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Chapter 4

Optimising selection systems

4.1 Introduction

Chapter 3 documented the development of the Sugarcane Selection Simulation Model (SSSM) and it showed its accuracy in representing the selection system from the Burdekin breeding region. However, using this tool to identify an optimal selection system would require testing all possible combinations of selection system design variables (Section 1.1.2) and identify the those that maximise the $\widetilde{G}$ value for any given cost limitation. As there are a large number of possible combinations of selection variables, this would require large amount of CPU time and memory. Thus, the optimisation algorithm ASSSO (Algorithm for Sugarcane Selection System Optimisation) which, is a combination of dynamic programming and branch-and-bound optimisation techniques was developed.

To document the development of the ASSSO, Section 4.2 discusses reasons for choosing branch-and-bound and dynamic programming to optimise the sugarcane selection system. Section 4.3 formulates the problem, through redefining the selection variables for the optimisation problem (Section 4.3.1) as well as giving the scope of the decision variables used for the optimisation of the simulation model. Section 4.3.2 details all the optimisation constraints. Next the general approach used in applying branch-and-bound and dynamic programming is described (Section 4.4). The upper bound is defined in Section 4.4.1. The reasoning behind the choice of the budget and total number of nodes to be branched limits used in optimisation are given in Section 4.4.2.

4.2 Optimisation techniques used in the study

The most obvious way to solve the sugarcane selection combinatorial optimisation problem would be an exhaustive search or complete enumeration. This is achieved by testing all possible combinations of selection variables (Section 1.1.2) using the SSSM, and choosing the one that yields the highest $\widetilde{G}$. However, this method would require large amount of CPU time and memory. If clonal selection was used, the number of stages n was four, and the set of all possible values each variable could take was limited to five, there would still be twenty one decision variables: starting number of genotypes k, four plot sizes, four site numbers, four number of replicates per site, four selection intensities, four selection indices. Thus, there would be $21^5 = 4{,}084{,}101$ possible selection system designs, not necessarily all feasible. If it takes 5 minutes to perform one hundred simulations for a selection system, it would be unpractical to test all the feasible combinations of selection variables using the SSSM. Alternatively one or a combination of optimisation techniques could be applied, whether conventional or heuristic.

Because most decision variables in designing sugarcane selection systems have integer restrictions set upon them (eg. number of sites, replicates, plot size), the problem belongs to the family of integer programming problems. Branch-and-bound methods are often used to solve the integer programming problems. It is a process of moving (branching) from one alternative solution (node) to another according to the magnitude of the objective function they yield. Branch-and-bound has been successfully applied to many optimisation problems, like the scheduling problem (Vasko *et al*, 1993; Hax and Candea, 1984 and Baker, 1974) or the travelling salesman problem (Wagner, 1975), and is the most efficient method for solving the combinatorial optimisation problem (Nemahuser and Wolsey, 1988).

The variables that completely describe the decisions to be made are called the decision variables. In the case of selection system optimisation the decisions to be made are how many stages selection should be comprised of, planting design for each stage as well as selection criteria and intensity at each stage. Thus, selection variables (Section 1.1.2) are the decision variables. A function of the decision variables to be optimised ie minimised or maximised is called the objective function. In the case of selection system optimisation, the genetic gain for economic value $\widetilde{G}$ is the objective function. However, it can not be computed from the decision variables. Thus the objective function in this case is not a function of the problems' decision variables. Hence, unlike a typical optimisation problem, instead of optimising a function of the decision variable given a set of variables such as population size and number of stages, the variables themselves are the decision variables.

Furthermore, the number of decision variables is a decision variable itself. To overcome this, branch-and-bound could be applied to optimise each stage independently. However, the selection system that comprises of the stages, each optimised independently, is not necessarily the optimal selection system itself. Thus, another optimisation technique was required to optimise across selection stages.

The optimisation problem is said to be "multistage" if it can be divided into stages, at each of which a decision is to be made that affects the objective function of the whole system (Mitten and Nemhauser, 1963). The problem of optimising sugarcane selection system is therefore, a multistage optimisation problem. Furthermore, there are a number of observed characteristics of the sugarcane selection optimisation problem:

(1) the problem consists of stages;
(2) at each stage there is a number of possible combinations of selection variables (alternatives) that can be chosen;
(3) at each stage a choice of selection variables has to be taken before proceeding to next stage;
(4) the choice of selection variables taken at any stage determines possible alternatives at following stages, as material available from a stage determines possible planting designs for the following stage, as well as the budget available for the next stage;
(5) the optimal combination of variables chosen at any stage does not depend on any previously reached combination of variables at that stage or any other stage;

(6) the population of genotypes selected at one stage is the starting population for the following stage thus, there is a connection (recursion) between stages.

The characteristics identified above are common to most applications of dynamic programming (Bellman and Dreyfus, 1962), which has singled out dynamic or multistage programming as the ideal primary candidate to optimise across selection stages.

Dynamic or multistage programming (Bellman, 1957) could be used to link stages together and ensure the optimality of the solution to the entire problem, thus ensuring the coherence of the solution. It is a technique designed for numerically solving multistage decision problems (Bellman and Dreyfus, 1962). Problems are solved in stages with stages being linked together with the recursive computations, that ensures the optimality of the solution to the entire problem. Being a multistage problem, dynamic programming could thus be used to optimise the sugarcane selection system.

4.3 Formulation of the selection system optimisation problem

Each stage z could be in a number of alternative states A_z, where a state defines a combination of selection variables. Accordingly, the overall selection system could be in a number of alternative states A depending on the combination of states A_z chosen for each stage $z = 1,2,3,..,n$.

The number of decision variables depends not only on the number of stages but on whether family selection is used in stage one or not. If family selection is used the decision variables could be represented in a vector form below:

$$(f,k,p_1,s_1,r_1,t_1,d_1,t_2,d_2,p_3,s_3,r_3,t_3,d_3,...,p_n,s_n,r_n,t_n,d_n) \qquad (4.1)$$

where f is the number of families at stage one, k the number of genotypes per family, and subscripts represent the stage of selection, where n is the total number of stages in the system. At a stage *z*, p_z is the number of rows in the p_z rows plot, s_z the number of sites, r_z is the number of replicates per site, t_z the selection intensity and d_z the selection index. Note that in order to represent the selection system mathematically, the second part of the stage one, when genotypes are selected from within families is considered as an independent stage ie stage two. Since in this stage, entire families are re-grown only two variables need to be identified: selection intensity t_2 and selection index d_2.

If family selection is not used the vector representing the decision variables becomes:

$$(k,0,1,1,t_1,d_1,p_2,s_2,r_2,t_2,d_2,p_3,s_3,r_3,t_3,d_3,...,p_n,s_n,r_n,t_n,d_n) \qquad (4.2)$$

where k is the starting number of genotypes, and all other variables are as explained above. Note that in stage one only one replicate of a single seedling can be planted on one site thus only selection intensity t_1 and selection index d_1 need to be identified.

Let $\widetilde{G}_z$ be the gain obtained through stages $1,2,3,..,z$. $\widetilde{G}_z$ depends on the population of genotypes P_{z-1} selected through stages $1,2,3,...z-1$. The alternative A_z to be used at stage z depends on the cost of previous $z-1$ stages $\overline{C}_{z-1}$, as well as on planting material available from the previous stage $\breve{M}_{z-1}$. The optimisation objective function could thus be written as:

$$\widetilde{G}_z = \max\{\widetilde{G}(P_{z-1}, A_z(\breve{M}_{z-1}, \overline{C}_{z-1}))\} \qquad (4.3)$$

ie the genetic gain for economic value chosen at a stage z is the maximum $\widetilde{G}$ obtained when all possible combinations of variables (alternatives) A_z are exhausted, given planting material available from the previous stage $\breve{M}_{z-1}$ and the cost $\overline{C}_{z-1}$ of stages $1,2,3,...z-1$, as well as the population of genotypes P_{z-1} selected through stages $1,2,3,...z-1$. The recursion formula for the problem could be written as:

$$P_z = P_{z-1}(A_z(\breve{M}_{z-1}, \overline{C}_{z-1})) \tag{4.4}$$

ie when the population of genotypes selected at stage $z-1$ goes through the selection stage z defined with the alternative $A_z(\breve{M}_{z-1}, \overline{C}_{z-1})$, the population of genotypes selected at stage z was obtained.

4.3.1 Definition of the decision variables

Options that could be chosen for the plot size p_z in the SSSM are limited to the plot sizes for which corresponding variance components were estimated (Table 2.9). However, for all other selection variables (Section 1.1.2) any desired numerical value is possible. For example, selection intensity t_z can be 16.50% and selection index d_z can be defined as $5 \cdot CCS + 7 \cdot TCH$, or selection can start with 12,547 genotypes. Contrary to the SSSM, optimisation requires that the set of the possible options that selection variables (Section 1.1.2) can take be limited to a finite set of values, given below:

- starting population range for clonal selection was proposed by two experienced sugarcane breeders: Phillip Jackson (CSIRO) and Mike Cox (BSES), as the most realistic starting populations of genotypes and the one that is most likely capturing the optimal starting number of genotypes:
  $k \in \{4000, 6000, 8000, 10000, 15000, 20000, 25000, 30000\}$

- starting population range for the number of families as well as the number of genotypes per family were also proposed by the plant breeders and are as follows:
  $f \in \{50, 100, 200, 300, 400\}$ and $k \in \{20, 40, 60, 80, 100, 200\}$

- plot size for each stage $z = 1, 2, ..., n$, $p_z \in \{0, 1, 2, 4\}$, where zero represents single seedling, one represents one row plot (10 meters long), two represents two row plot (10 meters long) and four represents four row plot (10 meters long). Note that options available for the number of rows of plots as well as the plot length was limited by the plot sizes for which variance components were estimated (Section 2.4.1).

- number of sites for each stage $z = 1,2,...,n$, was limited to $s_z \in \{1,2,3,4,5,6\}$. Due to the costs associated, it is unpractical to plant genotypes in selection trials at more than six sites and/or six replicates per site.

- thus, number of replications per site for each stage $z = 1,2,...,n$, was also limited to $r_z \in \{1,2,3,4,5,6\}$

- selection intensity for each stage $z = 1,2,...,n$, proposed by the plant breeders was: $t_z \in \{5\%,10\%,15\%,20\%,25\%,30\%,35\%,40\%,45\%,50\%,60\%,70\%,80\%,90\%,100\%\}$, with more intensity options given when selecting fewer genotypes.

- in the SSSM, the selection index d_z was defined by $\alpha \cdot CCS + \beta \cdot TCH$ ie it was defined with two values α and β. However, for the optimisation it was redefined to be expressible by a single value ie to be of a form $CCS + \alpha \cdot TCH$. For example the selection index d_z that was originally defined by $16 \cdot CCS + 3 \cdot TCH$ can be written as $CCS + 3/16 \cdot TCH$ ie $CCS + 0.1875 \cdot TCH$.

Therefore, the single number that defines such selection index was 0.1875. As suggested by plant breeders, selection index should be based more heavily on CCS than on cane yield thus, the following set was chosen for the optimisation: $\{0,0.0625,0.125,0.1875,0.25,0.375,0.5,0.75,1,2\}$. This together with cane yield, sugar yield and visual selection gives the following set:

$$d_z \in \{TSH, TCH, CCS, CCS + 0.0625 \cdot TCH, CCS + 0.125 \cdot TCH, CCS + 0.1875 \cdot TCH,\\ CCS + 0.25 \cdot TCH, CCS + 0.375 \cdot TCH, CCS + 0.5 \cdot TCH, CCS + 0.75 \cdot TCH, CCS + TCH,\\ CCS + 2 \cdot TCH, visual\}$$

i.e.

$$d_z \in \{TSH, TCH, CCS, 16 \cdot CCS + TCH, 8 \cdot CCS + TCH, 16 \cdot CCS + 3 \cdot TCH,\\ 4 \cdot CCS + TCH, 8 \cdot CCS + 3 \cdot TCH, 2 \cdot CCS + TCH, 4 \cdot CCS + 3 \cdot TCH, CCS + TCH,\\ CCS + 2 \cdot TCH, visual\}$$

Note that the option to use the visual selection is only available when selecting genotypes from within families (Section 2.3.5). Having a finite number of feasible solutions the problem of optimising selection systems belongs to a combinatorial optimisation problem.

4.3.2 Constraints on the problem

There are four constraints imposed on the system by practical considerations: cost constraint, planting material constraints, a minimal requirement for the final stage testing and the selected population size constraints.

4.3.2.1 Cost constraint

The budget, $\overline{B}$ available to perform selection had to be shared between all the stages. Decisions about the selection variables used at a stage determines its cost. This in turn determines the amount of resources available to perform remaining stages thus limiting the combination of variables that could be used.

If $\overline{C}_z$ is the total cost of stages $1,2,3,...,z$ ie the budget allocated to perform stages $1,2,3,...,z$ and C_z the cost of stage *z*, then $\overline{C}_z = \overline{C}_{z-1} + C_z$. Cost of stage z, C_z depends on the combination of selection variables used at stage *z*, comprising costs of planting, growing, sampling, harvesting, processing, data analysis and finally administration fees, including labour, machinery and compensation costs to farmers whose land was used for the trial (Section 3.3.2). Furthermore, the combination of variables that could be used at stages $z+1$ to n depends on the cost C_z and subsequently on the total budget $\overline{B}$. Cost thus, provides the link between stages. Finally, the total budget, $\overline{B}$ can not be exceeded during selection, $\overline{C}_n \leq \overline{B}$.

4.3.2.2 Planting material constraint

The values that plot size p_z, number of sites s_z and replicates per site r_z could take at any stage z depend on the amount of planting material ie meters of cane available from the previous stage. Thus, at each stage how many meters of cane were required $\widehat{M}_z$ to plant the stage and the how many meters of cane were available $\breve{M}_{z-1}$ from the previous stage, needs to be calculated to establish whether there is enough planting material to perform the stage ie whether:

$$\widehat{M}_z \leq \breve{M}_{z-1} \tag{4.5}$$

Generally, one meter of row produces eight stalks, each two meter long. It was assumed that plot lengths are ten meters. Then, planting material ie meters of cane $\breve{M}_z$ available from a stage z to be used in stage $z+1$ is given with:

$$\breve{M}_z = 8 \cdot 2 \cdot 10 \cdot p_z \cdot s_z \cdot r_z = 160 \cdot p_z \cdot s_z \cdot r_z \tag{4.6}$$

where p_z, s_z, r_z, are as before, respectively plot size, number of sites and replicates used at a stage z.

The combination of variables used at a stage z defines how many meters of cane $\widehat{M}_z$ were required for that stage. Assume that each plot is ten meters long. The formula for the length of cane required could then be written as:

$$\widehat{M}_z = 10 \cdot p_z \cdot s_z \cdot r_z \tag{4.7}$$

There are further restrictions when planting stage one for both clonal and family selection. When clonal selection is practiced, the plot size for stage one is limited to single seedling ie genotype, with one site and one replicate, because there is only a single seedling available for each genotype following germination of seeds from crossing. When family selection is practiced, on the other hand, each family is represented with a number of single seedlings, determined by the genotypes per family variable f. Although other options can be used, plant breeders suggested that twenty be the appropriate number of genotypes per family to form a one-row plot. Assuming thus, that twenty genotypes from a family form one-row plot, f defines how many one row plots can be planted. This in turn defines planting combinations of plot size p_1, number of sites s_1, and number of replicates r_1. For example if $f = 80$, four one row plots are available for planting. Therefore, one of the following combinations of stage-one planting variables can be adopted:

1) one one-row plot replicated once on a site, $p_1 = 4, s_1 = 1, r_1 = 1$;
2) one two row plot replicated twice on a site, $p_1 = 2, s_1 = 1, r_1 = 2$;
3) one two row plot replicated once on two sites, $p_1 = 2, s_1 = 2, r_1 = 1$;
4) one one-row plot replicated four times on a site, $p_1 = 1, s_1 = 1, r_1 = 4$;
5) one one-row plot replicated once on four sites, $p_1 = 1, s_1 = 4, r_1 = 1$;
6) one one-row plot replicated twice on two sites, $p_1 = 1, s_1 = 2, r_1 = 2$.

4.3.2.3 Last stage testing constraint

Before proposing a genotype for commercial use, an industry requirement that is generally adhered to is that the genotype should have been evaluated at least at four sites, in at least four row plots, and with at least two replicates per site. Thus, more sites and replicates per site could be used throughout selection but at least once the resulting genotypes should be tested for their performance in four row plots, planted at minimum four sites and two replicates per site.

4.3.2.4 Population size constraint

Because genotypes selected through the proposed selection system need to be further tested for their ratoon performance and disease resistance, the requirement imposed within this study is to have at least ten genotypes selected at the end of the selection process. Let k be the starting population and k_z be the size of the population selected at stage z to entering stage $z+1$. Then $k_1 = k \cdot t_1$, where t_1 is the selection intensity at stage one and the recursive formulae for $z = 2,3,..,n$ is $k_z = k_{z-1} \cdot t_z$, $0 < t_z \leq 1$. Thus

$k_n = k_{n-1} \cdot t_k$, is the size of the population to result the selection program. Thus, $k_n = k \cdot t_1 \cdot t_2 \cdots t_k \geq 10$, or $k_n = k\prod_{z=1}^{n} t_z \geq 10$.

4.4 Application of dynamic programming and branch-and-bound to the selection system optimisation

For the selection problem, the dynamic programming optimises across stages, using the embedded branch-and-bound to optimise the selection variables (Section 1.1.2) within each stage. The nature of the dynamic programming is to partition the problem into smaller problems. Thus, the vector 4.1 ie 4.2, depending on whether family selection is used in stage one or not, can be observed as a number of vectors of smaller size, each defining a single stage of selection. For example, vector $(1000,0,1,1,50\%,TSH)$ defines a stage one of selection, vector $(1,1,1,30\%,TSH)$ defines stage two and vector $(2,2,1,10\%,TSH)$ defines stage three. Independently these vectors represent nodes for branch-and-bound method, and together they define the state of the selection system.

The branch-and-bound method therefore searches through each stage independently and identifies the stage vectors that yield the optimal $\widetilde{G}$ at the time. The stage vectors identified then give the state of the system on which dynamic programming performs. Dynamic programming uses the information from the state of the system and searches for the combination of stage vectors that yield the optimal $\widetilde{G}$ given all previous stages (Figure 4.1). Thus, if a selection system is a global problem and its stages local problems, then dynamic programming solves the global problem whereas branch-and-bound solves the associated local problems. Different stages influence one another in multiple ways. The most obvious connection is in the population of genotypes that passes from one stage to another as shown with the recursive formula 4.4. Similarly, resources used at a stage determine the amount of resources available for future stages.

The flow chart of the ASSSO for the family selection is given in Figure 4.1 with its pseudo code in Appendix D. The flow chart of the ASSSO for the clonal selection is similar to that of family selection. To start the optimisation process the total budget and

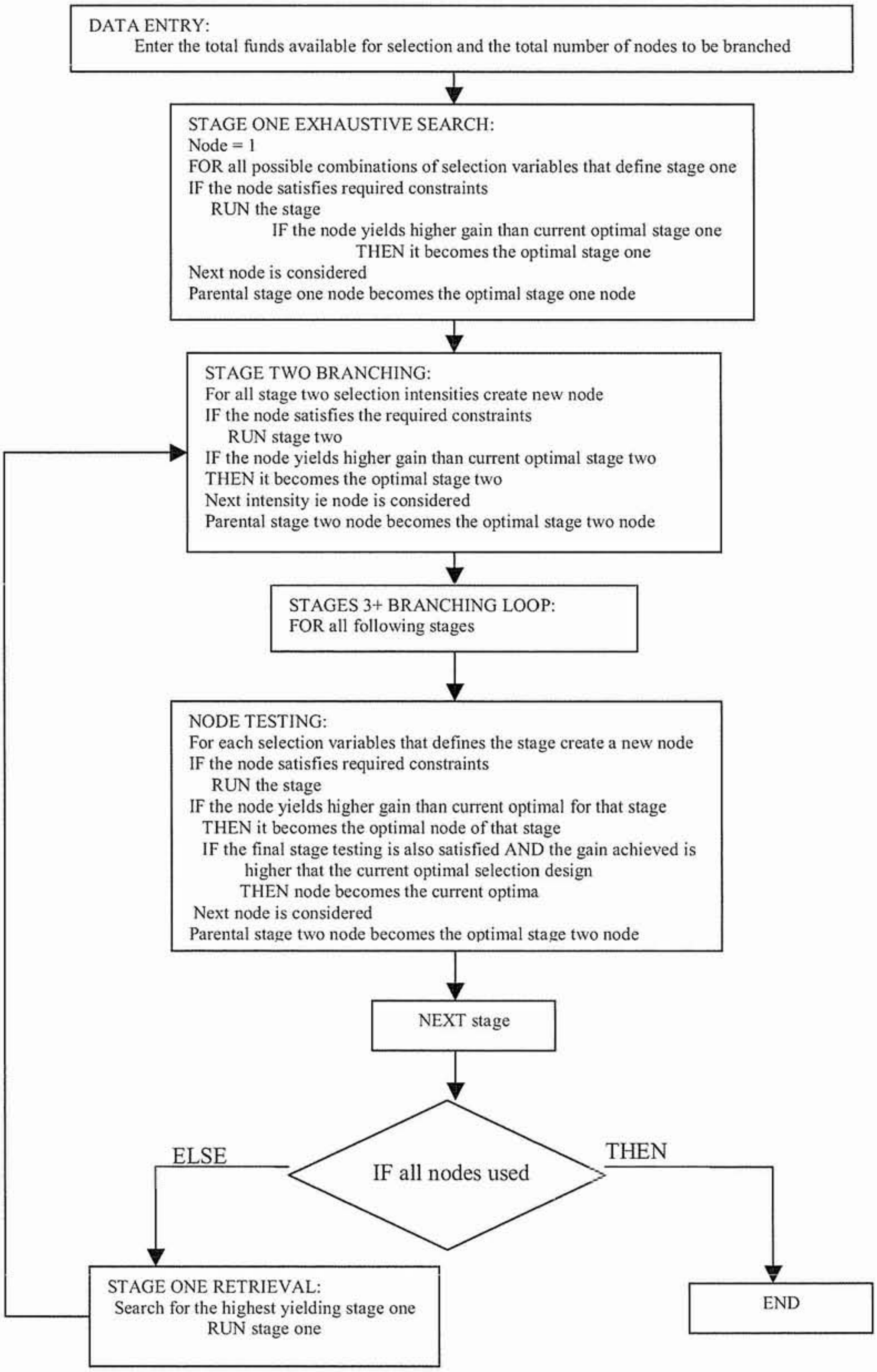

Figure 4.1: The flow-chart of the ASSSO for the family selection

the number of nodes to be branched need to be specified. With that information, the algorithm starts with testing all feasible combinations of stage-one selection variables (Section 1.1.2).

A combination of selection variables ie node is declared feasible and thus is performed using the SSSM if it satisfies relevant constraints (Section 4.3.2). If the gain it yields is greater then the current highest yielding stage-one node then it becomes the highest yielding stage one node. Once all feasible combinations have been tested, the information that defines the highest yielding stage-one node as well as all the populations of effects that define the genotypes selected through that stage were brought forward to stage two.

Given the stage-one definition brought forward and the population of genotypes, stage two performance was tested for all possible values of selection intensity. Note that at stage two of family selection genotypes were regrown thus planting design selection variables do not need to be branched for. Furthermore, only visual evaluation (Section 2.3.6) is available at this stage of selection, as there is no way to compare visual evaluation to other selection indices (Section 3.2.4). Thus, at stage two only selection intensities are branched for. The highest yielding stage-two node together with the population of genotypes it selects is brought forward to stage three.

In stage three, similar to all the stages that follow it, depth first branch-and-bound was performed to identify the highest yielding node. Given the particulars from stage-two and the population of genotypes selected at stage two, nodes three are branched for plot sizes. The highest yielding stage-three node identified while branching for different plot sizes that satisfies relevant constraints is then branched for the number of sites. The highest yielding node identified while branching for the number of sites that satisfies all relevant constraints is then branched for the number of replicates within each site and the process goes on until all selection variables have been branched for. Furthermore, if a node satisfies the final stage constraint (Section 4.3.2.4), it is compared to the current highest yielding selection system identified through the optimisation algorithm. At the beginning of the algorithm the gain to compare selection systems is set to $3372.86 (Section 3.4.1), the average performance of a typical selection system currently practiced in the Burdekin region (Section 1.1.1).

At the end of the stage-three branching, the particulars regarding the highest yielding stage-three node identified through branching and the population of genotypes selected from stage three are then brought forward to stage four and the process is repeated for stage four and five.

Once all stages have been branched, all stage one nodes are searched for the next highest yielding node that has not been branched, and the process is repeated until all stage-one nodes have been branched, after which stage-two, stage-three, four and five are branched. The process stops when the total number of nodes gets exhausted or there are no active nodes left to branch. Note that each node is simulated 100 times (Section 3.4.1) and compared to other nodes based on the gain obtained. Appendix E details a part of an optimisation storage file.

4.4.1 Definition of the upper bound

To save on time it takes to execute the ASSSO a mechanism was needed that identifies inferior nodes prior to their simulation and thus reduce the number of potentially active nodes. That mechanism was provided by an upper bound.

According to the definition of the genetic effect for economic value G_i of a genotype i (Section 3.3.1), its magnitude depends solely on its genetic values g_i for CCS and cane yield. The genetic values g_i, in turn are generated at the beginning of selection and stay the same throughout the selection (Section 3.2.3.2). Thus, the magnitude of the G_i for each genotype i can be computed at the beginning of selection and it also stays the same throughout the selection. Taking therefore, the starting population of genotypes and selecting $k\prod_{z=1}^{m} t_z$ genotypes based on their G_i rather than their phenotypic values gives the highest achievable gain $\widetilde{G}$ for a selection stage m and given the starting population of genotypes. Such genetic gain for economic value is the upper bound U_{m,P_0} for the selection stage m, given starting population P_0. If the computed U_{m,P_0} exceeds the currently highest yield $\tilde{G}$ for the stage m, it indicates that the selection stage has a potential to be superior to the current "optima", and thus the stage can be performed.

To illustrate the concept, assume that a stage-three node is being tested for its upper bound. Assume that the selection intensities for the three selection stages are $t_1 = 90\%, t_2 = 70\%, t_3 = 80\%$. Note that other particulars of the node could be omitted since the upper bound does not depend on them. Assume that there are six genotypes to start the selection (Table 4.1). Because only genetic values g_i for CCS and cane yield are needed to compute the genetic effect for economic value G_i, each genotype is defined by $\mu + g_i$ values. Assume that the highest gain $\tilde{G}$ achieved so far at stage three equals to \$702.80.

To calculate the upper bound U_{3,P_0} for the three stages, select three genotypes from the starting population of six ($6\prod_{z=1}^{3} t_z = 6 \cdot (0.90 \cdot 0.70 \cdot 0.80) = 3.024 \cong 3$) based on their G_i values. Genotypes 1,3 and 6 are thus, selected giving an average G_i value of \$3,515.21. The gain $\tilde{G}$ that these three genotypes yield is the upper bound U for this node and it equals to \$657.99 ($\overline{G}_{sel} - \overline{G}_{start}$ =\$3515.21-\$2857.22). The upper bound of \$657.99 is lower then the highest gain achieved so far for stage three of \$702.80, and subsequently there is no need to simulate this stage three, thus saving on computer time and memory.

Table 4.1

A sample of the computer generated population of genotype values for CCS and cane yield (TCH), expressed as the sum of $\mu + g_i$, where g_i is the genetic effect; their sugar yield (TSH) values; and genetic effect for economic value G_i for each genotype i

	CCS			TCH			TSH	
i	μ	g_i	$\mu + g_i$	μ	g_i	$\mu + g_i$		G_i
1	12	-1.49	10.51	150	7.29	157.29	16.52	\$3,377.41
2	12	-1.02	10.98	150	-16.09	133.91	14.70	\$1,957.23
3	12	0.34	12.34	150	20.15	170.15	20.99	\$3,570.89
4	12	0.79	12.79	150	-2.92	147.08	18.82	\$3,183.96
5	12	0.45	12.45	150	-17.14	132.86	16.54	\$2,617.47
6	12	0.87	12.87	150	10.06	160.06	20.61	\$3,597.33
							$\overline{x} =$	\$2,857.22

To prove that U is indeed the highest achievable genetic gain for economic value such a starting population can possibly yield, assume that there are three genotypes from the same starting population of genotypes that are yielding a higher $\widetilde{G}$. According to the definition of U and $\widetilde{G}$ this means that there are three genotypes such that $\frac{\sum_{i=1}^{3} G_i}{3} - \frac{\sum_{i=1}^{6} G_i}{6} > \$657.99$ ie $\frac{\sum_{i=1}^{3} G_i}{3} - \frac{\sum_{i=1}^{6} G_i}{6} > \frac{(G_1 + G_3 + G_6)}{3} - \frac{\sum_{i=1}^{6} G_i}{6}$, since 1, 3 and 6 are the three highest yielding genotypes. Manipulating the inequality, this means that $\frac{\sum_{i=1}^{3} G_i}{3} > \frac{(G_1 + G_3 + G_6)}{3} \Rightarrow \sum_{i=1}^{3} G_i > G_1 + G_3 + G_6$. This in turn means that there are some other three genotypes that yield higher G_i than genotypes 1, 3, and 6, which is a contradiction to the assumption that 1, 3, and 6 are the highest yielding ones. Therefore, U is the highest $\widetilde{G}$ such a starting population can possibly yield.

4.4.2 The budget and the comparison of the node limits

To execute the ASSSO: (1) the total capital available for selection, need to be entered by the user and (2) the number of nodes to be branched. According to the cost assumptions (Section 3.3.2), a typical selection system currently practiced in the Burdekin region (Section 1.1.2) costs \$231,292. Based on this, it was decided that a reasonable budget limit would be \$250,000. However, to avoid the situation in which a selection system that costs for example \$252,000 was discarded although it could have a $\widetilde{G}$ value that is superior to the current optima, a more generous budget limit of \$280,000 was used. By changing the budget limit one could investigate whether and how the budget makes a difference to what is a proposed optimal design.

To establish the sufficient number of nodes required for the ASSSO to reach the optima, a number of options were tested. A shorter version of the ASSSO that simulates each node only five times was run for each of the following node limits: 50,000; 100,000; 150,000 and 200,000. Table 4.2 records the node at which the highest yielding node was reached separately for family and clonal selection given the node limit.

Table 4.2

The total number of nodes branched together with the node number at which the highest yielding node was reached

	Highest yielding node reached	
Total nodes branched	Clonal selection	Family selection
50,000	30,120	25,004
100,000	66,024	59,262
150,000	89,198	58,194
200,000	91,552	83,142

For all options of node limits the highest yielding node was found within the first 100,000 nodes for both family and clonal selection. The limit of nodes to be branched was therefore, set at 100,000.

Chapter 5

Identifying an optimal selection system for the Burdekin region

5.1 Introduction

The optimisation algorithm ASSSO that is a combination of two optimisation techniques: dynamic programming and branch-and-bound, was described in Chapter 4. To illustrate how the combination of dynamic programming and branch-and-bound can be applied to solve the problem of designing efficient selection systems in breeding programs, the ASSSO was used in an attempt to maximise gains in the sugarcane selection system model (SSSM) within a set of constraints.

This chapter firstly details the hierarchical clustering and regression tree methods (Section 5.2) used to analyse the outputs of the ASSSO. It further defines the new selection system representation needed to allow the analyses of the optimisation results (Section 5.2.1). The three selection systems used in the comparison are given in Section 5.2.2. Sensitivity analysis of changing parameters is given in Section 5.3, with a general analysis of convergence was given in Section 5.4. Results were first (Section 5.5) compared to the three selection systems defined in Section 5.2.2. Results were then analysed to identify characteristics of a favourable selection system (Section 5.6). A comparison between individual and family selection is given in Section 5.7, and finally optimisation results were summarised proposing superior selection designs for the Burdekin region (Section 5.8).

5.2 Analysis methods used

Every time the ASSSO moves from one node to another it calls the SSSM to give it an estimate of the nodes performance. Because the performance of any selection strategy simulated on the SSSM depends on the randomly generated populations of effects that form the phenotypic values for CCS and cane yield, each node is simulated one hundred times (Section 3.4.1). By simulating 100 times each of the 100,000 (Section 4.4.3) nodes it further adds to the time required to run the algorithm, which took close to three months to evaluate only family selection optimisation part.

To utilise this long optimisation process to the fullest rather than obtaining one selection system design that yield maximal $\widetilde{G}$, a number of data files were stored throughout the ASSSO execution. Each of these files was used for different types of analysis. Some were used to analyse the optimisation process by investigating the distribution of $\widetilde{G}$ and follow the movement of the solution as the ASSSO progresses. Some were used to identify which selection systems, out of many, present a significant improvement to the selection system currently practiced in the Burdekin region (Section 1.1.1).

The information on all selection systems that satisfy the optimisation constraints (Section 4.3.2) and give a higher yield than the selection system currently used in the Burdekin region were stored. The information on the designs for those selection systems that are significantly improving the current practices, were collected. These were then analysed to give a better insight into any possible grouping of selection systems. Further analysis was performed to identify the most important decision points in achieving higher values for $\widetilde{G}$. The two methods used to analyse selection designs: hierarchical clustering (Seber, 1984) and regression tree method (Venables and Ripley, 1994) were explained below.

Hierarchical clustering was used to group different selection systems according to how similar they are to one another. By grouping selection systems it is possible to get a clearer picture of a typical selection system that yields higher $\widetilde{G}$. Furthermore, when applying the optimisation results to designing actual selection trials, by creating groups of similar selection systems, a greater freedom is given to the process of designing a selection system to be used in the region.

Hierarchical clustering attempts to identify relatively homogenous groups of selection systems based on selected characteristics. The clustering is given by the agglomerative schedule and can be displayed graphically by a tree of clusters, called a dendogram. The tree is normally constructed from the bottom up using an agglomerative method, which starts with as many clusters as there are objects, selection systems in this case, say n. Firstly, the proximity matrix of distances or similarities between clusters is formed. The two nearest clusters are then fused into one, so that there are $n-1$ clusters. The process goes on for these $n-1$ clusters until the last two clusters are fused into a single one. Different selection systems are grouped in clusters based on different methods. Two of these methods were used to test the robustness of the findings. Firstly, the average linkage between groups was used to measure the distance between clusters. Thus, the distance between two clusters is based according to the average dissimilarity between its members. And secondly, the furthest neighbour was used to measure the distance between clusters. In this case the distance between two clusters is defined as the furthest dissimilarity between its members.

The distance between clusters can be measured using different methods. For each of the two clustering methods, two related measuring techniques were used: Minkovsky differences and its special case Euclidean distance ($p = 2$). Minkovsky difference is the pth root of the sum of the absolute differences to the pth power between values for the object $\sqrt[p]{\sum |x_1 - x_2|^p}$ ($p = 1$) and the Euclidean distance is the square root of the sum of the squared differences between values for the object $\sqrt{\sum (x_1 - x_2)^2}$. To standardise the data before computing proximities, the data values were transformed to be between 0 and 1. The SPSS© 10.0 was used to identify relatively homogeneous groups of cases based on selected characteristics.

To identify the selection variables (Section 1.1.2) and their values that represent the most important decisive points in achieving the highest $\widetilde{G}$, the regression tree method was used. Construction of the regression tree may be seen as a type of variable classification. If X is the set of selection systems to be analysed i.e. the space of observations, then the task of the tree construction is to find the tree that describes the space X most concisely. Theoretically it is assumed that there is a classification of the space X that will correctly classify all observations, however statistically the distribution of the classes over the space X overlaps. Using cross-validation, the number of classes of the space X to base the computations and the construction of the tree can be chosen.

The regression tree was run using the statistical package SPLUS©, which as a part of its output offers the best fitting regression tree for a given data. For the regression tree analysis, selection variables (Section 1.1.2) were used as the exploratory variables and the genetic gain for economic value $\widetilde{G}$ was used as the response variable. Thus, the selection variables were classified based on how significant they are and for what values, based on the $\widetilde{G}$ they yield.

5.2.1 Selection system representation

The same representation of the selection systems that was adopted for the optimisation study (Section 4.3) was also used for the hierarchical clustering and regression tree methods. Selection system vectors (4.1) for family selection and (4.2) for individual selection accompanied by the genetic gain for economic value $\widetilde{G}$ the yield and its cost $\overline{C}$ represent rows of the data matrix:

$$\begin{pmatrix} f_1 & k_1 & p_{11} & s_{11} & r_{11} & t_{11} & d_{11} & t_{12} & d_{12} & p_{13} & \cdot & \cdot & \cdot & p_{1n} & s_{1n} & r_{1n} & t_{1n} & d_{1n} & \widetilde{G}_1 & \overline{C}_1 \\ f_2 & k_2 & p_{21} & s_{21} & r_{21} & t_{21} & d_{21} & t_{22} & d_{22} & p_{23} & \cdot & \cdot & \cdot & p_{2n} & s_{2n} & r_{2n} & t_{2n} & d_{2n} & \widetilde{G}_2 & \overline{C}_2 \\ f_3 & k_3 & p_{31} & s_{31} & r_{31} & t_{31} & d_{31} & t_{32} & d_{32} & p_{33} & \cdot & \cdot & \cdot & p_{3n} & s_{3n} & r_{3n} & t_{3n} & d_{3n} & \widetilde{G}_3 & \overline{C}_3 \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \\ \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot & \cdot \end{pmatrix} \tag{5.1}$$

where f is the number of families at stage one, k the number of genotypes per family, and the matrix with n rows and five columns, where n rows represent the number of stages of selection and five columns represent each variable that can vary at each stage.

At a stage *z*, p_z is the number of rows in the p_z rows plot, s_z the number of sites, r_z is the number of replicates per site, t_z the selection intensity and d_z the selection index. However, depending on whether individual or family selection was used in stage one, the data matrix (5.1) changes. Consequently, two data sets were obtained: one giving solutions for individual selection and one for family selection.

Note that all selection variables (Section 1.1.2) but selection index d_z are quantitative and as such are appropriate for the two described analyses. Selection index d_z on the other hand could be either calculated as a product of cane yield and CCS in sugar yield (TSH), solely cane yield, or in a linear combination of the two measured characters CCS and cane yield in $CCS + \alpha \cdot TCH$. Thus, the distance between them is not expressible by a number. For example the distance between any two intensities, like 50% and 90% is an exact value, but between cane yield and $CCS + 0.125 \cdot TCH$ it can not be expressed as an exact number. Therefore, to allow for statistical analyses of the relationship of the resulting selection designs to one another, which measure the distance in each selection variable, it was necessary to break the selection index from a single variable into three variables. Thus rather than having the selection index d_z alone, further two variables were added in the above matrix (5.1): TSH_z and TCH_z. The TSH_z equals 0 or 1 depending whether sugar yield (TSH) was used at the stage z or not, and TCH_z equals 0 or 1 depending whether cane yield was used at the stage z or not.

Note that although family selection is routinely practiced in the Australian sugarcane breeding programs, there is a continuing debate whether individual clonal selection or family should be used (Section 2.3.1). The emphasis of this chapter was thus, on analysing alternative family selection designs, with the sole purpose of the analysis of alternative individual clonal selections (Section 5.7) being in adding to the existing debate between the two selection practices.

5.2.2 Summary of the three selection systems from the Burdekin region to which the ASSSO solutions were compared to

The aim of the thesis was to evaluate alternative selection systems against those currently practiced in the region. A description of the typical selection system currently used in the Burdekin region (Section 1.1.1) is given below (Table 5.1) together with its average gain $\widetilde{G}$ and cost. Further, two selection systems were used in the comparison; the two selection systems that according to the breeders' experience and intuition should yield optimal gains for the region. The three selection systems denoted B for the design currently used in the region and PB1 and PB2 for the two proposed optimal selection systems were simulated using the SSSM.

Table 5.1

Summary of the typical selection system practiced in the Burdekin region (B) together with the two selection systems proposed by breeders to be the optimal for the region (PB1, PB2), where f is number of families, k genotypes per family, p_z are plot sizes, s_z number of sites, r_z number of replicates per site, t_z selection intensity and d_z selection index used at stages z, $\widetilde{G}$ is genetic gain for economic value and $\overline{C}$ the cost

	f	k	p_1	s_1	r_2	t_1	d_1	t_2	d_2	p_3	s_3	r_3	t_3	d_3	p_4	s_4	r_4	t_4	d_4	p_5	s_5	r_5	t_5	d_5	$\widetilde{G}$	$\overline{C}$
B	200	60	1	1	4	0.30	TSH	0.50	vs	1	1	2	0.05	TSH	4	4	2	0.20	TSH						\$3,372	\$231,292
PB1	200	60	1	1	4	0.30	TSH	0.50	vs	1	1	2	0.10	CCS	4	1	2	0.15	TSH	4	4	2	0.30	TSH	\$3,280	\$236,293
PB2	200	60	1	1	4	0.30	TSH	0.50	vs	1	1	2	0.10	0.1	4	1	2	0.15	TSH	4	4	2	0.30	TSH	\$3,464	\$276,053

5.3 Sensitivity analysis of changing parameters

Because an exhaustive search was practiced at stage one to identify nodes to be branched through to stage two, the data file storing all 100,000 nodes was examined. Note that it was impracticable to give the file that stored all nodes because of its size, thus only some information from it has been extracted here.

Thirty three percent of stage-one nodes have been branched and because it is only after all stage-one nodes have been branched that the algorithm goes to stage two, the ASSSO ends with many nodes still active. The first stage-one node branched was that with the highest $\widetilde{G}$ value of \$858.72 and the last branched stage-one node was that yielding the $\widetilde{G}$ value of $354.58. The lowest yielding stage-one node had the $\widetilde{G}$ value of $32.29. Thus, all high yielding and medium yielding stage-one nodes have been branched in the course of the ASSSO execution. However, the narrower intensity the bigger the $\widetilde{G}$ (Table 5.2). Thus selecting for example 5% families at stage one yields $\widetilde{G}$ of $622.37 whereas selecting 50% families yields almost its third at $230.40, indicating that at stage one those nodes that select fewer families have been branched.

Table 5.2

An example of the change in the $\widetilde{G}$ with the change in the selection intensity t at stage one

t	$\widetilde{G}$
5%	$622.37
10%	$534.94
15%	$475.51
20%	$415.82
25%	$377.71
30%	$336.99
35%	$299.46
40%	$274.81
45%	$252.33
50%	$230.40
60%	$185.25
70%	$141.86
80%	$96.54
90%	$51.56

Whether one selects 5% or 50% at stage one has no impact on the cost at that stage, however it has a great impact on the costs of all following stages. For example if stage one starts with 200 families and 60 genotypes per family, selecting 5% of families means that at stage two $(200 \cdot 0.05) \cdot 60 = 600$ genotypes needs to be evaluated for selection in comparison to $(200 \cdot 0.50) \cdot 60 = 6000$ genotypes when 50% of families are selected, which accordingly increases the cost of stage two as well as that of all the following stages. This in turn limits the resources available for the later stages of selection when genotypes need to be planted in larger plot sizes and with more replicates. Thus, the higher selection intensity used at stage one the less possibility remains at finding selection systems that satisfy optimisation constraints (Section 4.3.2), especially that of the last stage testing (Section 4.3.2.3).

Generally, the lower yielding stage one nodes were branched, more families were selected and in turn more resources was required to perform stage two and subsequently less resources available for remaining stages, when more demanding testing needs to be performed on each genotype. Therefore, as lower stage one are left to be branched the less frequently would these nodes be giving selection systems that satisfy all constraints. Indeed, the lowest stage-one node branched that gave a selection system that satisfies all constraints had the $\widetilde{G}$ value of \$407.65, whereas the last stage-one node branched had $\widetilde{G}$ of \$354.58. Thus, among the stage-one nodes that yielded between \$407.65 and \$354.58 there were no selection systems that satisfy all optimisation constraints.

Generally, when lower yielding stage-one nodes are branched the available budget would get used before the required conditions are meet. On the other hand, when selection intensity is too narrow in stages one and two, too many genotypes would be discarded from selection too early, which in turn would not allow sufficient selection material to test future stages. This indicates that optimal selection systems would probably be branched from a medium yielding stage-one nodes rather then the extreme yielding stage-one nodes. This finding is also confirmed, with the highest yielding node 57,165 (Figure 5.1) was branched from the medium yielding stage-one node with $\widetilde{G}$ being equal to \$464.67.

The impact that different selection indices have on the magnitude of $\widetilde{G}$ when different plot sizes are used can also be seen from the file of nodes. At stage one selecting for $16 \cdot CCS + 1 \cdot TCH$ yields $\widetilde{G}$ of \$752.50, whereas selecting for cane yield, CCS only \$488.44, \$500.68 respectively (Table 5.3). This indicates that at stage one when genotypes are grown in small plots, selection indices that put more emphasis to CCS than cane yield are preferred, confirming thus the view of Jackson and McRae (2001, 1998) that early in selection, CCS should be used as a primary selection index. Nevertheless, selecting for sugar yield, which gives an equal importance to CCS and cane yield still yields the highest $\widetilde{G}$ of \$744.66.

Table 5.3

An illustration of the change in the $\widetilde{G}$ with the change in selection index d for stage one and stage four

d	$\widetilde{G}$	
	Stage one	Stage four
TSH	\$ 744.66	\$ 3,675.10
TCH	\$ 488.44	\$ 3,126.05
CCS	\$ 500.68	\$ 3,465.13
$16\cdot CCS+1\cdot TCH$	\$ 752.50	\$ 3,662.76
$8\cdot CCS+1\cdot TCH$	\$ 668.34	\$ 3,654.04
$17\cdot CCS+3\cdot TCH$	\$ 615.96	\$ 3,563.65
$4\cdot CCS+1\cdot TCH$	\$ 576.01	\$ 3,478.58
$8CCS+3\cdot TCH$	\$ 539.39	\$ 3,306.27
$2\cdot CCS+1\cdot TCH$	\$ 522.06	\$ 3,234.33
$4\cdot CCS+3\cdot TCH$	\$ 493.35	\$ 3,129.01
$1\cdot CCS+1\cdot TCH$	\$ 489.55	\$ 3,203.09
$1\cdot CCS+2\cdot TCH$	\$ 488.25	\$ 3,128.22

Similarly, at stage four, when genotypes are planted in larger plot sizes, cane yield and those selection indices that put more emphasis on CCS were preferred (Table 5.3). For example, when $1\cdot CCS+2\cdot TCH$ was used the $\widetilde{G}$ value of \$3,128.22 was achieved, and when $16\cdot CCS+1\cdot TCH$ was used the $\widetilde{G}$ value of \$3,662.76 was achieved. Either way, regardless whether smaller or larger plot sizes were used, a combination of CCS and cane yield is preferred over using cane yield by itself. Thus, confirming Jackson and McRae (2001) findings that early in selection more emphasis should be given to CCS than cane yield as the magnitude of CCS is less inflated by the competition between neighbouring genotypes.

5.4 A general analysis of convergence

To analyse the movement of the solution, 100 gains $\widetilde{G}$ were stored for each selection systems that at some point of the ASSSO execution yielded the highest $\widetilde{G}$. The data was used to create the following graph (Figure 5.1).

There were nine selection systems that at some point of the ASSSO execution, yielded highest $\widetilde{G}$ (Figure 5.1). The first selection system that satisfied all the constraints (Section 4.3.2) was obtained at the node 10,276 yielding $\widetilde{G}$ of just under \$2,000. That node was significantly improved by the node 10,277 with the $\widetilde{G}$ of just under \$3,500.

The improvement continued, although not as significantly towards the node 57,165 that yielded the $\widetilde{G}$ of over \$5,000, after which there were no more improvements on the gain $\widetilde{G}$. Given the convergence curve (Figure 5.1), one would suggest a better solution would certainly be found after 100,000 node.

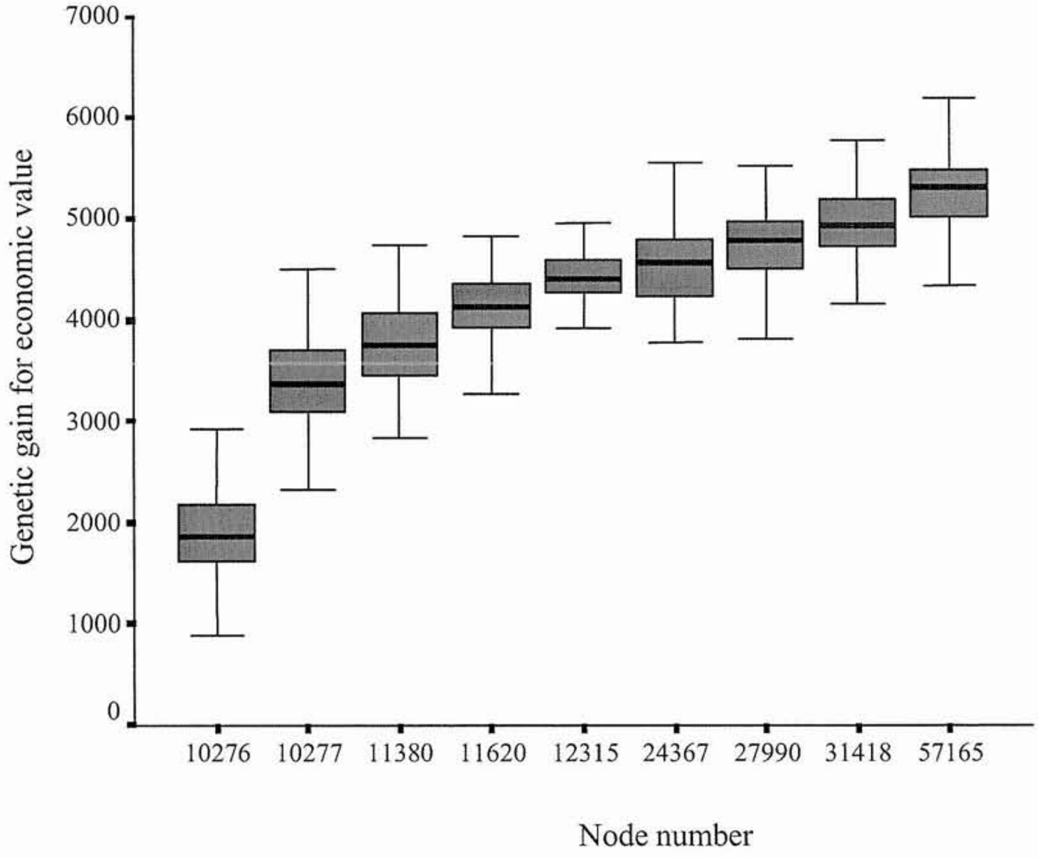

Figure 5.1: The box-plot for the populations of the genetic gains for economic value $\widetilde{G}$ showing the convergence characteristics of the solution, with the x-axis representing the branching node number and the y-axis representing the $\widetilde{G}$ values

There were 257 selection systems identified by the ASSSO that satisfied all constraints (Section 4.3.2) and provided gains greater than \$3372 (Table 5.1). This supports the assertion by Skinner (1961) that many combinations of selection variables (Section 1.1.2) will give approximately similar results. To identify selection systems that according to the ASSSO are superior to that currently used or suggested to be used in the region (Table 5.1), the error bar of the Burdekin selection system alongside error bars (Figure 5.2) of those 257 selection systems was created. Those selection systems that are 1 SE (standard error) away from the Burdekin selection system (Section 1.1.1) are superior to it at the 0.05 significance level and those that are away 2 SE are superior to it at the 0.005 significance level.

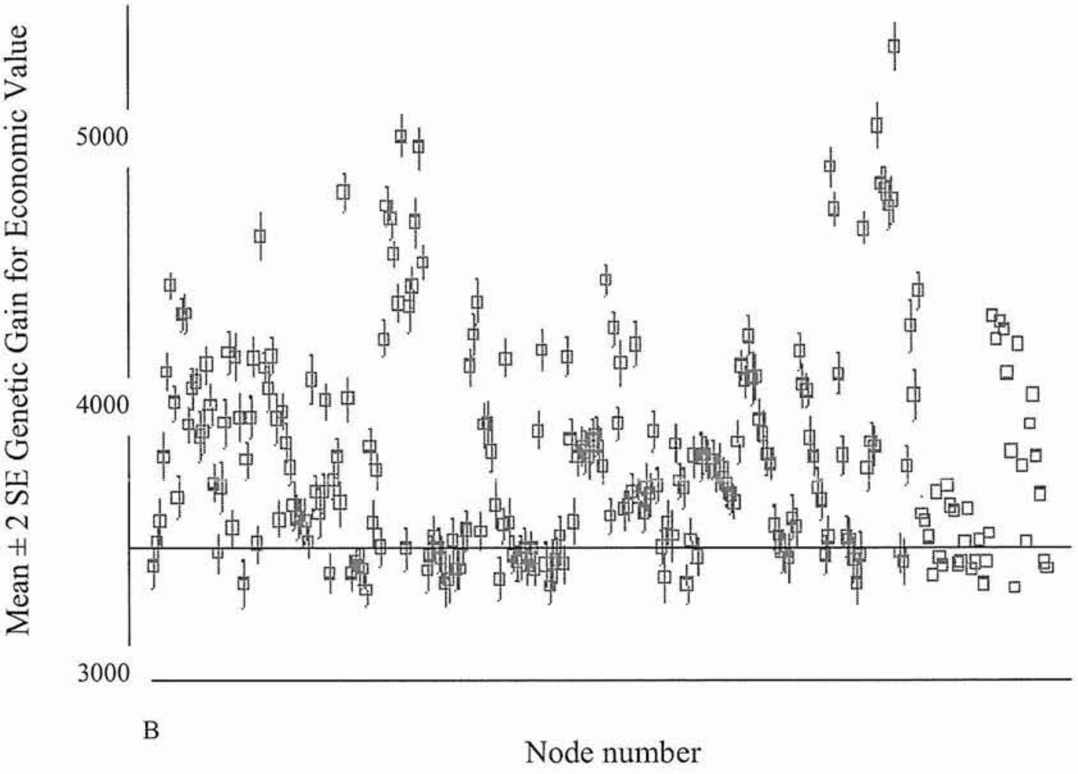

Figure 5.2: The error bars for the populations of the $\widetilde{G}$ for the alternative selection systems to the typical selection system currently practiced in the Burdekin region (Section 1.1.1), with the x-axis representing the branching node number and the y-axis representing the $\widetilde{G}$ values

There were 70 selection systems out of those 257 that represent significant improvements on selection system B (Table 5.1, Figure 5.1). The specifications of 43 selection system designs with the highest gains are given in Table 5.4.

Table 5.4

The selection system designs that are significant improvement to the typical selection system currently practiced in the Burdekin region (Section 1.1.1) ordered by gain where f is number of families, k number of genotypes per family, p_z are plot sizes, s_z number of sites, r_z number of replicates per site, t_z selection intensity and d_z selection index used at stages z, $\tilde{G}$ is genetic gain for economic value and $\overline{C}$ the cost

No.	f	k	p_1	s_1	r_2	t_1	d_1	t_2	d_2	p_3	s_3	r_3	t_3	d_3	p_4	s_4	r_4	t_4	d_4	$\tilde{G}$	$\overline{C}$
1	400	60	1	3	1	10%	0.375	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 5,302.68	$255,027
2	200	200	1	2	5	5%	CCS	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,991.06	$253,530
3	300	80	1	2	2	10%	0.375	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,969.04	$255,027
4	200	200	2	5	1	5%	0.75	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,836.88	$259,570
5	300	80	2	2	1	10%	0.5	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,826.32	$255,027
6	300	60	1	1	3	15%	0.1875	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,799.46	$ 265,775
7	100	80	1	1	4	20%	0.125	90%	VS	1	1	2	15%	TSH	4	4	2	5%	0.0625	$ 4,789.42	$271,740
8	400	60	1	1	3	10%	0.125	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,782.63	$255,027
9	100	80	1	1	4	20%	0.125	90%	VS	1	1	2	15%	TSH	4	4	2	5%	TSH	$ 4,722.80	$271,740
10	100	80	1	4	1	25%	TSH	90%	VS	1	1	2	10%	TSH	4	4	2	5%	TSH	$ 4,648.99	$259,755
11	300	80	2	2	1	10%	0.1875	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,624.31	$255,027
12	300	80	2	2	1	10%	0.75	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,619.13	$255,027
13	200	200	2	5	1	5%	0.5	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,611.15	$259,570
14	400	100	1	5	1	5%	0.375	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,604.10	$259,570
15	200	200	2	5	1	5%	CCS	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,603.80	$253,530
16	300	80	4	1	1	10%	0.125	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,484.29	$250,815
17	200	200	2	1	5	5%	0.5	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,471.59	$259,570
18	400	60	1	1	3	10%	0.375	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,436.73	$255,027
19	200	200	1	2	5	5%	TSH	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,425.08	$259,570
20	400	100	1	1	5	5%	0.375	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,402.94	$259,570
21	100	80	1	1	4	20%	0.125	90%	VS	1	1	2	15%	TSH	4	4	2	5%	TCH	$ 4,388.87	$233,084
22	300	80	1	2	2	10%	0.0625	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,379.79	$255,027
23	400	80	4	1	1	5%	0.25	90%	VS	1	1	2	10%	TSH	4	4	2	5%	TSH	$ 4,347.51	$262,310
24	300	60	1	1	3	15%	0.125	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,308.93	$265,775
25	300	80	2	1	2	10%	CCS	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,306.08	$251,403
26	300	80	1	4	1	10%	0.1875	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,299.08	$255,027
27	200	200	1	2	5	5%	0.75	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,296.90	$259,570
28	300	60	1	1	3	15%	CCS	90%	VS	1	1	2	5%	TSH	4	4	2	5%	0.125	$ 4,286.43	$263,057
29	300	80	4	1	1	10%	TSH	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,284.16	$250,815
30	300	60	1	3	1	15%	CCS	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,276.17	$263,057
31	300	60	1	1	3	15%	CCS	90%	VS	1	1	2	5%	TSH	4	4	2	5%	0.0625	$ 4,251.81	$263,057
32	200	200	2	1	5	5%	0.125	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,246.97	$259,570
33	300	60	1	1	3	15%	CCS	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,237.59	$263,057
34	300	80	2	2	1	10%	0.25	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,214.62	$255,027
35	400	60	1	1	3	10%	TSH	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,207.06	$255,027
36	300	60	1	1	3	10%	CCS	90%	VS	1	1	2	10%	TSH	4	4	2	5%	0.125	$ 4,192.60	$256,541
37	400	60	1	3	1	10%	CCS	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,179.27	$255,027
38	100	100	1	5	1	20%	0.125	90%	VS	1	1	2	10%	TSH	4	4	2	5%	TSH	$ 4,176.65	$264,337
39	400	80	1	2	2	5%	CCS	90%	VS	1	1	2	10%	TSH	4	4	2	5%	TSH	$ 4,174.17	$263,094
40	300	80	1	1	4	10%	0.1875	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,170.35	$255,027
41	100	80	2	1	2	35%	0.0625	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,161.13	$250,486
42	200	200	2	1	5	5%	CCS	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,159.87	$253,530
43	400	80	1	2	2	5%	0.75	90%	VS	1	1	2	10%	TSH	4	4	2	5%	TSH	$ 4,150.12	$267,926

No.	f	k	p_1	s_1	r_2	t_1	d_1	t_2	d_2	p_3	s_3	r_3	t_3	d_3	p_4	s_4	r_4	t_4	d_4	$\tilde{G}$	$\overline{C}$
44	300	60	1	1	3	10%	CCS	90%	VS	1	1	2	10%	TSH	4	4	2	5%	TSH	$ 4,130.54	$256,541
45	100	80	2	2	1	0.35	TSH	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,121.72	$250,486
46	400	60	1	3	1	10%	0.1875	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,118.62	$255,027
47	400	60	1	3	1	10%	0.0625	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,112.83	$255,027
48	400	100	1	5	1	5%	0.25	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,111.00	$259,570
49	300	60	1	1	3	10%	CCS	90%	VS	1	1	2	10%	TSH	4	4	2	5%	0.1875	$ 4,101.30	$256,541
50	300	60	1	1	3	10%	CCS	90%	VS	1	1	2	10%	TSH	4	4	2	5%	0.0625	$ 4,096.94	$256,541
51	100	100	1	5	1	20%	0.125	90%	VS	1	1	2	10%	TSH	4	4	2	5%	0.0625	$ 4,094.47	$264,337
52	400	80	1	1	4	5%	0.75	90%	VS	1	1	2	10%	TSH	4	4	2	5%	TSH	$ 4,092.42	$267,926
53	300	80	2	2	1	10%	TSH	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,061.92	$255,027
54	400	100	1	5	1	5%	TSH	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,060.55	$259,570
55	200	200	2	5	1	5%	0.375	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,040.22	$259,570
56	300	80	2	1	2	10%	TSH	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 4,040.18	$255,027
57	300	60	1	1	3	10%	CCS	90%	VS	1	1	2	10%	TSH	4	4	2	5%	0.25	$ 4,030.40	$256,541
58	300	80	1	2	2	10%	0.125	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 4,017.19	$255,027
59	100	100	1	5	1	20%	0.125	90%	VS	1	1	2	10%	TSH	4	4	2	5%	0.125	$ 4,012.04	$264,337
60	400	60	1	3	1	10%	0.125	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 3,989.31	$255,027
61	300	80	1	4	1	10%	0.0625	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 3,981.63	$255,027
62	300	80	2	1	2	10%	0.125	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 3,971.66	$255,027
63	100	80	1	1	4	25%	CCS	90%	VS	1	1	2	10%	TSH	4	4	2	5%	TSH	$ 3,969.14	$258,547
64	300	60	1	3	1	15%	0.375	90%	VS	1	1	2	5%	TSH	4	4	2	5%	0.0625	$ 3,967.64	$265,775
65	300	60	1	3	1	15%	0.0625	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	0.0625	$ 3,966.49	$265,775
66	300	60	1	1	3	10%	0.25	90%	VS	1	1	2	10%	TSH	4	4	2	5%	TSH	$ 3,966.39	$259,259
67	200	200	1	5	2	5%	0.25	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 3,936.01	$259,570
68	200	200	1	5	2	5%	0.125	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 3,933.14	$259,570
69	400	100	1	1	5	5%	0.1875	90%	VS	1	1	2	5%	0.0625	4	4	2	5%	TSH	$ 3,924.73	$259,570
70	200	200	2	5	1	5%	0.125	90%	VS	1	1	2	5%	TSH	4	4	2	5%	TSH	$ 3,913.68	$259,570

5.5 Comparison to selection systems developed by breeders

The three selection designs (Table 5.1); one that describes the selection practices currently used in the Burdekin region (B) and two selection designs (PB1 and PB2) proposed by breeders to be optimal for the region; are compared to 70 selection designs (Table 5.4) superior to it.

All selection designs consist of four stages (Table 5.4), with the stage two being actually the second part of the stage one when genotypes from within selected families are selected to enter stage two. Thus for the real life application three stages of selection systems are optimal, confirming Skinner (1961) finding that most genetic gain is theoretically achievable through early selection stages. In comparison, the two proposed selection systems (PB1 and PB2) consist of five stages (ie four stages for the real life selection) and thus they could be compared to one another only based on the magnitude of the $\widetilde{G}$ they yield.

The average gain $\widetilde{G}$ yielded by the two proposed systems PB1 and PB2 equals \$3,280 and \$3,464 respectively (Table 5.1). Both selection designs yield gains close, in the case of (PB1) even lower to that achieved by the Burdekin selection (B) of \$3,372 (Table 5.1), to which those selection designs are significantly superior. Therefore, all selection designs from Table 5.4 are also significantly superior to the proposed selection design (PB1) and most of them are superior to the design (PB2).

Apart from the number of stages, there are a number of similarities between the alternative selection systems (Table 5.4) and the Burdekin selection (B) (Table 5.1). They all use the same planting design for stage three, and the minimal required planting scheme (Section 4.3.2.3) for stage four. Thus, they all progress to the larger plot sizes as soon as there was enough planting material available to do so, which were Jackson and McRae (2001, 1998) findings.

The choice of starting population ie combination of the number of families and genotypes used varies greatly from design to design (Table 5.4). There is however a general guideline, that the larger the starting population of families, the fewer families are selected at stage one. If 50 families and 20 genotypes per family was the smallest starting population and 400 families and 200 genotypes per family was the largest starting population, then the preferred starting populations (Table 5.4) are of a "moderate" size. Similarly, the Burdekin selection system (B) (Table 5.1) starts with 200 families and 60 genotypes per family, which can also be considered a "moderate" size, and is in fact one of the preferred starting populations options (Table 5.4).

Selection intensities of the alternative selection systems (Table 5.4) were kept at high levels ($\leq 15\%$) throughout selection with the only exception being at stage two, which selects most of the genotypes from within each selected family. The combination of selecting 5%-35% of families coincides with the choice of selection intensities proposed by Kimbeng *et al* (2001b). However selecting 90% of genotypes from within selected families (Table 5.4) is quite extreme, as Kimbeng *et al* (2001b) suggested 40% of genotypes to be selected from within families when 10% of families are selected, 30%

when 20% families are selected, 25% when 30% families are selected, and 10% when 40% families are selected.

The major difference between the selection system (B) currently practiced in the region (Table 5.1) and the alternative selection systems (Table 5.4) is in the selection intensities used at those two stages: one and two, i.e. in the actual stage one of selection where in the first year the best performing families were selected and in the second year the best performing genotypes from within selected families were selected. The selection system (B) selects ($(200 \cdot 30\%) \cdot 60 \cdot 50\% = 1800$) (Table 5.1) in comparison to the ($(200 \cdot 5\%) \cdot 200 \cdot 90\% = 1800$) genotypes selected by for example, the selection system defined under the number 13 (Table 5.4). For the alternative selection systems (Table 5.4) much more emphasis was put on selecting the very best performing families, with the second part of stage one selecting almost all genotypes available, thus being much more lenient in the selection. However, one would expect the higher percentage of families selected with less genotypes per family, as there is much more variability attributable to within families (70%) than to between families (30%) (Section 2.3.1). On the other hand, because the lower yielding stage one nodes, which select higher percentage of families, were not branched in the course of the ASSSO execution, the optimal selection system is yet to be identified after the $100{,}000^{th}$ node.

In the case of the alternative selection systems (Table 5.4) the preferred selection indices, vary from stage to stage. At stage one, although there is a number of selection indices used, they all have some similarity to one another in giving more emphasis to CCS than to cane yield. This confirms Jackson and McRae (2001) suggestions that when genotypes were planted in small plots selection index should be chosen more carefully as the expression of cane yield does not give an accurate picture of the genotypes potential and more emphasis should be put on CCS. Kimbeng *et al* (2000, 2001a,b) agrees by discovering that most elite genotypes were found from within families that score high CCS values and low cane yield.

Selection index used early in selection was another significant difference between the selection system (B) and that of alternative superior selection systems identified using ASSSO (Table 5.4). As suggested by Jackson and McRae (2001), Cuenya and Mariotti

(1994), and Skinner *et al* (1987), each stage should be addressed separately in relation to developing optimal selection indices because CCS and cane yield are affected differently by the plot size and experimental design used at each stage. Accordingly, superior selection systems (Table 5.4) use various weighing between CCS and cane yield in stage one and seldom they use sugar yield (TSH), which is the index used in the selection system (B).

5.6 An analysis to identify characteristics of a favourable selection system

There are a number of similarities identified between some selection systems, which can give an idea of the common characteristics required for the superior design. For example, selection systems 28, 31, 36, 49, 50 and 57 (Table 5.4) are all of the following form $(300,60,1,1,3,t_1,CCS,0.9,vs,1,1,2,t_3,TSH,4,4,2,0.05,d_4)$. Further there are limited choices for those unspecified selection variables (Section 1.1.2). For example, selection intensity t_1 being either 10% or 15%, selection intensity t_3 5% or 10%, and selection index d_4 being one of the four 0.0625, 0.125, 0.1875, or 0.25 (Table 5.4).

There are twenty-four systems: 4, 11, 13, 14, 15, 16, 17, 20, 24, 25, 26, 32, 34, 35, 37, 40, 42, 46, 48, 55, 56, 60, 67, 69 (Table 5.4) that differ in stage one only and are of the $(f,k,p_1,s_1,r_1,t_1,d_1,90\%,vs,1,1,2,5\%,0.0625,4,4,2,5\%,TSH)$ general form. Again the choices of values taken for the stage one variables is limited.

Nineteen selection systems: 1, 3, 5, 6, 8, 12, 18, 22, 30, 33, 39, 43, 44, 47, 52, 58, 61, 62, 66 (Table 5.4) that start with 300 or 400 families and 60 or 80 genotypes per family. They all select 20% or 15% families at stage one and use various selection indices. The rest of the stages are similar with the only difference being the percentage of genotypes selected at stage three, with some selecting 10% and some 5% (Table 5.4). Note that the selection program 1 that yielded the highest $\widetilde{G}$ differs in a single variable (the index used at stage one) from the selection system 47 that yielded much less, on average \$4,112.83 (Table 5.4). This suggests that such extreme $\widetilde{G}$ achieved in selection system 1 was achieved by chance.

Then there are some general rules followed throughout the seventy selection systems. If the number of families is larger like 400 or 300 select very few like 5% or 10%, and for smaller starting populations of families select more 15% or 20%.

To identify any significant grouping of the selection systems (Table 5.4) the hierarchical clustering was performed four times for all combinations of clusters being made using average linkage between groups and furthest neighbour, and the distance between clusters being measured using the Minkovsky differences and Euclidean distance. All four analyses gave similar clustering thus only one of them was given below, the one that made clusters using average linkage between groups and measured the distance between clusters with the Euclidean distance (Table 5.5).

The agglomeration schedule (Table 5.5) depicts the process of clustering. At first a number of clusters are created, one at the time, all with the same significant value for p of 0.063, meaning that the two clusters differ slightly in its design. For example, at step 3 selection design ie clusters 11 and 34 are fused together ie identified as having their average values "closest" to one another, where closeness is measured using the Euclidean distance. Indeed these two selection designs differ only in selection index used at stage one (Table 5.4). The selection system 11 uses $16 \cdot CCS + 3 \cdot TCH$ whilst 34 uses $4 \cdot CCS + TCH$, which are defined by values 0.1875 and 0.25 respectively, the two consecutive selection indices (Section 4.3.1). Since both clusters ie selection systems 11 and 34 are fused for the first time into a cluster, 0 is written as the first time cluster combined. The next time the cluster made out of clusters 11 and 34 is used is at step 22, when it was fused with the cluster ie selection system 25. The new cluster created is assigned the smaller out of two numbers, in this case 11. As an addition to Table 5.5, Appendix F gives the graphical representation of the clustering to help understand the process described above.

Table 5.5

Agglomeration schedule for the alternative selection systems (Table 5.4)

Step	Comb.		p	First time		Next Step	Step	Comb.		p	First time		Next Step
	Cluster 1	Cluster 2		Cluster 1	Cluster 2			Cluster 1	Cluster 2		Cluster 1	Cluster 2	
1	46	60	0.063	0	0	27	36	39	44	0.561	0	14	39
2	22	58	0.063	0	0	17	37	14	26	0.579	9	27	48
3	11	34	0.063	0	0	22	38	20	24	0.627	12	21	52
4	51	59	0.067	0	0	59	39	3	39	0.659	30	36	45
5	49	57	0.067	0	0	11	40	29	53	0.712	0	0	54
6	36	50	0.067	0	0	11	41	11	16	0.720	22	0	48
7	28	31	0.067	0	0	32	42	35	37	0.726	34	0	64
8	13	55	0.125	0	0	19	43	2	27	0.750	0	0	56
9	14	48	0.125	0	0	37	44	1	5	0.756	28	16	45
10	32	42	0.125	0	0	25	45	1	3	0.777	44	39	49
11	36	49	0.133	6	5	32	46	10	45	0.850	0	0	57
12	20	69	0.188	0	0	38	47	28	64	0.912	32	0	53
13	6	33	0.188	0	0	24	48	11	14	0.924	41	37	52
14	44	66	0.250	0	0	36	49	1	43	0.956	45	35	55
15	8	18	0.250	0	0	24	50	9	41	1.061	33	0	58
16	5	12	0.250	0	0	44	51	38	68	1.099	0	23	62
17	3	22	0.281	0	2	26	52	11	20	1.107	48	38	60
18	1	47	0.313	0	0	28	53	7	28	1.126	0	47	59
19	4	13	0.313	0	8	31	54	29	54	1.191	40	0	57
20	30	61	0.339	0	0	28	55	1	23	1.219	49	0	58
21	24	40	0.339	0	0	38	56	2	19	1.222	43	0	63
22	11	25	0.417	3	0	41	57	10	29	1.342	46	54	65
23	68	70	0.417	0	0	51	58	1	9	1.348	55	50	62
24	6	8	0.429	13	15	30	59	7	51	1.353	53	4	66
25	17	32	0.438	0	10	61	60	4	11	1.402	31	52	61
26	3	62	0.441	17	0	30	61	4	17	1.431	60	25	64
27	26	46	0.443	0	1	37	62	1	38	1.456	58	51	63
28	1	30	0.472	18	20	44	63	1	2	1.602	62	56	65
29	15	67	0.486	0	0	31	64	4	35	1.654	61	42	67
30	3	6	0.506	26	24	39	65	1	10	1.743	63	57	68
31	4	15	0.533	19	29	60	66	7	21	1.773	59	0	68
32	28	36	0.537	7	11	47	67	4	65	1.817	64	0	69
33	9	63	0.542	0	0	50	68	1	7	1.873	65	66	69
34	35	56	0.552	0	0	42	69	1	4	2.068	68	67	70
35	43	52	0.559	0	0	49	70	1	B	2.683	69	0	0

According to the agglomeration schedule thus, the first seven clusters fused are somewhat significant, just over 0.05 significance level, with all other clusters being not significant (Table 5.5). Those seven clusters are made out of selection systems that differ only in selection index used in one of its stages. Selection systems 46 and 60 (step 1), 22 and 58 (step 2), 11 and 34 all differ in selection index used at stage one (Table 5.4). Whereas 51 and 59 (step 4), 49 and 57 (step 5), 36 and 50 (step 6), 28 and 31 (step 7) all differ in selection index used in stage four (Table 5.4). Note also, that the selection system that represents current practices from the Burdekin region (Table 5.1) is the last cluster to be fused at step 70, indicating that despite all its similarities to the identified selection systems (Table 5.4) it still differs significantly from them.

To be able to identify selection variables (Section 1.1.2) and their values that have the greatest impact on the magnitude of $\widetilde{G}$ the regression tree was created for the alternative selection designs (Table 5.4). Figure 5.3 depicts the regression tree suggested by the SPLUS application to be the one with the smallest standard error compared to the size of the tree and thus considered the optimal regression tree, for the alternative selection systems (Table 5.4).

There are three criteria that make most impact on the magnitude of $\widetilde{G}$ ie three most important decision points for obtaining higher magnitudes of $\widetilde{G}$. The first and therefore the most important decision point is the selection intensity of 0.125 ie 12.5% used at stage three, t_3 (Figure 5.3). There are three selection systems that select 15% or more at stage three and the average gain $\widetilde{G}$ they yield equals \$4,630 (Figure 5.3). On the other hand sixty-seven (70-3) selection designs select 10% or 5% at stage three and the average gain they achieve is \$4,347 (average of \$4,210, \$4,270 and \$4,560, Figure 5.3).

There are only three selection systems identified by the regression tree analysis for achieving the highest gains. Those three selection systems are also the only ones that selected 20% of families in stage one, with the remaining selection systems selecting inferior numbers. This coupled with having many nodes still active after 100,000 nodes have been branched indicates that the optimal selection design is yet to be found after 100,000th node.

Then, the sixty-seven selection designs were divided further according the selection index they use at stage one, d_1. Forty-two selection systems select at stage one based on $0, 0.0625, 0.125, 0.1875, 0.25$ ie $CCS, 16 \cdot CCS + TCH, 8 \cdot CCS + TCH, 16 \cdot CCS + 3 \cdot TCH$, $4 \cdot CCS + TCH$ and yield on average \$4,210. The remaining twenty-five (67-42) selection systems that yield on average \$4,415 (average of \$4,270 and \$4,560) select at stage one based on $0.375, 0.5, 0.75, 1, 2, TSH$ ie $8 \cdot CCS + 3 \cdot TCH$, $2 \cdot CCS + TCH$, $4 \cdot CCS + 3 \cdot TCH$, $CCS + TCH, CCS + 2 \cdot TCH, TSH$.

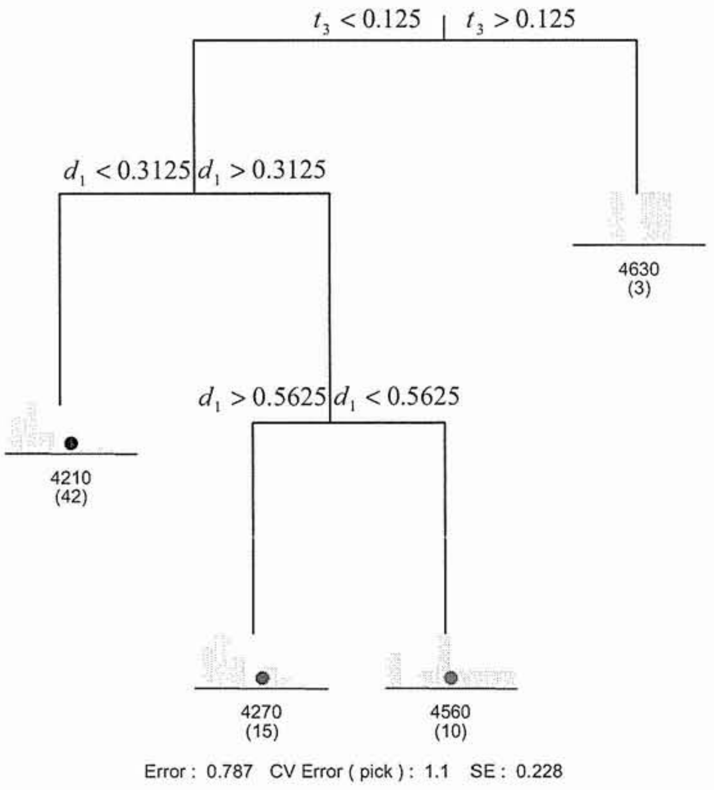

Figure 5.3 Regression tree for the alternative selection designs (Table 5.4), where t_3 is the selection intensity used at stage three and d_1 the selection index used at stage one, and each branch of the tree was given with the average genetic gain for economic value $\widetilde{G}$ of the alternative selection designs that belong to that branch and in brackets the total number of selection designs belonging to the branch

Finally, the twenty-two selection systems are divided based again on the selection index used at stage one, d_1. Ten selection designs that use 0.375 or 0.5 ie $8 \cdot CCS + 3 \cdot TCH$ or $2 \cdot CCS + TCH$ yield \$4,560, and those that use 0.75 ie $4 \cdot CCS + 3 \cdot TCH$ or TSH yield \$4,270. Note that other two selection indices $CCS + TCH, CCS + 2 \cdot TCH$ were not used by selection designs given in Table 5.4.

According to the regression tree results therefore, there are two rules to follow in order to achieve the highest gains $\widetilde{G}$. Firstly, select more than 10% of genotypes at stage three and secondly if 10% of genotypes or less are selected at stage three, at stage one select families based on either $8 \cdot CCS + 3 \cdot TCH$ or $2 \cdot CCS + TCH$.

Note that although stage one is the stage that alternative selection systems mostly differ amongst (Table 5.4), the regression tree method identified a stage-three variable (Section 1.1.2), selection intensity as one of the most important decisive points for obtaining maximal gain $\widetilde{G}$. Furthermore, note that clustering analysis (Table 5.5) identified groups of two selection systems that also differ only in selection index used in stage one.

5.7 A comparison between individual and family selection

Although many researchers (Hogarth and Mullins, 1989; Bull *et al,* 1992; Cox and Hogarth, 1993a; and Kimbeng *et al,* 2000) suggested that family selection is more efficient to be used early in selection, only Australia alongside breeding programs form Louisiana (United States of America) and South Africa practice family selection. Thus, it is an ongoing debate whether family selection is indeed superior to individual selection.

Unlike family selection, there are only three selection variables: the number of genotypes k, selection intensity t_1 and selection index d_1 to be branched at stage one, which allows for all stage-one nodes to be branched within 100,000 nodes. Because of this and because more emphasis is put throughout the thesis on family selection, as it is the selection used by Australian breeders, to shorten the time it takes to execute the algorithm only half 50,000 the nodes have been branched. Note that there is only a single seedling of each genotype available to start selection in stage one thus, only one replicate of a single seedling can be planted on one site.

The selection designs that yielded the highest $\widetilde{G}$ were summarised in Table 5.6 ordered in descending order by $\widetilde{G}$, with the highest yield being \$4909.22. Note that, similar to the family selection results, here too the distance from the highest yielding selection system 1 to its closest neighbour 2 is greater (\$364.83) than in other nodes, with the average distance being \$30.79, indicating again that such a high yield for $\widetilde{G}$ is happening by chance, which again emphasises the importance of analysing a set of resulting selection systems rather than a single highest yielding one.

Similar to family selection, by identifying three stages of selection as optimal, it also confirms Skinner (1961) findings that to achieve the highest gain the minimal number of stages that allow necessary field testing of genotypes suffices.

Table 5.6

The highest yielding systems that select individual genotypes, where k is number of genotypes, p_z are plot sizes, s_z number of sites, r_z number of replicates pre site, t_z selection intensity and d_z selection index used at stages z, $\widetilde{G}$ is genetic gain for economic value and $\overline{C}$ the cost

	k	p_1	s_1	r_2	t_1	d_1	p_2	s_2	r_2	t_2	d_2	p_3	s_3	r_3	t_3	d_3	$\widetilde{G}$	$\overline{C}$
1	25000	0	1	1	5%	0.75	1	2	1	5%	TSH	4	4	2	25%	TCH	\$ 4,909.22	\$261,740
2	10000	0	1	1	20%	0.125	2	1	1	5%	0.0625	4	4	2	10%	TSH	\$ 4,479.55	\$247,204
3	25000	0	1	1	5%	0.75	1	2	1	5%	TSH	4	4	2	25%	0.0625	\$ 4,451.87	\$265,708
4	25000	0	1	1	5%	0.75	1	2	1	5%	TSH	4	4	2	25%	TSH	\$ 4,386.52	\$273,292
5	25000	0	1	1	5%	0.75	1	2	1	5%	TSH	4	4	2	25%	CCS	\$ 4,365.03	\$252,132
6	25000	0	1	1	5%	1	1	2	1	5%	TSH	4	4	2	25%	TSH	\$ 4,318.63	\$273,292
7	10000	0	1	1	25%	0.125	2	1	1	5%	0.0625	4	4	2	15%	TSH	\$ 4,286.70	\$277,000
8	25000	0	1	1	10%	TSH	1	2	1	5%	TSH	4	4	2	15%	0.0625	\$ 4,171.72	\$270,150
9	25000	0	1	1	5%	2	1	1	2	5%	TSH	4	4	2	25%	TSH	\$ 4,170.99	\$273,292
10	25000	0	1	1	10%	TSH	1	2	1	5%	TSH	4	4	2	15%	TSH	\$ 4,139.79	\$270,150
11	20000	0	1	1	5%	0.0625	2	1	1	5%	0.0625	4	4	2	20%	1	\$ 4,123.44	\$220,432
12	25000	0	1	1	5%	2	1	1	2	5%	TSH	4	4	2	25%	0.125	\$ 4,122.50	\$273,292
13	25000	0	1	1	5%	2	1	1	2	5%	TSH	4	4	2	25%	0.0625	\$ 4,097.99	\$265,708
14	20000	0	1	1	10%	TCH	1	2	1	5%	TSH	4	4	2	10%	TSH	\$ 4,092.32	\$229,304
15	10000	0	1	1	25%	0.375	2	1	1	5%	0.0625	4	4	2	15%	0.0625	\$ 4,090.22	\$277,000
16	10000	0	1	1	25%	0.0625	2	1	1	5%	0.0625	4	4	2	15%	0.0625	\$ 4,083.71	\$277,000
17	25000	0	1	1	5%	0.75	1	2	1	5%	TSH	4	4	2	20%	TSH	\$ 4,079.88	\$273,292
18	10000	0	1	1	20%	0.0625	2	1	1	5%	0.0625	4	4	2	10%	0.125	\$ 4,075.22	\$235,364
19	10000	0	1	1	25%	0.375	2	1	1	5%	0.0625	4	4	2	15%	TSH	\$ 4,066.77	\$291,640
20	25000	0	1	1	5%	2	1	1	2	5%	TSH	4	4	2	25%	0.1875	\$ 4,056.31	\$265,708
21	10000	0	1	1	25%	0.125	2	1	1	5%	0.0625	4	4	2	10%	TSH	\$ 4,053.09	\$277,000
22	25000	0	1	1	5%	2	1	1	2	5%	TSH	4	4	2	25%	CCS	\$ 4,047.83	\$252,132
23	25000	0	1	1	5%	2	1	1	2	5%	TSH	4	4	2	25%	0.25	\$ 4,044.83	\$273,292
24	10000	0	1	1	25%	0.0625	2	1	1	5%	0.0625	4	4	2	15%	TSH	\$ 4,044.14	\$291,640
25	8000	0	1	1	30%	0.0625	2	1	1	5%	0.0625	4	4	2	10%	TSH	\$ 4,039.11	\$270,333
26	10000	0	1	1	20%	0.0625	2	1	1	5%	0.0625	4	4	2	10%	TSH	\$ 4,037.61	\$247,204
27	20000	0	1	1	10%	TSH	1	2	1	5%	TSH	4	4	2	15%	TSH	\$ 4,025.69	\$229,304
28	20000	0	1	1	10%	CCS	2	1	1	5%	TSH	4	4	2	10%	TSH	\$ 4,021.81	\$233,504
29	10000	0	1	1	20%	0.0625	2	1	1	5%	0.0625	4	4	2	10%	0.0625	\$ 4,016.22	\$247,204

Apart from the number of stages, there are other similarities between alternative family and individual selection designs. They all use the same minimal required planting design for stage three (Section 4.3.2.3) and progressing to it as soon as there was enough planting material available to do so, again confirming Jackson and McRae (2001, 1998) findings.

On the other hand contrary to family selection the preferred starting population of genotypes was not limited to the "moderate" size, but often one of the maximum allowed starting populations of 25,000 genotypes were used.

To answer the above question of whether there is enough evidence to suggest that family selection is more efficient than individual selection overall, the following error bars plot was created (Figure 5.4). The graph consists of the error bars for the distribution of $\widetilde{G}$ for the highest yielding 29 selection systems (Table 5.4) identified as significant improvement to the practices currently used in the Burdekin region (Section 1.1.1) alongside the highest yielding 29 individual selection system (Table 5.6). To allow for the comparison to the practices currently used in the region, the error bar of the selection system (B) (Table 5.1) described in Section 1.1.1 is also given.

On the individual level, some individual genotype selections present significant improvement (at 0.01 significant level) to some family selections and vice versa (Figure 5.4). However overall, error bars for family selection seem as a continuation of the upward trend of individual selections' error bars. Thus apart from indicating that similar to family selection an optimal individual selection is yet to be found after 50,000 nodes.

Furthermore and most importantly the error bars (Figure 5.4) are confirming that not only is the use of family selection at stage one more efficient than selection of individual genotypes, but selection systems that practice family selection in stage one also perform better as a whole.

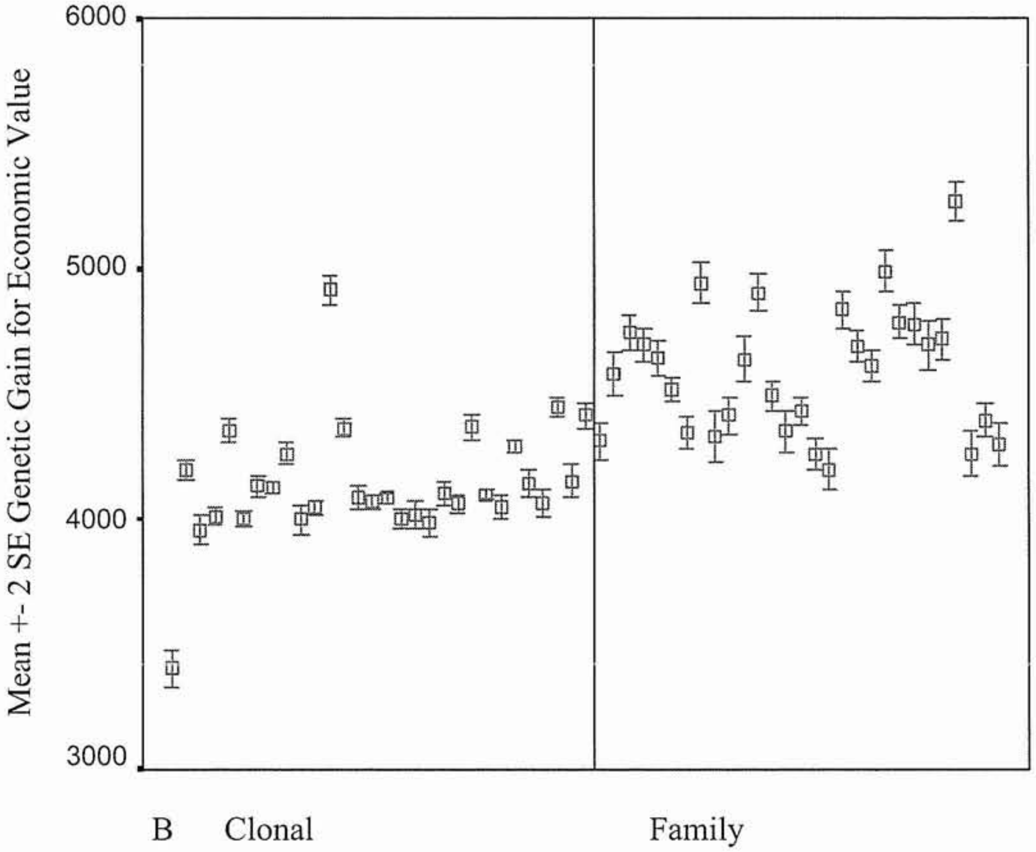

Figure 5.4: The error bars for the comparison between the populations of $\widetilde{G}$ for the alternative family selection systems (Table 5.4) and individual selection systems (Table 5.6). For the comparison reasons the selection system currently used in the Burdekin region, denote by B (Table 5.1) is also given

5.8 Proposed selection designs for the Burdekin region

The ASSSO has identified a number of alternative more efficient selection designs to the practices currently used in the region. To draw some more specific guideline, firstly family selection should be practiced in stage one. The selection design could be summarised as of the following form:

$$(f,k,p_1,s_1,r_1,t_1,d_1,90\%,vs,1,1,2,t_3,d_3,4,4,2,5\%,TSH) \tag{5.2}$$

with the unidentified variables being assigned to some of the limited set of values:

- the pair of number of families and the number of genotypes per family $(f,k) \in \{(100,80),(100,100),(200,60),(200,80),(200,100),(200,200),(300,60),(300,80),$ $(400,60),(400,80),(400,100),(200,60),(200,80)\}$;
- selection intensity at stage one $t_1 \in \{5\%,10\%,15\%,20\%,25\%,30\%,35\%\}$;
- selection index at stage one $d_1 \in \{CCS,TSH,0.0625,0.125,0.1875,0.25,0.375,0.5,0.75\}$ $$d_1 \in \{CCS,TSH,16\cdot CCS+TCH,8\cdot CCS+TCH,16\cdot CCS+3\cdot TCH,4\cdot CCS+TCH, \\ 8\cdot CCS+3\cdot TCH,2\cdot CCS+TCH,4\cdot CCS+3\cdot TCH\};$$
- selection intensity at stage three $t_3 \in \{5\%,10\%,15\%\}$;
- selection index at stage three $d_3 \in \{TSH,0.0625\} = \{TSH,16\cdot CCS+TCH\}$.

Note that those guidelines are generalised to encompass all the data from the highest yielding family selection designs (Table 5.4). According to the regression tree analysis results however, the guidelines to be followed are narrowed further to give:

$$(100,80,1,1,4,20\%,8\cdot CCS+TCH,90\%,vs,1,1,2,15\%,TSH,4,4,2,5\%,d_4) \tag{5.3}$$

where $d_4 \in \{TCH,TSH,16\cdot CCS+TCH\}$.

The chapter presented here has reported on the results of the ASSSO, which have identified some guidelines to be followed in order to achieve genetic gains for economic value that were higher than those currently obtained in the region. However, the ASSSO results also indicated that the optimal selection system for the Burdekin region is yet to be found, which highlighted limitations of the optimisation algorithm and rose new issues and questions for future detailed in the next chapter.

Chapter 6

Conclusion and future work

The research presented in this thesis investigated new methods for evaluating alternative sugarcane selection strategies and for designing efficient sugarcane selection systems. To achieve this, two new computational techniques have been developed: the simulation model SSSM and the optimisation algorithm ASSSO.

The simulation model SSSM is a method for the evaluation of alternative selection systems prior to their field trials and is of potential economic significance. The SSSM was verified for its accuracy and it was further analysed for its sensitiveness to any change in the initial set of estimated variance components. Being a user-friendly application the SSSM can be used independently, and thus be updated for other sugarcane breeding regions or for other crop.

Furthermore, this research has developed a new efficient measure of the performance of selection systems, the genetic gain for economic value $\widetilde{G}$ that utilises the "secret weapon" of the SSSM: the true yield of each genotype that it generates. Nevertheless, the SSSM have a number of limitations, which in a longer timeframe, with a larger number of breeders using it and thus expanding its use into other sugarcane breeding regions, could be addressed.

The optimisation algorithm ASSSO represents a new approach to designing and optimising efficient selection designs. It provides a new dimension to the application of mathematical optimisation techniques in breeding programs, maintaining the relevance and the applicability of its findings to the real-life problem. A set of industry related and other constraints were defined, as well as the optimisation upper bound, in order to increase the efficiency of the optimisation algorithm.

The principal constraint in effectiveness of the ASSSO is the execution time, which allied with a limited timeframe available precluded further investigations and improvement of its performance.

One way to make the ASSSO faster would be by lowering its precision and rather than simulating each node 100 times, using only 10 simulations for example. Another way to lower the execution time would be by narrowing down the selection variable options in some cases, thus allowing the optimisation process to go faster towards the optimum. On the other hand, not exploring selection index options for CCS greater than $16 \cdot CCS + TCH$ (Jackson and McRae, 2001) is a limitation of the ASSSO. Thus, it is questionable how cutting down options on one end and adding them elsewhere would help the ASSSO performance. Improving the performance of the algorithm by investigating more time and storage efficient objects and functions within its code, is another way of making it faster.

Making the algorithm perform faster would automatically address the problem of optimal selection system not being reached within 100,000 nodes, as more nodes could be used as a limit. Also being able to run the algorithm more times while changing and limiting its variable options would allow for an additional investigation of its performance as well as improving on its performance further.

Nevertheless, by applying both methods to the Burdekin region and having two plant breeders from the region involved in evaluating their performance, has suggested alternative selection designs that have the potential to achieve higher gains $\widetilde{G}$ for the Burdekin region than those currently used in the region. Thus, not only has the new method of evaluation of a selection system been developed, but it usefulness has also been verified for an existing breeding program. The approach is therefore, of potentially great significance in helping develop efficient breeding programs, and thus serves as an example how fruitful a cooperation across these two diverse disciplines: plant breeding and mathematics can be.

Furthermore, the results of this research validated the existing research on the effect of competition between neighbouring plants and the way different plot sizes affect the magnitudes of the two measured traits. The results further gave new evidence in favour of using family selection in early stages of selection and generally illustrated its wide application in all agricultural aspects of plant breeding.

6.2 Future directions

Being a multi-disciplinary research project, the research reported in this thesis is of relevance to both operations research and agriculture. The most important directions for future research are listed below, divided into two groups: mathematical applications future research points and agricultural ones.

From the viewpoint of the mathematical applications, future research directions would be:

- to expand the SSSM to include the ratoon crop simulation and thus encompass all aspects of selection, which due to its complexity, was not possible in the course of this research;

- to develop a faster application of the ASSSO, which due to the time limitations was not possible within the course of this research;

- to apply heuristic optimisation techniques such as tabu search, genetic algorithms or simulated annealing to optimise selection systems and thus compare their performance to the algorithm ASSSO developed in this thesis;

From a plant breeding point of view, future research directions are:

- to expand the SSSM to other sugarcane breeding regions, which would allow a larger group of plant breeders to use the tool developed, which in turn would provide with useful feedback to be used when developing newer versions of the SSSM prototype;

- more effort should be invested in estimating costs associated with all aspects of selection as well as the cost associated with changing the selection system within a region. This would provide scientists with a limit of how large the $\widetilde{G}$ value of the proposed selection system needs to be in order to justify the change of the selection design. Apart from the trade off between a selection system's performance and the costs associated with its implementation, the trade off between the cost of selection and what it achieves is also relevant to crop breeding.

- an investigation should be carried out to determine whether or not budget makes a difference to what is an optimal design. If for example, a million dollar budget was given, would the system design of an optimal system be the same as for a 250K budget, but simply allow the use of a larger starting population.

- to specifically design field experiments that would accurately estimate all the required variance components without which the simulation model would be of limited use. This should include the estimation of ratoon crop variance components as well as plot sizes other than those used in this study. Furthermore, in order to utilise the SSSM fully, ongoing research is required in any change of the effects identified in sensitivity analysis.

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Appendix A

Derivation of the correlation from MANOVA output

To show the way a correlation was calculated, let the following two tables (Table A.1 and Table A.2 respectively), represent the between-group covariance matrix and the tests of between-group effects matrix.

The correlation formula used was:

$$\rho_{l,c} = \frac{\operatorname{cov}(l,c)}{\sqrt{\sigma^2_{g_l}}\sqrt{\sigma^2_{g_c}}}$$

where $\operatorname{cov}(l,c)$ was the covariance between the large row plot and the competition effect (difference between the small and the large row plot measurements for the traits), $\sigma^2_{g_l}, \sigma^2_{g_c}$ were respectively the genetic variances for the large row plots and competition.

Table A.1

Example of the Between-group SSCP (Sum of Squares Cross Product) matrix for CCS between large plot size measurements and the competition (difference between the large plot and small plot measurements), data set A

Source	Dependant Variable	Large Plot	Competition
Genotype	Large Plot	312.775	-120.382
	Competition	-120.382	521.026
Error	Large Plot	187.115	-35.190
	Competition	-35.190	36.620

The two variances were calculated using the mean square estimates from the Table A.2 in the following formula:

$$\text{MS Genotype} = \text{MS Error} + 2\sigma_g^2$$

Table A.2

Example of the tests of between-groups effects for CCS between large plot measurements and the competition (difference between the large plot and small plot measurements), data set A

Source	Dependent Variable	Type III SS	df	Mean Square	F	Sign
Genotype	Large Plot	512.026	52	10.020	14.502	0.000
	Competition	312.775	52	6.015	1.704	0.028
Error	Large Plot	36.620	53	0.691		
	Competition	187.115	53	3.530		

The covariance was calculated using the results from the Table A.1 in the following formula:

$$\frac{Between(Competition \times L\arg ePlot)}{df} = \frac{Within(Comeptition \times L\arg ePlot)}{df} + 2\operatorname{cov}(l,c)$$

So, $$\frac{-120.382}{52} = \frac{-35.190}{53} + 2\operatorname{cov}(l,c)$$

to give $$\operatorname{cov}(l,c) = -0.8255\,.$$

Finally, according to the correlation formula:

$$\rho_{l,c} = -0.3429\,.$$

Appendix B

A detailed illustration of the simulation of the selection system from the Burdekin region

A selection system from the Burdekin region was simulated using the simulation model SSSM. Tables B.1 to B.10 illustrate the way the simulation model SSSM works.

Table B.1

Starting population of two hundred families of stage one generated in SSSM, where g_i is the genetic effect, c_{ik} competition effect, x_{ij} genotype by environment interaction effect, e_{ijk} error effect, and G_i the genetic gain for economic value for a family i planted in environment j and plot size k

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
1	0.57	0.13	0.05	1.76	14.50	-22.84	3.48	3.58	16.31	150.53	21.83	$ 2,113.34
2	0.29	0.14	0.67	0.64	13.74	-3.09	-15.25	1.65	9.38	142.69	19.61	$ 2,467.46
3	-0.64	-0.78	-0.03	0.14	10.69	16.76	-11.63	-2.04	-8.81	144.27	15.42	$ 2,436.09
4	-0.93	-0.63	-0.15	-0.91	9.38	10.56	-10.18	-3.03	-13.50	133.86	12.55	$ 2,155.61
5	-0.39	-0.66	0.22	1.14	12.31	-8.21	-1.00	-3.58	3.94	141.15	17.38	$ 2,034.43
6	-1.90	-0.18	0.40	1.23	11.54	2.81	-30.70	-4.74	-15.19	102.19	11.79	$ 1,523.39
7	-0.81	0.17	-0.10	1.71	12.97	-5.47	-10.13	2.26	-21.38	115.28	14.96	$ 1,898.06
8	-1.19	-0.12	-0.79	0.64	10.55	-21.33	-9.30	-7.11	12.19	124.45	13.13	$ 1,419.68
9	0.80	-0.09	0.15	-1.12	11.74	19.16	-5.12	5.24	-18.38	150.90	17.71	$ 3,273.10

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
10	0.51	-0.48	0.30	0.92	13.26	2.92	-21.54	0.00	14.44	145.82	19.33	$ 2,720.47
11	0.29	0.84	0.46	1.12	14.71	-22.62	-19.63	-0.66	6.38	113.47	16.70	$ 2,006.92
12	0.83	-0.38	-0.38	-0.60	11.47	6.91	-5.60	-1.10	-27.94	122.27	14.03	$ 2,979.78
13	-0.78	-0.44	0.09	-1.50	9.37	-12.79	-5.18	-2.04	8.81	138.80	13.01	$ 1,762.25
14	1.06	0.01	0.60	-0.39	13.28	12.72	23.02	0.77	-9.38	177.14	23.52	$ 3,246.55
15	0.17	0.33	0.01	-1.07	11.45	-9.28	-15.66	3.86	-14.06	114.86	13.15	$ 2,268.55
16	-0.77	0.29	-0.49	0.96	11.99	19.11	-11.48	-4.69	18.75	171.70	20.58	$ 2,410.80
17	-0.38	-1.20	0.27	-0.73	9.96	11.80	-10.09	-6.06	-1.50	144.14	14.35	$ 2,468.64
18	0.82	-0.30	-0.69	-0.09	11.74	-22.00	-11.98	1.38	5.25	122.65	14.40	$ 2,240.82
19	-0.14	-0.35	0.72	-1.53	10.71	-1.31	-8.78	0.44	11.63	151.98	16.28	$ 2,304.72
20	-0.38	-0.93	-0.26	-1.37	9.07	3.76	-6.74	10.69	-19.13	138.58	12.57	$ 2,298.42
21	-0.51	-0.29	0.50	-0.37	11.33	-18.17	1.30	-0.77	13.88	146.23	16.57	$ 1,768.76
22	1.58	0.42	1.01	0.96	15.97	-8.95	-19.98	-1.82	-5.63	113.63	18.14	$ 2,917.99
23	0.20	0.07	0.40	-0.77	11.89	-10.30	17.95	-2.81	-9.75	145.09	17.26	$ 2,255.57
24	-0.53	0.42	0.20	-0.74	11.35	13.73	-3.14	-3.36	7.13	164.36	18.65	$ 2,429.16
25	-0.15	0.41	0.04	-0.53	11.76	1.81	-2.52	-4.46	-11.25	133.58	15.71	$ 2,367.75
26	-1.40	-0.77	-0.11	0.05	9.77	6.98	8.68	-5.84	-18.75	141.07	13.78	$ 1,847.29
27	0.04	-0.23	-0.33	-1.39	10.10	-2.44	9.93	-6.72	16.31	167.08	16.87	$ 2,365.76
28	-0.95	0.08	0.13	-0.94	10.33	-14.11	31.51	-9.09	9.56	167.87	17.34	$ 1,662.37
29	0.19	0.13	0.71	-0.21	12.82	29.07	-28.99	3.14	-9.00	144.23	18.49	$ 3,171.93
30	-2.04	-0.66	0.05	0.34	9.70	-10.06	10.36	-0.61	-1.31	148.39	14.39	$ 1,246.95
31	0.41	-0.63	0.50	1.60	13.88	15.72	14.06	-1.54	-8.44	169.79	23.56	$ 2,978.24
32	-0.48	0.14	0.31	-0.51	11.47	10.79	16.07	0.77	-15.19	162.44	18.63	$ 2,395.04
33	-0.65	0.17	-0.55	0.09	11.07	0.24	16.93	-2.76	-6.00	158.41	17.53	$ 2,089.92
34	-0.90	0.16	0.23	0.84	12.32	5.47	4.39	10.80	-12.19	158.47	19.52	$ 2,068.52
35	0.90	-0.49	-0.82	0.20	11.79	-3.97	5.33	7.44	-5.81	152.99	18.03	$ 2,734.41
36	0.62	0.61	0.62	0.36	14.22	10.51	7.98	-2.09	51.56	217.96	30.99	$ 2,964.35
37	-0.29	0.21	-0.30	1.33	12.96	6.78	9.44	-3.09	-7.13	156.01	20.21	$ 2,406.10
38	0.20	-0.52	0.09	1.47	13.23	3.76	-1.00	3.75	13.69	170.20	22.52	$ 2,583.19
39	-0.71	-0.13	-0.07	0.09	11.17	-5.82	-0.38	2.70	22.88	169.37	18.93	$ 1,934.08
40	1.13	-0.43	0.37	0.72	13.80	-0.29	1.22	-6.28	0.19	144.84	19.98	$ 2,944.49
41	0.89	-0.45	0.18	0.76	13.38	16.23	-6.55	-8.32	27.00	178.36	23.86	$ 3,247.84
42	-0.05	0.75	1.01	-0.93	12.78	2.99	-7.10	0.39	2.06	148.34	18.95	$ 2,441.76
43	-0.32	-0.47	0.52	0.38	12.12	9.29	-20.19	-0.55	7.88	146.43	17.74	$ 2,448.27
44	-2.17	0.82	-0.37	1.34	11.63	5.97	-16.37	1.76	16.13	157.48	18.31	$ 1,436.95
45	1.66	-0.38	0.36	1.45	15.09	-2.91	-4.84	-1.93	-3.38	136.95	20.66	$ 3,125.25
46	0.25	0.26	0.17	-1.30	11.38	-13.70	20.68	-2.92	-31.31	122.74	13.97	$ 2,199.70
47	0.02	-0.03	0.01	0.73	12.73	1.96	26.35	10.09	27.75	216.15	27.52	$ 2,454.07
48	1.64	0.00	-0.73	-0.99	11.92	21.87	40.37	-1.71	3.75	214.28	25.54	$ 3,810.29
49	-1.45	0.70	-0.47	0.16	10.95	-13.77	-29.60	-7.83	8.25	107.05	11.72	$ 1,448.32
50	-0.78	-0.49	0.28	0.31	11.32	13.08	-5.67	-3.20	-36.00	118.21	13.38	$ 2,284.96
51	1.07	0.77	-0.19	1.19	14.85	2.01	4.32	-4.30	6.94	158.97	23.60	$ 2,974.18
52	0.73	-0.05	-0.04	-0.09	12.55	8.92	6.32	6.56	1.31	173.12	21.72	$ 2,978.71
53	-0.20	0.26	0.06	0.47	12.59	5.43	7.65	5.35	7.31	175.74	22.12	$ 2,421.98
54	-0.39	0.92	0.55	-0.44	12.65	-4.52	8.24	-13.83	-25.88	114.01	14.42	$ 2,115.62
55	-2.09	-0.10	-0.34	0.12	9.59	-21.26	8.86	3.47	9.75	150.82	14.46	$ 1,042.27
56	-0.85	0.25	0.40	0.15	11.95	22.65	1.16	-1.21	-29.44	143.16	17.10	$ 2,437.83
57	0.97	0.28	-0.09	-0.28	12.88	5.14	1.27	1.49	-17.25	140.64	18.11	$ 3,006.31
58	-0.03	0.24	-0.78	-0.13	11.29	-16.06	1.44	-9.15	15.38	141.60	15.98	$ 2,019.51
59	-1.10	0.29	0.15	-0.11	11.23	29.43	-4.60	3.20	-14.63	163.40	18.35	$ 2,430.26
60	-1.44	-0.43	-0.33	0.45	10.26	-9.75	17.06	2.15	18.00	177.46	18.21	$ 1,523.49
61	2.05	-0.38	0.06	0.00	13.74	14.57	-3.55	-6.34	31.31	185.99	25.55	$ 3,827.54
62	0.32	0.31	0.17	0.14	12.95	1.45	-15.58	0.83	3.38	140.08	18.13	$ 2,591.36

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
63	-0.59	0.27	0.90	0.16	12.75	-8.06	-13.87	0.00	-15.94	112.14	14.30	$ 1,946.87
64	0.47	0.26	-0.15	0.82	13.39	26.17	-9.16	-5.51	15.94	177.44	23.76	$ 3,263.47
65	-0.46	-0.37	0.22	0.99	12.37	-2.82	11.61	-1.98	10.88	167.68	20.74	$ 2,115.36
66	-1.90	-0.43	0.34	-0.11	9.91	-19.11	-32.12	-8.54	-7.69	82.53	8.18	$ 1,157.28
67	0.41	-1.20	0.60	1.71	13.51	-1.32	-24.14	15.16	33.00	172.69	23.33	$ 2,566.68
68	-0.37	0.35	0.00	-0.49	11.50	4.28	-19.58	-4.63	-5.81	124.25	14.29	$ 2,313.50
69	-0.62	0.33	0.43	0.08	12.21	-5.28	-5.31	6.23	11.63	157.26	19.20	$ 1,986.83
70	-0.92	0.30	0.65	-1.23	10.80	-20.76	16.49	-6.89	19.50	158.35	17.11	$ 1,541.73
71	0.88	-0.32	0.03	-0.87	11.71	8.07	6.42	4.13	-1.13	167.50	19.62	$ 3,035.08
72	1.74	-0.27	0.17	-0.17	13.47	4.58	7.75	3.03	-6.56	158.79	21.38	$ 3,376.43
73	0.26	-0.32	-0.30	-0.15	11.49	11.01	-10.92	2.04	0.38	152.50	17.53	$ 2,785.94
74	-1.60	0.36	0.09	-0.06	10.79	0.67	-1.04	-6.23	23.44	166.84	18.01	$ 1,633.31
75	1.92	0.43	-0.02	-0.43	13.90	-9.92	-0.80	0.88	-11.81	128.35	17.85	$ 3,047.86
76	0.30	0.08	0.38	0.13	12.89	-15.04	0.11	-3.97	22.13	153.22	19.74	$ 2,188.05
77	-1.84	-0.29	-0.11	0.15	9.92	-7.68	-23.31	-5.18	-33.94	79.89	7.92	$ 1,375.47
78	0.44	-0.25	0.27	0.24	12.70	-36.93	-21.65	-1.76	-3.56	86.10	10.93	$ 1,720.43
79	-0.29	0.06	0.41	1.00	13.18	6.06	-5.50	-7.88	-32.81	109.86	14.48	$ 2,393.65
80	-1.84	-0.24	0.74	1.54	12.19	13.22	-3.48	-3.20	7.69	164.22	20.02	$ 1,726.74
81	-0.90	0.46	0.05	1.76	13.37	-23.35	-4.31	8.93	-26.63	104.64	13.99	$ 1,500.09
82	0.27	-0.71	0.51	0.12	12.19	21.51	-1.24	-1.10	27.56	196.73	23.97	$ 3,039.89
83	-0.60	0.55	0.32	0.78	13.05	4.76	-0.78	-6.45	2.44	149.97	19.58	$ 2,207.27
84	-0.91	0.51	-0.57	0.82	11.86	0.90	-10.80	4.41	34.31	178.82	21.21	$ 1,976.91
85	-1.16	0.11	0.71	1.08	12.74	-8.48	-10.95	0.17	3.56	134.30	17.11	$ 1,673.80
86	0.67	-0.14	0.37	0.40	13.30	-3.12	-28.91	-4.96	-15.94	97.08	12.91	$ 2,647.21
87	-0.85	-0.19	0.56	1.51	13.03	-5.82	-23.03	-1.16	-22.50	97.49	12.71	$ 1,869.02
88	0.26	0.16	0.00	0.61	13.03	-19.63	1.67	-7.39	-1.31	123.35	16.07	$ 2,063.30
89	-0.64	0.65	-0.16	-1.19	10.66	9.33	16.44	-10.86	-25.13	139.79	14.90	$ 2,283.13
90	0.51	0.63	0.73	0.77	14.64	16.09	19.82	-0.06	-47.06	138.80	20.32	$ 3,039.10
91	-0.42	-0.55	0.08	0.30	11.42	2.21	-3.89	8.05	6.00	162.37	18.54	$ 2,244.84
92	2.11	0.78	-0.41	1.14	15.61	-1.47	-14.99	6.01	-12.75	126.80	19.80	$ 3,381.98
93	-0.86	-0.13	0.32	-0.62	10.71	6.11	8.62	-2.32	7.88	170.29	18.23	$ 2,103.17
94	0.96	-0.54	0.07	1.31	13.80	-11.12	9.21	-0.39	12.56	160.27	22.11	$ 2,577.20
95	1.64	0.75	0.25	-0.48	14.16	3.88	12.20	-3.97	4.88	166.99	23.65	$ 3,308.49
96	-0.18	0.31	0.12	-0.26	11.99	21.68	39.43	2.43	-30.19	183.35	21.98	$ 2,792.72
97	-1.45	1.07	0.67	0.29	12.59	-3.23	10.96	1.43	8.25	167.41	21.07	$ 1,637.72
98	-0.58	-0.05	0.37	0.31	12.05	2.87	11.83	-7.88	-25.13	131.68	15.87	$ 2,176.15
99	1.40	0.33	-0.44	-0.56	12.73	-7.69	1.21	-12.62	-15.00	115.89	14.76	$ 2,870.17
100	0.16	0.01	-0.90	0.02	11.28	-11.80	2.49	-0.72	-24.56	115.41	13.02	$ 2,202.30
101	0.02	0.00	-0.17	0.63	12.48	3.15	4.86	7.55	38.81	204.38	25.52	$ 2,481.53
102	-0.20	-0.35	0.20	0.20	11.85	-7.17	-5.90	5.73	20.63	163.29	19.35	$ 2,146.61
103	-1.50	-0.97	0.08	-0.23	9.37	-0.62	-3.76	0.28	40.69	186.58	17.49	$ 1,659.08
104	0.52	-1.01	0.56	0.31	12.39	-3.74	-2.57	3.80	-20.25	127.24	15.76	$ 2,561.84
105	0.38	-0.30	0.22	-0.06	12.25	-16.63	6.06	6.89	12.94	159.25	19.51	$ 2,185.26
106	0.69	-0.97	0.39	-0.64	11.47	-5.64	0.56	5.02	18.19	168.13	19.28	$ 2,594.48
107	0.40	-1.35	-0.10	-0.03	10.91	25.34	-21.94	-3.03	41.06	191.43	20.89	$ 3,201.21
108	-1.21	-0.36	0.00	-1.23	9.20	-2.98	-7.95	3.25	-23.25	119.06	10.95	$ 1,754.60
109	0.66	-0.87	0.14	-1.15	10.79	-15.39	-7.21	2.26	11.25	140.91	15.20	$ 2,338.70
110	0.51	0.05	0.75	-0.30	13.00	-28.70	-20.18	1.32	-19.88	82.57	10.74	$ 1,949.24
111	0.27	0.40	0.40	0.25	13.32	-11.20	-18.57	-8.21	13.50	125.51	16.72	$ 2,268.92
112	-0.64	0.07	-0.40	-0.65	10.38	5.59	19.61	-15.16	22.50	182.54	18.95	$ 2,204.43
113	1.26	0.09	-0.79	-0.62	11.95	2.51	23.44	-5.13	-9.56	161.26	19.27	$ 3,082.60
114	0.99	0.11	-0.15	-0.01	12.94	-7.34	23.73	7.28	7.50	181.17	23.45	$ 2,690.52
115	-0.02	0.07	0.77	-1.15	11.67	-0.09	30.87	5.51	1.88	188.17	21.96	$ 2,389.14

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
116	-0.26	-0.73	0.09	-1.09	10.00	-7.45	-32.92	0.33	7.69	117.66	11.77	$ 2,109.26
117	1.04	0.16	-0.38	0.27	13.09	-28.87	-28.57	3.86	-24.75	71.67	9.38	$ 2,151.28
118	-3.04	0.05	0.02	-0.10	8.94	6.25	-8.28	-0.94	-2.44	144.59	12.92	$ 1,003.11
119	0.34	-0.71	0.46	-0.67	11.42	-1.92	14.15	-1.82	-8.06	152.35	17.40	$ 2,519.65
120	0.90	-0.20	0.29	-0.55	12.44	4.18	16.88	-9.70	-16.50	144.86	18.02	$ 2,946.81
121	-0.08	-0.61	-0.64	0.59	11.26	1.29	19.79	3.53	15.94	190.54	21.46	$ 2,389.01
122	-0.23	-0.64	0.19	-1.21	10.11	17.36	-15.63	-4.41	-14.06	133.26	13.48	$ 2,669.81
123	-1.55	0.52	0.36	0.87	12.20	-3.76	6.74	6.45	18.75	178.18	21.73	$ 1,580.63
124	0.52	0.20	-0.12	0.29	12.88	-22.60	7.22	-7.61	-1.31	125.71	16.19	$ 2,099.53
125	-0.21	0.16	-0.34	1.12	12.74	-1.27	-0.55	4.30	-5.63	146.86	18.70	$ 2,268.13
126	0.14	0.61	-0.62	2.40	14.53	-9.84	38.31	11.96	-57.75	132.68	19.28	$ 2,240.28
127	-0.83	0.16	0.64	-2.15	9.83	12.76	-8.64	7.44	-7.31	154.25	15.16	$ 2,254.70
128	0.95	-0.52	0.35	0.60	13.38	-8.28	-7.83	1.10	-13.88	121.11	16.20	$ 2,646.23
129	-0.59	-0.15	0.13	-1.23	10.17	21.05	-4.37	4.91	21.94	193.53	19.69	$ 2,554.44
130	-0.86	0.18	-1.02	0.87	11.16	5.06	3.90	-0.17	13.50	172.30	19.22	$ 2,080.57
131	-0.41	0.21	-0.19	-0.82	10.80	-20.95	-18.59	-1.05	-5.25	104.17	11.25	$ 1,751.91
132	0.73	-0.44	0.66	-0.68	12.27	7.35	-14.11	-5.51	-9.56	128.16	15.73	$ 2,939.88
133	-0.20	-0.48	-0.24	-2.40	8.68	-11.50	-4.16	-2.43	-4.88	127.04	11.03	$ 2,049.59
134	-0.42	0.25	0.53	-1.73	10.63	-17.34	-2.99	-3.47	-10.88	115.32	12.26	$ 1,825.24
135	-0.58	0.27	-0.02	-0.42	11.26	9.26	0.14	3.36	-3.19	159.57	17.96	$ 2,313.06
136	1.40	0.30	0.39	0.87	14.95	22.92	-9.84	2.37	16.88	182.33	27.25	$ 3,705.04
137	0.94	0.00	0.23	0.91	14.08	13.50	-8.59	-6.89	-3.00	145.03	20.41	$ 3,204.12
138	0.03	0.34	-0.75	-0.13	11.50	1.19	-8.30	1.16	20.63	164.67	18.94	$ 2,440.28
139	1.28	0.81	-0.54	0.43	13.98	9.23	-6.07	12.62	-3.56	162.21	22.68	$ 3,270.92
140	0.11	-0.01	0.82	1.88	14.80	-0.36	4.01	2.26	-31.88	124.04	18.35	$ 2,444.41
141	-0.85	-0.04	-0.19	0.01	10.92	14.86	6.55	1.32	-3.19	169.55	18.52	$ 2,283.98
142	0.33	0.32	0.18	0.60	13.43	2.83	7.48	-10.03	-30.94	119.34	16.02	$ 2,629.07
143	-1.65	1.04	-0.29	-0.34	10.76	-6.01	21.33	0.00	-1.31	164.01	17.65	$ 1,495.10
144	0.48	-0.03	0.09	-0.85	11.70	6.46	-1.13	-0.83	-25.50	129.01	15.09	$ 2,792.04
145	0.24	-0.33	0.86	1.06	13.82	4.21	0.27	-6.72	10.13	157.89	21.82	$ 2,615.56
146	-0.66	-0.01	0.37	-0.66	11.04	11.13	13.76	4.85	-6.75	172.99	19.10	$ 2,307.82
147	-0.86	-0.02	-0.12	-0.06	10.95	-8.86	2.22	3.64	37.31	184.31	20.18	$ 1,805.33
148	-1.23	1.03	0.25	-0.05	12.00	-10.08	2.45	8.54	3.94	154.85	18.58	$ 1,612.17
149	0.60	-1.03	-0.55	-1.29	9.74	-13.43	4.09	-5.90	-15.19	119.58	11.64	$ 2,359.99
150	-0.32	-1.27	0.67	-0.35	10.73	-6.01	6.28	5.51	-21.75	134.04	14.38	$ 2,112.47
151	0.94	1.34	0.03	-0.19	14.12	8.77	21.05	-9.20	12.19	182.81	25.81	$ 3,081.65
152	-0.70	0.04	0.17	-0.16	11.35	17.00	26.25	3.14	-24.19	172.20	19.55	$ 2,408.00
153	0.44	0.05	0.97	-0.67	12.79	10.75	-11.09	-4.91	-40.69	104.06	13.31	$ 2,876.49
154	-0.44	0.01	-0.17	-0.48	10.92	-7.45	8.67	6.67	6.38	164.26	17.94	$ 2,025.29
155	1.81	0.13	-0.36	-0.45	13.12	-12.51	-0.81	0.77	-12.19	125.26	16.43	$ 2,921.44
156	-1.21	-0.84	-0.66	0.12	9.41	12.84	2.08	-2.98	8.25	170.19	16.02	$ 2,052.29
157	0.90	-0.23	-0.12	-0.85	11.71	-21.27	-10.39	9.70	-10.13	117.92	13.80	$ 2,292.70
158	-0.08	-0.68	-0.24	-0.16	10.83	7.58	-6.80	-1.38	8.63	158.02	17.11	$ 2,529.59
159	-1.14	-0.70	0.14	-0.12	10.19	3.68	-5.97	-2.09	3.56	149.18	15.20	$ 1,915.82
160	-1.46	0.49	-0.34	1.60	12.29	-6.85	-21.86	4.91	-1.50	124.70	15.33	$ 1,566.62
161	0.55	0.18	0.06	-0.43	12.35	-0.56	-18.04	3.75	-25.69	109.47	13.52	$ 2,652.09
162	1.22	0.63	-0.46	0.13	13.52	19.68	-14.08	-1.05	-15.38	139.18	18.82	$ 3,517.55
163	0.08	0.58	0.33	0.16	13.14	16.12	-11.99	5.90	17.25	177.28	23.30	$ 2,810.60
164	-0.78	0.14	-0.15	-0.88	10.34	10.29	-10.50	-8.43	-13.13	128.23	13.26	$ 2,230.69
165	-1.13	0.12	0.22	-0.12	11.10	10.05	31.22	-3.47	4.31	192.11	21.32	$ 2,041.15
166	-1.80	-0.17	-0.20	0.44	10.27	-13.57	-34.09	-4.57	10.50	108.27	11.12	$ 1,295.29
167	0.46	0.20	0.61	1.91	15.19	-6.59	-25.41	-5.24	-20.81	91.95	13.97	$ 2,463.18
168	0.31	0.18	-0.30	-1.16	11.03	8.63	-7.66	-6.89	12.56	156.64	17.28	$ 2,755.64

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
169	-0.59	0.70	0.14	0.16	12.41	23.89	16.45	-2.92	-6.56	180.86	22.45	$ 2,612.69
170	0.50	-0.49	-0.04	0.80	12.76	14.66	5.45	15.87	-10.88	175.12	22.35	$ 3,001.90
171	0.26	-0.53	-0.21	1.10	12.62	1.19	-17.77	-4.63	6.19	134.98	17.03	$ 2,552.02
172	0.68	0.28	-0.40	-0.65	11.90	6.92	-14.91	6.23	-12.38	135.86	16.17	$ 2,901.91
173	-0.82	0.23	-0.78	-0.62	10.01	5.29	-2.14	1.43	8.06	162.64	16.28	$ 2,105.47
174	0.99	0.25	0.49	0.62	14.34	-2.52	23.89	-9.65	14.81	176.54	25.32	$ 2,817.10
175	0.69	0.32	-0.28	-1.15	11.57	-7.12	8.07	3.03	8.44	162.42	18.79	$ 2,556.48
176	0.49	-0.40	0.09	-0.30	11.88	7.00	10.85	2.04	17.44	187.33	22.26	$ 2,810.96
177	-0.40	-0.05	-0.40	-0.27	10.89	15.35	0.84	-6.50	-2.44	157.25	17.12	$ 2,537.08
178	2.23	0.34	0.04	1.17	15.78	3.56	12.96	-8.93	-9.56	148.02	23.36	$ 3,589.86
179	0.32	-0.36	-0.11	-0.62	11.23	0.74	15.10	-0.11	-16.50	149.23	16.76	$ 2,572.05
180	1.00	1.15	0.29	-0.55	13.88	-10.56	15.92	10.25	-7.13	158.48	22.00	$ 2,612.49
181	-0.01	-0.34	-0.48	0.69	11.86	-3.83	3.63	7.17	-13.31	143.65	17.04	$ 2,309.29
182	-1.04	0.35	0.79	-1.05	11.06	-7.20	4.96	1.05	-6.75	142.06	15.71	$ 1,755.39
183	0.19	-1.00	-0.23	0.27	11.21	23.36	19.68	4.80	13.88	211.71	23.74	$ 3,035.85
184	2.84	-0.24	0.53	-0.72	14.41	6.49	21.99	8.93	-8.06	179.35	25.84	$ 3,986.78
185	-1.19	0.34	-0.34	1.12	11.94	5.10	34.78	6.61	31.13	227.62	27.17	$ 1,919.30
186	0.14	0.35	-0.62	0.41	12.28	-24.91	-1.78	1.65	21.00	145.97	17.93	$ 1,888.33
187	-0.86	-1.38	0.58	0.02	10.37	7.26	1.56	4.41	-0.56	162.66	16.86	$ 2,127.38
188	0.99	-0.31	0.00	0.63	13.31	-3.12	-8.12	3.31	-5.81	136.26	18.14	$ 2,800.47
189	-0.64	-0.32	0.14	-1.15	10.04	-15.39	-7.21	-1.38	45.94	171.96	17.26	$ 1,771.15
190	-0.94	0.40	-0.35	-0.94	10.18	1.44	18.41	-2.48	4.88	172.24	17.53	$ 1,971.96
191	-0.41	0.37	-0.76	-0.92	10.29	-8.06	22.13	0.77	-12.19	152.66	15.70	$ 2,029.60
192	1.99	0.40	-0.08	1.12	15.43	16.02	-13.54	-4.08	21.38	169.77	26.19	$ 3,836.54
193	-0.27	-0.26	0.31	-0.64	11.14	10.08	-11.91	-5.35	-0.19	142.63	15.89	$ 2,488.12
194	0.94	-0.25	-0.16	-0.03	12.50	-28.07	8.41	1.82	25.13	157.29	19.66	$ 2,133.66
195	-0.06	-0.29	0.91	0.62	13.19	9.01	36.12	0.94	-34.69	161.38	21.28	$ 2,576.33
196	-0.27	-0.22	0.08	-0.33	11.26	1.25	-30.02	-13.83	-2.25	105.15	11.84	$ 2,295.52
197	-1.46	0.44	0.58	0.22	11.77	-21.20	9.79	-0.33	15.75	154.02	18.13	$ 1,307.66
198	-0.67	0.43	-0.80	1.10	12.05	23.54	14.88	-1.21	-3.38	183.83	22.16	$ 2,557.69
199	1.22	0.57	-0.50	-0.65	12.64	-12.74	14.69	-2.15	2.06	151.87	19.20	$ 2,651.39
200	-0.41	0.50	-0.05	-0.04	12.00	12.96	19.15	-2.65	32.81	212.29	25.48	$ 2,476.51

Table B.2

Selected (based on their TSH values) sixty families from those generated in Table B.1, where g_i is the genetic effect, c_{ik} competition effect, x_{ij} genotype by environment interaction effect, e_{ijk} error effect, and G_i the genetic gain for economic value for a family i planted in environment j and plot size k

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
1	0.57	0.13	0.05	1.76	14.50	-22.84	3.48	3.58	16.31	150.54	21.83	$ 2,113.34
14	1.06	0.01	0.60	-0.39	13.28	12.72	23.02	0.77	-9.38	177.14	23.52	$ 3,246.55
16	-0.77	0.29	-0.49	0.96	11.99	19.11	-11.48	-4.69	18.75	171.70	20.58	$ 2,410.80
31	0.41	-0.63	0.50	1.60	13.88	15.72	14.06	-1.54	-8.44	169.79	23.56	$ 2,978.24
36	0.62	0.61	0.62	0.36	14.22	10.51	7.98	-2.09	51.56	217.96	30.99	$ 2,964.35
37	-0.29	0.21	-0.29	1.33	12.96	6.78	9.44	-3.09	-7.13	156.01	20.21	$ 2,406.10
38	0.20	-0.52	0.09	1.47	13.23	3.76	-1.00	3.75	13.69	170.19	22.52	$ 2,583.19
40	1.13	-0.43	0.37	0.72	13.80	-0.29	1.22	-6.29	0.19	144.84	19.98	$ 2,944.49
41	0.89	-0.46	0.18	0.76	13.38	16.23	-6.55	-8.32	27.00	178.36	23.86	$ 3,247.84
45	1.66	-0.38	0.36	1.45	15.09	-2.91	-4.84	-1.93	-3.38	136.95	20.66	$ 3,125.25
47	0.02	-0.03	0.01	0.73	12.73	1.96	26.35	10.09	27.75	216.15	27.52	$ 2,454.07
48	1.64	0.00	-0.73	-0.99	11.92	21.87	40.37	-1.71	3.75	214.28	25.54	$ 3,810.29
51	1.07	0.77	-0.19	1.19	14.85	2.01	4.32	-4.29	6.94	158.97	23.60	$ 2,974.18
52	0.73	-0.05	-0.04	-0.09	12.55	8.92	6.32	6.56	1.31	173.12	21.72	$ 2,978.71
53	-0.20	0.26	0.06	0.47	12.59	5.43	7.65	5.35	7.31	175.74	22.12	$ 2,421.98
61	2.05	-0.38	0.06	0.00	13.74	14.57	-3.55	-6.34	31.31	185.99	25.55	$ 3,827.54
64	0.47	0.26	-0.16	0.82	13.39	26.17	-9.16	-5.51	15.94	177.44	23.76	$ 3,263.47
65	-0.46	-0.38	0.22	0.99	12.37	-2.82	11.61	-1.98	10.88	167.68	20.74	$ 2,115.36
67	0.41	-1.20	0.60	1.71	13.51	-1.32	-24.14	15.16	33.00	172.69	23.33	$ 2,566.68
71	0.88	-0.32	0.03	-0.87	11.71	8.07	6.42	4.13	-1.13	167.49	19.62	$ 3,035.08
72	1.74	-0.27	0.17	-0.17	13.47	4.57	7.75	3.03	-6.56	158.79	21.38	$ 3,376.43
76	0.30	0.08	0.38	0.13	12.89	-15.04	0.11	-3.97	22.13	153.22	19.74	$ 2,188.05
80	-1.84	-0.25	0.74	1.54	12.19	13.22	-3.48	-3.19	7.69	164.22	20.02	$ 1,726.74
82	0.27	-0.71	0.51	0.12	12.19	21.51	-1.24	-1.10	27.56	196.72	23.97	$ 3,039.89
84	-0.91	0.52	-0.57	0.82	11.86	0.90	-10.80	4.41	34.31	178.82	21.21	$ 1,976.91
90	0.51	0.63	0.73	0.77	14.64	16.09	19.82	-0.05	-47.06	138.79	20.32	$ 3,039.10
92	2.11	0.78	-0.41	1.14	15.61	-1.47	-14.99	6.01	-12.75	126.79	19.80	$ 3,381.98
94	0.96	-0.54	0.07	1.31	13.80	-11.12	9.21	-0.39	12.56	160.27	22.11	$ 2,577.20
95	1.64	0.75	0.25	-0.48	14.16	3.88	12.20	-3.97	4.88	166.99	23.65	$ 3,308.49
96	-0.18	0.31	0.12	-0.26	11.99	21.69	39.43	2.43	-30.19	183.35	21.98	$ 2,792.72
97	-1.45	1.07	0.68	0.29	12.59	-3.23	10.96	1.43	8.25	167.41	21.07	$ 1,637.72
101	0.02	0.00	-0.17	0.63	12.48	3.15	4.86	7.55	38.81	204.38	25.52	$ 2,481.53
107	0.40	-1.36	-0.10	-0.03	10.91	25.34	-21.94	-3.03	41.06	191.43	20.89	$ 3,201.21
114	0.99	0.11	-0.15	-0.01	12.94	-7.34	23.73	7.28	7.50	181.17	23.45	$ 2,690.52
115	-0.02	0.07	0.77	-1.16	11.67	-0.09	30.87	5.51	1.88	188.17	21.96	$ 2,389.14
121	-0.08	-0.61	-0.64	0.59	11.26	1.29	19.79	3.53	15.94	190.54	21.46	$ 2,389.01
123	-1.55	0.52	0.36	0.87	12.20	-3.76	6.74	6.45	18.75	178.18	21.73	$ 1,580.63
129	-0.59	-0.15	0.13	-1.23	10.17	21.06	-4.37	4.91	21.94	193.53	19.69	$ 2,554.44
136	1.40	0.30	0.39	0.87	14.95	22.92	-9.84	2.37	16.88	182.33	27.25	$ 3,705.04
137	0.94	0.00	0.23	0.91	14.08	13.50	-8.59	-6.89	-3.00	145.03	20.41	$ 3,204.12
139	1.28	0.81	-0.54	0.43	13.98	9.23	-6.07	12.62	-3.56	162.21	22.68	$ 3,270.92
145	0.24	-0.33	0.86	1.06	13.82	4.21	0.27	-6.73	10.13	157.89	21.82	$ 2,615.56
147	-0.86	-0.02	-0.12	-0.06	10.95	-8.86	2.22	3.64	37.31	184.31	20.18	$ 1,805.33
151	0.94	1.34	0.03	-0.19	14.12	8.77	21.05	-9.20	12.19	182.81	25.81	$ 3,081.65
163	0.08	0.58	0.33	0.16	13.14	16.12	-11.99	5.90	17.25	177.28	23.30	$ 2,810.60
165	-1.13	0.12	0.23	-0.12	11.10	10.05	31.22	-3.47	4.31	192.11	21.32	$ 2,041.15
169	-0.59	0.70	0.14	0.16	12.41	23.89	16.45	-2.92	-6.56	180.86	22.45	$ 2,612.69

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
170	0.50	-0.49	-0.04	0.80	12.76	14.66	5.45	15.87	-10.88	175.12	22.35	$ 3,001.90
174	0.99	0.25	0.49	0.62	14.34	-2.52	23.89	-9.65	14.81	176.54	25.32	$ 2,817.10
176	0.49	-0.40	0.09	-0.30	11.88	7.00	10.85	2.04	17.44	187.33	22.26	$ 2,810.96
178	2.23	0.34	0.04	1.17	15.78	3.56	12.96	-8.93	-9.56	148.02	23.36	$ 3,589.86
180	1.00	1.15	0.29	-0.56	13.88	-10.56	15.92	10.25	-7.13	158.48	22.00	$ 2,612.49
183	0.19	-1.01	-0.23	0.27	11.21	23.36	19.68	4.80	13.88	211.71	23.74	$ 3,035.85
184	2.84	-0.24	0.53	-0.72	14.41	6.49	21.99	8.93	-8.06	179.35	25.84	$ 3,986.78
185	-1.19	0.34	-0.34	1.12	11.94	5.10	34.78	6.61	31.13	227.62	27.17	$ 1,919.30
192	1.99	0.40	-0.08	1.12	15.43	16.02	-13.54	-4.08	21.38	169.77	26.19	$ 3,836.54
194	0.94	-0.25	-0.16	-0.03	12.50	-28.07	8.41	1.82	25.13	157.29	19.66	$ 2,133.66
195	-0.06	-0.29	0.91	0.62	13.19	9.01	36.12	0.94	-34.69	161.38	21.28	$ 2,576.33
198	-0.67	0.43	-0.80	1.10	12.05	23.54	14.88	-1.22	-3.38	183.83	22.16	$ 2,557.69
200	-0.41	0.51	-0.05	-0.04	12.00	12.96	19.15	-2.65	32.81	212.29	25.48	$ 2,476.51

Table B.3

Sixty genotypes generated for one of selected families from Table B.2, where g_i is the genetic effect, c_{ik} competition effect, x_{ij} genotype by environment interaction effect, e_{ijk} error effect, and G_i the genetic gain for economic value for a genotype i planted in environment j and plot size k

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
201	-1.40	0.46	1.22	-0.41	11.87	-27.46	22.33	-8.17	-0.45	136.26	16.17	$ 1,220.66
202	-2.25	-0.33	0.10	-0.07	9.46	-53.34	19.27	-4.21	9.45	121.17	11.46	$ 482.49
203	0.36	0.78	-0.68	3.20	15.66	-38.52	-13.38	-14.90	-3.15	80.05	12.54	$ 1,654.47
204	0.50	-2.44	0.52	0.14	10.73	6.23	11.88	-6.82	47.25	208.54	22.37	$ 2,796.08
205	-0.53	0.01	0.14	-3.62	8.00	-15.71	11.50	-8.76	-2.25	134.79	10.78	$ 1,811.58
206	1.50	2.30	0.36	-2.34	13.82	-50.79	9.57	-11.70	-58.50	38.58	5.33	$ 1,727.58
207	0.81	0.24	-0.32	-0.50	12.23	-15.73	-24.17	-15.57	2.70	97.23	11.89	$ 2,396.38
208	-2.77	-0.34	0.24	-1.75	7.38	-1.79	-1.15	0.00	16.65	163.70	12.08	$ 1,027.55
209	1.22	0.27	0.42	3.46	17.36	-20.07	-0.70	3.62	-27.90	104.96	18.22	$ 2,456.42
210	1.67	-1.18	-0.29	-1.19	11.01	-31.66	21.74	-12.04	13.50	141.54	15.59	$ 2,322.12
211	0.29	-0.55	0.96	1.12	13.81	9.54	-9.60	7.24	-31.50	125.68	17.36	$ 2,764.68
212	0.03	0.06	0.53	-3.06	9.57	-48.43	-48.93	-0.42	48.60	100.82	9.65	$ 1,308.38
213	-3.14	-1.00	-0.70	-0.81	6.35	-57.98	-42.36	-1.77	34.20	82.09	5.22	$ 144.20
214	0.39	0.21	-0.04	0.45	13.02	-14.42	-29.47	-2.44	-11.25	92.42	12.03	$ 2,245.00
215	-2.11	-2.12	0.57	-1.89	6.46	14.31	-20.81	6.74	-1.35	148.88	9.62	$ 1,603.86
216	3.65	0.08	-0.17	-1.80	13.76	-13.24	21.00	-0.84	15.75	172.67	23.76	$ 3,716.37
217	0.15	-0.52	0.38	2.72	14.73	-42.12	49.51	11.53	31.05	199.98	29.45	$ 1,494.59
218	-2.22	-1.97	0.18	-5.54	2.44	-10.79	81.70	2.53	-14.85	208.59	5.10	$ 1,151.89
219	1.49	1.01	-0.15	-1.40	12.94	-36.65	6.40	-4.63	98.55	213.67	27.65	$ 2,114.45
220	0.10	1.80	-1.85	1.26	13.30	-24.22	10.90	4.29	-63.45	77.53	10.31	$ 1,888.73
221	-0.73	-0.77	0.56	-1.26	9.80	-50.72	-33.40	1.43	22.95	90.26	8.84	$ 1,009.81
222	2.63	2.27	-0.18	0.09	16.82	-24.51	44.39	-4.29	-21.15	144.44	24.29	$ 2,914.06
223	0.91	1.85	0.46	1.71	16.93	-49.82	49.34	-5.89	-42.30	101.33	17.15	$ 1,560.60
224	-0.73	1.45	0.61	0.32	13.66	-7.70	29.71	-1.85	-71.10	99.06	13.53	$ 1,889.39
225	0.71	-0.69	-0.70	-0.50	10.81	-34.85	-57.37	-3.28	20.70	75.20	8.13	$ 1,871.53
226	0.51	0.07	0.05	0.76	13.39	-1.74	11.05	-17.60	-23.85	117.86	15.78	$ 2,605.22
227	-1.22	-0.23	-0.26	-0.25	10.05	-20.55	11.73	-6.06	-35.55	99.57	10.01	$ 1,422.49
228	1.67	-0.53	1.06	2.75	16.96	-12.36	-5.70	-8.08	-73.35	50.51	8.57	$ 2,865.67
229	0.41	0.67	0.11	-4.12	9.07	-42.04	-6.56	-3.45	19.35	117.29	10.64	$ 1,585.92

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
230	-1.37	-0.25	0.86	-3.49	7.74	-51.76	-5.20	-4.97	41.40	129.47	10.02	$ 784.86
231	1.86	1.58	-0.65	1.31	16.10	-58.11	-72.25	-1.77	-54.00	-36.13	-5.82	$ 1,632.21
232	0.93	-0.10	0.00	0.07	12.90	-7.27	9.04	-3.12	-138.60	10.06	1.30	$ 2,663.93
233	0.58	-0.19	0.09	0.13	12.61	-64.08	-11.52	5.81	41.40	121.61	15.33	$ 1,102.35
234	-0.19	-1.31	0.81	-0.88	10.44	-42.39	-30.09	-1.43	-36.45	39.64	4.14	$ 1,368.96
235	-0.32	0.27	0.52	0.40	12.86	-1.48	-20.01	9.26	7.20	144.98	18.64	$ 2,212.21
236	-0.84	-1.22	-0.83	1.98	11.09	-9.45	-16.87	0.59	25.20	149.47	16.58	$ 1,802.91
237	2.19	-0.09	0.34	2.00	16.43	-34.57	-15.87	-0.67	36.45	135.34	22.24	$ 2,432.88
238	3.49	0.83	-1.37	-0.40	14.56	-8.36	32.97	-2.11	-9.90	162.61	23.68	$ 3,814.06
239	0.37	1.10	0.20	-1.57	12.10	-22.40	35.55	9.26	-19.80	152.61	18.47	$ 2,043.19
240	0.00	0.99	-0.09	-1.12	11.79	-25.15	-36.48	-4.29	73.80	157.88	18.61	$ 1,827.00
241	0.26	-1.09	0.65	-1.04	10.77	-39.11	-32.06	-5.89	7.65	80.58	8.68	$ 1,603.10
242	-1.42	-0.52	0.23	1.26	11.55	19.90	65.94	-7.75	64.35	292.45	33.79	$ 2,072.61
243	1.81	1.27	-1.31	-0.76	13.02	-39.12	17.93	-10.19	39.15	157.77	20.54	$ 2,160.81
244	1.18	-0.16	0.71	-0.70	13.03	-49.14	19.86	6.57	65.70	192.99	25.14	$ 1,667.66
245	-1.16	0.94	-0.08	2.21	13.90	-6.22	29.62	-17.60	-17.10	138.71	19.29	$ 1,715.51
246	-0.52	-0.42	0.51	0.94	12.50	-24.68	5.05	4.04	81.90	216.31	27.04	$ 1,625.49
247	-0.02	-0.37	-0.78	-0.14	10.68	-33.89	-37.41	-10.44	38.25	106.51	11.37	$ 1,619.92
248	-1.49	0.06	1.38	3.49	15.44	-50.08	6.62	1.43	-4.95	103.02	15.90	$ 777.05
249	1.58	0.51	-0.27	-2.99	10.84	-7.63	15.70	-19.87	-64.80	73.40	7.95	$ 2,956.03
250	0.06	-0.26	-0.15	1.48	13.12	-28.67	-4.67	-8.67	78.75	186.74	24.49	$ 1,769.51
251	0.70	0.39	0.42	1.57	15.07	7.64	54.75	2.44	8.55	223.39	33.67	$ 2,931.60
252	-0.89	0.09	-0.77	-2.12	8.32	-39.55	62.38	1.09	-37.35	136.58	11.36	$ 1,182.88
253	-0.09	-0.30	1.14	-0.45	12.29	10.10	-57.08	-6.31	-20.70	76.00	9.34	$ 2,583.15
254	0.71	0.45	0.08	2.79	16.03	-20.89	-44.71	-0.84	28.35	111.90	17.94	$ 2,221.74
255	3.01	0.80	0.79	-0.05	16.54	-30.91	-13.82	-2.19	-58.95	44.13	7.30	$ 2,859.07
256	1.60	-0.99	0.42	-1.31	11.72	-33.70	-8.43	0.59	24.75	133.21	15.61	$ 2,236.10
257	-0.67	-0.45	-1.06	-4.18	5.65	-63.87	32.10	-5.47	43.20	155.96	8.82	$ 760.70
258	-1.18	0.08	-0.69	1.57	11.77	-10.42	17.13	-9.43	-6.30	140.98	16.60	$ 1,628.30
259	-0.51	0.15	-0.03	0.23	11.84	-27.13	2.26	8.00	-19.80	113.33	13.42	$ 1,580.04
260	-1.14	-1.95	0.07	1.75	10.73	-15.89	6.30	6.15	-45.90	100.65	10.80	$ 1,542.46

Table B.4

Thirty genotypes selected (based on visual selection) from among the family whose clones were generated in Table B.3, where g_i is the genetic effect, c_{ik} competition effect, x_{ij} genotype by environment interaction effect, e_{ijk} error effect, and G_i the genetic gain for economic value for a genotype i planted in environment j and plot size k

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
201	-1.40	0.46	1.22	-0.41	11.87	-27.46	22.33	-8.17	-0.45	136.26	16.17	$ 1,220.66
204	0.50	-2.44	0.52	0.14	10.72	6.23	11.88	-6.82	47.25	208.54	22.37	$ 2,796.08
209	1.22	0.27	0.42	3.46	17.36	-20.07	-0.70	3.62	-27.90	104.96	18.22	$ 2,456.42
210	1.67	-1.18	-0.29	-1.19	11.01	-31.66	21.74	-12.04	13.50	141.54	15.59	$ 2,322.12
211	0.29	-0.55	0.96	1.12	13.81	9.54	-9.60	7.24	-31.50	125.68	17.36	$ 2,764.68
216	3.65	0.08	-0.17	-1.80	13.76	-13.24	21.00	-0.84	15.75	172.67	23.76	$ 3,716.37
217	0.15	-0.52	0.38	2.72	14.73	-42.12	49.51	11.53	31.05	199.98	29.45	$ 1,494.59
219	1.49	1.01	-0.16	-1.40	12.94	-36.64	6.40	-4.63	98.55	213.67	27.65	$ 2,114.45
222	2.63	2.27	-0.18	0.09	16.82	-24.51	44.40	-4.29	-21.15	144.44	24.29	$ 2,914.06
223	0.91	1.85	0.46	1.71	16.93	-49.82	49.34	-5.89	-42.30	101.33	17.15	$ 1,560.60
224	-0.73	1.45	0.61	0.32	13.66	-7.70	29.71	-1.85	-71.10	99.06	13.53	$ 1,889.39
226	0.51	0.07	0.05	0.76	13.39	-1.74	11.05	-17.60	-23.85	117.86	15.78	$ 2,605.22
233	0.58	-0.19	0.09	0.13	12.61	-64.07	-11.52	5.81	41.40	121.61	15.33	$ 1,102.35
235	-0.32	0.27	0.52	0.40	12.86	-1.48	-20.01	9.26	7.20	144.98	18.64	$ 2,212.21
236	-0.84	-1.22	-0.83	1.98	11.09	-9.45	-16.87	0.59	25.20	149.46	16.58	$ 1,802.91
237	2.19	-0.10	0.34	2.00	16.43	-34.57	-15.87	-0.67	36.45	135.34	22.24	$ 2,432.88
238	3.49	0.83	-1.37	-0.40	14.56	-8.36	32.97	-2.11	-9.90	162.61	23.68	$ 3,814.06
239	0.37	1.10	0.20	-1.57	12.10	-22.40	35.55	9.26	-19.80	152.61	18.47	$ 2,043.19
240	0.00	0.99	-0.09	-1.12	11.79	-25.15	-36.48	-4.29	73.80	157.88	18.61	$ 1,827.00
242	-1.42	-0.52	0.23	1.26	11.55	19.90	65.95	-7.75	64.35	292.45	33.79	$ 2,072.61
243	1.81	1.27	-1.31	-0.76	13.02	-39.12	17.93	-10.19	39.15	157.77	20.54	$ 2,160.81
244	1.18	-0.16	0.71	-0.70	13.03	-49.14	19.86	6.57	65.70	192.99	25.14	$ 1,667.66
245	-1.16	0.94	-0.08	2.21	13.90	-6.22	29.62	-17.60	-17.10	138.71	19.29	$ 1,715.51
246	-0.52	-0.43	0.51	0.94	12.50	-24.67	5.05	4.04	81.90	216.31	27.04	$ 1,625.49
248	-1.49	0.06	1.38	3.49	15.44	-50.08	6.62	1.43	-4.95	103.02	15.90	$ 777.05
250	0.06	-0.26	-0.16	1.48	13.12	-28.67	-4.67	-8.67	78.75	186.74	24.49	$ 1,769.51
251	0.70	0.39	0.42	1.57	15.07	7.64	54.75	2.44	8.55	223.39	33.67	$ 2,931.60
254	0.71	0.45	0.08	2.79	16.03	-20.89	-44.71	-0.84	28.35	111.90	17.94	$ 2,221.74
256	1.60	-0.99	0.42	-1.31	11.72	-33.70	-8.43	0.59	24.75	133.21	15.61	$ 2,236.10
258	-1.18	0.08	-0.69	1.57	11.78	-10.42	17.13	-9.43	-6.30	140.98	16.60	$ 1,628.30

Table B.5

Some of the one thousands and eight hundred generated and selected (based on TSH) genotypes (Table B.3 and Table B.4), from within selected families (Table B.2), where g_i is the genetic effect, c_{ik} competition effect, x_{ij} genotype by environment interaction effect, e_{ijk} error effect, and G_i the genetic gain for economic value for a genotype i planted in environment j and plot size k

	CCS					TCH						
i	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	TSH	G_i
201	-1.40	0.46	1.22	-0.41	11.87	-27.46	22.33	-8.17	-0.45	136.26	16.17	$1,220.66
204	0.50	-2.44	0.52	0.14	10.72	6.23	11.88	-6.82	47.25	208.54	22.37	$2,796.08
209	1.22	0.27	0.42	3.46	17.36	-20.07	-0.70	3.62	-27.90	104.96	18.22	$2,456.42
210	1.67	-1.18	-0.29	-1.19	11.01	-31.66	21.74	-12.00	13.50	141.54	15.59	$2,322.12
211	0.29	-0.55	0.96	1.12	13.81	9.54	-9.60	7.24	-31.50	125.68	17.36	$2,764.68
216	3.65	0.08	-0.17	-1.80	13.76	-13.24	21.00	-0.84	15.75	172.67	23.76	$3,716.37
217	0.15	-0.52	0.38	2.72	14.73	-42.12	49.51	11.53	31.05	199.98	29.45	$1,494.59
219	1.49	1.01	-0.16	-1.40	12.94	-36.64	6.40	-4.63	98.55	213.67	27.65	$2,114.45
222	2.63	2.27	-0.18	0.09	16.82	-24.51	44.39	-4.29	-21.15	144.44	24.29	$2,914.06
223	0.91	1.85	0.47	1.71	16.93	-49.82	49.34	-5.89	-42.30	101.33	17.15	$1,560.60
224	-0.73	1.46	0.61	0.32	13.66	-7.70	29.71	-1.85	-71.10	99.06	13.53	$1,889.39
226	0.51	0.07	0.05	0.76	13.39	-1.74	11.05	-17.60	-23.85	117.86	15.78	$2,605.22
233	0.58	-0.19	0.09	0.13	12.61	-64.07	-11.50	5.81	41.40	121.61	15.33	$1,102.35
235	-0.32	0.27	0.52	0.40	12.86	-1.48	-20.00	9.26	7.20	144.98	18.64	$2,212.21
236	-0.84	-1.22	-0.83	1.98	11.09	-9.45	-16.90	0.59	25.20	149.46	16.58	$1,802.91
237	2.19	-0.10	0.34	2.00	16.43	-34.57	-15.90	-0.67	36.45	135.34	22.24	$2,432.88
238	3.49	0.83	-1.37	-0.40	14.56	-8.36	32.97	-2.10	-9.90	162.61	23.68	$3,814.06
239	0.37	1.11	0.20	-1.57	12.10	-22.40	35.55	9.26	-19.80	152.61	18.47	$2,043.19
240	0.00	1.00	-0.09	-1.12	11.79	-25.15	-36.50	-4.29	73.80	157.88	18.61	$1,827.00
242	-1.42	-0.52	0.23	1.26	11.55	19.90	65.94	-7.75	64.35	292.45	33.79	$2,072.61
243	1.81	1.27	-1.31	-0.76	13.02	-39.12	17.93	-10.20	39.15	157.77	20.54	$2,160.81
244	1.18	-0.16	0.71	-0.70	13.03	-49.14	19.86	6.57	65.70	192.99	25.14	$1,667.66
245	-1.16	0.94	-0.08	2.21	13.90	-6.22	29.62	-17.60	-17.10	138.71	19.29	$1,715.51
246	-0.52	-0.43	0.51	0.94	12.50	-24.67	5.05	4.04	81.90	216.31	27.04	$1,625.49
248	-1.49	0.06	1.38	3.49	15.44	-50.08	6.62	1.43	-4.95	103.02	15.90	$777.05
250	0.06	-0.26	-0.16	1.48	13.12	-28.67	-4.67	-8.67	78.75	186.74	24.49	$1,769.51
251	0.70	0.39	0.42	1.57	15.07	7.64	54.75	2.44	8.55	223.39	33.67	$2,931.60
254	0.71	0.45	0.08	2.79	16.03	-20.89	-44.70	-0.84	28.35	111.90	17.94	$2,221.74
256	1.60	-0.99	0.42	-1.31	11.72	-33.70	-8.43	0.59	24.75	133.21	15.61	$2,236.10
258	-1.18	0.08	-0.69	1.57	11.78	-10.42	17.13	-9.43	-6.30	140.98	16.60	$1,628.30
262	2.04	1.35	0.05	-0.79	14.65	18.24	42.09	-5.98	63.45	267.80	39.23	$3,929.35
266	1.30	-0.93	-0.09	0.02	12.30	23.66	-17.20	17.60	67.50	241.57	29.71	$3,672.59
267	0.78	0.09	0.43	0.88	14.18	20.21	41.46	2.61	-38.25	176.02	24.96	$3,288.77
271	-0.49	1.12	0.24	-0.52	12.35	35.08	94.78	3.96	-71.55	212.27	26.22	$2,906.76
273	2.09	-0.06	-0.21	-0.04	13.78	8.85	43.20	-10.40	8.55	200.16	27.58	$3,677.86
274	2.27	0.36	0.19	2.38	17.19	-0.07	69.98	-8.59	-65.70	145.62	25.04	$3,500.48
275	-1.39	-0.49	-0.71	0.27	9.67	35.71	-16.70	-3.79	64.35	229.57	22.21	$2,373.87
276	-0.03	1.01	-0.21	0.18	12.95	1.71	57.42	-2.10	17.55	224.58	29.08	$2,425.28
277	1.72	-1.58	0.79	1.08	14.01	58.00	55.97	-1.09	-40.50	222.38	31.16	$4,880.70
281	3.54	0.15	-0.29	0.99	16.39	34.63	9.97	0.59	3.15	198.34	32.51	$5,306.84
284	2.62	0.44	0.11	1.12	16.29	9.07	-4.02	6.90	46.35	208.30	33.93	$3,956.36
285	1.66	0.04	-1.18	0.56	13.07	10.18	-13.30	2.19	51.30	200.36	26.20	$3,493.87
286	-0.08	0.77	0.07	0.47	13.22	2.51	1.14	-5.72	67.05	214.97	28.43	$2,416.71
287	-0.08	-0.82	0.51	0.09	11.69	-3.35	52.13	-4.55	18.45	212.69	24.87	$2,286.49
288	2.49	0.62	-0.39	2.41	17.13	38.04	8.93	9.43	63.90	270.30	46.31	$4,785.34

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
290	3.40	1.69	-0.45	-3.02	13.62	29.40	28.43	0.42	-2.70	205.55	28.00	$5,049.48
291	0.92	0.19	-0.04	-0.34	12.73	-12.46	34.07	-3.11	104.40	272.90	34.74	$2,525.35
293	-1.25	0.76	-0.54	0.40	11.37	10.04	39.71	6.31	34.20	240.26	27.31	$1,978.90
294	2.97	1.04	-0.09	-1.44	14.48	26.01	56.00	2.53	-78.75	155.79	22.56	$4,690.08
300	3.02	0.64	0.16	-1.01	14.81	51.57	21.22	7.49	-49.50	180.78	26.77	$5,547.04
305	-0.46	0.03	0.59	2.57	14.73	13.03	50.19	-14.40	4.95	203.77	30.02	$2,451.81
307	2.38	1.46	0.08	-3.37	12.55	73.13	42.57	-1.43	3.15	267.42	33.57	$5,787.75
309	3.06	1.94	-0.38	0.59	17.21	20.80	64.10	-2.44	-12.60	219.86	37.84	$4,568.03
310	-0.01	0.82	0.46	1.62	14.89	-8.05	20.37	13.64	12.60	188.56	28.07	$2,211.52
311	3.88	1.05	1.35	4.18	22.47	37.92	-1.14	-0.08	-50.40	136.29	30.62	$5,630.30
313…	2.53	0.20	0.38	1.48	16.58	26.18	0.54	11.45	17.10	205.27	34.04	$4,442.12

Table B.6

Some of the one thousands and eight hundred genotypes from Table B.5 regenerated in stage two, where g_i is the genetic effect, c_{ik} competition effect, x_{ij} genotype by environment interaction effect, e_{ijk} error effect, and G_i the genetic gain for economic value for a genotype i planted in environment j and plot size k

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
201	-1.40	0.20	0.23	2.04	13.07	-27.46	2.57	-8.45	1.95	118.61	15.51	$1,220.66
204	0.50	-2.52	0.22	-0.80	9.40	6.23	-7.28	-0.70	15.21	163.46	15.37	$2,796.08
209	1.22	0.02	1.33	3.51	18.07	-20.07	-19.12	11.67	25.55	148.03	26.75	$2,456.42
210	1.67	-1.34	0.28	1.06	13.67	-31.66	2.01	1.81	19.50	141.66	19.37	$2,322.12
211	0.29	-0.75	-0.44	0.03	11.12	9.54	-27.51	3.02	16.19	151.24	16.82	$2,764.68
216	3.65	-0.16	-0.31	-0.36	14.82	-13.24	1.31	-7.95	3.51	133.63	19.80	$3,716.37
217	0.15	-0.73	1.34	0.36	13.13	-42.12	28.17	-5.23	11.51	142.32	18.69	$1,494.59
219	1.49	0.71	-0.25	-0.69	13.27	-36.64	-12.44	8.15	-19.11	89.95	11.93	$2,114.45
222	2.63	1.89	0.84	-1.65	15.71	-24.51	23.35	0.81	-26.33	123.32	19.37	$2,914.06
223	0.91	1.50	-1.11	1.19	14.48	-49.82	28.00	9.86	23.99	162.03	23.46	$1,560.60
224	-0.73	1.13	1.15	-1.51	12.04	-7.70	9.52	-0.40	14.82	166.24	20.02	$1,889.39
226	0.51	-0.17	0.72	2.29	15.36	-1.74	-8.06	-7.95	-5.46	126.79	19.48	$2,605.22
233	0.58	-0.41	0.65	-1.05	11.77	-64.07	-29.32	-9.86	-21.06	25.69	3.02	$1,102.35
235	-0.32	0.02	0.16	0.58	12.43	-1.48	-37.31	6.94	37.83	155.99	19.40	$2,212.21
236	-0.84	-1.38	-0.69	1.12	10.21	-9.45	-34.36	12.98	14.24	133.41	13.63	$1,802.91
237	2.19	-0.32	-0.44	-0.81	12.61	-34.57	-33.41	-11.20	36.47	107.32	13.54	$2,432.88
238	3.49	0.55	0.08	0.58	16.70	-8.36	12.59	14.19	33.35	201.76	33.69	$3,814.06
239	0.37	0.80	0.19	-0.84	12.52	-22.40	15.02	-8.75	14.63	148.49	18.60	$2,043.19
240	0.00	0.70	-0.12	0.72	13.30	-25.15	-52.82	11.17	7.80	91.00	12.10	$1,827.00
242	-1.42	-0.72	-0.27	2.51	12.10	19.90	43.64	1.51	14.24	229.29	27.75	$2,072.61
243	1.81	0.96	0.60	1.11	16.48	-39.12	-1.58	-4.93	-38.81	65.57	10.80	$2,160.81
244	1.18	-0.38	0.20	0.66	13.65	-49.14	0.24	-10.80	18.33	108.67	14.84	$1,667.66
245	-1.16	0.64	0.44	-0.73	11.18	-6.22	9.43	-16.20	26.72	163.73	18.31	$1,715.51
246	-0.52	-0.63	0.68	0.19	11.72	-24.67	-13.71	0.30	20.28	132.20	15.49	$1,625.49
248	-1.49	-0.18	-1.35	-0.39	8.59	-50.08	-12.23	6.14	-7.80	86.02	7.39	$777.05
250	0.06	-0.48	0.78	-0.11	12.25	-28.67	-22.86	2.31	26.13	126.91	15.55	$1,769.51
251	0.70	0.13	-0.11	2.17	14.90	7.64	33.11	-0.60	10.34	200.48	29.87	$2,931.60
254	0.71	0.19	0.08	-1.39	11.59	-20.89	-60.58	3.52	6.83	78.88	9.14	$2,221.74
256	1.60	-1.16	-1.72	2.40	13.12	-33.70	-26.40	-2.01	24.18	112.07	14.70	$2,236.10
258	-1.18	-0.16	0.15	1.54	12.35	-10.42	-2.33	-0.40	6.63	143.48	17.72	$1,628.30
262	2.04	1.04	-0.30	-3.10	11.68	18.24	21.18	2.42	-12.68	179.16	20.92	$3,929.35

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
266	1.30	-1.10	0.08	-0.86	11.42	23.66	-34.66	-15.70	-3.32	120.00	13.71	$3,672.59
267	0.78	-0.15	1.36	-2.65	11.34	20.21	20.58	-4.23	23.21	209.77	23.78	$3,288.77
271	-0.49	0.82	-1.79	-1.44	9.11	35.08	70.80	2.62	27.50	285.99	26.06	$2,906.76
273	2.09	-0.29	-0.29	-1.76	11.74	8.85	22.22	-21.30	-32.96	126.79	14.89	$3,677.86
274	2.27	0.11	-0.10	1.48	15.76	-0.07	47.44	20.02	-17.36	200.04	31.52	$3,500.48
275	-1.39	-0.69	0.37	-1.44	8.85	35.71	-34.19	-2.01	-18.33	131.17	11.61	$2,373.87
276	-0.03	0.71	-0.06	-0.95	11.68	1.71	35.62	-22.30	-14.24	150.75	17.60	$2,425.28
277	1.72	-1.71	0.15	-1.37	10.79	58.00	34.25	4.03	0.98	247.26	26.67	$4,880.70
281	3.54	-0.09	-0.74	-1.37	13.33	34.63	-9.07	-2.82	-14.63	158.12	21.08	$5,306.84
284	2.62	0.18	1.10	1.00	16.90	9.07	-22.25	-4.13	-15.41	117.29	19.82	$3,956.36
285	1.66	-0.20	-0.65	-0.62	12.18	10.18	-31.00	18.01	-2.15	145.04	17.67	$3,493.87
286	-0.08	0.49	0.03	-3.03	9.41	2.51	-17.39	1.11	3.51	139.73	13.15	$2,416.71
287	-0.08	-1.01	-0.17	-2.45	8.30	-3.35	30.64	0.20	-13.26	164.23	13.63	$2,286.49
288…	2.49	0.35	1.12	1.37	17.33	38.04	-10.05	-5.53	-56.16	116.29	20.16	$4,785.34

Table B.7

Ninety-nine genotypes from table B.6 selected at stage two, where g_i is the genetic effect, c_{ik} competition effect, x_{ij} genotype by environment interaction effect, e_{ijk} error effect, and G_i the genetic gain for economic value for a genotype i planted in environment j and plot size k

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
294	2.97	0.74	-0.81	2.14	17.04	26.01	34.28	-8.15	2.54	204.68	34.87	$4,690.08
300	3.02	0.37	-0.94	1.39	15.84	51.57	1.52	-5.13	18.14	216.10	34.22	$5,547.04
307	2.38	1.13	-0.82	2.85	17.55	73.13	21.63	2.92	23.21	270.88	47.54	$5,787.75
309	3.06	1.58	0.99	0.19	17.82	20.80	41.91	-9.96	16.97	219.71	39.15	$4,568.03
419	1.18	0.05	1.18	3.76	18.16	44.26	45.11	-3.32	-8.97	227.08	41.23	$4,148.29
422	2.54	-1.04	0.68	2.09	16.28	25.69	19.94	0.30	22.62	218.55	35.58	$4,432.88
423	3.68	1.12	1.02	2.09	19.91	7.55	36.18	-0.50	-9.17	184.06	36.65	$4,453.85
448	2.19	-0.29	1.09	2.57	17.57	12.00	38.63	-8.15	36.47	228.95	40.23	$3,824.40
496	1.89	0.82	1.24	0.53	16.48	47.07	52.80	8.35	-23.01	235.21	38.75	$4,678.98
497	2.27	0.14	1.72	1.08	17.21	22.99	1.05	5.43	30.03	209.50	36.05	$4,194.28
538	2.96	2.13	1.23	0.86	19.18	22.35	11.75	18.31	1.17	203.58	39.04	$4,561.68
627	0.78	-2.05	1.06	4.29	16.08	22.04	29.03	2.31	30.03	233.41	37.54	$3,338.03
637	3.16	0.83	-0.71	2.07	17.35	26.43	22.15	9.36	-11.70	196.24	34.05	$4,807.38
805	1.30	-1.19	1.97	1.28	15.36	35.11	56.15	1.31	3.90	246.46	37.86	$3,980.69
818	2.35	0.62	0.77	2.18	17.93	58.14	37.70	-7.95	-14.24	223.66	40.11	$5,311.92
864	4.20	-0.42	0.39	1.62	17.79	21.18	9.99	13.48	0.00	194.65	34.62	$5,214.95
865	1.62	-0.40	-1.50	1.31	13.03	40.45	110.47	-4.53	-26.33	270.07	35.20	$4,322.92
869	1.69	0.44	0.89	0.33	15.34	59.97	47.62	-7.14	31.59	282.04	43.27	$4,916.66
886	4.83	1.42	-0.98	-1.09	16.17	48.10	83.07	-4.23	-7.22	269.73	43.62	$6,596.75
898	4.91	0.27	-0.91	0.27	16.53	46.46	18.83	0.50	2.34	218.13	36.07	$6,583.62
913	3.33	-0.42	1.41	2.98	19.30	33.87	30.93	10.06	-0.98	223.89	43.21	$5,155.19
915	1.31	-1.62	-0.13	0.94	12.49	32.42	63.46	-2.82	51.68	294.74	36.82	$3,910.02
916	1.92	1.52	0.45	1.67	17.56	16.97	25.51	15.50	-1.56	206.41	36.25	$3,828.50
958	2.11	0.38	0.24	1.45	16.18	25.86	40.76	22.64	-2.15	237.11	38.38	$4,193.59
965	4.14	0.37	0.03	2.20	18.74	40.91	14.07	-7.45	23.79	221.32	41.48	$5,894.86
973	2.95	1.24	1.15	2.78	20.12	26.33	25.32	3.82	-20.28	185.20	37.25	$4,688.02
1115	1.86	1.17	1.15	0.92	17.11	41.24	2.43	0.70	9.17	203.54	34.82	$4,495.10
1191	-0.75	1.25	0.02	3.31	15.83	45.24	27.43	-1.51	6.63	227.79	36.06	$2,957.44

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
1433	5.06	-0.13	-0.03	-1.09	15.80	19.59	58.60	12.88	0.39	241.45	38.16	$5,629.02
1533	-0.08	0.23	1.27	3.23	16.65	38.25	15.19	2.62	6.44	212.49	35.38	$3,223.81
1714	-0.88	1.58	-0.23	1.23	13.70	53.38	51.42	6.04	-5.46	255.37	34.97	$3,033.12
1720	2.20	1.07	0.63	-1.69	14.22	40.20	38.46	-0.70	17.16	245.11	34.84	$4,670.67
1743	1.92	1.24	-0.51	1.58	16.23	21.02	22.97	24.65	8.39	227.03	36.84	$3,942.77
1750	2.82	0.83	0.06	2.54	18.25	34.20	17.27	-2.11	11.31	210.66	38.44	$4,861.19
1754	0.36	0.24	0.92	0.31	13.83	50.47	47.01	12.98	28.67	289.12	39.98	$3,783.78
1756	2.69	1.05	-0.64	0.67	15.77	15.71	38.63	2.01	18.14	224.49	35.39	$4,200.70
1767	2.23	2.10	0.52	1.54	18.38	10.85	15.57	-4.33	20.28	192.37	35.37	$3,810.24
1784	4.33	-0.69	0.82	-0.25	16.22	36.79	36.27	2.42	-4.29	221.19	35.87	$5,861.57
1818	4.46	1.38	-0.19	2.11	19.76	49.44	-23.76	5.23	11.70	192.61	38.05	$6,408.87
1896	0.84	0.16	0.55	1.73	15.28	40.63	56.80	16.70	-14.82	249.31	38.08	$3,841.73
1904	0.56	0.42	-0.76	3.68	15.89	67.24	31.08	10.57	-16.38	242.51	38.54	$4,323.42
1956	1.54	1.06	0.95	-0.03	15.52	33.24	77.93	7.04	-19.70	248.51	38.57	$4,074.38
1967	2.92	1.92	-0.39	3.00	19.45	67.81	20.54	0.70	5.66	244.70	47.58	$6,008.23
1972	-1.08	1.18	0.88	2.59	15.57	32.77	50.01	-9.06	15.80	239.53	37.30	$2,506.78
1993	1.19	-0.29	1.06	1.84	15.81	36.70	33.89	-0.70	-0.20	219.69	34.73	$3,955.42
2101	0.97	-1.52	-0.65	2.59	13.39	48.54	62.53	10.57	45.24	316.88	42.42	$4,126.42
2228	4.27	0.27	1.54	0.67	18.75	16.56	12.25	6.04	15.02	199.87	37.48	$5,084.52
2277	0.69	1.17	1.11	-0.94	14.04	25.18	47.87	0.00	19.89	242.94	34.11	$3,364.95
2290	2.04	1.54	-0.35	0.51	15.74	17.83	35.12	-8.96	26.72	220.71	34.75	$3,918.46
2298	1.81	1.06	1.15	0.11	16.13	25.59	45.63	3.42	0.00	224.64	36.24	$4,012.18
2443	-0.42	0.57	0.47	3.62	16.24	44.28	17.28	12.68	15.41	239.64	38.92	$3,141.21
2495	3.55	0.78	0.54	-1.56	15.32	68.95	-6.64	8.15	7.61	228.06	34.93	$6,492.50
2514	4.53	1.18	-0.73	0.64	17.62	57.01	-3.93	-15.30	34.91	222.68	39.24	$6,738.62
2526	2.03	2.31	1.22	0.62	18.18	70.09	13.32	1.71	17.16	252.28	45.87	$5,446.92
2611	2.29	1.60	1.05	2.46	19.41	17.56	13.68	14.99	-14.43	181.80	35.29	$4,046.66
2813	2.48	2.69	-0.43	-0.50	16.25	31.13	34.21	3.52	0.20	219.06	35.59	$4,567.73
2819	2.32	1.11	-0.27	2.62	17.79	16.75	17.08	-4.63	28.47	207.67	36.94	$4,035.76
2832	0.19	1.18	-0.91	2.46	14.93	46.49	67.85	5.03	-14.43	254.94	38.07	$3,582.00
2948	1.49	0.73	-0.69	-0.16	13.37	42.25	48.27	12.68	3.90	257.09	34.37	$4,290.03
2972	-1.03	1.23	1.22	3.00	16.40	18.33	40.79	17.91	-12.48	214.55	35.19	$2,253.41
2986	4.17	0.55	0.52	1.31	18.55	34.52	-4.42	-4.43	30.03	205.71	38.16	$5,680.93
2993	1.12	0.71	-0.56	1.44	14.71	36.41	9.33	18.82	37.44	251.99	37.06	$3,907.58
3008	1.08	-0.15	-0.41	0.84	13.36	54.68	47.37	5.53	3.51	261.10	34.88	$4,362.01
3115	1.58	0.12	0.98	0.44	15.12	23.37	49.13	0.60	14.24	237.34	35.88	$3,820.58
3122	5.75	0.12	0.28	2.31	20.46	11.12	22.51	-7.55	3.32	179.40	36.71	$5,656.82
3208	2.05	0.65	-0.55	3.76	17.91	31.69	38.84	7.04	-21.65	205.93	36.88	$4,327.25
3214	2.87	-0.21	-0.10	-0.34	14.22	30.33	44.69	-5.03	23.79	243.78	34.66	$4,767.02
3229	2.16	0.66	0.45	0.30	15.57	54.89	30.18	15.40	-12.48	237.99	37.05	$5,082.68
3239	5.66	2.10	-1.20	-1.58	16.99	-5.21	33.62	-1.31	50.12	227.22	38.61	$4,941.89
3298	2.93	2.14	0.53	0.69	18.29	13.71	29.63	3.82	-6.83	190.34	34.82	$4,268.90
3300	2.04	2.59	0.52	1.34	18.49	17.13	7.70	13.79	5.07	193.68	35.82	$3,896.08
3317	2.30	2.15	-0.36	2.32	18.42	6.21	51.88	-2.42	-11.90	193.78	35.69	$3,708.36
3344	1.01	0.48	-0.02	2.20	15.68	33.47	17.50	20.83	3.12	224.92	35.26	$3,762.71
3370	1.67	-1.27	0.87	2.23	15.50	45.76	36.94	4.33	5.85	242.88	37.65	$4,504.48
3375	0.99	0.37	-0.28	1.26	14.34	31.07	53.64	-3.72	25.55	256.52	36.79	$3,688.35
3386	4.68	0.78	0.26	3.46	21.18	15.89	34.80	11.67	14.82	227.18	48.12	$5,279.39
3396	4.53	0.52	0.78	0.51	18.34	68.73	57.66	-3.12	4.49	277.76	50.93	$7,174.80
3405	2.03	-0.41	0.37	0.61	14.60	48.08	26.19	-1.41	29.84	252.69	36.90	$4,798.34
3408	5.15	0.54	0.08	1.34	19.11	31.86	42.68	5.63	5.07	235.24	44.96	$6,160.13
3413	6.38	0.31	0.02	0.09	18.80	18.60	20.52	7.04	8.00	204.16	38.39	$6,312.89
3422	2.90	-0.60	1.32	2.11	17.73	14.36	42.06	-10.97	7.80	203.26	36.04	$4,274.76
3424	4.58	-0.32	1.52	1.29	19.08	17.07	51.32	-1.51	10.34	227.22	43.36	$5,271.31
3438	2.74	-1.45	1.50	0.55	15.34	15.94	46.29	16.10	5.27	233.59	35.83	$4,238.33
3442	2.76	0.08	0.17	0.69	15.70	23.18	83.32	3.52	40.76	300.78	47.21	$4,479.55

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
3503	4.13	1.47	0.74	0.06	18.40	6.84	-16.37	15.90	56.16	212.53	39.11	$4,655.53
3510	3.23	1.52	-2.32	3.51	17.94	39.32	29.03	0.70	-13.26	205.80	36.93	$5,277.83
3520	4.12	1.06	0.84	1.90	19.92	37.17	2.33	11.77	25.74	227.01	45.22	$5,745.52
3535	4.78	1.84	-0.35	-0.25	18.01	49.32	-10.11	-8.35	21.26	202.12	36.41	$6,609.75
3549	2.29	0.46	-0.78	1.87	15.84	33.15	25.33	8.45	0.59	217.53	34.45	$4,515.73
3558	5.19	0.25	0.27	-0.69	17.02	26.44	15.54	-7.65	16.77	201.10	34.23	$5,973.02
3610	2.54	0.61	0.41	2.28	17.83	1.41	29.87	8.45	2.73	192.46	34.33	$3,680.24
3630	1.04	-0.59	0.41	1.36	14.22	29.53	53.62	3.22	24.57	260.94	37.11	$3,676.31
3646	3.20	1.33	0.43	2.61	19.57	17.45	56.59	-7.55	-22.23	194.26	38.02	$4,534.01
3686	0.20	2.37	0.15	2.32	17.05	12.71	82.53	-6.24	5.27	244.26	41.65	$2,795.75
3690	0.95	0.72	0.91	1.31	15.89	30.17	4.76	-3.52	31.20	212.61	33.78	$3,639.35
3698	2.40	1.29	-1.31	1.15	15.53	22.87	14.69	4.83	28.47	220.87	34.29	$4,264.32
3730	3.09	0.12	-0.64	0.66	15.22	57.92	42.35	2.01	17.94	270.22	41.13	$5,799.44
3744	0.31	1.94	-0.74	-1.00	12.51	28.85	56.54	13.28	26.13	274.80	34.38	$3,236.69
3790	4.04	2.45	-0.21	1.29	19.58	15.92	11.74	-25.86	28.86	180.67	35.37	$4,937.59

Table B.8

Ninety-nine genotypes (Table B.7) regenerated in stage three, where g_i is the genetic effect, c_{ik} competition effect, x_{ij} genotype by environment interaction effect, e_{ijk} error effect, and G_i the genetic gain for economic value for a genotype i planted in environment j and plot size k

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
294	2.97	0.00	-0.22	0.04	14.79	26.01	0.00	-4.23	-2.93	168.86	24.98	$4,690.08
300	3.02	0.00	0.48	-0.11	15.39	51.57	0.00	1.21	-1.71	201.07	30.95	$5,547.04
307	2.38	0.00	0.07	-0.19	14.26	73.13	0.00	-6.64	-0.93	215.56	30.75	$5,787.75
309	3.06	0.00	0.02	0.03	15.11	20.80	0.00	5.63	-0.45	175.99	26.59	$4,568.03
419	1.18	0.00	-0.57	0.16	12.77	44.26	0.00	2.16	1.52	197.95	25.28	$4,148.29
422	2.54	0.00	-0.18	-0.29	14.07	25.69	0.00	2.92	-5.27	173.33	24.38	$4,432.88
423	3.68	0.00	0.67	-0.08	16.27	7.55	0.00	-0.60	1.78	158.73	25.83	$4,453.85
448	2.19	0.00	-0.30	-0.02	13.87	12.00	0.00	-3.32	-2.86	155.82	21.61	$3,824.40
496	1.89	0.00	0.32	-0.22	13.99	47.07	0.00	2.82	1.78	201.67	28.22	$4,678.98
497	2.27	0.00	-0.29	-0.63	13.35	22.99	0.00	-1.26	-4.49	167.24	22.32	$4,194.28
538	2.96	0.00	-0.35	-0.35	14.26	22.35	0.00	7.40	1.97	181.71	25.91	$4,561.68
627	0.78	0.00	0.02	-0.49	12.31	22.04	0.00	4.08	-0.19	175.93	21.65	$3,338.03
637	3.16	0.00	-0.18	-0.28	14.70	26.43	0.00	-4.13	0.93	173.23	25.46	$4,807.38
805	1.30	0.00	-0.53	0.25	13.03	35.11	0.00	-5.84	-4.97	174.29	22.71	$3,980.69
818	2.35	0.00	-0.40	0.07	14.03	58.14	0.00	1.06	-2.34	206.86	29.02	$5,311.92
864	4.20	0.00	0.27	-0.28	16.19	21.18	0.00	1.71	5.83	178.71	28.93	$5,214.95
865	1.62	0.00	0.13	-0.03	13.72	40.45	0.00	5.94	-3.16	193.23	26.52	$4,322.92
869	1.69	0.00	-0.35	-0.11	13.24	59.97	0.00	-11.87	-2.30	195.79	25.91	$4,916.66
886	4.83	0.00	0.52	0.36	17.70	48.10	0.00	-3.02	-6.24	188.85	33.43	$6,596.75
898	4.91	0.00	0.50	-0.60	16.81	46.46	0.00	-1.66	3.34	198.14	33.30	$6,583.62
913	3.33	0.00	-0.72	-0.09	14.52	33.87	0.00	-0.20	5.72	189.39	27.49	$5,155.19
915	1.31	0.00	-0.35	0.46	13.42	32.42	0.00	-0.70	4.27	185.99	24.95	$3,910.02
916	1.93	0.00	0.21	0.01	14.15	16.97	0.00	-3.82	3.56	166.71	23.59	$3,828.50
958	2.11	0.00	0.20	-0.45	13.86	25.86	0.00	-10.21	-0.89	164.75	22.83	$4,193.59
965	4.14	0.00	-0.11	0.01	16.04	40.91	0.00	3.97	-3.60	191.29	30.69	$5,894.86
973	2.95	0.00	0.69	0.26	15.90	26.33	0.00	3.37	1.82	181.52	28.86	$4,688.02
1115	1.87	0.00	0.00	0.36	14.22	41.24	0.00	-3.67	-3.86	183.71	26.12	$4,495.10

	CCS					TCH						
i	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	TSH	G_i
1191	-0.75	0.00	0.59	-0.48	11.37	45.24	0.00	-2.21	6.16	199.19	22.64	$2,957.44
1433	5.06	0.00	-0.21	0.22	17.07	19.59	0.00	-3.52	0.67	166.73	28.46	$5,629.02
1533	-0.08	0.00	-0.30	-0.24	11.38	38.25	0.00	-6.19	2.04	184.10	20.96	$3,223.81
1714	-0.88	0.00	-0.38	-0.47	10.26	53.38	0.00	-4.53	2.26	201.11	20.64	$3,033.12
1720	2.20	0.00	0.70	0.12	15.02	40.20	0.00	-2.92	-1.93	185.35	27.84	$4,670.67
1743	1.92	0.00	0.39	-0.07	14.24	21.02	0.00	-4.38	1.78	168.43	23.98	$3,942.77
1750	2.82	0.00	0.97	-0.28	15.51	34.20	0.00	0.70	1.15	186.05	28.85	$4,861.19
1754	0.36	0.00	-0.06	0.50	12.80	50.47	0.00	-2.06	-6.05	192.35	24.63	$3,783.78
1756	2.69	0.00	-0.30	0.00	14.38	15.71	0.00	-1.21	4.45	168.96	24.30	$4,200.70
1767	2.23	0.00	-0.13	-0.24	13.86	10.85	0.00	0.60	-3.42	158.03	21.90	$3,810.24
1784	4.33	0.00	0.33	0.14	16.79	36.79	0.00	-8.60	-0.78	177.41	29.80	$5,861.57
1818	4.46	0.00	0.25	0.00	16.71	49.44	0.00	-3.22	3.16	199.38	33.31	$6,408.87
1896	0.84	0.00	-0.25	0.26	12.85	40.63	0.00	12.33	4.75	207.70	26.68	$3,841.73
1904	0.56	0.00	0.25	0.12	12.93	67.24	0.00	3.22	1.48	221.95	28.71	$4,323.42
1956	1.55	0.00	-0.76	-0.08	12.71	33.24	0.00	-1.86	2.30	183.68	23.34	$4,074.38
1967	2.92	0.00	-0.44	-0.49	14.00	67.81	0.00	0.35	0.00	218.16	30.53	$6,008.23
1972	-1.08	0.00	0.61	-0.45	11.08	32.77	0.00	-0.25	-2.78	179.74	19.91	$2,506.78
1993	1.19	0.00	0.03	0.13	13.35	36.70	0.00	-0.35	-5.46	180.89	24.15	$3,955.42
2101	0.97	0.00	-0.19	0.16	12.93	48.54	0.00	-4.23	-9.32	185.00	23.93	$4,126.42
2228	4.27	0.00	1.01	-0.17	17.12	16.56	0.00	-0.25	0.52	166.83	28.55	$5,084.52
2277	0.69	0.00	-0.65	0.14	12.18	25.18	0.00	-2.97	-2.27	169.94	20.70	$3,364.95
2290	2.04	0.00	-0.01	0.33	14.37	17.83	0.00	-7.95	3.01	162.89	23.41	$3,918.46
2298	1.81	0.00	-0.38	0.14	13.57	25.59	0.00	1.66	-1.78	175.47	23.81	$4,012.18
2443	-0.42	0.00	0.34	-0.43	11.48	44.28	0.00	2.47	-1.34	195.41	22.44	$3,141.21
2495	3.55	0.00	0.24	0.06	15.86	68.95	0.00	-3.72	-4.38	210.84	33.44	$6,492.50
2514	4.53	0.00	0.06	-0.54	16.06	57.01	0.00	-2.92	-10.21	193.88	31.13	$6,738.62
2526	2.03	0.00	0.21	0.22	14.46	70.09	0.00	-11.87	-1.11	207.10	29.94	$5,446.92
2611	2.30	0.00	-0.06	0.73	14.96	17.56	0.00	-0.10	4.64	172.10	25.75	$4,046.66
2813	2.48	0.00	-0.29	0.10	14.29	31.13	0.00	2.72	-0.15	183.69	26.26	$4,567.73
2819	2.32	0.00	-0.22	-0.22	13.89	16.75	0.00	4.83	-3.23	168.35	23.38	$4,035.76
2832	0.20	0.00	-0.69	0.14	11.64	46.49	0.00	10.21	0.71	207.41	24.15	$3,582.00
2948	1.49	0.00	-0.25	-0.24	13.00	42.25	0.00	-5.28	2.12	189.08	24.58	$4,290.03
2972	-1.03	0.00	-0.43	-0.16	10.38	18.33	0.00	-4.18	-2.64	161.52	16.77	$2,253.41
2986	4.17	0.00	-0.28	-0.07	15.83	34.52	0.00	7.70	-1.71	190.51	30.15	$5,680.93
2993	1.12	0.00	-0.79	-0.34	11.99	36.41	0.00	-8.15	-3.94	174.32	20.90	$3,907.58
3008	1.08	0.00	-0.26	-0.34	12.49	54.68	0.00	1.06	1.00	206.74	25.81	$4,362.01
3115	1.58	0.00	0.66	-0.34	13.90	23.37	0.00	-2.47	0.74	171.65	23.86	$3,820.58
3122	5.75	0.00	0.68	0.08	18.51	11.12	0.00	-7.85	3.56	156.84	29.03	$5,656.82
3208	2.05	0.00	-0.13	-0.32	13.59	31.69	0.00	-3.67	0.78	178.80	24.30	$4,327.25
3214	2.87	0.00	-0.03	0.39	15.22	30.33	0.00	2.06	2.23	184.62	28.10	$4,767.02
3229	2.16	0.00	0.01	0.26	14.43	54.89	0.00	-0.96	0.97	204.90	29.56	$5,082.68
3239	5.67	0.00	0.37	0.38	18.42	-5.21	0.00	-13.33	2.23	133.69	24.62	$4,941.89
3298	2.93	0.00	-0.20	-0.40	14.34	13.71	0.00	-9.76	5.16	159.11	22.81	$4,268.90
3300	2.04	0.00	-0.48	0.41	13.97	17.13	0.00	3.52	0.07	170.73	23.86	$3,896.08
3317	2.30	0.00	0.70	0.10	15.11	6.21	0.00	2.21	-5.53	152.89	23.10	$3,708.36
3344	1.01	0.00	-0.27	0.12	12.86	33.47	0.00	3.57	3.16	190.20	24.46	$3,762.71
3370	1.68	0.00	0.13	0.49	14.29	45.76	0.00	-2.97	0.52	193.31	27.63	$4,504.48
3375	0.99	0.00	-0.02	-0.35	12.62	31.07	0.00	-7.20	-1.60	172.27	21.75	$3,688.35
3386	4.68	0.00	0.25	0.05	16.97	15.89	0.00	-0.15	-0.15	165.59	28.11	$5,279.39
3396	4.53	0.00	-0.35	-0.15	16.02	68.73	0.00	5.28	5.20	229.21	36.72	$7,174.80
3405	2.03	0.00	0.10	-0.09	14.05	48.08	0.00	-5.53	-1.15	191.40	26.88	$4,798.34
3408	5.15	0.00	-0.40	0.20	16.94	31.86	0.00	-3.67	5.09	183.27	31.05	$6,160.13
3413	6.38	0.00	-0.25	0.34	18.47	18.60	0.00	-2.01	3.12	169.71	31.34	$6,312.89
3422	2.90	0.00	-0.04	-0.05	14.81	14.36	0.00	4.33	-3.01	165.68	24.54	$4,274.76
3424	4.58	0.00	-0.10	-0.29	16.19	17.07	0.00	-2.77	6.50	170.80	27.65	$5,271.31
3438	2.74	0.00	-0.54	0.10	14.30	15.94	0.00	-5.48	0.04	160.49	22.95	$4,238.33

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
3442	2.76	0.00	0.38	-0.35	14.79	23.18	0.00	5.94	-7.31	171.81	25.42	$4,479.55
3503	4.13	0.00	-0.04	0.04	16.13	6.84	0.00	2.31	1.63	160.79	25.93	$4,655.53
3510	3.23	0.00	-0.33	-0.24	14.66	39.32	0.00	4.68	3.01	197.01	28.89	$5,277.83
3520	4.12	0.00	-0.07	0.19	16.24	37.17	0.00	11.87	5.53	204.57	33.21	$5,745.52
3535	4.78	0.00	-0.11	-0.14	16.52	49.32	0.00	10.11	3.04	212.48	35.11	$6,609.75
3549	2.29	0.00	0.71	0.13	15.14	33.15	0.00	-5.08	5.12	183.20	27.73	$4,515.73
3558	5.19	0.00	-0.11	-0.28	16.80	26.44	0.00	1.06	-2.38	175.12	29.42	$5,973.02
3610	2.54	0.00	-0.14	-0.03	14.37	1.41	0.00	4.88	-8.06	148.24	21.30	$3,680.24
3630	1.04	0.00	0.06	-0.11	12.99	29.53	0.00	2.52	0.74	182.79	23.75	$3,676.31
3646	3.20	0.00	0.10	0.46	15.76	17.45	0.00	6.29	1.89	175.63	27.68	$4,534.01
3686	0.20	0.00	-0.29	-0.43	11.48	12.71	0.00	-6.24	-0.85	155.62	17.86	$2,795.75
3690	0.95	0.00	0.33	0.08	13.35	30.17	0.00	0.40	0.71	181.28	24.21	$3,639.35
3698	2.40	0.00	0.03	0.14	14.57	22.87	0.00	8.55	1.19	182.61	26.60	$4,264.32
3730	3.09	0.00	-0.75	0.24	14.58	57.92	0.00	-8.10	-4.60	195.21	28.46	$5,799.44
3744	0.31	0.00	-0.10	0.57	12.78	28.85	0.00	-4.83	-2.38	171.65	21.94	$3,236.69
3790	4.04	0.00	-0.17	0.44	16.31	15.92	0.00	-0.76	-3.79	161.38	26.33	$4,937.59

Table B.9

Nineteen genotypes from Table B.8 selected at stage three, where g_i is the genetic effect, c_{ik} competition effect, x_{ij} genotype by environment interaction effect, e_{ijk} error effect, and G_i the genetic gain for economic value for a genotype i planted in environment j and plot size k

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
300	3.02	0.00	0.48	-0.11	15.39	51.57	0.00	1.21	-1.71	201.07	30.95	$5,547.04
307	2.38	0.00	0.07	-0.19	14.26	73.13	0.00	-6.64	-0.93	215.56	30.75	$5,787.75
886	4.83	0.00	0.52	0.36	17.70	48.10	0.00	-3.02	-6.24	188.85	33.43	$6,596.75
898	4.91	0.00	0.50	-0.60	16.81	46.46	0.00	-1.66	3.34	198.14	33.30	$6,583.62
965	4.14	0.00	-0.11	0.01	16.04	40.91	0.00	3.97	-3.60	191.29	30.69	$5,894.86
1784	4.33	0.00	0.33	0.14	16.79	36.79	0.00	-8.60	-0.78	177.41	29.79	$5,861.57
1818	4.46	0.00	0.25	0.00	16.71	49.44	0.00	-3.22	3.16	199.38	33.31	$6,408.87
1967	2.92	0.00	-0.44	-0.49	14.00	67.81	0.00	0.35	0.00	218.16	30.53	$6,008.23
2495	3.55	0.00	0.24	0.06	15.86	68.95	0.00	-3.72	-4.38	210.84	33.43	$6,492.50
2514	4.53	0.00	0.06	-0.54	16.06	57.01	0.00	-2.92	-10.21	193.88	31.13	$6,738.62
2526	2.03	0.00	0.21	0.22	14.46	70.09	0.00	-11.87	-1.11	207.10	29.94	$5,446.92
2986	4.17	0.00	-0.28	-0.07	15.83	34.52	0.00	7.70	-1.71	190.51	30.15	$5,680.93
3229	2.16	0.00	0.01	0.26	14.43	54.89	0.00	-0.96	0.97	204.90	29.56	$5,082.68
3396	4.53	0.00	-0.35	-0.15	16.02	68.73	0.00	5.28	5.20	229.21	36.72	$7,174.80
3408	5.15	0.00	-0.40	0.20	16.94	31.86	0.00	-3.67	5.09	183.27	31.05	$6,160.13
3413	6.38	0.00	-0.25	0.34	18.47	18.60	0.00	-2.01	3.12	169.71	31.34	$6,312.89
3520	4.12	0.00	-0.07	0.19	16.24	37.17	0.00	11.87	5.53	204.57	33.21	$5,745.52
3535	4.78	0.00	-0.11	-0.14	16.52	49.32	0.00	10.11	3.04	212.48	35.11	$6,609.75
3558	5.19	0.00	-0.11	-0.28	16.80	26.44	0.00	1.06	-2.38	175.12	29.42	$5,973.02

Table B.10

The final ten genotypes selected, where g_i is the genetic effect, c_{ik} competition effect, x_{ij} genotype by environment interaction effect, e_{ijk} error effect, and G_i the genetic gain for economic value for a genotype i planted in environment j and plot size k

i	CCS					TCH					TSH	G_i
	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}	g_i	c_{ik}	x_{ij}	e_{ijk}	y_{ijk}		
3396	4.53	0.00	-0.35	-0.15	16.02	68.73	0.00	5.28	5.20	229.21	36.72	$7,174.80
3535	4.78	0.00	-0.11	-0.14	16.52	49.32	0.00	10.11	3.04	212.48	35.11	$6,609.75
2495	3.55	0.00	0.24	0.06	15.86	68.95	0.00	-3.72	-4.38	210.84	33.43	$6,492.50
886	4.83	0.00	0.52	0.36	17.70	48.10	0.00	-3.02	-6.24	188.85	33.43	$6,596.75
1818	4.46	0.00	0.25	0.00	16.71	49.44	0.00	-3.22	3.16	199.38	33.31	$6,408.87
898	4.91	0.00	0.50	-0.60	16.81	46.46	0.00	-1.66	3.34	198.14	33.30	$6,583.62
3520	4.12	0.00	-0.07	0.19	16.24	37.17	0.00	11.87	5.53	204.57	33.21	$5,745.52
3413	6.38	0.00	-0.25	0.34	18.47	18.60	0.00	-2.01	3.12	169.71	31.34	$6,312.89
2514	4.53	0.00	0.06	-0.54	16.06	57.01	0.00	-2.92	-10.21	193.88	31.13	$6,738.62
3408	5.15	0.00	-0.40	0.20	16.94	31.86	0.00	-3.67	5.09	183.27	31.05	$6,160.13

Appendix C

The experimental matrix for the SSSM screening process

Table C.1 gives the factorial experimental matrix for fourteen factors at three levels obtained from NEMROD-W software.

Table C.1

Experimental matrix for the fractional factorial analyses with 14 factors at three levels derived by Nemrod-W; the genetic variance σ_g^2, correlation between genotypic value and competition $\rho_{g,c}$, proportion of variation between families δ, the error variance σ_e^2 in single seedling and one row plot, σ_x^2/σ_g^2 ratio; and genetic correlation between plots $\rho_{g,g+c}$ in the three plot sizes considered as a single factor

	σ_g^2 CCS	σ_g^2 TCH	$\rho_{g,c}$ CCS	$\rho_{g,c}$ TCH	δ CCS	δ TCH	σ_e^2 CCS seed	σ_e^2 TCH seed	σ_e^2 CCS 1row	σ_e^2 TCH 1row	σ_x^2/σ_g^2 CCS	σ_x^2/σ_g^2 TCH	$\rho_{g,g+c}$ CCS	$\rho_{g,g+c}$ TCH	$\widetilde{G}$
1	1	1	1	1	1	1	1	1	1	1	1	1	1	1	\$ 1,845.74
2	1	1	1	1	1	1	1	1	1	1	1	1	1	2	\$ 2,058.73
3	1	1	1	1	1	1	1	1	1	1	1	1	1	3	\$ 2,215.26
4	1	1	1	1	2	2	2	2	2	2	2	2	2	1	\$ 1,914.33
5	1	1	1	1	2	2	2	2	2	2	2	2	2	2	\$ 2,075.08
6	1	1	1	1	2	2	2	2	2	2	2	2	2	3	\$ 2,188.11
7	1	1	1	1	3	3	3	3	3	3	3	3	3	1	\$ 1,865.38
8	1	1	1	1	3	3	3	3	3	3	3	3	3	2	\$ 1,920.40
9	1	1	1	1	3	3	3	3	3	3	3	3	3	3	\$ 2,151.56
10	1	2	2	2	1	1	1	2	2	2	3	3	3	1	\$ 2,701.71
11	1	2	2	2	1	1	1	2	2	2	3	3	3	2	\$ 2,713.52
12	1	2	2	2	1	1	1	2	2	2	3	3	3	3	\$ 2,755.21
13	1	2	2	2	2	2	2	3	3	3	1	1	1	1	\$ 2,616.38
14	1	2	2	2	2	2	2	3	3	3	1	1	1	2	\$ 2,708.18
15	1	2	2	2	2	2	2	3	3	3	1	1	1	3	\$ 2,816.06

	σ_g^2 CCS	σ_g^2 TCH	$\rho_{g,c}$ CCS	$\rho_{g,c}$ TCH	δ CCS	δ TCH	σ_e^2 CCS seed	σ_e^2 TCH seed	σ_e^2 CCS 1row	σ_e^2 TCH 1row	σ_x^2/σ_g^2 CCS	σ_x^2/σ_g^2 TCH	$\rho_{g,g+c}$ CCS	$\rho_{g,g+c}$ TCH	$\widetilde{G}$
16	1	2	2	2	3	3	3	1	1	1	2	2	2	1	$ 2,614.08
17	1	2	2	2	3	3	3	1	1	1	2	2	2	2	$ 2,727.24
18	1	2	2	2	3	3	3	1	1	1	2	2	2	3	$ 2,792.21
19	1	3	3	3	1	1	1	3	3	3	2	2	2	1	$ 3,270.81
20	1	3	3	3	1	1	1	3	3	3	2	2	2	2	$ 3,321.53
21	1	3	3	3	1	1	1	3	3	3	2	2	2	3	$ 3,346.19
22	1	3	3	3	2	2	2	1	1	1	3	3	3	1	$ 3,312.57
23	1	3	3	3	2	2	2	1	1	1	3	3	3	2	$ 3,238.39
24	1	3	3	3	2	2	2	1	1	1	3	3	3	3	$ 3,370.01
25	1	3	3	3	3	3	3	2	2	2	1	1	1	1	$ 3,351.43
26	1	3	3	3	3	3	3	2	2	2	1	1	1	2	$ 3,372.68
27	1	3	3	3	3	3	3	2	2	2	1	1	1	3	$ 3,382.30
28	2	1	2	3	1	2	3	1	2	3	1	2	3	1	$ 3,280.71
29	2	1	2	3	1	2	3	1	2	3	1	2	3	2	$ 3,291.38
30	2	1	2	3	1	2	3	1	2	3	1	2	3	3	$ 3,309.28
31	2	1	2	3	2	3	1	2	3	1	2	3	1	1	$ 3,162.30
32	2	1	2	3	2	3	1	2	3	1	2	3	1	2	$ 3,154.70
33	2	1	2	3	2	3	1	2	3	1	2	3	1	3	$ 3,196.33
34	2	1	2	3	3	1	2	3	1	2	3	1	2	1	$ 3,196.85
35	2	1	2	3	3	1	2	3	1	2	3	1	2	2	$ 3,149.86
36	2	1	2	3	3	1	2	3	1	2	3	1	2	3	$ 3,237.49
37	2	2	3	1	1	2	3	2	3	1	3	1	2	1	$ 3,304.06
38	2	2	3	1	1	2	3	2	3	1	3	1	2	2	$ 3,511.88
39	2	2	3	1	1	2	3	2	3	1	3	1	2	3	$ 3,643.56
41	2	2	3	1	2	3	1	3	1	2	1	2	3	2	$ 3,568.88
42	2	2	3	1	2	3	1	3	1	2	1	2	3	3	$ 3,837.73
43	2	2	3	1	3	1	2	1	2	3	2	3	1	1	$ 3,335.58
44	2	2	3	1	3	1	2	1	2	3	2	3	1	2	$ 3,541.58
45	2	2	3	1	3	1	2	1	2	3	2	3	1	3	$ 3,866.21
46	2	3	1	2	1	2	3	3	1	2	2	3	1	1	$ 4,012.72
47	2	3	1	2	1	2	3	3	1	2	2	3	1	2	$ 4,144.78
48	2	3	1	2	1	2	3	3	1	2	2	3	1	3	$ 4,257.76
49	2	3	1	2	2	3	1	1	2	3	3	1	2	1	$ 3,941.44
50	2	3	1	2	2	3	1	1	2	3	3	1	2	2	$ 4,151.25
51	2	3	1	2	2	3	1	1	2	3	3	1	2	3	$ 4,320.00
52	2	3	1	2	3	1	2	2	3	1	1	2	3	1	$ 4,140.85
53	2	3	1	2	3	1	2	2	3	1	1	2	3	2	$ 4,327.53
54	2	3	1	2	3	1	2	2	3	1	1	2	3	3	$ 4,306.60
55	3	1	3	2	1	3	2	1	3	2	1	3	2	1	$ 4,084.90
56	3	1	3	2	1	3	2	1	3	2	1	3	2	2	$ 4,212.53
57	3	1	3	2	1	3	2	1	3	2	1	3	2	3	$ 4,222.84
58	3	1	3	2	2	1	3	2	1	3	2	1	3	1	$ 4,259.99
59	3	1	3	2	2	1	3	2	1	3	2	1	3	2	$ 4,303.27
60	3	1	3	2	2	1	3	2	1	3	2	1	3	3	$ 4,223.40
61	3	1	3	2	3	2	1	3	2	1	3	2	1	1	$ 4,105.88
62	3	1	3	2	3	2	1	3	2	1	3	2	1	2	$ 4,098.92
63	3	1	3	2	3	2	1	3	2	1	3	2	1	3	$ 4,209.47
64	3	2	1	3	1	3	2	2	1	3	3	2	1	1	$ 4,608.71
65	3	2	1	3	1	3	2	2	1	3	3	2	1	2	$ 4,492.59
66	3	2	1	3	1	3	2	2	1	3	3	2	1	3	$ 4,647.59
67	3	2	1	3	2	1	3	3	2	1	1	3	2	1	$ 4,887.58
68	3	2	1	3	2	1	3	3	2	1	1	3	2	2	$ 4,859.02
69	3	2	1	3	2	1	3	3	2	1	1	3	2	3	$ 4,914.56
70	3	2	1	3	3	2	1	1	3	2	2	1	3	1	$ 4,860.49
71	3	2	1	3	3	2	1	1	3	2	2	1	3	2	$ 4,907.49
72	3	2	1	3	3	2	1	1	3	2	2	1	3	3	$ 4,904.36
73	3	3	2	1	1	3	2	3	2	1	2	1	3	1	$ 4,622.91
74	3	3	2	1	1	3	2	3	2	1	2	1	3	2	$ 5,188.22
75	3	3	2	1	1	3	2	3	2	1	2	1	3	3	$ 5,372.97
76	3	3	2	1	2	1	3	1	3	2	3	2	1	1	$ 4,648.30
77	3	3	2	1	2	1	3	1	3	2	3	2	1	2	$ 4,983.61
78	3	3	2	1	2	1	3	1	3	2	3	2	1	3	$ 5,183.00
79	3	3	2	1	3	2	1	2	1	3	1	3	2	1	$ 4,683.70
80	3	3	2	1	3	2	1	2	1	3	1	3	2	2	$ 4,954.10
81	3	3	2	1	3	2	1	2	1	3	1	3	2	3	$ 5,434.25

Appendix D

The ASSSO pseudo code

The optimisation algorithm ASSSO pseudo code detailing the connection between branch-and-bound and dynamic programming as well as its execution is given below. The optimisation algorithm is divided into two parts, one that optimises clonal selection and one that optimises family selection, ie there are two functions: *optimise clonal* and *optimise family*. Because computations repeat themselves from stage to stage and because the two main functions differ only in the execution of stage one, further four functions were developed as subroutines for the two main functions; these are: *stage 1*, *stage*, *selecting clones families* and *branch2to6*.

```
# stage 1 routine

FUNCTION Stage 1

    calculate cost of stage 1
    IF cost ≤ Budget THEN
            FOR counter = 1 TO 10 (the average value of ten generated populations was
                                  used rather than a single generation)
            Generate population of clones given selection parameters defining the stage
            and perform selection
        NEXT counter
        Calculate the average yield for the stage
        IF stage yields better then the current best THEN
            best stage 1 yield = this stage yield
            best stage 1 node = this stage node
        END IF
        node number = node number + 1
        parent node = best stage 1 node
        parent yield = best stage 1 yield

    END IF
```

```
END FUNCTION
```

```
# stage 1 routine selecting clones from within families part

FUNCTION Select clones families

    FOR each selected family value
        FOR counter = 1 TO 10
            Generate population of clones given selection parameters defining the stage and perform selection
        NEXT counter
    NEXT family
    Calculate the average yield for the stage
    IF stage yields better then the current best THEN
        best stage 1 yield = this stage yield
        best stage 1 node = this stage node
    END IF
    node number = node number + 1
    parent node = best stage 1 node
    parent yield = best stage 1 yield

    END IF

END FUNCTION
```

```
# general stage routine
FUNCTION stage
    calculate overall cost  = cost previous stage + cost current stage
    IF (planting material required ≤ Planting material available) AND (cost ≤ budget available) AND (population size * selection intensity) ≥ 3) (at least three clones were selected)THEN
        calculate the upper bound for the population of clones coming from the previous stage
        IF upper bound was greater then the current best yield THEN
            FOR counter = 1 TO 10
                Regenerate population of clones given selection parameters defining the stage and perform selection
            NEXT counter
            Calculate the average yield for the stage
            IF stage yield was greater then best yield stage THEN
                best yield stage = stage yield
                best node stage = stage node
            END IF
            IF plot size = 4 AND number of sites ≥ 4 AND number of replicates ≥ 2 (test that clones were tested in large plot size on at least four sites and two replicates per site) THEN
                IF best yield stage > best yield selection THEN
                    best yield selection = best yield stage
                    best node selection = best node stage
                END IF
            END IF
        END IF
    END IF
    Node number = Node number + 1
    IF Node number > Node limit THEN GO TO END
    Parent = best node stage
    Parent yield = best yield stage
END FUNCTION
```

```
# branch-and-bound routine for stages 2-6 selection
```

```
FUNCTION Branching2to6
    FOR each stage
        get the best performing previous stage combination of parameters
        collect the population of clones selected at this stage to  continue selection
        calculate planting material available
        Population size = parent node population size * parent node selection intensity
        FOR each combination of plot size, number of sites and replicates per site that satisfies
            material available ≥ material required
            CALL stage
        FOR each selection intensity
            CALL stage
        FOR each selection index
            CALL stage
END FUNCTION
```

```
# family selection optimisation algorithm routine
FUNCTION Optimise Family

    # branch-and-bound routine for stage 1 selection, selecting best performing families
    FOR each clones per family size
        calculate all possible combination of plots, sites and replicates such that
        plot size * number of sites * number of replicates = clones pre family /20
        FOR each such combination
            CALL Stage 1
    111
    # branch-and-bound routine for the starting population size: number of families
    FOR each number of families
        CALL Stage 1

    # branch-and-bound routine for the selection intensities
    FOR each selection intensity
        CALL Stage 1

    # branch-and-bound routine for the selection indices
    FOR each selection index
        CALL Stage 1
        get the best performing stage 1 combination of parameters
        collect the population of families selected to continue selection
        population size = parent number of families * parent selection intensity

    # branch-and-bound routine for the stage 1 selection: ratoon crop selection of clones from within selected families

    FOR each selection intensity
        calculate overall cost stage 1 (selecting families part + selecting clones from within selected families)
        IF ((cost ≤ budget available) and (population size * intensity) ≥ 1) THEN
            CALL selection clones families
            IF selected yield was greater then best ratoon stage 1 yield THEN
                best ratoon stage yield = this stage yield
                best ratoon stage 1 node = this stage node
            END IF
        END IF
    node number = node number + 1
    IF node number  > Node limit THEN GO TO END
    Parent node = best ratoon stage 1
    Parent yield = best ratoon stage yield
    CALL Stage2to6
```

```
    # search the next best  node to start branching routines all over again
    search for the next best performing node to branch down
    Parent = next best stage node
    Node number = node number + 1
    IF  Node number  > Node limit THEN GO TO END
    ELSE GO TO 111
    END IF
    END
    read best node results through parent nodes
END FUNCTION
```

```
#clonal  selection optimisation algorithm routine
FUNCTION Optimise Clonal

    # exhaustive search of stage 1 parameters
    FOR each population of clones size
        FOR each election intensity
            FOR each selection index
                CALL Stage 1
    111
    get the best performing stage 1 combination of parameters
    collect the population of clones to continue selection
    population size = parent number of clones * parent selection intensity

    CALL Stage2to6
    # search the next best node to start branching routines all over again
    search for the next best performing node to branch down
    Parent = next best stage node
    Node number = node number + 1
    IF Node number  > Node limit THEN GO TO END
    ELSE GO TO 111
    END IF
    END
    read best node results through parent nodes
END FUNCTION
```

Appendix E

An illustration of the optimisations node storage file

Table E.1 gives a sample of the optimisation algorithm ASSSO nodes storage file illustrating the way the algorithm runs. Only first 536 nodes were given that involve those nodes used in Table 4.3 to illustrate branching of the nodes and retrieval of results.

Table E.1

A sample of the optimisation algorithm ASSSO nodes storage file clonal selection. Only the first 536 nodes are given. Columns represent node number m, parenting node number m_z, stage number z_m also the branching level, number of clones k_m, plot size p_m, number of sites s_m, number of replicates r_m, selection intensity t_m, selection index d_m, cost of stages $1,2,3,\ldots,z_m$ $\overline{C}_m$, genetic gain for economic value $\widetilde{G}_m$, whether m was feasible F_m, whether m had been branched B_m, and previous branching level parenting node m_{z-1}

m	m_z	z_m	k_m	p_m	s_m	r_m	t_m	d_m	$\overline{C}_m$	$\widetilde{G}_m$	F_m	B_m	m_{z-1}
1	0	1	4000	0	1	1	0.9	3	27080	19.24	TRUE	TRUE	0
2	0	1	4000	0	1	1	0.9	4	11080	2.58	TRUE	TRUE	0
3	0	1	4000	0	1	1	0.9	0	8480	19.60	TRUE	TRUE	0
4	0	1	4000	0	1	1	0.9	0.0625	27080	19.75	TRUE	TRUE	0
5	0	1	4000	0	1	1	0.9	0.125	27080	19.61	TRUE	TRUE	0
6	0	1	4000	0	1	1	0.9	0.187	27080	18.31	TRUE	TRUE	0
7	0	1	4000	0	1	1	0.9	0.25	27080	17.47	TRUE	TRUE	0
8	0	1	4000	0	1	1	0.9	0.375	27080	14.30	TRUE	TRUE	0
9	0	1	4000	0	1	1	0.9	0.5	27080	12.44	TRUE	TRUE	0
10	0	1	4000	0	1	1	0.9	0.75	27080	9.42	TRUE	TRUE	0

m	m_z	z_m	k_m	p_m	s_m	r_m	t_m	d_m	$\overline{c}_m$	$\widetilde{G}_m$	F_m	B_m	m_{z-1}
11	0	1	4000	0	1	1	0.8	3	27080	33.71	TRUE	TRUE	0
12	0	1	4000	0	1	1	0.8	4	11080	3.17	TRUE	TRUE	0
13	0	1	4000	0	1	1	0.8	0	8480	34.89	TRUE	TRUE	0
14	0	1	4000	0	1	1	0.8	0.0625	27080	33.65	TRUE	TRUE	0
15	0	1	4000	0	1	1	0.8	0.125	27080	31.84	TRUE	TRUE	0
16	0	1	4000	0	1	1	0.8	0.187	27080	29.67	TRUE	TRUE	0
17	0	1	4000	0	1	1	0.8	0.25	27080	26.65	TRUE	TRUE	0
18	0	1	4000	0	1	1	0.8	0.375	27080	22.23	TRUE	TRUE	0
19	0	1	4000	0	1	1	0.8	0.5	27080	18.57	TRUE	TRUE	0
20	0	1	4000	0	1	1	0.8	0.75	27080	14.91	TRUE	TRUE	0
21	0	1	4000	0	1	1	0.7	3	27080	48.03	TRUE	TRUE	0
22	0	1	4000	0	1	1	0.7	4	11080	4.20	TRUE	TRUE	0
23	0	1	4000	0	1	1	0.7	0	8480	49.40	TRUE	TRUE	0
24	0	1	4000	0	1	1	0.7	0.0625	27080	47.91	TRUE	TRUE	0
25	0	1	4000	0	1	1	0.7	0.125	27080	45.00	TRUE	TRUE	0
26	0	1	4000	0	1	1	0.7	0.187	27080	40.80	TRUE	TRUE	0
27	0	1	4000	0	1	1	0.7	0.25	27080	36.46	TRUE	TRUE	0
28	0	1	4000	0	1	1	0.7	0.375	27080	30.24	TRUE	TRUE	0
29	0	1	4000	0	1	1	0.7	0.5	27080	25.84	TRUE	TRUE	0
30	0	1	4000	0	1	1	0.7	0.75	27080	18.45	TRUE	TRUE	0
31	0	1	4000	0	1	1	0.6	3	27080	60.88	TRUE	TRUE	0
32	0	1	4000	0	1	1	0.6	4	11080	3.64	TRUE	TRUE	0
33	0	1	4000	0	1	1	0.6	0	8480	62.74	TRUE	TRUE	0
34	0	1	4000	0	1	1	0.6	0.0625	27080	61.73	TRUE	TRUE	0
35	0	1	4000	0	1	1	0.6	0.125	27080	57.48	TRUE	TRUE	0
36	0	1	4000	0	1	1	0.6	0.187	27080	52.31	TRUE	TRUE	0
37	0	1	4000	0	1	1	0.6	0.25	27080	47.68	TRUE	TRUE	0
38	0	1	4000	0	1	1	0.6	0.375	27080	39.58	TRUE	TRUE	0
39	0	1	4000	0	1	1	0.6	0.5	27080	31.89	TRUE	TRUE	0
40	0	1	4000	0	1	1	0.6	0.75	27080	23.94	TRUE	TRUE	0
41	0	1	4000	0	1	1	0.5	3	27080	74.91	TRUE	TRUE	0
42	0	1	4000	0	1	1	0.5	4	11080	3.19	TRUE	TRUE	0
43	0	1	4000	0	1	1	0.5	0	8480	79.97	TRUE	TRUE	0
44	0	1	4000	0	1	1	0.5	0.0625	27080	76.29	TRUE	TRUE	0
45	0	1	4000	0	1	1	0.5	0.125	27080	69.24	TRUE	TRUE	0
46	0	1	4000	0	1	1	0.5	0.187	27080	63.71	TRUE	TRUE	0
47	0	1	4000	0	1	1	0.5	0.25	27080	57.02	TRUE	TRUE	0
48	0	1	4000	0	1	1	0.5	0.375	27080	47.45	TRUE	TRUE	0
49	0	1	4000	0	1	1	0.5	0.5	27080	40.30	TRUE	TRUE	0
50	0	1	4000	0	1	1	0.5	0.75	27080	26.13	TRUE	TRUE	0
51	0	1	4000	0	1	1	0.4	3	27080	91.15	TRUE	TRUE	0
52	0	1	4000	0	1	1	0.4	4	11080	5.57	TRUE	TRUE	0
53	0	1	4000	0	1	1	0.4	0	8480	93.52	TRUE	TRUE	0
54	0	1	4000	0	1	1	0.4	0.0625	27080	91.98	TRUE	TRUE	0
55	0	1	4000	0	1	1	0.4	0.125	27080	85.77	TRUE	TRUE	0
56	0	1	4000	0	1	1	0.4	0.187	27080	77.22	TRUE	TRUE	0
57	0	1	4000	0	1	1	0.4	0.25	27080	69.14	TRUE	TRUE	0
58	0	1	4000	0	1	1	0.4	0.375	27080	57.31	TRUE	TRUE	0
59	0	1	4000	0	1	1	0.4	0.5	27080	49.04	TRUE	TRUE	0
60	0	1	4000	0	1	1	0.4	0.75	27080	36.14	TRUE	TRUE	0
61	0	1	4000	0	1	1	0.3	3	27080	108.81	TRUE	TRUE	0
62	0	1	4000	0	1	1	0.3	4	11080	9.19	TRUE	TRUE	0
63	0	1	4000	0	1	1	0.3	0	8480	108.44	TRUE	TRUE	0

m	m_z	z_m	k_m	p_m	s_m	r_m	t_m	d_m	$\overline{c}_m$	$\widetilde{G}_m$	F_m	B_m	m_{z-1}
64	0	1	4000	0	1	1	0.3	0.0625	27080	107.67	TRUE	TRUE	0
65	0	1	4000	0	1	1	0.3	0.125	27080	104.16	TRUE	TRUE	0
66	0	1	4000	0	1	1	0.3	0.187	27080	95.72	TRUE	TRUE	0
67	0	1	4000	0	1	1	0.3	0.25	27080	85.96	TRUE	TRUE	0
68	0	1	4000	0	1	1	0.3	0.375	27080	68.48	TRUE	TRUE	0
69	0	1	4000	0	1	1	0.3	0.5	27080	58.89	TRUE	TRUE	0
70	0	1	4000	0	1	1	0.3	0.75	27080	48.75	TRUE	TRUE	0
71	0	1	4000	0	1	1	0.2	3	27080	128.66	TRUE	TRUE	0
72	0	1	4000	0	1	1	0.2	4	11080	11.65	TRUE	TRUE	0
73	0	1	4000	0	1	1	0.2	0	8480	131.36	TRUE	TRUE	0
74	0	1	4000	0	1	1	0.2	0.0625	27080	129.26	TRUE	TRUE	0
75	0	1	4000	0	1	1	0.2	0.125	27080	121.40	TRUE	TRUE	0
76	0	1	4000	0	1	1	0.2	0.187	27080	114.99	TRUE	TRUE	0
77	0	1	4000	0	1	1	0.2	0.25	27080	104.48	TRUE	TRUE	0
78	0	1	4000	0	1	1	0.2	0.375	27080	86.85	TRUE	TRUE	0
79	0	1	4000	0	1	1	0.2	0.5	27080	74.06	TRUE	TRUE	0
80	0	1	4000	0	1	1	0.2	0.75	27080	60.97	TRUE	TRUE	0
81	0	1	4000	0	1	1	0.1	3	27080	164.34	TRUE	TRUE	0
82	0	1	4000	0	1	1	0.1	4	11080	20.15	TRUE	TRUE	0
83	0	1	4000	0	1	1	0.1	0	8480	162.05	TRUE	TRUE	0
84	0	1	4000	0	1	1	0.1	0.0625	27080	164.18	TRUE	TRUE	0
85	0	1	4000	0	1	1	0.1	0.125	27080	159.74	TRUE	TRUE	0
86	0	1	4000	0	1	1	0.1	0.187	27080	51.96	TRUE	TRUE	0
87	0	1	4000	0	1	1	0.1	0.25	27080	134.70	TRUE	TRUE	0
88	0	1	4000	0	1	1	0.1	0.375	27080	111.27	TRUE	TRUE	0
89	0	1	4000	0	1	1	0.1	0.5	27080	91.03	TRUE	TRUE	0
90	0	1	4000	0	1	1	0.1	0.75	27080	70.29	TRUE	TRUE	0
91	0	1	4000	0	1	1	1	3	1600	0.00	TRUE	TRUE	0
92	0	1	6000	0	1	1	0.9	3	39500	19.95	TRUE	TRUE	0
93	0	1	6000	0	1	1	0.9	4	15500	2.87	TRUE	TRUE	0
94	0	1	6000	0	1	1	0.9	0	11920	20.87	TRUE	TRUE	0
95	0	1	6000	0	1	1	0.9	0.0625	39500	20.69	TRUE	TRUE	0
96	0	1	6000	0	1	1	0.9	0.125	39500	19.59	TRUE	TRUE	0
97	0	1	6000	0	1	1	0.9	0.187	39500	17.76	TRUE	TRUE	0
98	0	1	6000	0	1	1	0.9	0.25	39500	16.39	TRUE	TRUE	0
99	0	1	6000	0	1	1	0.9	0.375	39500	13.88	TRUE	TRUE	0
100	0	1	6000	0	1	1	0.9	0.5	39500	12.27	TRUE	TRUE	0
101	0	1	6000	0	1	1	0.9	0.75	39500	10.32	TRUE	TRUE	0
102	0	1	6000	0	1	1	0.8	3	39500	33.97	TRUE	TRUE	0
103	0	1	6000	0	1	1	0.8	4	15500	4.83	TRUE	TRUE	0
104	0	1	6000	0	1	1	0.8	0	11920	4.79	TRUE	TRUE	0
105	0	1	6000	0	1	1	0.8	0.0625	39500	34.26	TRUE	TRUE	0
106	0	1	6000	0	1	1	0.8	0.125	39500	31.47	TRUE	TRUE	0
107	0	1	6000	0	1	1	0.8	0.187	39500	28.53	TRUE	TRUE	0
108	0	1	6000	0	1	1	0.8	0.25	39500	25.78	TRUE	TRUE	0
109	0	1	6000	0	1	1	0.8	0.375	39500	22.14	TRUE	TRUE	0
110	0	1	6000	0	1	1	0.8	0.5	39500	18.40	TRUE	TRUE	0
111	0	1	6000	0	1	1	0.8	0.75	39500	15.31	TRUE	TRUE	0
112	0	1	6000	0	1	1	0.7	3	39500	45.53	TRUE	TRUE	0
113	0	1	6000	0	1	1	0.7	4	15500	4.97	TRUE	TRUE	0
114	0	1	6000	0	1	1	0.7	0	11920	47.62	TRUE	TRUE	0
115	0	1	6000	0	1	1	0.7	0.0625	39500	46.43	TRUE	TRUE	0
116	0	1	6000	0	1	1	0.7	0.125	39500	43.15	TRUE	TRUE	0

m	m_z	z_m	k_m	p_m	s_m	r_m	t_m	d_m	$\bar{c}_m$	$\tilde{G}_m$	F_m	B_m	m_{z-1}
117	0	1	6000	0	1	1	0.7	0.187	39500	39.05	TRUE	TRUE	0
118	0	1	6000	0	1	1	0.7	0.25	39500	35.46	TRUE	TRUE	0
119	0	1	6000	0	1	1	0.7	0.375	39500	28.48	TRUE	TRUE	0
120	0	1	6000	0	1	1	0.7	0.5	39500	24.15	TRUE	TRUE	0
121	0	1	6000	0	1	1	0.7	0.75	39500	19.05	TRUE	TRUE	0
122	0	1	6000	0	1	1	0.6	3	39500	58.31	TRUE	TRUE	0
123	0	1	6000	0	1	1	0.6	4	15500	5.88	TRUE	TRUE	0
124	0	1	6000	0	1	1	0.6	0	11920	61.00	TRUE	TRUE	0
125	0	1	6000	0	1	1	0.6	0.0625	39500	60.22	TRUE	TRUE	0
126	0	1	6000	0	1	1	0.6	0.125	39500	54.77	TRUE	TRUE	0
127	0	1	6000	0	1	1	0.6	0.187	39500	49.93	TRUE	TRUE	0
128	0	1	6000	0	1	1	0.6	0.25	39500	44.71	TRUE	TRUE	0
129	0	1	6000	0	1	1	0.6	0.375	39500	37.67	TRUE	TRUE	0
130	0	1	6000	0	1	1	0.6	0.5	39500	30.38	TRUE	TRUE	0
131	0	1	6000	0	1	1	0.6	0.75	39500	22.44	TRUE	TRUE	0
132	0	1	6000	0	1	1	0.5	3	39500	70.72	TRUE	TRUE	0
133	0	1	6000	0	1	1	0.5	4	15500	6.23	TRUE	TRUE	0
134	0	1	6000	0	1	1	0.5	0	11920	74.01	TRUE	TRUE	0
135	0	1	6000	0	1	1	0.5	0.0625	39500	71.92	TRUE	TRUE	0
136	0	1	6000	0	1	1	0.5	0.125	39500	68.40	TRUE	TRUE	0
137	0	1	6000	0	1	1	0.5	0.187	39500	63.40	TRUE	TRUE	0
138	0	1	6000	0	1	1	0.5	0.25	39500	57.44	TRUE	TRUE	0
139	0	1	6000	0	1	1	0.5	0.375	39500	44.93	TRUE	TRUE	0
140	0	1	6000	0	1	1	0.5	0.5	39500	37.82	TRUE	TRUE	0
141	0	1	6000	0	1	1	0.5	0.75	39500	27.39	TRUE	TRUE	0
142	0	1	6000	0	1	1	0.4	3	39500	88.51	TRUE	TRUE	0
143	0	1	6000	0	1	1	0.4	4	15500	3.48	TRUE	TRUE	0
144	0	1	6000	0	1	1	0.4	0	11920	9.07	TRUE	TRUE	0
145	0	1	6000	0	1	1	0.4	0.0625	39500	90.23	TRUE	TRUE	0
146	0	1	6000	0	1	1	0.4	0.125	39500	85.17	TRUE	TRUE	0
147	0	1	6000	0	1	1	0.4	0.187	39500	76.20	TRUE	TRUE	0
148	0	1	6000	0	1	1	0.4	0.25	39500	66.96	TRUE	TRUE	0
149	0	1	6000	0	1	1	0.4	0.375	39500	53.41	TRUE	TRUE	0
150	0	1	6000	0	1	1	0.4	0.5	39500	44.73	TRUE	TRUE	0
151	0	1	6000	0	1	1	0.4	0.75	39500	32.55	TRUE	TRUE	0
152	0	1	6000	0	1	1	0.3	3	39500	10.14	TRUE	TRUE	0
153	0	1	6000	0	1	1	0.3	4	15500	3.57	TRUE	TRUE	0
154	0	1	6000	0	1	1	0.3	0	11920	110.90	TRUE	TRUE	0
155	0	1	6000	0	1	1	0.3	0.0625	39500	112.12	TRUE	TRUE	0
156	0	1	6000	0	1	1	0.3	0.125	39500	105.08	TRUE	TRUE	0
157	0	1	6000	0	1	1	0.3	0.187	39500	92.80	TRUE	TRUE	0
158	0	1	6000	0	1	1	0.3	0.25	39500	82.06	TRUE	TRUE	0
159	0	1	6000	0	1	1	0.3	0.375	39500	63.83	TRUE	TRUE	0
160	0	1	6000	0	1	1	0.3	0.5	39500	52.50	TRUE	TRUE	0
161	0	1	6000	0	1	1	0.3	0.75	39500	39.31	TRUE	TRUE	0
162	0	1	6000	0	1	1	0.2	3	39500	34.41	TRUE	TRUE	0
163	0	1	6000	0	1	1	0.2	4	15500	9.07	TRUE	TRUE	0
164	0	1	6000	0	1	1	0.2	0	11920	36.54	TRUE	TRUE	0
165	0	1	6000	0	1	1	0.2	0.0625	39500	136.89	TRUE	TRUE	0
166	0	1	6000	0	1	1	0.2	0.125	39500	127.82	TRUE	TRUE	0
167	0	1	6000	0	1	1	0.2	0.187	39500	113.10	TRUE	TRUE	0
168	0	1	6000	0	1	1	0.2	0.25	39500	97.43	TRUE	TRUE	0
169	0	1	6000	0	1	1	0.2	0.375	39500	77.32	TRUE	TRUE	0

m	m_z	z_m	k_m	p_m	s_m	r_m	t_m	d_m	$\overline{c}_m$	$\widetilde{G}_m$	F_m	B_m	m_{z-1}
170	0	1	6000	0	1	1	0.2	0.5	39500	60.48	TRUE	TRUE	0
171	0	1	6000	0	1	1	0.2	0.75	39500	44.51	TRUE	TRUE	0
172	0	1	6000	0	1	1	0.1	3	39500	170.86	TRUE	TRUE	0
173	0	1	6000	0	1	1	0.1	4	15500	17.33	TRUE	TRUE	0
174	0	1	6000	0	1	1	0.1	0	11920	181.57	TRUE	TRUE	0
175	0	1	6000	0	1	1	0.1	0.0625	39500	176.30	TRUE	TRUE	0
176	0	1	6000	0	1	1	0.1	0.125	39500	162.41	TRUE	TRUE	0
177	0	1	6000	0	1	1	0.1	0.187	39500	149.16	TRUE	TRUE	0
178	0	1	6000	0	1	1	0.1	0.25	39500	130.31	TRUE	TRUE	0
179	0	1	6000	0	1	1	0.1	0.375	39500	98.12	TRUE	TRUE	0
180	0	1	6000	0	1	1	0.1	0.5	39500	83.48	TRUE	TRUE	0
181	0	1	6000	0	1	1	0.1	0.75	39500	67.16	TRUE	TRUE	0
182	0	1	6000	0	1	1	1	3	1600	0.00	TRUE	TRUE	0
183	0	1	8000	0	1	1	0.9	3	51920	17.21	TRUE	TRUE	0
184	0	1	8000	0	1	1	0.9	4	19920	-3.08	TRUE	TRUE	0
185	0	1	8000	0	1	1	0.9	0	15360	19.49	TRUE	TRUE	0
186	0	1	8000	0	1	1	0.9	0.0625	51920	19.63	TRUE	TRUE	0
187	0	1	8000	0	1	1	0.9	0.125	51920	18.62	TRUE	TRUE	0
188	0	1	8000	0	1	1	0.9	0.187	51920	17.78	TRUE	TRUE	0
189	0	1	8000	0	1	1	0.9	0.25	51920	16.15	TRUE	TRUE	0
190	0	1	8000	0	1	1	0.9	0.375	51920	12.65	TRUE	TRUE	0
191	0	1	8000	0	1	1	0.9	0.5	51920	10.56	TRUE	TRUE	0
192	0	1	8000	0	1	1	0.9	0.75	51920	7.59	TRUE	TRUE	0
193	0	1	8000	0	1	1	0.8	3	51920	4.87	TRUE	TRUE	0
194	0	1	8000	0	1	1	0.8	4	19920	0.83	TRUE	TRUE	0
195	0	1	8000	0	1	1	0.8	0	15360	36.89	TRUE	TRUE	0
196	0	1	8000	0	1	1	0.8	0.0625	51920	35.47	TRUE	TRUE	0
197	0	1	8000	0	1	1	0.8	0.125	51920	32.90	TRUE	TRUE	0
198	0	1	8000	0	1	1	0.8	0.187	51920	30.98	TRUE	TRUE	0
199	0	1	8000	0	1	1	0.8	0.25	51920	27.89	TRUE	TRUE	0
200	0	1	8000	0	1	1	0.8	0.375	51920	22.86	TRUE	TRUE	0
201	0	1	8000	0	1	1	0.8	0.5	51920	18.96	TRUE	TRUE	0
202	0	1	8000	0	1	1	0.8	0.75	51920	13.32	TRUE	TRUE	0
203	0	1	8000	0	1	1	0.7	3	51920	46.99	TRUE	TRUE	0
204	0	1	8000	0	1	1	0.7	4	19920	1.87	TRUE	TRUE	0
205	0	1	8000	0	1	1	0.7	0	15360	48.62	TRUE	TRUE	0
206	0	1	8000	0	1	1	0.7	0.0625	51920	47.63	TRUE	TRUE	0
207	0	1	8000	0	1	1	0.7	0.125	51920	45.33	TRUE	TRUE	0
208	0	1	8000	0	1	1	0.7	0.187	51920	40.77	TRUE	TRUE	0
209	0	1	8000	0	1	1	0.7	0.25	51920	37.07	TRUE	TRUE	0
210	0	1	8000	0	1	1	0.7	0.375	51920	29.35	TRUE	TRUE	0
211	0	1	8000	0	1	1	0.7	0.5	51920	24.02	TRUE	TRUE	0
212	0	1	8000	0	1	1	0.7	0.75	51920	18.21	TRUE	TRUE	0
213	0	1	8000	0	1	1	0.6	3	51920	60.12	TRUE	TRUE	0
214	0	1	8000	0	1	1	0.6	4	19920	4.07	TRUE	TRUE	0
215	0	1	8000	0	1	1	0.6	0	15360	62.19	TRUE	TRUE	0
216	0	1	8000	0	1	1	0.6	0.0625	51920	60.90	TRUE	TRUE	0
217	0	1	8000	0	1	1	0.6	0.125	51920	56.51	TRUE	TRUE	0
218	0	1	8000	0	1	1	0.6	0.187	51920	51.86	TRUE	TRUE	0
219	0	1	8000	0	1	1	0.6	0.25	51920	45.36	TRUE	TRUE	0
220	0	1	8000	0	1	1	0.6	0.375	51920	37.03	TRUE	TRUE	0
221	0	1	8000	0	1	1	0.6	0.5	51920	31.41	TRUE	TRUE	0
222	0	1	8000	0	1	1	0.6	0.75	51920	24.38	TRUE	TRUE	0

m	m_z	z_m	k_m	p_m	s_m	r_m	t_m	d_m	$\overline{c}_m$	$\widetilde{G}_m$	F_m	B_m	m_{z-1}
223	0	1	8000	0	1	1	0.5	3	51920	72.67	TRUE	TRUE	0
224	0	1	8000	0	1	1	0.5	4	19920	6.53	TRUE	TRUE	0
225	0	1	8000	0	1	1	0.5	0	15360	74.62	TRUE	TRUE	0
226	0	1	8000	0	1	1	0.5	0.0625	51920	74.00	TRUE	TRUE	0
227	0	1	8000	0	1	1	0.5	0.125	51920	68.27	TRUE	TRUE	0
228	0	1	8000	0	1	1	0.5	0.187	51920	60.76	TRUE	TRUE	0
229	0	1	8000	0	1	1	0.5	0.25	51920	54.45	TRUE	TRUE	0
230	0	1	8000	0	1	1	0.5	0.375	51920	45.38	TRUE	TRUE	0
231	0	1	8000	0	1	1	0.5	0.5	51920	38.78	TRUE	TRUE	0
232	0	1	8000	0	1	1	0.5	0.75	51920	28.91	TRUE	TRUE	0
233	0	1	8000	0	1	1	0.4	3	51920	88.23	TRUE	TRUE	0
234	0	1	8000	0	1	1	0.4	4	19920	8.50	TRUE	TRUE	0
235	0	1	8000	0	1	1	0.4	0	15360	89.05	TRUE	TRUE	0
236	0	1	8000	0	1	1	0.4	0.0625	51920	89.91	TRUE	TRUE	0
237	0	1	8000	0	1	1	0.4	0.125	51920	81.58	TRUE	TRUE	0
238	0	1	8000	0	1	1	0.4	0.187	51920	72.77	TRUE	TRUE	0
239	0	1	8000	0	1	1	0.4	0.25	51920	66.17	TRUE	TRUE	0
240	0	1	8000	0	1	1	0.4	0.375	51920	55.02	TRUE	TRUE	0
241	0	1	8000	0	1	1	0.4	0.5	51920	46.78	TRUE	TRUE	0
242	0	1	8000	0	1	1	0.4	0.75	51920	35.72	TRUE	TRUE	0
243	0	1	8000	0	1	1	0.3	3	51920	104.34	TRUE	TRUE	0
244	0	1	8000	0	1	1	0.3	4	19920	13.78	TRUE	TRUE	0
245	0	1	8000	0	1	1	0.3	0	15360	107.61	TRUE	TRUE	0
246	0	1	8000	0	1	1	0.3	0.0625	51920	107.07	TRUE	TRUE	0
247	0	1	8000	0	1	1	0.3	0.125	51920	98.56	TRUE	TRUE	0
248	0	1	8000	0	1	1	0.3	0.187	51920	90.55	TRUE	TRUE	0
249	0	1	8000	0	1	1	0.3	0.25	51920	79.94	TRUE	TRUE	0
250	0	1	8000	0	1	1	0.3	0.375	51920	66.17	TRUE	TRUE	0
251	0	1	8000	0	1	1	0.3	0.5	51920	54.73	TRUE	TRUE	0
252	0	1	8000	0	1	1	0.3	0.75	51920	43.22	TRUE	TRUE	0
253	0	1	8000	0	1	1	0.2	3	51920	24.74	TRUE	TRUE	0
254	0	1	8000	0	1	1	0.2	4	19920	14.41	TRUE	TRUE	0
255	0	1	8000	0	1	1	0.2	0	15360	134.31	TRUE	TRUE	0
256	0	1	8000	0	1	1	0.2	0.0625	51920	127.11	TRUE	TRUE	0
257	0	1	8000	0	1	1	0.2	0.125	51920	121.30	TRUE	TRUE	0
258	0	1	8000	0	1	1	0.2	0.187	51920	109.62	TRUE	TRUE	0
259	0	1	8000	0	1	1	0.2	0.25	51920	97.74	TRUE	TRUE	0
260	0	1	8000	0	1	1	0.2	0.375	51920	77.92	TRUE	TRUE	0
261	0	1	8000	0	1	1	0.2	0.5	51920	67.24	TRUE	TRUE	0
262	0	1	8000	0	1	1	0.2	0.75	51920	53.26	TRUE	TRUE	0
263	0	1	8000	0	1	1	0.1	3	51920	161.06	TRUE	TRUE	0
264	0	1	8000	0	1	1	0.1	4	19920	6.61	TRUE	TRUE	0
265	0	1	8000	0	1	1	0.1	0	15360	165.40	TRUE	TRUE	0
266	0	1	8000	0	1	1	0.1	0.0625	51920	164.20	TRUE	TRUE	0
267	0	1	8000	0	1	1	0.1	0.125	51920	155.06	TRUE	TRUE	0
268	0	1	8000	0	1	1	0.1	0.187	51920	134.71	TRUE	TRUE	0
269	0	1	8000	0	1	1	0.1	0.25	51920	117.44	TRUE	TRUE	0
270	0	1	8000	0	1	1	0.1	0.375	51920	90.84	TRUE	TRUE	0
271	0	1	8000	0	1	1	0.1	0.5	51920	70.52	TRUE	TRUE	0
272	0	1	8000	0	1	1	0.1	0.75	51920	52.51	TRUE	TRUE	0
273	0	1	8000	0	1	1	1	3	1600	0.00	TRUE	TRUE	0
274	0	1	10000	0	1	1	0.9	3	64340	12.42	TRUE	TRUE	0
275	0	1	10000	0	1	1	0.9	4	24340	0.51	TRUE	TRUE	0

m	m_z	z_m	k_m	p_m	s_m	r_m	t_m	d_m	$\overline{c}_m$	$\widetilde{G}_m$	F_m	B_m	m_{z-1}
276	0	1	10000	0	1	1	0.9	0	18800	18.78	TRUE	TRUE	0
277	0	1	10000	0	1	1	0.9	0.0625	64340	18.68	TRUE	TRUE	0
278	0	1	10000	0	1	1	0.9	0.125	64340	18.52	TRUE	TRUE	0
279	0	1	10000	0	1	1	0.9	0.187	64340	17.37	TRUE	TRUE	0
280	0	1	10000	0	1	1	0.9	0.25	64340	15.90	TRUE	TRUE	0
281	0	1	10000	0	1	1	0.9	0.375	64340	13.41	TRUE	TRUE	0
282	0	1	10000	0	1	1	0.9	0.5	64340	11.36	TRUE	TRUE	0
283	0	1	10000	0	1	1	0.9	0.75	64340	8.17	TRUE	TRUE	0
284	0	1	10000	0	1	1	0.8	3	64340	31.57	TRUE	TRUE	0
285	0	1	10000	0	1	1	0.8	4	24340	0.28	TRUE	TRUE	0
286	0	1	10000	0	1	1	0.8	0	18800	32.20	TRUE	TRUE	0
287	0	1	10000	0	1	1	0.8	0.0625	64340	31.96	TRUE	TRUE	0
288	0	1	10000	0	1	1	0.8	0.125	64340	30.82	TRUE	TRUE	0
289	0	1	10000	0	1	1	0.8	0.187	64340	27.86	TRUE	TRUE	0
290	0	1	10000	0	1	1	0.8	0.25	64340	25.13	TRUE	TRUE	0
291	0	1	10000	0	1	1	0.8	0.375	64340	20.63	TRUE	TRUE	0
292	0	1	10000	0	1	1	0.8	0.5	64340	17.59	TRUE	TRUE	0
293	0	1	10000	0	1	1	0.8	0.75	64340	13.32	TRUE	TRUE	0
294	0	1	10000	0	1	1	0.7	3	64340	43.92	TRUE	TRUE	0
295	0	1	10000	0	1	1	0.7	4	24340	0.47	TRUE	TRUE	0
296	0	1	10000	0	1	1	0.7	0	18800	44.68	TRUE	TRUE	0
297	0	1	10000	0	1	1	0.7	0.0625	64340	44.24	TRUE	TRUE	0
298	0	1	10000	0	1	1	0.7	0.125	64340	42.10	TRUE	TRUE	0
299	0	1	10000	0	1	1	0.7	0.187	64340	38.86	TRUE	TRUE	0
300	0	1	10000	0	1	1	0.7	0.25	64340	35.09	TRUE	TRUE	0
301	0	1	10000	0	1	1	0.7	0.375	64340	28.83	TRUE	TRUE	0
302	0	1	10000	0	1	1	0.7	0.5	64340	24.23	TRUE	TRUE	0
303	0	1	10000	0	1	1	0.7	0.75	64340	18.34	TRUE	TRUE	0
304	0	1	10000	0	1	1	0.6	3	64340	57.16	TRUE	TRUE	0
305	0	1	10000	0	1	1	0.6	4	24340	4.25	TRUE	TRUE	0
306	0	1	10000	0	1	1	0.6	0	18800	57.23	TRUE	TRUE	0
307	0	1	10000	0	1	1	0.6	0.0625	64340	57.29	TRUE	TRUE	0
308	0	1	10000	0	1	1	0.6	0.125	64340	54.26	TRUE	TRUE	0
309	0	1	10000	0	1	1	0.6	0.187	64340	50.07	TRUE	TRUE	0
310	0	1	10000	0	1	1	0.6	0.25	64340	45.69	TRUE	TRUE	0
311	0	1	10000	0	1	1	0.6	0.375	64340	37.16	TRUE	TRUE	0
312	0	1	10000	0	1	1	0.6	0.5	64340	30.52	TRUE	TRUE	0
313	0	1	10000	0	1	1	0.6	0.75	64340	23.19	TRUE	TRUE	0
314	0	1	10000	0	1	1	0.5	3	64340	68.89	TRUE	TRUE	0
315	0	1	10000	0	1	1	0.5	4	24340	5.80	TRUE	TRUE	0
316	0	1	10000	0	1	1	0.5	0	18800	70.55	TRUE	TRUE	0
317	0	1	10000	0	1	1	0.5	0.0625	64340	70.63	TRUE	TRUE	0
318	0	1	10000	0	1	1	0.5	0.125	64340	66.65	TRUE	TRUE	0
319	0	1	10000	0	1	1	0.5	0.187	64340	61.37	TRUE	TRUE	0
320	0	1	10000	0	1	1	0.5	0.25	64340	56.01	TRUE	TRUE	0
321	0	1	10000	0	1	1	0.5	0.375	64340	47.08	TRUE	TRUE	0
322	0	1	10000	0	1	1	0.5	0.5	64340	38.00	TRUE	TRUE	0
323	0	1	10000	0	1	1	0.5	0.75	64340	27.21	TRUE	TRUE	0
324	0	1	10000	0	1	1	0.4	3	64340	84.04	TRUE	TRUE	0
325	0	1	10000	0	1	1	0.4	4	24340	8.46	TRUE	TRUE	0
326	0	1	10000	0	1	1	0.4	0	18800	86.68	TRUE	TRUE	0
327	0	1	10000	0	1	1	0.4	0.0625	64340	85.01	TRUE	TRUE	0
328	0	1	10000	0	1	1	0.4	0.125	64340	79.66	TRUE	TRUE	0

m	m_z	z_m	k_m	p_m	s_m	r_m	t_m	d_m	$\bar{c}_m$	$\tilde{G}_m$	F_m	B_m	m_{z-1}
329	0	1	10000	0	1	1	0.4	0.187	64340	73.36	TRUE	TRUE	0
330	0	1	10000	0	1	1	0.4	0.25	64340	67.36	TRUE	TRUE	0
331	0	1	10000	0	1	1	0.4	0.375	64340	53.66	TRUE	TRUE	0
332	0	1	10000	0	1	1	0.4	0.5	64340	45.95	TRUE	TRUE	0
333	0	1	10000	0	1	1	0.4	0.75	64340	34.80	TRUE	TRUE	0
334	0	1	10000	0	1	1	0.3	3	64340	101.70	TRUE	TRUE	0
335	0	1	10000	0	1	1	0.3	4	24340	10.70	TRUE	TRUE	0
336	0	1	10000	0	1	1	0.3	0	18800	103.92	TRUE	TRUE	0
337	0	1	10000	0	1	1	0.3	0.0625	64340	102.29	TRUE	TRUE	0
338	0	1	10000	0	1	1	0.3	0.125	64340	98.80	TRUE	TRUE	0
339	0	1	10000	0	1	1	0.3	0.187	64340	90.40	TRUE	TRUE	0
340	0	1	10000	0	1	1	0.3	0.25	64340	82.10	TRUE	TRUE	0
341	0	1	10000	0	1	1	0.3	0.375	64340	65.50	TRUE	TRUE	0
342	0	1	10000	0	1	1	0.3	0.5	64340	54.76	TRUE	TRUE	0
343	0	1	10000	0	1	1	0.3	0.75	64340	43.38	TRUE	TRUE	0
344	0	1	10000	0	1	1	0.2	3	64340	121.88	TRUE	TRUE	0
345	0	1	10000	0	1	1	0.2	4	24340	10.18	TRUE	TRUE	0
346	0	1	10000	0	1	1	0.2	0	18800	125.79	TRUE	TRUE	0
347	0	1	10000	0	1	1	0.2	0.0625	64340	123.40	TRUE	TRUE	0
348	0	1	10000	0	1	1	0.2	0.125	64340	118.22	TRUE	TRUE	0
349	0	1	10000	0	1	1	0.2	0.187	64340	109.25	TRUE	TRUE	0
350	0	1	10000	0	1	1	0.2	0.25	64340	98.31	TRUE	TRUE	0
351	0	1	10000	0	1	1	0.2	0.375	64340	81.01	TRUE	TRUE	0
352	0	1	10000	0	1	1	0.2	0.5	64340	68.57	TRUE	TRUE	0
353	0	1	10000	0	1	1	0.2	0.75	64340	52.86	TRUE	TRUE	0
354	0	1	10000	0	1	1	0.1	3	64340	153.60	TRUE	TRUE	0
355	0	1	10000	0	1	1	0.1	4	24340	16.75	TRUE	TRUE	0
356	0	1	10000	0	1	1	0.1	0	18800	162.61	TRUE	TRUE	0
357	0	1	10000	0	1	1	0.1	0.0625	64340	154.83	TRUE	TRUE	0
358	0	1	10000	0	1	1	0.1	0.125	64340	148.26	TRUE	TRUE	0
359	0	1	10000	0	1	1	0.1	0.187	64340	131.82	TRUE	TRUE	0
360	0	1	10000	0	1	1	0.1	0.25	64340	115.27	TRUE	TRUE	0
361	0	1	10000	0	1	1	0.1	0.375	64340	93.68	TRUE	TRUE	0
362	0	1	10000	0	1	1	0.1	0.5	64340	82.67	TRUE	TRUE	0
363	0	1	10000	0	1	1	0.1	0.75	64340	64.26	TRUE	TRUE	0
364	0	1	10000	0	1	1	1	3	1600	0.00	TRUE	TRUE	0
365	0	1	15000	0	1	1	0.9	3	95390	17.69	TRUE	TRUE	0
366	0	1	15000	0	1	1	0.9	4	35390	-2.61	TRUE	TRUE	0
367	0	1	15000	0	1	1	0.9	0	27400	20.71	TRUE	TRUE	0
368	0	1	15000	0	1	1	0.9	0.0625	95390	20.83	TRUE	TRUE	0
369	0	1	15000	0	1	1	0.9	0.125	95390	19.11	TRUE	TRUE	0
370	0	1	15000	0	1	1	0.9	0.187	95390	17.67	TRUE	TRUE	0
371	0	1	15000	0	1	1	0.9	0.25	95390	15.92	TRUE	TRUE	0
372	0	1	15000	0	1	1	0.9	0.375	95390	12.84	TRUE	TRUE	0
373	0	1	15000	0	1	1	0.9	0.5	95390	10.68	TRUE	TRUE	0
374	0	1	15000	0	1	1	0.9	0.75	95390	7.85	TRUE	TRUE	0
375	0	1	15000	0	1	1	0.8	3	95390	35.04	TRUE	TRUE	0
376	0	1	15000	0	1	1	0.8	4	35390	0.90	TRUE	TRUE	0
377	0	1	15000	0	1	1	0.8	0	27400	36.45	TRUE	TRUE	0
378	0	1	15000	0	1	1	0.8	0.0625	95390	35.07	TRUE	TRUE	0
379	0	1	15000	0	1	1	0.8	0.125	95390	33.13	TRUE	TRUE	0
380	0	1	15000	0	1	1	0.8	0.187	95390	28.91	TRUE	TRUE	0
381	0	1	15000	0	1	1	0.8	0.25	95390	25.77	TRUE	TRUE	0

m	m_z	z_m	k_m	p_m	s_m	r_m	t_m	d_m	$\overline{c}_m$	$\widetilde{G}_m$	F_m	B_m	m_{z-1}
382	0	1	15000	0	1	1	0.8	0.375	95390	20.43	TRUE	TRUE	0
383	0	1	15000	0	1	1	0.8	0.5	95390	16.42	TRUE	TRUE	0
384	0	1	15000	0	1	1	0.8	0.75	95390	11.55	TRUE	TRUE	0
385	0	1	15000	0	1	1	0.7	3	95390	49.61	TRUE	TRUE	0
386	0	1	15000	0	1	1	0.7	4	35390	0.55	TRUE	TRUE	0
387	0	1	15000	0	1	1	0.7	0	27400	50.86	TRUE	TRUE	0
388	0	1	15000	0	1	1	0.7	0.0625	95390	50.56	TRUE	TRUE	0
389	0	1	15000	0	1	1	0.7	0.125	95390	46.56	TRUE	TRUE	0
390	0	1	15000	0	1	1	0.7	0.187	95390	41.72	TRUE	TRUE	0
391	0	1	15000	0	1	1	0.7	0.25	95390	36.67	TRUE	TRUE	0
392	0	1	15000	0	1	1	0.7	0.375	95390	27.66	TRUE	TRUE	0
393	0	1	15000	0	1	1	0.7	0.5	95390	21.97	TRUE	TRUE	0
394	0	1	15000	0	1	1	0.7	0.75	95390	14.96	TRUE	TRUE	0
395	0	1	15000	0	1	1	0.6	3	95390	63.89	TRUE	TRUE	0
396	0	1	15000	0	1	1	0.6	4	35390	0.70	TRUE	TRUE	0
397	0	1	15000	0	1	1	0.6	0	27400	65.47	TRUE	TRUE	0
398	0	1	15000	0	1	1	0.6	0.0625	95390	64.90	TRUE	TRUE	0
399	0	1	15000	0	1	1	0.6	0.125	95390	60.81	TRUE	TRUE	0
400	0	1	15000	0	1	1	0.6	0.187	95390	54.11	TRUE	TRUE	0
401	0	1	15000	0	1	1	0.6	0.25	95390	46.70	TRUE	TRUE	0
402	0	1	15000	0	1	1	0.6	0.375	95390	35.99	TRUE	TRUE	0
403	0	1	15000	0	1	1	0.6	0.5	95390	28.16	TRUE	TRUE	0
404	0	1	15000	0	1	1	0.6	0.75	95390	19.31	TRUE	TRUE	0
405	0	1	15000	0	1	1	0.5	3	95390	77.70	TRUE	TRUE	0
406	0	1	15000	0	1	1	0.5	4	35390	4.64	TRUE	TRUE	0
407	0	1	15000	0	1	1	0.5	0	27400	81.36	TRUE	TRUE	0
408	0	1	15000	0	1	1	0.5	0.0625	95390	79.67	TRUE	TRUE	0
409	0	1	15000	0	1	1	0.5	0.125	95390	72.94	TRUE	TRUE	0
410	0	1	15000	0	1	1	0.5	0.187	95390	65.83	TRUE	TRUE	0
411	0	1	15000	0	1	1	0.5	0.25	95390	58.07	TRUE	TRUE	0
412	0	1	15000	0	1	1	0.5	0.375	95390	45.10	TRUE	TRUE	0
413	0	1	15000	0	1	1	0.5	0.5	95390	36.72	TRUE	TRUE	0
414	0	1	15000	0	1	1	0.5	0.75	95390	27.37	TRUE	TRUE	0
415	0	1	15000	0	1	1	0.4	3	95390	94.67	TRUE	TRUE	0
416	0	1	15000	0	1	1	0.4	4	35390	8.44	TRUE	TRUE	0
417	0	1	15000	0	1	1	0.4	0	27400	99.34	TRUE	TRUE	0
418	0	1	15000	0	1	1	0.4	0.0625	95390	96.96	TRUE	TRUE	0
419	0	1	15000	0	1	1	0.4	0.125	95390	87.19	TRUE	TRUE	0
420	0	1	15000	0	1	1	0.4	0.187	95390	77.21	TRUE	TRUE	0
421	0	1	15000	0	1	1	0.4	0.25	95390	68.17	TRUE	TRUE	0
422	0	1	15000	0	1	1	0.4	0.375	95390	53.71	TRUE	TRUE	0
423	0	1	15000	0	1	1	0.4	0.5	95390	44.06	TRUE	TRUE	0
424	0	1	15000	0	1	1	0.4	0.75	95390	34.40	TRUE	TRUE	0
425	0	1	15000	0	1	1	0.3	3	95390	112.26	TRUE	TRUE	0
426	0	1	15000	0	1	1	0.3	4	35390	10.26	TRUE	TRUE	0
427	0	1	15000	0	1	1	0.3	0	27400	119.96	TRUE	TRUE	0
428	0	1	15000	0	1	1	0.3	0.0625	95390	115.61	TRUE	TRUE	0
429	0	1	15000	0	1	1	0.3	0.125	95390	105.56	TRUE	TRUE	0
430	0	1	15000	0	1	1	0.3	0.187	95390	93.84	TRUE	TRUE	0
431	0	1	15000	0	1	1	0.3	0.25	95390	81.48	TRUE	TRUE	0
432	0	1	15000	0	1	1	0.3	0.375	95390	64.85	TRUE	TRUE	0
433	0	1	15000	0	1	1	0.3	0.5	95390	55.10	TRUE	TRUE	0
434	0	1	15000	0	1	1	0.3	0.75	95390	41.61	TRUE	TRUE	0

m	m_z	z_m	k_m	p_m	s_m	r_m	t_m	d_m	$\overline{c}_m$	$\widetilde{G}_m$	F_m	B_m	m_{z-1}
435	0	1	15000	0	1	1	0.2	3	95390	137.08	TRUE	TRUE	0
436	0	1	15000	0	1	1	0.2	4	35390	9.62	TRUE	TRUE	0
437	0	1	15000	0	1	1	0.2	0	27400	143.57	TRUE	TRUE	0
438	0	1	15000	0	1	1	0.2	0.0625	95390	140.83	TRUE	TRUE	0
439	0	1	15000	0	1	1	0.2	0.125	95390	130.59	TRUE	TRUE	0
440	0	1	15000	0	1	1	0.2	0.187	95390	112.33	TRUE	TRUE	0
441	0	1	15000	0	1	1	0.2	0.25	95390	97.84	TRUE	TRUE	0
442	0	1	15000	0	1	1	0.2	0.375	95390	76.77	TRUE	TRUE	0
443	0	1	15000	0	1	1	0.2	0.5	95390	62.57	TRUE	TRUE	0
444	0	1	15000	0	1	1	0.2	0.75	95390	46.62	TRUE	TRUE	0
445	0	1	15000	0	1	1	0.1	3	95390	175.02	TRUE	TRUE	0
446	0	1	15000	0	1	1	0.1	4	35390	7.12	TRUE	TRUE	0
447	**0**	**1**	**15000**	**0**	**1**	**1**	**0.1**	**0**	**27400**	**184.95**	**TRUE**	**TRUE**	**0**
448	0	1	15000	0	1	1	0.1	0.0625	95390	180.70	TRUE	TRUE	0
449	0	1	15000	0	1	1	0.1	0.125	95390	162.71	TRUE	TRUE	0
450	0	1	15000	0	1	1	0.1	0.187	95390	144.09	TRUE	TRUE	0
451	0	1	15000	0	1	1	0.1	0.25	95390	125.57	TRUE	TRUE	0
452	0	1	15000	0	1	1	0.1	0.375	95390	96.86	TRUE	TRUE	0
453	0	1	15000	0	1	1	0.1	0.5	95390	79.55	TRUE	TRUE	0
454	0	1	15000	0	1	1	0.1	0.75	95390	55.47	TRUE	TRUE	0
455	0	1	15000	0	1	1	1	3	1600	0.00	TRUE	TRUE	0
456	447	2	1500	1	1	1	0.9	3	60420	192.23	TRUE	FALSE	447
457	**447**	**2**	**1500**	**2**	**1**	**1**	**0.9**	**3**	**101700**	**194.56**	**TRUE**	**TRUE**	**447**
458	457	2	1500	2	1	1	0.5	3	112840	218.47	TRUE	FALSE	447
459	457	2	1500	2	1	1	0.4	3	112840	204.59	TRUE	FALSE	447
460	**457**	**2**	**1500**	**2**	**1**	**1**	**0.3**	**3**	**112840**	**269.26**	**TRUE**	**TRUE**	**447**
461	457	2	1500	2	1	1	0.2	3	112840	244.59	TRUE	FALSE	447
462	457	2	1500	2	1	1	1	3	49250	84.95	TRUE	FALSE	447
463	460	2	1500	2	1	1	0.3	4	89700	196.12	TRUE	FALSE	447
464	460	2	1500	2	1	1	0.3	0	81500	267.87	TRUE	FALSE	447
465	460	2	1500	2	1	1	0.3	0.0625	101700	262.91	TRUE	FALSE	447
466	460	2	1500	2	1	1	0.3	0.125	101700	264.82	TRUE	FALSE	447
467	460	2	1500	2	1	1	0.3	0.187	101700	222.74	TRUE	FALSE	447
468	460	2	1500	2	1	1	0.3	0.25	101700	245.44	TRUE	FALSE	447
469	460	2	1500	2	1	1	0.3	0.375	101700	181.80	TRUE	FALSE	447
470	460	2	1500	2	1	1	0.3	0.5	101700	152.21	TRUE	FALSE	447
471	460	2	1500	2	1	1	0.3	0.75	101700	92.35	TRUE	FALSE	447
472	460	2	1500	2	1	1	0.3	1	101700	212.56	TRUE	FALSE	447
473	460	2	1500	2	1	1	0.3	2	101700	205.78	TRUE	FALSE	447
474	460	3	450	1	1	1	0.9	3	124314	244.61	TRUE	FALSE	460
475	460	3	450	2	1	1	0.9	3	136698	281.64	TRUE	FALSE	460
476	**460**	**3**	**450**	**4**	**1**	**1**	**0.9**	**3**	**154716**	**283.21**	**TRUE**	**TRUE**	**460**
477	**476**	**3**	**450**	**4**	**2**	**1**	**0.9**	**3**	**194352**	**285.73**	**TRUE**	**TRUE**	**460**
478	476	3	450	4	3	1	0.9	3	233988	246.28	TRUE	FALSE	460
479	477	3	450	4	2	1	0.5	3	207592	303.33	TRUE	FALSE	460
480	**477**	**3**	**450**	**4**	**2**	**1**	**0.4**	**3**	**207592**	**363.76**	**TRUE**	**TRUE**	**460**
481	477	3	450	4	2	1	0.1	3	207592	103.75	TRUE	FALSE	460
482	477	3	450	4	2	1	1	3	126590	69.26	TRUE	FALSE	460
483	480	3	450	4	2	1	0.4	4	187152	233.93	TRUE	FALSE	460
484	480	3	450	4	2	1	0.4	0	170240	136.29	TRUE	FALSE	460
485	480	3	450	4	2	1	0.4	0.0625	194352	352.20	TRUE	FALSE	460
486	480	3	450	4	2	1	0.4	0.125	194352	352.90	TRUE	FALSE	460
487	480	3	450	4	2	1	0.4	0.187	194352	352.43	TRUE	FALSE	460

m	m_z	z_m	k_m	p_m	s_m	r_m	t_m	d_m	$\overline{c}_m$	$\widetilde{G}_m$	F_m	B_m	m_{z-1}
488	480	3	450	4	2	1	0.4	0.25	194352	353.84	TRUE	FALSE	460
489	480	3	450	4	2	1	0.4	0.375	194352	255.27	TRUE	FALSE	460
490	480	3	450	4	2	1	0.4	0.5	194352	315.38	TRUE	FALSE	460
491	480	3	450	4	2	1	0.4	0.75	194352	240.52	TRUE	FALSE	460
492	480	3	450	4	2	1	0.4	1	194352	308.19	TRUE	FALSE	460
493	480	3	450	4	2	1	0.4	2	194352	309.87	TRUE	FALSE	460
494	480	4	180	1	1	1	0.9	3	213526	350.74	TRUE	FALSE	480
495	480	4	180	2	1	1	0.9	3	218479	353.64	TRUE	FALSE	480
496	**480**	**4**	**180**	**4**	**1**	**1**	**0.9**	**3**	**225686**	**357.59**	**TRUE**	**TRUE**	**480**
497	496	4	180	4	1	1	0.4	3	228846	444.25	TRUE	FALSE	480
498	496	4	180	4	1	1	0.3	3	228846	449.24	TRUE	FALSE	480
499	**496**	**4**	**180**	**4**	**1**	**1**	**0.1**	**3**	**228846**	**626.96**	**TRUE**	**TRUE**	**480**
500	496	4	180	4	1	1	1	3	211622	363.76	TRUE	FALSE	480
501	499	5	18	1	1	1	0.9	3	231455	432.19	TRUE	FALSE	499
502	499	5	18	2	1	1	0.9	3	231951	591.07	TRUE	FALSE	499
503	**499**	**5**	**18**	**4**	**1**	**1**	**0.9**	**3**	**232671**	**610.39**	**TRUE**	**TRUE**	**499**
504	**503**	**5**	**18**	**4**	**2**	**1**	**0.9**	**3**	**234257**	**624.54**	**TRUE**	**TRUE**	**499**
505	503	5	18	4	3	1	0.9	3	235842	453.32	TRUE	FALSE	499
506	503	5	18	4	4	1	0.9	3	237428	622.19	TRUE	FALSE	499
507	504	5	18	4	2	2	0.9	3	239076	612.76	TRUE	FALSE	499
508	504	5	18	4	2	1	0.5	3	235401	825.41	TRUE	FALSE	499
509	504	5	18	4	2	1	0.4	3	235401	820.84	TRUE	FALSE	499
510	504	5	18	4	2	1	0.3	3	235401	819.14	TRUE	FALSE	499
511	**504**	**5**	**18**	**4**	**2**	**1**	**0.2**	**3**	**235401**	**974.92**	**TRUE**	**TRUE**	**499**
512	504	5	18	4	2	1	1	3	230932	626.96	TRUE	FALSE	499
513	511	5	18	4	2	1	0.2	4	233969	978.46	TRUE	FALSE	499
514	511	5	18	4	2	1	0.2	0	232678	899.27	TRUE	FALSE	499
515	511	5	18	4	2	1	0.2	0.0625	234257	1013.39	TRUE	FALSE	499
516	511	5	18	4	2	1	0.2	0.125	234257	1760.66	TRUE	FALSE	499
517	**511**	**5**	**18**	**4**	**2**	**1**	**0.2**	**0.187**	**234257**	**1884.54**	**TRUE**	**TRUE**	**499**
518	511	5	18	4	2	1	0.2	0.25	234257	1856.10	TRUE	FALSE	499
519	511	5	18	4	2	1	0.2	0.375	234257	1729.97	TRUE	FALSE	499
520	511	5	18	4	2	1	0.2	0.5	234257	1693.13	TRUE	FALSE	499
521	511	5	18	4	2	1	0.2	0.75	234257	987.73	TRUE	FALSE	499
522	511	5	18	4	2	1	0.2	1	234257	1685.25	TRUE	FALSE	499
523	511	5	18	4	2	1	0.2	2	234257	1817.51	TRUE	FALSE	499
524	**517**	**6**	**4**	**1**	**1**	**1**	**0.9**	**3**	**234257**	**945.74**	**TRUE**	**TRUE**	**517**
525	**524**	**6**	**4**	**1**	**1**	**1**	**1**	**3**	**235911**	**1884.54**	**TRUE**	**TRUE**	**517**
526	525	6	4	1	1	1	1	4	235911	1884.54	TRUE	FALSE	517
527	525	6	4	1	1	1	1	0	235911	1884.54	TRUE	FALSE	517
528	525	6	4	1	1	1	1	0.0625	235911	1884.54	TRUE	FALSE	517
529	525	6	4	1	1	1	1	0.125	235911	1884.54	TRUE	FALSE	517
530	525	6	4	1	1	1	1	0.187	235911	1884.54	TRUE	FALSE	517
531	525	6	4	1	1	1	1	0.25	235911	1884.54	TRUE	FALSE	517
532	525	6	4	1	1	1	1	0.375	235911	1884.54	TRUE	FALSE	517
533	525	6	4	1	1	1	1	0.5	235911	1884.54	TRUE	FALSE	517
534	525	6	4	1	1	1	1	0.75	235911	1884.54	TRUE	FALSE	517
535	525	6	4	1	1	1	1	1	235911	1884.54	TRUE	FALSE	517

Appendix F

The graphical representation of the hierarchical clustering process

Figure F.1 gives a graphical representation of the hierarchical clustering detailed in Table 5.5.

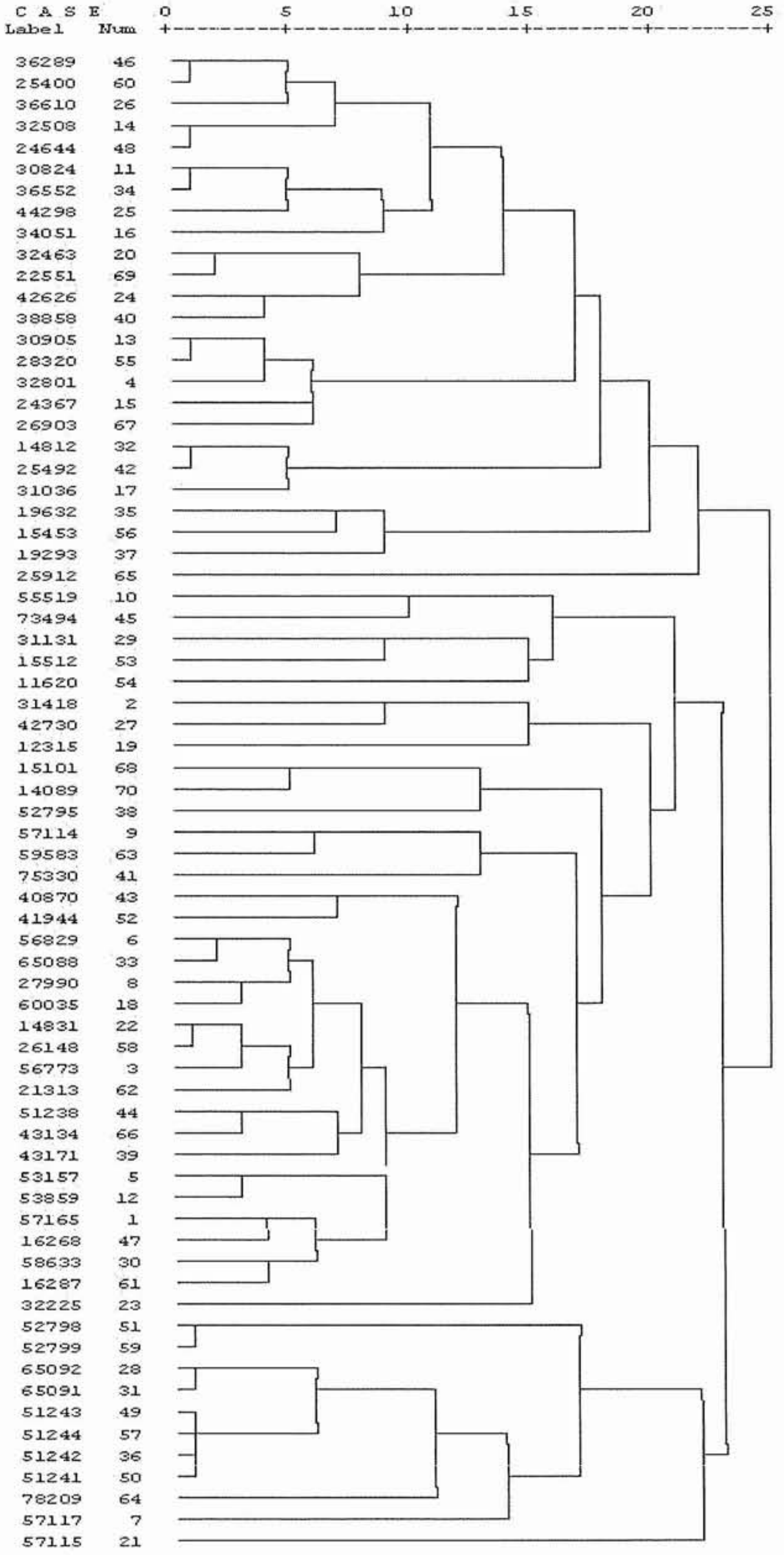

Figure F.1 **Graphical representation of the process of hierarchical clustering**