livestock and agronomy officers. Systems that make short-term predictions (e.g. StockPlan and BeefSpecs) will also continue assisting producers.

ACKNOWLEDGMENTS

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