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Overview

MateSel is a tool available to Sheep Genetics clients to help with mate selection. The program created by Brian Kinghorn assists in balancing emphasis on genetic gain and maintenance of diversity.

Mating outcomes will be reported by submitting a list of possible males, possible females, desired gains as well as constraints on long term and short term inbreeding (coancestry). The program will run a number of scenarios to get the best possible choice of individuals to select and the best arrangement of mate selection.

Access will be given to service providers and breeders who successfully complete the MateSel training. The following information should assist you in running MateSel on the Sheep Genetics website.

Background – Strategy and Logistics

MateSel is a tool available to make selection decisions on that allows a balance between genetic gain and inbreeding.

When using MateSel, inbreeding is defined as the mating of related animals, where co ancestry is defined as a measure of the degree of common ancestry of two or more individuals. Managing in-breeding and co-ancestry are different but not mutually exclusive.

A sound breeding objective is the basis of effectively using MateSel and the mating outcomes it suggests. By identifying the traits of interest, the direction of gain and the time frame, or pressure in which you want to select for these traits you can set up a MateSel run that will complement your breeding objectives. The effective use of MateSel is underpinned by having the rest of the breeding program correct and stable. This includes pedigree and recording of key traits in the objective.

MateSel can be used for allocation and selection. Allocation is the program assigning the ewes to the rams with no selection pressure attributed. Selection allows a surplus of either ewes or rams to be included in the animal lists and based on the run parameters and traits of interest selected, will calculate the best joining combinations to suit the breeding objective. To get the most out of MateSel, allow selection and allocation to be used in conjunction with each other.

First observation

If you attach no limitations to your mating scenario, MateSel will produce the best mating/selection result obtainable for the candidates available. However, a joining program without some form of constraint is rarely feasible.

Therefore, before you begin you should establish some basic strategic and logistic measures that will guide the outcome.

Strategic

- What is the breeding objective within the flock?
- What is the current genetic profile of the flock?
- What are the average ASBV values for the current drop - for the traits that affect the breeding objective?
- What traits (if any) need particular emphasis?

NOTE: “ You can’t make a silk purse out of a sow’s ear” MateSel can only produce a result using the candidates presented. Do not expect it to produce an unrealistic “dream” result.

Logistic (What resources do you have available?)

For example

- How many joining paddocks are available?
- Is AI involved. If so how many doses are available?
- Is ET/Jivet involved?
- Are there different ewe joining groups?
- Are the ewes all at one location?

Second observation

Do not logistically constrain the process too much.

For example

Let us say you are joining 100 ewes and you have four sire candidates. If you set sire usage to a strict 25 each, the result will more than likely be well below the best achievable with the candidates available.

You must give the program “room to breathe – don’t choke it”

MateSel Instructions

To complete a MateSel run you have to complete the following steps:

1. Select Dataset and Analysis
2. Create or Select a Run
3. Set the Run
4. Start the Run

1. Choose a dataset and an analysis

Datasets are aligned with the Sheep Genetics products: LAMBPLAN (incorporates Terminals, Maternals, First cross sires, Sheddars, SAMMS and Corriedale analyses), MERINOSELECT, KIDPLAN and DOHNES have their own dataset and analysis.

Use the drop down menu to choose a dataset ¹ and the analysis ² relevant to the flock you are running MateSel.

Figure 1 – Select dataset & analysis

The screenshot shows the Sheep Genetics website interface. At the top, there's a navigation bar with 'SG HOME', 'Search home', and 'Tools'. Below this is a header with 'SHEEP GENETICS' and a search bar. The main content area is titled 'MATESEL at Sheep Genetics'. It contains two sections. The first section, 'Select Dataset & Analysis', has two dropdown menus: 'Dataset:' (marked with a red 1) and 'Analysis:' (marked with a red 2). The second section, 'Create/Select Run', has two buttons: 'Create New run' and 'Select Existing Run'.

2. Create or Select a Run

To create or select existing run both dataset and analysis MUST be selected as described above.

2.1 Create a Run

To create a new run, go to the “**Create/Select Run**” section and click “**Create New Run**”. Under the “Create New Run”, do the following:

- i. **Select Run Parameters** ¹ - Select Run Parameters from the drop down menu, only one is available at the moment which is: “DEFAULT”).
- ii. **Choose Index** ² - Choose Index from the drop down menu, which is populated with the available Indexes or ASBVs. This will become the y-axis on the frontier graph created.
- iii. **Run name** ³ - Write MateSel run name, call it something you can remember and is descriptive of the run you are doing (i.e. the name of the flock and year of joining).
- iv. **Custom Column (Optional)** ⁴ - Select Custom Column. This section is for you to select a custom column in your dam and sire lists to be used as the main ‘index’. To see more on Custom Columns go to “[How to use Custom Columns](#)” section.

The red text message tells you what you should do.

Figure 2 - Create new run

MATESEL at Sheep Genetics

Select Dataset & Analysis

Dataset:

MATESEL

Analysis:

MATESEL EXERCISES

Create/Select Run

[Create New Run](#)

Run template must be selected

Select Run Parameters:

1

Choose Index:

2

Run name:

3

Custom Column:

4

Create matesel run

[Select Existing Run](#)

Once the run has been created, it will be available in the 'Select Existing Run' to be selected to go to the next step as it is mentioned in the green text¹.

Figure 3 - New run created

Create/Select Run

[Create New run](#)

Template:

DEFAULT

Choose Index:

Postweaningt clean fleece wt

Run name:

509999_AI_2017

Custom Column:

Create matesel run

... Run id 5593 created as 509999_AI_2017

1

GO TO 'Select Existing Run' SECTION BELOW & SELECT YOUR NEW RUN!

[Select Existing Run](#)

2.2 Select a Run

To select existing run or the run you just created click "**Select Existing Run**" and from the drop down menu of the **Select from existing run**¹ select your run.

Figure 4 - Select existing run

Create/Select Run

[Create New run](#)

[Select Existing Run](#)

Select from existing run:

Once a run is selected the “Run Detail” section and the other sections will appear. The “Run Detail” section tells all the details of the run including its run id, status and the index selected as shown below.

Figure 5 - Run detail

Run ID	User	Date	Description	Status	Index
5593	ezerazion	3/13/18 3:26 PM	509999_AI_2017	INIT	PCFW (Postweaning clean fleece weight) (pcfw)

3. Set Run

This section is where you upload your animal lists, make the link between your male and female groups, set the basic & advanced run parameters and select a trait you want to put additional emphasis on. Each section is set as a tab under the “Set Run” section and will be described one by one.

Figure 6 - Set run

Set Run: 509999_AI_2017

[Animal Lists](#) [Mating Groups](#) [Basic Run Parameters](#) [Advanced Run Parameters](#) [Traits](#) [End Uses](#)

[Create New List](#)

[Modify Existing Lists](#)

3.1 Animals Lists

In this **Animals Lists** ¹ section, you can either create new list or modify existing list.

Figure 7 - Animals Lists

Set Run: 509999_AI_2017

¹ [Animal Lists](#) [Mating Groups](#) [Basic Run Parameters](#) [Advanced Run Parameters](#) [Traits](#) [End Uses](#)

[Create New List](#)

[Modify Existing Lists](#)

Sheep Genetics’ version of MateSel requires two groups of animal list at a minimum. One list needs to contain your proposed sires and the second list the available dams. To create a mating group, you first have to create a list by clicking “Create New List”. To modify an existing list click the “Modify Existing Lists”.

3.1.1 Create New List

How to create a new Animal list:

Using Text File ¹ - Create a text file of your animals list and upload it into this page,

Figure 8 - Create a new list

1. Create List Using Text File

To create list using a text file you should have the 16 digits animal id in text file, one animal per line.

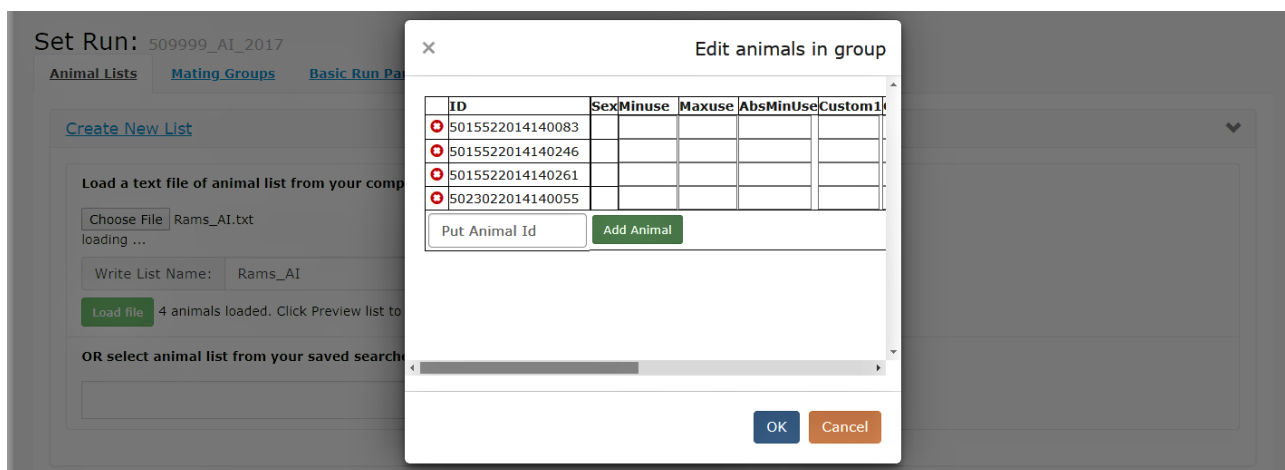
NOTE: You do not need any of the extended pedigree in your lists; the information will be automatically taken from the Sheep Genetics database

Figure 9 - Create a new list using text file

- Click the “**Choose File**” ¹ button and select your file from your computer. Once you select a file, the “**Write List Name**” field will appear.
- Write your list name in the “**Write List Name**” ² field. When creating a new list, type a memorable name for the list. A tip is to make sure the list name has what sex the animals in the list are. Once you put the list name, the “**Load file**” button will appear.
- Click the “**Load file**” ³ button to load the animals. When the animals are loaded, you will receive a message next to the button and the “**Preview list**” and “**Create list**” buttons will appear.
- Preview the file before creating the list by clicking the “**Preview list**” ⁴ button. Animals can be removed from the list as well as minimum and maximum uses can be set, which will override parameters set later on. (See figure 10)
- Click the “**Create list**” ⁵ button to create the list. If there are no errors, it will be created and ‘List created ...’ message will appear in green (see figure 11). If there are errors in the list, it will not be created and an error message followed by “Show errors” button will appear (see figure 12). Press the “Show errors” button to see the reasons (see figure 13). The sheep with errors need to be fixed. You can either edit your input file then re-upload it or you can selectively remove animals from the list by clicking “**Preview list**” again and removing those animals that have an exclamation mark next to them by clicking the red ✖ icon before the ID (see figure 14).

Preview list

Figure 10 - Preview list



NOTE:

- Minuse = minimum number of matings. If Matesel wants to use a sire for fewer matings than 'Minuse' value then the sire will not be used at all.
- Maxuse = maximum number of matings.
- AbsMinUse = Absolute minimum number of matings (effectively MUSTUSE). AbsMinUse can be helpful when talking about AI, where if you have 20 doses of a ram you want all 20 doses to be used.

Figure 11 - Create list without error

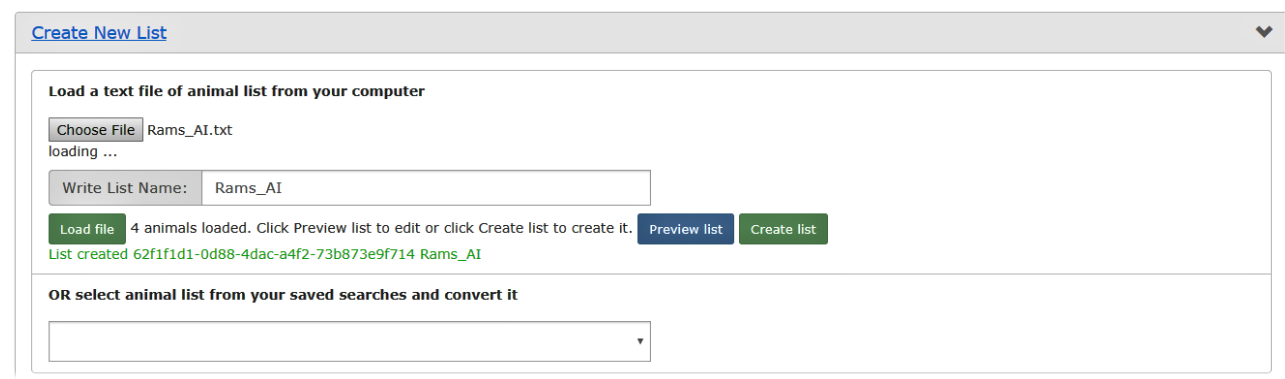


Figure 12 - Create list with error

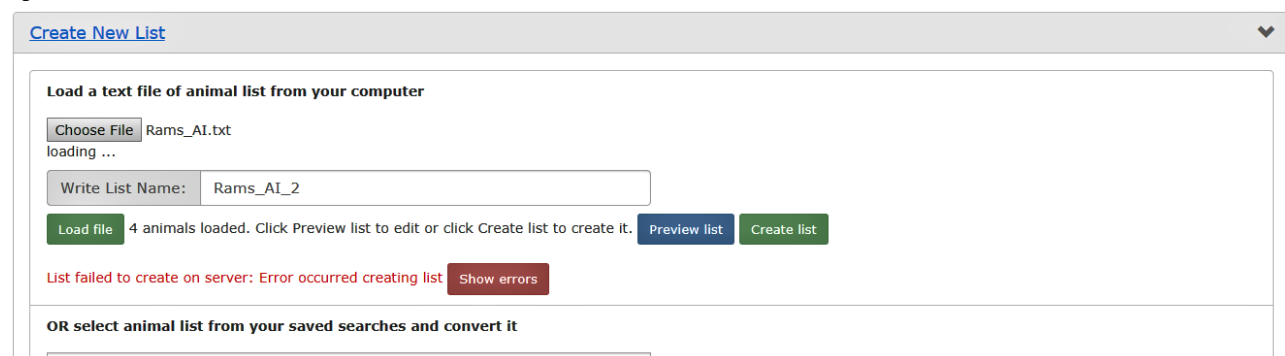


Figure 13 - Viewing reason of error for the animals with error

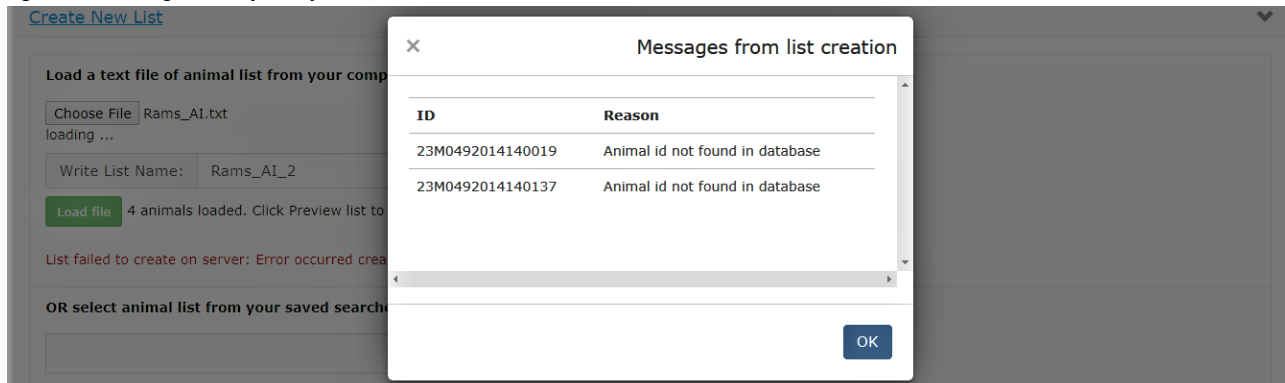
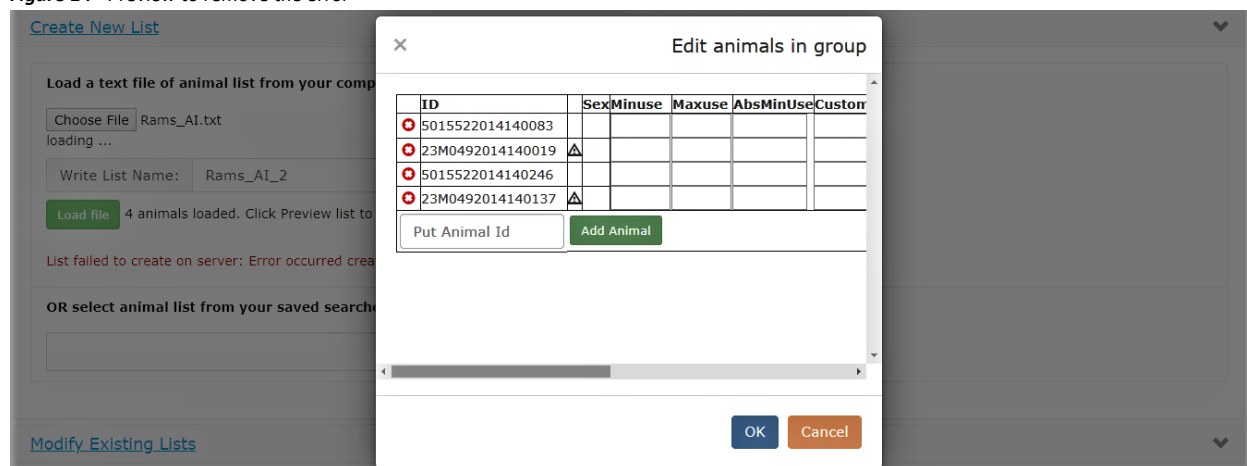


Figure 14 - Preview to remove the error



3.1.2 Modify Existing List

The Modify Existing List is used to edit an existing list or add custom column headings.

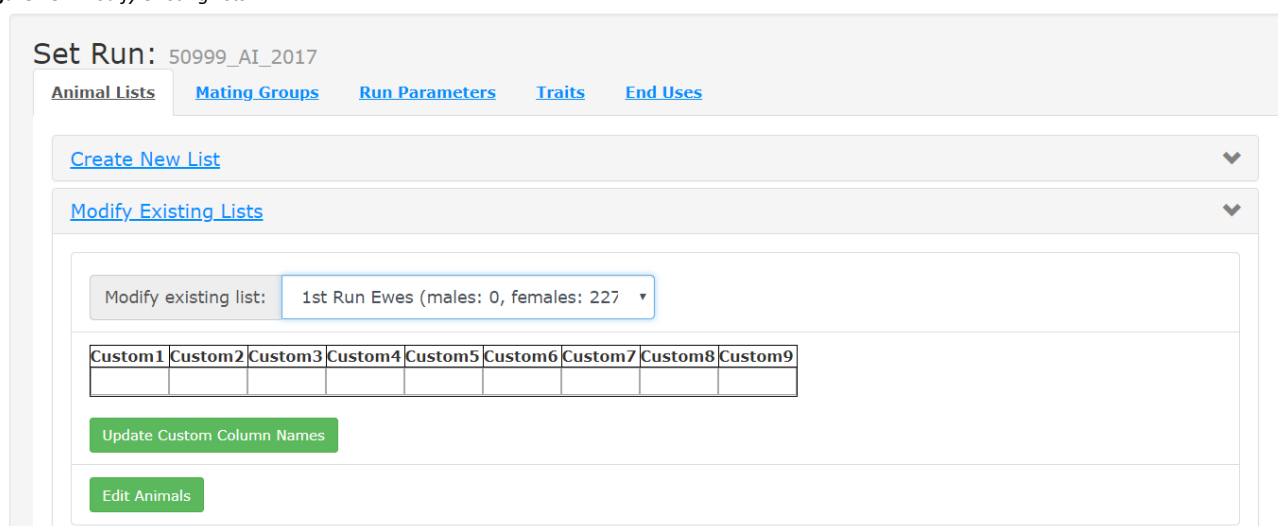
Figure 17 - Drop down menu of existing lists



To modify existing list:

- Select the list from the drop down box that needs editing.
- Once you select a list, a table to add custom column headings and few buttons will appear (see figure 18).
- Add your custom heading if needed and click the “Update Custom Column Names” button.
- The “**Edit Animals**” button is used to edit, remove or add animals as explained previously (see figure 10).

Figure 18 - Modify existing lists



3.2 Mating Groups

At least one male and female group need to be linked for MateSel to run. The male groups are added from the “Add Male Group” drop down menu while the female groups are added from the “Add Female Group” drop down menu (see figure below).

Figure 19 - Male & Female groups

Add Male and Female groups to the run

- To add male group select the male group from the “**Add Male Group:**” ¹ drop down menu and click the “**Add male group to run**” ² button. Similarly to add the female groups select the female group from the “Add Female Group:” ³ drop down menu and click the “Add female group to run” ⁴ button (see figure 19).
- Once you select the list and add it, the group detail (which includes group number, M for male/ F for female, list name and male & female animal count) will appear under each section as shown in the figure below. If you have selected more than one group for each sex you will see multiple groups listed.

Figure 20 - Male & Female groups

- By clicking on the Male group title ¹, you can set the usage guidelines for the male group (see figure 20 below). If you click the title again, it will collapse the form.

Figure 20 - Setting guidelines for Male groups

- ✓ The main strategies to think about are minimum use ², maximum use ³ and absolute minimum use ⁴.
- ✓ If you have set maximum use for any sire higher than 30 you must do the same here otherwise it will limit usage to 30

NOTE: If changes are made, press the “**Update**” ⁵ button for it to be implemented in the next run.

The “Delete” ⁶ button removes the group from the run.

- By clicking on the Female group title ¹, you can set the usage guidelines for the female group (see figure 21 below). If you click the title again, it will collapse the form.

Figure 21 - Setting guidelines for Female groups

- ✓ The main parameters to consider are minimum use ² and maximum use ³.
- ✓ If you want to run a MOET or JIVET scenario, the maximum use of the ewe list has to be greater than one.

NOTE: If changes are made press the “Update” button for it to be implemented in the next run.

The “Delete” ⁶ button removes the group from the run.

Linking Male and Female groups

There are two ways to join the male and female groups. Both processes create the input files that MateSel needs.

Way 1 of linking Male and Female groups.

Drag the male group title on to the female group title.

Figure 22 - Drag the Male group to the Female group

When a Male and Female groups are linked you will see the information which male group is linked to which female group next to each groups title as shown in the figure 23 ¹.

NOTE: One Male group can be linked to more than one Female groups and vice versa.

You can click the red circle with ✕ ² to remove the link.

Figure 23 – Remove linkage

Set Run: 509999_AI_2017

[Animal Lists](#) [Mating Groups](#) [Basic Run Parameters](#) [Advanced Run Parameters](#) [Traits](#) [End Uses](#)

Add Male Group: CP_Link (males: 5, females: 0) Add male group to run

[1 M \(CP_AI\(males: 6, females: 0\)\)](#)

Male group: 1 is linked with Female group: 2 2

Male group: 1 is linked with Female group: 3 3

Add Female Group: CP_RBN_Ewes (males: 0, females: 1113) Add female group to run

[2 F \(CP_Female\(males: 0, females: 318\)\)](#)

Female group: 2 is linked with Male group: 1 1

[3 F \(CP_RBN_Ewes\(males: 0, females: 1113\)\)](#)

Female group: 3 is linked with Male group: 1 1

Way 2 of Linking Male and Female groups

Clicking on the Female Group title, choose the appropriate male group in the drop down list next to “Select male to join” 1 and click the “JOIN” 2 button.

Figure 24 - Linking Male to the Female group

Add Female Group: Add female group to run

[2 F \(CP_Female\(males: 0, females: 318\)\)](#)

Group number: 2

Sex: F

List: CP_Female(males: 0, females: 318) (ba5a6809-686b-4aac-8416-9f377ec5b276)

Minimum use: 1

Maximum use: 1

Absolute Minimum use: 0

Preselection: 1

Number of matings or selection proportion

Number of matings or selection proportion value

Invoke female nums or props

Maximum backups

Select male to join 1

Join 2

Update Delete

NOTE: To ensure that the mating groups are correct you can run MateSel before setting any other parameters or traits. It only takes a few minutes.

3.3 Basic Run Parameters

All parameters, ‘Basic run parameters’ and ‘Advanced run parameters’ have been set to a sensible default setting.

NOTE: See the glossary at the back for definitions of the basic and advanced parameters. For more detail go to Instructions for MateSel by Brian and Sandy Kinghorn.

The Basic Run Parameters are the main parameters you will need to use. These parameters include Balance Strategy, Grouping, Matings to be made if not grouping, MaxNewGens, AbsMin-NewGens, Enduses, Target degrees, Pressure on inbreeding, Threshold on progeny inbreeding and pressure on progeny inbreeding.

You can change the values by selecting from the drop down menu or by typing on the field.

NOTE: To see a brief explanation/hint about the parameter hover you mouse on the parameter's name ¹.

Figure 25 – Basic Run Parameters brief explanation/hint

Set Run: 509999_AI_2017

Animal Lists Mating Groups **Basic Run Parameters** Advanced Run Parameters Traits End Uses

Balance Strategy (Hard constraint on target degrees) Hard constraint on target degrees Update ¹

Grouping (Off) Off

Number of matings to be generated (2000) 2000 Update

Maximum number of Generations (10000) 10000 Update

Absolute Minimum New Generations (1000) 1000 Update

Multiple EndUses (Off) Off Update

TargetDegrees (10) 10 Update

Coancestry Limit (0.075) Update

Pressure on Coancestry (xAx/2) (-10) Update

Pressure on progeny inbreeding (0) 0 Update

Threshold for Progeny inbreeding level (0.24) 0.24 Update

Pressure on inbreeding threshold (0) 0 Update

NOTE: If changes are made to a parameter, press the **“Update”** button for the change to be implemented in the run.

Balance Strategy

MateSel needs a Balance strategy to be selected for it to run. The different balance strategies related to different balances between genetic gain (predicted index value in progeny) and parental coancestry. The different strategies are listed on the next page. Select the balance strategy from the drop down box. Depending on what strategy you choose determines what parameters are available underneath. Set these accordingly.

NOTE: the below table has been sourced from **“Instructions for MateSel”** by Brian and Sandy Kinghorn.

Table 1 – Description of Basic Run Parameters

1. Hard constraint on coancestry	This maintains the solution at or below a given value of parental coancestry. Set the limit at parameter “Max permissible coancestry (xAx/2)”. You should specify a value that is greater than the minimum value – this is the minimum value on the horizontal axis of the Frontier Graph, that only appears after “Run” has been clicked.
2. Soft constraint on coancestry	As above, except that exceeding the limit by a small amount is permitted, but heavily penalised. This can help with speed of convergence.
3. Hard constraint on Target Degrees	This maintains the solution at or “above” a given value of Target Degrees (TD, see below). In fact, this component simply aims to “maximise gain”, but also severely penalises solutions that break the TD constraint. * For TD > 45 degrees, substitute “below” and “minimise coancestry” respectively.
4. Soft constraint on Target Degrees	As above, except that undercutting the limit is permitted, but heavily penalised beyond a 2 degree deviation. This can help with speed of convergence.
5. Project to Target Degrees line	This aims for a solution that is most deviated from the origin when projected to the TD line. [Hold a ruler perpendicular to the TD line and move it out to where it last coincides with the frontier – that is where a solution should go with no other issues included.] For non-circular frontier shapes, this projected point can be outside the frontier, with the solution exploiting the prevailing shape of the frontier to maximise the index implied by the TD line.
6. Projection plus deviation penalty	As above, except that a weighting is applied against deviations of more than 5 degrees from the TD line. [Note: Some danger of settling on a local optimum. You can check this by moving to strategy 5, waiting for good convergence, then change back to strategy 6]

Grouping

Grouping is used to define different group membership for animals, which allows different mating numbers and mating group links to be set.

NOTE: If you are grouping animals instead of running all rams and ewes through as one list you have to turn grouping 'On' ¹ (see figure 26).

For more information on Grouping, see "[How to use Grouping](#)" section.

Number of matings to be generated

If grouping is 'Off' the "Number of matings to be generated" ² has to be set. This should be set to the number of matings that you want to occur during the run (see figure 26).

Figure 26 – Grouping and Number of matings to be generated

Set Run: 509999_AI_2017

[Animal Lists](#) [Mating Groups](#) **Basic Run Parameters** [Advanced Run Parameters](#) [Traits](#) [End Uses](#)

NOTE: To see a brief explanation/hint about the parameter hover you mouse on the parameter name.

Balance Strategy (Hard constraint on target degrees)	Hard constraint on target degrees	Update
Grouping (Off)	Off ¹	Update
Number of matings to be generated (2000)	2000 ²	Update

Maximum number of Generations

This is the maximum number of joining scenarios for MateSel to process ¹ (see figure 27). This number has to be greater than the Absolute Minimum New Generations number below.

Absolute Minimum New Generations

The minimum number of joining scenarios for MateSel to process. A larger value here is applicable to larger data sets ² (see figure 27).

Target Degrees

Target degrees is used to target a relationship between Genetic Gain and parental coancestry ⁴ (see figure 27). It is only used for Balance Strategies 3 to 6 (see **table 1** above).

Pressure on progeny inbreeding

This is the weighting value used to penalise inbreeding in the progeny derived from the matings to be made. Use a negative value to put downward pressure on short-term inbreeding ⁵ (see figure 27).

Suggestion: if this is used start with a value of -1

Threshold for Progeny inbreeding level

This is the value of progeny inbreeding, which you **prefer** not to exceed for any individual mating ⁶ (see figure 27).

Pressure on inbreeding threshold

This is the weighting applied for breaking the progeny inbreeding threshold. Suggestion: if you use this, start with a value of -1 ⁷ (see figure 27).

Figure 27 – Basic Run Parameters

Set Run: 509999_AI_2017

[Animal Lists](#) [Mating Groups](#) [Basic Run Parameters](#) [Advanced Run Parameters](#) [Traits](#) [End Uses](#)

NOTE: To see a brief explanation/hint about the parameter hover you mouse on the parameter name.

Balance Strategy (Hard constraint on target degrees)	Hard constraint on target degrees	Update
Grouping (Off)	Off	Update
Number of matings to be generated (2000)	2000	Update
Maximum number of Generations (10000)	10000 1	Update
Absolute Minimum New Generations (1000)	1000 2	Update
Multiple EndUses (Off)	Off 3	Update
TargetDegrees (10)	10 4	Update
Coancestry Limit (0.075)		Update
Pressure on Coancestry (xAx/2) (-10)		Update
Pressure on progeny inbreeding (0)	0 5	Update
Threshold for Progeny inbreeding level (0.24)	0.24 6	Update
Pressure on inbreeding threshold (0)	0 7	Update

NOTE: If changes are made to a parameter, press the “Update” button for the change to be implemented in the run.

3.4 Advanced Run Parameters

Advanced parameters should not need changing the first time you start the MateSel run unless you want to run a MOET or JIVET scenario.

Breeding program. MOET/JIVET

If a ewe lists maximum use has been set to greater than one the program assumes a JIVET scenario.

- **JIVET** scenario allows the program to allocate more than one sire to an individual ewe that has a maximum use >1, as long as it is the best scenario.
- **MOET** will only allocate one sire to all progeny from any one ewe. **Tip:** Do not forget to take into account the maximum use of the females when calculating the total number of matings.

Example: An ET program with 5 ewes, where you plan 10 embryos per ewe. Max use = 10. Number of matings to be generated per ewe =10. Ten matings multiplied by 5 ewes = 50 matings to be generated if not grouping.

Figure 28 – Advanced Run Parameters

Set Run: 509999_AI_2017

[Animal Lists](#) [Mating Groups](#) [Basic Run Parameters](#) [Advanced Run Parameters](#) [Traits](#) [End Uses](#)

NOTE: To see a brief explanation/hint about the parameter hover you mouse on the parameter name.

Minimum New Generations (10)	10	Update
Generations between reporting point (1000)	1000	Update
Frontier 0 degree generations (1000)	1000	Update
Frontier 90 degree generations (1500)	1500	Update
Frontier xx degree generations (1000)	1000	Update
Back Pedigree considered (999)	999	Update
Reporting level (2)	2	Update
Breeding program. MOET / JIVET (JIVET)	JIVET	Update
Target % converged (99.9)	99.9	Update
No improvement in last x% of generations (20)	20	Update
Frontier degree gap (10)	10	Update

3.5 Traits

Breeding objectives that have extra emphasis on certain traits or a custom column can be entered into MateSel using the 'Traits' tab. You can select the basic traits from the first drop down menu and press '**Add trait to run**' button¹ to add it to the run. Similarly, you can add your Custom Column from the second drop down and press '**Add custom column to run**' button² to add it to the run (see figure 29).

NOTE: you can only have up to 5 traits of interest selected at one time.

Figure 29 – Additional Traits

Set Run: 509999_AI_2017

Animal Lists Mating Groups Basic Run Parameters Advanced Run Parameters **Traits** End Uses

¹ Add trait to run ² Add custom column to run

Every added trait will be listed below the drop down menu as shown in figure 30.

Figure 30 – List of added Traits

Set Run: 509999_AI_2017

Animal Lists Mating Groups Basic Run Parameters Advanced Run Parameters **Traits** End Uses

¹ Add trait to run Add custom column to run

bwt (active)
pfd (active)
pgfw (active)

Once a trait is added its parameters need to be set. To set the parameters click on the trait link¹ (see figure 31).

- ✓ The first step is to indicate the desired direction of the trait by selecting a control type⁴ e.g. YWT - Increase Mean
- ✓ Depending on the Control type selected set the "Optimum value" or "Minimum value" or "Maximum value" or "Lower mean, Upper mean & Percentage in upper group" (see **table 2** which describes the different control types)
- ✓ The second is to apply an appropriate weighting⁵. This is how much emphasis MateSel puts on the trait parameters.
- ✓ If more than one trait has been added the order that they are ranked can be updated by inserting a 1, 2, 3 etc. into 'Trait Order'².
- ✓ To turn the trait on in the MateSel run make sure that it is active, or if you want the program to ignore the trait make it inactive³. This is useful if you want to keep track of traits but do not want any control type, weighting or target to effect the result.
- ✓ Click the "**Update**"⁶ button to implement the change or "**Delete**"⁷ button to remove the trait from the run.

Figure 31 –Trait Parameters

Set Run: 509999_AI_2017

Animal Lists Mating Groups Basic Run Parameters Advanced Run Parameters **Traits** End Uses

Yearling Weight
Add trait to run
Add custom column to run

ywt (active) 1

Trait name: ywt

Trait order: 1 2

Active: Yes 3

Control type: Increase Mean 4

Weighting: 1 5

Update Delete 6 7

Table 2 – Description of Control types

1. Increase Mean <i>No Values are needed</i>	‘Increase Mean’ will put extra emphasis on selecting matings that increase the trait average of the progeny (mid-parents) calculated for that drop.
2. Decrease Mean <i>No Values are needed</i>	‘Decrease Mean’ will put extra emphasis on selecting matings that decrease the trait average of the progeny (mid-parents) calculated for that drop.
3. Increase Variation <i>No Values are needed</i>	‘Increase Variation’ emphasises that a greater range in the mid-parents of the progeny created is desired for the trait.
4. Decrease Variation <i>No Values are needed</i>	‘Decrease Variation’ is used when less range in the mid-parents of the progeny created is desired for the trait.
5. Increase Variation about an Optimum <i>Optimum value (mean value as centre)</i>	MateSel can centre the variation of progeny mid-parents around a value this is the ‘Optimum’. This control type will ask for a greater range in mid-parents with the Optimum value being the mean.
6. Decrease Variation about an Optimum <i>Optimum value (mean value as centre)</i>	MateSel can centre the variation of progeny mid-parents around a value this is the ‘Optimum’. This control type will ask for a less range in mid-parents around the optimum value.
7. Set a Minimum Value Boundary <i>Minimum value desired for progeny</i>	A limit can be set for MateSel to recognise and aim to keep above or below. ‘Set a Minimum Value Boundary’ will aim to keep all progeny created above the minimum value set.
8. Set a Maximum Value Boundary <i>Maximum value desired for progeny</i>	A limit can be set for MateSel to recognise and aim to keep above or below. ‘Set a Maximum Value Boundary’ will aim to keep all progeny created above the minimum value set.
9. Target Bimodality <i>Lower mean value</i> <i>Upper mean value</i> <i>Percentage of progeny in upper group</i>	Bimodality can be used when you have two distinct markets. Aiming for matings to be selected towards two means a lower and upper mean. The proportion desired for each market can be identified by the percentage in upper group.

How to use Grouping

Grouping is useful when you have candidate animals (especially ewes) divided into different groups for any reason. For example, you may have ewes running at different locations and obviously, a ram mated naturally is only able to service one group. Alternately, you may have a group of ewes that for some reason you do not want to AI.

You could run all these groups separately and combine the results to give a joining solution for the flock. However, it is important to remember that you are wanting to maximise genetic gain whilst limiting co-ancestry across the flock so it is important that MateSel is run for all groups together.

Generally female groups will be defined by some logistic/management factor. In turn, these ewe groups will define how the male candidates are grouped and how many groups of females the male candidates might be joined to.

The minimum requirement for running a group scenario would be 1 male group and 2 female groups. This might be the case where only natural mating was used and the ewes are running at 2 separate locations. The groups for this scenario would look like:

FLOCK 1

The flock has 2 groups of ewes at different locations

1. Ewes at Stud North
2. Ewes at Stud South

One group of rams to be joined naturally

3. Stud Rams

In this scenario, the Ram group would be joined to both ewe groups but individual rams will only be used in 1 group of ewes.

A second scenario might look like this:

FLOCK 2

A flock has 3 ewe groups

1. Mature ewes to be AI'd.
2. Maiden ewes that may be AI'd or joined naturally.
3. Mature ewes to be joined naturally.

The male candidates would be allocated to 2 groups

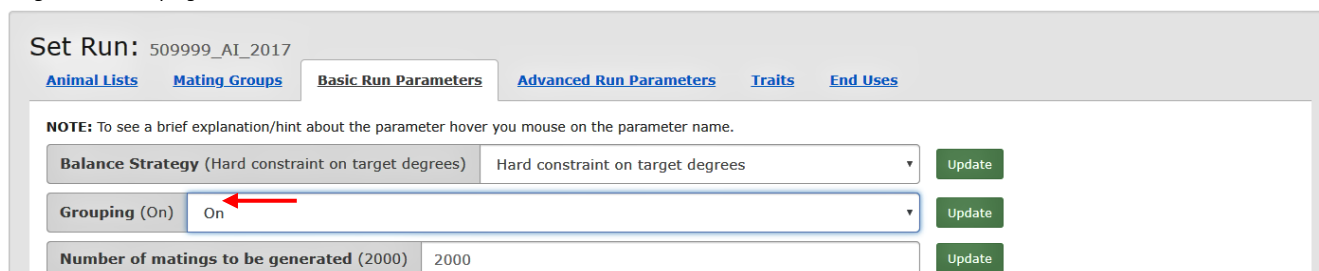
4. Potential AI sires.
5. Potential natural sires.

In this scenario, Male group 4 would be joined to Female groups 1 & 2, and Male group 5 would be joined to Female groups 2 & 3. Male usage is set in the same way as previously described but joining numbers are set by allocating target numbers of females to mate in each group.

The settings for both these examples are outlined in the following discussion.

NOTE: If you are running a group scenario, you have to turn grouping 'On' (see figure 32).

Figure 32 - Grouping On



Set Run: 509999_AI_2017

[Animal Lists](#) [Mating Groups](#) [Basic Run Parameters](#) [Advanced Run Parameters](#) [Traits](#) [End Uses](#)

NOTE: To see a brief explanation/hint about the parameter hover you mouse on the parameter name.

Balance Strategy (Hard constraint on target degrees)	Hard constraint on target degrees	Update
Grouping (On)	On	Update
Number of matings to be generated (2000)	2000	Update

In “Male Groups” adjust “Maximum use”¹ if required. This is required if individual sire use for any ram is set higher than the default 30 set in group usage.

If rams are to be used in only one ewe group then set “Male natural mating vector”² to 1 (if it is set to 0 then rams may be used in more than one group).

In the two examples given earlier “Male natural mating vector” would be set to 1 in **FLOCK 1** only allowing rams to be used at one of the two locations. In **FLOCK 2** however it would be set at 0, allowing rams from Male Group 4 to be used in Female Groups 1 & 2 and rams from Male Group 5 to be used in Female Groups 2 & 3.

Figure 33 – Updating Male Group

Add Male Group: CP_AI (males: 6, females: 0) Add male group to run

1 M (CP_AI(males: 6, females: 0))

Group number: 1

Sex: M

List: CP_AI(males: 6, females: 0) (50eb0ea8-4549-41ab-8598-0b14afc484f4)

Minimum use: 1

Maximum use: 30¹

Absolute Minimum use: 0

Preselection: 1

Males can be backups: 1

Male natural mating vector: 0²

Update Delete

In addition, you will have to change some of the settings in the “Female Groups” you are using. You have the option of using “Number of matings or selection proportion”¹ to describe the matings per female group. If “Number of matings or selection proportion” is set to 1, then this number of matings is used. This would probably be the most common setting. (0 = selection proportions)

You must also set the “Number of matings or selection proportion value”² In most cases this would mean setting the number of matings to be made within the ewe group

You must also set “Invoke female nums or props”³ to 1.

Figure 33 – Updating Female Group

Add Female Group: CP_Female (males: 0, females: 318) Add female group to run

2 F (CP_Female(males: 0, females: 318))

Group number: 2

Sex: F

List: CP_Female(males: 0, females: 318) (ba5a6809-686b-4aac-8416-9f377ec5b276)

Minimum use: 1

Maximum use: 1

Absolute Minimum use: 0

Preselection: 1

Number of matings or selection proportion: 1¹

Number of matings or selection proportion value: 30²

Invoke female nums or props: 1³

Maximum backups: 2

Update Delete

After making some changes, remember to click the “Update” button to implement the change.

How to use Custom Columns

Custom columns allow you to use numerical selection criteria that is outside those in the Sheep Genetics database. For example, you may have a customised selection index, or a numerical value for a trait that is important to your breeding objective.

When you create a new run select from the “**Custom Column**” ¹ drop down menu.

Figure 34 – Create a run with Custom Index

Create/Select Run

Create New Run

Template: DEFAULT

Choose Index:

Run name: 509999_customIndex

Custom Column: custom_column1 ¹

Create mateset run ... Run id 5609 created as 509999_customIndex

GO TO 'Select Existing Run' SECTION BELOW & SELECT YOUR NEW RUN!

To import an ID list with custom column values create an Excel file with the IDs in column A and the custom values in column B. (You can have more than one custom column, put them in consecutive columns.)

Figure 35 – Excel file with IDs and custom index values

	A	B	C	D	E
1	5046372012120652	123.3			
2	6000012015150026	122.1			
3	6011512015150106	121.5			
4	6014422014140961	124.6			
5	6090402012122295	125.7			
6	6091472014140474	122.9			

Save the file as a CSV (comma-separated variable) file. Open with Notepad and save as a text (.txt) file. When you build an animal list with this file the “custom” values will import into the custom columns.

Figure 36 – Text file with IDs and custom index values

CustomColumn.txt ...

File Edit Format View Help

5046372012120652,123.3
6000012015150026,122.1
6011512015150106,121.5
6014422014140961,124.6
6090402012122295,125.7
6091472014140474,122.9

Custom column values can also be used as traits (as opposed to the main selection criteria).

Figure 36 – Traits with custom column

Set Run: 509999_customIndex

Animal Lists Mating Groups Basic Run Parameters Advanced Run Parameters Traits End Uses

Yearling Weight Add trait to run custom_column1 Add custom column to run

custom_column1 (active)

Under “Modify Existing Lists”, you can update custom column names

Figure 37 – Update custom column name

Modify Existing Lists

Modify existing list: Ram_CustomColumn (males: 6, females: 0)

Custom1	Custom2	Custom3	Custom4	Custom5	Custom6	Custom7	Custom8	Custom9
MyIndex								

Update Custom Column Names

Edit AnimalsDelete list

Similarly, by clicking the “Edit Animals” button you can edit custom column values.

Figure 38 – Change custom column values

Create New List

Modify Existing Lists

Modify existing list: Ram_CustomColumn

Custom1	Custom2	Custom3	Custom4	Custom5
MyIndex				

Update Custom Column Names

Edit AnimalsDelete list

Edit animals in group

ID	Sex	Minuse	Maxuse	AbsMinUse	Custom1
5046372012120652	1				123.3
6000012015150026	1				122.1
6011512015150106	1				121.5
6014422014140961	1				124.6
6090402012122295	1				125.7
6091472014140474	1				122.9

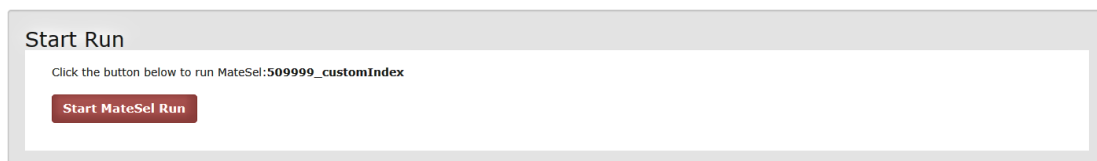
Put Animal IdAdd Animal

OKCancel

4. Start Run

Once the lists and parameters have been finalised click the “**Start MateSel Run**” button under the **Start Run** section to generate the input files and run MateSel.

Figure 40 – Start MateSel



Once you click the button, it can take anywhere from 10 minutes to hours to finish the process depending on the number of animals in the run and the structure of the parameters. The status of the run will be updated in the Run Detail as the process progresses.

The main status description:

- **INIT** = the run is created.
- **PREPARED** = All preparation of the Matesel is finished and it is ready to run.
- **RUNNING** = The Matesel is running. At this point, the Frontier starts to build.
- **COLLATE** = The Matesel finishes running and starts to organize the result.
- **FINISHED** = The Matesel finishes and the output is ready.
- **FAILED** = The Matesel failed. See the Console output to diagnose the error.

The frontier will be built under the “View Output” section, which is found under Run Output.

5. Run Output

The Run Output has two section: “View Output” and “Download Output”.

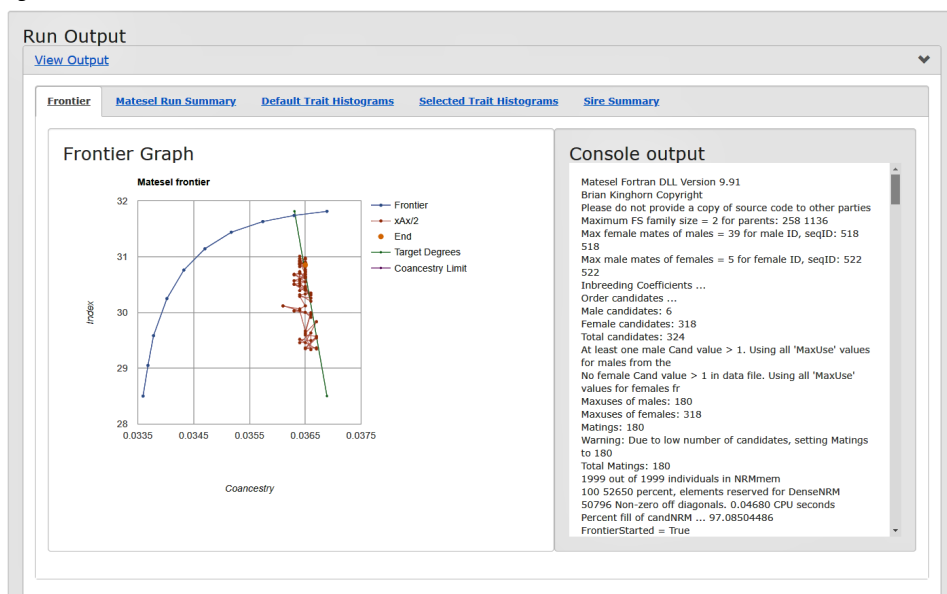
5.1 View Output

The View Output section categorizes the output in different tabs, which are Frontier, MateSel Run Summary, Default Trait Histograms, Selected Trait Histograms and Sire Summary.

5.1.1 Frontier

This section shows the frontier being built and Console output which helps you to diagnose any problems.

Figure 41 – Frontier



5.1.2 Matesel Run Summary

The Matesel Run Summary shows the parameters and constraints set for the run.

1. Parameters

Figure 42 – Parameters

Parameters	
Balance Strategy	Hard constraint on target degrees
Grouping	Off
Number of matings to be generated	2000
Maximum number of Generations	10000
Absolute Minimum New Generations	1000
Multiple EndUses	Off
TargetDegrees	10
Coancestry Limit	
Pressure on Coancestry ($\times A\% / 2$)	
Pressure on progeny inbreeding	0
Threshold for Progeny inbreeding level	0.24
Pressure on inbreeding threshold	0

2. Candidates

Figure 43 – Candidates

Candidates 	
Male candidates	6
Female candidates	318
Selected sires	6
Selected dams	180
Matings used	180
Balance Strategy	3
DE Generations	10001
Generations since last Update	10001

3. Targets

Target degrees and Achieved target degrees

If the MateSel run was set using a target degrees balance strategy these two figures are important.


- ✓ Target degrees describes the level you set and
- ✓ Achieved target degrees describes the exact level of target degrees that was achieved.

Target Coancestry and Achieved Coancestry

If the MateSel run was set using Coancestry as a balance strategy these two figures are important.

- ✓ Target Coancestry describes the level of Coancestry you set and
- ✓ Achieved Coancestry describes the level of coancestry that was achieved.

Figure 44 – Targets

Targets 	
Fitness	12.3977321386
Target degrees	10.000000
Achieved degrees	10.080457
Effective weight on Coancestry	-10.000000
Target Coancestry	0.075000
Achieved Coancestry	0.036472

4. Index constraints

Achieved Mean Progeny index: This indicates the mean index of all output matings achieved for the run. When you change parameters in the run this is a good indication if the result is going to achieve greater genetic gain or not.

Lowest selected male and Lowest selected female index: This gives the index value of the lowest performing animals selected to use in the run

Achieved Progeny Mean F: Mean F is the mean progeny inbreeding across all matings. Remember coancestry describes the level of inbreeding on a flock basis, whereas progeny Inbreeding (F) describes the progeny inbreeding for individual matings

Figure 45 – Index constraints


Index constraints 	
Weighting on Mean Progeny Index	1.000000
Achieved Mean Progeny Index	30.850054
Achieved Std Dev Progeny Index	5.968127
Lowest selected male index	22.680000
Lowest selected female index	11.530001

5. Inbreeding constraints

Maximum F achieved: The maximum F (Progeny Inbreeding) describes the maximum inbreeding level achieved for an individual mating.

Proportion of Matings over Max F: If you set a Max F threshold and use a soft balance strategy this number indicates the number matings that were over the maximum F thresh hold.

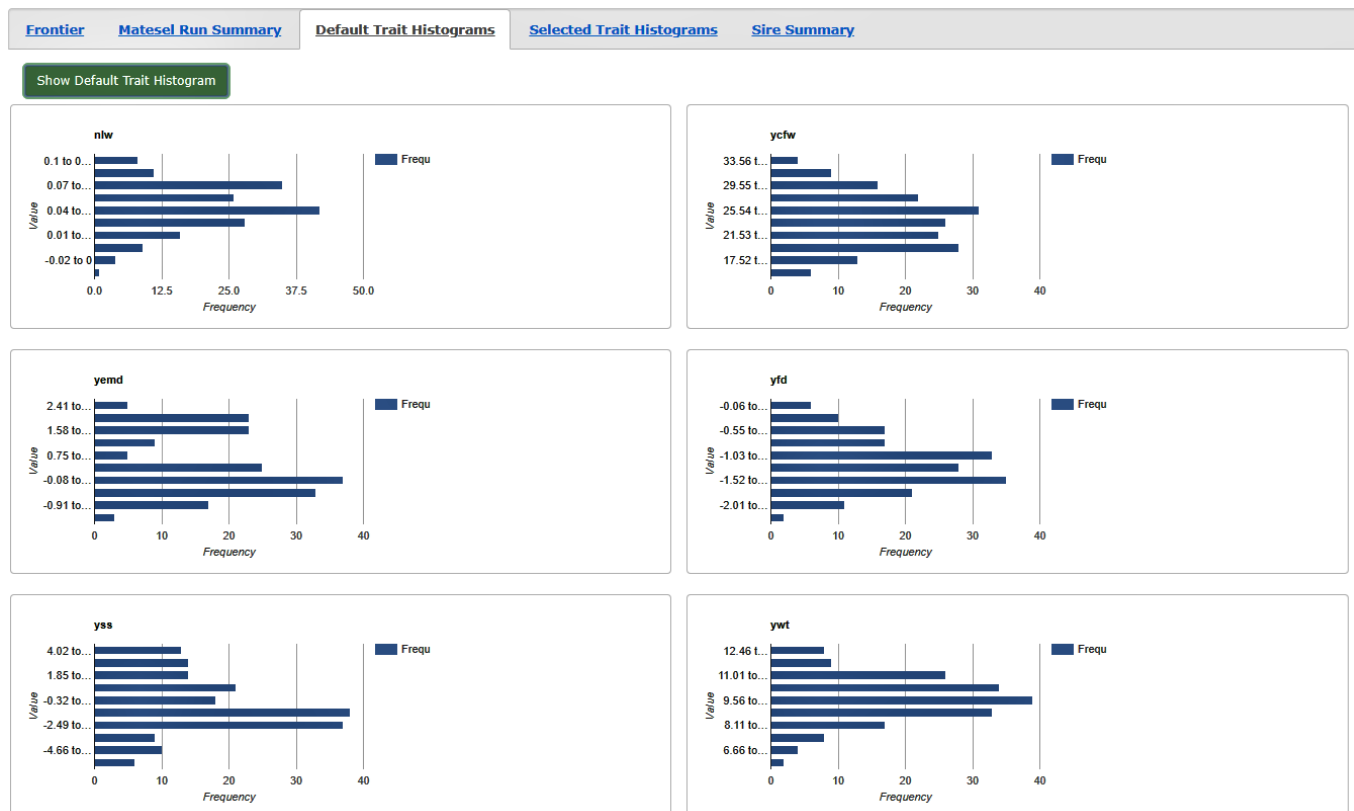
Figure 46 – Inbreeding constraints

Inbreeding constraints 	
Weighting on Progeny Mean F	0.000000
Achieved Progeny Mean F	0.008625
Random mating F	0.009181
MaxF weight	0.000000
MaxF threshold	0.240000
Maximum F achieved	0.080519
Proportion of matings over MaxF	0.000000
MaxF component criterion	0.000000

5.1.3 Default Trait Histograms

This section show Histograms of the main six traits for the analysis type. Click the “Show Default Traits Histogram” button to show the histograms.

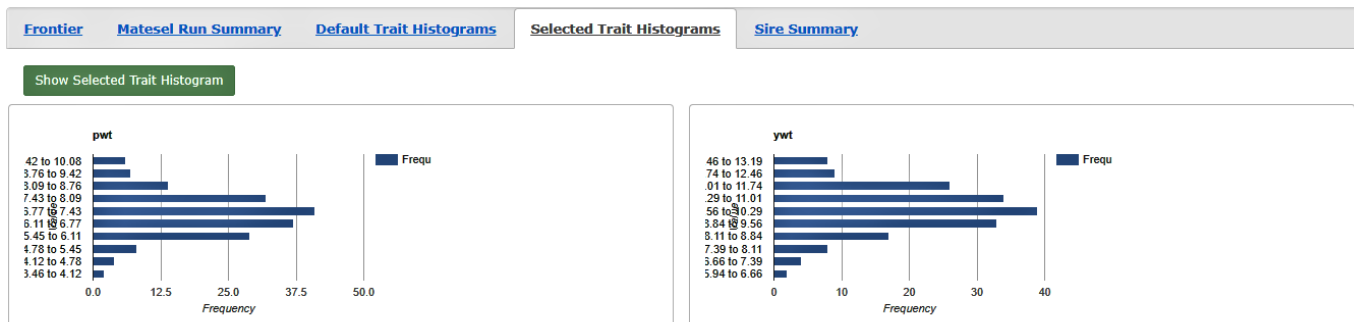
Figure 47 – Default Trait Histograms



5.1.4 Selected Trait Histograms

This section show Histograms of the selected traits. Click the “Show Selected Traits Histogram” button to show the histograms.

Figure 48 – Selected Trait Histograms



5.1.5 Sire Summary

This section summarises the usage of each of the sires and include groups and sire constraints.

Figure 49 – Sire Summary

Frontier Matesel Run Summary Default Trait Histograms Selected Trait Histograms Sire Summary										
Grouped usage					Group constraints			Sire constraints		
Sire	Sire group	Dam group	Index	Usage	Max Use	Min Use	Abs Min Use	Max Use	Min Use	Abs Min Use
504637-2012-120652	1	1		30	30	1	0			
600001-2015-150026	1	1		30	30	1	0			
601151-2015-150106	1	1		30	30	1	0			
601442-2014-140961	1	1		30	30	1	0			
609040-2012-122295	1	1		30	30	1	0			
609147-2014-140474	1	1		30	30	1	0			

5.2 Download Output

In the Download Output section, there are two output files that can be downloaded.

1. MateselMatings.xlsx – this is an Excel file which contains the mating list and mid-parent values.
2. MateselSettings.zip – zipped file that contains the Matesel configuration files.

Figure 50 – Download Output

Run Output	
View Output	
Download Output	
Link	Output file description
MateselMatings.xlsx	Mating list and midparent figures from run
MateselSettings.zip	Matesel configuration files from run

NOTE: The results will also be emailed to you, which includes a sire summary, the list of matings and the output console of the system so you can diagnose any problems.

The list of out-matings emailed contains all of the information for individual matings. This includes the sire and the dam, the predicted ASBVs and index values for each mating and the level of inbreeding per mating (ms_prog_f).

5.3 Print Output

The Print Output section shows all of the above results in a printable format. You can directly print it by clicking the “Print Output” button.

5.4 Visually analysing the output

Through the use of the MateSel Results Tool, you are able to import the OutMatings file from the MateSel run and visually analysis the results.

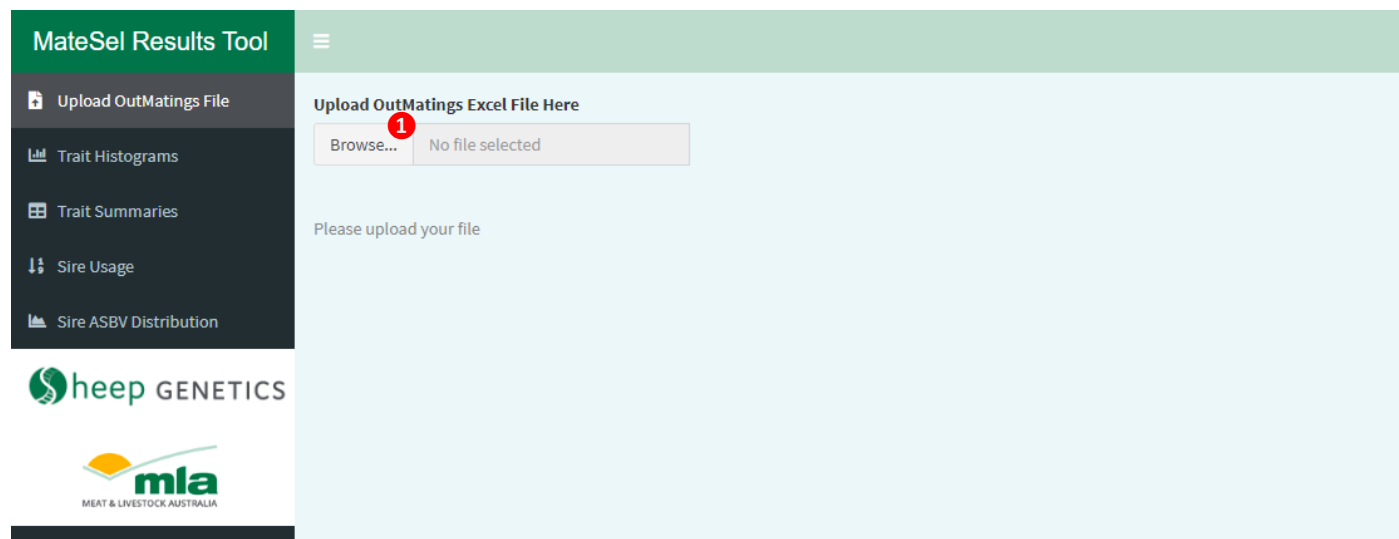
The link to this tool can be found below, or contact Sheep Genetics.

[MateSel Results Tool \(shinyapps.io\)](#)

Download and save the OutMatings file from the MateSel run as described above

Open the Result tool and upload the file from your desktop ¹ (see Figure 51)

Figure 51: Upload the Outmatings file to the MateSel results tool.



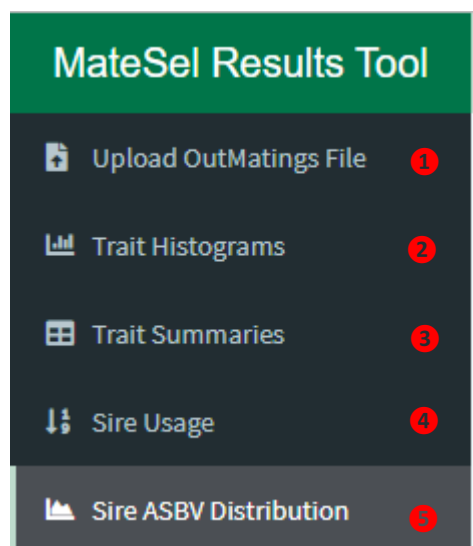
Once the file is uploaded it will display the Mating allocations as well as the estimated progeny ASBV outcome from that mating.

On the right hand side of the screen are tab options to investigate and analysis the results further (see Figure 52)

These include:

- Upload Outmating file ¹ (described above)
- Trait histograms ² (described below)
- Traits summaries ³, the minimum, maximum and average mid-parent ASBV for each trait. Can search for the trait of interest using the search bar.
- Sire usage ⁴, number of times each sire is used within the mating outcomes.
- Sire ASBV Distributions ⁵ (described below).

Figure 52: Investigation tabs available



Selecting on the **“Trait Histograms”** tab ¹ (see Figure 53) you can graphically see the distribution and frequency of the mid parent breeding value for the trait selected. Select the trait of interest from the drop down ².

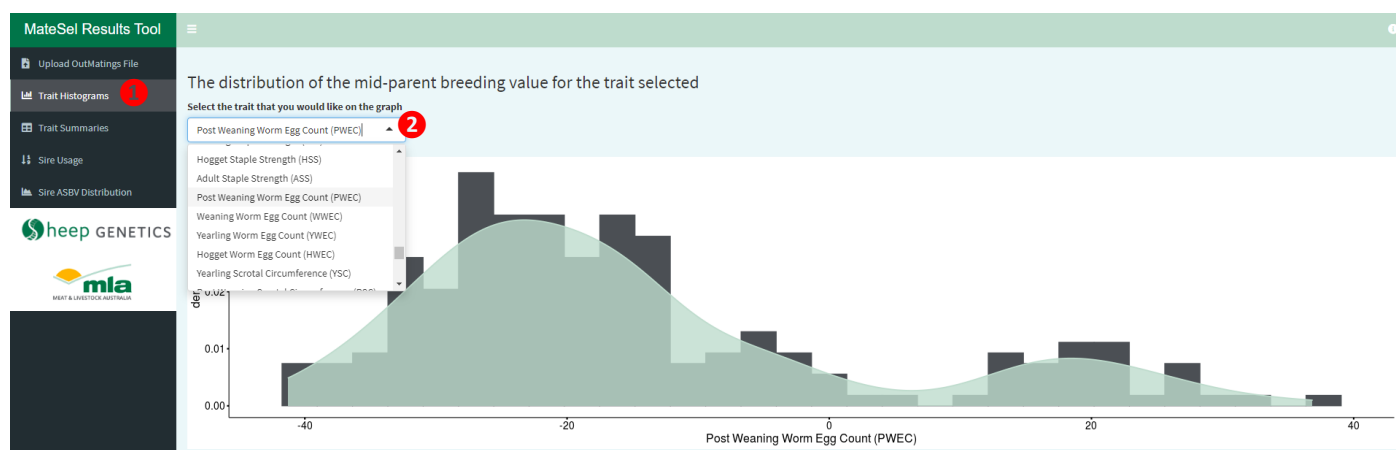
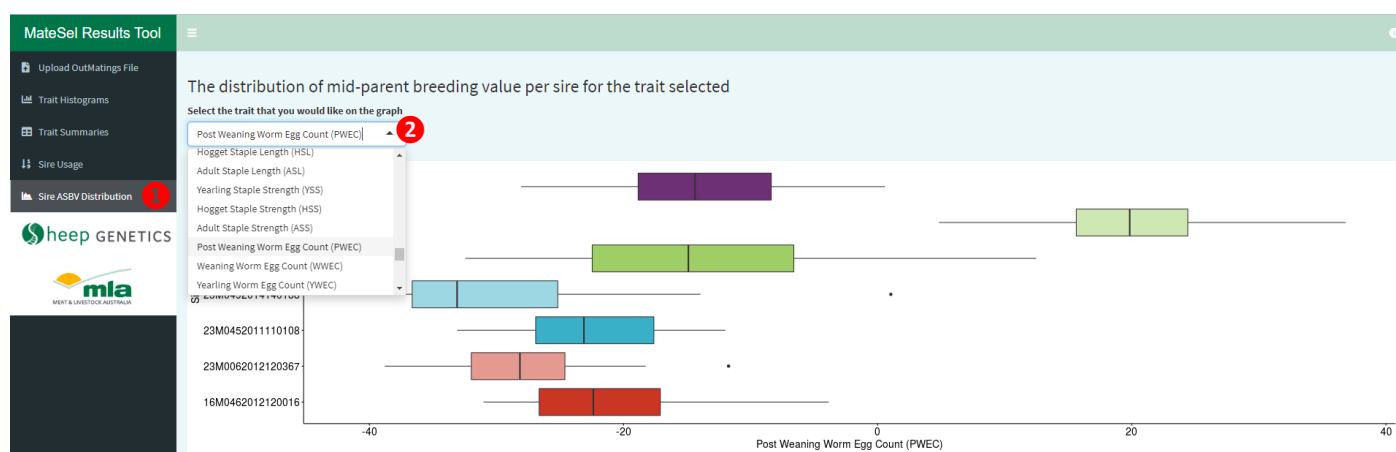


Figure 53:

Selecting on the **“Sire ASBV Distribution”** tab ¹ you can graphically see the distribution of the mid parent breeding value per sire for the trait selected. Select the trait of interest from the drop down ².



More information

- Why use Matesel— MateSel pre-reading guide
- Technical information—Instructions for MateSel by Brian and Sandy Kinghorn.
- Technical support—Sheep Genetics

Glossary/Definitions

Inbreeding (F)

The mating of closely related individuals, as cousins, sire-daughter, brother-sister, or self-fertilized plants, which tends to increase the number of individuals that are homozygous for a trait and therefore increases the appearance of recessive traits.

Coancestry

A measure of the degree of common ancestry of two (more) individuals.

Balance Strategy

This relates to management of the balance between genetic gain (predicted index value in progeny) and parental coancestry, whose outcome is illustrated in the graph to the upper right of the MateSel window.

Weight on coancestry ($xAx/2$)

This is weighting value I, which is only invoked for Balance Strategy 0.

Max permissible coancestry ($xAx/2$)

This is the limit on parental coancestry, which is only used in Balance Strategies 1 and 2.

Target Degrees (TD)

TD is used to target a relationship between Genetic Gain (Progeny Index, xG) and parental coancestry ($xAx/2$). It is only used for Balance Strategies 3 to 6.

Weight on progeny inbreeding (F)

This is the weighting value used to penalise inbreeding (F) in the progeny that derive from the matings to be made. Use a negative value to put downward pressure on short-term inbreeding. Suggestion: start with a value of -1. [Note that this has little impact on long-term inbreeding. In fact if you aim for *high progeny inbreeding* the program will usually seek many males as parents in order to achieve widespread full-sib mating, and this increases effective population size so that *long-term inbreeding goes down*. The importance of progeny inbreeding is often exaggerated.]

Progeny inbreeding (F) threshold

This is the value of progeny inbreeding that you prefer not to exceed for any individual mating.

Weight on inbreeding (F) threshold

This is the weighting applied for breaking of the Progeny F threshold. The criterion to which it is applied is the mean across all matings of the squared deviation from half of the threshold for matings that break the threshold.

Suggestion: if you use this feature, start with a value of -1.

Matings to be made

This is the number of matings to be made. It is typically the number of breeding females, but for IVF matings it is the number of oocytes fertilized. [Under Grouping, the numbers of matings is calculated from grouping information provided, overriding what you enter here.]

NRM

Numerator Relationship Matrix.

NRM limit

[Use only if needed, else leave at zero] For large problems you can speed up operation by setting to zero any numerator relationship value (between two individuals) that is below this value. Elements with a value of zero are not addressed in calculating $x'Ax$, and so setting low values to zero speeds up operation.

NRM generations

This is the number of generations back from each candidate in the supplied pedigree that is used in the calculation of relationships between individuals. Fewer generation gives faster calculation of relationships at the start of the program, and probably faster operation thereafter due to a higher proportion of relationship values that are perceived to be zero. [Note: You can also invoke this reduction in Pedigree Viewer, using Prune Pedigree on the Tools Menu, whereby you can save your pruned file.]

Grouping

This feature gives ability to define group membership for each candidate, set mating numbers for each group, set mating permissions on a male group by female group basis, and other grouping functions. See “Grouping” for more details.

Frontier degree gap

This is the gap between points generated to draw the frontier of possible responses in Index and coancestry.

Frontier 0 degree generations

The number of generations of the Differential Evolution algorithm to be used to generate the 0 degree point, which reflects full emphasis on high Progeny Index. [This is only used when Grouping = True, else a truncation selection approach is used.]

Frontier 90 degree generations

The number of generations of the Differential Evolution algorithm to be used to generate the 90 degree point, which reflects full emphasis on low coancestry.

Frontier xx degree generations

The number of generations of the Differential Evolution algorithm to be used to generate each intermediate degree point.

Target % converged

This is a component of the overall stopping criterion. The percentage of the currently predicted asymptotic maximum fitness that has been reached is calculated each time a better solution is found, and also each 1000 generations. When the value in this textbox is exceeded, then this component criterion has been met. [Note that it can latterly be no longer met if the predicted asymptote increases sufficiently.] See “Diagnosis of Convergence” for details.

% since last change

This component criterion is met if there has not been a better solution over the last x% generations of the last generation when there was an improvement in DE algorithm fitness

No change generations

This component criterion is met if there has not been a better solution over the last x generations.

Minimum generations

This is the absolute minimum number of generation that has to be completed before stopping of the DE algorithm.

Maximum generations

This is the maximum number of generation that the algorithm will run for. However, this number can be overrun if “Do not stop till “Stop” clicked” is checked.