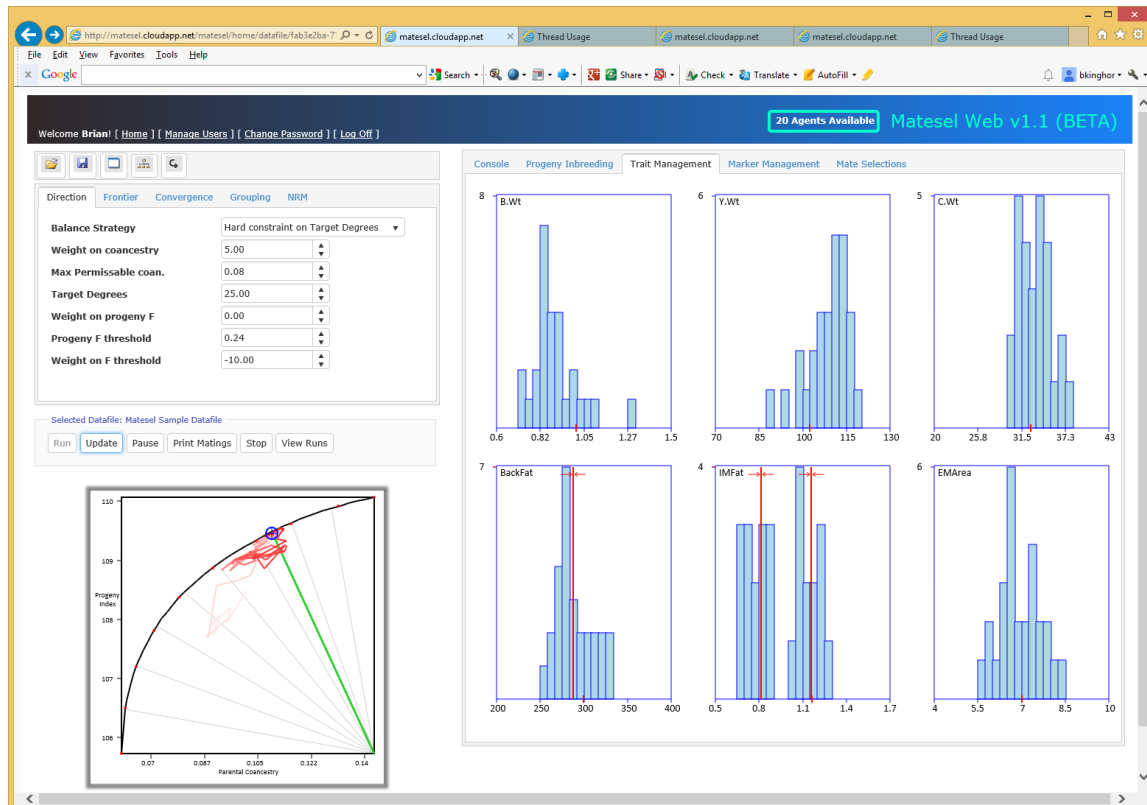


Practical Examples for Matesel

20 February 2019



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Getting started

Read the instruction manual for a good description of this. But here are a few words by way of a short-cut.

The Windows version

To run the program, launch Matesel.exe. You will be prompted for your username and password. If you are in a group workshop, this information should be supplied to you at the workshop. Once logged in, open a main data file and edit parameters or simply hit "Run".

The Web version

Open your web browser and go to your Matesel server. This is probably matesel.une.edu.au or www.matesel.com

Username and Password

You will be prompted for your username and password. If you are in a group workshop, this information should be supplied to you at the workshop.

Follow the instruction manual to get ready to run

Read and follow instructions in the instruction manual. Start with the Open Folder icon. After clicking "Upload new datafile..." you should select the project zip file that you want to use, from your local computer, probably on your hard drive. Once uploaded, click the Open button for the project you have just uploaded.

Click the Run button when you see "Ready" on the console

If you run a small project (such as TinyTest) things should happen pretty quickly. When the Frontier picture stops changing click the Pause button so you can catch your breath.

Notes

- Whenever you aim to do a series of parameter Updates (changes of direction) during a single run, then click the Convergence tab and set "Do not stop until 'Stop' clicked" to selected or True.
- Click the Stop button when you have the result you want and do not want to change direction with an Update of parameters. This frees up a processor for others to use.
- Click the Pause button each time the run settles on a result you want to inspect before any further Updating – this stops Matesel looking for better solutions and frees up resources for

others. You can click the Resume button just before entering your changed parameters with the Update button.

Accessing files for these exercises

The required files for these exercises can be downloaded from www.matesel.com or <http://matesel.une.edu.au>, in the file Matesel_Sample_Datafiles.zip

Save this zip file in a folder on the computer you are working on. Double-click on it to see the contents, which are several zip files, one zip file for each data scenario or project. Extract these zip files into a folder on your computer.

If you run Matesel on the web you can upload these zip files to the server to carry out the runs required, as described above.

If you run the Windows version of Matesel you can put the group of files for each project into its own folder.

How this document is organised

There are several exercises listed, but the numbering of questions is continuous across exercises, for ease of reference.

There is no particular order for the exercises, except that there is more hand-holding in Exercise 1, to help get you going. So you can scan through all exercises, then choose what you want to do, and in what order.

Exercise 1: TinyTest: Just a few animals, to help see what is going on

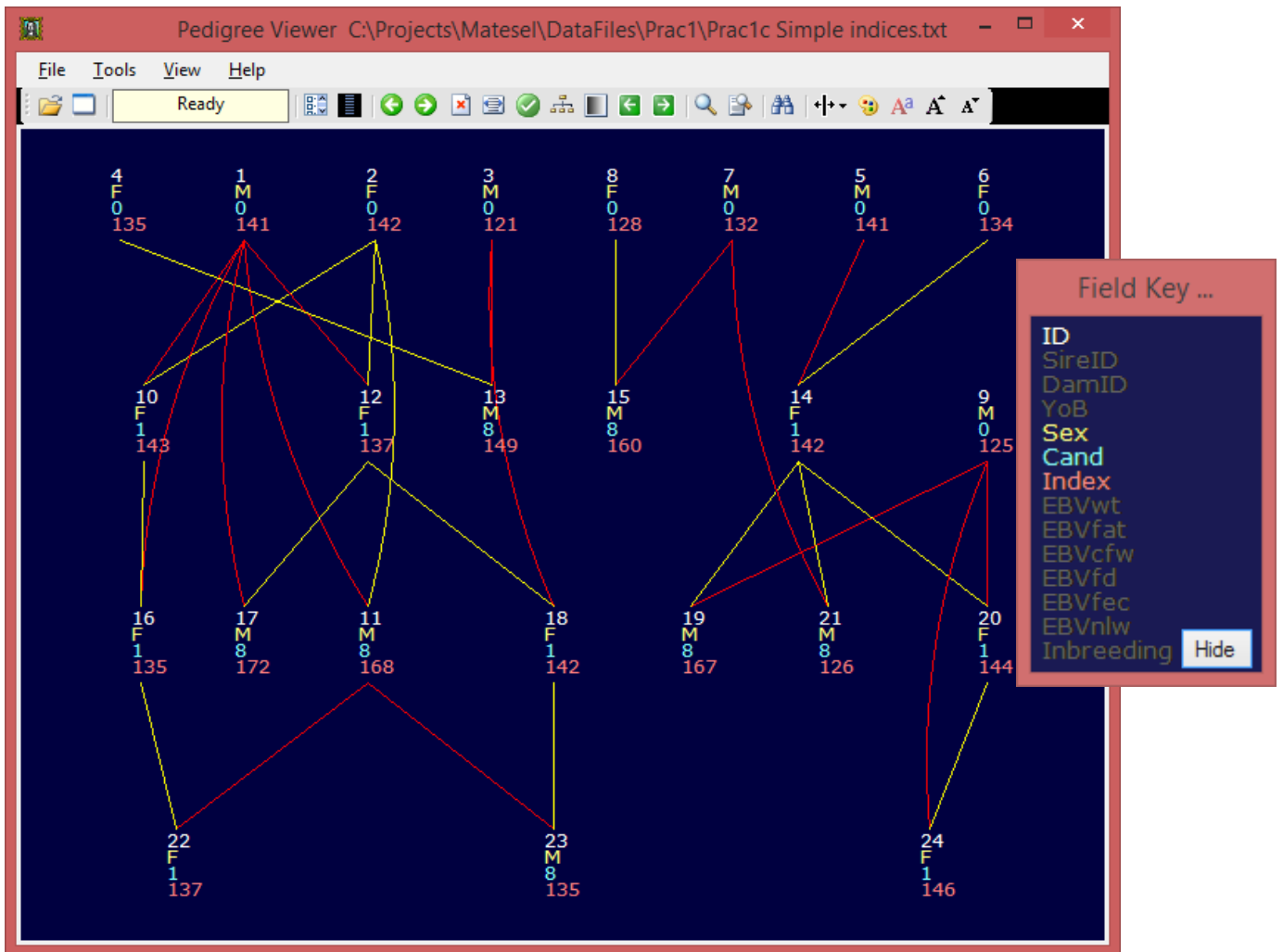
Introduction

The main technical emphasis in this practical is on balancing faster genetic gains with maintenance of genetic diversity.

We will use a trivially small example to help make the process manageable, and to help show why the results come out as they do. We can move on to more realistic examples in later practical exercises.

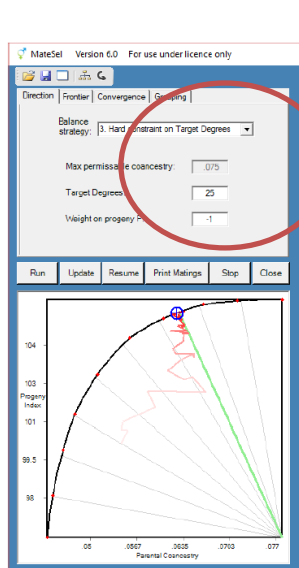
The scenario


We have a tiny flock of sheep, as shown in the pedigree diagram below, with a total of 24 animals in the pedigree. For each animal, the diagram shows identity ID (1 to 24), sex (males “M” are odd-numbered, just for convenience), candidate status (=MaxUse, maximum number of uses or matings) and selection index.



The pedigree for Exercise 1

There are 7 rams available for selection and 8 ewes. We will aim for just 7 matings, such that there is a small amount of selection on females, and more in males – in fact as Maxuse for males is 8, one ram can serve all 7 selected ewes.



Open () TinyTest.txt in Matesel. The Balance Strategy should be set at 3 (Hard constraint on Target Degrees) with Target Degrees=25.

The main data file, TinyTest.txt

Here is our very simple example.

ID	SireID	DamID	Sex	Maxuse	Index
1	0	0	M	0	141
2	0	0	F	0	142
3	0	0	M	0	121
4	0	0	F	0	135
5	0	0	M	0	141
6	0	0	F	0	134
7	0	0	M	0	132
8	0	0	F	0	128
9	0	0	M	0	125
10	1	2	F	1	143
11	1	2	M	8	168
12	1	2	F	1	137
13	3	4	M	8	149
14	5	6	F	1	142
15	7	8	M	8	160
16	1	10	F	1	135
17	1	12	M	8	172
18	3	12	F	1	142
19	9	14	M	8	167
20	9	14	F	1	144
21	7	14	M	8	126
22	11	16	F	1	137
23	11	18	M	8	135
24	9	20	F	1	146

InpOneGroup.txt

We are not using grouping here, so just one group per sex. The Matesel instructions show how we could use this file to control backup matings, preselection and use constraints. But we do none of these things here, so we can leave this file as it is.

Matesel.ini

This file sets the default parameters that Matesel will adopt. You can edit most of these on the interface before you click the run button. However, editing Matesel.ini will save you making the same old edits every time.

Questions

1. Click Run, then when the solution has settled down, click Print Matings.
 - a. You should see the 7 matings for the current solution.
 - b. Do you think the result is sensible? The pedigree diagram and data file shown above may help here.
 - c. Is the best ram well used? Why was he not used more?
 - d. Some of the matings would result in quite highly inbred progeny. How might you avoid that? (If you want to test your answer on the side, then please revert to the original weightings after doing that, so we can proceed).
2. Set the Target Degrees to 0, Update, Print Matings.
 - a. Is the result sensible? For both sexes?

3. Set the Target Degrees to 90, then look at the resulting matings.
 - a. What do you notice about the best sire, number 17 (Index=172)? Can you explain this? (Hint: Read section “The Mate Selections tab” in the instructions, or peek at the very next question)
 - b. For male candidates, “Coan” (Mean coancestry with female candidates) seems quite important for describing the extent to which they are “new blood”. Matesel actually uses something better. What might that be?
4. Now move downwards in steps from 90 degrees – **you can choose what values to test, but filling out the table below with the number of uses of each sire** might help. To see results more concisely, it is useful to select “Show sire use”, sort on Index, and click the Update button in the Mate Selections tab as required.
 - a. If you inspect the pedigree diagram above you might see that this pedigree has two distinct parts, labelled L and R in the table above. *[Aside, of course, there being no pedigree connection that we have recorded between these two parts does not really tell us about how related they might actually be. We can use genomics to help with that. You can use the GRM feature in Matesel to let genetic markers manage such underlying relationships.]* It can be useful to observe how these two sides are represented in results for differing emphasis on diversity (Target Degrees).
 - b. At 50 Target Degrees you should find that ram 19 (Index 167) is used more than ram 11 (Index 168). At what Target Degrees does this ranking change? 25, I found, but what happens a bit below that? Why?

ID	Index	Coan	Ped	Degrees				
				50	25	24	10	0
17	172	0.166	L					
11	168	0.154	L					
19	167	0.092	R					
15	160	0.045	R					

5. If you have not already done so, see if you can do something to sort out that problem of inbred progeny.
 - a. In this case it could be worth putting a lot of emphasis on reducing progeny inbreeding. [Progeny inbreeding can be seen in the mating list.] What do you find?
 - b. With large weightings against progeny inbreeding, do you ever get a solution that is far from the optimal Frontier? The reason for your answer is probably that with such a shallow pedigree it is quite easy to find unrelated mating pairs.
 - c. However, if you were aggressively aiming at genetic gain, is there a compromise in putting a lot of emphasis against progeny inbreeding? It is worth it?
6. Lastly, six sheep traits have been included in the main data file, simulated using PopSim with Sheep Genetics Parameters (see appendix just FYI). With only 7 matings made, the histograms on the Trait management tab do not make a pretty sight – but we can work with them.
 - a. Consider that some ram buyers are in a bad parasite region, and for others this is no problem. Try generating a bimodal output for FEC – so you can offer rams tailored to buyers’ needs. Click left on the EBVfec histogram and set up bimodality around the two EBVfec levels you choose (the instructions will help), and choose what proportion of matings

you want targeted at each group. After clicking Resume you should see a bimodal distribution of predicted progeny genetic means, and the result on the Frontier will change.

- b. Is the compromise in genetic gain and diversity worth the bimodality you get? You can change the weighting on achieving bimodality so that you get a balance that you prefer.
- c. Consider that fat levels are about right, but you don't want to have too much variation in the fat EBVs of future rams. Try "Decrease variation about optimum" for EBVfat. Do you get the desired result?
- d. If you can be bothered ... look at the trait EBVs in datafile TinyTest.txt together with the mating list (also stored in OutMatings.csv), and check how these predicted trait distributions have been achieved.

In the last part you manipulated individual traits. Later on we will look at managing all traits simultaneously so that we can target different outcomes (eg different markets targeted) as affected by multiple traits.

Exercise 2: Balancing genetic gain and genetic diversity using a bigger dataset.

7. Open MateselClassicDemo

Set the Target Degrees at 90 degrees and use Balance Strategy 3 (Hard constraint on Target Degrees). This puts maximal emphasis on reducing the rate of inbreeding ("long-term" inbreeding). Set the weightings on progeny F and F threshold to zero (these relate to "short-term" inbreeding). When the solution has settled reasonably at the bottom left of the frontier graph, click "Print Matings" and look at the matings in the Mate Selections tab that pops open. Notice the pattern of use of sires.

- a. Why does a minimum co-ancestry solution, with little or no emphasis on genetic gain, generally not make equal use of sires?
 - b. If you have Pedigree Viewer (free install from <http://www-personal.une.edu.au/~bkinghor/pedigree.htm>), make a note of at least one little-used sire and at least one much-used sire. Open MateselClassicDemo.txt, then click on the main PV window and use the search tool to find these sires, one at a time, and investigate how well they are connected to the rest of the population, and to the rest of the selection candidates.
8. Observe the frontier of genetic gain versus co-ancestry. If you were a breeder, where would you want to be on this graph? Why? What are the key issues to consider? Try and achieve a mating set solution that is close to your aims for these components.

Exercise 3: Minuse: Accommodating minimum use constraints.

9. If this is sheep or cattle you would not want a solution that allocates just one of two females to a natural mating sire. Use "Minuse" on male candidates to handle this. The instruction manual tells you that there are two ways to set Minuse constraints:

- a. Edit the data file (MateselClassicDemo.txt) to set all Maxuse levels to just “1” for male candidates, then globally set male Minuse and Maxuse values in the file “InpOneGroup.txt”. (This way, you do not need a Minuse field in the data file).
- b. Edit the data file (MateselClassicDemo.txt) to add a field called “Minuse”, and enter the Minuse value you want for each male candidate.

The first of these is easier, but only works where you want the Minuse values (and the Maxuse values) to be equal across male candidate. To save you doing the editing, you might file a file “Matesel_Minuse.txt” available for you to open – this has all Maxuse values set to 1.

As a suggestion, set Minuse = 20 and Maxuse = 40 for all male candidates and number of matings = 100 (in Matesel.ini, or under the Grouping tab in Matesel, just before hitting Run).

- a. Take a note of the range of values on the Parental Coancestry scale. Then re-run with Minuse values set to zero. Explain the big difference you see. Hint: You can copy the frontier points from the console, they look something like this:

Target	Realised	Prog Index	Par.Coan.
0.00	0.00	110.001190	0.108537
10.00	10.37	109.811409	0.096533
20.00	20.70	109.440804	0.084375
30.00	31.32	108.601204	0.071931
40.00	40.53	107.321091	0.062026
50.00	48.99	105.632698	0.054728
60.00	58.68	103.283905	0.049024
70.00	69.02	100.633690	0.045238
80.00	80.04	97.794006	0.043096
90.00	89.90	95.242889	0.042069

- b. Under Minuse=20, why do you see compromise at 90 Degrees, but no compromise at 0 degrees?
- c. Change Minuse to 30. Why is there now compromise at zero degrees?
- d. Change Minuse to 40. What happens? View the file OutErrorMessage.txt. Explain what is illogical in your constraints.

10. [You could try some trait manipulations on this bigger dataset – or just move on if time is short]

Exercise 4: Managing a recessive mutation

11. Consider that a recessive gene has been found to cause black fibers in our breed of sheep. Continuing to use MateselClassicDemo, make a run and Pause after the frontier has been built so that you can look under the Marker Management tab. The offending mutation is labelled as M1 (Marker 1), in the left hand column. The top histogram (M1-1) shows the distribution of frequency of the **favourable** variant (number 1) in progeny. The bottom histogram (M1-22) shows the distribution of frequency of recessive homozygous progeny carrying two copies of the **unfavourable** variant (number 2) in progeny. (See the instructions for more detail).

First try selecting for high frequency of the favourable variant (=selecting against the bad variant) by increasing the mean in the top histogram (left-click that histogram and follow as for managing trait distributions as described in the Instructions.). You should see the histogram change. Is that change worth the compromise in gain and diversity? You can change the weighting on marker selection to perhaps achieve better balance.

Selecting against the recessive mutation is a longer-term strategy. We can also aim to reduce incidence in the next drop of lambs. Do this by Decreasing the Mean in M-22. Again you can seek good balance, and can also include pressure upwards on M-1.

Just for interest, if you have time, you could read the first few paragraphs of “Handling multiple lethal recessives” in the instructions.

Exercise 5: IVF and MOET

12. Test the effect on limits that can be reached with reproductive technologies to boost female fecundity: If MateSel is still running then Stop it, but probably keep the window open so you can make a further run without JIVET (Juvenile In Vitro Embryo Transfer) or MOET.

[The Instructions tell you how to choose between MOET and JIVET. We will stick to JIVET here, but you could try MOET if you want. The only difference is that under MOET, all progeny of a female are all by the same male.]

[For this exercise it helps if you can have two windows (or tabs) open at the same time, so you can compare results from different runs on-screen. But you can more simply, work with a friend, or take screen captures, or even make notes on relevant results to make that comparisons required.]

Open JIVETtest, click “Run” and compare the new frontier with the first one. Does it make sense? (Hint: look at the axis values).

- a. Can this reproductive technology help genetic diversity as well as genetic gain? Suggestion: On the no-JIVET (MateSelClassicDemo) job, set Balance Strategy = 1 (Hard constraint on coancestry) and set Max permissible coancestry to 0.1. Note the gain achieved, in column “xG” in the MateSel console.

Then do a run using JIVETtest, with Balance Strategy = 3, and adjust Target Degrees to achieve an outcome with a similar gain value as you noted from the no-JIVET run. Has setting female Maxuse to 50 given you much of a decrease in parental coancestry? Can you explain this result?

Exercise 6: Managing inbreeding in progeny

13. (This question is perhaps a bit of a repeat from question 5) Using MateSelClassicDemo, choose 25 degrees with Balance Strategy = 3. Let the solution converge close to the frontier. Set Weight on progeny F to -100 and click “Update”. Notice the changes in progeny inbreeding (Fbar) on the Progeny inbreeding tab, the F value of the most inbred progeny (Fmax), and on gain and coancestry.

- Is the balance between gain and coancestry suitably maintained near the chosen target Degrees?
- Is the reduction in progeny inbreeding worth the compromises made in gain and coancestry?
- Find a “Weighting on progeny F” that gives you a result that you find satisfying.

14. Open FullSibInbreedingTest

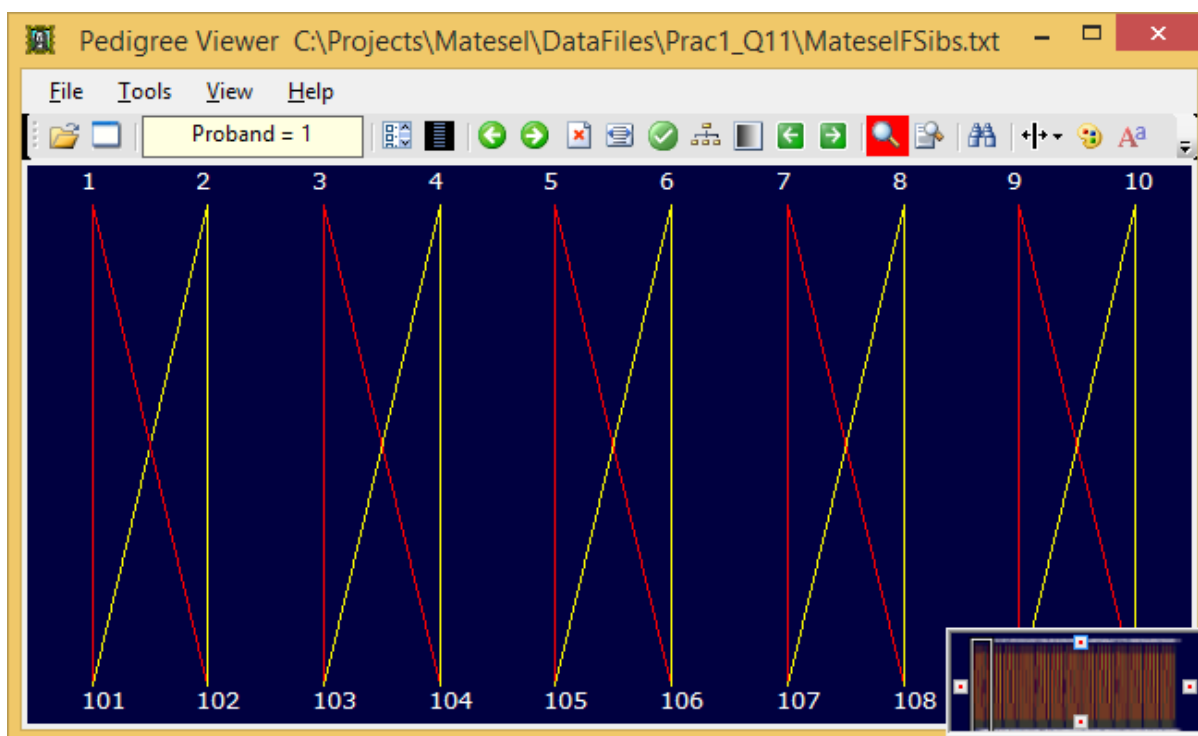
The pedigree diagram below shows part of the pedigree in this file. It is just a set of full sib families.

You should set Target Degrees and Weight on progeny F both to zero, and Matings to be made = 50. You could check in “InpOneGroup.txt” that Male Maxuse numbers = 50 and Female Maxuse numbers = 1.

- Click “Run” and you should get quick convergence.
- Click “Print Matings” then “Show sire use” and convince yourself that the result is sensible. For the next bit, be sure to set “Do not stop until ‘Stop’ clicked” to Checked or True, under the Convergence tab.
- Change “Weight on progeny F” to 1000 (positive – aiming for high progeny inbreeding) and click the Progeny Inbreeding tab to watch how the red line progresses. Click Update to send your new direction to the Matesel engine in the cloud. You should see progeny inbreeding increase. What is the impact on parental coancestry? Why do you get the result that you see? [Hint: Have a look at “Show sire use”].

[Note: Convergence can be slow when aiming to increase mean progeny inbreeding. This relates to the fact that there are very many solutions that involve very low levels of progeny inbreeding, but very few that involve the highest levels of progeny inbreeding.]

- Do your observations tell you anything about the value of avoiding the mating of relatives? This is a very important message that many breeders seem to miss.



Part of the pedigree for Question 13

Exercise 7: Satisfying diverse customer needs

Introduction

The main technical emphasis in this practical is on targeting multiple end uses of the progeny that result from the matings to be made. The Instruction Manual gives details on how to do this.

[Currently the switch for invoking Multiple EndUses is only in Matesel.ini – not on the Matesel interface. This means running two separate jobs, with and without EndUses, if you need to compare results. However, we will proceed only with Multiple EndUses invoked.]

The scenario

PopSim was used to generate a pedigree file with animals born over the period 1997 to 2015. Over this period, 200 ewes were mated each year by 8 rams, with age of both sexes at first drop of lambs being two years, and culling for age after 2 matings for rams and 7 matings for ewes. Weaning rate was 80% and adult mortality was 5% for rams and 10% for ewes. Selection was on the DP+ index using BLUP EBVs with Sheep Genetics Parameters (see appendix just FYI) to calculate selection index values. The traits and DP+ weightings used were:

Trait	Index Wt	St.Dev.
Body weight	0.890049	5.56
Body fat	0	2.83
Clean Fleece Wt	0.283209	0.4575
Fibre Diameter	-1.56956	1.225
Fecal Egg Count	0	2.828
# lambs weaned	125.29	0.649

The current task is to make 200 matings. The breeder is keen to keep the most appropriate Rams for his own flock, based on DP+ index and other issues such as genetic diversity. He is keen to retain the best 50% of matings aiming directly at that outcome – considering that to be his “nucleus” (Although the other 50% of matings will produce progeny that can compete to stay in his nucleus flock).

Consider that the breeder has three groups of ram-buying customers that he wants to target from his single breeding program, and he is willing to deviate somewhat from the DP+ index in parts of his overall flock:

- One group takes 30% of the rams he sells. They get most of their income from wool, and they struggle with high parasite loads.
- A second group takes 25% of the rams he sells. They get most of their income from wool, but they have essentially no parasite problems.
- A third group takes 45% of the rams he sells. They get most of their income from meat, and aim for fast lean growth.

[Note that you could do a good job with setting index weights if you could work out the economic weights involved. But an approximate job is good enough for this exercise. It may be worth noting that if standard deviation doubles then index weights halve, and standard deviations are given for these traits in the table above.]

1. Edit EndUses.txt, eg. in Notepad. [Web version: Extract the EndUses.txt file from EndUsesSheepTest.zip, so that you can edit it then put it back in the zip ready for Matesel to use.] You will find the file in a somewhat virgin state, ready for you to make sensible changes. Read the Instructions on Multiple Enduses and edit the file accordingly.
2. Open the EndUsesSheepTest project.
3. Set “Do not stop until ‘Stop’ clicked” to Checked or True. Make the run and don’t Stop until the run is very well converged. This is required as noted in the second-last dot point on the relevant page of the instructions, only up to the Results section, if time is tight.
4. View OutSummary.txt. This file shows summary output for the run. At the end you will find the mean trait indices for each of your End Uses.
5. Do the results look sensible, given what you set out to achieve? If not, consider editing EndUses.txt on your local PC and setting up a new job to see if you can achieve the sort of outcome that you hope for.

Exercise 8: Generating ram lambs for genetics research

[If you have had enough of Multiple EndUses, you could jump this one.]

The Research Organisation is running a test of the practical value of its EBVs for parasite resistance, and it has asked the county’s top breeders (including you) to send their most extreme EBVfec young rams from the next drop to the Experimental Farm for FEC evaluation and later mating.

You want to help, but you don’t want to compromise your own breeding program.

Use the Multiple EndUses feature to set up your matings for this. You can edit EndUses.txt as you think best. Consider that the CRC asks for 5 ram lambs of high EBVfec and 5 ram lambs of low EBVfec. Recall that not all matings result in a lamb and not all lambs are rams.

Make the run and inspect the results in OutSummary.txt. Are you happy with the result? If not, you could try again with different settings.

Exercise 9: Simple Grouping

You can use the MateselClassicDemo job for this one. First have a look at InpGroups.txt, and look at the description given in the instructions. [Look also at MateselClassicDemo.txt, if it has numerical IDs (the old version) then note that for both sexes MatingGroup is 1 for odd-numbered animals and 2 for even-numbered animals. This means that when you look at a resulting mating list you will easily see whether mating permissions you have declared have been adhered to.]

Run Matesel and open the MateselClassicDemo job. On the Grouping tab, set grouping to True. [Setting Target Degrees low will cause few males to be selected and so there will be less evidence that grouping has worked – maybe keep Target Degrees up a bit]. Make the run and stop when you seem to have convergence. Look at the mating list and check that the mating permissions matrix has been adhered to.

You can then replace InpGroups.txt inside MateselClassicDemo.zip with one you have edited to change the permission pattern. For example you might consider there are AI and Natural mating rams, with AI rams only to be mated to adult ewes and Natural mating rams can be used for both maiden and adult ewes (In this case the MatingGroups column entries in the Matesel.txt file may not fit exactly with maiden-adult scenario, but that is OK just for this exercise).

Make a Grouping run on this second job and check that the permissions you invoke are adhered to.

Exercise 10: Committed Matings

You might want to first read about Committed Matings in the Matesel manual.

You can construct your own CommittedMatings.txt file, or use those supplied with the MateselClassicDemo project.

Edit the CommittedMatings switch in Matesel.ini (it is the last of the integer parameters) from 0 to 1 or 2 (see the manual for details). It seems more popular to use a setting of 1 (Automatic setting of Maxuse - set Committed Matings switch to value 1), rather than a setting of 2 (Manual setting of Maxuse - set Committed Matings switch to value 2).

Two example files are included:

CommittedMatings1.txt ...	This works with Automatic setting of Maxuse. Maxuse values are automatically increased to accommodate the previous or committed matings.
CommittedMatings2.txt ...	The Maxuse values that you supply have to cover the committed matings in this list. This is OK with the starting Maxuse values used in this project. So you can use this file with both settings: Automatic (1) and Manual (2) setting of Maxuse values.

In both cases, ***you need to rename your chosen file to CommittedMatings.txt before you make the run.***

A useful exercise is to make all four runs (both files under both settings = 4 runs).

You should find errors when using CommittedMatings1.txt with manual setting of Maxuse, as these values are in some cases not enough to cover both old and new matings. Typically, it will be reported that a sire in the committed matings list is not a candidate (he is not currently a candidate for new matings so his Maxuse is set to zero – and his Maxuse has not been automatically increased to cover his “old” committed matings.)

For each run look at the top of the console to see the reporting of numbers of candidates, number of new matings, total matings, and the total Maxuses for each sex. You should see higher Maxuse values for the Automatic setting.

The Automatic setting is probably easier to work with here – but the manual will tell that the manual setting is useful for several mating sessions over a mating season.

Next Compare two runs – No Committed Matings (setting = 0 in Matesel.ini) and Committed Matings using CommittedMatings1.txt with setting = 1 in Matesel.ini. [You can make the two runs each in a separate folder with their own Matesel.exe + associated files – then you can compare results with both jobs running. Never run Matesel concurrently from a single folder!!]

Compare the frontiers between the two runs. What key difference do you notice? Why do you get such a strong result?

We have increased the effective population size by adding Committed Matings - by taking account of a larger proportion of the full life cycle – and so our comparison is not quite fair. In the end, it is the rate of increase in coancestry is the key factor

(<http://www.wcgalp.org/system/files/proceedings/2018/accommodating-recent-contributions-under-optimal-contribution-selection.pdf>).

Look at results for the standard run at Target Degrees=25. Note which is the most used sire – I think you will find he is used for 25 matings. Now look at the mating results under the Committed Matings run. How many matings is he allocated ... and how many of the 50 new matings is he allocated (look in OutMatings.txt and count how many of his matings are NOT Enduse = -1 {which indicates a Committed Mating}).

You should find that accommodation of Committed Matings has significantly reduced the new mate allocations to this sire. Why has this happened?

Exercises 11-19 use the datafile “DavisAngusHerdDec18.txt”

Suggestion: Copy of DavisAngusHerdDec18.txt to DavisAngusHerdDec18.csv and open this copy in Excel to be able to view the data. [Excel locks an opened file so it cannot be used by other applications – hence the copy.]

This file and the associated questions have been developed by Alison Van Eenennaam with assistance from colleagues at the University of California, Davis, the American Angus Association, and Brian Kinghorn.

In this file there are female selection candidates (43) of which 33 are cows (female mating group 1) and 10 are heifers (female mating group 2), and 24 male candidates from the UC Davis herd. Five of these are coded as AI (male mating group 1) meaning they can be used with either heifers or cows, and the remaining 19 are natural service candidates (male mating group 2) which can only be put out with one group of females. The selection index in this case has been arbitrarily set to \$W

Davis Cow Herd from DavisAngusHerdDec18.txt

AnID	Sire	Dam	Sex	YEAR	\$W	\$F	\$G	\$QG	\$YG	\$B
15426632	13868010	13878897	F	2005	39.25	43.55	24.14	21.39	2.75	94.48
15431586	14712091	14695607	F	2005	46.19	6.06	40.17	33.47	6.70	82.39
15448922	14403369	12539776	F	2005	27.19	-1.24	48.92	43.61	5.31	70.63
15846586	15289239	14429952	F	2007	32.55	-6.90	31.68	25.63	6.05	74.36
15846588	15289239	14695611	F	2007	35.41	16.27	39.06	32.12	6.94	88.76
15846589	15289239	14695612	F	2007	30.66	-3.36	18.65	16.11	2.54	45.43
15850147	13687063	13878897	F	2007	29.36	19.70	32.06	28.37	3.69	81.94
15850157	13592905	15426630	F	2007	54.64	53.87	35.80	34.27	1.53	105.99
16246408	15289239	15426628	F	2008	24.96	9.22	36.09	29.68	6.41	93.10
16264464	13724351	15063191	F	2008	24.55	35.09	40.89	33.47	7.42	110.74
16264466	13009379	15431586	F	2008	52.97	21.00	46.76	39.44	7.32	102.57
16264467	13009379	15448922	F	2008	44.03	29.01	46.98	42.18	4.80	91.81
16672598	15850154	14695611	F	2009	23.78	4.00	34.03	27.07	6.96	61.50
16673551	13592905	15850146	F	2009	52.35	53.81	29.57	31.29	-1.72	126.50
16673553	13592905	15846586	F	2009	51.15	35.80	26.91	22.80	4.11	101.18
16880382	15109865	16246409	F	2010	44.16	13.22	30.32	24.70	5.62	94.27
16880412	14963730	15431586	F	2010	51.68	50.40	42.18	36.03	6.15	127.32
17293803	13588640	15448922	F	2011	36.43	27.41	50.80	44.05	6.75	103.52
17293806	16676759	15846589	F	2011	29.73	-26.37	22.00	18.82	3.18	34.26
17299314	15313140	15846588	F	2011	46.36	44.45	32.22	30.88	1.34	108.88
17299483	16458143	16673553	F	2011	46.12	56.01	26.51	22.80	3.71	108.17
17362721	16458143	15850147	F	2011	44.33	41.13	33.18	29.23	3.95	108.97
17576363	16880413	15555316	F	2012	23.69	32.71	30.35	24.70	5.65	108.34
17770834	16880433	16880382	F	2012	42.68	8.38	24.90	23.29	1.61	77.51
17794847	14691231	16880436	F	2012	49.08	67.82	24.06	22.80	1.26	109.43
17794853	14691231	16261647	F	2012	25.74	-22.76	28.24	21.85	6.39	64.32
17794878	15313140	16874138	F	2012	41.80	22.04	32.83	29.31	3.52	95.17
17794919	15832750	15846588	F	2012	49.69	38.03	31.74	28.77	2.97	91.28
17794963	16858775	15846586	F	2012	45.62	23.93	29.08	26.07	3.01	128.01
17812135	17293804	16264464	F	2013	32.33	5.50	39.93	33.35	6.58	100.26
17888351	17293804	16246409	F	2013	26.36	-19.86	35.94	30.56	5.38	89.10
17903825	16207085	16673553	F	2013	52.57	41.51	22.96	20.39	2.57	101.25
17903826	16207085	16673551	F	2013	55.15	66.36	24.27	24.70	-0.43	116.81
18069759	17631147	15431586	F	2014	43.96	13.55	34.01	28.77	5.24	93.19
18069760	17631147	15850147	F	2014	38.51	29.53	31.30	27.94	3.36	106.41
18069763	17631147	16264467	F	2014	36.64	5.50	38.57	34.27	4.30	90.74
18069764	17631147	16672595	F	2014	44.66	67.75	37.86	34.62	3.24	143.16
18081077	14691231	16880382	F	2014	42.70	-0.71	37.39	30.48	6.91	77.26
18081078	15109865	16880412	F	2014	43.16	44.23	45.61	40.03	5.58	125.88
18081084	14691231	16672598	F	2014	27.24	8.55	31.55	26.07	5.48	69.21
18081090	14691231	15448922	F	2014	37.00	24.06	40.47	35.72	4.75	77.30
18081123	16270340	16264466	F	2014	66.76	73.61	48.86	41.88	6.98	139.36
18211726	16270340	15846586	F	2014	40.30	14.80	45.88	38.58	7.30	106.99

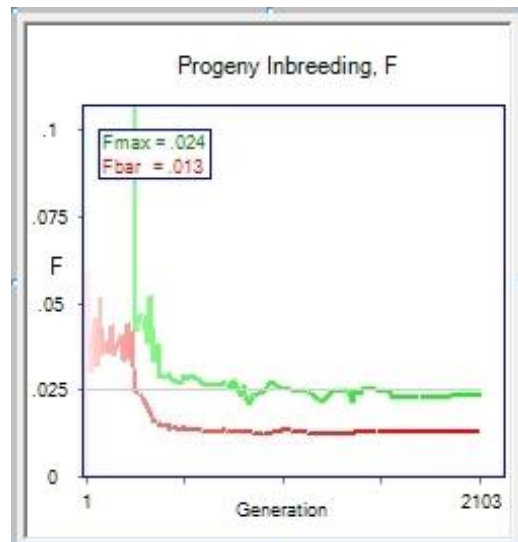
17888185	17293804	16880382	M	2013	41.41	-26.80	34.65	28.97	5.68	92.02
17888354	17293804	17293803	M	2013	36.66	17.45	44.89	38.64	6.25	96.65
17888356	17293804	17299483	M	2013	36.91	14.36	32.74	28.02	4.73	98.97
18069755	17631147	16880390	M	2014	38.62	4.81	18.84	16.64	2.20	66.38
18069756	17631147	17299314	M	2014	40.59	37.11	29.24	26.84	2.40	109.05
18069758	17631147	17794878	M	2014	37.64	14.92	29.54	26.06	3.48	102.19
18069761	17631147	15850157	M	2014	47.65	56.73	31.83	29.23	2.60	109.62
18069762	17631147	15555316	M	2014	44.47	38.82	24.82	22.33	2.49	102.64
18069765	17631147	16264464	M	2014	32.13	26.55	34.39	28.77	5.62	104.92
18081057	15109865	17794853	M	2014	29.77	-11.12	30.70	25.25	5.46	82.46
18081059	15109865	17770834	M	2014	48.47	26.77	29.03	25.97	3.07	89.05
18081070	14691231	17299483	M	2014	55.76	37.96	21.30	18.30	3.00	79.23
18081071	14691231	17293803	M	2014	58.49	42.95	43.16	37.09	6.07	108.43
18081079	14691231	16673553	M	2014	51.51	50.29	21.44	17.17	4.27	111.13
18081105	14691231	15426632	M	2014	47.64	54.09	26.77	23.29	3.48	89.38
18081145	16270340	16246408	M	2014	43.10	30.92	45.17	39.75	5.42	120.76
18204142	16270340	15846588	M	2014	45.62	68.44	51.39	43.87	7.52	144.39
18228929	17631147	17293806	M	2014	34.92	3.79	24.13	20.81	3.32	71.74

Exercise 11: Balancing gain and diversity: Simple case

- Run Matesel.exe, login as instructed at the workshop, then open DavisAngusHerdDec18.txt. Have a look at the yellow ListBox that tells you some details about the file that you have just opened. You can generally ignore this information – but it sometimes contains warning messages.
- Set the Target Degrees at 0 degrees and use Balance Strategy 3 (Hard constraint on Target Degrees (**TD**)). This puts maximal emphasis on maximizing genetic gain. Set the weighting on progeny F to zero (this relates to “short-term” inbreeding). You should see the number of matings requested as 35, under the grouping tab.
- Click Run, and let the solution settle reasonably at the top right of the frontier graph, then click “Pause”. Scroll to the top of the blue ListBox under the tab “Console for FortranDLL.dll”. Here you can read some key factors to do with this run. Look through these to get an idea about this simple run. It is useful to look in this area, especially for more complex runs. Warning messages can sometimes appear here.
- Click “Resume” then “Print Matings” and look at the matings in the Mate Selections tab that pops open. Notice the pattern of use of sires (Click “Show sire use”). Does this pattern of sire use make sense? (Hint: you can look at the list of sire candidates in your copy of DavisAngusHerdDec18.txt). Take a note of the Index value and “Coan.” of the best sire.
- Change Target Degrees to 90 then click “Update”. Wait until the frontier settles again and then click print matings. What has happened to the best sire? Why?
- Observe the frontier of genetic gain versus co-ancestry. Where would you want to be on frontier of genetic gain versus co-ancestry? Why? What are the key issues to consider? Change Target Degrees to a few different values and observe the impact on sire use. Can you find a solution that satisfies you? Do you see a practical problem?

Exercise 12: Managing inbreeding in progeny

This graph under the “Progeny Inbreeding” tab plots the mean value of the inbreeding coefficients of the progeny that would arise from the matings in the best solution, graphed over the progression of the analysis (the generations of the DE algorithm). The mean inbreeding coefficient (**Fbar**) is shown in **red**. And the inbreeding coefficient for the most highly inbred individual (**Fmax**) is shown in **green**.



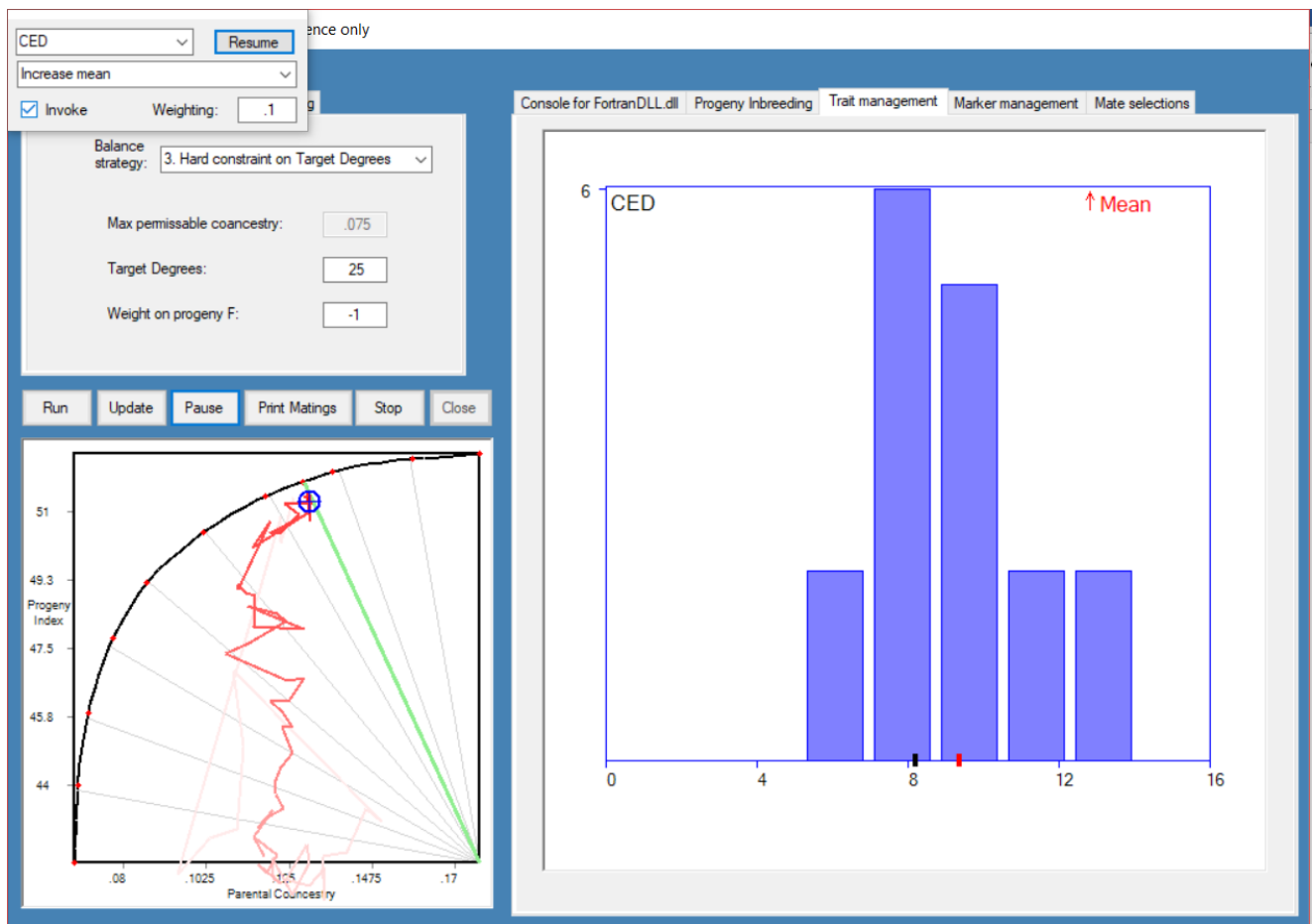
21. Choose 25 degrees with Balance Strategy = 3 and click run. Let the solution converge to the frontier. If you pause the run, you can scroll up on the blue window to see which column is “MeanF”, which is the mean progeny inbreeding coefficient (column 7). You can also click the Progeny Inbreeding tab to see this in a graph.
22. Set Weight on progeny F to -100 and click “Resume” (if Paused) then “Update”. Notice the changes in progeny inbreeding (Fbar) on the Progeny inbreeding tab, the F value of the most inbred progeny (Fmax), and on gain and coancestry on the frontier graph.
 - a. Is the balance between gain and coancestry suitably maintained near the chosen target Degrees (or at least, to the left of the green line)? (Note that, as before, in a small dataset there might not be any solutions close to the green line)
 - b. Is the reduction in progeny inbreeding worth the compromises made in gain and coancestry
 - c. Find a “Weighting on progeny F” that gives you a result that you find satisfying

Exercise 13: Impact of single trait selection emphasis

Go to the trait management window. The horizontal line on each histogram shows two tick marks:



- Black tick: Sex-balanced mean of all candidates. This should remain fixed for the duration of your run.
- Red tick: Mean of progeny for the current solution. This will change as your settings change and as the solution evolves.



23. Set target degrees to 25. Select the trait CED – to make this large use the shift key while the mouse pointer is on the trait you want to manage, then Click-Left. To see all traits hit the control key while clicking on the trait management screen. Select increase mean for CED and put a heavy emphasis of on this with a weighting of 10, then invoke, and click “Resume”.
- What did this do to genetic progress in \$Index (on the Y-axis on the frontier graph)? Is this a reasonable strategy?
 - Now change the weighting to 1, and then to 0.1 and see the impact on progress towards \$Index.
 - Choose your favorite trait and watch the correlated responses as you put increased selection pressure on that specific trait.
 - Try some of the other trait constraint options (down arrow to the right of “Increase mean”). You might choose the trait and the constraint(s) in a manner that seems potentially useful to you. For example, you should find that “Tactical Desired Gains upwards” gives you much nicer control than “Increase mean”.

Exercise 14: Applying Animal Grouping Constraints

First have a look at InpGroups.txt and look at the description given in the instructions (starting on page 24). Look also at your copy of DavisAngusHerdDec18.txt and note the MatingGroup entries for the male and female candidates.


```
2, (# of Male Groups)   This file: AI then Natural
1,      1
1,      2
2, (# of Female Groups) This file: Cows then Heifers
1,      1
1,      2
Use number of matings (1) or selection proportions (0) to describe matings per female
group
```

```

1
Number of matings per female group, or proportion selected out of preselected females.
Numbers can be > #candidates, or proportions>1, to drive MOET and JIVET
28,7
Invoke Female mating numbers or proportions (Enter 1, else enter 0 to use above line to
calculate total #matings only)
1
Male group could be backup sires
0, 1
Max number of backup sires reported per mating for each female group
3, 3
Male preselection. 1 for no preselection, <1 for proportion preselected, >1 for number
preselected ...
1,1
Female preselection. ... Any preselection is on the main (first) Index only, Ignores
maxuse. Set these values to 1 in a 'pre-run' to see candidates per group.
1, 1
Male ABS-Minuse numbers
0, 0
Male Minuse numbers
0, 0
Male Maxuse numbers
100, 30
Female ABS-Minuse numbers
0, 0
Female Minuse numbers
0, 0
Female Maxuse numbers
1, 1
Male natural mating vector (1 = constrain to one female group)
0,1
Mating permission matrix: Male x Female ...
1, 1
1, 0

```

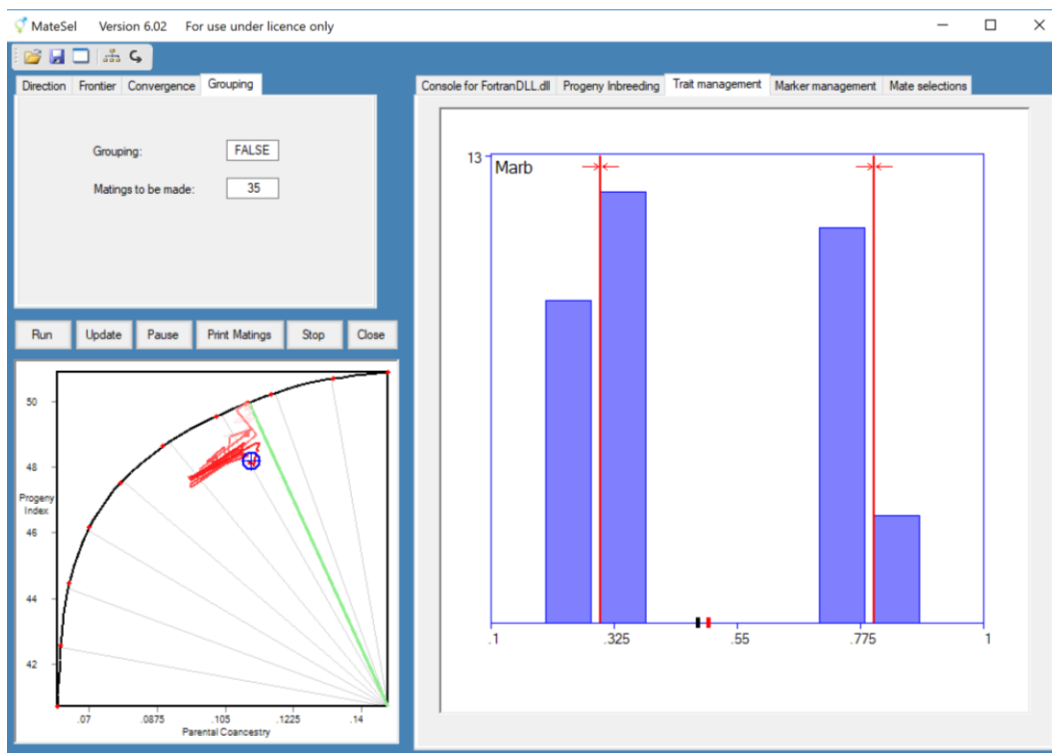
AI sires can be bred to both cows and heifers, but natural service only cows



24. On the Grouping tab, set Grouping to True. (If you set Grouping to 1 in Matesel.ini, then Grouping will be True by default, and you will not have to make this change each time you make a run). [Setting Target Degrees to a low value will cause fewer males to be selected and so there will be less evidence that grouping has worked – maybe keep Target Degrees a bit higher for this example]. Make the run and pause when you seem to have convergence. Look at the mating list and check that the mating permissions matrix has been adhered to.
25. You can then edit InpGroups.txt to change the permission pattern. For example, you might permit Heifers to be mated only by AI sires, rather than by natural mating sires – as shown above.
26. Make a Grouping run on this second job that requires cows to be bred by a natural service sire and the heifers to be bred by AI sires and check that the permissions you invoke are adhered to. How did this affect genetic gain?
27. Make a Grouping run so that all the cows have to be bred to a single herd sire.

Exercise 15: Targeting multiple product endpoints or diverse bull buyers' needs

Traits can be managed for bimodality. Imagine you would like to have a set of bulls with high marbling for customers who are targeting a premium and another group who is supplying a speciality lean market. Select marbling and target bimodality with a .3 and .8 targets and invoke.



28. What markets could you envision where you would be targeting two separate markets? Perhaps you want to select your own replacements using \$W, and yet you are producing bulls for commercial producers who are using a different index (\$I). The total number of matings to be made was set at 35, with 20 of these being dedicated Nucleus matings (i.e., producing animals that are targeted to return to the seedstock nucleus herd), plus 15 targeted to customers who buy bulls that will sire replacement heifers for cow-calf production
29. The overall weighting for these two groups were set at 1, and 0.85, ensuring that the nucleus end-use attracts the best candidates mated in the best manner to maximize the nucleus index for these 20 matings. Essentially, we direct the head of the breeding program at our long-term genetic goals for the nucleus, and we direct the tail of the breeding program at our customers' needs.
30. Change the following switch from 0 to 1 in the file Matesel.ini:

```
0      , Switch to control Multiple EndUses (1, else just one EndUse only - nucleus)
```

Edit EndUses.txt, eg. in Notepad. Read the Instructions on Multiple Enduses and edit the file accordingly.

```
Number of EndUses, including nucleus breeding program as EndUse number 1:
2
Relative Trait Weightings on the Index then each trait:
1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
0 0 0 0 0 0 1 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
Number of Matings in each EndUse (enter in one row):
20 15
Relative EndUse Weighting of each EndUse for genetic merit (enter in one row):
1 0.75
```

Exercise 16: Controlling for CED

Sometimes producers place an absolute requirement on CED for heifer bulls – however this may not always make sense as some heifers, especially those born early in the calving season, can be large enough to handle a bull with a lower CED score. One way this could be achieved would be to have a threshold weight below which there is a requirement to use a high CED bull. Look at the Davis file at the column CEDcontrol.

If your average cow weighs 1,390 lbs. (and many do), a heifer would need to weigh 904 lbs. at breeding in a traditional system, but recent research suggest they can be as little as 709-806 lbs. The smaller ones are the ones we most need to breed to a high CED EPD bull – if they are over 750 lbs at yearling weigh in, then there is a much lower CED threshold on bull choice.

There is a column in the Davis file that is called “CEDcontrol”. This is the yearling weight for the females in the herd. Younger heifers tend to be lighter than older heifers. The following small table represents one breeder’s opinion about the CED levels required for Heifers of different yearling weights:

Female body weight, Lbs	minimum EPD_CED
600	15
625	12

From these constraints we developed a simple equation for male CEDcontrol = -725 + (8.333) CED

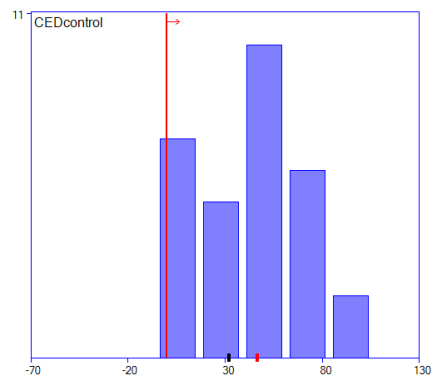
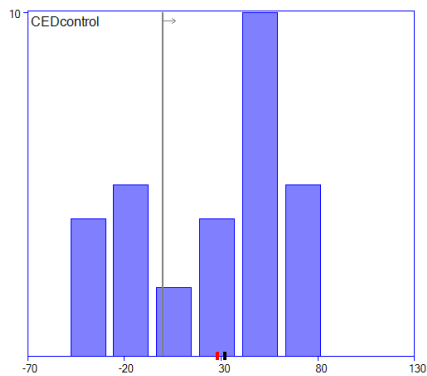
AnID	Sex	YEAR	DOB	MatingGroup	CEDcontrol	CED
18069763	F	2014	11/20/2014	2	603	13
18069760	F	2014	9/24/2014	2	604	5
18069764	F	2014	9/18/2014	2	611	9
18069759	F	2014	9/15/2014	2	617	12
18081084	F	2014	8/25/2014	2	621	14
18081090	F	2014	8/18/2014	2	629	5
18081077	F	2014	8/18/2014	2	632	6
18081123	F	2014	8/16/2014	2	633	9
18081078	F	2014	8/5/2014	2	648	10
18211726	F	2014	8/5/2014	2	654	15
17903826	F	2013	8/10/2013	1	608	4
17888351	F	2013	9/30/2013	1	642	10
17903825	F	2013	8/8/2013	1	673	12
16673551	F	2009	8/15/2009	1	698	8
15448922	F	2005	9/12/2005	1	725	5
15850157	F	2007	7/27/2007	1	734	10
15431586	F	2005	9/8/2005	1	738	12
17794853	F	2012	8/12/2012	1	739	12
16672598	F	2009	9/9/2009	1	739	11
17576363	F	2012	9/2/2012	1	741	1
17362721	F	2011	8/17/2011	1	741	6
17794963	F	2012	8/16/2012	1	747	12
17794919	F	2012	8/12/2012	1	758	14
17794847	F	2012	8/10/2012	1	759	10
15850147	F	2007	8/24/2007	1	759	10
16880382	F	2010	8/23/2010	1	762	8
16246408	F	2008	9/25/2008	1	764	12
16673553	F	2009	8/11/2009	1	769	13
15846588	F	2007	10/13/2007	1	772	8
17293806	F	2011	9/18/2011	1	783	16
15846586	F	2007	10/16/2007	1	783	15
16880412	F	2010	8/16/2010	1	784	6
17299483	F	2011	8/16/2011	1	786	4
15426632	F	2005	9/27/2005	1	789	4
16264464	F	2008	8/16/2008	1	791	6

17812135	F	2013	9/4/2013	1	793	8
16264467	F	2008	8/16/2008	1	794	6
17299314	F	2011	8/14/2011	1	803	8
17293803	F	2011	8/13/2011	1	807	4
17794878	F	2012	9/5/2012	1	808	10
17770834	F	2012	10/2/2012	1	821	9
15846589	F	2007	9/19/2007	1	829	13
16264466	F	2008	8/17/2008	1	832	10

18069761	M	2014	10/20/2014	2	-708.333	2
18069756	M	2014	9/4/2014	2	-708.333	2
18069765	M	2014	9/14/2014	2	-691.667	4
17888356	M	2013	9/24/2013	2	-691.667	4
17631147	M	2012	3/10/2012	2	-691.667	4
16680293	M	2009	10/1/2009	2	-691.667	4
18081105	M	2014	8/18/2014	2	-683.333	5
17888354	M	2013	8/28/2013	2	-683.333	5
18069762	M	2014	9/10/2014	2	-675	6
18069758	M	2014	10/2/2014	2	-666.667	7
18069755	M	2014	9/14/2014	2	-658.333	8
18228929	M	2014	8/30/2014	2	-658.333	8
17888185	M	2013	9/4/2013	2	-658.333	8
17812132	M	2013	9/24/2013	2	-650	9
17812136	M	2013	9/3/2013	2	-650	9
18081059	M	2014	8/13/2014	2	-641.667	10
17812134	M	2013	9/3/2013	2	-641.667	10
18081057	M	2014	8/10/2014	2	-633.333	11
17812129	M	2013	9/24/2013	2	-591.667	16
18204142	M	2014	8/24/2014	1	-725	0
18081070	M	2014	8/24/2014	1	-675	6
18081071	M	2014	8/16/2014	1	-666.667	7
18081079	M	2014	8/8/2014	1	-608.333	14
18081145	M	2014	8/25/2014	1	-600	15

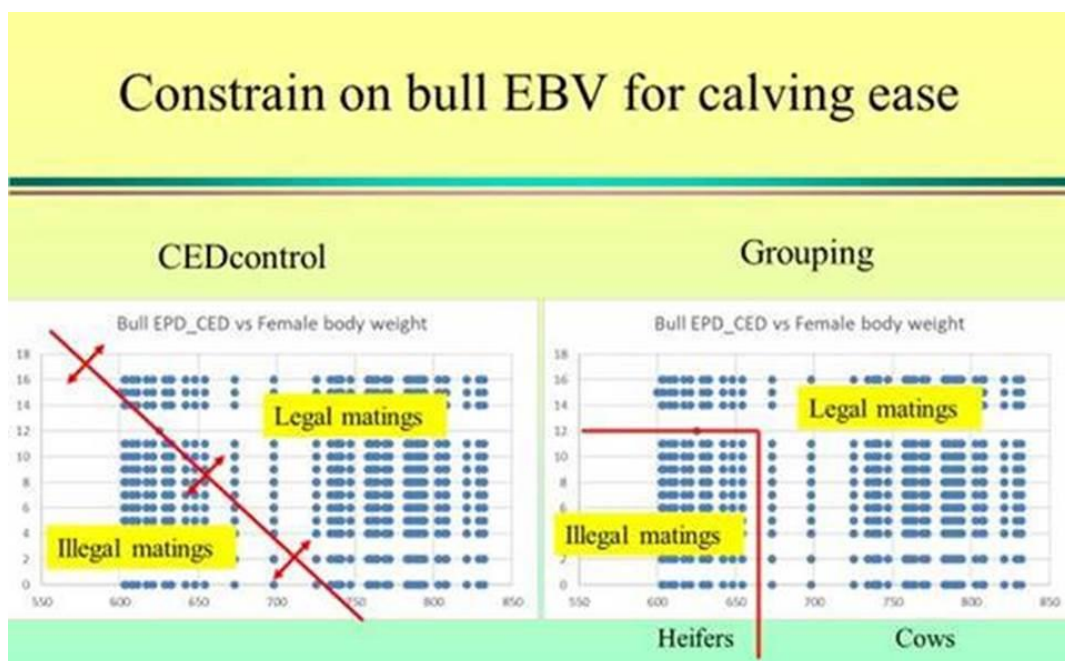
CEDcontrol for each bull is a negative value of the smallest sized heifer is should be allowed to mate, and this is calculated by the system according to that small table that represents the breeder's opinion . This means that if adding female and male CED together results in a value greater than zero , then this is an allowable mating. , then this is an allowable mating. Eg. For the first heifer and bull in the data above this sum is $603 + (-708.333) = -105.333$... Very much below 0 and a very bad allocation (low CED bull over a very light heifer).

With this setup, a mating between any bull and any cow gives a predicted progeny value for CEDcontrol that needs to be at least 0 to satisfy the breeders desires in relation to calving ease for that female. We can use Matesel's Trait Management tab to control this:



Setting CEDcontrol boundary at zero to ensure that all matings conform to the breeder's calving ease policy with respect to female body weights. Left: Boundary not invoked (9 matings do not conform). Right: Boundary invoked (all matings conform). This is a small example with just 30 matings.

The following slide shows how this is in fact a sliding scale.



31. By changing the CEDcontrol threshold from zero you can put more or less emphasis on management of calving ease, and let it compete with all other issues in the Matesel run. Try doing this in the DavisAngusHerdDec18.txt dataset. You can do this by changing the minimum boundary for CEDcontrol (set to 0 in the example here):

CEDcontrol
Resume

Set minimum value at boundary

☒ Invoke
Weighting:

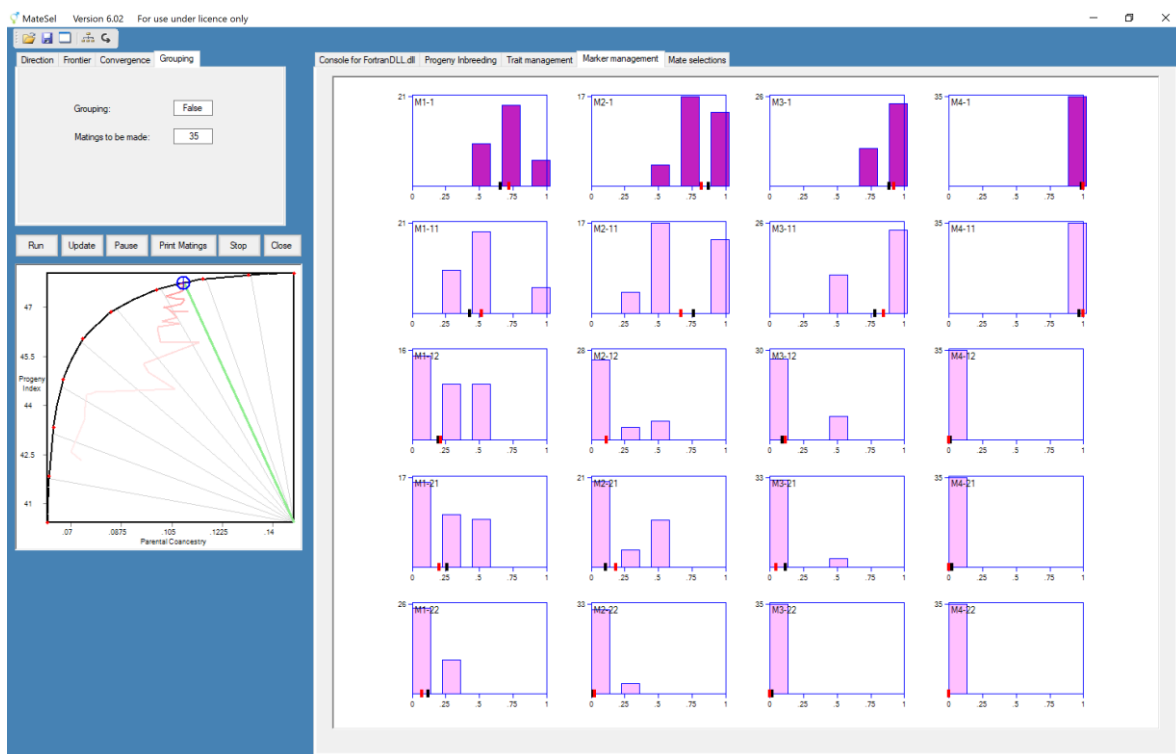
Minimum value (Click-L):

Managing genetic markers

Start a new run by stopping the previous run; and clicking run. After your job has passed the frontier building stage, click on the “Marker Management” tab to manage marker allele and genotype probability distributions. You will see four columns corresponding to 4 genetic conditions.

Each genetic condition on the display can be manipulated as described under “Managing trait distributions”, above.

Each column of distributions relates to one marker locus. The top row of distributions shows the allele frequency distributions in progeny for the first allele at each locus (each column is a locus). This is typically the predominate and favourable allele – the minor allele is typically the “2” allele and affected individuals can be seen as M-22 in the bottom row. There are 4 genetic markers shown here – M1, M2, M3 and M4. The marker 1 minor allele is present at quite high frequencies as can be seen by the presence of M1-22 predicted animals i.e. affected individuals in the bottom row.



Exercise 17: Managing genetic conditions

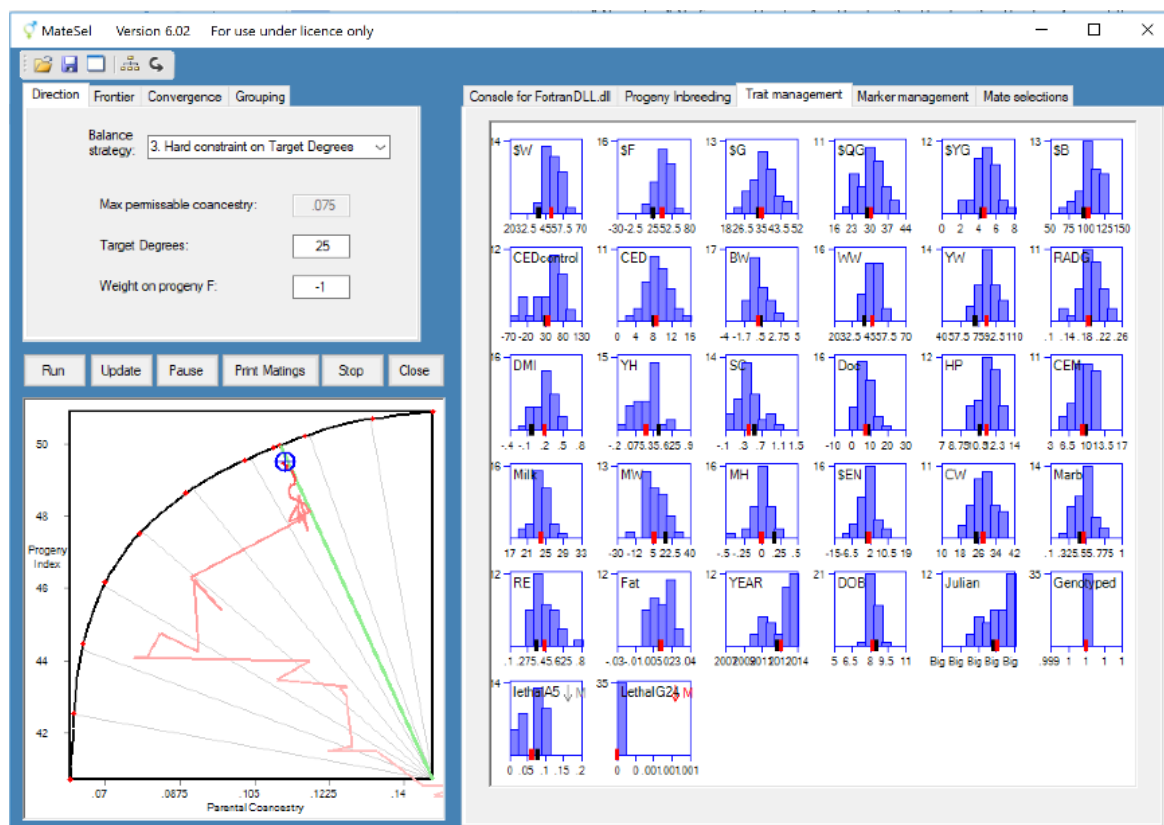
32. Develop an approach to avoid obtaining affected animals. One approach would be to select M1-1 and attempt to increase the frequency of the predominate favourable allele. Select M1-1 and invoke “Increase mean” with a high weighting. What happens to genetic gain, why is the program having a hard time coming to a solution? Which bulls got selected and why?
33. Change the selection strategy to try to avoid affected animals – set M1-22 and M2-22 to decrease mean – what happens to M3-22? Set M3-22 to decrease mean. This approach removes all affected animals at little cost to genetic gain – what are the pros and cons of this approach?

Exercise 18: Avoiding the production of homozygous calves in the case of recessive lethals (i.e. reducing embryo mortality)

34. Go to the trait management window. Notice there are two histograms at the bottom called lethalA5 and LethalG24 – this represents 20 hypothetical low-frequency recessive lethals loci with ‘missing homozygotes’ in the population(s) of interest (Locus 5 to locus 24 – 20 in total). With 20 in the file we need a special way to manipulate them as they cannot be easily handled on a case-by-case basis.

LethalA: Use this for longer-term objectives, by selecting against recessive lethal alleles in the population. LethalA for each progeny is the probability of mortality in their offspring (i.e. in grand-progeny of the current candidates), given that the progeny will be randomly mated to the population at large, with recessive allele frequencies equal to those observed (or implied from genotype probabilities) among the current candidates.

LethalG: Use this for short-term objectives by selecting against the incidence of lethally affected progeny from the current matings. LethalG for each progeny is the probability of mortality due to lethal homozygosity at one or more of the loci concerned. Given that the parents have zero probability of being homozygous lethal at any locus, the minimum predicted probability of *survival* is $(1 - 0.5 * 0.5) = 0.75$ for each locus, where both parents are heterozygotes. Across n loci, the minimum probability of survival is thus 0.75^n , giving a maximum value for LethalG of $1 - 0.75^n$. So LethalG ranges 0 to $1 - 0.75^n$ for n loci considered.



You can manipulate LethalA and LethalG using their histograms under Trait Management. As frequencies are generally very low, the scales shown will be well below the maximum possible. Rescaling will occur as you find success in reducing allele and genotypes frequencies to very low levels. But look out for the impact on other issues!!

35. Decrease the mean of lethalA – this is akin to selecting against carrier parents. What happens to genetic progress? Un-invoke selection to decrease lethalA5 and invoke selection to decrease LethalG – is this a better short term solution? What are the long term consequences of this approach?

36. Play around with the 4 genetic conditions under marker management and also the 20 low frequency lethal recessives – if you avoid all affected progeny – what does the solution look like? Which marker is the one that has the biggest effect on decreased rates of genetic gain to achieve zero affected progeny? What would be the cost versus the benefit of avoiding affected calves?

Exercise 18: Controlling the production of phenotypes determined by a single locus.

[Note: You will need to find an appropriate dataset for this exercise. We used it with cattle breeders using their own datasets with one of the marker loci simulated into these datasets having a frequency high enough for this question to be a good fit.]

[Background: BK worked at Trangie Research Station, Australia, on a project selecting up and also DOWN on yearling weight in Angus cattle – in the early 1980's. When the project finished the cattle were sold, and the "Low" selection line of small cattle fetched much higher prices at auction. The hobby farm market is big!! See https://en.wikipedia.org/wiki/Australian_Lowline]

- a. Consider that marker 1 is found to be in your herd, and that this is a recessive condition that in recessive "22" form gives a much smaller but perfectly formed animal, perhaps "Lowline".
- b. Are you able to get rid of this gene in this single mating round? (Of course, in the next year or two you would also have to pay some attention to this in what are currently your juvenile cattle)
- c. Can you engineer a predicted outcome of say 10 calvings that give Lowline cattle – as you find that you can sell these for a very high price?
- d. Can you do both ... generate 10 lowline cattle but otherwise get rid of the Lowline gene, with no carrier progeny produced? (If not, why not?)
- e. How would you use Matesel to move towards having essentially two pure lines – normal and Lowline – within your herd?

Appendix: PopSim settings and example output

PopSim Version 1.5 default.gnp [Merino example from Daniel Brown parameters]

File Edit Options

Parameters 1 Parameters 2 Mate Selection Results

Population Structure

Breeding males: 20 Male survival rate: 0.95 Age at first drop: 2 2
 Breeding Females: 400 Female surv rate: 0.9 Age at last drop: 3 8
 Weaning rate: 1

Trait parameters:

	Full Trait Name	Short	Units	SD	h2	EconWt	IndexWt	HetD	HetM	YearSD	SexEff	QTLef1	QTLef2
►	Body weight	Ywt	Kg	5.56	0.43	4	0.89004	0	0	0	0	0	0
	Body fat	Yfat	mm	2.83	0.21	-1	0	0	0	0	0	0	0
	Clean Fleece Wt	Ycfw	Kg	.4575	0.36	10	0.28320	0	0	0	0	0	0
	Fibre Diameter	Yfd	micron	1.225	0.77	-5	-1.56956	0	0	0	0	0	0
	Fecal Egg Count	Yfec	Log	2.828	0.25	-1	0	0	0	0	0	0	0
	# lambs weaned	Nlw	lambs	.649	0.07	20	125.29	0	0	0	0	0	0

Breed means: direct effects (D) and maternal deviations (M)

Breed	Ywt(D)	Yfat(D)	Ycfw(D)	Yfd(D)	Yfec(D)	Nlw(D)	Ywt(M)	Yfat(M)	Ycfw(M)	Yfd(M)	Yfec(M)	Nlw(M)
► Merino	46.65	2.33	2.6	18.06	9.65	1.62	0	0	0	0	0	0

Correlations: phenotypic above diagonal, genetic below

Trait	Ywt	Yfat	Ycfw	Yfd	Yfec	Nlw
► Body weight	-	.023158	.295029	.198998	.056035	.101263
Body fat	1E-05	-	.010752	-.01784	-.04385	-.0137
Clean Fleece Wt	.24953	1E-05	-	.308837	.032972	.028982
Fibre Diameter	.19878	1E-05	.29504	-	-.04968	.025798
Fecal Egg Count	.09671	1E-05	.04993	-.09708	-	-.04549
# lambs weaned	.14987	1E-05	-.0961	-.00167	-.00054	-

PopSim Version 1.5 default.gnp [Merino example from Daniel Brown parameters]

File Edit Options

Parameters 1 Parameters 2 Mate Selection Results

Mean Phenotypes

Year	Ywt	Yfat	Ycfw	Yfd
1992	-	-	-	-
1993	-	-	-	-
1994	-	-	-	-
1995	-	-	-	-
1996	-	-	-	-

Replicates

☐ Run replicates First Replicate: 1
☐ Crt Rep Last Replicate: 5

Age Structure Table

Breeding animals mated in year 2009 are in **blue** . and juveniles are in **red**

Birth year: 2009 2008 2007 2006 2005 2004 2003 2002

Males: 225 11 9 0 0 0 0 0
 Females: 246 203 157 112 61 41 18 8

Total animals weaned in each year, before any death or culling:

Males: 225 248 230 239 245 240 227 218
 Females: 246 241 244 239 240 245 258 236

Graph: Body weight

Start/Restart
 Zip + show
 Zip to end
 End of run

Y X
 Phen Year
 QTL Phen
 P-Q Sex
 QTLf EBV
 Crit TBV
 EBV INB
 TBV
 INB
 1 2
 Line only

Show
☐ Males
☐ Females
☒ Both
☐ Survivors
☒ All