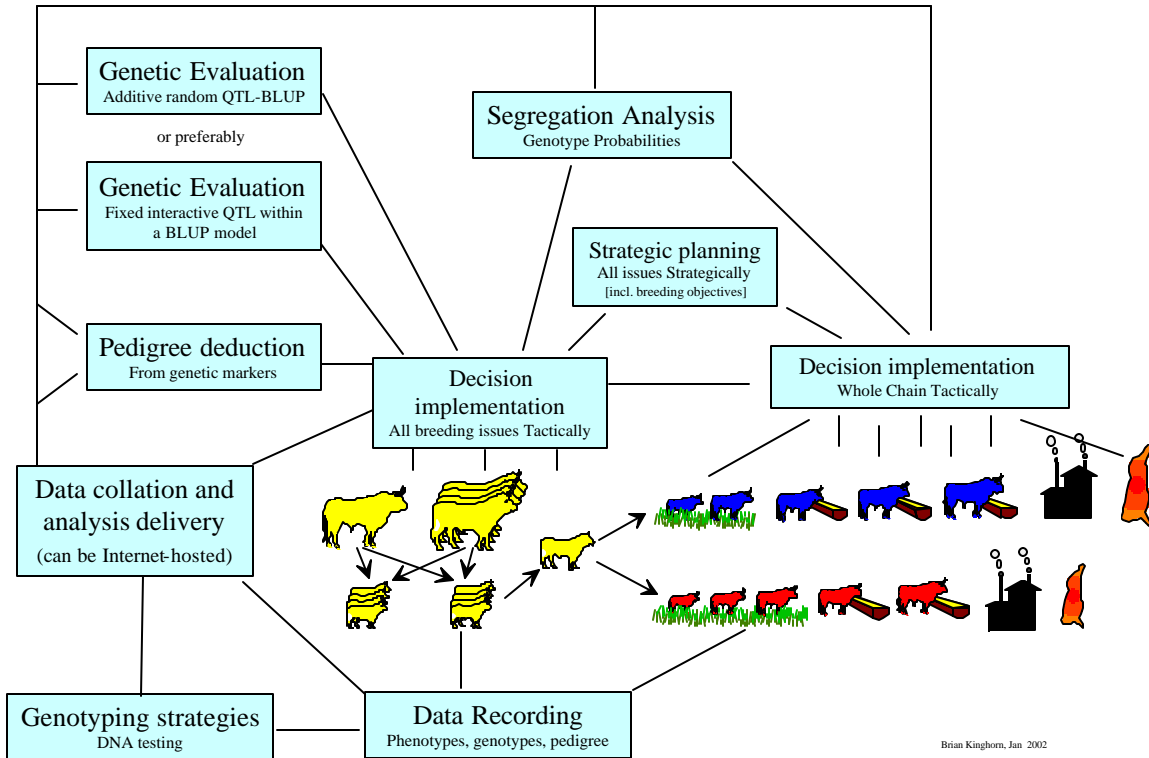Defining and realizing breeding objectives

Desired gains
and other desired outcomes

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Some key information systems

Genetic Evaluation
Additive random QTL-BLUP

or preferably

Genetic Evaluation
Fixed interactive QTL within a BLUP model

Pedigree deduction
From genetic markers

Data collation and analysis delivery
(can be Internet-hosted)

Genotyping strategies
DNA testing

Segregation Analysis
Genotype Probabilities

Strategic planning
All issues Strategically
[incl. breeding objectives]

Decision implementation
All breeding issues Tactically

Decision implementation
Whole Chain Tactically

Data Recording
Phenotypes, genotypes, pedigree

Brian Kinghorn, Jan 2002

Animal Breeding ...

Where to go?

Corporate objectives

Breeding objectives → Economically Rational approach

Biological approach

Desired gains approach

How to get there?

Introduction

Breeding Objectives are all about Where to go? John Gibson has tacked this largely from an "Economically Rational" viewpoint. I will touch on a more biological approach (which is still economically rational!) and discuss the Desired Gains approach in more detail. The Desired Gains approach will also be extended to cover Desired Outcomes in general, covering not just desires in trait changes, but other breeding program outcomes such as costs and logistics, using Total Genetic Resource Management.

Breeding objectives stipulate the animal characteristics to be improved and the desired direction for genetic change. They should be constructed in a manner which allows them to play an appropriate role, together with parameters such as heritability and correlations, as part of a genetic evaluation system. This is done in order to facilitate ranking of animals on genetic merit and implementation of effective breeding program design.

To this end, breeding objectives are generally expressed as economic weightings that describe the economic impact of a unit change in each trait of commercial importance. These economic weightings can be used directly to help evaluate different breeds and crosses, or, more commonly, they can be used in conjunction with genetic parameters and knowledge of population structure to rank animals on an index of genetic merit in monetary units.

The breeding objective traits are not necessarily the same as the selection criterion traits that are measured and used to make selection decisions. For example, lean percent may be a breeding objective, and ultrasonically measured backfat thickness a

selection criterion. Knowing the genetic relationship between these two traits permits selection index methods to target the former using data on the latter.

There are two approaches to calculating these weightings - the Economically Rational approach, and the Desired Gains approach.

The Economically Rational approach – a brief review

This approach has already been presented in this course by John Gibson and Julius van der Werf. Did you enjoy it? I imagine they have done an excellent job. I will only give an outline here to maintain context.

The classic approach to calculating economic weightings is economically rational - it takes no account of genetic parameters.   This makes sense in that the value of making a unit change in a given trait should not be influenced by how difficult it is to generate this change. These difficulties can be handled appropriately at the genetic evaluation phase. In this setting, breeding objectives should reflect the costs and returns involved in a *production* system, and should not consider costs and gains generated in a *breeding* program.

A simple example (for beginners only)

A very simple breeding objective is presented here. The reader is directed to Ponzoni (1988) for a comprehensive worked example. The key tactical objective of a selection program is to choose animals of high breeding value to be used as parents.   An animal's breeding value (A) is the value of its genes to its progeny. The breeding objective is simply a multi-trait breeding value, with each trait weighted by a relative economic weight, for example:

Breeding objective: 6 x Fleece weight   +   -1 x Fibre diameter

Units = $: $/kg .   kg   + $/μ .   μ

In order to combine different traits into such a single score, they have to be converted to a common scale. This is generally dollars or some other monetary unit.   The economic weights in this simple example are taken to have been calculated from market prices of $6 per kilogram of wool and -$1 per micron for an average fleece. The units of expression are thus 'dollars [per unit (kg or μ)] per head shorn'. Note that these weights involve no consideration of genetic parameters.

Units of expression

All economic weightings in a breeding objective should have the same basis for units of expression, such as 'dollars per head shorn' as used above. Choice of this basis can have an important influence on the consequences of using the breeding objective.

A simple basis for unit of expression, such as 'dollars per head shorn' can be used for situations in which all traits are *directly* related to economic costs or returns, and thus

excludes reproductive traits, whose effect is at least partly manifested through progeny.

A less simple basis is 'dollars per breeding ewe per year', which accommodates both production and reproduction traits. In all cases, each trait should use this same basis, such that an objective might be, for example:

   $7.20 per kilogram   per breeding ewe per year   x   Clean fleece weight
+ $-1.20 per micron   per breeding ewe per year   x   Fibre diameter
+ $7.20 per lamb weaned per breeding ewe per year   x   Number of lambs weaned

This means that in a flock of 150 breeding ewes, a marginal increase of 1kg in clean fleece weight would increase profit by $7.20 x 150 = $1,080 per year. This accommodates wool shorn from all classes of stock, through the way in which the economic weight is calculated. The economic weight for an increase of one lamb weaned is more difficult to calculate, due to expression via progeny, but in this case it is the same as for clean fleece weight. Delays in returns due to expression in progeny can be accommodated by considering the pattern of flow of genes through the population, and discounting future returns to give current values (McClintock and Cunningham, 1974).

Economic weights calculated on a 'dollars per head shorn' or 'dollars per breeding ewe per year' basis suffer a potentially important drawback. They relate to dollars per livestock unit, rather than dollars per resource unit, such as 'dollars per hectare'. As an example, consider two breeds of meat sheep:

Breed	Value of weight at slaughter	Value of food consumed	Profit per head	Dollar efficiency
Small	$200	$100	$100	2:1
Large	$350	$200	$150	1.75:1

The large breed would be targeted by a breeding objective based on 'dollars per head'. However, a breeding objective based on 'dollars per hectare' would target the small breed. A breeding objective based on dollars per resource unit will usually be more appropriate, as long as proper account is made of any fixed costs per head.

Economic values can be calculated from several different perspectives, eg with the aim of maximising the profitability of an enterprise for an individual producer, or with the aim of improving the efficiency of a national livestock industry. Amer (1994) and Weller (1994) discuss these different approaches and the attempts to unify them.

Matching environment and genotype

It is possible to derive inappropriate breeding objectives by not taking account of the fact that different genotypes, for example different breeds, perform most economically under different environments or management policies. As an extreme example, consider the two breeds in Figure 1.
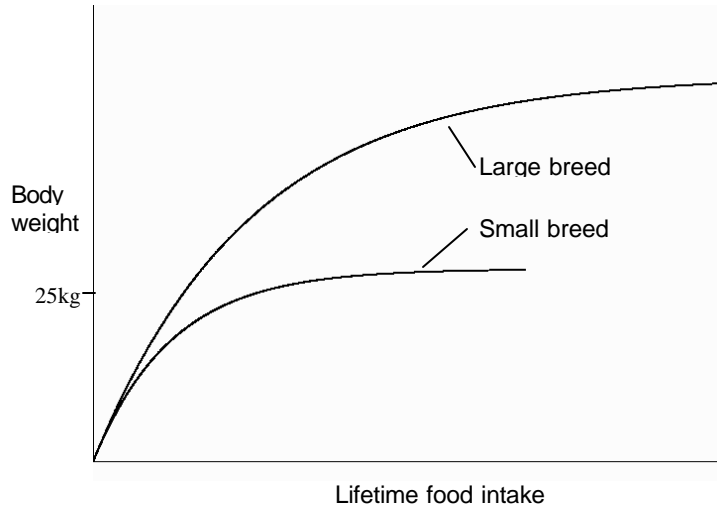
Figure 1. Growth efficiency curves for two breed sizes

If food intake to a fixed slaughter weight of 25 kg is taken as a key objective trait, then the small breed cannot compete, as it is very old when it reaches this weight. Also, if body weight achieved for a given level of accumulated food intake is taken as a key objective trait, then the small breed cannot compete. These apparently convincing arguments have lead to widespread selection for increased body size in meat producing species.

However, if we consider two small animals as a single large individual, then they will compete equally well on both these objective traits. In fact, when we consider that smaller animals reach mature size more quickly than larger animals (Taylor, 1980) then the small breed comes into favour under an objective that accounts for timely use of resources. But even this is an illusion - larger animals consume less per kilogram of body weight (Taylor, 1980), such that fixed food resources can carry more kilograms of large animals, and the net result is that the two breed sizes are of equal value (Kinghorn, 1985).
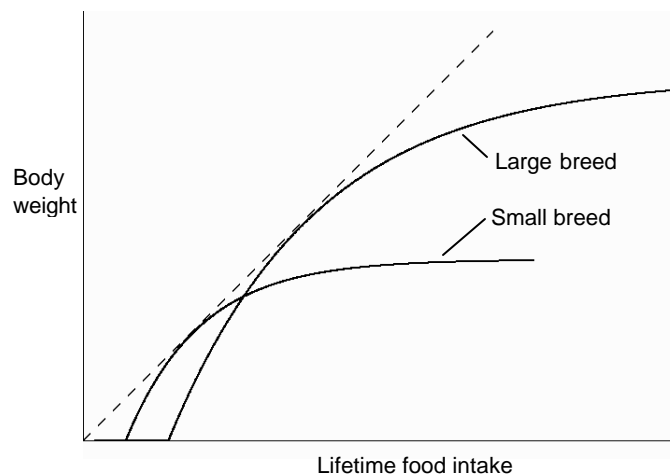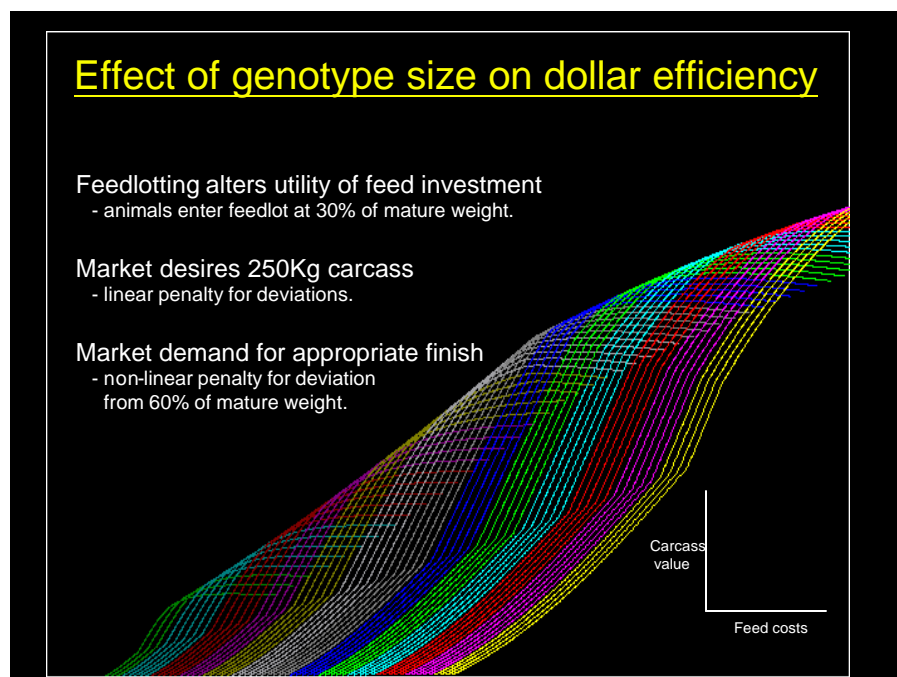

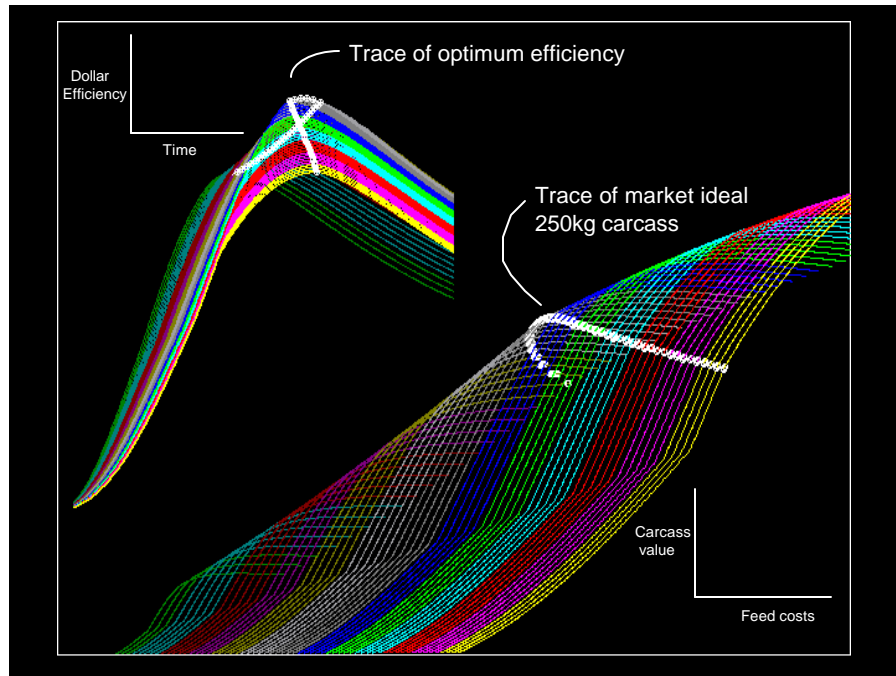Figure 2. Growth efficiency curves accounting for maternal food costs.

This sort of debate can be avoided wherever it is possible to match the production system to the prevailing environment. For example, if the curves in Figure 2 were a close reflection of the patterns for dollar output plotted on dollar input, now accounting for maternal food costs, the production system should be to slaughter at a fixed proportion of mature size, about 60 percent in the current simplified example, and this should feature as the key breeding objective trait.

However, such a simple solution is rarely possible, because, for example:

- the market places a strong premium on a given slaughter weight, carcass weight, or level of fatness, or

- the supply of grass or other food varies in magnitude or cost, such that slaughter within a given time period has a large effect on profitability.

The following two figures give a simple example that addresses such a situation:

Trace of optimum efficiency

Trace of market ideal 250kg carcass

Dollar Efficiency

Time

Carcass value

Feed costs

> Even considering just one trait (size/growth rate) leads to complexity.
> Understanding the biology is critical
> We must consider:
>> o all important traits
>> o details of market requirements.
>> o resource implications

The best genotype depends on environment/management, and the best management regime depends on genotype. This means that we should ideally co-optimise genetic and environmental (management) changes (Sivarajasingam *et al.*, 1984b).

The breeding objective calculations should in many cases accommodate non-linear value surfaces (eg. Sivarajasingam *et al.*, 1984a). The value of a micon reduction in fibre diameter depends on fleece weight. There are optimal values for backfat thickness and birthweight.

The Desired Gains approach

An alternative approach to developing breeding objectives, the 'Desired Gains' approach, involves declaration of the relative magnitudes of genetic gain desired in the traits of importance. The breeding objective calculations still result in relative economic weights, but these are now influenced by genetic parameters, with generally greater economic weightings for traits which are more difficult to change.

A convenient way of doing this is to view the range of possible outcomes, as in figure 3. This figure is achieved by looping through combinations of economic weights for two traits and plotting the predicted response in each trait to get an ellipse. Changing

genetic parameters changes the shape of the ellipse. The selection index will continue to do the best job possible, as shown in figure zz, but the direction of desired gain might well change in the light of different possible outcomes.
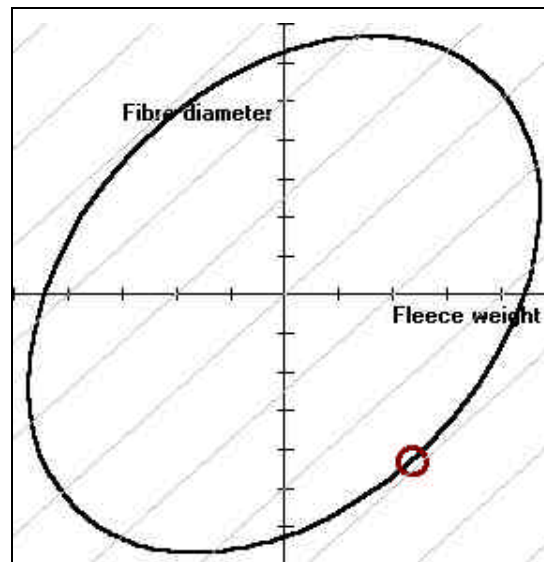

Figure 3. Example output from GENUP module ELLIPSE. The genetic merit of the population starts at the origin, and can progress over a given number of years to any point on the ellipse, depending on the economic weights chosen. The diagonal lines are lines of equal economic merit. The result from using an economically rational selection index is shown by the small circle, with an optimal combination of high fleece weight and low fibre diameter.

A simple subset of the Desired Gains approach is the restricted index, in which the objective is set up to give a predicted zero genetic change in one or more nominated traits. Examples are restrictions for no change in fibre diameter, backfat, and milk fat.

Brascamp (1984) describes methods which can be used for restriction and desired gains. He also shows how to use a mixture of the economically rational and the desired gains approaches, with some traits constrained to pre-chosen levels of response, and others influenced just by production economics. In all cases, relative economic weights are calculated, which is useful for demonstrating the 'effective economic weights' which nominated desired gains or restrictions imply.

A key problem with the desired gains approach is that initial desires in a specified direction will not be achievable in most cases. The program Desire has been written to discover the range of possible outcomes, and arrive at a theoretically achievable set of predicted responses, and economic weightings to target these (Kinghorn, 2000a).

Desire, shown in Figure 4, is largely based on the approach of Brascamp (1984), which uses genetic parameters to handle predictions of selection response per generation. This is an algebraic approach – not somple to implement but fast to execute. Julius van der Werf will probably have shown you his excel solution, which

uses an Evolutionary Algorithm to discover economic weights that give predicted responses that are at close as possible to those desired.
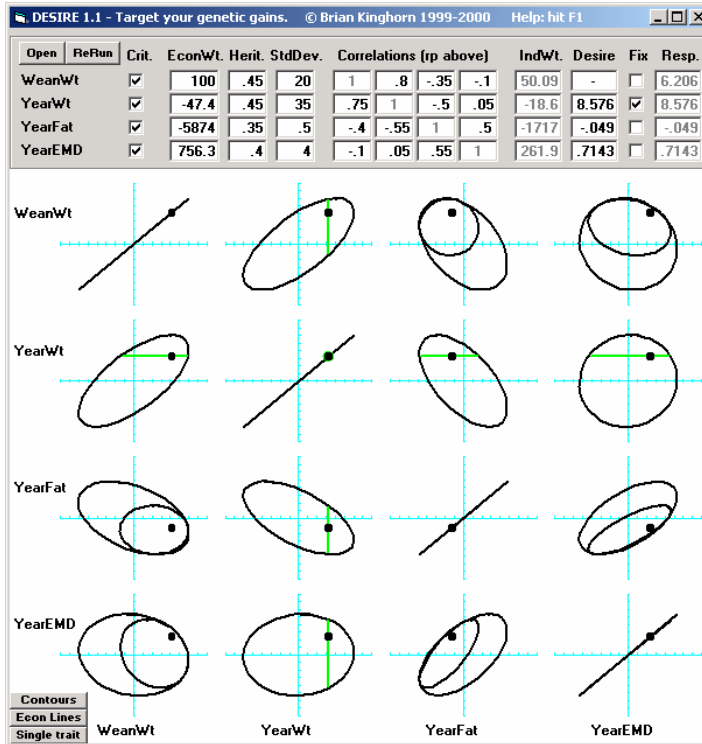

Figure 4. Screen capture from program DESIRE. The outer ellipses show limits of response for pairs of traits. "Fix"ing YearWt to +8.576Kg response constrains responses in other traits to within the inner ellipses. Parameter values were chosen for illustration only, to approximately match the pattern found in Figure 2.

Tactical implementation of the desired gains approach

This section presents a different approach, which makes predictions based not on genetic parameters, but on the prevailing list of estimated breeding values of candidate animals for selection. This approach has been written into an application called "Progeny Explorer", named because it explores the possible range of outcomes in the progeny generation.

Progeny Explorer uses the same data input file as used in the Total Genetic Resource Management (TGRM) system (eg. Kinghorn, 2000b). This includes all estimated breeding values (EBVs) for traits of interest, as well as any limits on number of matings for each candidate animal. For any set of relative economic weightings on these traits, the optimal selection set (animals to be used as parents, and the number of matings per animal) can be found. Optimisation was carried out using a form of Differential Evolution, adapted from Price and Storn (1997).

In contrast to Desire, Progeny Explorer (Figure 5) makes predictions for the next progeny crop, based not on genetic parameters, but on the prevailing list of estimated breeding values of candidate animals for selection. Predicted progeny merit is simply the average of parental EBVs, and there is no need to involve estimated genetic parameters.
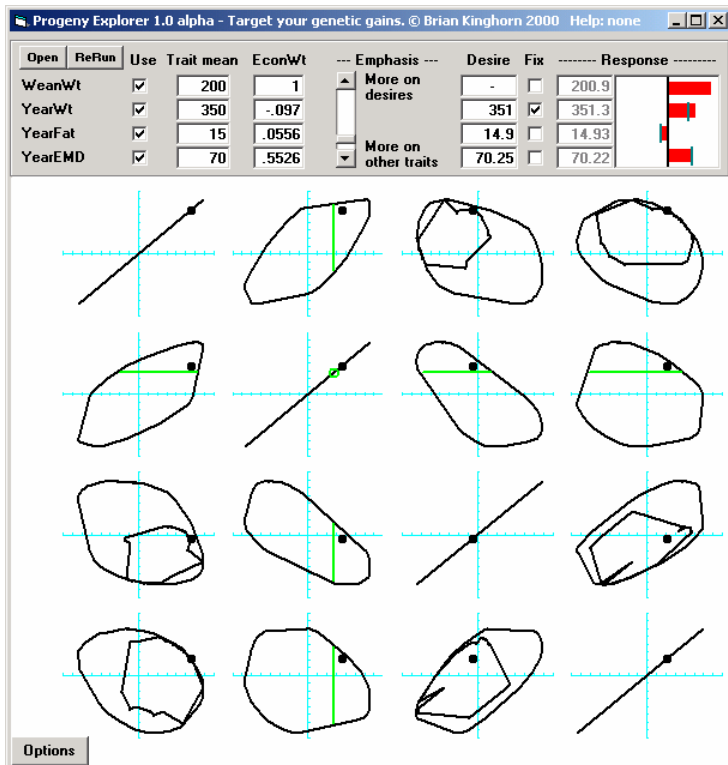
Figure 5. Screen capture from program Progeny Explorer. Inner ellipses especially are of irregular shape due to the vagaries of individual animal EBVs. Implied economic weights are relative to the first trait. Data for this example, other than trait means, come from an Australian beef cattle herd, courtesy of David Murray.

Desire helps the user to visualise the multi-dimensional response surface by providing 2-dimensional slices through this. The outer ellipses illustrate maximal responses achievable for each pair of traits, and the inner ellipses illustrate slices through the multi-dimensional space that adhere to constraints placed on other traits.

Notice that the ideally-shaped ellipses from Desire, based on predictions based on genetic parameters, are imperfect under Progeny Explorer. This is because they reflect responses in progeny that can be made with the exact candidates available for the current selection decision, and there is a finite number of parents available with an imperfect distribution of EBVs.

A degree of emphasis on desired gains needs to be declared. This is because with individual animal EBVs, desired gains are generally not exactly met, and very high emphasis on achieving desired gains will unacceptably compromise response in other traits. Placing more emphasis on desired gains in Figure 5 will make the inner constrained shapes even smaller and less regular. Given this, these inner shapes should be used as a guide only.

Progeny Explorer should be used in conjunction with an economically rational tool such as BreedObject (Barwick and Henzell 1998). A planned feature is to show ranges of response that are constrained to expressing, for example, at least 95% of the predicted response under unadulterated use of an economically rational approach. This should be appealing to both 'rationalists' and 'free spirits', as the shape of response surfaces is such that there is usually quite a wide range of response directions possible within a few percent of theoretically maximum economic response.

Progeny Explorer could usefully be run as a precursor to TGRM (Kinghorn et al. 2002), to help users set their overall breeding direction. Implied economic weights from Progeny Explorer can be used to calculate indices for selection candidates. This approach will help avoid current tendencies to manipulate selection direction through the means of predicted progeny genetic distributions in TGRM. These distributions should be used to influence variation and other distribution properties, as suggested in Figure 6.
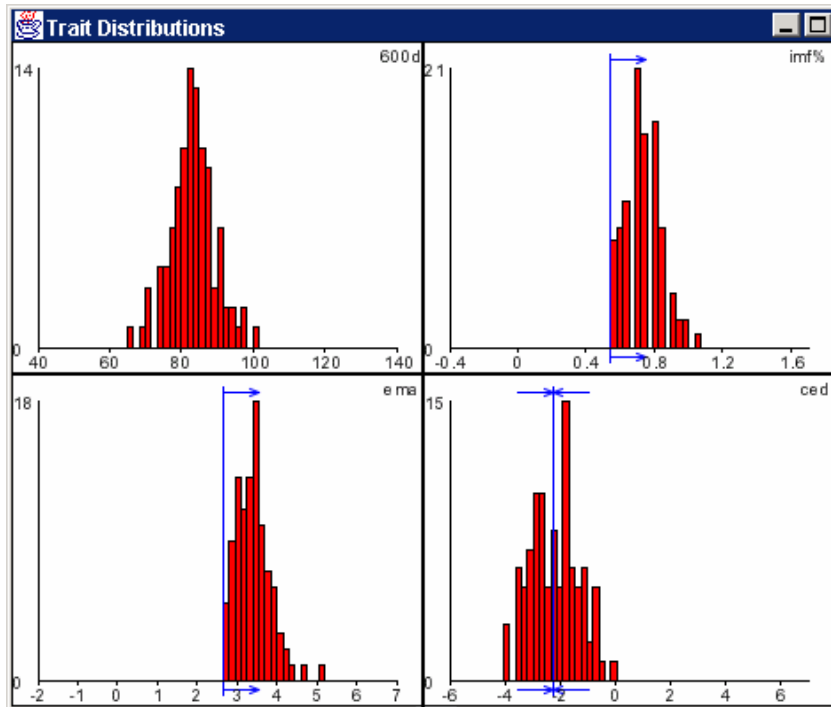

Figure 6. Trait Distributions window from TGRM Control Center, showing predicted genetic merits of prospective progeny from the current solution. This feature should be used to manipulate distribution properties other than the mean. Progeny Explorer is well suited to influencing means via implied economic weights.

Economically rational v. Desired gains – a balance.

The classical Economically Rational calculation of economic weights for use in a selection index framework ignores genetic parameters. This means that the resulting direction of genetic gain is not fully addressed. The Desired Gains approach handles this and accommodates practitioner feelings that the best direction to take depends on how far you can go in each direction. Moreover, the Economically Rational approach usually assumes linearity, which may not be the case, usually ignores the reality of the seedstock marketplace, and can have difficulty in handling some traits such as disease resistance. On the other hand, Desired Gains can be hampered by irrational and dogmatic opinions. The Economically Rational approach is ideal where there is a strong knowledge about product value in the marketplace. The best solution is probably a mix of each, using Desired Gains to explore solutions that are at least, say, 90% efficient on the Economically Rational scale. There is generally a lot of room to move in that top 10%.

A portfolio of gene tic resources?

Should we breed a number of different selection lines in different directions, to give us a resource for fast access in the future? The answer to this question depends partly on the relationship among the key breeding objective traits. Figure 7 illustrates this.
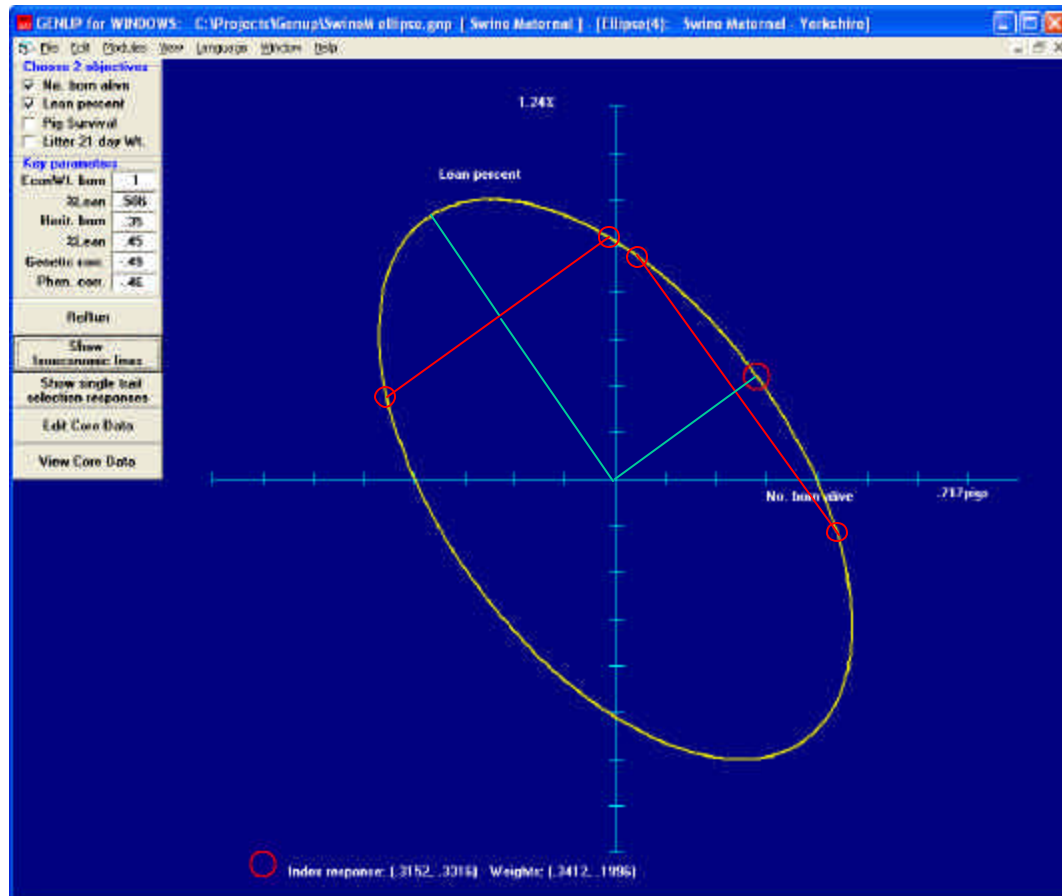
Figure 7. We are at the origin. We can be anywhere on yellow ellipse in say 5 or 10 years time. [This actually assumes mass selection on both sexes (!), and is response per unit of (selection intensity divided by gen. Int).]. The biggest red circle is where the index takes us. There is only a small compromise after crossing diversely selected lines about that general direction. However there is a big compromise if our general direction was with the favourable correlation.

Targeting breeding objectives (for beginners only)

Once relative economic weights have been calculated, we can use them to drive breeding programs in an appropriate direction. This can be done at a simple level for decisions on breeds and crosses to farm. However, for selection programs the process is more complex. This complexity arises from the flexibility that we need in order to use information from a range of traits, including traits not included in the breeding objective, and a range of different relatives.

> **Criterion and objective traits:** Traits such as scrotal circumference are *criterion traits* - they are used as judgement criteria to help rank animals, and are of no economic importance in their own right. However, this ranking is constructed in the best way to select animals on *breeding objective traits*, such

as female fertility. It is the correlations between the two sets of traits that makes the *selection index* system work well.

Pedigree information gives higher selection accuracy: We want to select animals with the best genes because they will leave the best progeny. Relatives share some of their genes – for example full sibs (which share the same father and mother) share half their genes in common (see Figure 8). This means that how well an animal's relatives perform tells us something about the quality of that animal's own genes. BLUP manages to balance the information from relatives to make the best estimates of breeding value (EBV).
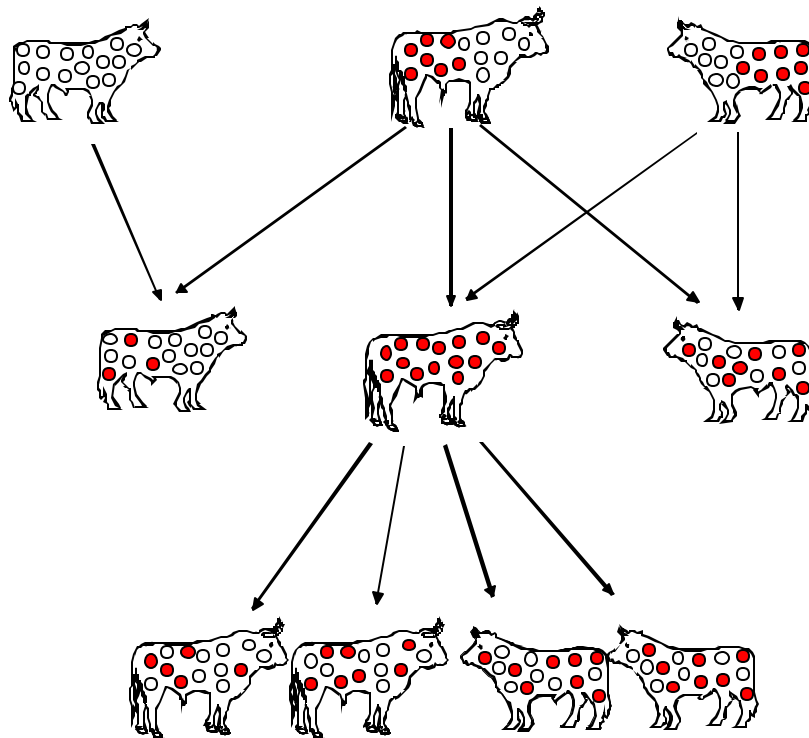
Figure 8.. The bull in the middle of this pedigree shares his genes with his relatives (shaded circles represent the genes which the bull carries). So the performance of these relatives helps us to estimate the value of his genes. The more distant the relationship, the lower the proportion of genes shared.

Selection index

The selection index is a simple method to integrate information from different traits and different relatives. This section briefly illustrates the extension to handling multiple traits.

As described for a single trait in lecture notes, EBV = heritability * phenotypic deviation, or $\hat{A} = h^2 P$ in trait units, or $a\hat{A} = ah^2 P$ in dollar units, where a is the economic weight of the single trait. Thus the overall weighting factor on phenotype is ah^2, and by extension for multiple traits, the selection index is $\hat{A}_\$ = a_1 h_1^2 P_1 + a_2 h_2^2 P_2 + ...$ for traits 1, 2 etc. However, this is only true where traits are uncorrelated with each other, and the breeding objective traits are the same as the measured criterion traits (the difference between these is described above). These factors can be accommodated by calculating appropriate index weights $b_1, b_2 ...$ etc., and this is illustrated here by analogy with the simple single trait case:

For a single trait: $\quad b \quad = \quad\quad h^2 \quad\quad\quad a$

$$b \quad = \quad \frac{Cov_{AP}}{V_P} \quad\quad a$$

$$b \quad = \quad Cov_{PP}^{-1} \ Cov_{PA} \quad\quad a$$

For multi-trait: $\quad \mathbf{b} \ = \ \mathbf{P^{-1}} \quad\quad \mathbf{G} \quad\quad \mathbf{a}$

- where $\mathbf{b}$ is the vector of weights $b_1, b_2 ...$ etc., which are used to calculate the selection index for animal i as follows: $\hat{A}_{\$_i} = b_1 P_{1_i} + b_2 P_{2_i} + ...$ $\mathbf{P}$ is the (co)variance of all criterion traits, $\mathbf{G}$ is the covariance matrix of criterion traits with breeding values for objective traits, and $\mathbf{a}$ is the vector of economic weights for objective traits. The traits in $\mathbf{b}$ can be totally different from the traits in $\mathbf{a}$, and their can be different numbers of traits in $\mathbf{b}$ and $\mathbf{a}$.

This selection index framework can be used to accommodate information from relatives, as outlined in lecture notes, and detailed in Brascamp (1984). However, Best Linear Unbiased Prediction of breeding values is more flexible and powerful than classical selection index, and software for its implementation has become widely available.

Multi-trait BLUP

The extension from single-trait BLUP to multi-trait BLUP is conceptually simple. The model is unchanged, $\mathbf{Y} = \mathbf{Xb} + \mathbf{Zu} + \mathbf{e}$, where $\mathbf{Y}$ now includes observations on all traits recorded for each individual, $\mathbf{b}$ includes fixed effects for all traits, and $\mathbf{u}$ contains a breeding value for each trait for each individual.

The mixed model equations now involve genetic and environmental correlations. The result includes EBV's (or $\hat{A}$'s) for the each of the traits fitted - which can include both measured criterion traits and breeding objective traits, even if there is missing information on the latter. The breeder only needs to weight EBV's for the objective traits by their economic weights to provide an index which s/he can select on: Index $= a_1\hat{A}_1 + a_2\hat{A}_2 + a_3\hat{A}_3 + ...$. The index is itself an EBV - an estimate of breeding value for economic merit.

Unscored traits

In many cases, EBV's from selection index or BLUP analyses must compete with unscored traits such as body conformation, leg weakness and pigmented fibres. This is not ideal. If these other traits have economic significance, they should be scored and included in the breeding objective and genetic evaluation steps. Not only will this give some 'economic balance', but it provides the framework to use information from correlated traits and information from candidates' relatives to speed up favourable genetic change for these traits.

Desired Outcome s - Total Genetic Resource Management

Breeding program design can be pre-determined and implemented through sets of rules, or it can emerge as a consequence of decisions made at the level of individual matings. This latter approach is the tactical approach, with decisions made tactically in the face of prevailing animals and other resources.

This approach lends itself to "Desired Outcomes". This is because any one solution is a set of actions – for which we can predict the outcomes – genetic merit of progeny, cost of semen purchse, number of mating paddocks required, etc.

Tactical implementation of breeding programs provides a practical means to integrate technical, logistical and cost issues facing animal breeders. Moreover, tactical implementation benefits from opportunistic use of prevailing animals and other resources, resulting in better outcomes.

In any breeding operation, there is an almost infinite range of actions that can be made, involving decisions on issues such as animal selection, semen collection and purchase, and mate allocations. Each set of actions is predicted to have a given utility to the breeder - based on factors such as genetic gains, risk, costs and constraints satisfied. The tactical approach described in this section works by searching across all these possible routes ahead, and finding the one that is predicted to best suit the breeder's needs. This has only recently become possible because of development of efficient computing algorithms that mimic evolutionary processes to find the best solution.

The animal breeder must juggle many issues when s/he makes decisions resulting in implementation of the breeding program, including concerns about breeding objectives, genetic gains, crossbreeding, inbreeding, logistical constraints, and various types of operational cost.

One approach to solving these problems is to follow sets of rules recommended by geneticists and other practitioners. However, such rules are derived from generalised theories and concepts - and these are usually not well integrated with each other. For example, theories and rules about

selection, crossbreeding and inbreeding have been developed largely in isolation from each other, such that it is difficult to mix them in real applications, and we are likely to miss the best overall strategy.

Mate Selection is an approach that can be used both to integrate all the key issues facing animal breeders, and to implement the program tactically. A simple example involving selection, crossbreeding and running costs is given eg in Kinghorn et al. (2000). Mate selection incorporates decisions on animal selection and mate allocation. Because the best animals to select depends on pattern of mate allocation, and vice versa, we can best make these decisions simultaneously as mate selection - we just decide what mating pairs and groups to make.

Moreover, there can be added advantage in making decisions tactically, rather than following a pre-set strategy. This is because a tactical approach will make use of knowledge of the full range of actual animals available for breeding at the time of decision making, as well as other factors such as availability of mating paddocks, current costs of specified semen, current quarantine restrictions on animal migration, current or projected market prices, etc. Tactical implementation of breeding programs gives the power to capitalise on prevailing opportunities - opportunities that would often be missed when adhering to a set of rules.

The Mate Selection Index (MSI)

The MSI quantifies the value to the breeder of matings made. It is in fact equivalent to the objective function of Kinghorn and Shepherd (1994).

In some cases, the consequences of a particular mating might be simple and quantifiable. For example, if the predicted merit of progeny from a mating is, say, 310Kg yearling weight, or +$12 in breeding objective units, then either of these figures constitutes an MSI *for that mating*. This can be done because the value of a mating in such a scheme is independent from what other matings might be made. However, in most progressive programs this is not the case - the value of a mating depends on what other matings are actually going to be made. For example, the value of a mating using a 'new blood' imported sire to help reduce inbreeding depends on how many other matings will be made using sires from the same outside source.

This means that for most applications the MSI cannot be specified at the level of individual matings - we can only calculate an overall MSI that characterises the combined value of all matings in the mating set. Examples of such an MSI are given by Kinghorn (1998), Shepherd and Kinghorn (1998) and Kinghorn *et al.* (1999), and a further example will be given later in this paper.

Implementation of Mate Selection

The mate selection approach to breeding is driven by specifying desired outcomes. An outline of the approach is shown in figure 9. For each mating set tested, the component outcomes evaluated constitute the overall Mate

Selection Index (MSI). Each component must be evaluated on the same scale, typically the scale of the breeding objective in units of, for example, dollars profit per breeding cow per year. The MSI can be set to an arbitrarily low and uncompetitive value for mating sets that break a constraint - for example mating sets that imply migration against a hard quarantine barrier, or greater use of liquid funds than a limit specified by the breeder or group.

Figure 9. An outline for implementation of a mate selection index. The set of matings shown is an hypothetical test mating set. The matings specified imply the need for collection of semen, etc., as shown. The mating set is evaluated for all components in the MSI.
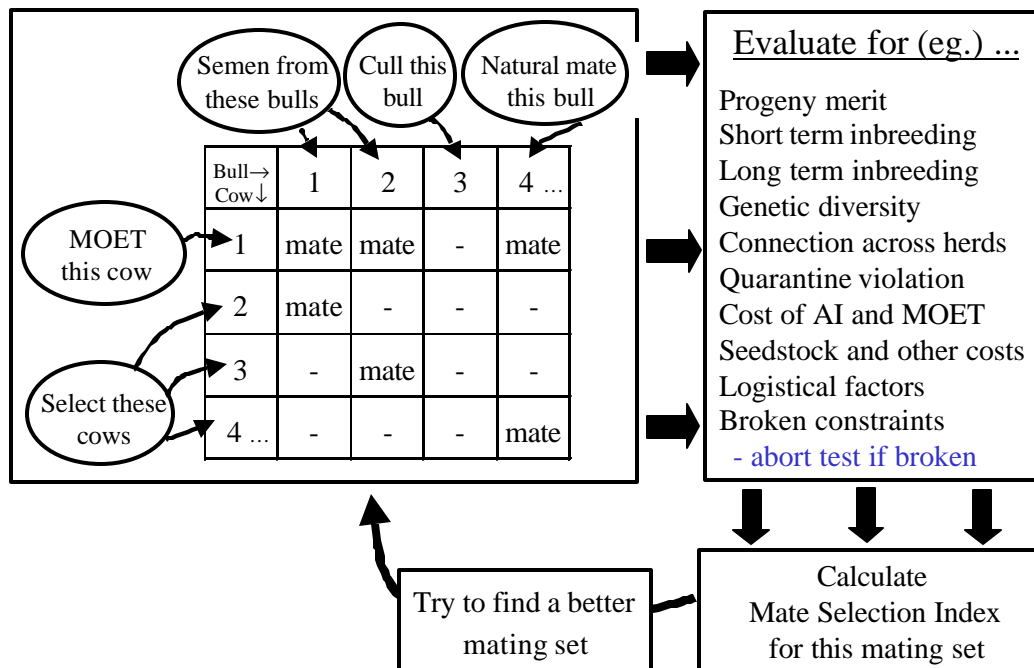
An efficient algorithm for finding the best mating set is required. The computing challenge is to find the mating set that gives the best MSI. For this purpose, an evolutionary algorithm was developed (Kinghorn 1998), based on Differential Evolution (Price and Storn 1997).

An Example Mate Selection Index

The following example MSI pays attention to genetic gain, long-term inbreeding, short-term inbreeding, crossbreeding effects, running costs and logistical constraints. This section is included for completeness. It adds little in concept to what is shown in figure 1, and so this section can be skipped by those not wanting to know more about the nuts and bolts of an MSI.

For any given mate selection set (list of matings to be made):

$$\text{MSI} = \frac{x'G}{2M} + \mathbf{1}\frac{x'Ax}{4M^2} + \mathbf{f}F + \mathbf{c}C - \cos t \qquad \text{when no logistical constraint is broken, or}$$

> MSI = a very low value when a logistical constrain is broken. This low value is sufficienly low to ensure that the mating set is not the solution of the mate selection algorithm.

- *M* is the total number of matings to be made. This is typically the number of breeding females, unless MOET or some other form of reproductive boosting is to be an option, whence some breeding females will effectively be mated more than once.

- *x* is a vector of number of matings to be made for each candidate, over both sexes. These numbers are the same as 'number of uses' in table 1. Thus, for each sex of candidate, the elements of *x* are restricted to sum to the total number of matings to be made, giving a total sum of 2*M* for the elements of *x*. Meuwissen (1997) and Grundy et al. (1999) treat elements of *x* as proportional contributions, with *x* restricted to sum to ½ for each sex of candidates. However, using number of matings as elements of *x* is useful for practical application of selection and mate allocation. The difference is handled by dividing by 2M for each instance of *x* in the MSI. Restrictions on the maximum value of each element of *x* are made as described later. Vector *x* could also be extended to accommodate predicted future contributions from existing juveniles and adults, following Meuwissen and Sonesson (1998) or Grundy et al. (1999).

- *G* is a vector of selection index values for candidates based on multi-trait EBV's, typically in dollar units.

- $\frac{x'G}{2M}$ is the weighted mean EBV of selected parents - it is in fact an estimate of the mean genetic value of progeny arising from the mating set.

- *1* is a weighting factor on mean coancestory for selected parents (see next item). *1* is typically negative, to discourage low effective population sizes. Meuwissen (1997) calculates *1* to give a constrained value of *x'Ax*. However, different values of *1* can be chosen, effectively giving different index weights on genetic gain (1) and long-term inbreeding (*1*), to give a range of results for these two factors, as shown in figure 3.

- *A* is the numerator relationship matrix for candidates.

- $\dfrac{x'Ax}{4M^2}$ is the weighted mean coancestry of selected parents. This reflects long-term inbreeding, reliability of predicted selection response, and risk of poor response achieved. Just as the numerator relationship between two animals is twice the inbreeding predicted in their progeny, this value is equivalent to half the rate of inbreeding, ½Δ*F*.

- *f* is a weighting factor on predicted progeny mean inbreeding coefficient. A small value for *f* is often sufficient to have a notable effect to reduce progeny inbreeding. This can also be true even when there are competing mate allocation issues in the MSI. Higher values of *f* will affect which animals are selected, as well as mate allocation (Kinghorn et al., 1999).

- *F* is predicted progeny mean inbreeding coefficient for the mating set under consideration.

- χ is a weighting factor on predicted progeny mean crossbreeding value *C*. A sensible value for χ is 1 - this is the implied weight on the genetic gain component $\dfrac{x'G}{2M}$, and both these components have direct effects on progeny merit, making them of equal importance if merit of later descendants does not feature in the objective.

- *C* is predicted progeny crossbreeding value - the value predicted using information on breed genotype alone. This is typically predicted using a dominance model of heterosis, incorporating direct and maternal components of both additive and dominance effects. Use of χ*C* aims just one generation ahead. A more involved approach is required in order to aim further ahead (Shepherd and Kinghorn, 1999), making investment matings (eg. to generate first cross females) as well as realisation matings (eg. terminal sire by first cross female). If χ*C* is included in the MSI then EBVs in *G* should be net of breed genotype effects, to avoid double counting of these effects.

- *cost* is the cost of the mating policy implied by *x.* This can include costs of AI and MOET. It can be calculated to discourage solutions that, for example, nominate allocation of just a few females to a natural mating male, as well as giving both genetic and economic consideration to use of reproductive manipulation. Figure 10 gives a simple example for females. In one mode of operation, the price of reproductive techniques used to drive figure 2 can be decreased until reproductive technology starts to feature in the best mating set, and this illustrates a break-even price for use of that technology. *cost* can include other components such as seedstock purchase prices and transport costs, expressed in the same units as the dollar EBV's in *G*.

Other MSI components not in this example include penalties on variation in progeny trait expression, attention to connection between flocks and optimising QTL expression in progeny.

Figure 10 An illustration of one way to formulate costs for female matings. Calculated costs are summed over all candidates, of both sexes, to contribute to the component *cost* in the MSI.
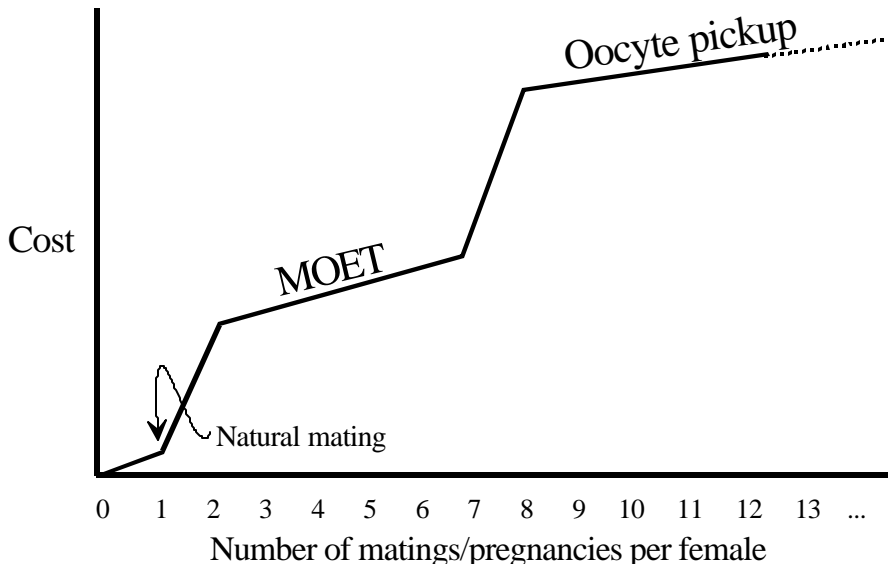

Logistical constraints are simply applied by examining each contending mating set and applying an MSI value of low value, or an overriding penalty, if any constraint is broken. A related strategy is to apply a moderate penalty - this means that matings sets that break a constraint but are otherwise of high merit can contribute to finding the best solution. However, the penalty must be applied in such a manner that the final solution contains no broken constraints. Here are some example constraints:

- Nominated maximum number of matings for each candidate. This might be, for example, 40 matings for males that cannot have semen taken from them, 1000 for males that can have semen taken, 1 for females that cannot enter a MOET program and 8 for females that can. The figure for dead males might be the number of semen doses available. Minimum numbers can also been set, where a minimum number of semen doses per animal must be purchased. Of course zero is an accepted value in such cases.

- Migration constraints include not permitting young rams to migrate from flock of birth, and restricting older natural mating rams to be used in just one flock alone. Quarantine barriers can also set set in a simple manner.

- Any factor in the MSI can be included as a constraint instead of an index component. For example, long-term inbreeding can be included as a constraint by using a simplified MSI, (MSI =

$$\frac{x'G}{2M} + fF + cC - \cos t)$$ and penalising any mating set for which $\frac{x'Ax}{4M^2}$

= ½ΔF exceeds a predetermined value. For example, to constrain ΔF to 0.02 per generation, this value should be set at ½ times 0.02 equals 0.01.

To calculate optimal values for MSI index weights χ, ϕ and λ would be a complex undertaking. However, these can be manipulated to give a desire outcome. An example of this is shown in figure 11, where λ is varied in order to give a frontier of outcomes for genetic gain and long-term inbreeding. (see also ' Dynamic control of desired outcomes, below).

Figure 11. Plot of predicted progeny merit (EBV Index) against mean predicted long-term inbreeding per generation, for 13 alternative mate selection sets generated by using 13 values of *l*. The chosen solution is circled.
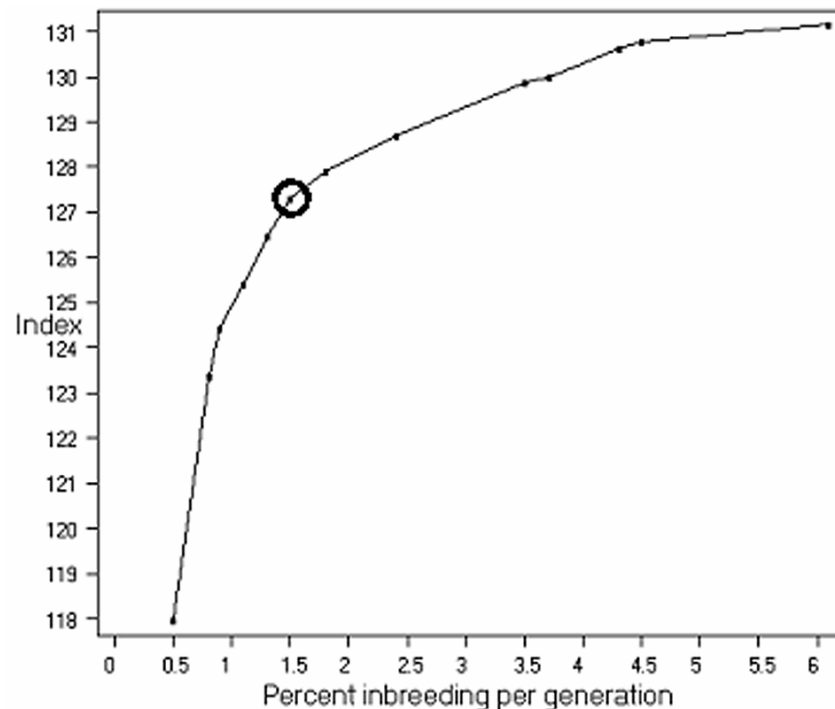
Application of the Mate Selection Approach

The mate selection approach outlined here has been implemented as Total Genetic Resource Management (TGRM, trademarked to LAMBPLAN). Information to implement TGRM includes parameters that describe conditions and desires, and data on animals.

Parameters that Describe Conditions and Desires

These currently include:

- Number of matings to be made, across all breeding units in the analysis
- Whether costs are to be applied
- Information on costs
- MSI weights

Plus, as required:

- Direct and maternal breed and heterosis effects
- Effects of know quantitative trait genes
- Mating contraints
- Constraints to be applied to trait expression
- Any other constraints

Data on Animals

If possible, pedigree data should be extensive, including all relatives of all animals that are candidates for breeding. This helps when calculating the numerator relationships among candidates. Pedigree data are simply animal's ID, sire's ID and dam's ID for each animal, with 0 or * entered for unknown parents.

Additional fields should be filled in for animals that are potential candidates for breeding. These fields must include:

- Sex of the animal. This is required in order to separate male and female candidates.

- EBV of the animal, or some other criterion of genetic merit. This is usually the multi-trait EBV calculated from a BLUP run followed by application of economic weights.

- Candidate status of the animal. This is the maximum number of matings that can be made by the animal, and reflects natural mating versus use of reproductive boosting (AI, MOET etc.). Values are typically higher for males (25 to 1000+) than for females (1 to 8+). Candidate status defines a limit, and does not mean that the animal will automatically be used for that number of matings.

Other information on each animal can be included as required, for example:

- Information on individual traits, in order to place restrictions on progeny expression of these traits, or simply to report expected outcomes in terms of these individual traits.

- Information on breed genotype of the animal, in order to accommodate crossbreeding effects.

- Information on the animal's genetic markers for known quantitative trait loci.

Output and Reporting

The mean value of key variables for the chosen mating set is reported, such as predicted genetic merit of progeny, long-term rate of inbreeding, progeny inbreeding, progeny heterosis and program costs.

The sires selected are listed together with their number of matings and distribution of these matings across flocks/herds.

The part of the report to be acted on is the mating list. This lists the male and female to be used for each mating, together with predicted merit, inbreeding etc. for progeny from each mating. This mating list constitutes decisions on all the breeding issues addressed in the mate selection run.

Dynamic Control of Desired Outcomes
As the mate selection analysis is running it is possible to view key aspects of the currently best solution in a visual manner. This means showing predicted progeny trait merit, trait distributions, inbreeding, heterosis, costs and structural components, such as the pattern of use of sires over flocks, using real-time graphical output. The user can then change weighting factors and constraints during the analysis so that these outcomes change in desired directions. This approach will give great flexibility to learn about the potential outcomes and to optimally balance them, without having to rely on theoretical calculations about what weighting factors to be used *a priori*.

This approach is similar to the desired gains selection index approach, except that here the index (MSI) covers much more ground than selection alone.

Use Over Multiple Stages
It is possible to carry out mate selection runs to make culling decisions well before joining time. In this way it is possible to undertake, for example, relatively heavy culling by castrating males, at a relatively early stage, while accommodating concerns about (lack of) relevance of early measures of merit, inbreeding, cost savings, etc.

A separate run can be made well before mating for the purpose of identifying semen, embryos and seedstock to purchase. A later run for the main mating round will benefit from knowledge of purchases made and any change in the candidate status of other animals. A further run can be made to make backup mating decisions in the light of knowledge of which females did not conceive.

Getting the Most out of the Tactical Approach
The tactical approach to breeding is driven by specifying desired outcomes. Although mate selection analysis is a very powerful computing tool, the results that it gives are closely aligned to the 'outcome instructions' that it receives. This means that the breeder can have a high degree of control, not by specifying which animals should be selected, but by specifying desires in terms of direction of genetic change, maintenance of genetic diversity, limits in money spent, constrains to be satisfied etc.

Using the tactical approach is like driving a good car in a competitive race. We have control of the steering wheel, accelerator and brakes, and we can drive in a manner that is fast, yet safe, economical and in the proper direction. We no longer need to have our head under the bonnet, monitoring every piston beat, and missing opportunities to overtake or avoid crashes. To make the most of mate selection, we should let it monitor the piston beats, and give it good head to find the best way ahead. There is plenty of opportunity to do test laps of the circuit before committing to a decision - if it does something we do not like, we need to adjust the way we steer it, rather than getting out and pushing it round the track. Here are some examples of how we can give mate selection room to maneuver:

- Pre-culling of animals should be restricted to 'definite culls'. The mate selection approach will only use competitive animals, but benefits from a bigger pool of candidates.

- It is worth considering the numerical scoring of important visually classed traits. This will permit the use of information from relatives to make faster progress in these traits and monitor their genetic change. It also gives more opportunity to make corrective matings.

- Consider a wide range of outside sires. These can help increase gains, lower inbreeding levels, and provide connections to outside seedstock sources that will result in better gains in the longer term.

- Include all key costs. These can include costs of semen, transport, quarantine holding and even fencing for natural mating paddocks. Limits on finances available can also be set.

- Make flock size variable. By factoring in the cost of maintaining breeding females, flock size can be an outcome of the analysis. This can provide a way to give controlled reduction of flock size through periods of drought or financial hardship, with parallel accommodation of concerns about genetic gains, inbreeding, etc.

- Select sires for commercial units as well as breeding units. This is likely to work well in large enterprises in which the breeding objectives differ between commercial units. This means that the fate of stud males can be use in the stud, use in any one of several production units, or culled.

- There is potential for constraining outcomes. For example, it could be declared that all progeny should be expected to be below a given fat thickness or micron diameter.   This is most relevant to breeding operations in which the value of product is high.

- Drive outcomes using a production model.   Mate selection could usefully be driven by a dynamic production model, with each mating set evaluated on profit from the optimal production and processing pathway(s) for prospective progeny, as described below.

Exercise: Desired Gains using "DESIRE"

NOTE: This version of DESIRE and the examples below assume no information from relatives, and measurement on both sexes. Please do not make specific conclusions from your results!

We have found that some breeders spend time using TGRM Control Centre (http://tgrm.une.edu.au) to set the direction of genetic change for the traits in the breeding objective. This is essentially a Desired Gains approach. However, this can be done much more quickly with a simpler tool – module DESIRE in GENUP (http://www-personal.une.edu.au/~bkinghor/genup.htm). DESIRE is also available as a stand-alone program (http://www-personal.une.edu.au/~bkinghor/desire.htm). This prac uses a recently updated version that may not yet be posted at these sites.

Questions:

1) Run DESIRE. To get help at any stage, hit key F1 and read the help file. Click on the "Open" button to open Beef2.txt. This is a two-trait Beef example. You will find that with two traits the module is very similar in function to ELLIPSE. The initial economic weights are $5/Kg for Yearling Weight (YW) and -$20/mm for Backfat (BF). The right-most column shows predicted response per generation per unit of selection intensity. (Note: we will simply use "response" to mean "predicted response" from here.)

    i) Take a note of the predicted responses in these two traits at these initial economic weights. Would you be happy with these responses?

    ii) Would you be happy with these responses, given knowledge of the genetic changes that could be made? [Look at the graphical output – yellow ellipses show the bounds of possible responses for pairs of traits.]

    iii) If your population was too fat, and you wanted to reduce backfat by say 3.5mm in 10 years, then about where on the ellipse would you target? (Click on the ellipse to get different results Note that response, as in the last column, is given per unit of selection intensity, per generation.)

    iv) Is any reduced response in YW worth this change in direction?

    v) Note the percentage figure at the top left of the blue part of the window. This is the value of the current solution compared to what the original economic weights would yield. [You can check this figure for yourself: Calculate the value of both the original responses and these new responses, both calculations based on the initial economic weights.] Comment on your percentage figure. What is the correct course of action?

    vi) Is the shape of the yellow ellipse for these two traits favourable or antagonistic for genetic change? (Temporarily increase the magnitude of the genetic correlation to exaggerate the effect). Is the shape favourable or

unfavourable for changing the direction of response with little effect on "theoretical" economic gains?

2) Open Beef4.txt – this will add the traits Feed Intake (FI) and Weaning Rate (WR). Read the help file and/or ask a demonstrator if you need help. Take a note of the initial economic weights and responses (There is now a reset button to the left of the EconWt column that restores original values).

    i) Looking at the initial results, note the extent to which each trait realizes its most favourable possible genetic change (take care – for two of these traits, small is usually good). Discover whether it is possible to make only small compromises in the 'best placed' trait while making sizable improvements in response for other traits. [Hitting 'Reset' restores original economic weights.] You could test the effect of changing parameters (particularly genetic correlations) on your conclusions.

    ii) "Fix" your desired response for one trait and discover how this restricts the possible range of outcomes for other pairs of traits (Restricted by red ellipses rather than yellow ellipses). Be progressively more greedy in your desire for this trait, and note the increasing constraints on what can be done for other traits.

    iii) Try restricting one (or more) trait(s) to zero genetic change, while keeping the economic weights for other traits in their original proportion:

- Click the "Fix" box for your chosen trait(s), then enter 0 in the Desire column – but do not click on the screen except as follows ...

- Click anywhere on the Trait x Trait subgraph (this is just a diagonal line) – by doing this you are not invoking a desired gain for any of the other traits.

- Note that the *relative* economic weights for the other traits have not changed.

- Note the percentage economic response and comment on the results.

    iv) Use the program to help find what outcomes are possible, then arrive at a set of responses that you feel happiest with.

    v) Evaluate these responses using the initial economic weights, and compare the result with that for the initial responses based on these economic weights. [This is now possible by simply looking at the percentage figure at the top left of the blue part of the window.] Comment on the result.

Exercise: Mate Selection using "TGRM"

In this practical we hope to have you running the TGRM Control Centre to drive the breeding decisions for an example real scenario - deciding on mate selection for a single mating period.

This will give you some experience in making selection and mating decisions driven by concerns for both gain and inbreeding.

Setup:

a) If you do not have TGRM Control Center installed on your computer, ask a demonstrator for help, or go to http://tgrm.une.edu.au/ccws/ and follow instructions.

b) Run TGRM Control Center with username and password both being "demo".

c) Enter Data ID as 0017 and click Set. This is an Angus cattle data set used for demonstration.

d) Use any Run ID that works (a separate RunID is needed for each person simultaneously accessing the same dataset).

e) Click "Edit Fixed" to see the parameters that are fixed for the duration of your run. It is possible to change these at this stage, but this is not recommended for this practical. Click "Set" to accept the current parameters.

f) You will now see the TGRM toolbar and some window that you will have seen in a demonstrated to you. Click to send the initial parameters to the TGRM server, then click in order to start your run.

g) Click "OK" in the New Frontier box, and you will see a frontier for the boundary of possible combinations of genetic gain and inbreeding rate, as described in your lectures or notes.

h) At any stage you can click and follow instructions to see your mating list and summary statistics.

Suggested investigations:

You should find that once you are familiar with the TGRM Control Centre, you will follow lines of investigation of your own accord. However, to get you going, here are some suggestions.

1. Set the TargetDegrees at (or very close to) 90 degrees. You can do this by clicking on the "Progeny Index vs Inbreeding Rate" window, or, for exactly 90

degrees, by entering 90 directly in the "Inbreeding" window. This puts maximal emphasis on reducing the rate of inbreeding. Look at the "Use" of sires in the table at the bottom of the main window. Why does a minimum co-ancestry solution, with little or no emphasis on genetic gain, generally not make equal use of sires?

2. Observe the frontier genetic gain versus co-ancestry. If you were a breeder, where would you want to be on this graph? Why? What are the key issues to consider? Try and achieve a mating set solution that is close to your aims.

3. Test the effect on limits that can be reached with reproductive technologies to boost female fecundity: Click the "Frontiers" button, and create a new frontier for which the "Maxuse" constraint on females in unticked.   Can this technology help genetic diversity as well as genetic gain? You can remove this new frontier graph by opening the "Frontiers" window again and unclicking the "Show" button for this new frontier.

4. Now try imposing some constraints, and see what effect this has on overall genetic gain (progeny index) and long-term inbreeding (coancestry).   For example, impose some limits on predicted progeny EBV, and/or impose greater or less use of certain sires. (You can see progeny predicted genetic merit distributions by clicking on the "Hist" checkboxes in the "Trait Constraints" window).

5. Imagine that you are a bull breeder wanting to breed bulls for two sets of customers – one wanting lighter 600-day weight EBV bulls and the other wanting heavier bulls. Try to manipulate the predicted progeny EBV distribution for 600-day weight to give a suitable outcome. [Hint – 'optimising' a trait (with a given positive emphasis or weighting) tends to make a narrower distribution.]

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