*2023 Beef Improvement Federation Symposium*
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# Precision Matching of Objectives and Technologies in the Implementation of Breeding Programs

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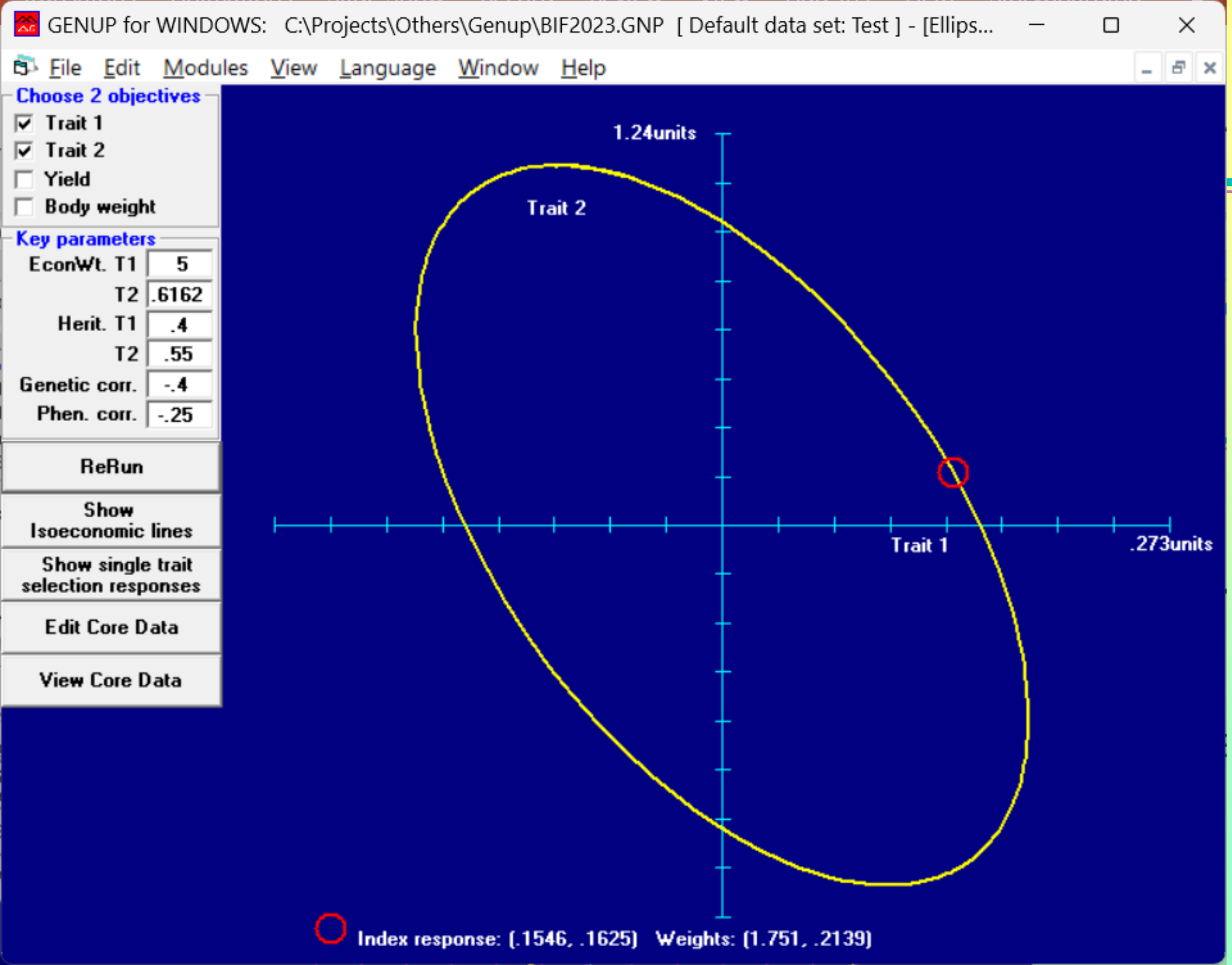
*[1] University of New England, Australia*
*[2] MateSel, Australia*

# We need ***precision*** in these key questions …

- Where to go ? … Objectives
- How to get there ? … Technologies

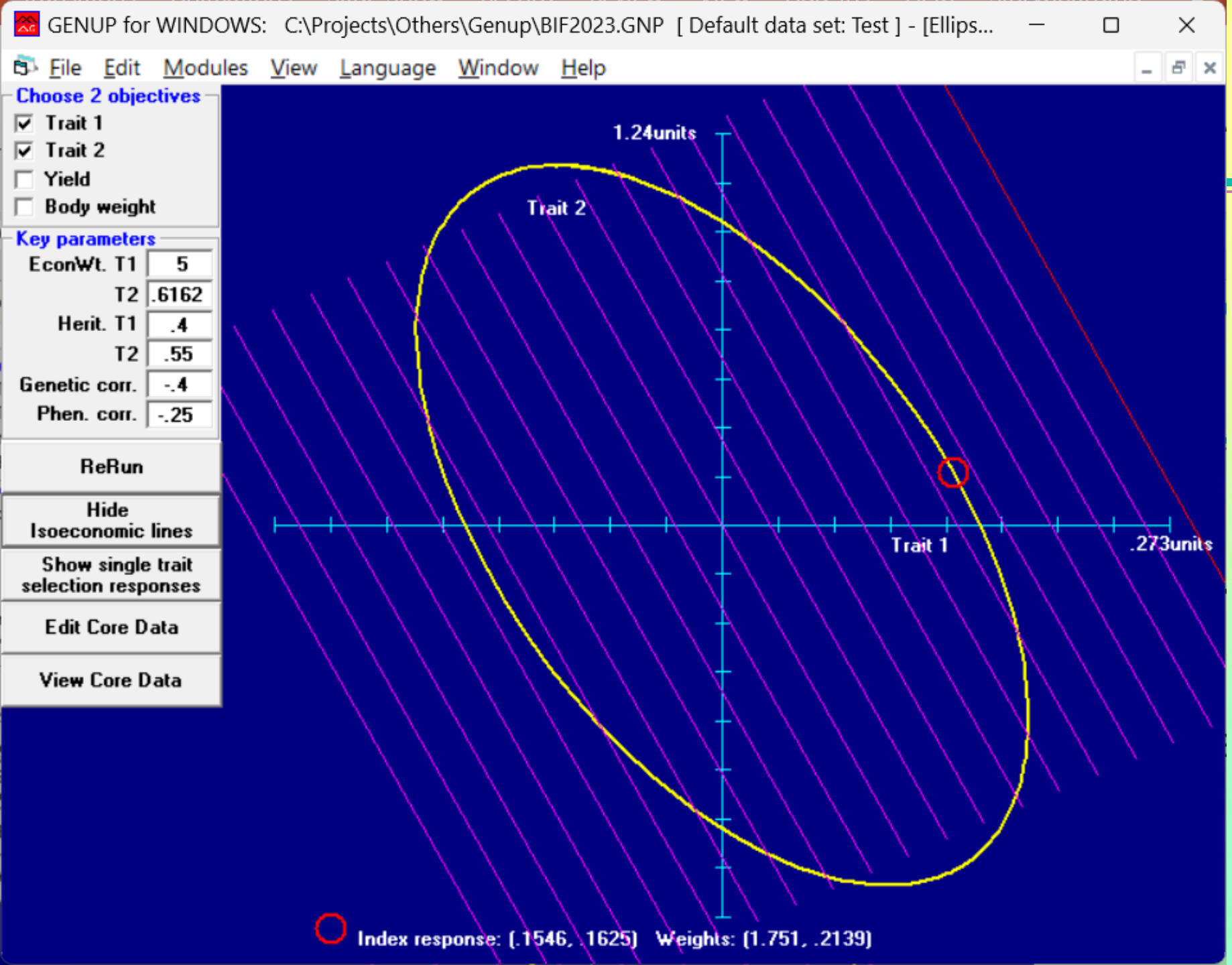
- How to get back ?




MateSel

# Where to go

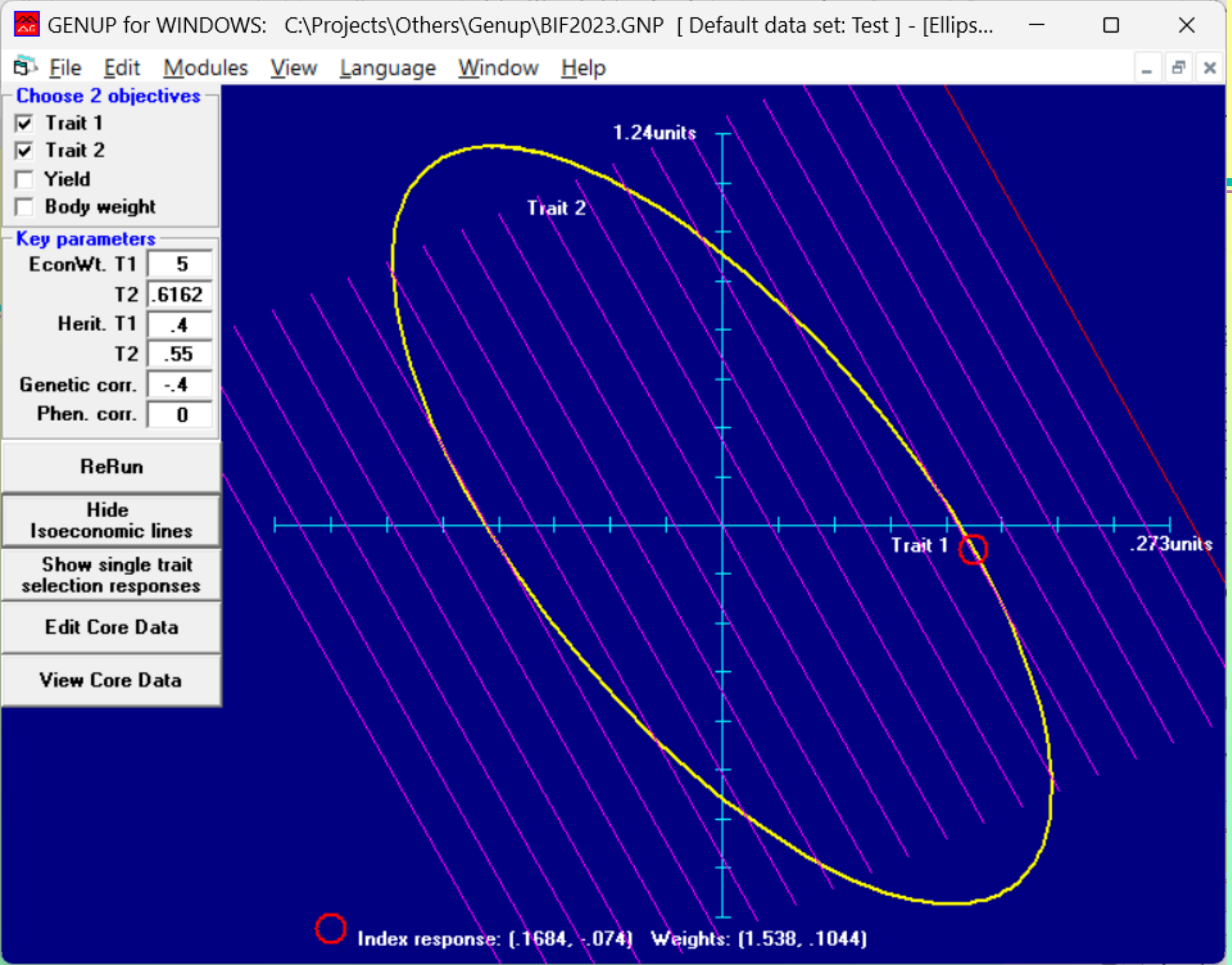
Just one example




MateSel

# Where to go

Just one example




MateSel

# Where to go

Just one example

# Animal Breeding questions ...

MateSel

- Where to go ? **Explore different directions** – different emphasis on each trait or genetic marker, different emphasis on diversity/inbreeding, different patterns of mating constraints, different patterns of use of AI & IVF, etc.
- How to get there ? **Be precise** – use all available information on EBVs/EPDs, genomic/pedigree relationships, animal locations, logistical constraints, costs etc. in a balanced manner to best target the chosen direction.

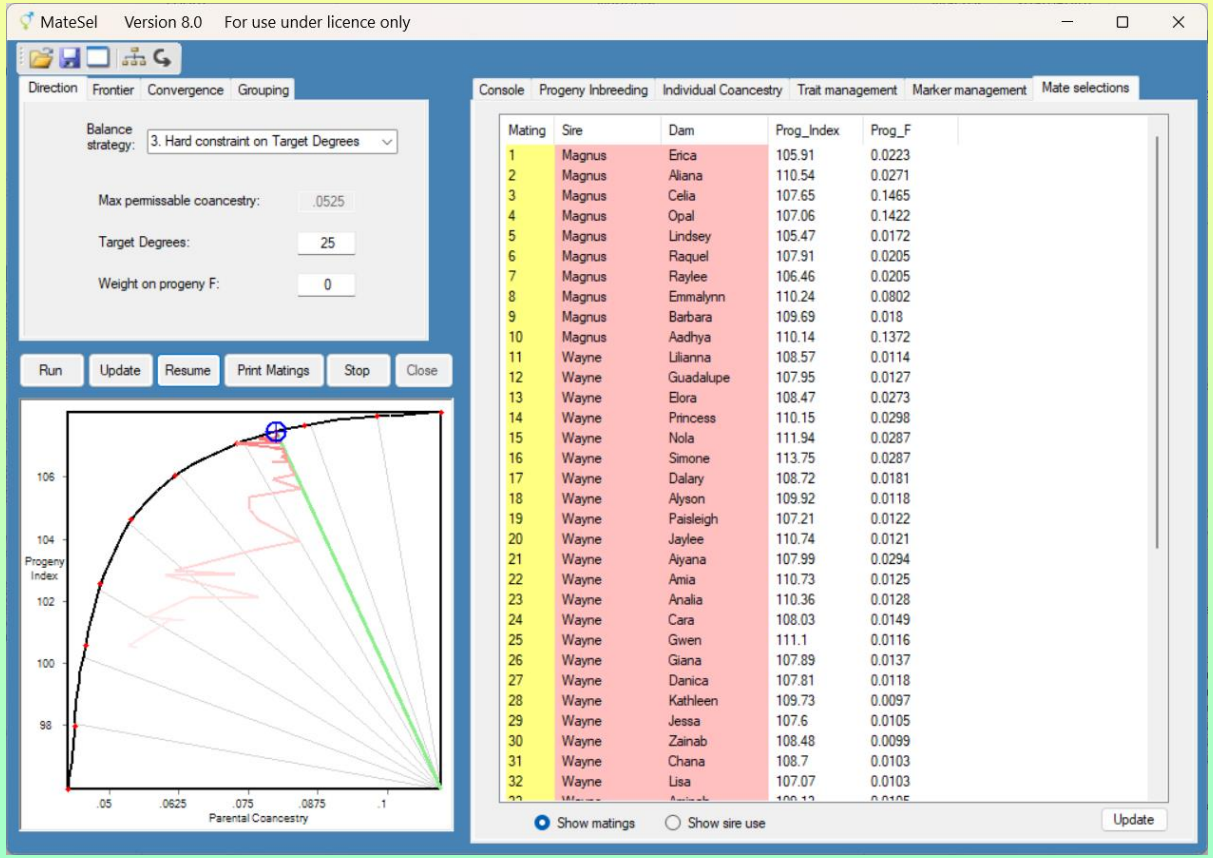
# Technical requirements

1. The breeder should have '**ownership**' of the result. This brings **relevance**.
   - a fancy computer tool is of little value if it is not **relevant** to the needs of the breeder.

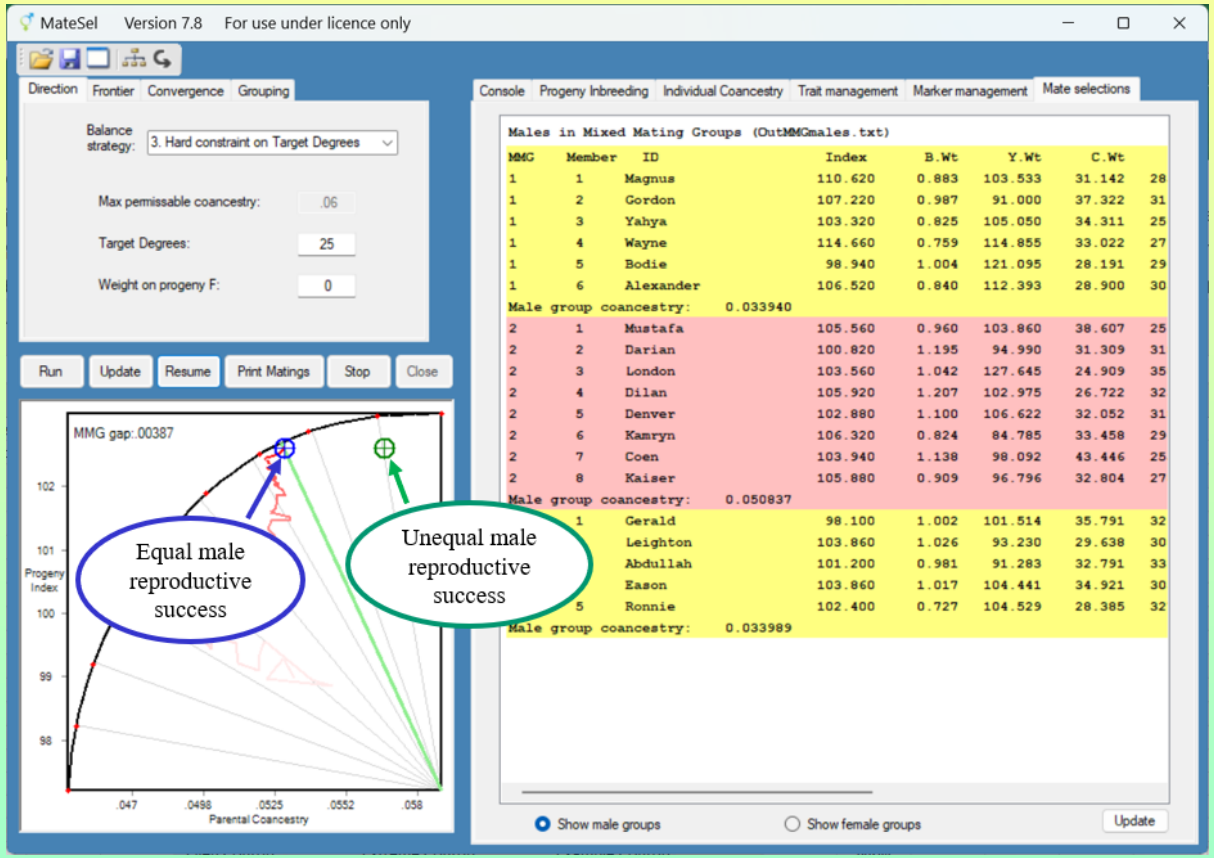
2. The breeder needs power to target **a wide range of possible outcomes**.
   - As simple as possible
   - As complex as necessary

# Example illustrations of MateSel features

## Basic operations: Single-sire mating *vs*. Multi-sire mating




Single-sire matings. You can dictate the range in number of females per bull




Multi-sire mating groups. Male syndicate groups only shown in this screenshot.

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Direction | Frontier | Convergence | Grouping

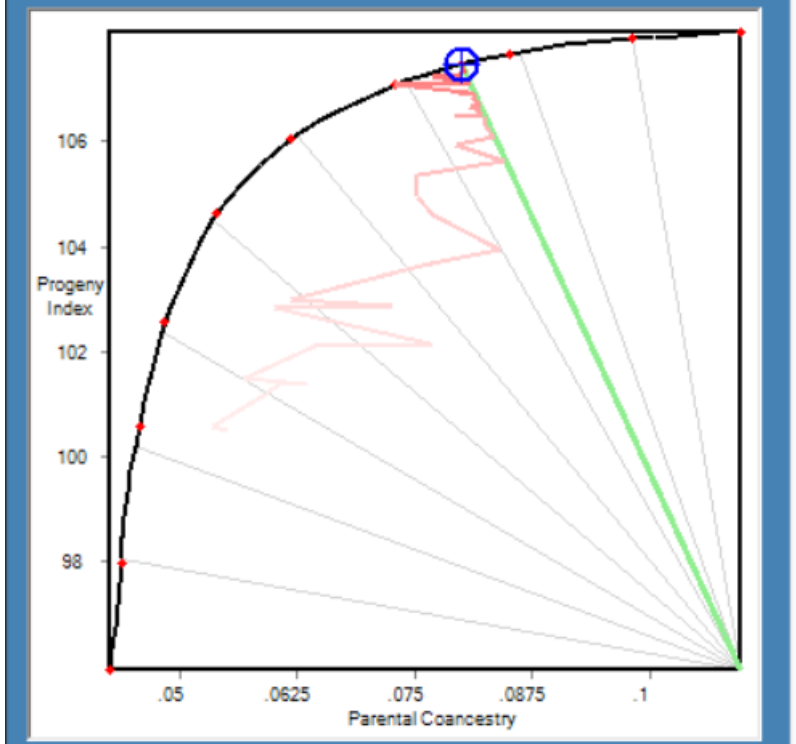
Balance strategy: 3. Hard constraint on Target Degrees

Max permissable coancestry: .0525

Target Degrees: 25

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections

| Mating | Sire | Dam | Prog_Index | Prog_F |
|---|---|---|---|---|
| 1 | Magnus | Lilianna | 106.55 | 0.0266 |
| 2 | Magnus | Meadow | 106.28 | 0.1418 |
| 3 | Magnus | Paisleigh | 105.19 | 0.027 |
| 4 | Magnus | Celia | 107.65 | 0.1465 |
| 5 | Magnus | Opal | 107.06 | 0.1422 |
| 6 | Magnus | Gwen | 109.08 | 0.0248 |
| 7 | Magnus | Sariyah | 106.71 | 0.1422 |
| 8 | Magnus | Chana | 106.68 | 0.0256 |
| 9 | Magnus | Lisa | 105.05 | 0.0256 |
| 10 | Magnus | Barbara | 109.69 | 0.018 |
| 11 | Wayne | Guadalupe | 107.95 | 0.0127 |
| 12 | Wayne | Elora | 108.47 | 0.0273 |
| 13 | Wayne | Clementine | 107.8 | 0.0323 |
| 14 | Wayne | Nola | 111.94 | 0.0287 |
| 15 | Wayne | Lina | 106.93 | 0.0099 |
| 16 | Wayne | Erica | 107.93 | 0.0111 |
| 17 | Wayne | Aliana | 112.56 | 0.0116 |
| 18 | Wayne | Alyson | 109.92 | 0.0118 |
| 19 | Wayne | Jaylee | 110.74 | 0.0121 |
| 20 | Wayne | Frankiee | 108.74 | 0.0143 |
| 21 | Wayne | Amia | 110.73 | 0.0125 |
| 22 | Wayne | Hadlee | 108.17 | 0.0294 |
| 23 | Wayne | Giana | 107.89 | 0.0137 |
| 24 | Wayne | Danica | 107.81 | 0.0118 |
| 25 | Wayne | Harleigh | 108.44 | 0.0105 |
| 26 | Wayne | Raquel | 109.93 | 0.0099 |
| 27 | Wayne | Raylee | 108.48 | 0.0099 |
| 28 | Wayne | Aminah | 109.13 | 0.0105 |
| 29 | Wayne | Emmalynn | 112.26 | 0.0184 |
| 30 | Wayne | Patricia | 108.11 | 0.011 |
| 31 | Wayne | Avalyn | 107.88 | 0.0213 |
| 32 | Wayne | Jana | 107.52 | 0.032 |

Show matings | Show sire use

Update

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Direction | Frontier | Convergence | Grouping

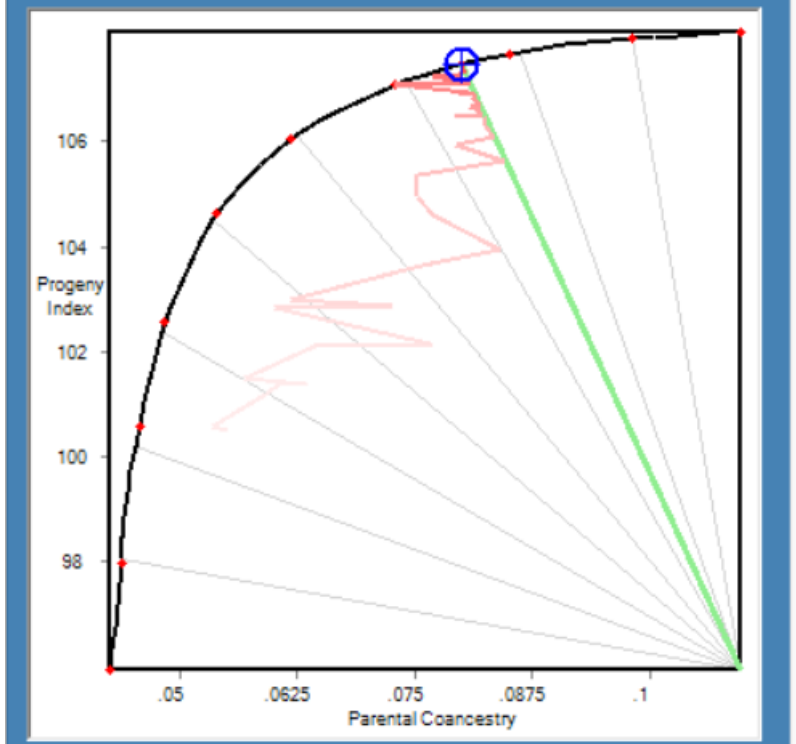
Balance strategy: 3. Hard constraint on Target Degrees

Max permissable coancestry: .0525

Target Degrees: 25

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections

| Females i... | Index | CoanCand | CoanSel | GrandSire | AbsMin | Min | Max | < Uses |
|---|---|---|---|---|---|---|---|---|
| Wayne | 114.66 | 0.0241 | 0.1438 | Gannon | 0 | 0 | 25 | 25 |
| Magnus | 110.62 | 0.0564 | 0.1 | Cassius | 0 | 0 | 25 | 10 |
| Gordon | 107.22 | 0.0547 | 0.067 | Rodney | 0 | 0 | 25 | 6 |
| Alexander | 106.52 | 0.0468 | 0.0618 | Rodney | 0 | 0 | 25 | 4 |
| Mustafa | 105.56 | 0.0542 | 0.045 | Xzavier | 0 | 0 | 25 | 2 |
| Dilan | 105.92 | 0.0567 | 0.0479 | Zyaire | 0 | 0 | 25 | 2 |
| Kamryn | 106.32 | 0.0553 | 0.0539 | Xzavier | 0 | 0 | 25 | 1 |

Show matings | Show sire use | Update

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Direction | Frontier | Convergence | Grouping

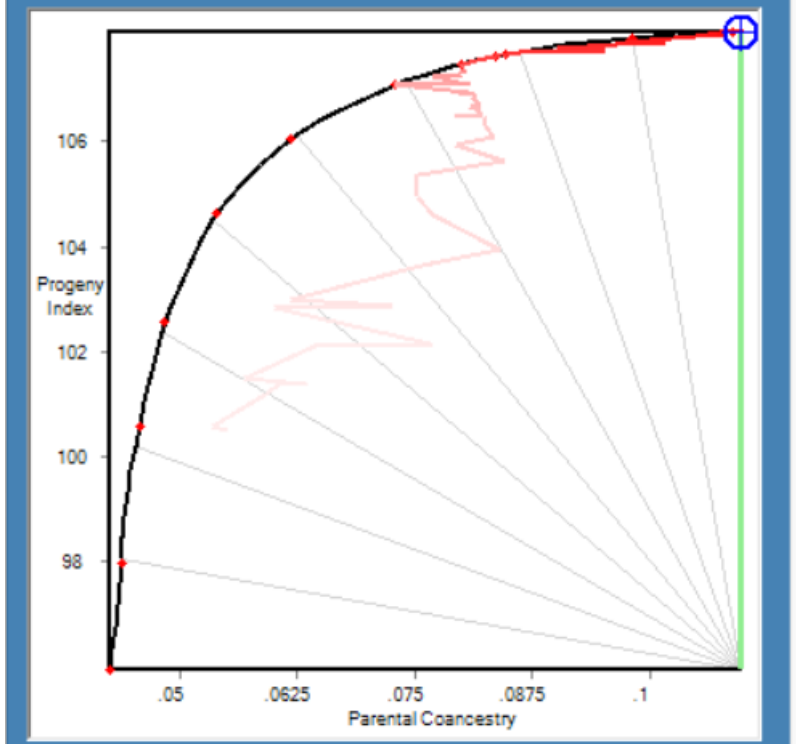
Balance strategy: 3. Hard constraint on Target Degrees

Max permissable coancestry: .0525

Target Degrees: 0

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections

| Females i... | Index | CoanCand | CoanSel | GrandSire | AbsMin | Min | Max | < Uses |
|---|---|---|---|---|---|---|---|---|
| Magnus | 110.62 | 0.0564 | 0.1757 | Cassius | 0 | 0 | 25 | 25 |
| Wayne | 114.66 | 0.0241 | 0.1469 | Gannon | 0 | 0 | 25 | 25 |

Show matings | Show sire use | Update

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Direction | Frontier | Convergence | Grouping

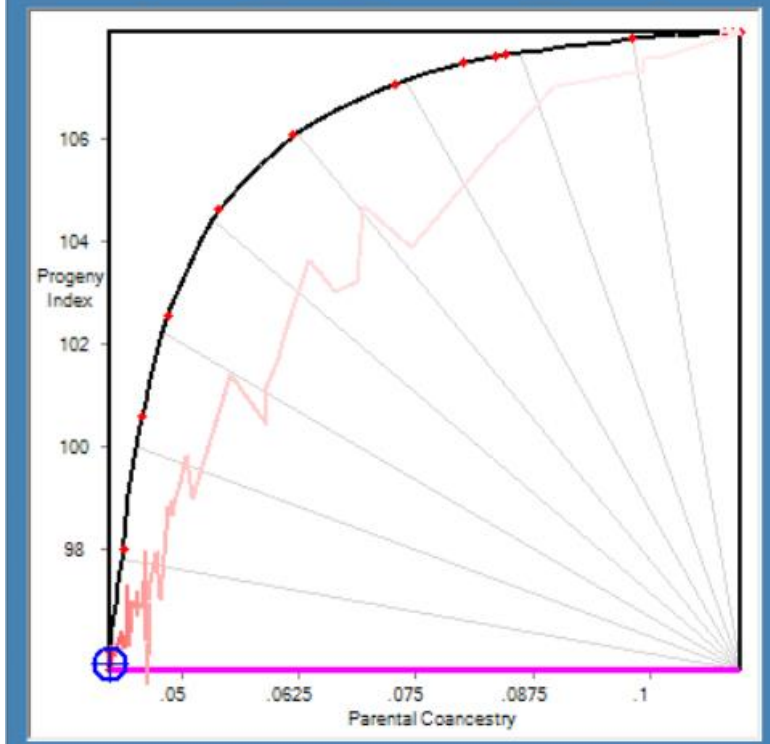
Balance strategy: 3. Hard constraint on Target Degrees

Max permissable coancestry: .0525

Target Degrees: 90

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections

| Females i... | Index | CoanCand | CoanSel | GrandSire | AbsMin | Min | Max | < Uses |
|---|---|---|---|---|---|---|---|---|
| Jordy | 83.04 | 0.019 | 0.0445 | Juelz | 0 | 0 | 25 | 6 |
| Wayne | 114.66 | 0.0241 | 0.0408 | Gannon | 0 | 0 | 25 | 4 |
| Will | 87.66 | 0.0344 | 0.0453 | Cory | 0 | 0 | 25 | 4 |
| Darian | 100.82 | 0.0266 | 0.0428 | Joziah | 0 | 0 | 25 | 3 |
| Bodie | 98.94 | 0.0266 | 0.0428 | Joziah | 0 | 0 | 25 | 3 |
| Gibson | 84.4 | 0.0373 | 0.0425 | Augustine | 0 | 0 | 25 | 3 |
| Shiloh | 89.38 | 0.0455 | 0.0445 | Rey | 0 | 0 | 25 | 2 |
| Denver | 102.88 | 0.0525 | 0.0437 | Zyaire | 0 | 0 | 25 | 2 |
| Gerald | 98.1 | 0.0416 | 0.042 | Terrance | 0 | 0 | 25 | 2 |
| Jaziel | 97.88 | 0.0523 | 0.0429 | Chris | 0 | 0 | 25 | 1 |
| Abdullah | 101.2 | 0.0523 | 0.0429 | Chris | 0 | 0 | 25 | 1 |
| Blaze | 94.54 | 0.0511 | 0.0445 | Aron | 0 | 0 | 25 | 1 |
| Gordon | 107.22 | 0.0547 | 0.0426 | Rodney | 0 | 0 | 25 | 1 |
| London | 103.56 | 0.0498 | 0.0432 | Emery | 0 | 0 | 25 | 1 |
| Merrick | 93.36 | 0.0437 | 0.0423 | Chris | 0 | 0 | 25 | 1 |
| Ronnie | 102.4 | 0.0492 | 0.0436 | Keanu | 0 | 0 | 25 | 1 |
| Konnor | 84.68 | 0.0512 | 0.045 | Shiloh | 0 | 0 | 25 | 1 |
| Dangelo | 83.6 | 0.0496 | 0.0452 | Shiloh | 0 | 0 | 25 | 1 |
| Kamryn | 106.32 | 0.0553 | 0.0434 | Xzavier | 0 | 0 | 25 | 1 |
| Shaun | 103.34 | 0.0562 | 0.0437 | Xzavier | 0 | 0 | 25 | 1 |
| Coen | 103.94 | 0.0556 | 0.0439 | Felipe | 0 | 0 | 25 | 1 |
| Leighton | 103.86 | 0.0542 | 0.044 | Xzavier | 0 | 0 | 25 | 1 |
| Mustafa | 105.56 | 0.0542 | 0.0431 | Xzavier | 0 | 0 | 25 | 1 |
| Nova | 88.8 | 0.0486 | 0.0423 | Darrell | 0 | 0 | 25 | 1 |
| Dilan | 105.92 | 0.0567 | 0.0447 | Zyaire | 0 | 0 | 25 | 1 |
| Yahya | 103.32 | 0.0487 | 0.0424 | Chris | 0 | 0 | 25 | 1 |
| Alexander | 106.52 | 0.0468 | 0.0433 | Rodney | 0 | 0 | 25 | 1 |
| Shepard | 100.2 | 0.0543 | 0.0429 | Xzavier | 0 | 0 | 25 | 1 |
| Eason | 103.86 | 0.0563 | 0.0441 | Zyaire | 0 | 0 | 25 | 1 |
| Leroy | 87.42 | 0.0501 | 0.0423 | Darrell | 0 | 0 | 25 | 1 |

○ Show matings ◉ Show sire use

Update

B.Wt

Resume

Decrease variation

- Increase mean
- Decrease mean
- Increase variation
- Decrease variation
- Increase variation about optimum
- Decrease variation about optimum
- Set minimum value at boundary
- Set maximum value at boundary
- Target bimodality
- Tactical Desired Gains upwards
- Tactical Desired Gains downwards
- Tactical Desired Gains stabilising

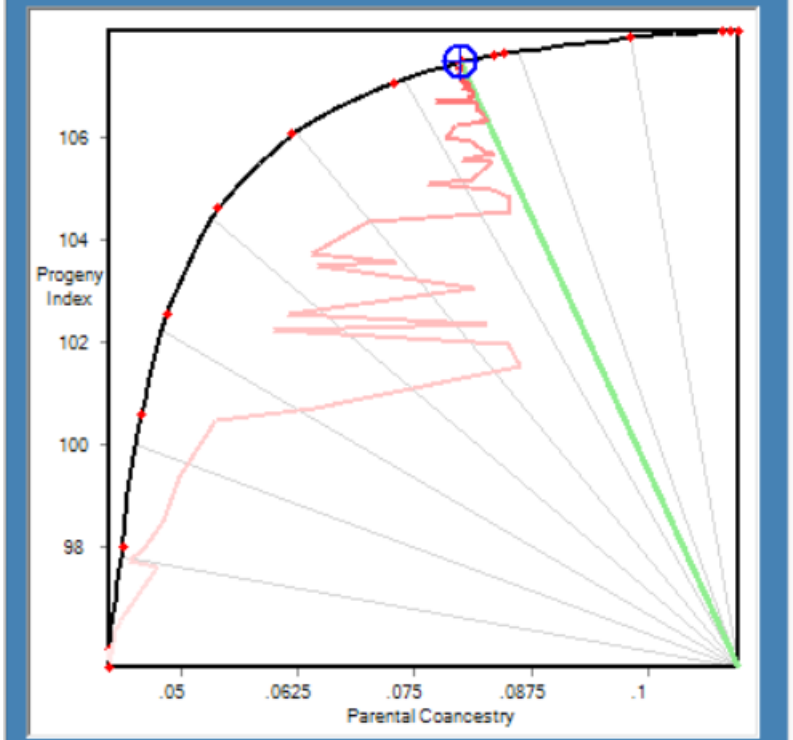
Target Degrees

.0525

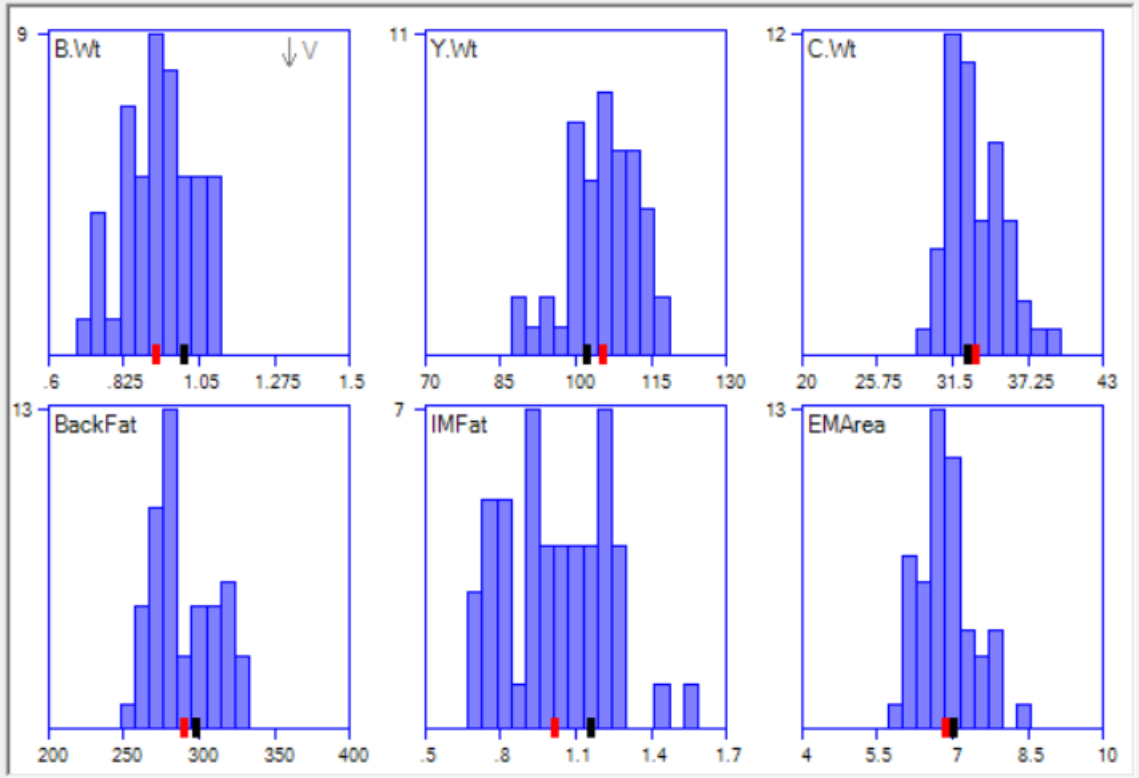
25

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections



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Direction | Frontier | Convergence | Grouping

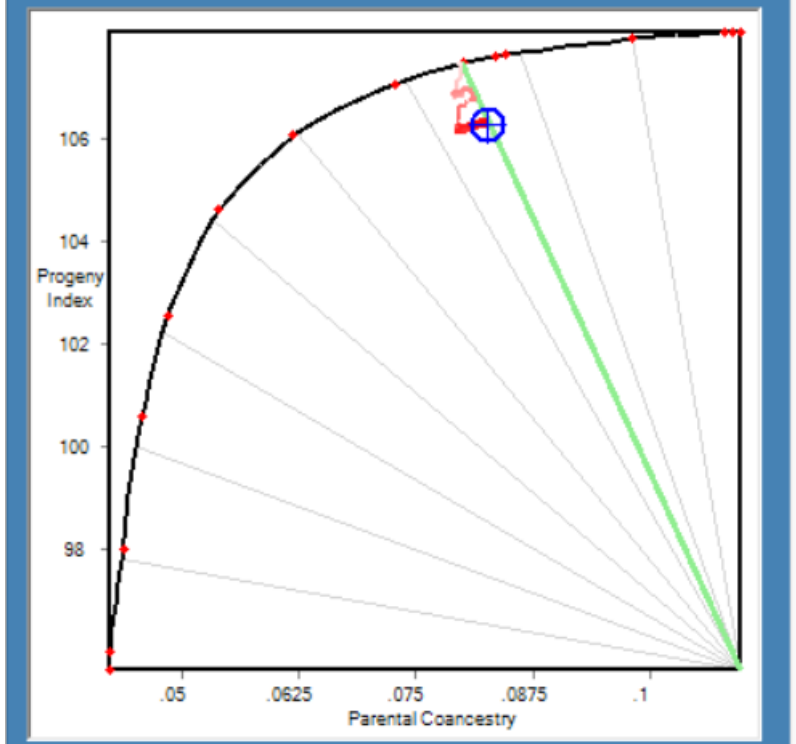
Balance strategy: 3. Hard constraint on Target Degrees

Max permissable coancestry: .0525

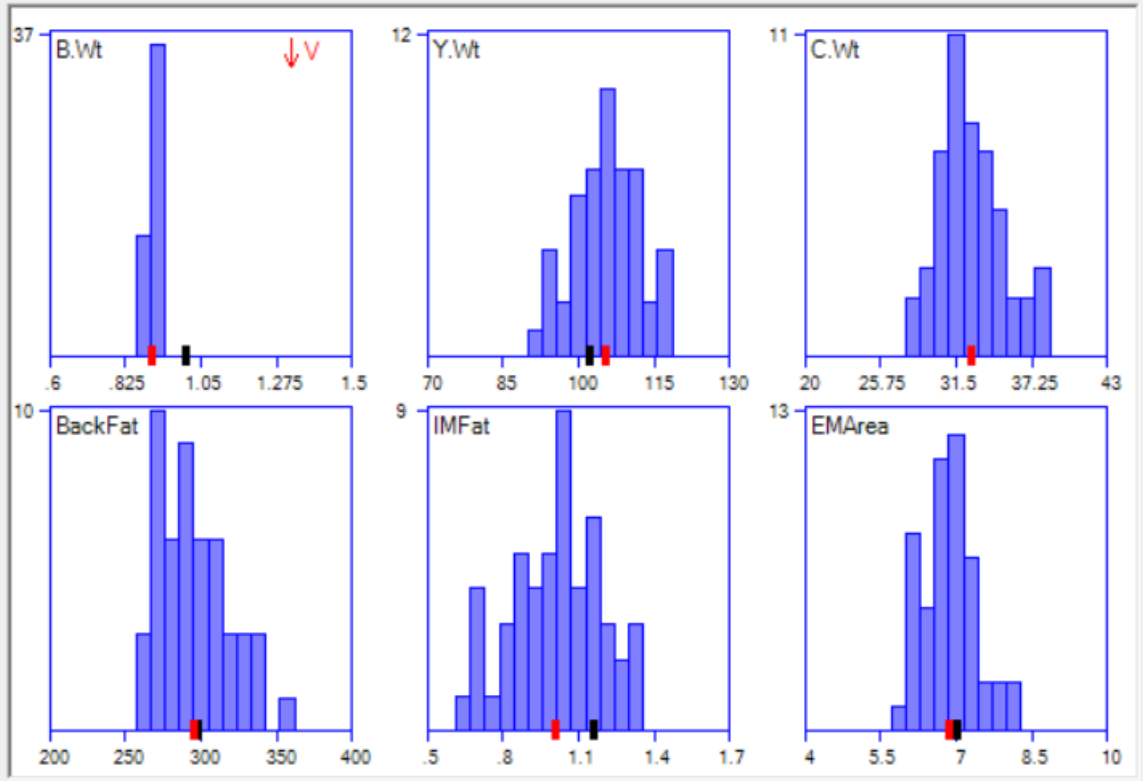
Target Degrees: 25

Weight on progeny F: 0

Run | Update | Resume | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections



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Direction | Frontier | Convergence | Grouping

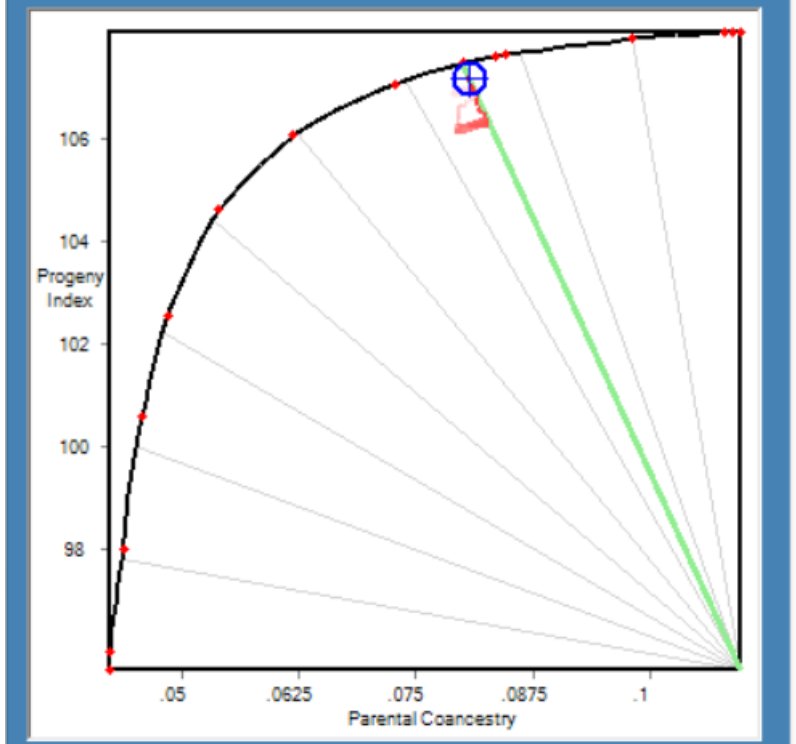
Balance strategy: 3. Hard constraint on Target Degrees

Max permissable coancestry: .0525

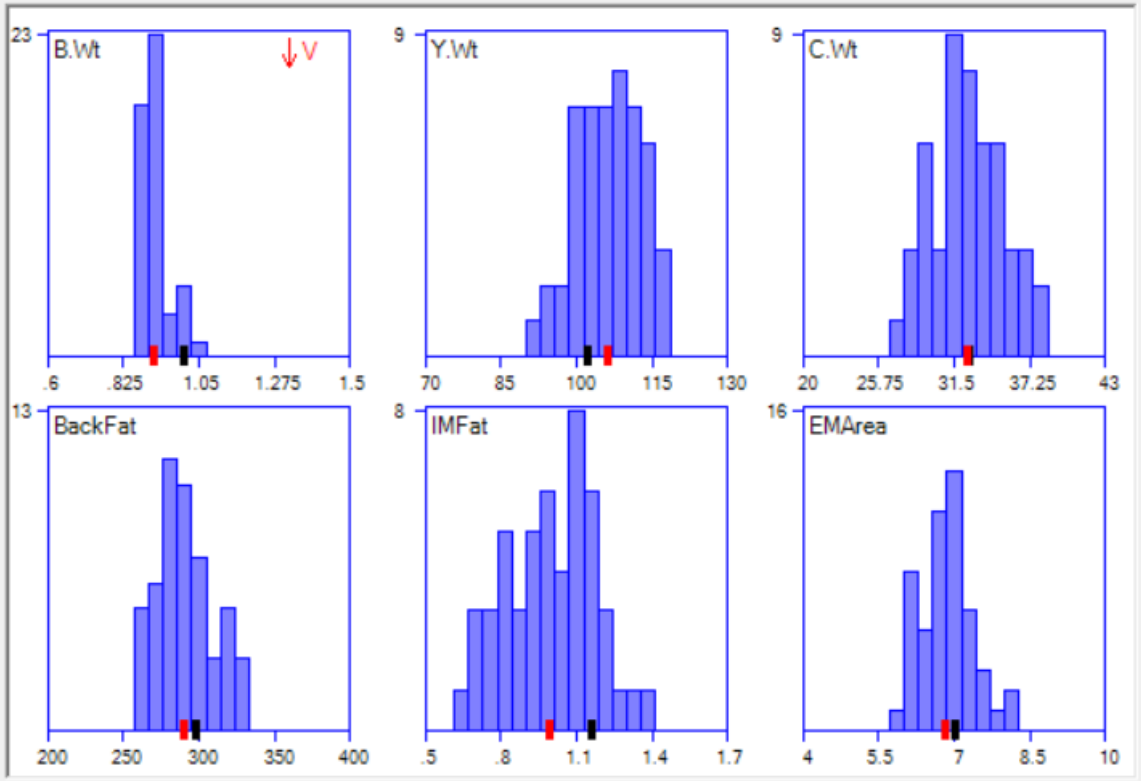
Target Degrees: 25

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections



IMFat | Resume

Target bimodality

Invoke | Weighting: 1

Target lower mean (Click-L): .8128

Target upper mean (Click-R): 1.172

Target percent in upper group: 50

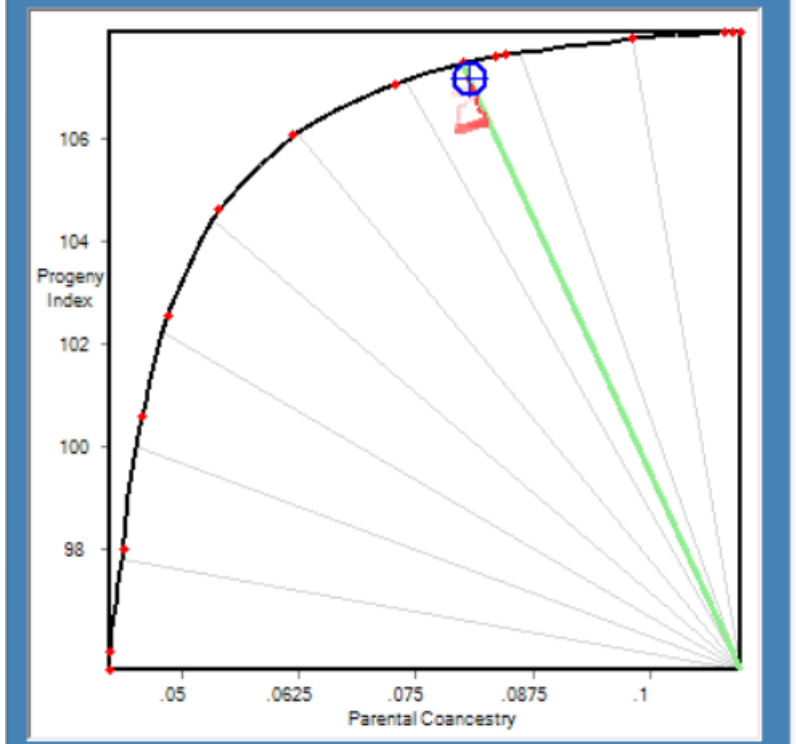
arget Degrees

.0525

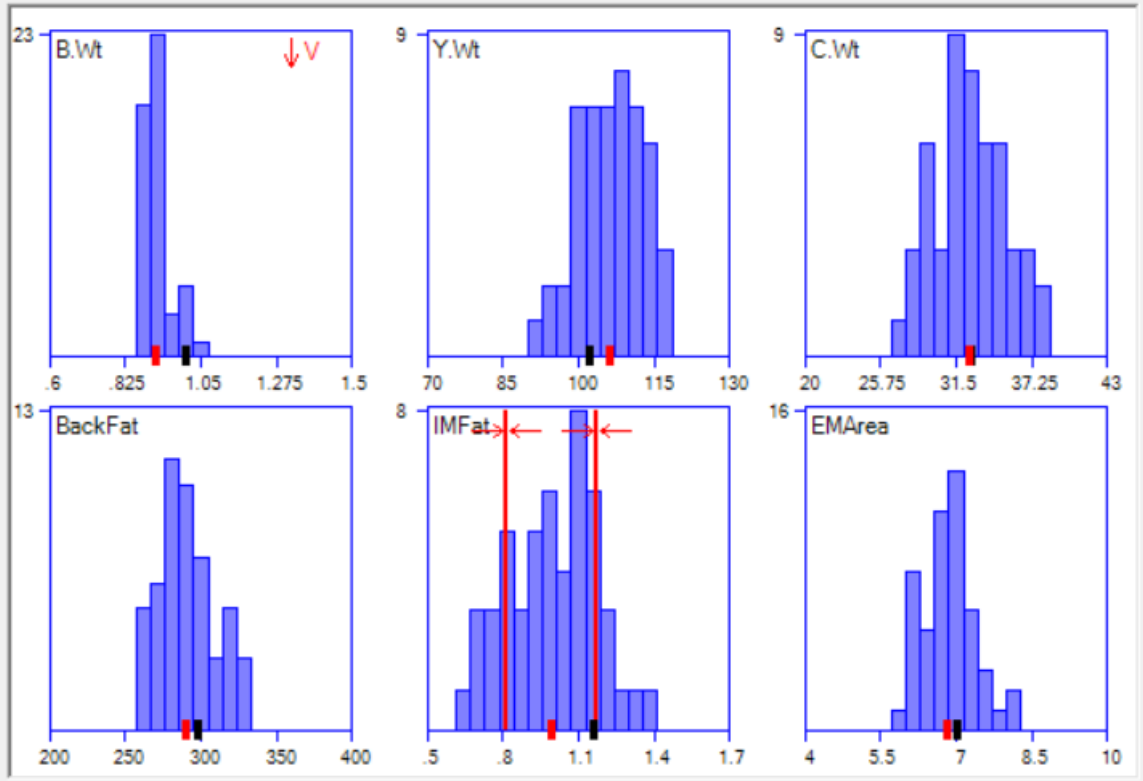
Target Degrees: 25

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections



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Direction | Frontier | Convergence | Grouping

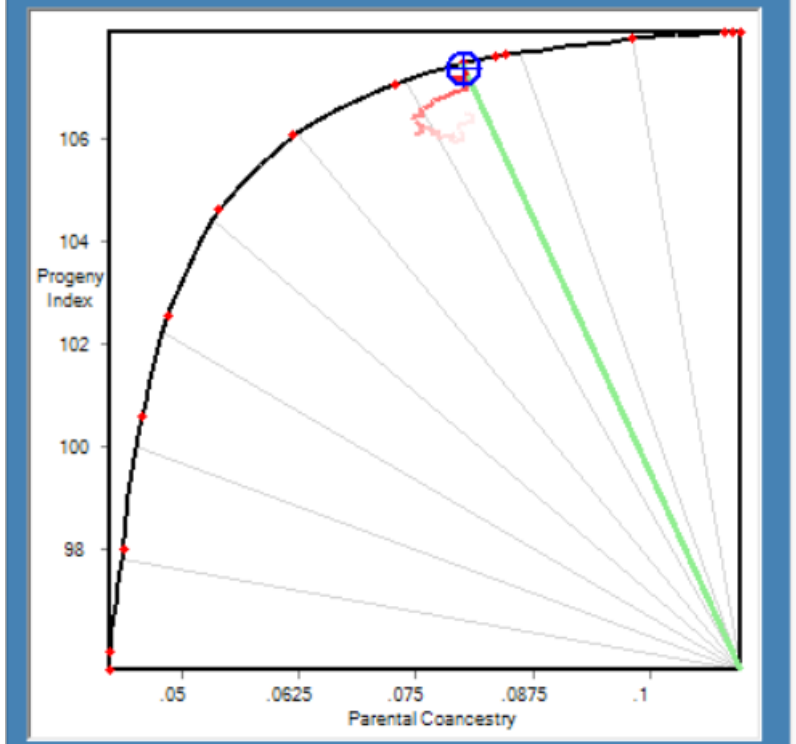
Balance strategy: 3. Hard constraint on Target Degrees

Max permissable coancestry: .0525

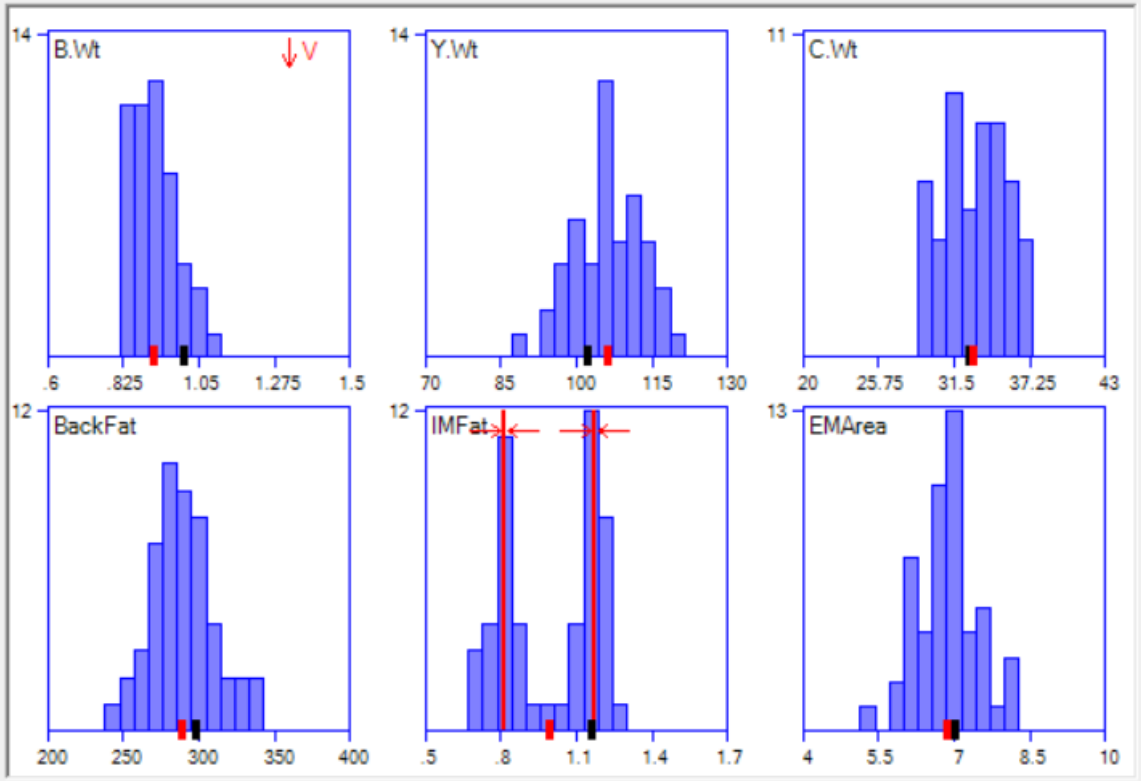
Target Degrees: 25

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections



EMArea | Resume

Tactical Desired Gains stabilising

Invoke | Weighting: 1

Target value (Click-L): 7.359

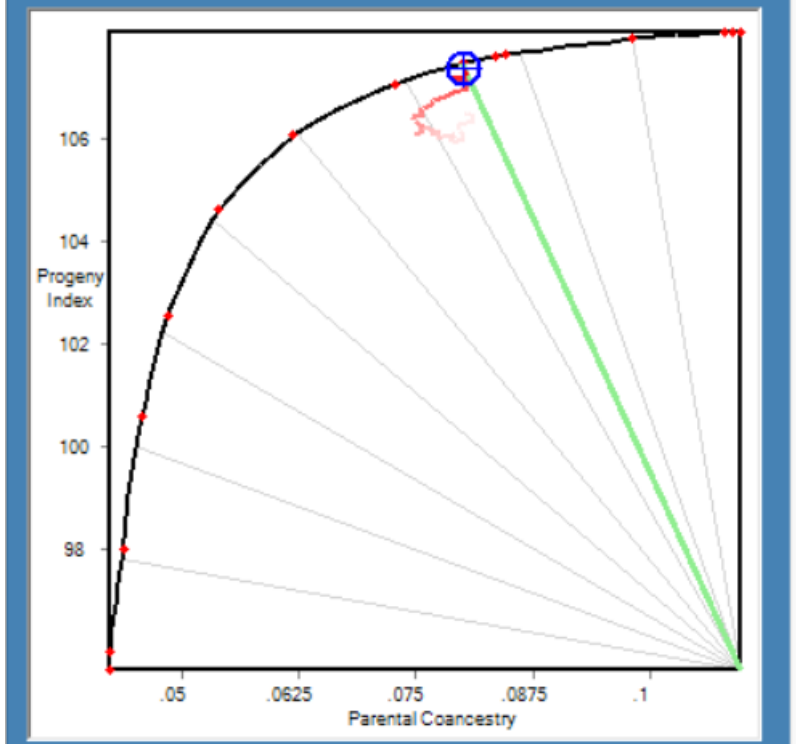
arget Degrees

Max permissable coancestry: .0525

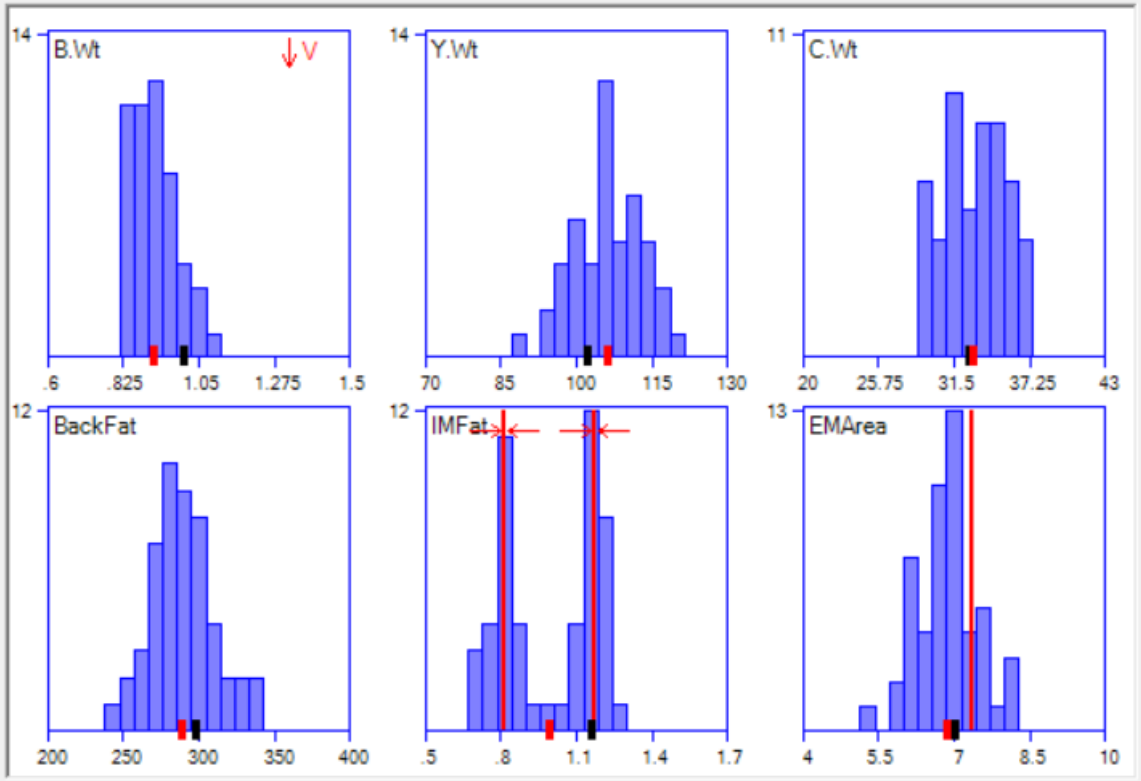
Target Degrees: 25

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections



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Direction | Frontier | Convergence | Grouping

Balance strategy: 3. Hard constraint on Target Degrees

Max permissable coancestry: .0525

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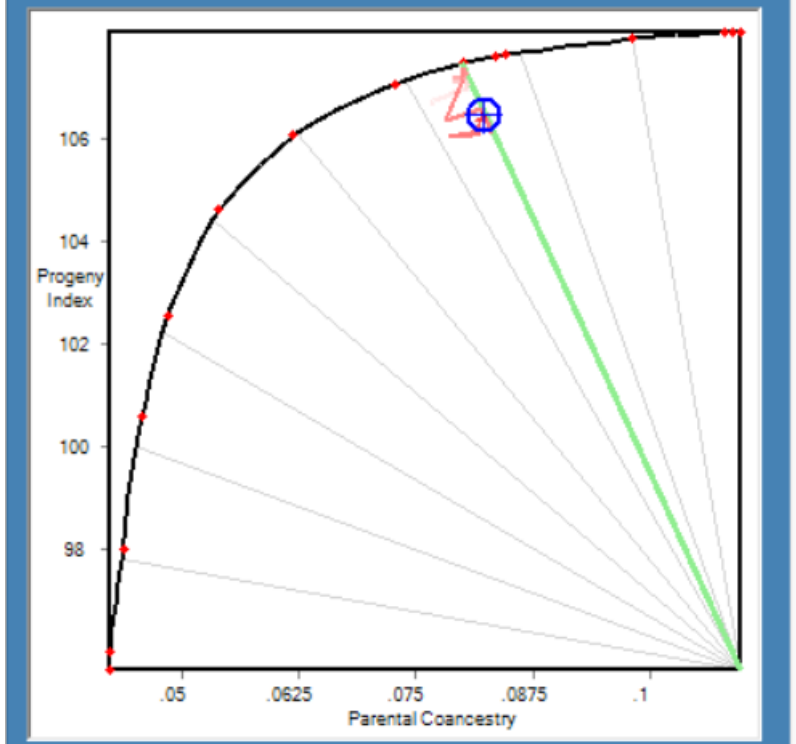
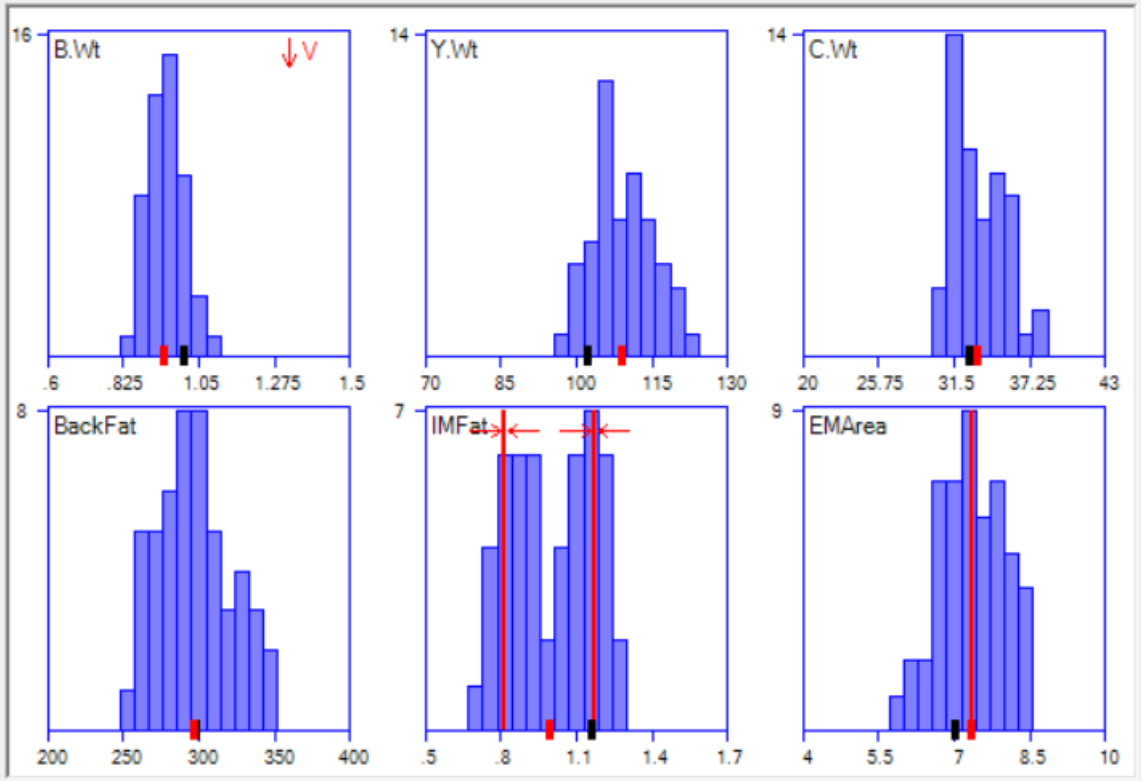
Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections



M2-22 | Resume

Decrease mean

Invoke | Weighting: 1

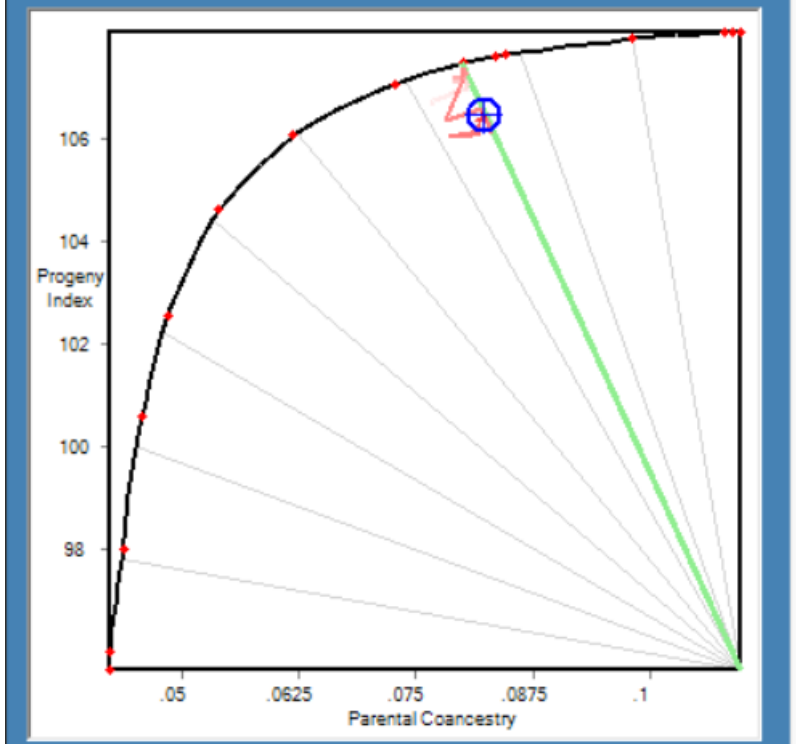
Balance strategy: 3. Hard constraint on Target Degrees

Max permissable coancestry: .0525

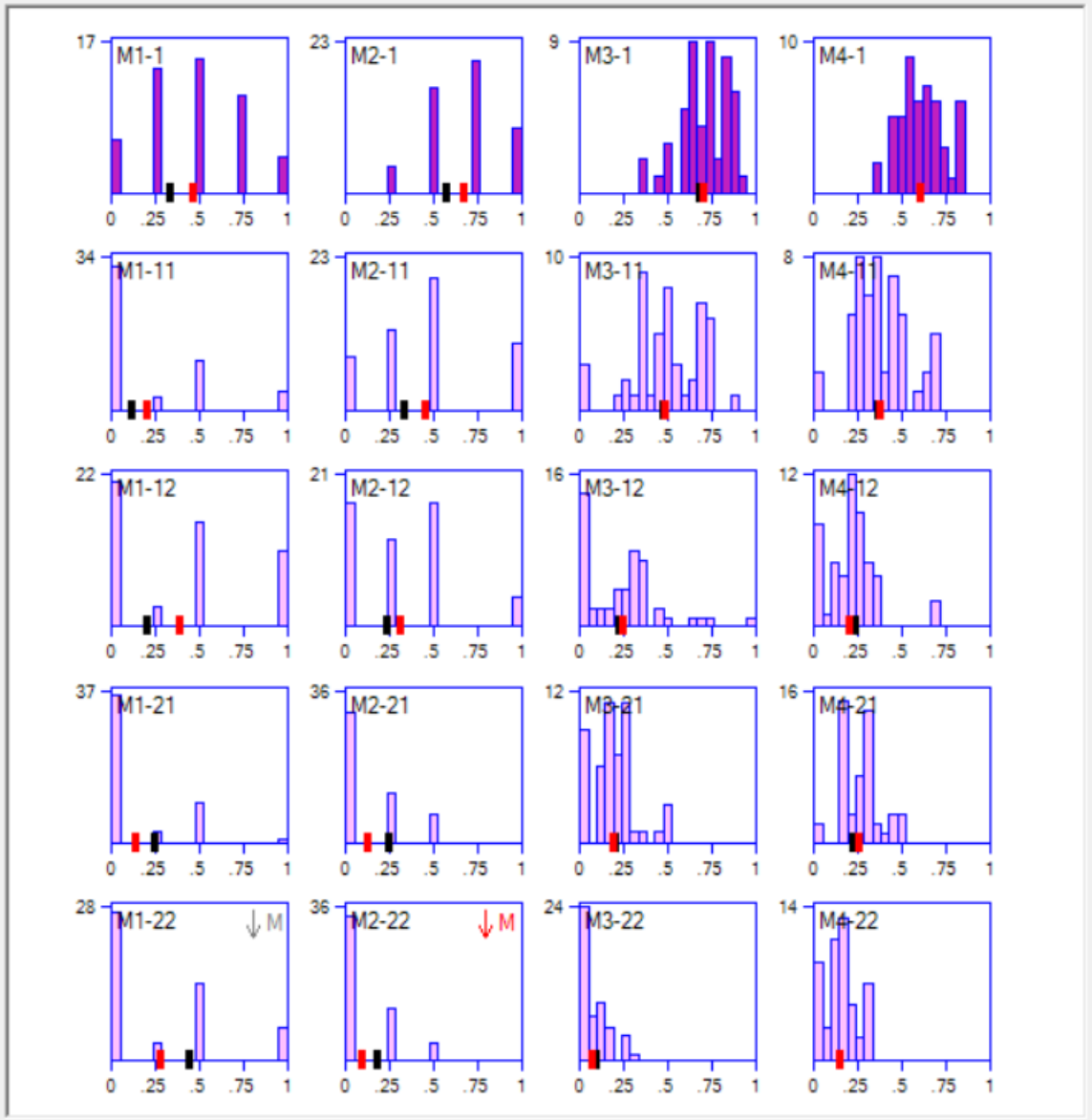
Target Degrees: 25

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections



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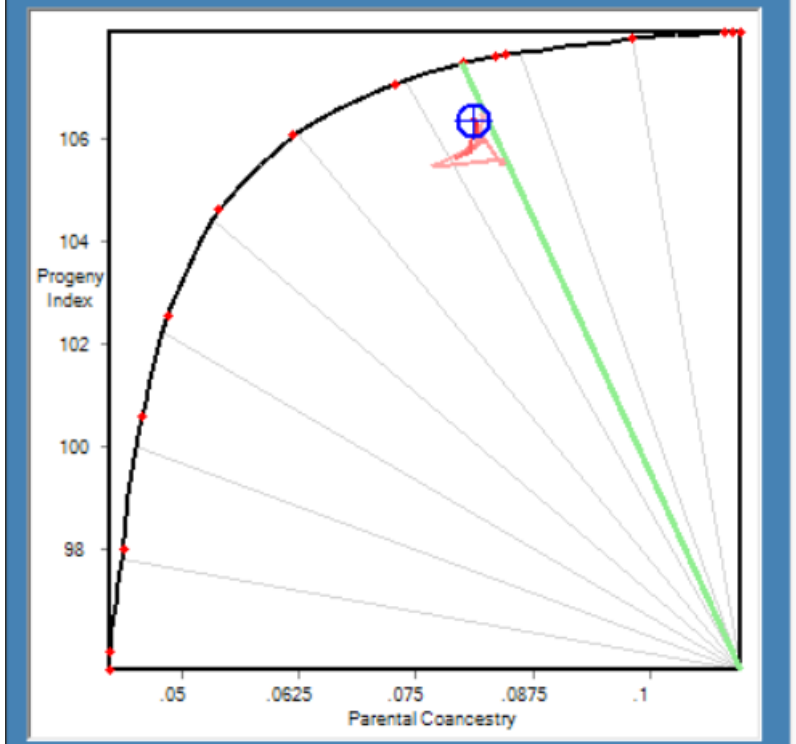
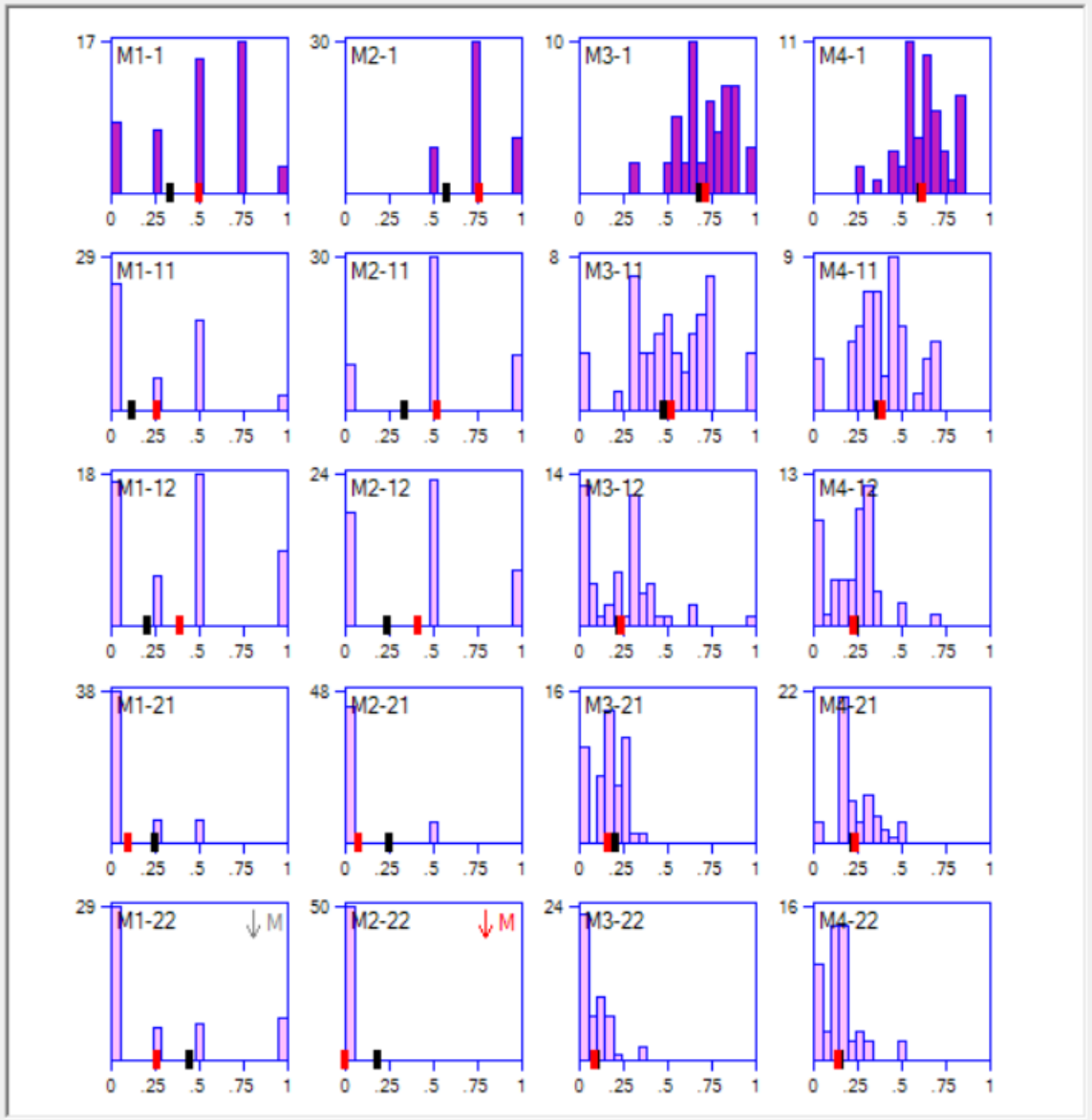



Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections



# Mixed Mating Groups

Multi-sire joining
Multi-sire pastures
Sire syndicates

Preparing matched groups for later matings
Multipliers herds
Groups of AI sires

Mass spawning fish
Open pollination

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Direction | Frontier | Convergence | Grouping

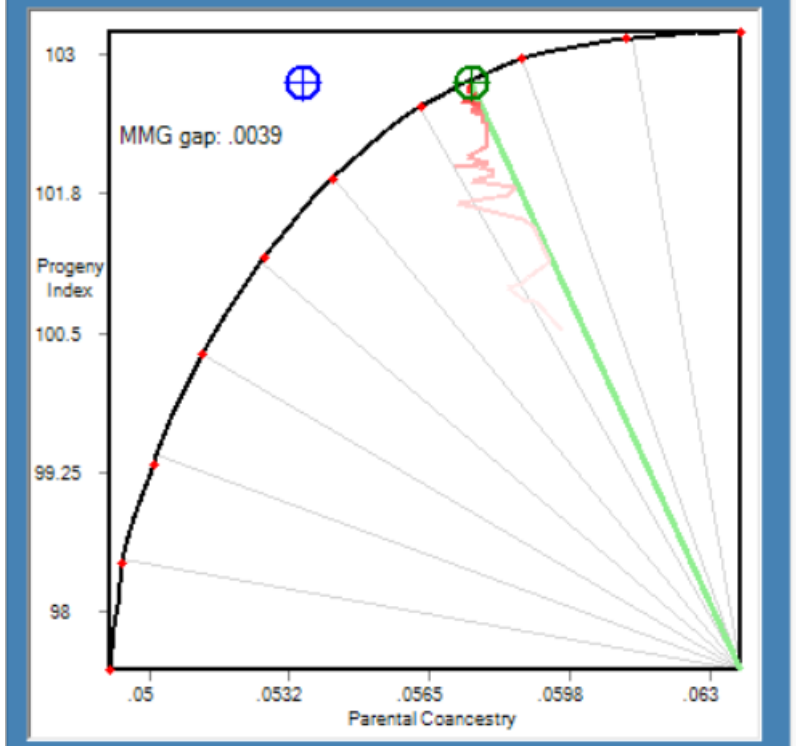
Balance strategy: 3. Hard constraint on Target Degrees

Max permissable coancestry: .0525

Target Degrees: 25

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close




Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections

Males in Mixed Mating Groups (OutMMGmales.txt)

| MMG | Member | ID | Index | B.Wt | Y.Wt | C.Wt | |
|---|---|---|---|---|---|---|---|
| 1 | 1 | Magnus | 110.620 | 0.883 | 103.533 | 31.142 | 28 |
| 1 | 2 | Bodie | 98.940 | 1.004 | 121.095 | 28.191 | 29 |
| 1 | 3 | Darian | 100.820 | 1.195 | 94.990 | 31.309 | 31 |
| 1 | 4 | London | 103.560 | 1.042 | 127.645 | 24.909 | 35 |
| 1 | 5 | Wayne | 114.660 | 0.759 | 114.855 | 33.022 | 27 |
| 1 | 6 | Coen | 103.940 | 1.138 | 98.092 | 43.446 | 25 |
| Male group coancestry: | | 0.055739 | | | | | |
| 2 | 1 | Dilan | 105.920 | 1.207 | 102.975 | 26.722 | 32 |
| 2 | 2 | Denver | 102.880 | 1.100 | 106.622 | 32.052 | 31 |
| 2 | 3 | Alexander | 106.520 | 0.840 | 112.393 | 28.900 | 30 |
| 2 | 4 | Frankie | 105.020 | 1.191 | 89.308 | 34.641 | 35 |
| 2 | 5 | Gordon | 107.220 | 0.987 | 91.000 | 37.322 | 31 |
| 2 | 6 | Eason | 103.860 | 1.017 | 104.441 | 34.921 | 30 |
| Male group coancestry: | | 0.093714 | | | | | |
| 3 | 1 | Shaun | 103.340 | 0.999 | 105.079 | 36.110 | 20 |
| 3 | 2 | Kamryn | 106.320 | 0.824 | 84.785 | 33.458 | 29 |
| 3 | 3 | Abdullah | 101.200 | 0.981 | 91.283 | 32.791 | 33 |
| 3 | 4 | Mustafa | 105.560 | 0.960 | 103.860 | 38.607 | 25 |
| 3 | 5 | Yahya | 103.320 | 0.825 | 105.050 | 34.311 | 25 |
| Male group coancestry: | | 0.080038 | | | | | |

*Thank you Alison !*

Show male groups | Show female groups | Update

MateSel Version 8.0 For use under licence only

Direction | Frontier | Convergence | Grouping

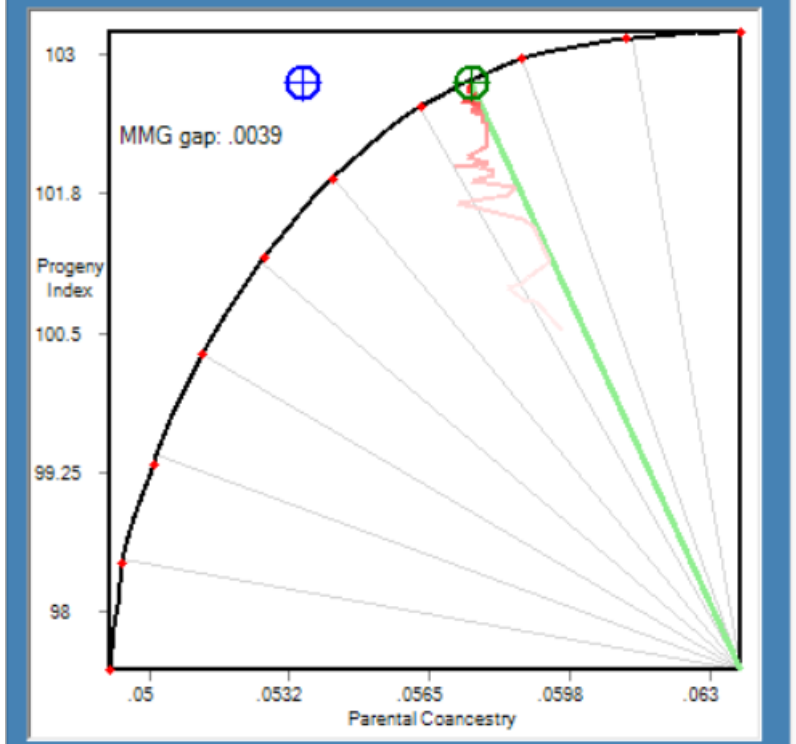
Balance strategy: 3. Hard constraint on Target Degrees

Max permissable coancestry: .0525

Target Degrees: 25

Weight on progeny F: 0

Run | Update | Pause | Print Matings | Stop | Close



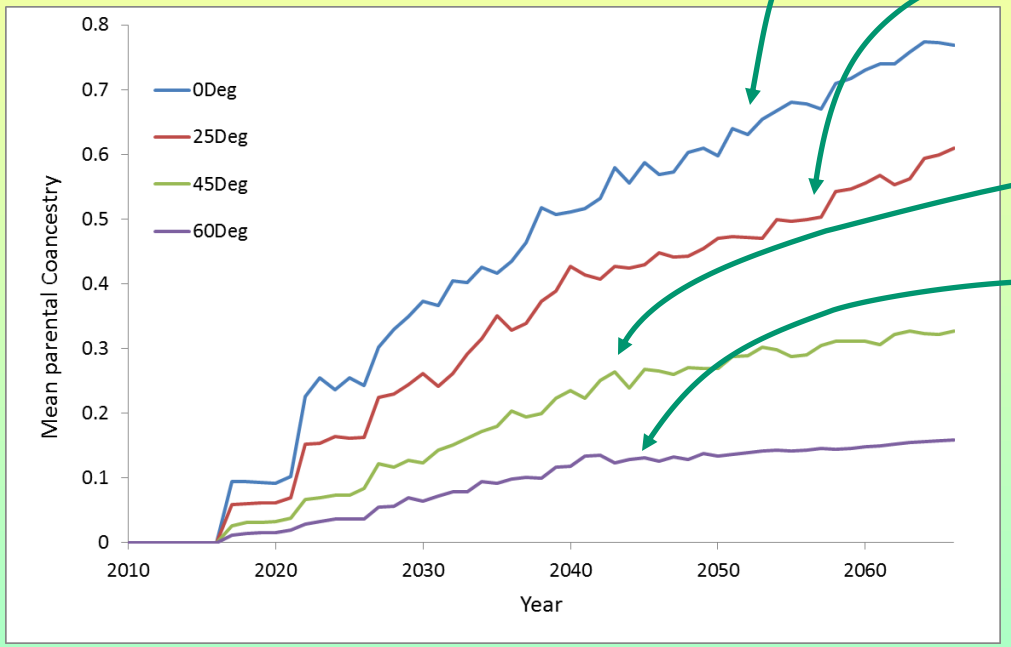

Console | Progeny Inbreeding | Individual Coancestry | Trait management | Marker management | Mate selections

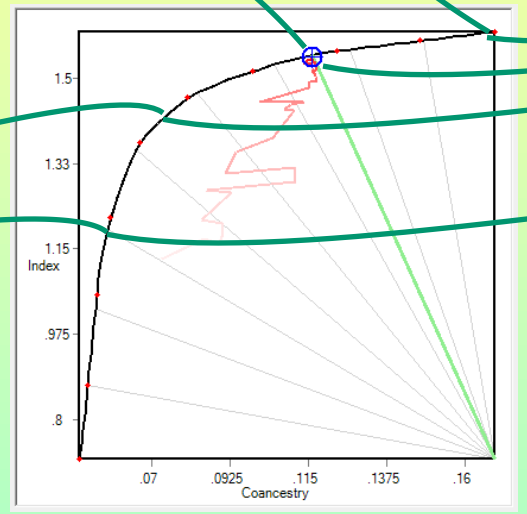
Females in Mixed Mating Groups (OutMMGfemales.txt)

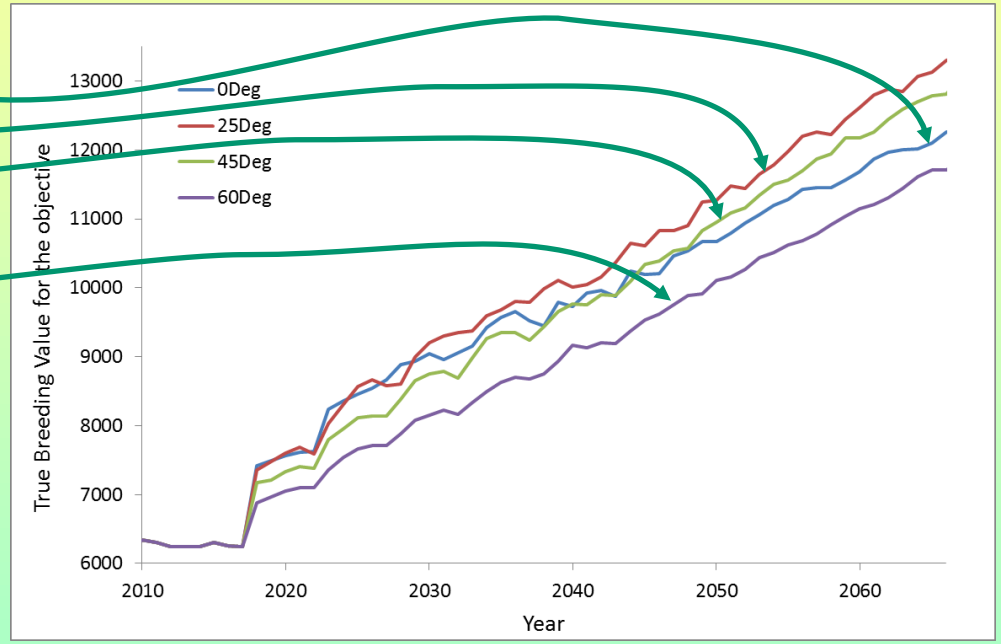
| | | | | | | |
|---|---|---|---|---|---|---|
| 1 | 21 | Carolyn | 95.720 | 0.792 | 106.999 | 25.674 |
| 1 | 22 | Simone | 112.840 | 0.972 | 97.294 | 36.363 |
| 1 | 23 | Jaylee | 106.820 | 1.241 | 110.851 | 39.824 |
| 1 | 24 | Estrella | 99.320 | 0.948 | 91.881 | 31.830 |
| 1 | 25 | Selene | 103.960 | 0.987 | 112.662 | 34.859 |
| 1 | 26 | Danica | 100.960 | 0.648 | 114.126 | 28.596 |
| 1 | 27 | Raylee | 102.300 | 1.125 | 98.378 | 32.501 |
| 1 | 28 | Kallie | 91.420 | 1.081 | 117.757 | 28.799 |
| 1 | 29 | Lina | 99.200 | 0.946 | 99.768 | 37.894 |
| 1 | 30 | Guadalupe | 101.240 | 1.224 | 84.665 | 33.386 |
| 2 | 1 | Clementine | 100.940 | 1.026 | 116.926 | 34.066 |
| 2 | 2 | Lyra | 95.220 | 0.980 | 118.088 | 32.476 |
| 2 | 3 | Nathalie | 97.740 | 0.986 | 101.327 | 32.754 |
| 2 | 4 | Sariyah | 102.800 | 0.966 | 84.795 | 37.526 |
| 2 | 5 | Clare | 94.400 | 1.233 | 98.711 | 31.464 |
| 2 | 6 | Nancy | 98.700 | 1.117 | 112.061 | 26.677 |
| 2 | 7 | Lilianna | 102.480 | 0.796 | 92.551 | 30.491 |
| 2 | 8 | Jaydene | 99.280 | 1.181 | 112.666 | 31.355 |
| 2 | 9 | Patricia | 101.560 | 1.111 | 102.071 | 35.140 |
| 2 | 10 | Chana | 102.740 | 0.886 | 108.346 | 31.649 |
| 2 | 11 | Audrina | 99.220 | 1.354 | 99.384 | 33.835 |
| 2 | 12 | Princess | 105.640 | 1.236 | 107.615 | 40.559 |
| 2 | 13 | Amaris | 97.220 | 0.970 | 88.575 | 29.130 |
| 2 | 14 | Claudia | 89.120 | 1.359 | 98.954 | 32.655 |
| 2 | 15 | Cara | 101.400 | 0.925 | 99.345 | 41.788 |
| 2 | 16 | Amia | 106.800 | 1.380 | 119.975 | 35.651 |
| 2 | 17 | Jessa | 100.540 | 1.231 | 91.296 | 36.619 |
| 2 | 18 | Jana | 100.380 | 1.248 | 82.488 | 37.078 |
| 2 | 19 | Zariyah | 96.600 | 0.957 | 118.634 | 34.750 |
| 2 | 20 | Aubrielle | 96.520 | 1.037 | 109.264 | 28.520 |

Show male groups | Show female groups | Update

# Balancing long-term and short-term genetic gains



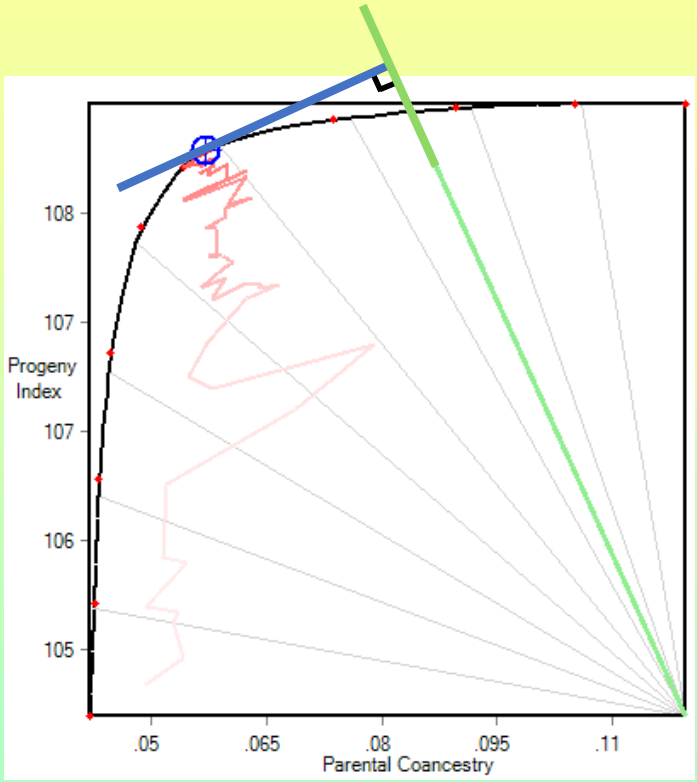



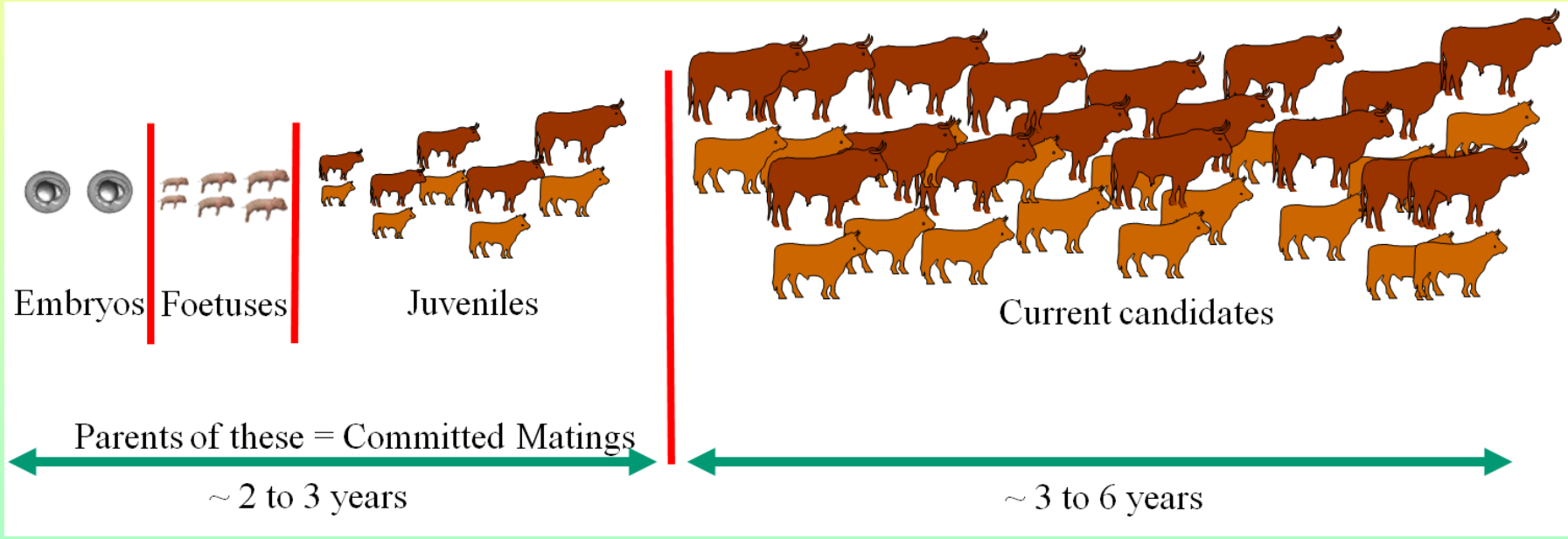




For a closed breeding program, ‘pedal to the metal’ is not best in the long run.

# Fine control of diversity and inbreeding outcomes

MateSel



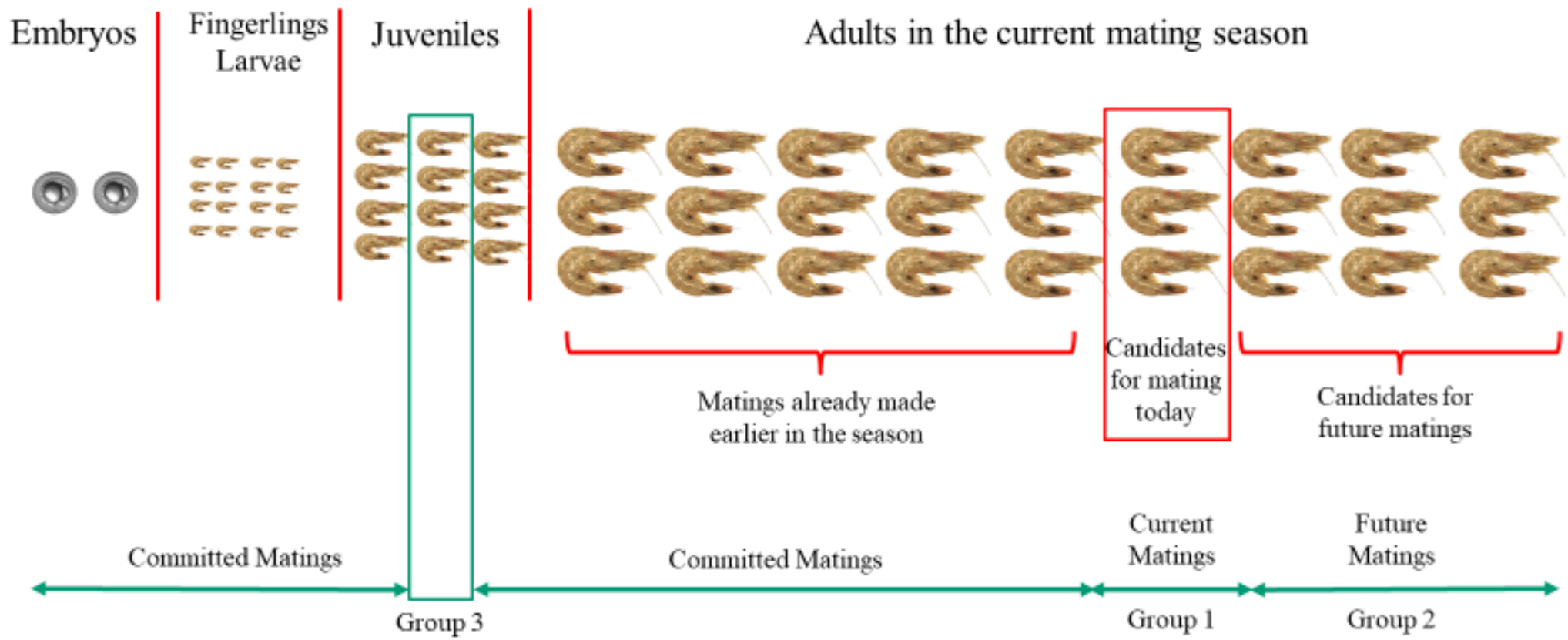

Exploiting prevailing opportunities

Managing the full life cycle. As explained here.

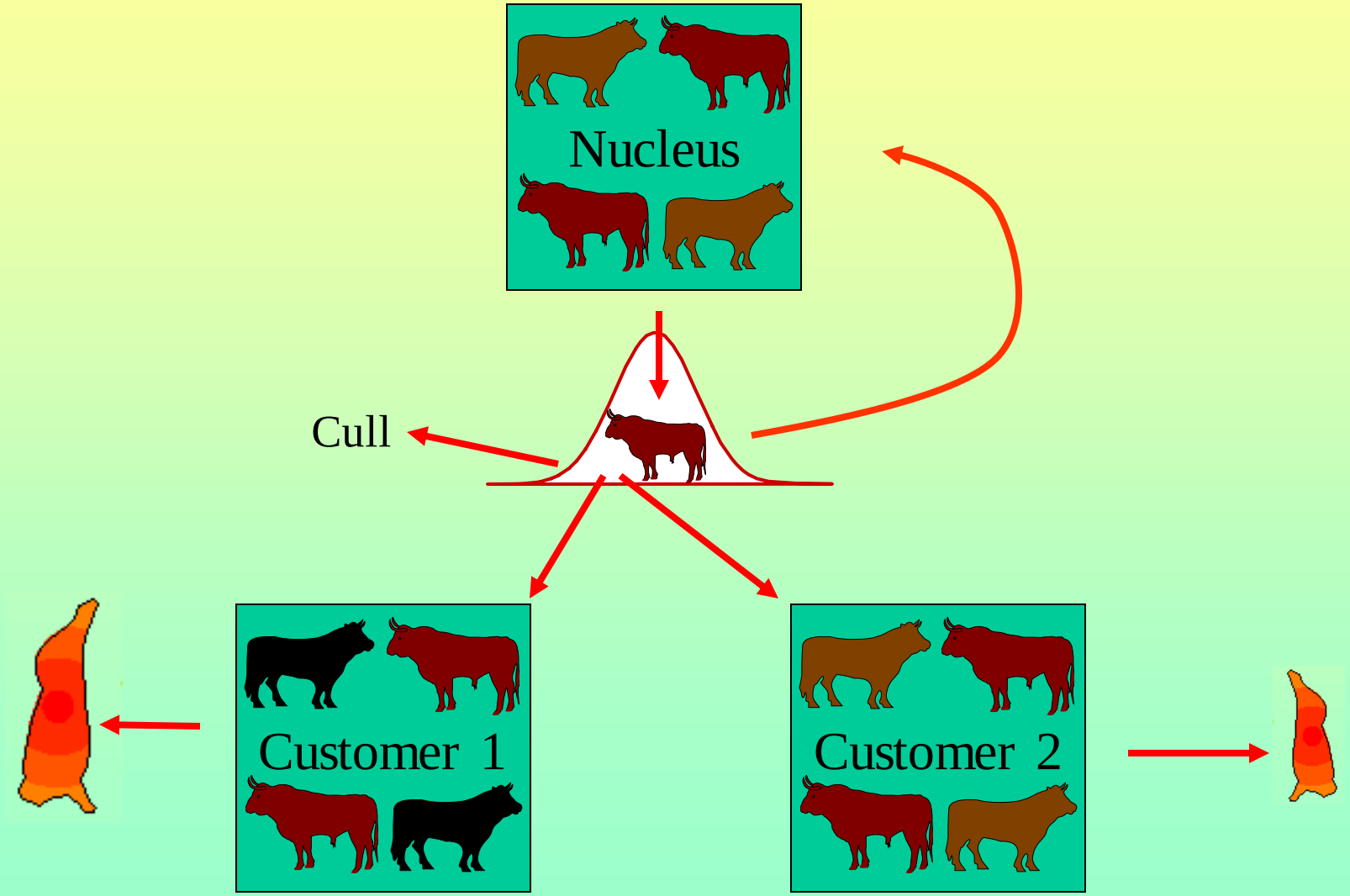
# Balance in use and costs of AI and IVF

MateSel

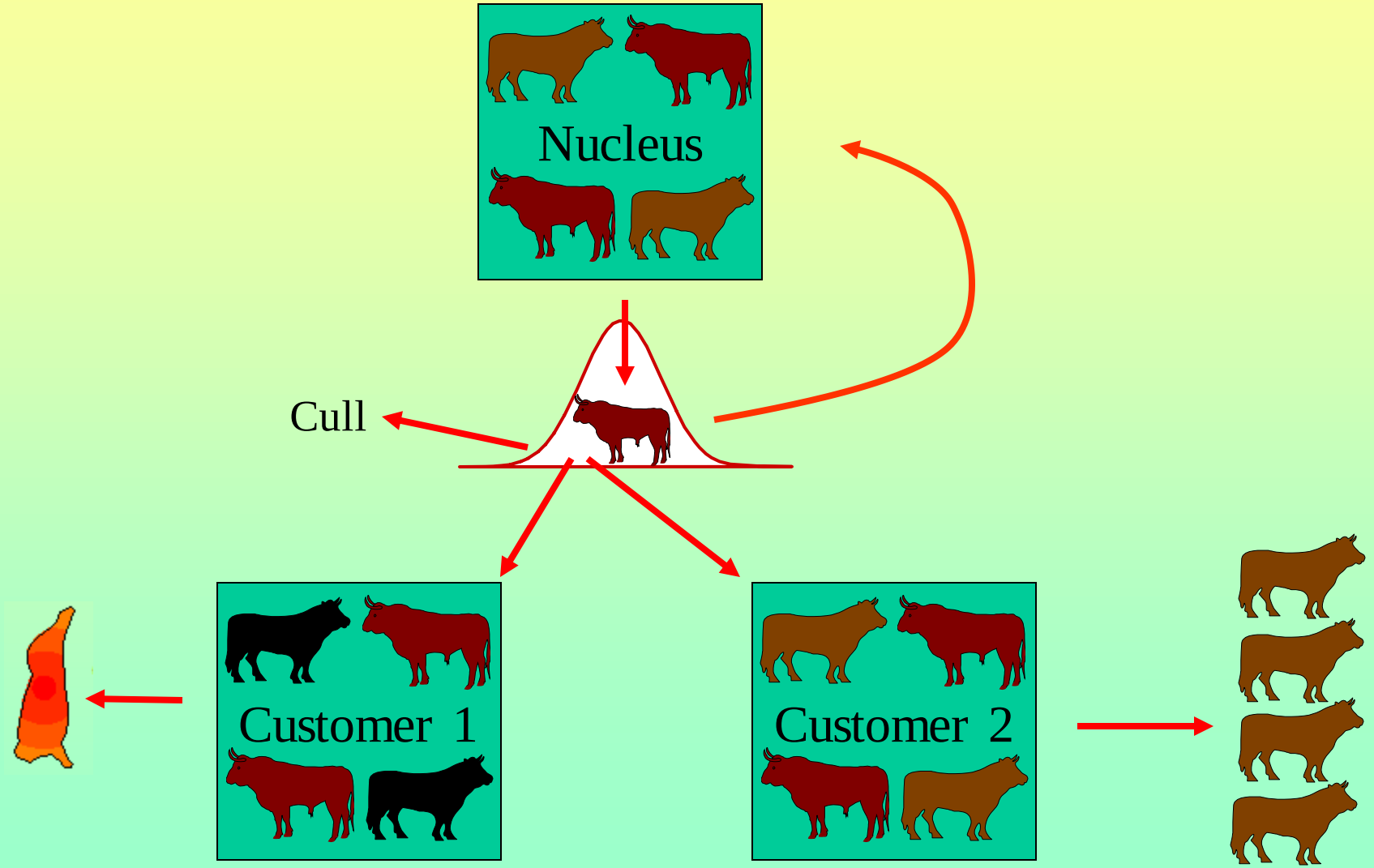
## Prawns and Salmon and advanced beef, sheep, dairy …



# Multiple EndUses

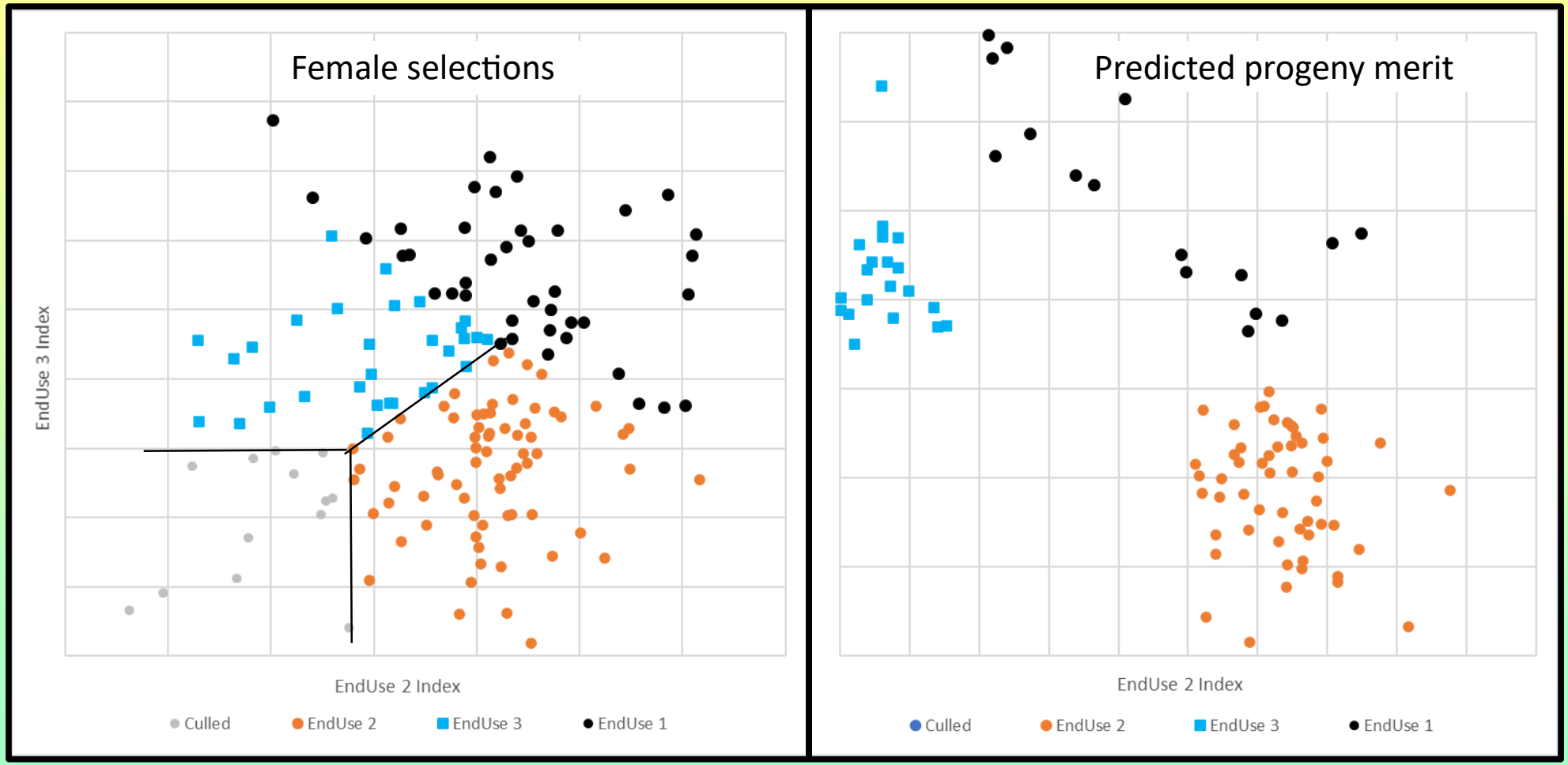


# Multiple EndUses




Plus sexed semen decisions

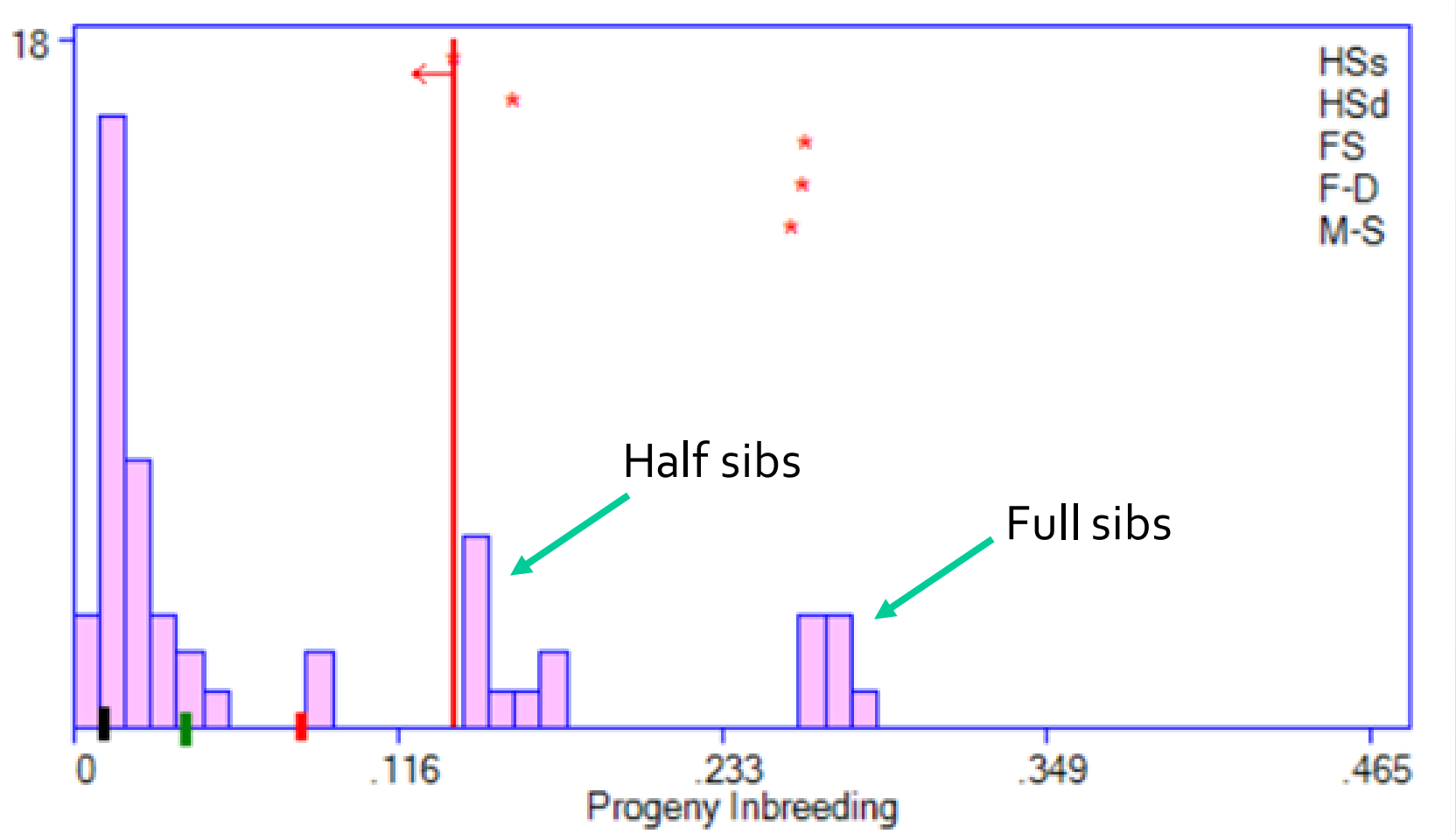
# Targeting Multiple EndUses to cater for the varied needs of bull-buying clients




Female EPDs plotted for two client indices with EndUse 2 and 3 targeted matings in orange and blue.

Useful separation in resulting progeny merit. Example nucleus matings are black, as seen here.
Thanks to ABS Global.

# Managing distribution of Progeny Inbreeding




When the red line is invoked, HS and FS matings will be quickly eliminated!

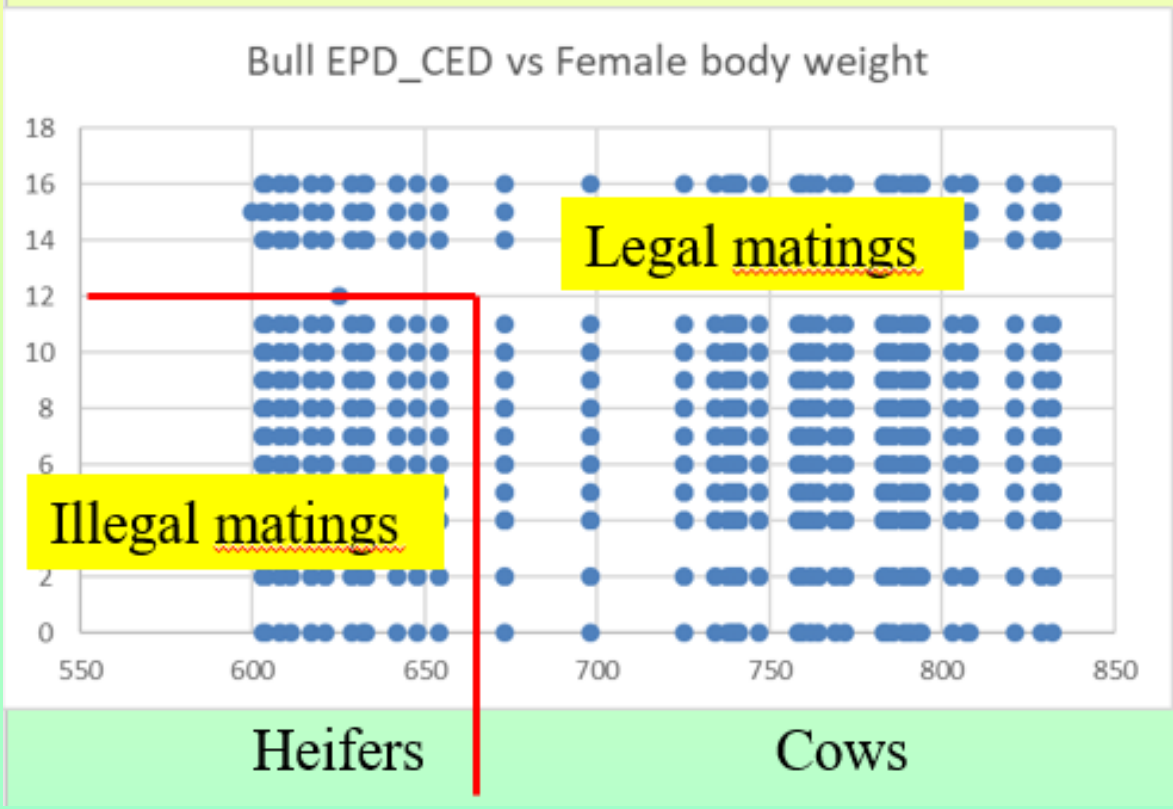
This should ***not*** replace a general weighting against mean Progeny Inbreeding.

https://doi.org/10.1093/jhered/esad027

# An efficient approach to using High Calving-Ease bulls

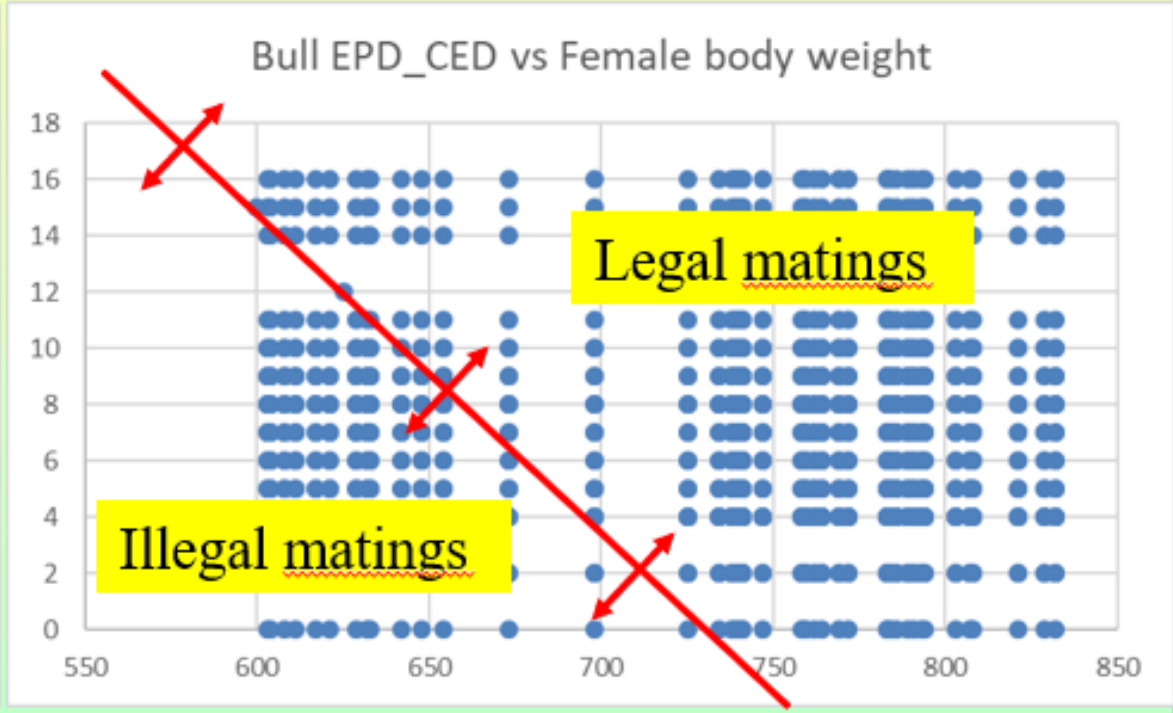
MateSel

## Grouping




The conventional use of Grouping to allow heifers to be mated only by High CE bulls.

## CEcontrol




CEcontrol makes better use of the CE EPD resources available, as seen here.

# Other issues can be handled, e.g.:

MateSel

- Management of **distribution of sires across herds**
  - sire referencing schemes
  - genomic reference populations
- Managing **backup sires**
- Creating harmonious **multi-sire mating syndicates**

# Other issues can be handled, e.g.:

MateSel

- Collective **management of multiple genetic markers** (recessive lethals, gene edits, QTL, etc) for both short-term and long-term objectives.
- Decisions on **generation and use of sexed semen** and embryos
- Genomic mate selection.

# Bringing MateSel to Beef Breeders

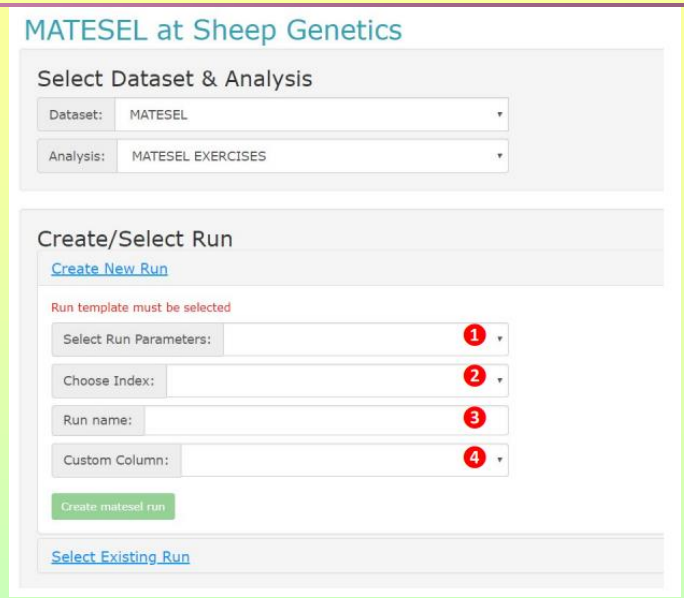
- Why do we have **300 sheep breeders** using MateSel,

  but probably under **100 beef breeders**?

- … the sheep breeders have a **system to extract the data**.

- The **breeders can operate independently**.

- We are now developing MSaaS (MateSel-as-a-Service) to make this available to other service providers:

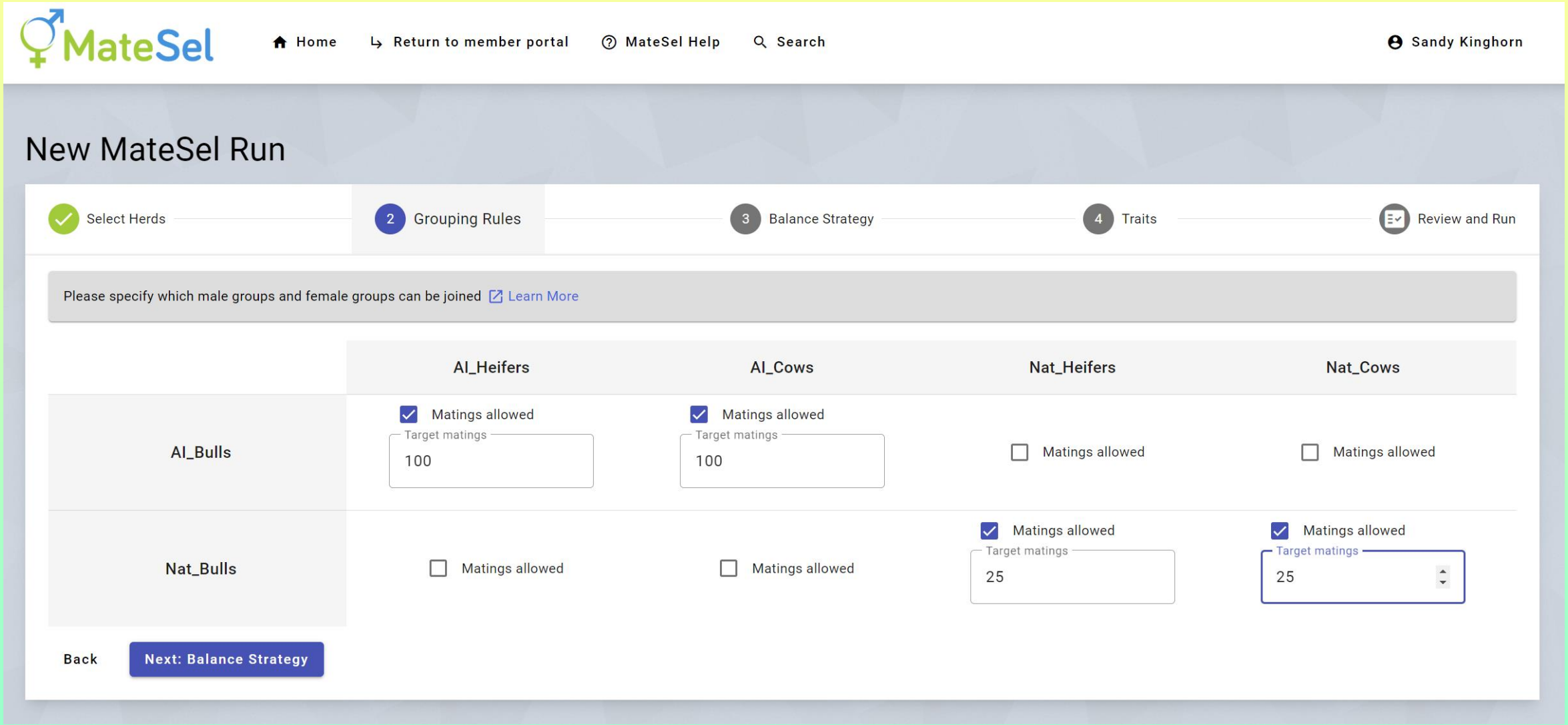



sheepgenetics.org.au/resources/matesel/

Service providers

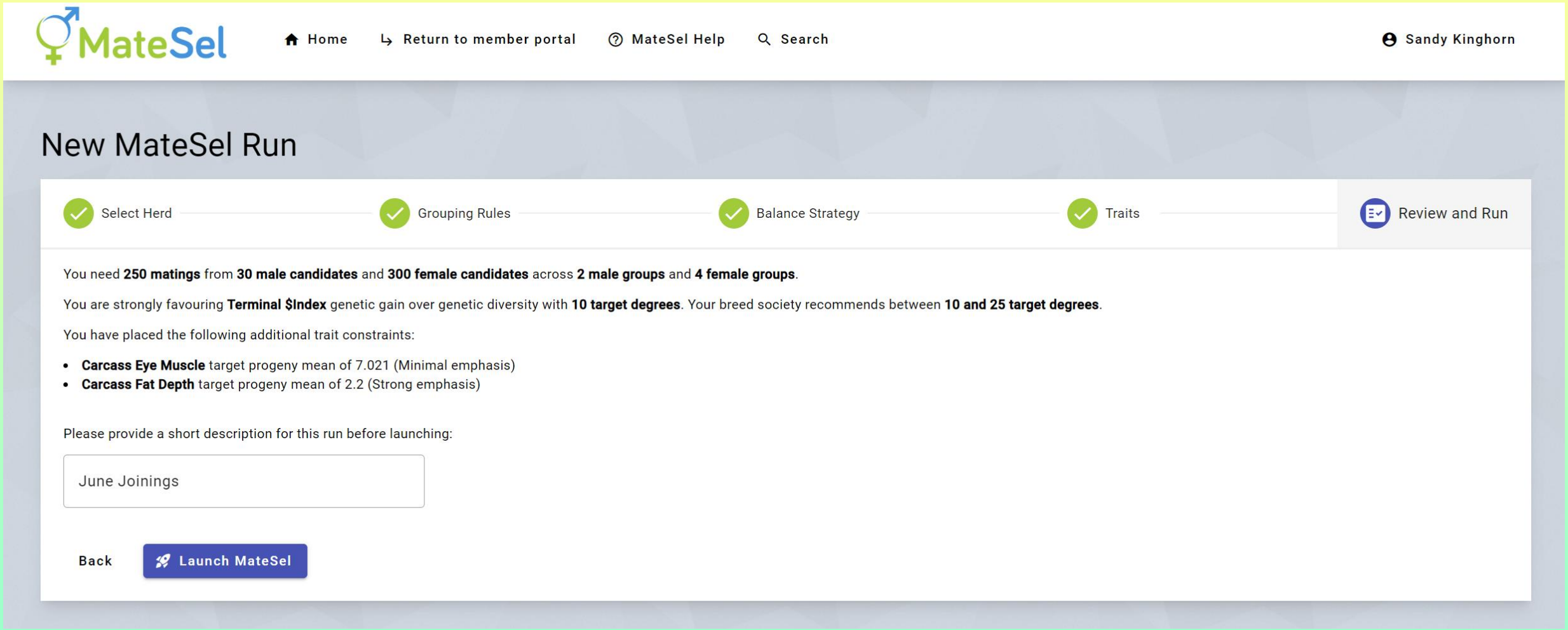
# Bringing MateSel to Beef Breeders

Breeders extracting data from their association database and configuring initial constraints



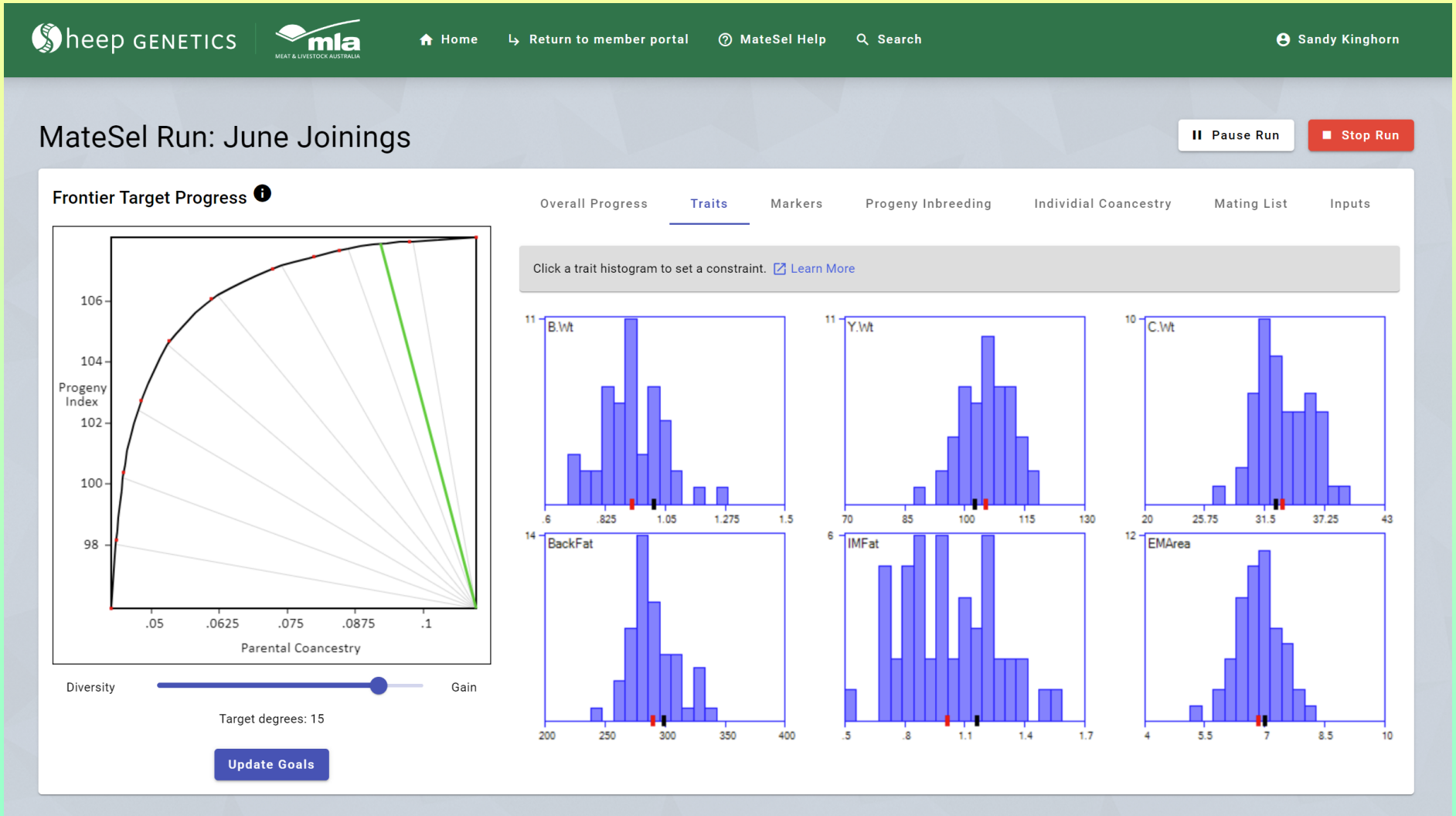
# Bringing MateSel to Beef Breeders

Breeders reviewing their inputs before launching MateSel



# Bringing MateSel to Beef Breeders

MateSel running with the ability to change targets in real-time to test different directions

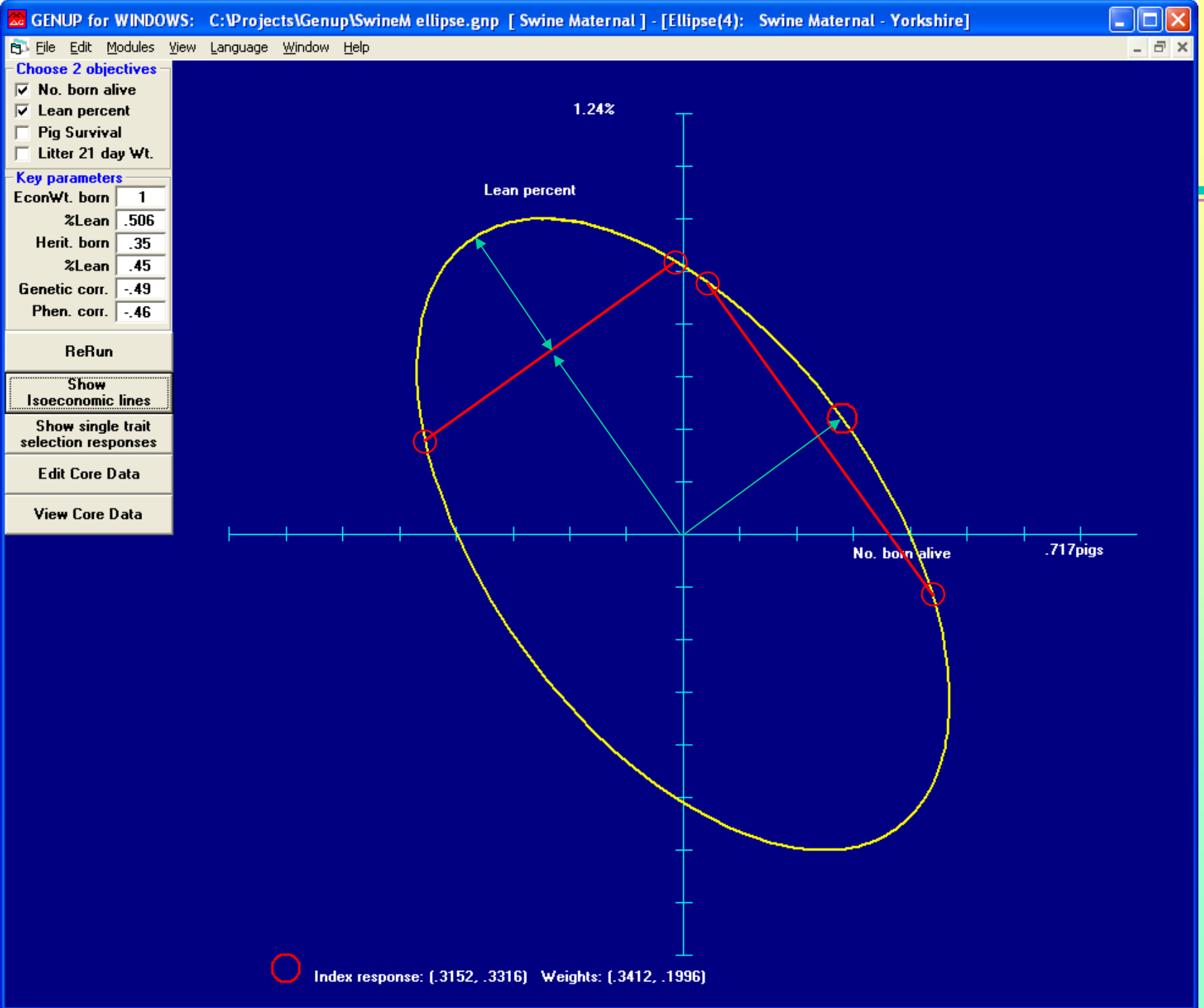


# Conclusion: The wide value of Precision

MateSel

- A system that brings ***precision*** in predicting the impact of your decisions …
- … can also bring ***power to discover*** a wide range of alternative directions.
- This gives more ***control and confidence*** in chosen directions.


The End




MateSel

# Where to go

How to get back ?

# Use a dummy individual to represent a large group

| | George | Mildred | Gabrielle | Females in Region 6 |
|---|---|---|---|---|
| George | 1 | 0 | 0 | 0.012 |
| Mildred | 0 | 1.02 | 0 | 0.043 |
| Gabrielle | 0 | 0 | 1 | 0.131 |
| Females in Region 6 | 0.012 | 0.043 | 0.131 | 1.09 |

| Index | AbsMinuse | Maxuse | Trait1 |
|---|---|---|---|
| 104.32 | 11393 | 11393 | 3.26 |

Or use Committed Matings

Or eg.

"All sows in multiplier herd 4"
"All 5 year old cows in Devon"
"Bulls in syndicate mating group 2"

Average relationship beween George and Females in Region 6

No pedigree available? See manual for a geneflow solution.

# Bringing MateSel to Beef Breeders

- Which buttons to press
- Demonstrations
- Discussions around opportunities

Manual = 133 pages … videos popular!

Video Series

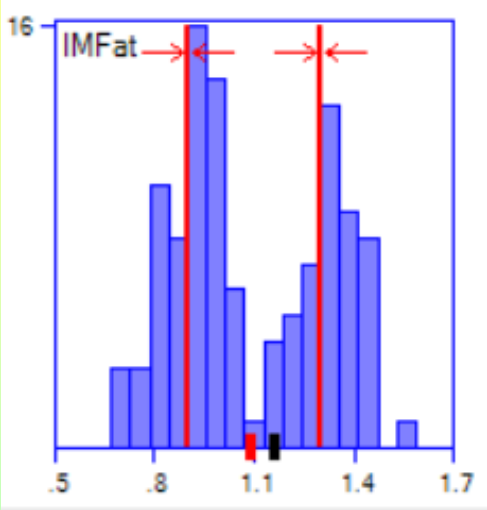
YouTube

The MateSel video series is hosted on YouTube. Click here or the YouTube logo to view the MateSel YouTube channel. An index of all videos can be found below.

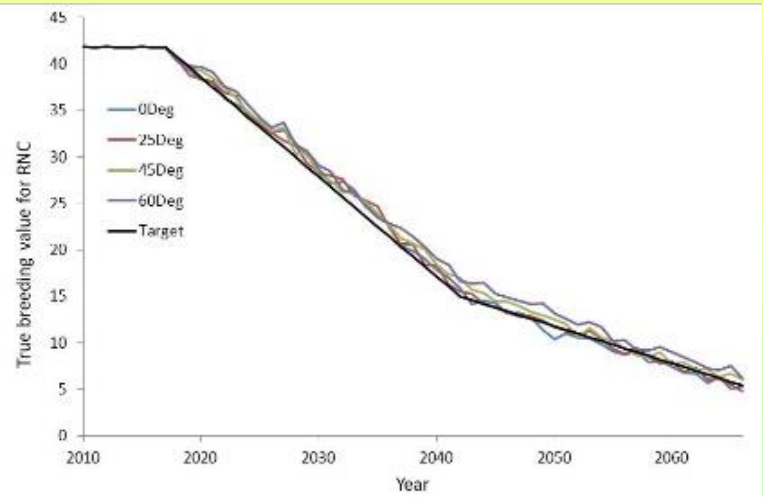
| | |
|---|---|
| **Category: 1. Introduction** | |
| General Introduction | A quick introduction to how MateSel works and its core functions and features. |
| Overview and Demo Project Test Drive | Provides a walkthrough of a demo project that comes with MateSel. |
| **Category: 2. Preparing your data files** | |
| Preparing your main data file | Comprehensive, except no detail on handling genetic markers. |
| Preparing Matesel.ini | Please also see Introduction to version 7.0.12.0 from about 6min, which shows the new format for Matesel.ini, including automatic upgrading. |
| Preparing InpOneGroup.txt | Setting constraints and other settings across all candidates.Includes basic discussion on what Groups are in MateSel. |
| Preparing InpGroups.txt - Standard Operations | Everything in this file up to the permission matrix, except for 'natural mating'.Example in beef cattle across US states. |
| Preparing InpGroups.txt - Advanced Operations | Features below the permission matrix in this file, plus 'natural mating'.Some discussion on method used for Grouping. |
| **Category: 3. The MateSel user interface** | |
| Windows Desktop | Coming soon... |
| Web Browser | Coming soon... |
| Batch Versions | Coming soon... |
| **Category: 4. The MateSel Frontier** | |
| Frontier fundamentals | Includes discussion of what parental coancestry is, and why relationships are important. Simple spreadsheet example. Desired outcomes discussion, including programs Desire and Diversity. |
| Where should I aim? | First, be sure to make a correct Frontier – by example. Your corporate position. Measuring and predicting inbreeding rate/diversity loss and its effect on long-term gains. |
| Working with Balance Strategies | First 4 mins is introduction – you could fast forward that. Walking through the different ways of balancing Progeny Index and Parental Coancestry, with discussion on what strategy might be most suitable. |
| **Category: 5. Managing Trait Distributions** | |
| Standard operations | What are these trait distributions? Worked example of using the different control types for manipulating traits. |
| Advanced operations | This includes a number of unusual tricks, eg showing distributions for sires and for dams, as well as for progeny. Also using dummy traits to manage ages, breed crossing, locations etc. Please also see Introduction to version 7.0.12.0 for the desired gains options when Committed Matings are being displayed, and also for some relevant updates to format of Matesel.ini. |
| Should I manage my traits? | Changing distribution means (responses), and shapes (eg variances). Managing genetic variation for individual traits, and planning for the splitting of breeding lines. Discussion on compromises caused by mating for desired trait distribution shapes. |
| **Category: 6. Genetic markers** | |
| Coding markers in the main data file | This video tells you how to enter genetic marker data into your dataset, so that you can manipulate these in Matesel. |
| Managing individual markers/QTL/Gene Edits | A guide to how marker information is displayed and how to use Matesel to manage allele and genotype distributions in the progeny. |

# Fine control of trait and marker outcomes

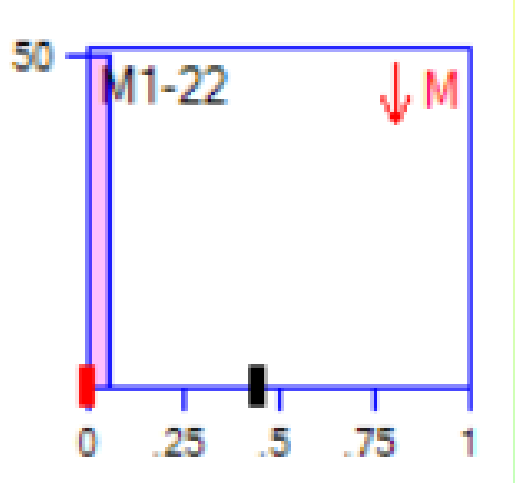
MateSel



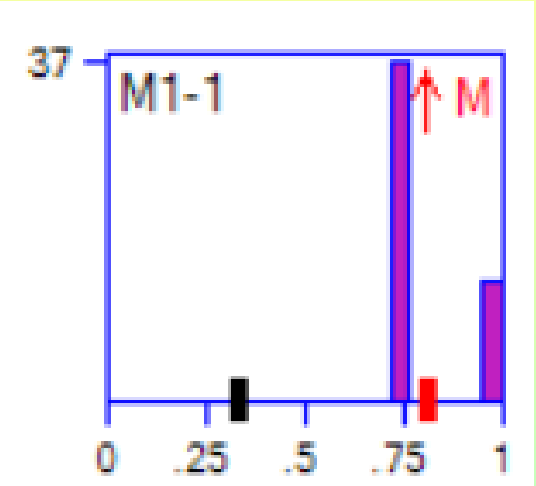

Bimodality in IMF to target two markets




Planned reduction in disease susceptibility




Decreasing expression of a genetic defect to zero




… while increasing the good allele frequency