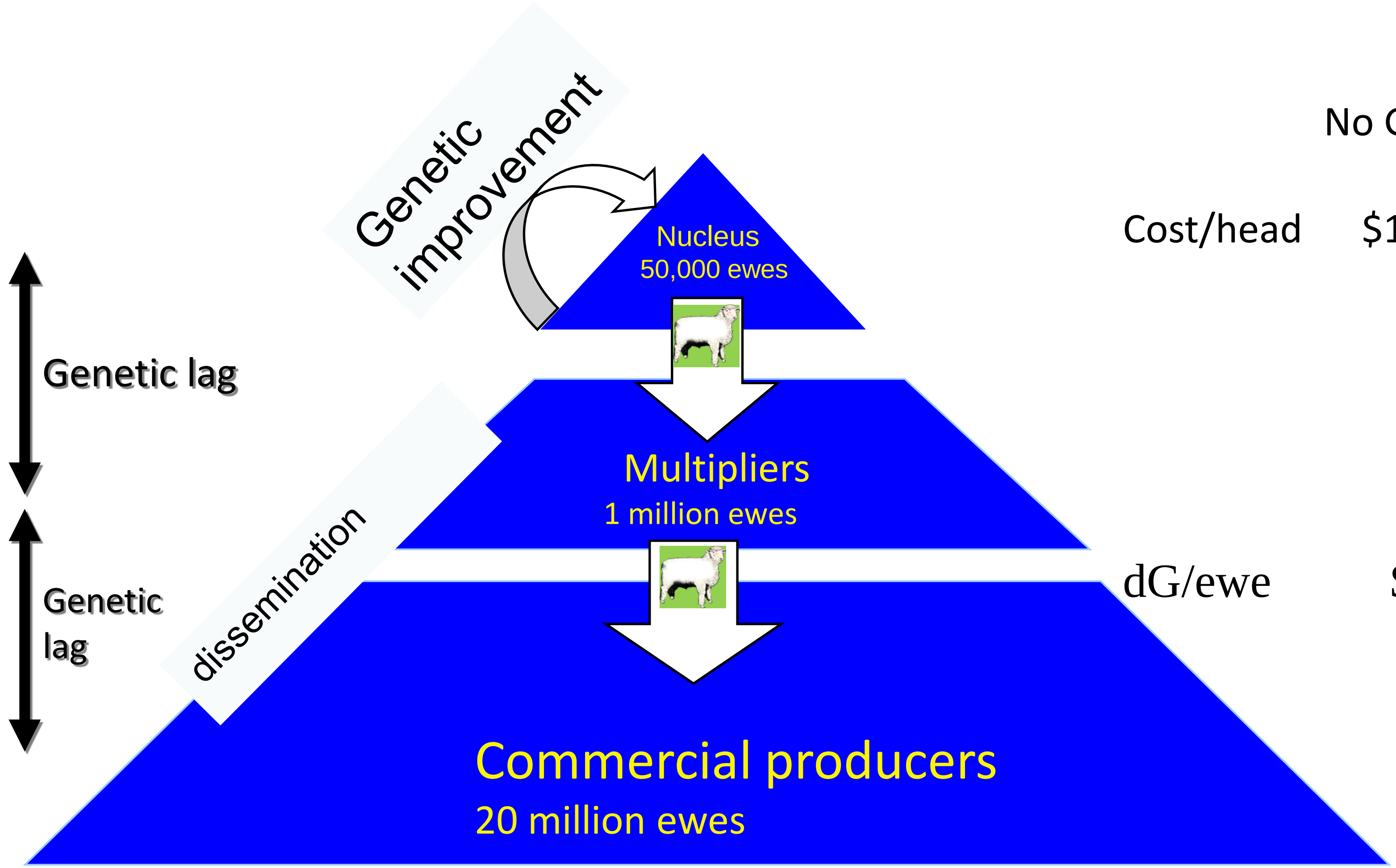
# Optimizing Breeding Programs

# COST-BENEFIT

Armidale Animal Breeding Summer Course 2014

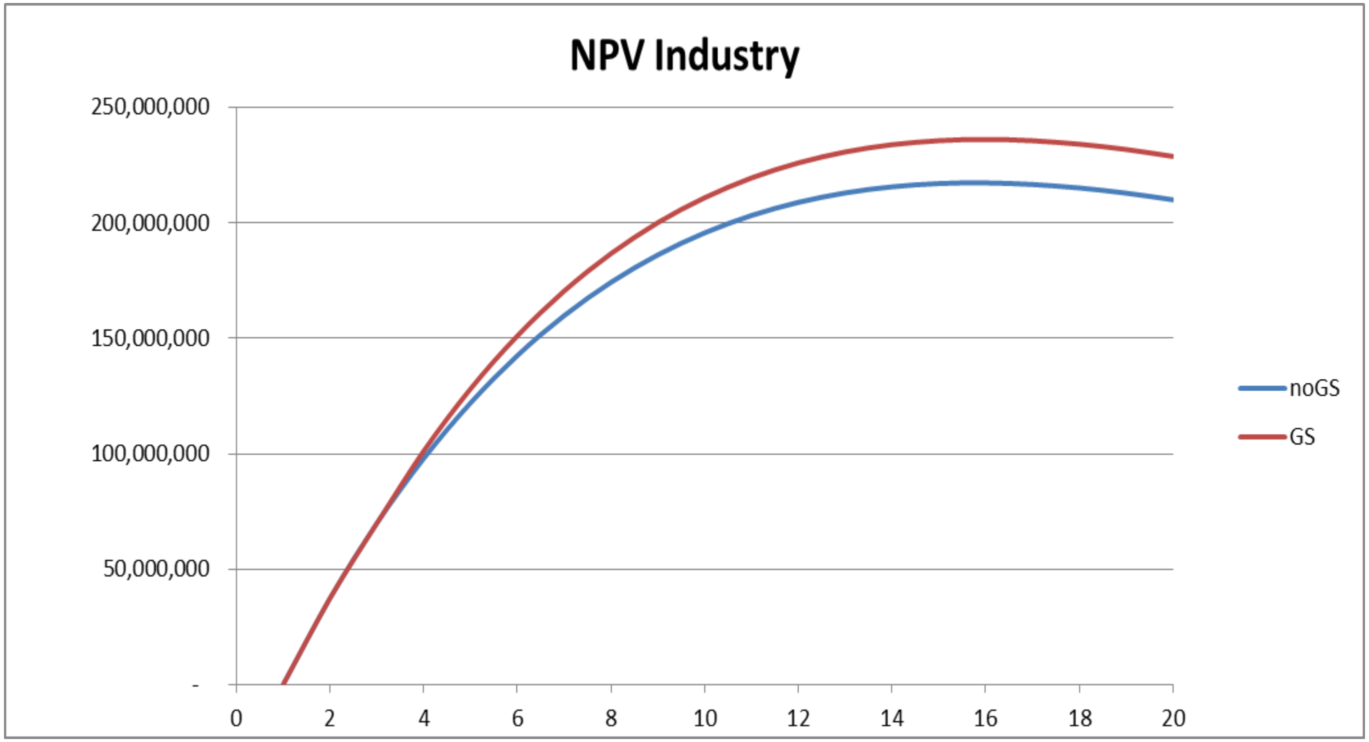
# Cost - Benefit




| | No GS | GS |
|---|---|---|
| Cost/head | $10 | $60 |
| dG/ewe | $2 | $2.2 |

# Cost-Benefit industry wide

| | No GS | GS |
|---|---|---|
| Cost | $0.5 M | $ 1.65 M |
| dG | $40 M | $ 44 M |

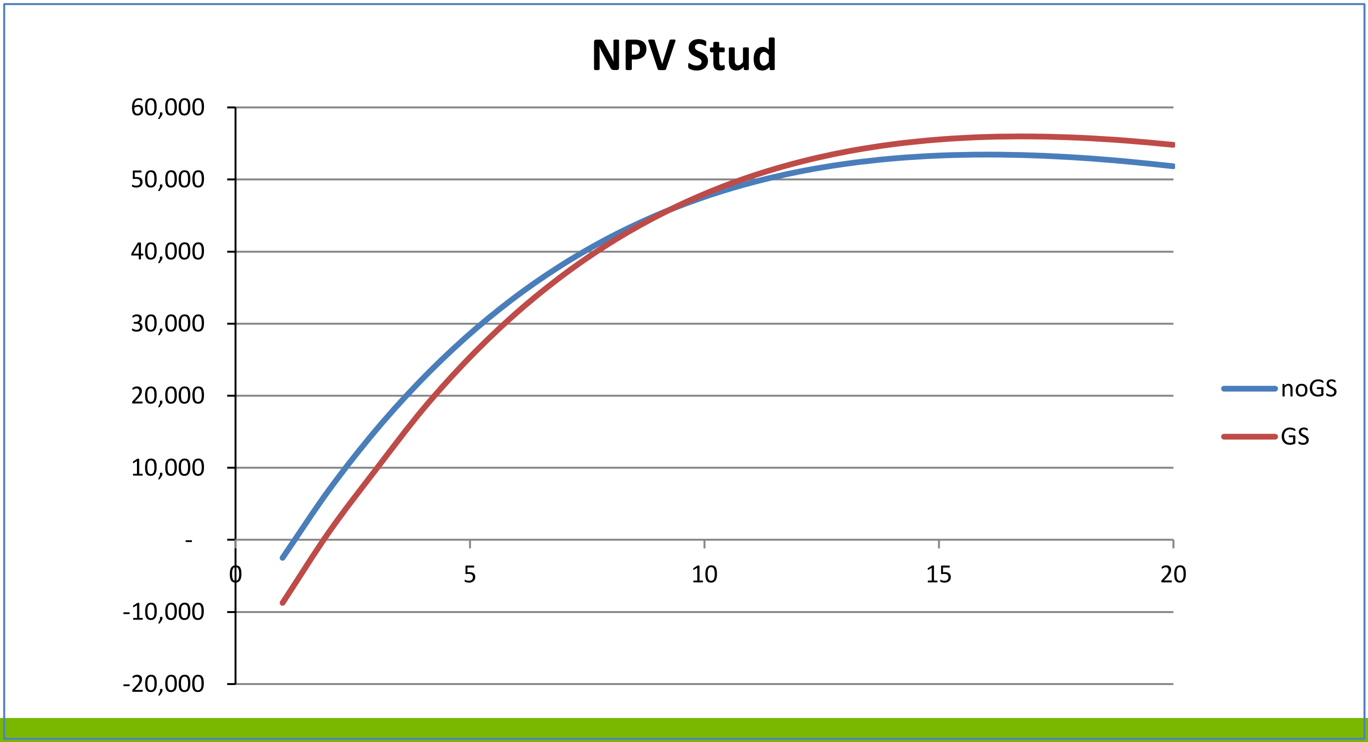



50k Nuc ewes
20M Comm

3 tier benefit

# Cost-Benefit Stud

| | No GS | GS |
|---|---|---|
| Cost | $ 5 k | $17.5 k |
| dG | $20 k | $ 22 k |




500 Nuc ewes
10k Comm

2 tier benefit

# Outline

- Economic value of genetic improvement
  - Value difference between two rams
  - Value of selecting better rams
      - Rams sold to Commercial
      - Rams used in Stud
  - Value of genetic improvement – whole flock

# Two Commercial Rams

| | ASBV PWWT |
|---|---|
| Ram 1: Kevin | +10 kg |
| Ram 2: Tony | +15 kg |

| | |
|---|---|
| Nr Progeny: | 100 |
| Value of 1 kg PWWT | $4 |
| Difference in progeny | 2.5 kg |

| | | | |
|---|---|---|---|
| Difference in value: as commercial rams | 5*$4 | * 100 | * 0.5 |
| | Selection Difference | Nr of Progeny | Expression per progeny |

= $1000.-

# Two Commercial Rams

| | $Index |
|---|---|
| Ram 1: Kevin | +190 |
| Ram 2: Tony | +180 |

Nr Progeny: 100

Difference in progeny $5

| | | | |
|---|---|---|---|
| Difference in value: as commercial rams | $10 | * 100 | * 0.5 |
| | Selection Difference | Nr of Progeny | Expression per progeny |

= $500.-

# Selecting Better Rams

| | | $Index |
|---|---|---|
| Average of 100 rams sold: | With Genomics | +182 |
| | No Genomics | +180 |

Nr Progeny: 100 per ram

Difference in progeny $1.0

| | | | |
|---|---|---|---|
| Difference in value: as commercial rams | $2 | * 100 | * 0.5 |
| | Selection Difference | Nr of Progeny | Expression per progeny |

= $100.- * 100 rams = $10,000.

# So principles are

Value of a superior ram

= Selection Difference * Nr.Progeny * expressions per progeny

We look at all expressions in <u>commercial</u> progeny

To evaluate benefit we need to predict

- the extra Selection Difference we can get

  *this will depend a lot on extra accuracy*

- the number of expressions

# How about selection of stud rams?

Value of a superior ram

= Selection Difference * Nr.Progeny * expression per progeny

Progeny in commercial,
so for a stud ram these
are actually
grand progeny,
great grand progeny, etc

# GENEFLOW

| | |
|---|---|
| males to males | females to males |
| males to females | females to females |

Donors of genes

Recipients of genes

| | Sires of Nucleus | | | | | Dams of Nucleus | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **P matrix** | 1 | 2 | 3 | 4 | 5 | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| 1 | 0 | 0.5 | 0 | 0 | 0 | 0 | 0.166667 | 0.166667 | 0.166667 | 0 | 0 | 0 | 0 | 0 | 0 |
| 2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 1 | 0 | 0.5 | 0 | 0 | 0 | 0 | 0.166667 | 0.166667 | 0.166667 | 0 | 0 | 0 | 0 | 0 | 0 |
| 2 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 3 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| 5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| 6 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| 7 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 | 0 |
| 8 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| 9 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| 10 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |

# GENEFLOW

Donors of genes

Recipients of genes

| | | | | | | | | |
|---|---|---|---|---|---|---|---|---|
| Sn<Sn | Sn<Dn | Sn<Sc | Sn<Cm | Sn<Cf | Sn | Sires of Nucleus | | |
| Dn<Sn | Dn<Dn | Sf<Sc | Dn<Cm | Dn<Cf | Dn | Dams of Nucleus | | |
| Sc<Sn | Sc<Dn | Sc<Sc | Sc<Cm | Sc<Cf | Sc | Stud born males to sire commercial | | |
| Cm<Sn | Cm<Dn | Cm<Sc | Cm<Cm | Cm<Cf | Cm | Commercial born males | | |
| Cf<Sn | Cf<Dn | Cf<Sc | Cf<Cm | Cf<Cf | Cf | Commercial born females | | |

# GENEFLOW

Donors of genes

| | P matrix | donors of genes: Sires of Nucleus 1 | 2 | 3 | 4 | 5 | Dams of Nucleus 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 | Stud born males to sire commercial 1 | 2 | 3 | 4 | 5 | Commercial born males 1 | 2 | 3 | 4 | 5 | Commercial born females 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| recipients of genes | 1 | 0 | 0.5 | 0 | 0 | 0 | 0 | 0.166667 | 0.166667 | 0.166667 | 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 |
| | 2 | 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 |
| | 3 | 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 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | 4 | 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 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| | 5 | 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 | 0 | 0 | 0 | 0 | 0 | 0 |
| | 1 | 0 | 0.5 | 0 | 0 | 0 | 0 | 0.166667 | 0.166667 | 0.166667 | 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 |
| | 2 | 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 | 0 | 0 | 0 | 0 |
| | 3 | 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 | 0 | 0 | 0 |
| | 4 | 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 | 0 | 0 |
| | 5 | 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 | 0 |
| | 6 | 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 |
| | 7 | 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 |
| | 8 | 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 |
| | 9 | 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 |
| | 10 | 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 |
| | 1 | 0 | 0.5 | 0 | 0 | 0 | 0 | 0.166667 | 0.166667 | 0.166667 | 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 |
| | 2 | 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 |
| | 3 | 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 |
| | 4 | 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 |
| | 5 | 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 |
| | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.166667 | 0.166667 | 0.166667 | 0 | 0 | 0 | 0 | 0 | 0 |
| | 2 | 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 |
| | 3 | 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 |
| | 4 | 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 |
| | 5 | 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 |
| | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.5 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.166667 | 0.166667 | 0.166667 | 0 | 0 | 0 | 0 | 0 | 0 |
| | 2 | 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 |
| | 3 | 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 |
| | 4 | 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 |
| | 5 | 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 |
| | 6 | 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 |
| | 7 | 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 |
| | 8 | 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 |
| | 9 | 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 |
| | 10 | 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 |

Recipients of genes

# GENEFLOW

- R = a matrix defining gene transmission of some superiority (or particular allele)

- Q= a matrix describing aging

- P = matrix describing transmission of genes
  - P=R+Q

$$m_t = P\ m_{t-1} + Rn_{t-1}$$

- m vector of allele frequency in each age class

- n vector to describe inserting allele or superiority

# GENEFLOW

| g1 | g2 | g3 | g4 | g5 | g6 | g7 | g8 | g9 | g10 | g11 | g12 | g13 | g14 | g15 | g16 | g17 | g18 | g19 | g20 | g21 | g22 | g23 | g24 | g25 |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 | 0.194699 | 0.20445 | 0.196265 |
| 1 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 | 0.194699 | 0.20445 |
| 0 | 1 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 | 0.194699 |
| 0 | 0 | 1 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 |
| 0 | 0 | 0 | 1 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 |
| 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 | 0.194699 | 0.20445 | 0.196265 |
| 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 | 0.194699 | 0.20445 |
| 0 | 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 | 0.194699 |
| 0 | 0 | 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 |
| 0 | 0 | 0 | 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 |
| 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 | 0.194699 | 0.20445 | 0.196265 |
| 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 | 0.194699 | 0.20445 |
| 0 | 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 | 0.194699 |
| 0 | 0 | 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 | 0.206315 |
| 0 | 0 | 0 | 0 | 0 | 0.5 | 0 | 0.333333 | 0.083333 | 0.305556 | 0.111111 | 0.273148 | 0.138889 | 0.251543 | 0.156636 | 0.236368 | 0.169496 | 0.225609 | 0.178498 | 0.21805 | 0.184849 | 0.212718 | 0.189324 | 0.208962 | 0.192477 |
| 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 | 0.206188 | 0.190297 | 0.204567 | 0.193304 | 0.203333 | 0.195378 |
| 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 | 0.206188 | 0.190297 | 0.204567 | 0.193304 | 0.203333 |
| 0 | 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 | 0.206188 | 0.190297 | 0.204567 | 0.193304 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 | 0.206188 | 0.190297 | 0.204567 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 | 0.206188 | 0.190297 |
| 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 | 0.206188 | 0.190297 | 0.204567 | 0.193304 | 0.203333 | 0.195378 |
| 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 | 0.206188 | 0.190297 | 0.204567 | 0.193304 | 0.203333 |
| 0 | 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 | 0.206188 | 0.190297 | 0.204567 | 0.193304 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 | 0.206188 | 0.190297 | 0.204567 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 | 0.206188 | 0.190297 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 | 0.206188 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 | 0.185905 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 | 0.208424 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 | 0.179479 |
| 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.25 | 0 | 0.208333 | 0.083333 | 0.229167 | 0.104167 | 0.22338 | 0.138889 | 0.218557 | 0.156057 | 0.214989 | 0.170332 | 0.211072 |

Allele frequency in the limit, from on ‘insertion’ of superiority (or an allele) = $1/(L_m + L_f)$

Geneflow mainly useful for initial part of an action, otherwise can use Rendel and Robertson

# Cumulative Discounted Expressions CDE

Value (V) in year t is worth now V.c where $c=1/(1+d)^t$

d = discount rate

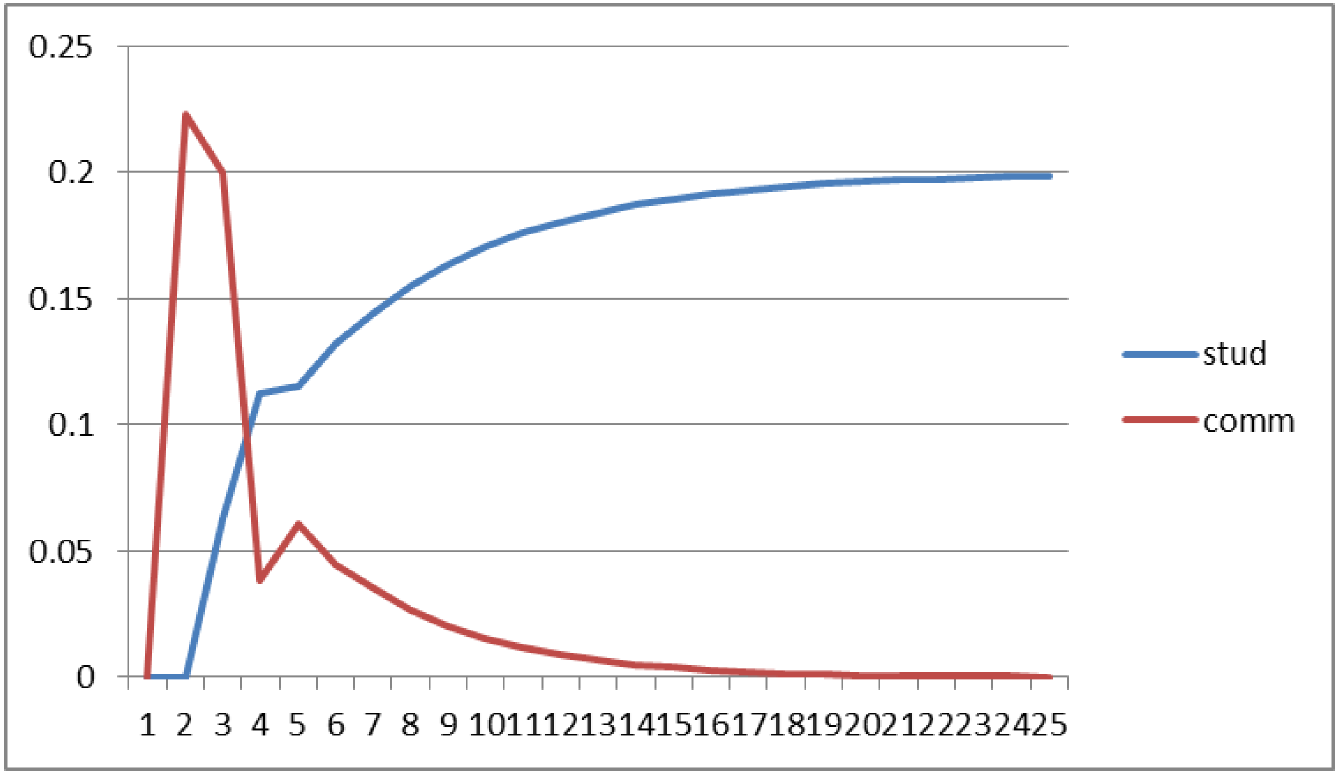
c = discount factor

Expression in age class i in year t is $m(i)_t = E_{it}$

Net Present Value of Sum of expression over 25 years

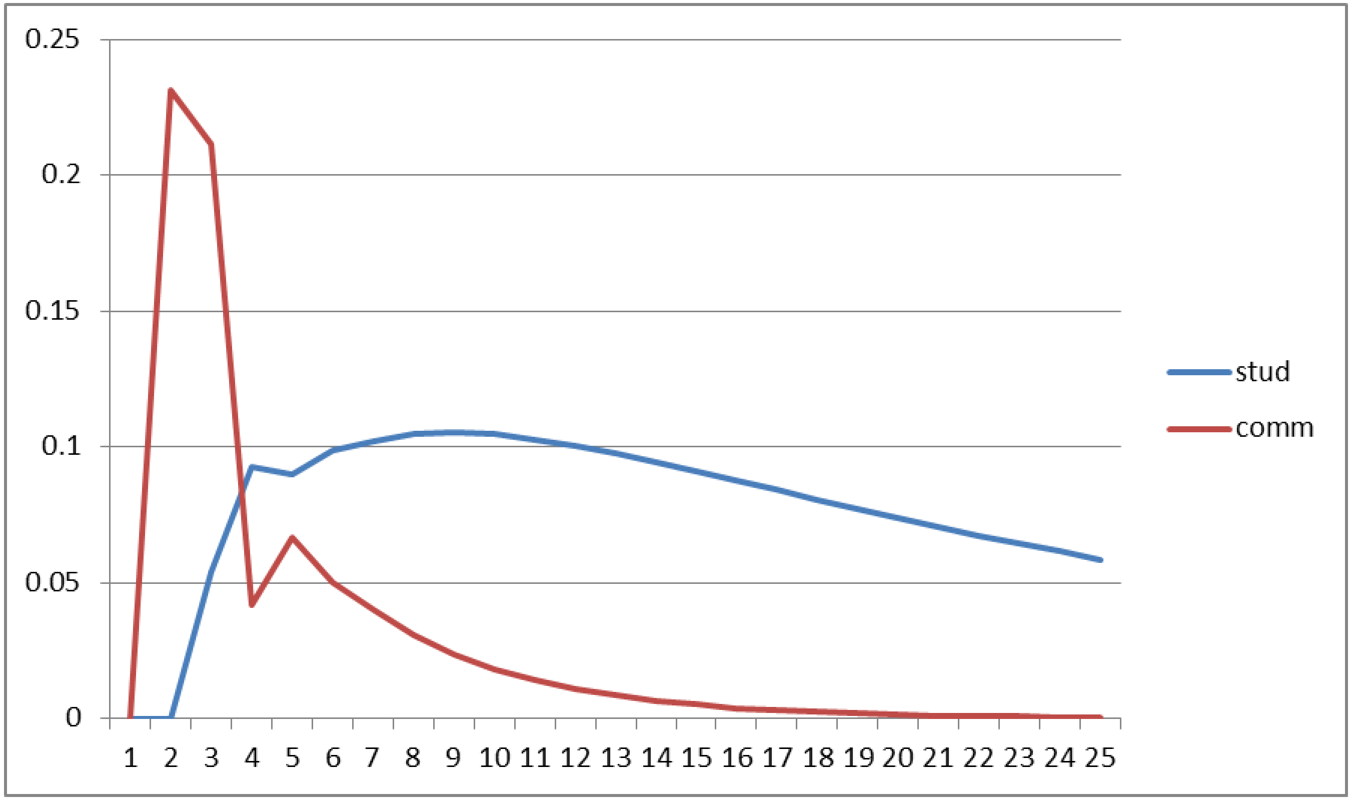
$$CDE = \sum_{t=1}^{25} \sum_{i=1}^{nac} E_{it} c_t$$

# (allele) frequency of one unit of superiority as expressed in commercial flock




| Discount rate | CDE flock rams | CDE stud rams |
|---|---|---|
| 0 | 0.99 | 3.93 |
| 0.05 | 0.78 | 1.96 |
| 0.08 | 0.68 | 1.37 |

# (allele) frequency of one unit of superiority as expressed in commercial flock




| Discount rate | CDE flock rams | CDE stud rams |
|---|---|---|
| 0 | 0.99 | 3.93 |
| 0.05 | 0.78 | 1.96 |
| 0.08 | 0.68 | 1.37 |

une

# Value of selecting Stud Rams and Flock Rams

## Value of a superior ram

CDE

= Selection Difference * Nr.Progeny * expression per progeny

| | | | | |
|---|---|---|---|---|
| Flock Ram | + 1.4 | 100 | 0.55 | = $ 77 |
| Stud Ram | + 3.0 | 400 | 1.35 | = $ 1,620 |

# Flock structure

| | |
|---|---|
| Nr Sheep Commercial Flock | 12,000 |
| Comm Dams/sire | 50 |
| Comm Sire replacem. rate | 0.5 |
| Comm Weaning rate | 1 |
| Nr new rams needed for comm flock/yr | 120 |
| Nr lifetime Progeny per commercial sire | 100 |
| Prop. Nucl.Males sold as breeding ram | 0.2000 |
| Nucleus weaning rate | 1 |
| Nuleus dams/sire | 40 |
| Nr Nucleus females | 1200 |
| Nr. Nucleus born progeny tested/yr | 600 |
| Nr. of Nucleus sires needed/yr | 30 |

100 prog/flock ram

400prog/stud ram

# Some real data

| | | |
|---|---|---|
| Commerical Flock | Nr Sheep Commercial Flock | 34,280 | |
| | Comm Dams/sire | 40 | |
| | Comm Sire replacem. rate | 0.33333 | |
| | Comm Weaning rate | 1.1 | |
| | Nr new rams needed for comm flock/yr | 286 | |
| | Nr lifetime Progeny per commercial sire | | 132 |

| | | | |
|---|---|---|---|
| Stud Flock | Prop. Stud.Males sold as breeding ram | 40% | |
| | Stud weaning rate | 1.28 | |
| | Stud dams/sire | 20 | |
| | Nr stud breeding ewes | 1116 | |
| | Nr. Of stud sires | 56 | |
| | Nr of flock rams sold per year | 286 | |
| | | | |
| | | | |
| | Nr of commercial rams sold per Stud male | 5.12 | |
| | | | |
| | Nr of commercial progeny receiving genes from a stud male | | 676 |

# Value of selecting Stud Rams and Flock Rams

Value of a superior ram = Selection Difference * Nr.Progeny * CDE

- Selection differential within the cohort: “The result of one round of selection”

| | | | | | | |
|---|---|---|---|---|---|---|
| Breeding performance | | | | | | |
| | | | SD of breeding Objective | 10.82 | | |
| | | | Male Selection intensity | 2.06 | | |
| | | | Female Selection intensity | 0.2 | | |
| | | | | | | |
| | | | Male Selection accuracy *without* genomics | 0.358 | increase | |
| | | | Male Selection accuracy *with* genomics | 0.432 | 21% | |
| | | | Female Selection accuracy | 0.358 | | |
| | | | Generation Interval Stud males | 1.53 | | |
| | | | Gneration Interval stud females | 2.97 | | |
| | approximaley | 1.90 | CDE stud sires | 1.90 | | |
| | | | CDE flock sires | 0.6 | | |
| | | | | no GS | GS | |
| | | | Sire superiority | 7.979534 | 9.628934 | |
| | | | Dam Superiority | 0.774712 | 0.774712 | increase |
| | | | Rate of gain/year | 1.945 | 2.312 | 19% |

# Comparing geneflow with dG/year method

| group | int | acc | | Sup | L | | dG/year |
|---|---|---|---|---|---|---|---|
| sires | 2.1543 | 0.53 | | 10.27622255 | 1.0 | | 3.233294535 |
| dams | 0.7979 | 0.37 | | 2.656955587 | 3.0 | | |

| | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | | Calculations based on dG/year | | | | calculations based on GFLOW | | | | |
| | | | | | | | sire | dam | | |
| | | dG/gen | | | | | selection | selection | | |
| | | 3.23 | | | dG/yr | superiority | 10.2762 | 2.6570 | | GFLOW |
| year | disc fact | genetic mean | cum benefit | cost | disc retruns | | Expr_SS | Expr_DS | cum benefit | disc retruns |
| 1 | 1.000 | 0 | $ - | $0 | $0 | | 0.000 | 0.000 | $ - | $ - |
| 2 | 0.935 | 0 | $ - | $0 | $0 | | 0.000 | 0.000 | $ - | $ - |
| 3 | 0.873 | 0 | $ - | $0 | $0 | | 0.119 | 0.000 | $ 14,694 | $ 12,834 |
| 4 | 0.816 | 0 | $ - | $0 | $0 | | 0.174 | 0.048 | $ 37,679 | $ 30,757 |
| 5 | 0.763 | 0 | $ - | $0 | $0 | | 0.131 | 0.105 | $ 57,158 | $ 43,606 |
| 6 | 0.713 | $3.23 | $ 38,800 | $0 | $27,664 | | 0.157 | 0.128 | $ 80,610 | $ 57,474 |
| 7 | 0.666 | $6.47 | $ 77,599 | $0 | $51,708 | | 0.185 | 0.149 | $ 108,155 | $ 72,068 |
| 8 | 0.623 | $9.70 | $ 116,399 | $0 | $72,487 | | 0.196 | 0.165 | $ 137,537 | $ 85,651 |
| 9 | 0.582 | $12.93 | $ 155,198 | $0 | $90,327 | | 0.197 | 0.178 | $ 167,514 | $ 97,494 |
| 10 | 0.544 | $16.17 | $ 193,998 | $0 | $105,522 | | 0.206 | 0.190 | $ 198,976 | $ 108,230 |
| 11 | 0.508 | $19.40 | $ 232,797 | $0 | $118,342 | | 0.213 | 0.199 | $ 231,559 | $ 117,713 |
| 12 | 0.475 | $22.63 | $ 271,597 | $0 | $129,034 | | 0.217 | 0.206 | $ 264,833 | $ 125,820 |
| 13 | 0.444 | $25.87 | $ 310,396 | $0 | $137,820 | | 0.220 | 0.211 | $ 298,645 | $ 132,602 |
| 14 | 0.415 | $29.10 | $ 349,196 | $0 | $144,904 | | 0.223 | 0.216 | $ 332,996 | $ 138,182 |
| 15 | 0.388 | $32.33 | $ 387,995 | $0 | $150,471 | | 0.225 | 0.220 | $ 367,735 | $ 142,614 |
| 16 | 0.362 | $35.57 | $ 426,795 | $0 | $154,690 | | 0.227 | 0.222 | $ 402,772 | $ 145,983 |
| 17 | 0.339 | $38.80 | $ 465,594 | $0 | $157,713 | | 0.228 | 0.225 | $ 438,053 | $ 148,384 |
| 18 | 0.317 | $42.03 | $ 504,394 | $0 | $159,678 | | 0.229 | 0.226 | $ 473,539 | $ 149,910 |
| 19 | 0.296 | $45.27 | $ 543,193 | $0 | $160,711 | | 0.230 | 0.228 | $ 509,179 | $ 150,648 |
| 20 | 0.277 | $48.50 | $ 581,993 | $0 | $160,926 | | 0.231 | 0.229 | $ 544,943 | $ 150,681 |
| 21 | 0.258 | $51.73 | $ 620,793 | $0 | $160,425 | | 0.231 | 0.230 | $ 580,808 | $ 150,092 |
| 22 | 0.242 | $54.97 | $ 659,592 | $0 | $159,300 | | 0.232 | 0.231 | $ 616,754 | $ 148,954 |
| 23 | 0.226 | $58.20 | $ 698,392 | $0 | $157,636 | | 0.232 | 0.231 | $ 652,763 | $ 147,337 |
| 24 | 0.211 | $61.43 | $ 737,191 | $0 | $155,508 | | 0.232 | 0.232 | $ 688,823 | $ 145,305 |
| 25 | 0.197 | $64.67 | $ 775,991 | $0 | $152,984 | | 0.233 | 0.232 | $ 724,923 | $ 142,916 |
| | | | | | | | | | | |
| | | | | NPV | $2,607,849 | | | | NPV | $ 2,645,255 |

Expressed in 12,000 ewes

20 nucleus sires

i.e. 600 per sire

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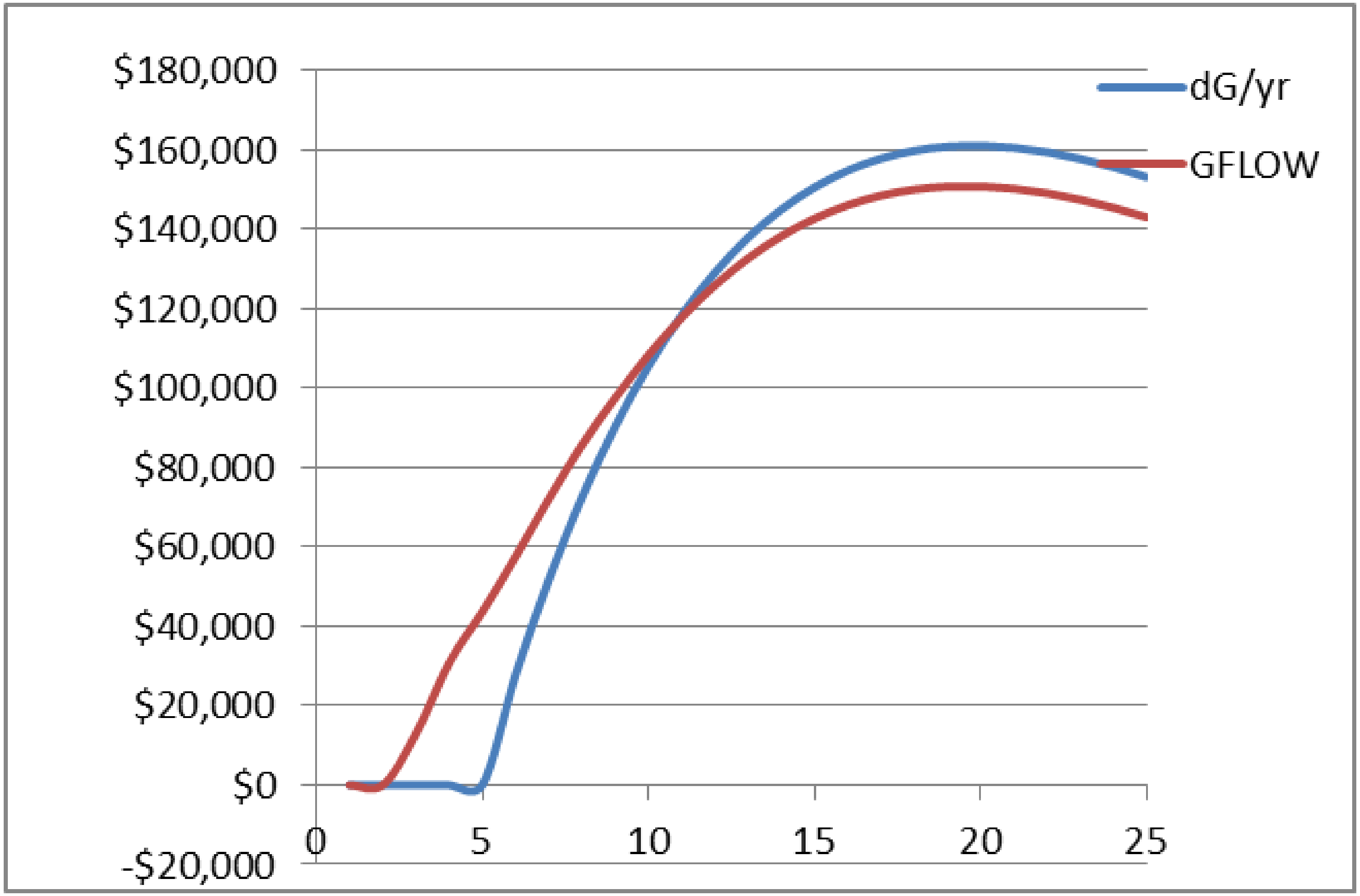
$180,000
$160,000
$140,000
$120,000
$100,000
$80,000
$60,000
$40,000
$20,000
$0
-$20,000
0
5
10
15
20
25
dG/yr
GFLOW

# Value of selecting Stud Rams and Flock Rams

## Value of a superior ram

= Selection Difference * Nr.Progeny * expression per progeny

| | | | | | |
|---|---|---|---|---|---|
| Flock Ram | + 1.4 | 100 | 0.55 | = $ 77 | |
| With Genomics | +1.6 | | | = $ 88 | +11 |
| Stud Ram | + 3.0 | 400 | 1.35 | = $ 1,620 | |
| With Genomics | +3.4 | | | = $ 1,836 | +216 |

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# Cost benefit analysis

- Extra benefit 120 * $11 + 30* $216 = $ 7,800
- If all young stud males tested: 600
- Break even: $13.00 per DNA test

# Merino: Breakeven ($) for testing

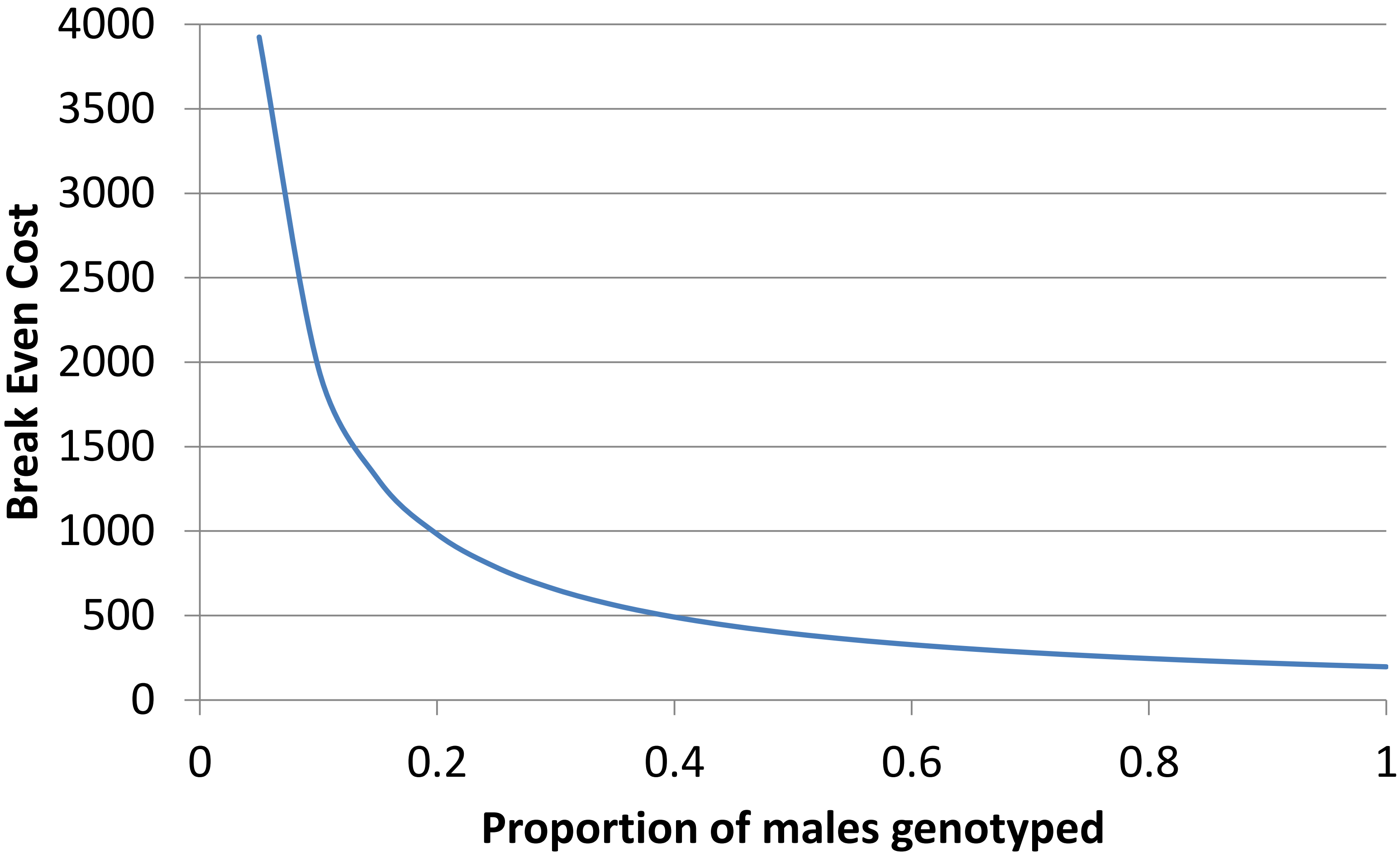
| Proportion tested | 100% | | 20% | |
|---|---|---|---|---|
| Age at first progeny | 1yo | 2yo | 1yo | 2yo |
| Breakeven ($/test) | 196 | 83 | 981 | 415 |

- assumes 40% males sold as rams

| % males born sold as rams | 40% | | 20% | |
|---|---|---|---|---|
| Age at first progeny | 1yo | 2yo | 1yo | 2yo |
| Breakeven ($/test) | 196 | 83 | 98 | 41 |

- assumes 100% of males tested

Breakeven cost and proportion genotyped  (no loss assumed!)




1yo male, 2yo female, Fine10% + SS, 40% males sold as rams

# What increase in price received per ram sold do you need to cover costs?

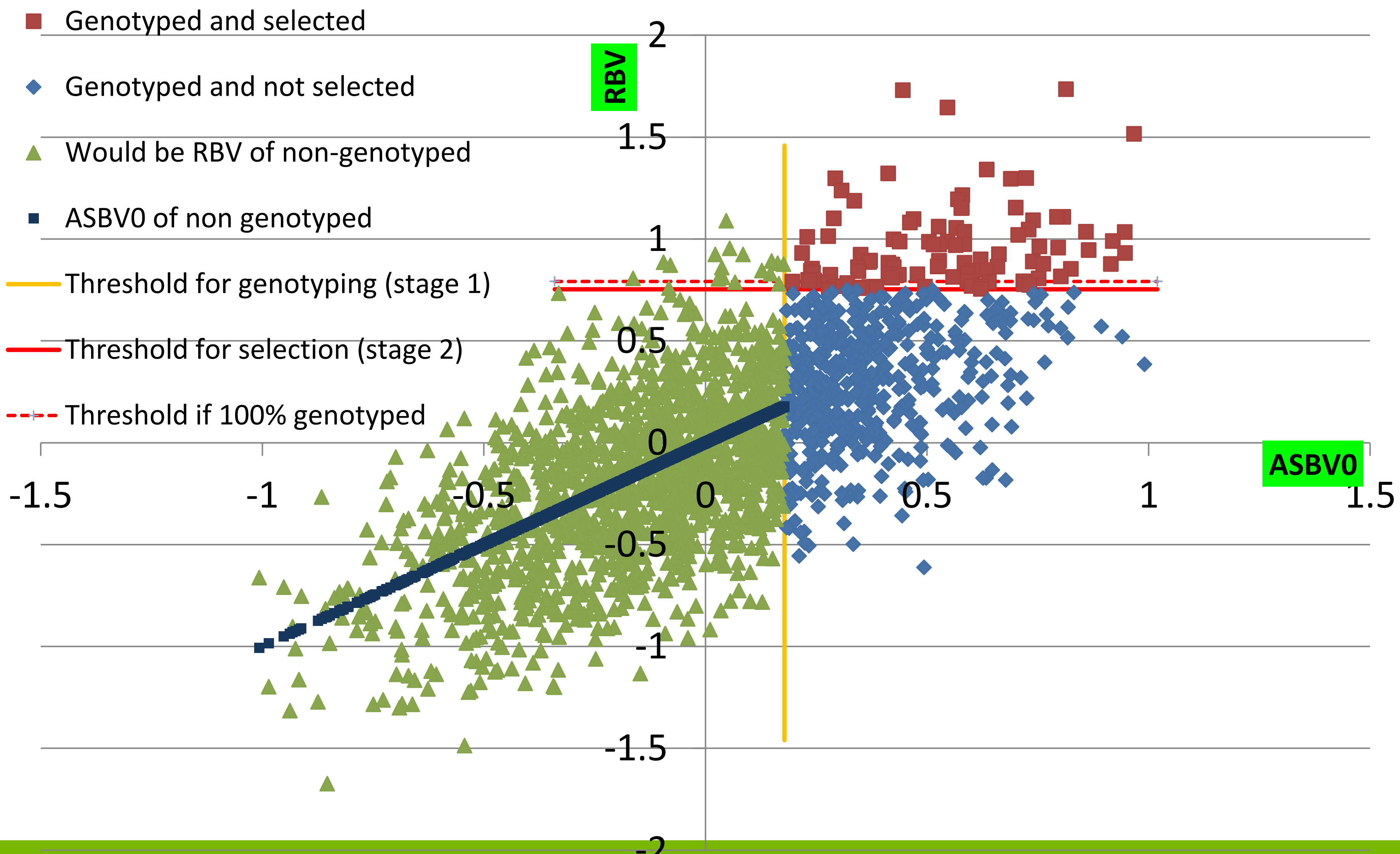
- total cost of genotyping/total nr of rams sold
  - 444 ewes @ 0.9 weaning rate = 200 ram lambs
  - Assume $50 genotype cost
  - Doesn’t account for collection costs etc.

| **Total ram lambs weaned** | **200** | **200** | **200** | **200** |
|---|---|---|---|---|
| % tested | 20 | 100 | 20 | 100 |
| nr tested (for use in nucleus) | 40 | 200 | 40 | 200 |
| Total test cost | 2000 | 10000 | 2000 | 10000 |
| % sold as flock rams | 20 | 20 | 40 | 40 |
| nr rams sold | 40 | 40 | 80 | 80 |
| Cost of test per ram sold | $50 | $250 | $25 | $125 |

# 2 stage selection

How many rams to genotype?

# 30% genotyped, 5% selected, correlation ASBV to RBV of 0.7

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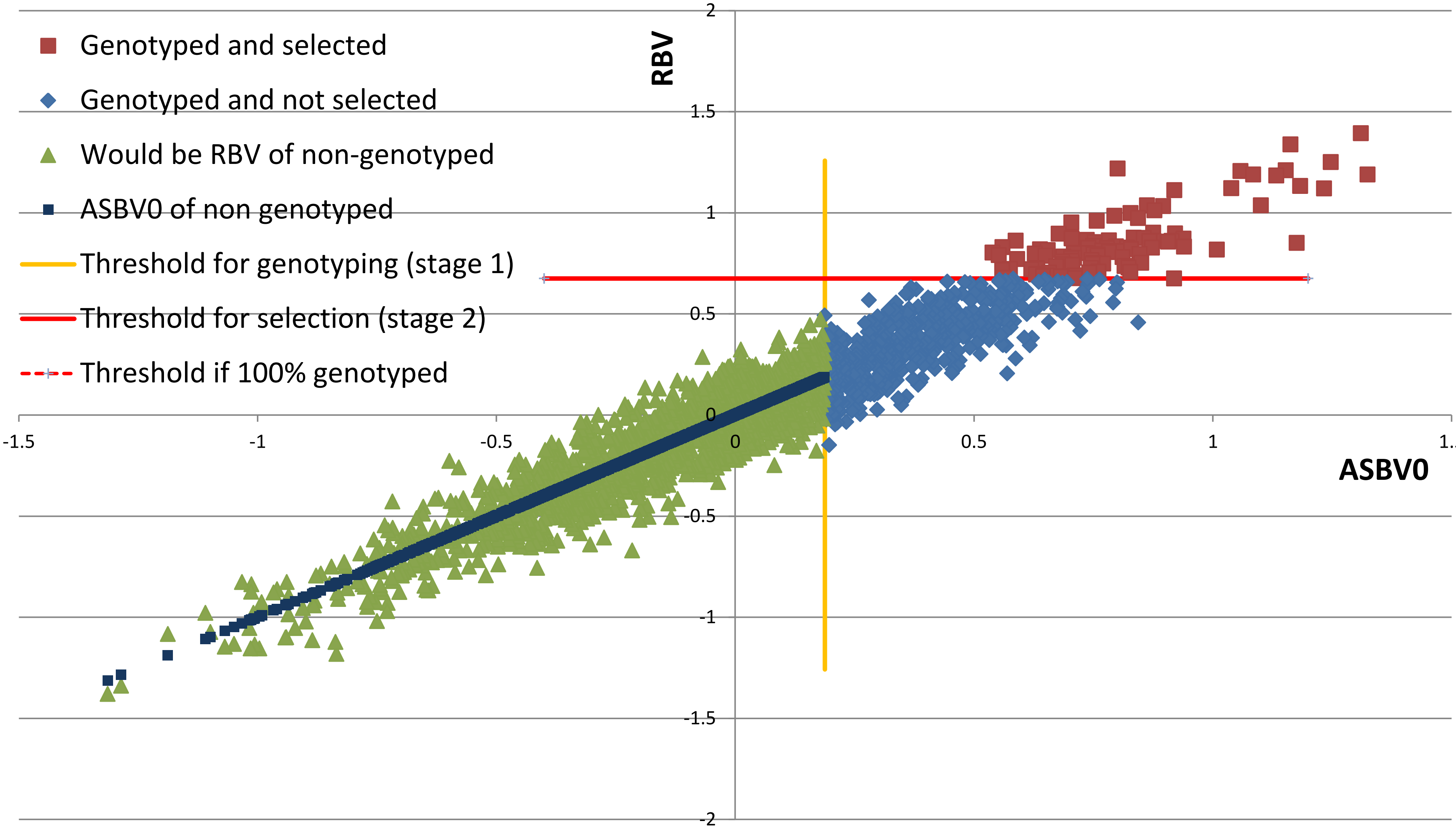
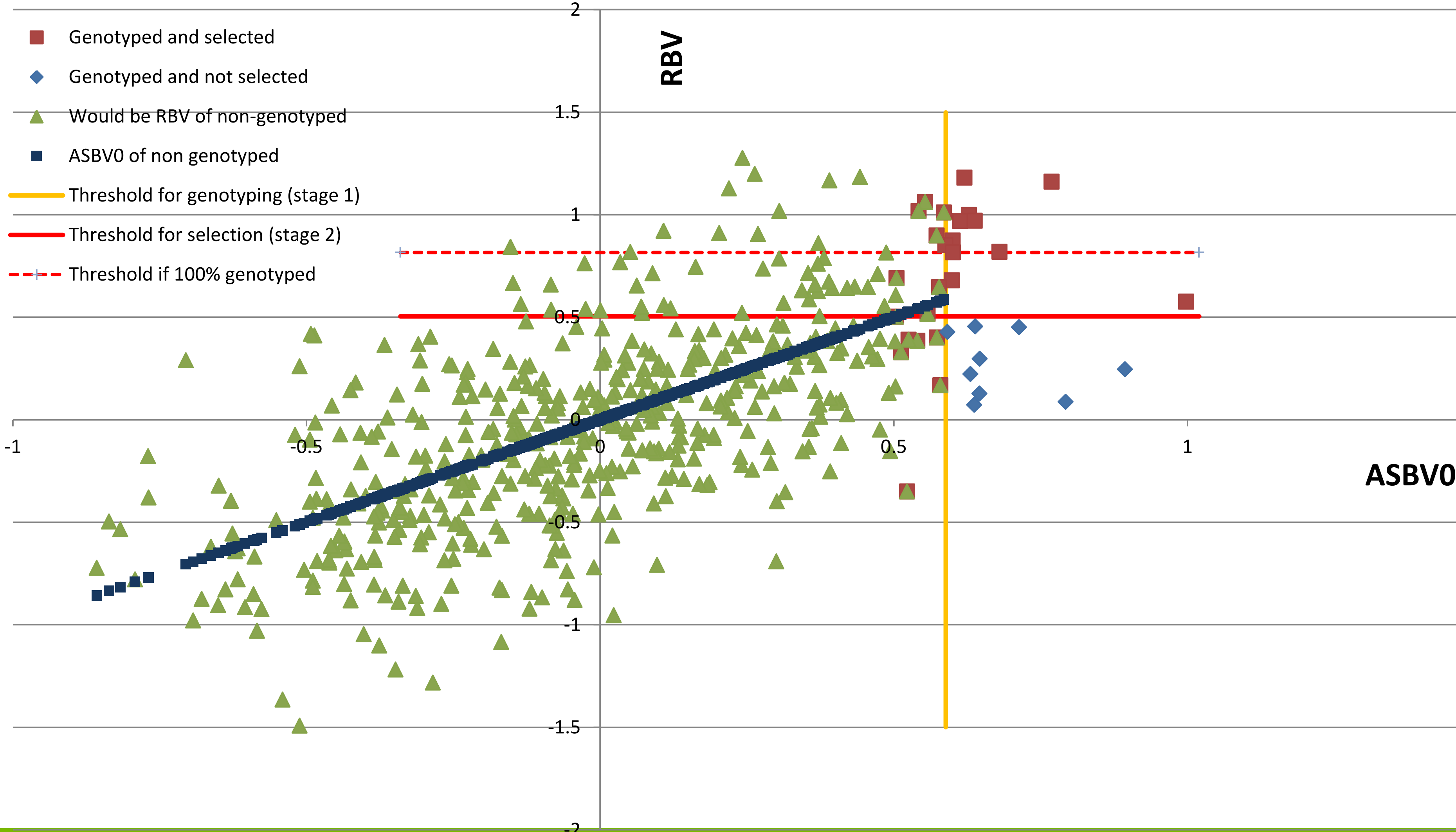
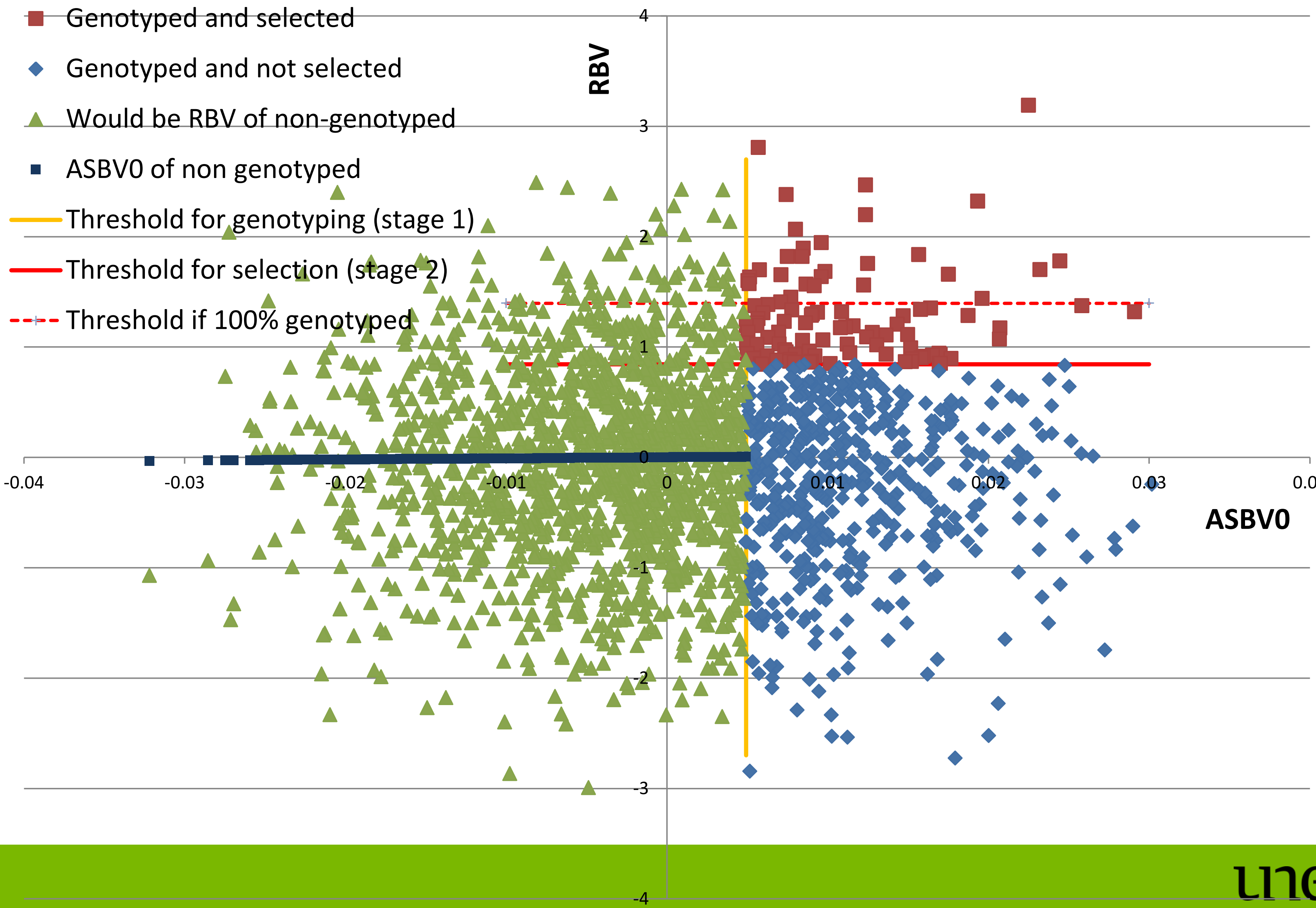
# 30% genotyped, 5% selected with very high correlation ASBV to RBV



# Very low proportion tested



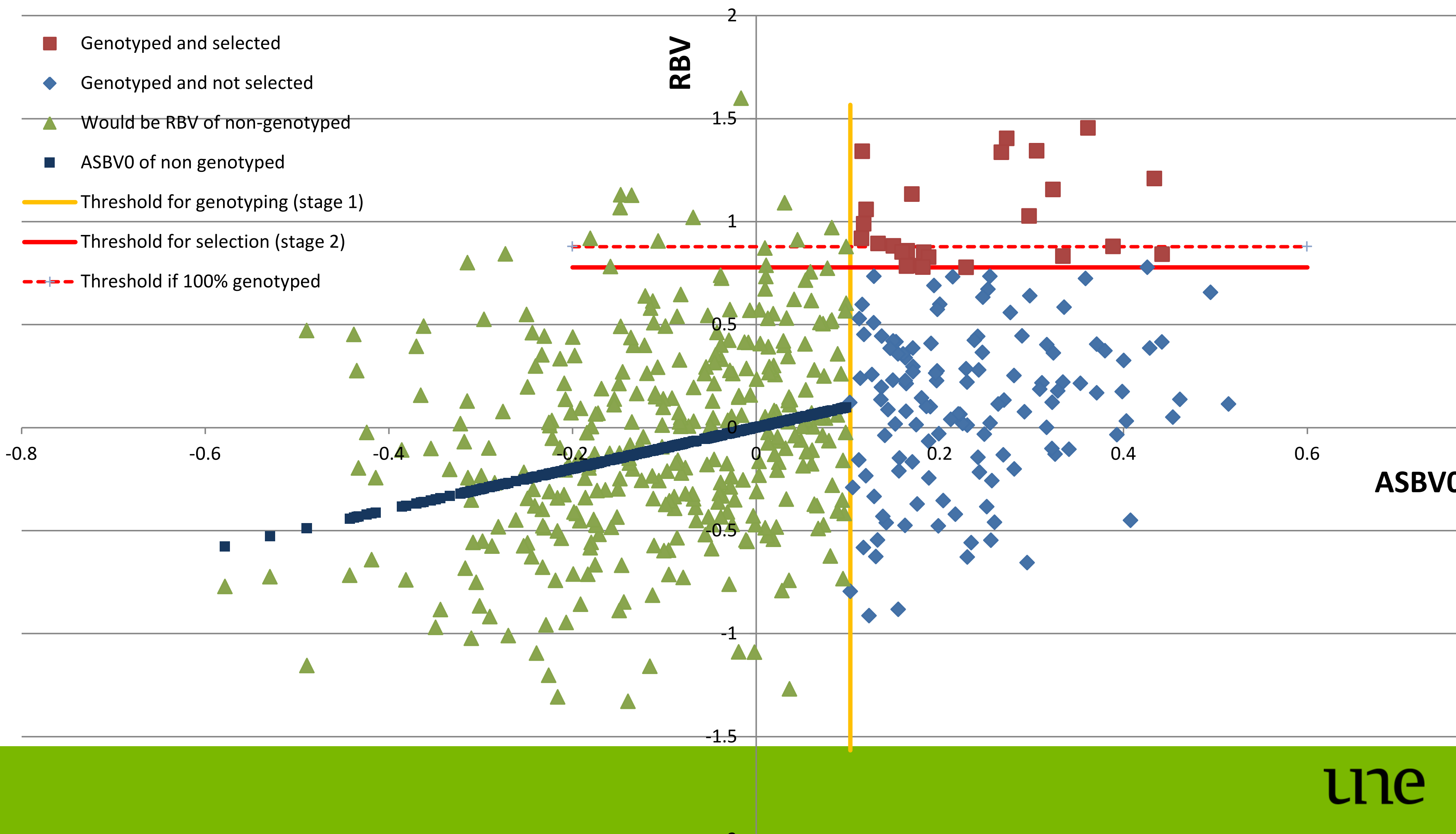
# 0.01 ASBV, 0.90 GBV, r = 0.9



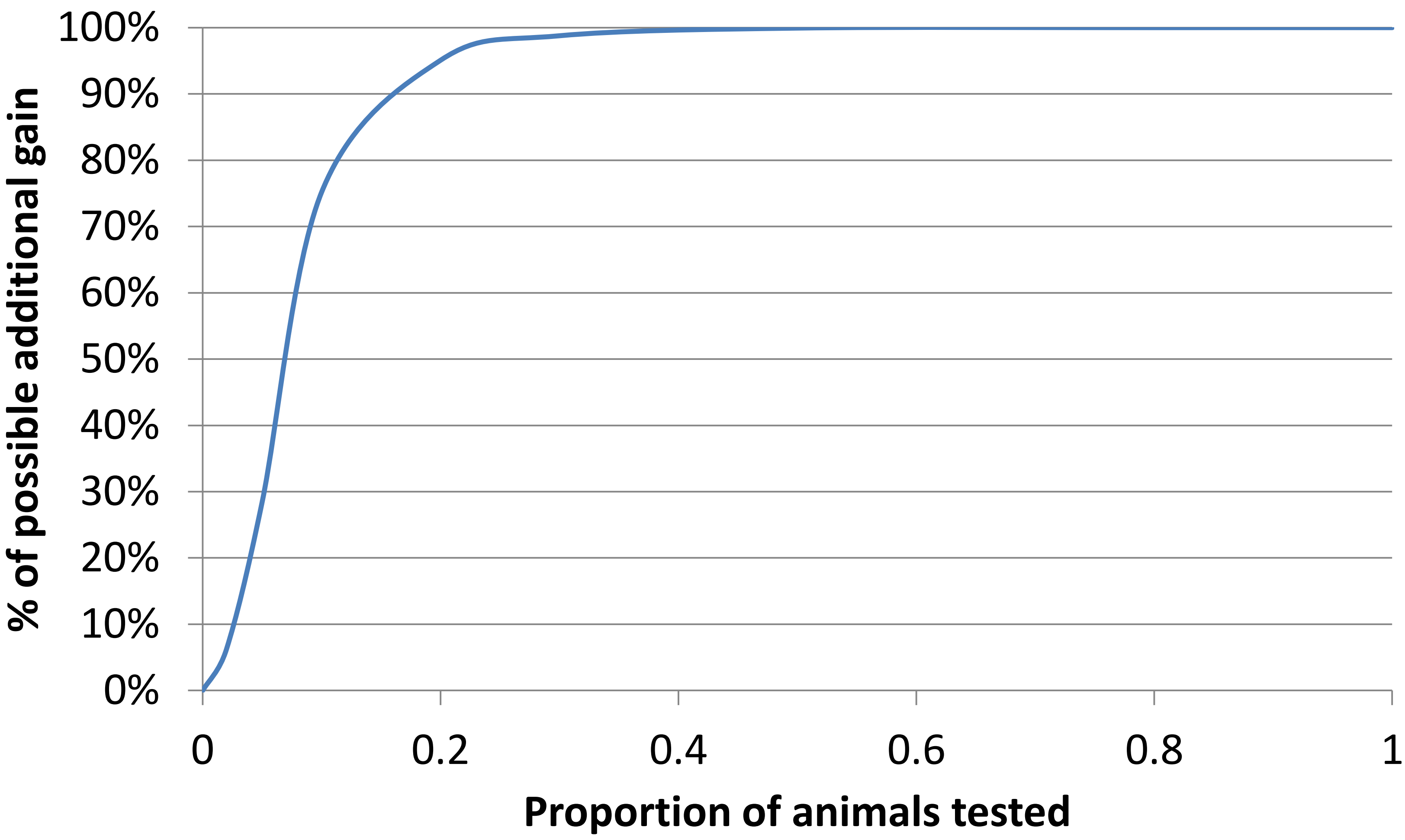
# Low ASBV acc% & high GBV

| | |
|---|---|
| ASBV0 | 0.20 |
| GBV | 0.50 |
| RBV | 0.52 |
| correlation ASBV0-RBV | 0.38 |
| | |
| prop genotyped | 0.3 |
| prop selected final | 0.05 |
| | |
| Selection Differential | 0.96 |
| SelDiff 100% genotyping | 1.08 |
| SelDiff 0% genotyping | 0.40 |
| % of possible additional gain | 82% |

# Low ASBVO acc% & high GBV



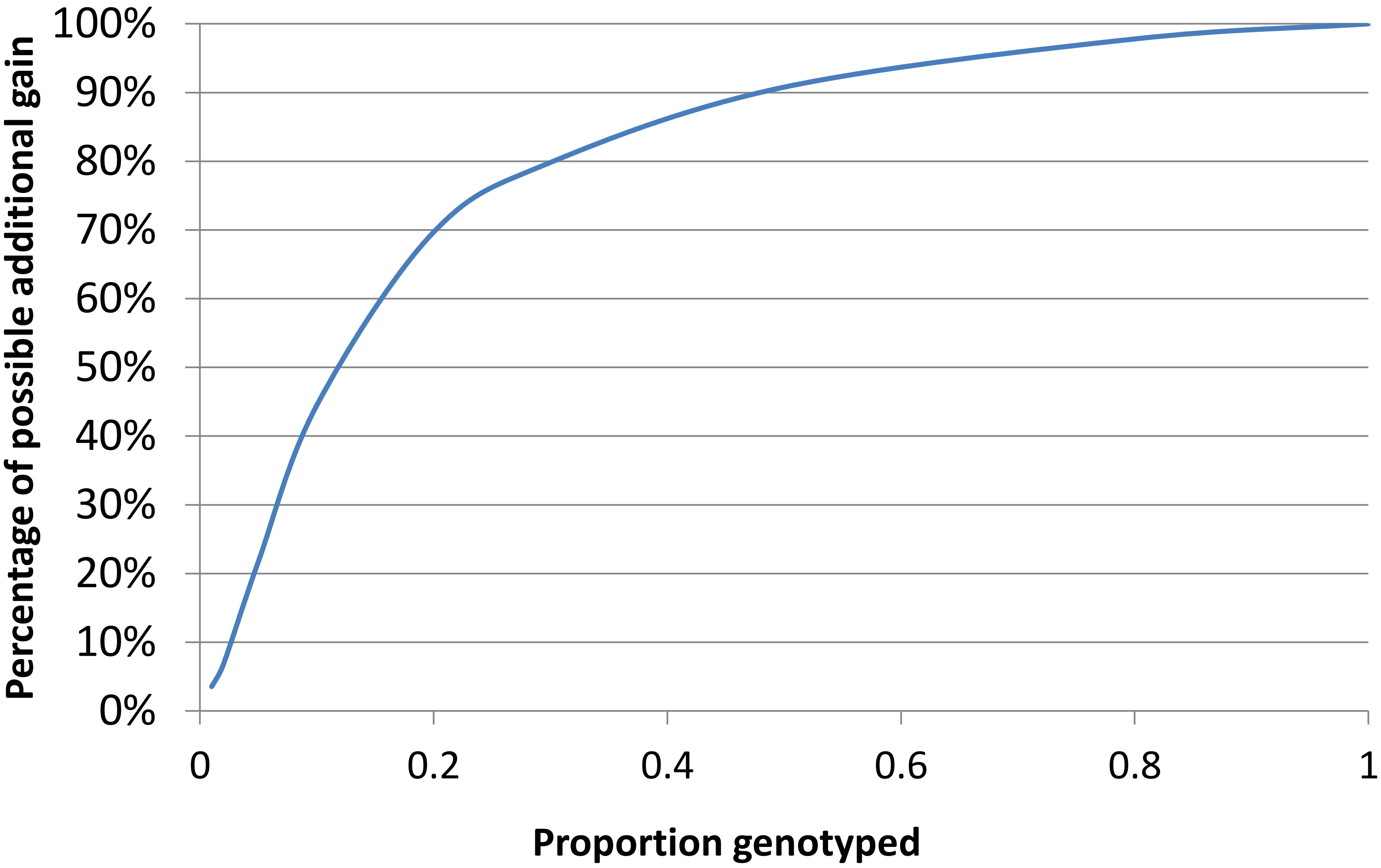
# % gain compared with 100% genotyping ASBV 0.34, GBV 0.39, RBV = 0.50, r = 0.7




At high(ish) correlation between ASBV and RBV only need to genotype ~20%

Fine SS10% for 1yo males with/without genomics testing

# % gain compared with 100% genotyping ASBV 0.10, GBV = 0.39, RBV 0.40, r = 0.25




At low(er) correlation between ASBV and RBV need to genotype more

# summary

- Can calculate additional gain on a per ram basis, assuming returns in commercial progeny

- Those figures depend on
  - Additional accuracy
  - Age structure
  - Flock parameters such as weaning rate, mating rate, prop. Sold
  - Can have strategies to save costs, e.g. test top 50%
  - Sonja will show many more examples