Multiple Trait Breeding Objectives

Multiple Trait breeding values

Selection on multiple traits

Predicting multi trait selection response

manipulating Multi Trait response

Multiple Trait Breeding Objectives

- Animals have many characteristics

» Do we want to improve them all ?

Issues with Multiple Trait selection

- We have to spread our selection efforts over several traits
- Not all traits are equally important economically
- Not all traits are equally heritable
- There are correlations between traits
    - Selection for one trait gives also a correlated response for other traits

  – How to weight optimally the different traits?

Multiple Trait Selection

- Setting the Breeding Objective
- Defining MT Selection Weights
- Predicting MT Selection Response
- Manipulating MT Selection Response

Breeding Objectives

To optimise genetic improvement we need to know:

- Where do we want to go?

AND

- How are we going to get there?

Introduction to Breeding Objectives

Where do we want to go?

Many possible traits to improve

Many possible traits to record

What is the value of improving different traits?

How do we combine information on different traits to get to where we want to go?

What is a Breeding Objective?

Overall statement about what we want to achieve

e.g.

- Maximise profit
- Minimise costs
- Maximise bad temper and ugliness
- Maximise gross national happiness (Kingdom of Bhutan)

How Much is Each Animal Worth in Terms of the Breeding Objective?

Each individual has many traits that might have some value in relation to the breeding objective.

We need a way of determining the value of each trait and then combining those values into an overall value of the individual in relation to the breeding objective

What is an Aggregate Genotype?

A function of genetically controlled traits that contribute value to the breeding objective, that, if maximised (or minimised) will achieve the breeding objective.

$$H = v_1g_1 + v_2g_2 + v_3g_3 \ldots\ldots etc$$

Note:
linearity assumed here
(big assumption?)

Where:

v_i are ***economic weights***

g_i are additive genetic values of an individual animal

What is a Selection Index?

A function of genetically controlled phenotypes (or EBV) that if maximised will maximise the aggregate genotype which will achieve the breeding objective.

$$I = b_1x_1 + b_2x_2 + b_3x_3 \ldots\ldots etc$$

Where b_i are ***selection index weights*** and x_i are the phenotypes (or EBV) of an individual animal

The Logical Process

Define breeding objective

Develop the aggregate genotype

Develop selection index

Defining an Aggregate Genotype

$H = v_1g_1 + v_2g_2 + v_3g_3$……etc

Which traits are included?

- All ***genetically controlled*** traits that contribute to profit
- Exclude traits that only indirectly associated with profit (eg conformation traits)
- Can exclude traits with very little genetic variation (not the same as low heritability)

Note: Not all traits in H may be measured, and there is limited cost associated with including them in H.

Defining an Aggregate Genotype

$$H = v_1g_1 + v_2g_2 + v_3g_3 \ldots\ldots etc$$

An **economic weight**, v_i , is a partial weight; it is the value of increasing trait i by one unit when all other traits remain unchanged.

An **economic weight** is the rate of change in profit as the genetic mean of the trait changes, when all other traits remain unchanged

Selection Index / Selection Criteria Traits

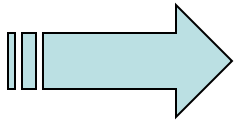
$I = b_1x_1 + b_2x_2 + b_3x_3$……etc

Which traits are included?

- Traits that are relatively easy to measure
- Traits that are included in H
- Traits that are correlated with traits in H

Note: These traits require measurement (=cost) so need to do cost-benefit on whether worth while to include them

Selection Index Concept

Selection Criteria  Breeding Objective

Own performance X_{11}

Performance on relatives X_{12}

Breeding Value (g_1)

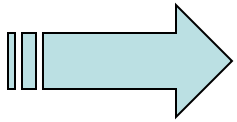
X_{12} = phenotypic measurement (2^{nd} source on Trait 1)

g_1 = breeding value for trait 1

Selection Index (multiple regression)

$$EBV_1 = b_1X_{11} + b_2X_{12} + ...$$

Selection Index Concept

Selection Criteria  Breeding Objective

Own performance X_{11}

Performance on relatives X_{12}

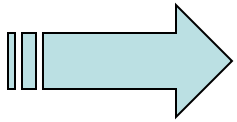
Correlated Trait **X_{21}**

Breeding Value (g_1)

Selection Index (multiple regression)

$$EBV_1 = b_1X_{11} + b_2X_{12} + b_3X_{21} + ...$$

Selection Index Concept

Selection Criteria  Breeding Objective

Own performance X_{11}

Performance on relatives X_{12}

Correlated Trait **X_{21}**

Breeding Value (g_1)

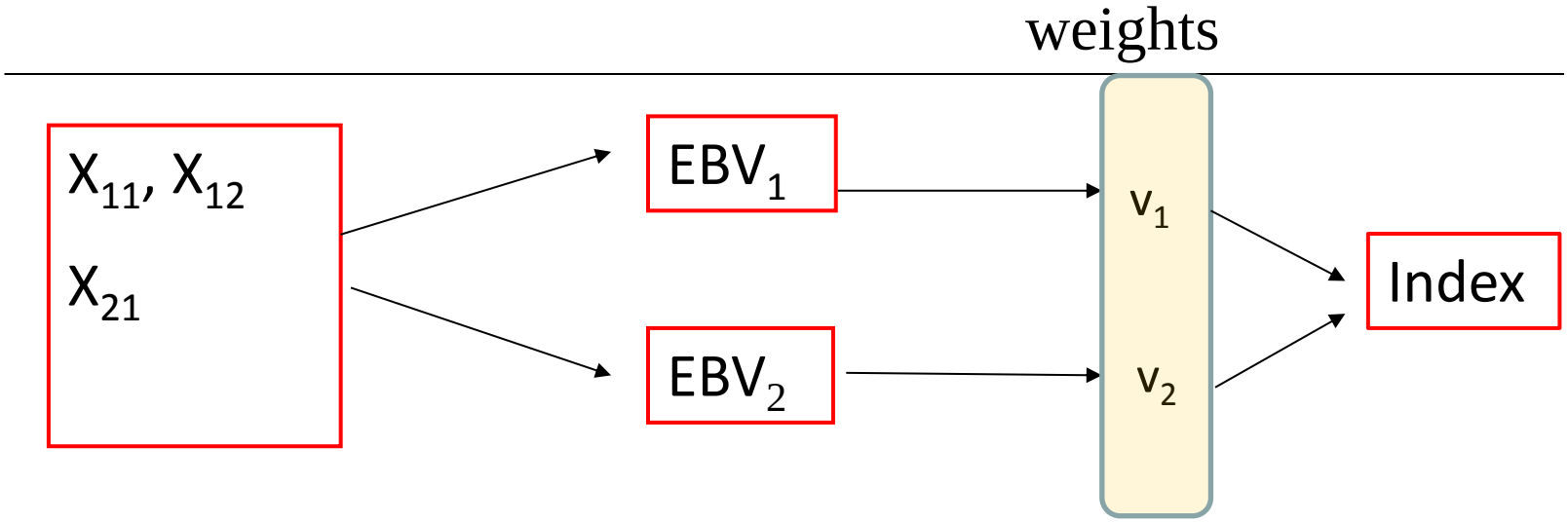
Breeding Value (g_2)

Selection Index (multiple regression)

$$EBV_2 = b_1X_{11} + b_2X_{12} + b_3X_{21} + ...$$

Selection Index Concept

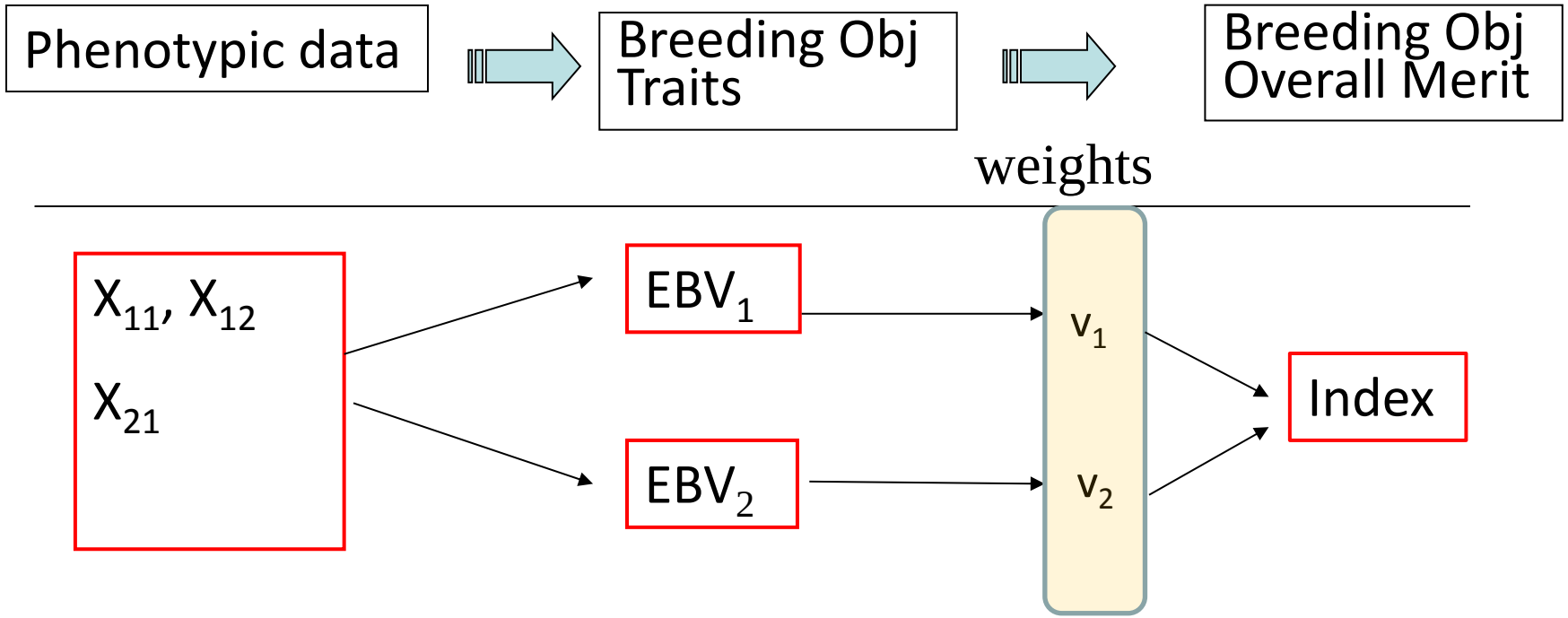
Phenotypic data → Breeding Obj Traits → Breeding Obj Overall Merit



Selection Index (multiple regression)

$$\text{Index} = b_1X_{11} + b_2X_{12} + b_3X_{21} + \ldots.$$

Selection Index Concept



Selection Index (multiple regression)

$$\text{Index} = I = \begin{matrix} v_1\,EBV_1 \\ + \\ v_2\,EBV_2 \end{matrix} = \begin{matrix} v_1\,[\,b_{11}X_{11} + b_{12}X_{12} + b_{13}X_{21} + \ldots..] \\ + \\ v_2\,[\,b_{21}X_{11} + b_{22}X_{12} + b_{23}X_{21} + \ldots..] \end{matrix}$$

Some formal definitions

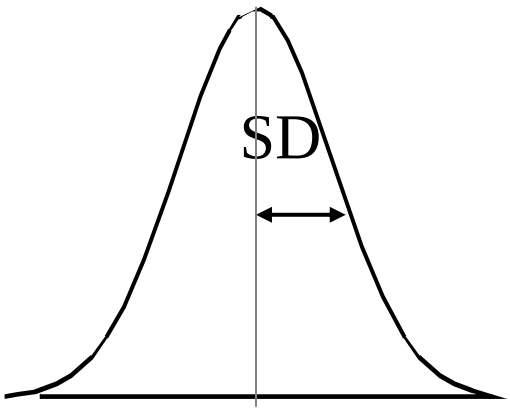
Aggregate Genotype / Breeding Goal

$$H = v_1g_1 + v_2g_2 + v_3g_3 \ldots\ldots \text{etc} = v'g$$

Var (H) = σ_H^2 = v'Cv where C = var(g)

σ_H = SD of breeding objective = SD in profit

$\sigma_H \cong$ \$10 (sheep)
\$30 (beef)
\$50 (dairy)



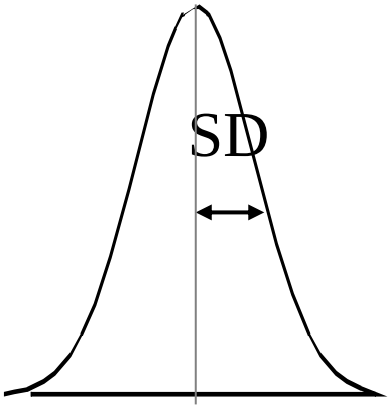
SD of genetic merit for 'profit'

Some formal definitions

$H = v_1g_1 + v_2g_2 + v_3g_3 \ldots\ldots etc = v'g$

$I = b_1x_1 + b_2x_2 + b_3x_3 \ldots\ldots etc$

σ_I = SD of Index



SD of $index

Var (H) = $\sigma_H^2 = v'Cv$

Var(I) = b'Pb

where P = var(x)

cov(x,g) = G

$b = P^{-1} G$

accuracy = σ_I / σ_H

note: $\sigma_I < \sigma_H$

Some basic Quantitative Genetic Theory

single trait

$P = A + E$ → General Model

$Var(P) = var(A) + var(E) = V_A + V_E$ no cov. between A and E

$cov(A_i,P_i) = cov(A_i, A_i) + cov(A_i, E_i) = V_A$ if A same animal as P

$cov(A_i,P_i) = cov(A_j, A_i) + cov(A_j, E_i) = a_{ij}V_A$ aij = additive genetic relationship between i and j

$cov(P_i, P_j) = a_{ij}V_A$ as E's are uncorrelated if not same animal

Some basic Quantitative Genetic Theory

multi trait

$cov(P_{1i}, P_{2i}) = r_p \sigma_{P1} \sigma_{P2}$

phenotypic covariance as

E's are correlated if same animal

$cov(P_{1i}, P_{2j}) = a_{ij} r_g \sigma_{g1} \sigma_{g2}$

genetic covariance as

E's are uncorrelated if not same animal

$cov(A_{1i}, P_{2i}) = r_g \sigma_{g1} \sigma_{g2}$

if A_1 same animal as P_2

$cov(A_{1i}, P_{2j}) = a_{ij} r_g \sigma_{g1} \sigma_{g2}$

if A1 not same animal as P2

In general,
when between traits, replace variance by covariance

Types of correlations

- Phenotypic correlations
  - measure association between observed performance
  - Cows that produce more milk tend to have lower fertility

- Genetic correlations
  - measure association between breeding values
  - Bulls with daughters that produce more milk tend to have daughters with lower fertility

  - Due to pleiotropy or linkage (may be +ve or –ve)

Types of correlations

- Phenotypic correlations (r_p)
  - measure association between observed performance
- Genetic correlations (r_g)
  - measure association between breeding values
- Environmental correlations (r_e)
  - measure association between random environmental effects

$P = A + E$

- Recall Variances add up $V_P = V_A + V_E$
- Similarly Covariances add up $Cov_P = Cov_A + Cov_E$

But correlations do not add up! $r_p \neq r_A + r_E$

Selection index with more information sources (multiple regression)

p = vector with phenotypes (criteria)

g = breeding objective (single trait BV here)

var*(p)* = P = matrix = $\begin{bmatrix} \text{var}(x_1) & \text{cov}(x_1, x_2) \\ \text{cov}(x_2, x_1) & \text{var}(x_2) \end{bmatrix}$

cov*(p,*g) = G = vector = $\begin{bmatrix} cov(x_1, g) \\ cov(x_2, g) \end{bmatrix}$

weights: $b = P^{-1}G$

Selection index with more information sources and with more objective traits (multiple regression)

p = vector with phenotypes (criteria)

H = breeding objective (multiple traits here)

= $v_1 g_1 + v_2 g_2$

var(*p*) = P = matrix =

$$\begin{bmatrix} \text{var}(x_1) & \text{cov}(x_1, x_2) \\ \text{cov}(x_2, x_1) & \text{var}(x_2) \end{bmatrix}$$

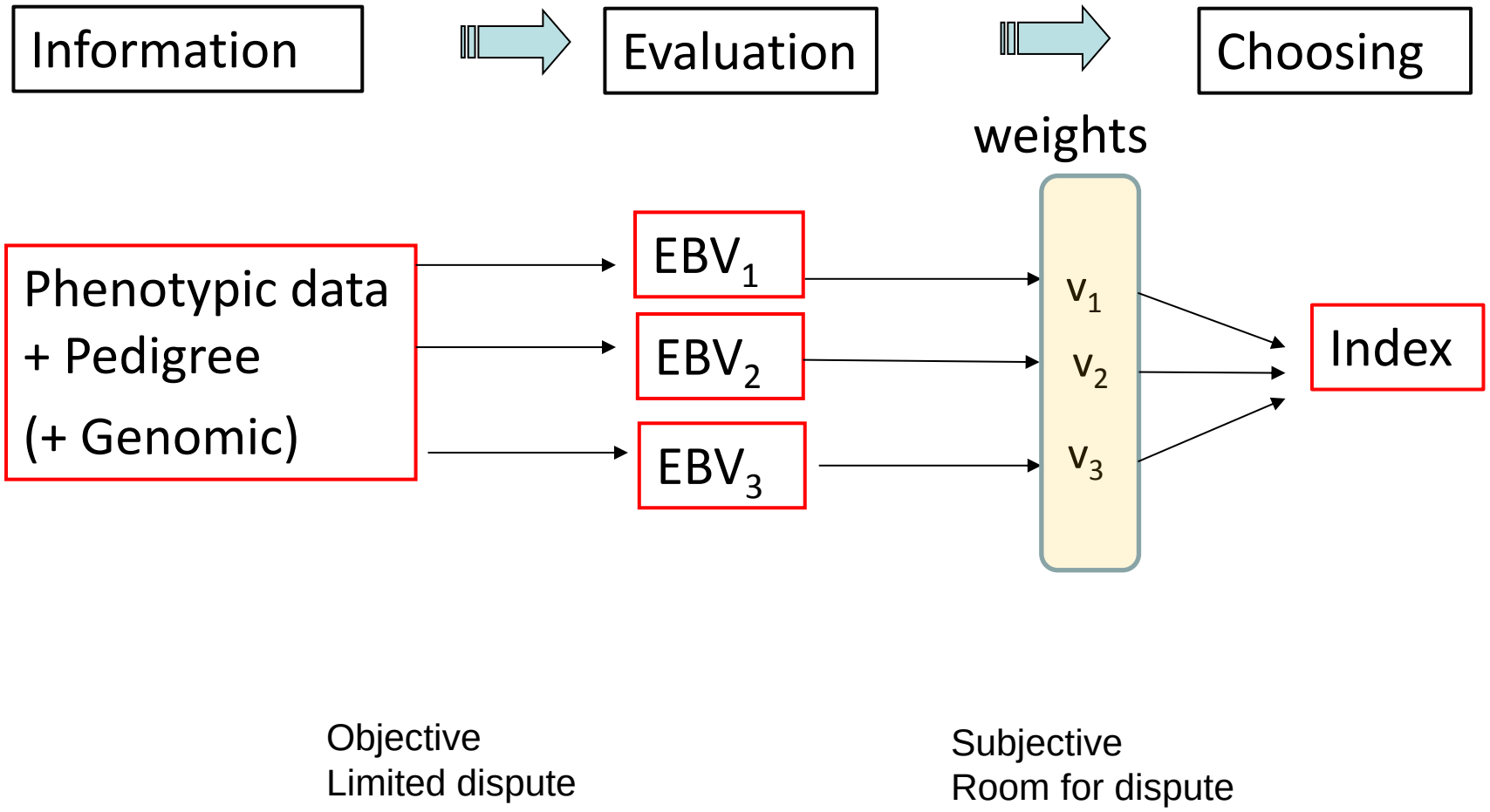
cov(*p*,A) = G = matrix =

$$\begin{bmatrix} cov(x_1, g_1) & cov(x_1, g_2) \\ cov(x_2, g_1) & cov(x_2, g_2) \end{bmatrix}$$

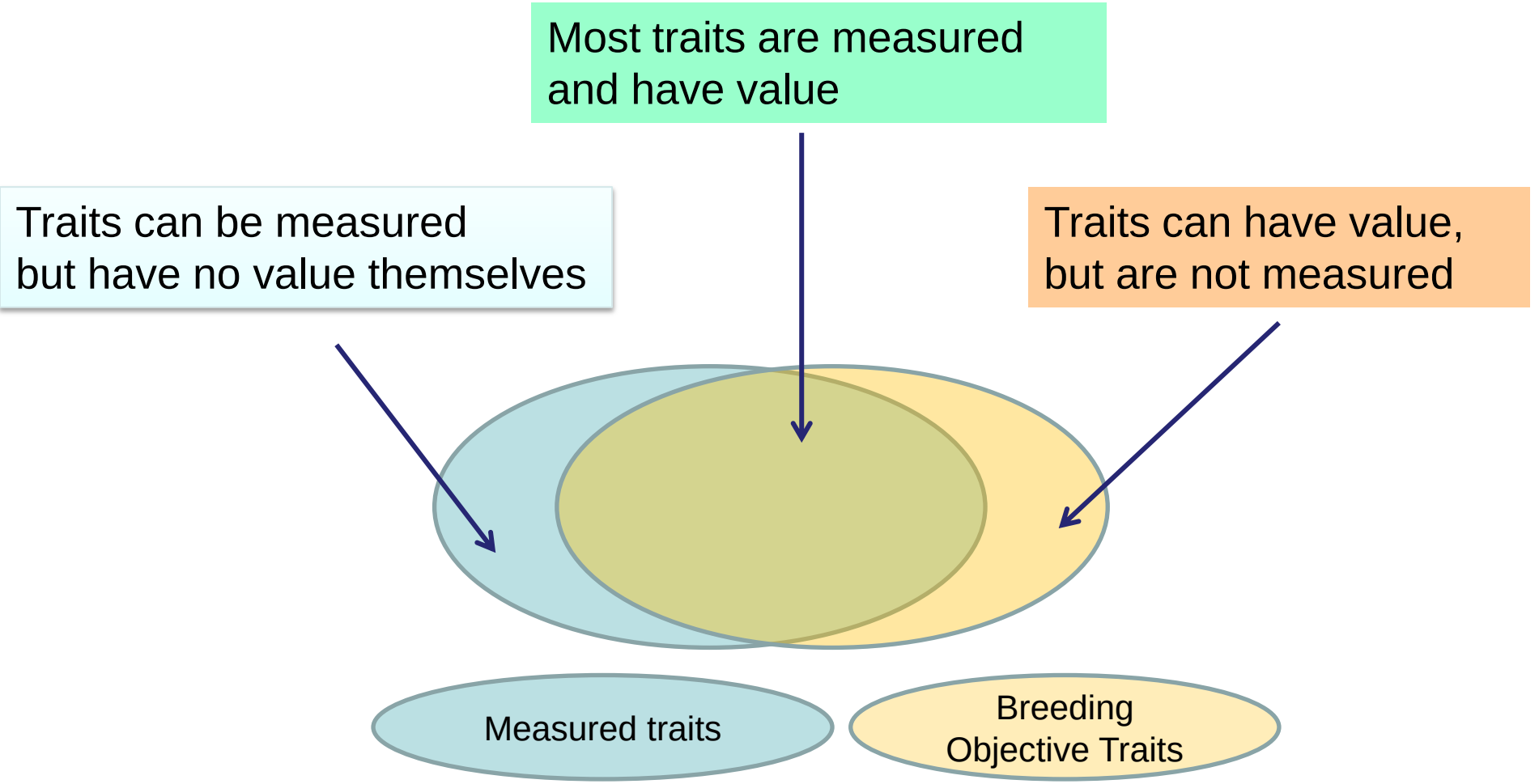
weights: $b = P^{-1}Gv$

V are economic values

Back to Selection Index Concept

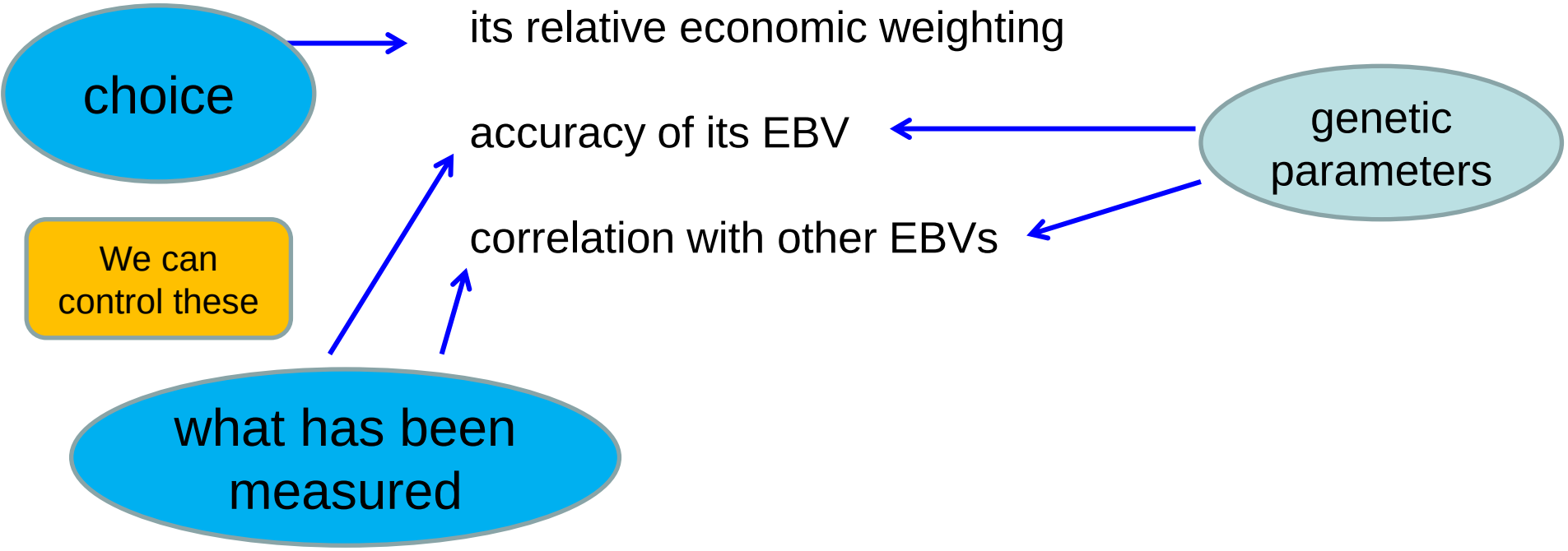


Breeding objective traits and selection criteria traits



Some important points about MT selection

1 The ultimate response of a trait will depend on:



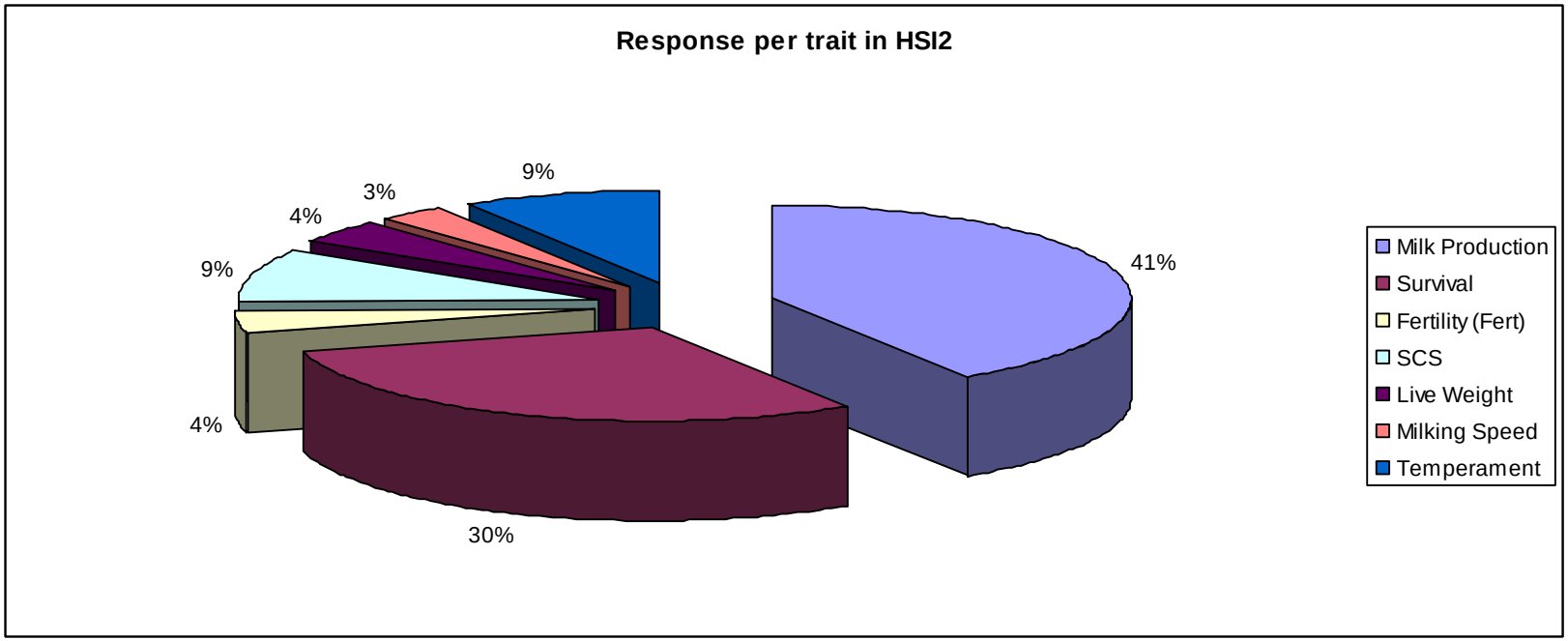
Some important points

The index weight is not always reflecting the response

Some traits are easier to improve than others

Some traits are easier to improve *jointly* than others

What is this “percent emphasis”



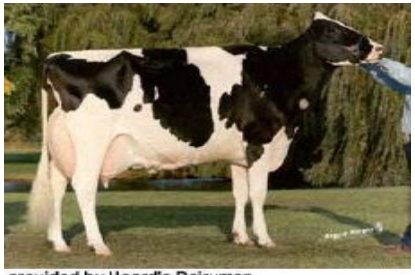
e.g. UK: “55% focus on fitness traits” ; “remaining 45% of index covering production”

Index weights?

Selection response?

Index weight vs Selection response

	weights	response	weights	response
Milk Kg	0	321	1	368
Protein Kg	1	11.0	0	9.6



provided by Hoard's Dairyman

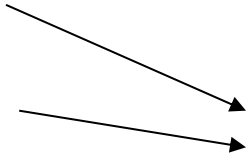
	weights	response	weights	response
Protein Kg	4	9.0	4	11.0
Live Weight Kg	-1	12.5	0	24.9

Some important points

The EBV of a trait can reflect another trait

Body Weight X_{11}

Body Weight on relatives X_{12}



EBV for fertility (g_2)

In this case, selection of $EBV_{fertility}$ will increase fertility,
but it will even more increase body weight!

Can predict changes from MT selection using selection index

Need to understand some important MT principles → ellipse

Predicting genetic change to multiple trait selection

- Single trait selection response
- Correlated response to selection
- Response to multi trait index selection
  - Predicting response per trait
  - How can multiple trait response be manipulated by varying index weights
  - Can we go anywhere we want?

Predicting Selection Response

- Total Response to selection (in $$)

$$R = i.r_{IH}.\sigma_A = i.\sigma_I \text{ in \$\$}$$

- Response for each trait (in trait units)

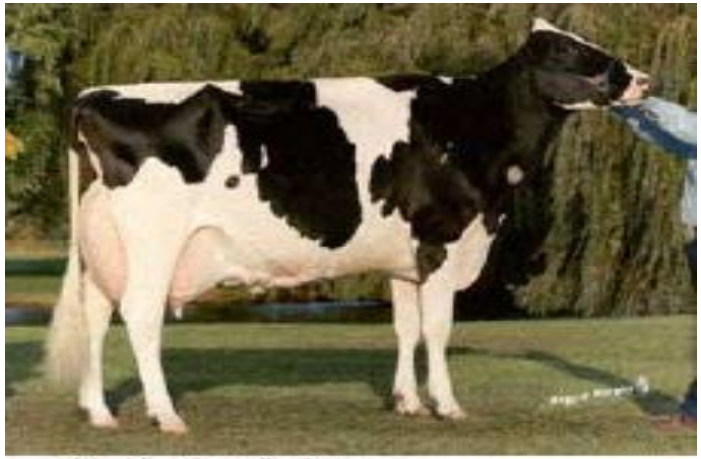
$$\delta g_i = b_{gi,I}\, R \quad = i.b'G_i/\sigma_I$$

Regression of g_i on Index

Case study 1

Dairy: select bulls (50 prog) on

- milk production
- feed intake



provided by Hoard's Dairyman

	μ	σ_P	h^2
Milk (kg/day)	25	2.5	.3
Feed intake (kg/day)	20	2.0	.2

r_g=.70 r_p= 0.40

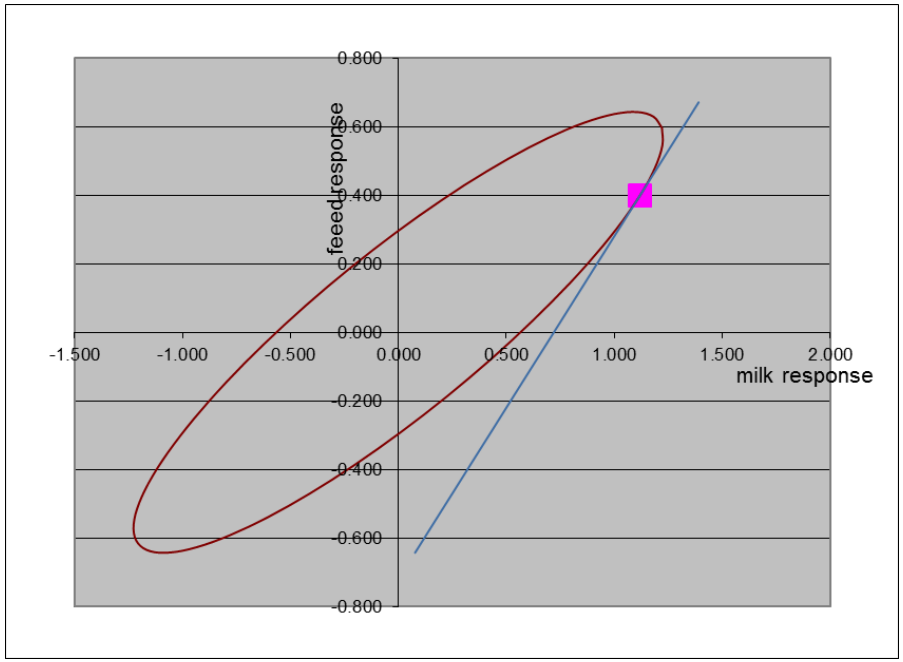
Selection for Milk Yield and Feed Intake

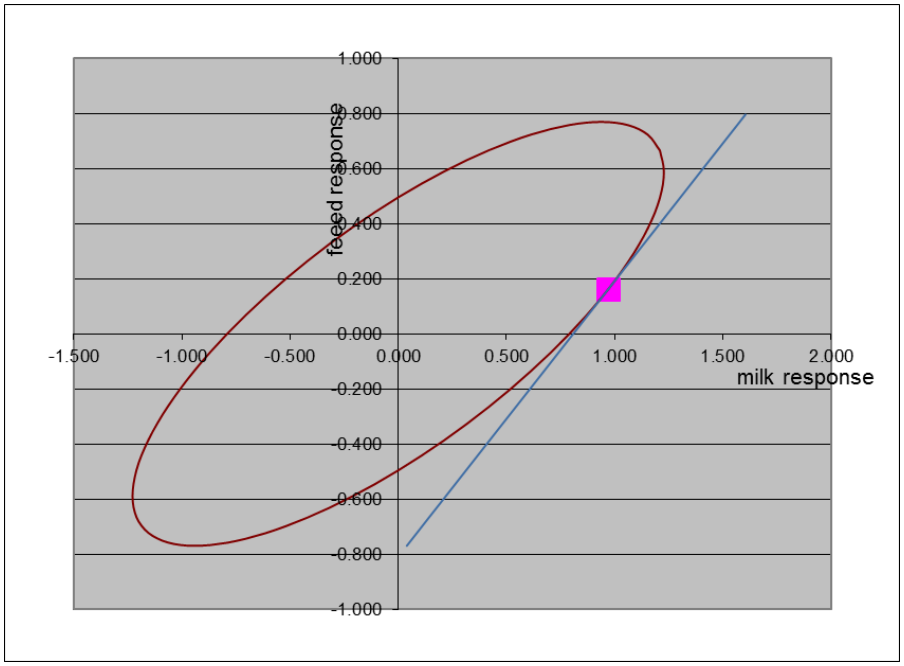
economic	*weights*	*progeny*	*measured*	*response*	*(4 yrs)*
milk	*feed*	*milk*	*feed*	*milk*	*feed*
0.2	0	50	-	1.23	0.56
0.2	0	50	50	1.23	0.59
0.2	**-0.2**	50	-	1.23	0.56
0.2	**-0.2**	50	50	0.97	0.16
0.2	**-0.3**	50	-	1.23	0.56
0.2	**-0.3**	50	50	0.52	-0.20
0.2	**-0.3**	50	10	0.79	0.14

To achieve response for a trait, we need to give it some weight

but we also need some data!

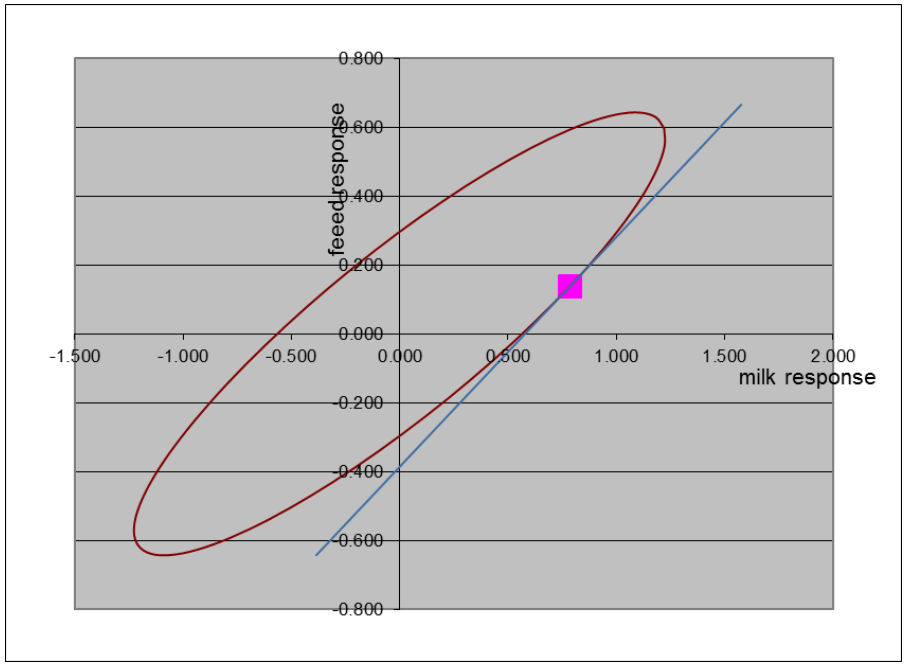
Selection for Milk Yield and Feed Intake

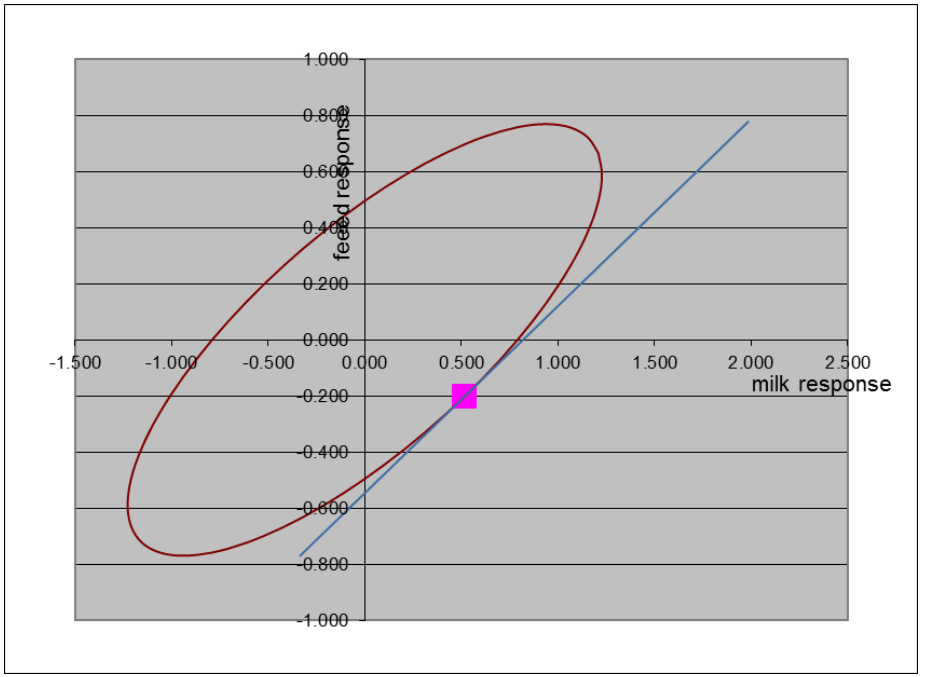




	economic	*weights*	*progeny*	*measured*	*response*	*(4 yrs)*
	milk	*feed*	*milk*	*feed*	*milk*	*feed*
left	0.2	**-0.2**	50	**10**	1.23	0.56
right	0.2	**-0.2**	50	**50**	0.97	0.16

Selection for Milk Yield and Feed Intake



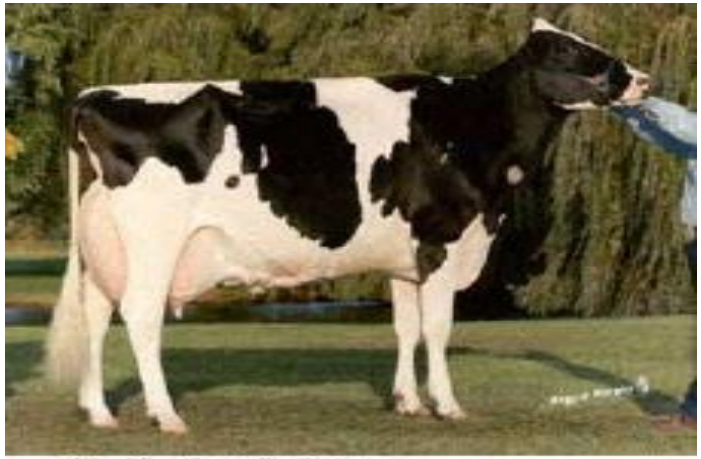


	economic	*weights*	*progeny*	*measured*	*response*	*(4 yrs)*
	milk	*feed*	*milk*	*feed*	*milk*	*feed*
left	0.2	**-0.3**	50	**10**	0.79	0.14
right	0.2	**-0.3**	50	**50**	0.52	-0.20

Case study 2

Dairy: select bulls (50 prog) on

- milk production
- fertility



provided by Hoard's Dairyman

	μ	σ_P	h^2
Milk (kg/lac)	8,000	800	.3
Fertility(%)	70	46	.03
	r_g= -.25	r_p= -0.1	

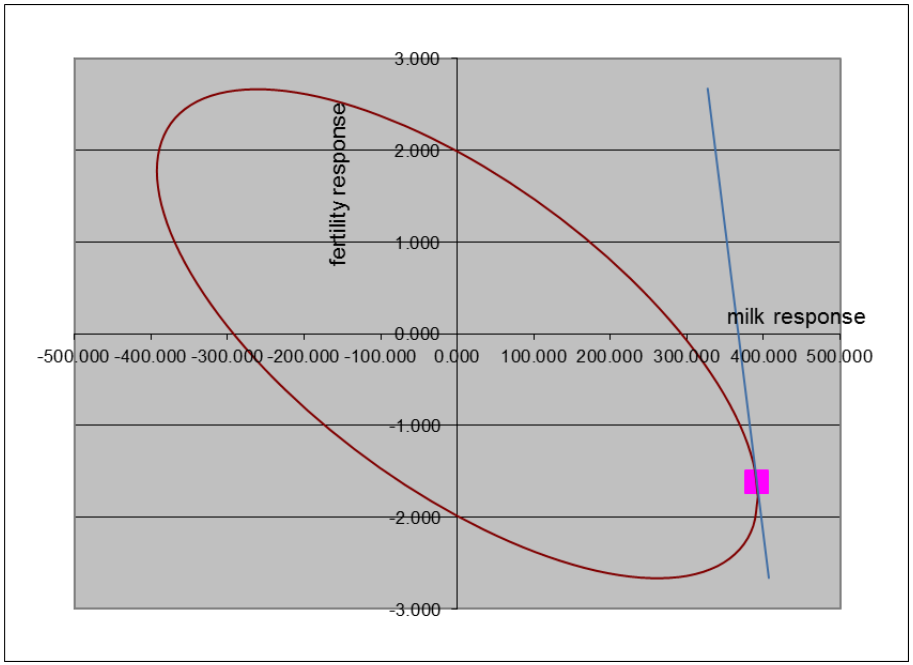
Selection for milk Yield and Fertility

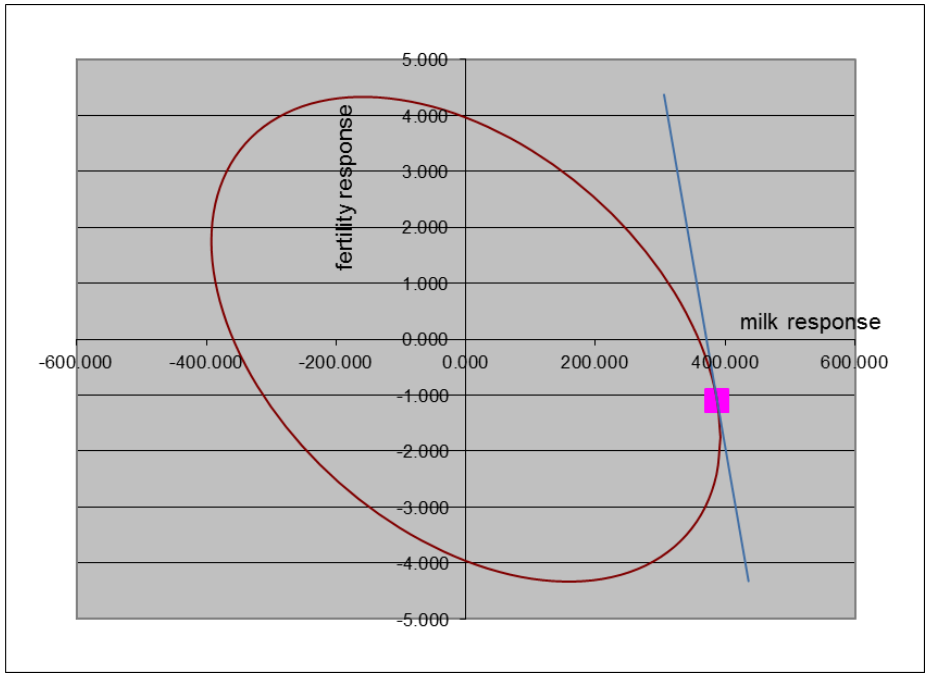
economic weights		*progeny*	*measured*	*response*	*(4 yrs)*
milk	*fertility*	*milk*	*fertility*	*milk*	*fertility*
0.2	0	50	-	392	-1.78
0.2	0	50	50	392	-1.75
0.2	**3**	50	-	392	-1.78
0.2	**3**	50	50	387	-1.09
0.2	**8**	50	-	392	-1.78
0.2	**8**	50	50	352	0.17
0.2	**8**	50	10	381	-1.25

To achieve response for a trait, we need to give it some weight

but we also need some data!

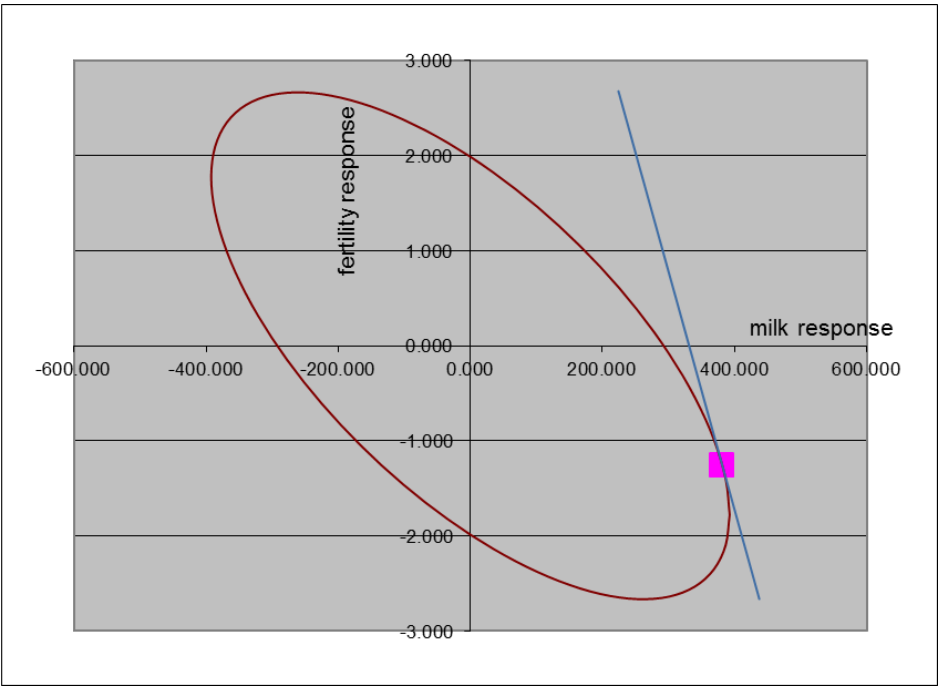
Selection for milk Yield and Fertility

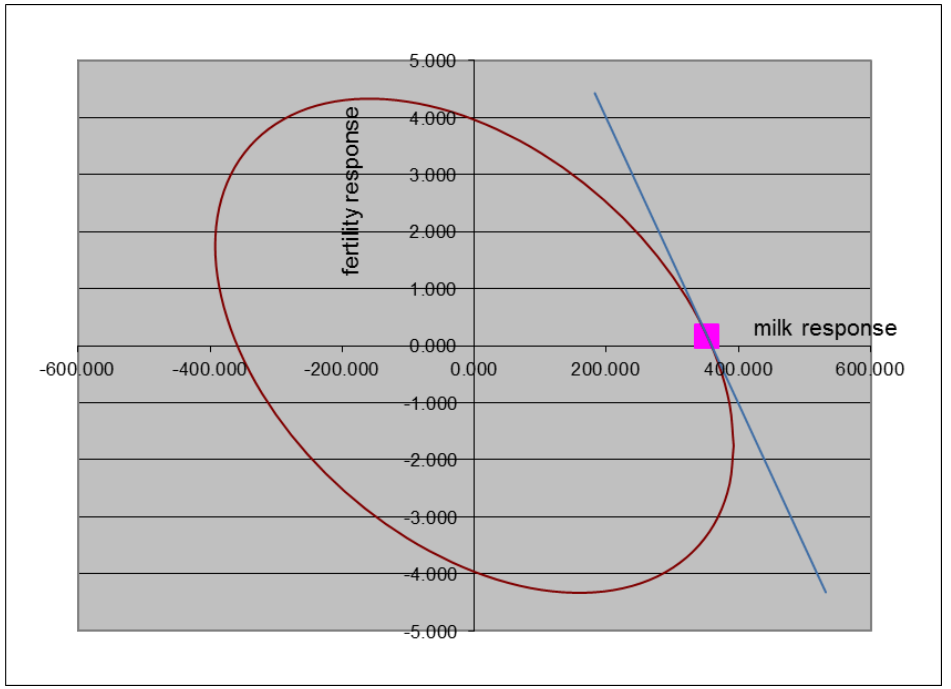




	economic weights		*progeny*	*measured*	*response*	*(4 yrs)*
	milk	*fertility*	*milk*	*fertility*	*milk*	*fertility*
left	0.2	**3**	50	10	391	-1.61
right	0.2	**3**	50	50	387	-1.09

Selection for milk Yield and Fertility



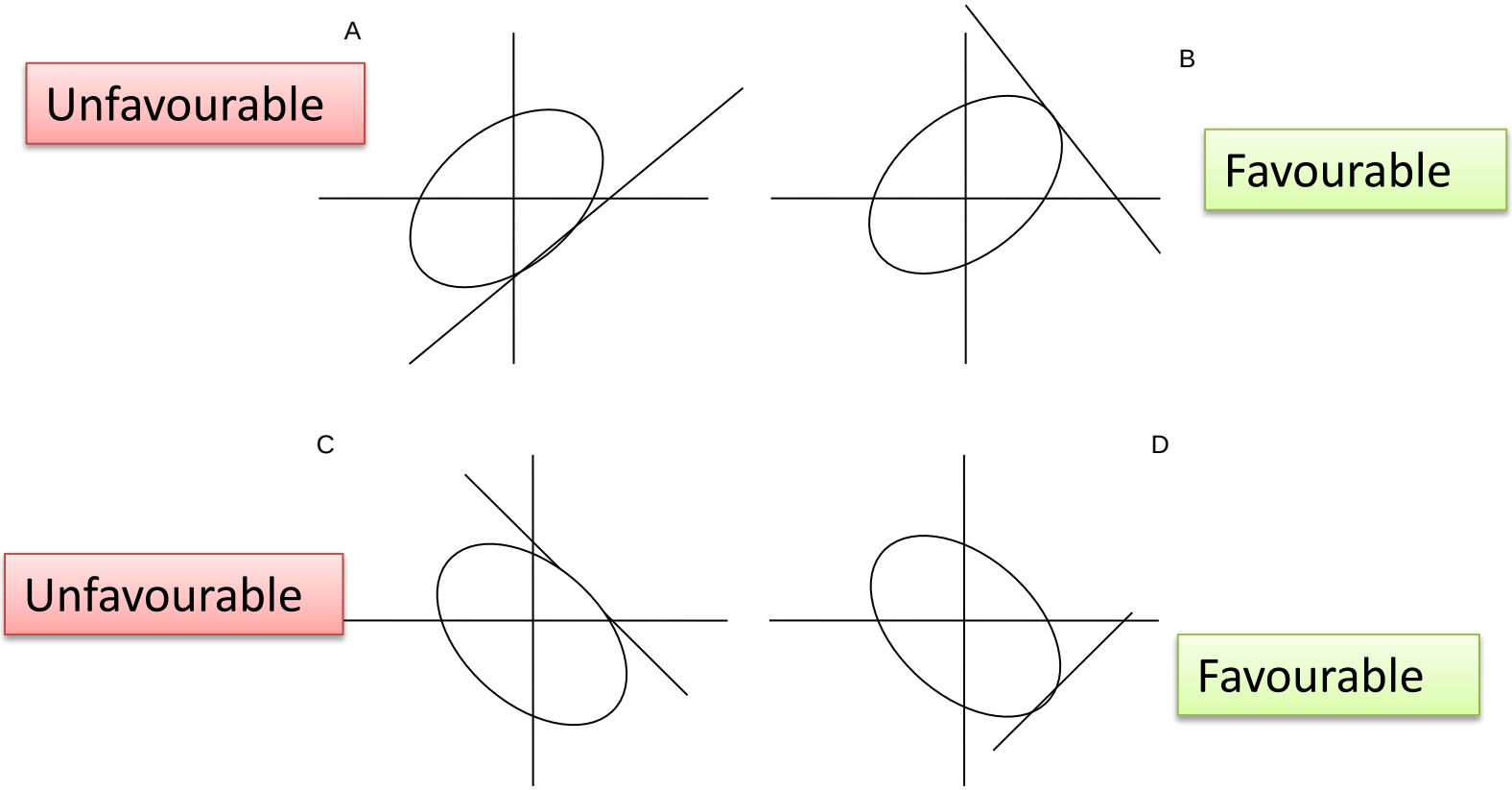


	economic	*weights*	*progeny*	*measured*	*response*	*(4 yrs)*
	milk	*feed*	*milk*	*feed*	*milk*	*feed*
left	0.2	**8**	50	10	381	-1.25
right	0.2	**8**	50	50	352	0.17

A challenge

- Assume two traits have a positive economic values
- Why is selection for these traits less sensitive to economic values when they are positively correlated compared to when they are negatively correlated

Correlation	Sign of economic weights	
	Equal	Opposite
Positive	Favourable (B)	Unfavourable (A)
Negative	Unfavourable (C)	Favourable (D)



Are selection indices always linear?

- nonlinear profit function
- optimal traits
- threshold values for profit

Selection index with ‘desired gains’

- Rather than
  - determine econ. values >>>> response
  - We desire a response >>>> economic values (implicit)

When useful?

Using EBVs as Selection Criteria

1) Define the overall objective (e.g. profit per animal).

2) Develop a linear breeding goal: $H = v_1g_1 + v_2g_2 \ldots v_ng_n = \mathbf{v'g}$

3) Derive the economic value (v) for each trait in H

3) Derive a linear index (I) of information sources that maximizes the accuracy of the index with H: $\mathbf{b = P^{-1}Gv}$

   a. Based on phenotypes: $I = b_1x_1 + b_2x_2 \ldots b_mx_m = \mathbf{b_x'x}$

   a. Based on EBV: $I = b_1\hat{g}_1 + b_2\hat{g}_2 \ldots b_m\hat{g}_m = \mathbf{b_{EBV}'\hat{g}}$

Maximize Response in Overall Objective

Optimize Response in Individual Traits

Selection Index Theory

$H = v_1g_1 + v_2g_2 \ldots v_ng_n = \mathbf{v}'\mathbf{g}$ $\qquad$ $I = b_1\hat{g}_1 + b_2\hat{g}_2 \ldots b_m\hat{g}_m = \mathbf{b}_{EBV}'\hat{\mathbf{g}}$

Optimal Index Weights (multi-trait EBV)**: $\mathbf{b} = \mathbf{P}^{-1}\mathbf{G}\mathbf{v}$**

- if traits in I = traits in H: $\mathbf{b}_{EBV} = \mathbf{v}$
- if traits in $I \neq$ traits in H: $\mathbf{b}_{EBV} = \mathbf{b}_{g_H,g_I}'\mathbf{v}$ function of genetic parameters

(Schneeberger et al. 1992)

Responses to selection:

- **in individual traits:** $\mathbf{S_g} = [S_{g_1}, S_{g_2}, \ldots, S_{g_m}] = \mathbf{b}_{g_H,g_I}'\mathbf{b}_{EBV}'\mathbf{G}_{EBV}/\sigma_I \overset{\text{traits } I = H}{=} \mathbf{v}'\mathbf{G}_{EBV}/\sigma_I$

with $\sigma_I = \mathbf{b}_{EBV}'\mathbf{G}_{EBV}\mathbf{b}_{EBV}$

Trait responses depend on:

- Genetic parameters, economic values
- Variance-covariance matrix of EBV $= \mathbf{G}_{EBV} =$

$$\begin{bmatrix} r_1^2\sigma_{g_1}^2 & & \\ & r_2^2\sigma_{g_2}^2 & \\ & & r_m^2\sigma_{g_m}^2 \end{bmatrix}$$

EBV covariances
genet.param.
- Information
  - phenotypes
  - genomics

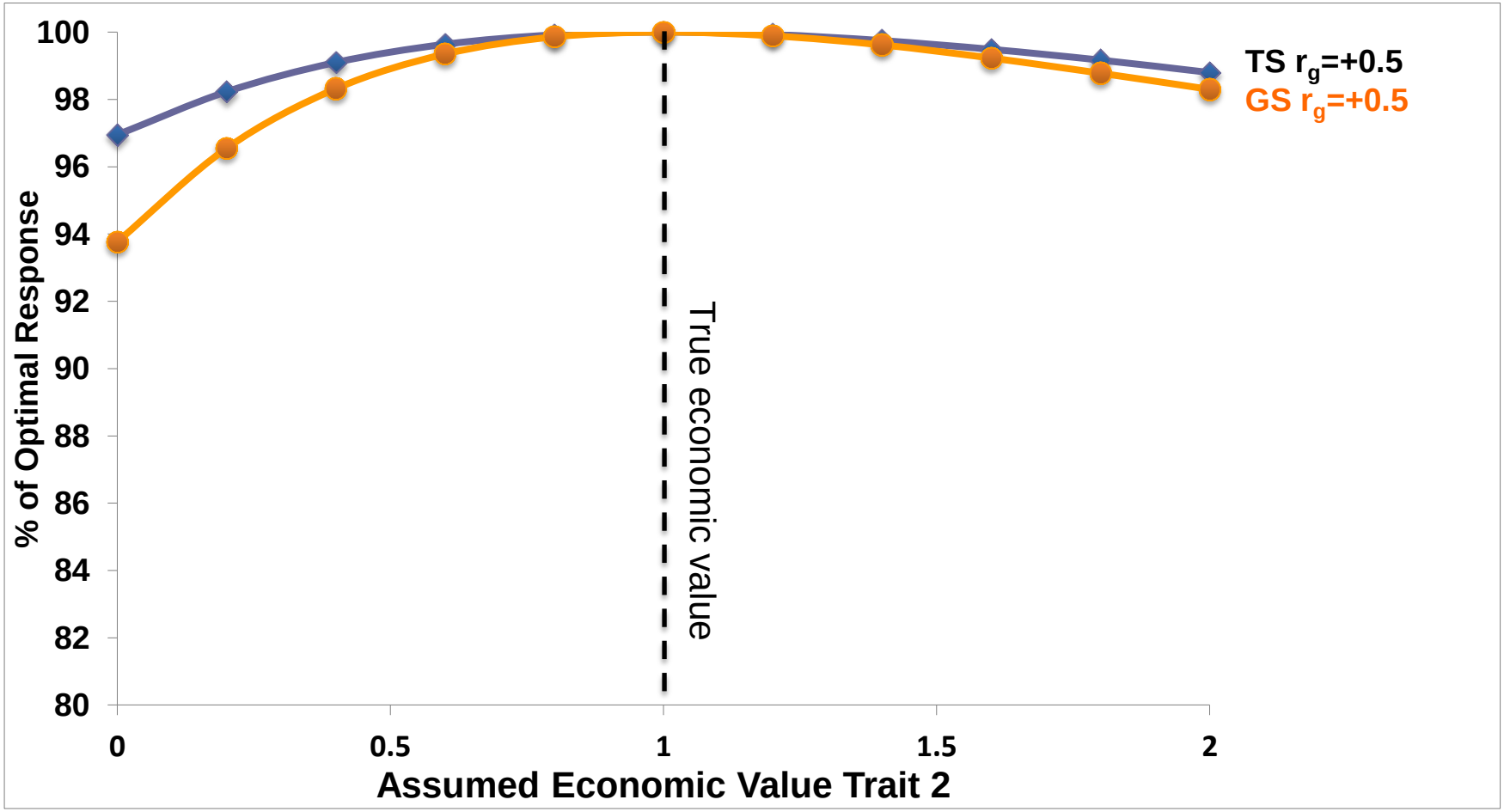
$\mathbf{G}_{EBV}$ captures the impact of alternate breeding program and phenotyping designs on trait responses – 'artificial evolution' (Gibson 1989)

une

Lost Responses from Uncertainty about Economic Values

TS = traditional selection $r_1 = 0.64$ $r_2 = 0.43$

GS = genomic selection $r_1 = 0.90$ $r_2 = 0.90$



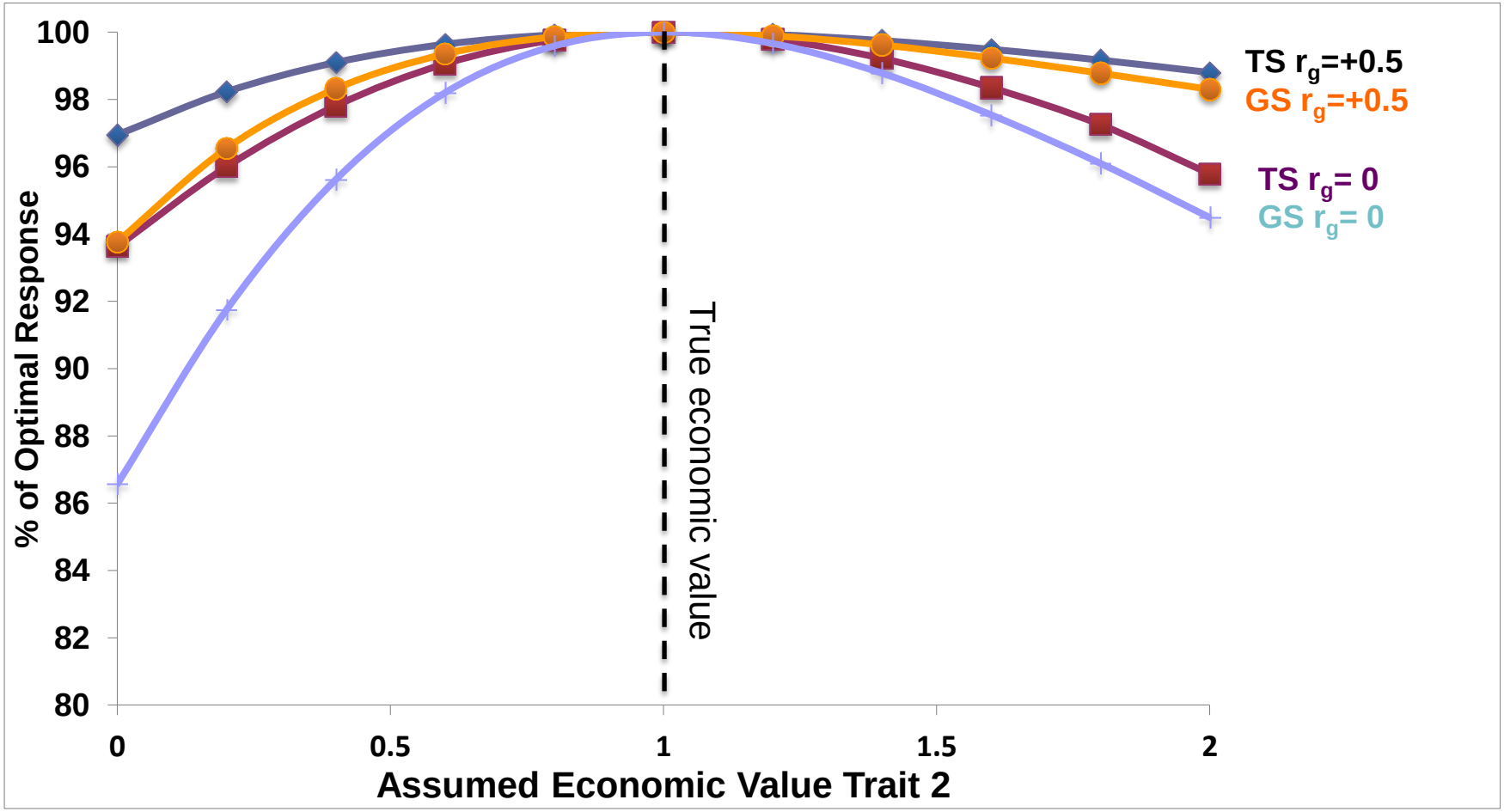
True economic values = 1 for both traits

une

Lost Responses from Uncertainty about Economic Values

TS = traditional selection $r_1 = 0.64$ $r_2 = 0.43$

GS = genomic selection $r_1 = 0.90$ $r_2 = 0.90$

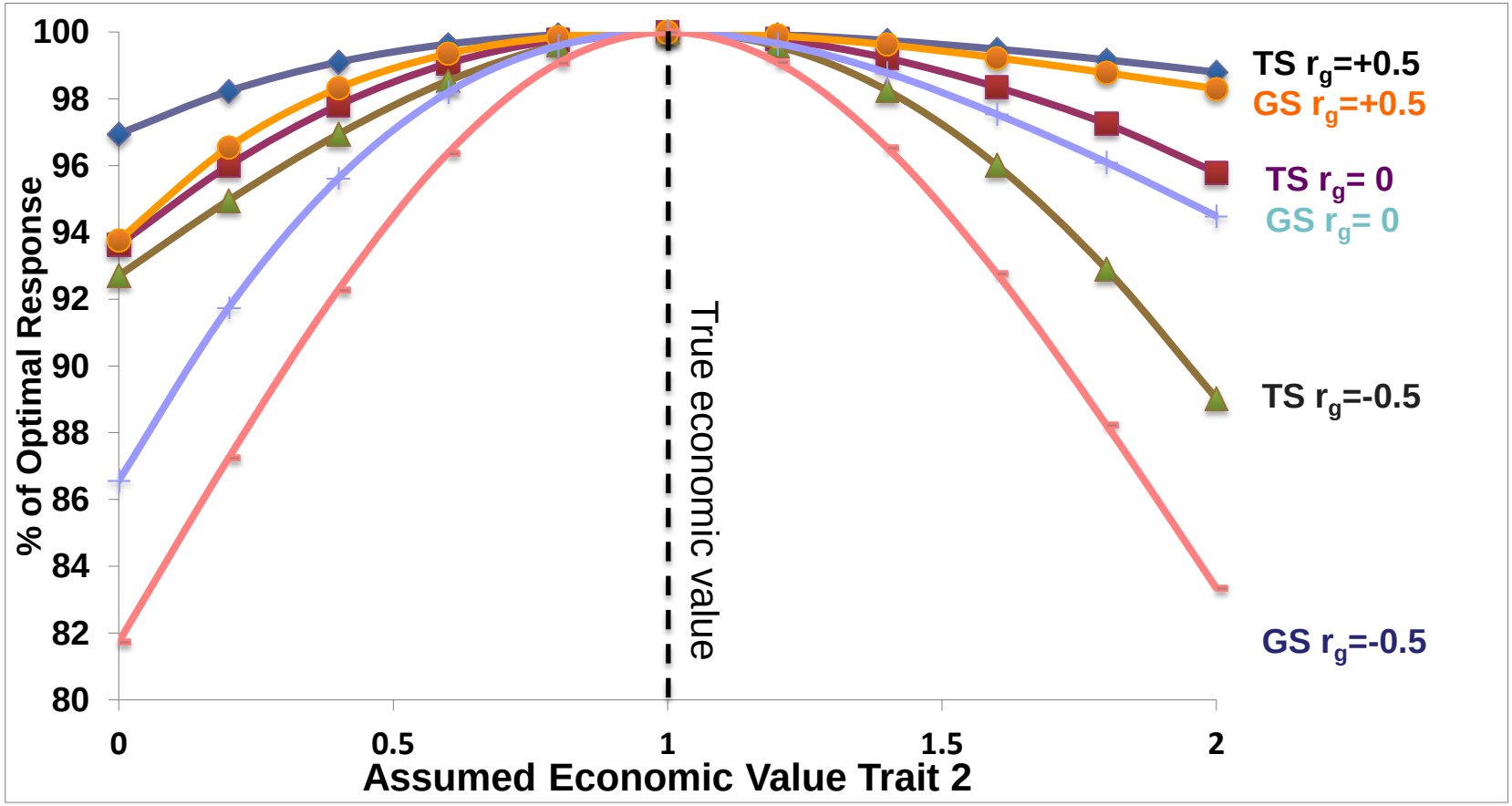


True economic values = 1 for both traits

Lost Responses from Uncertainty about Economic Values

TS = traditional selection $r_1 = 0.64$ $r_2 = 0.43$

GS = genomic selection $r_1 = 0.90$ $r_2 = 0.90$

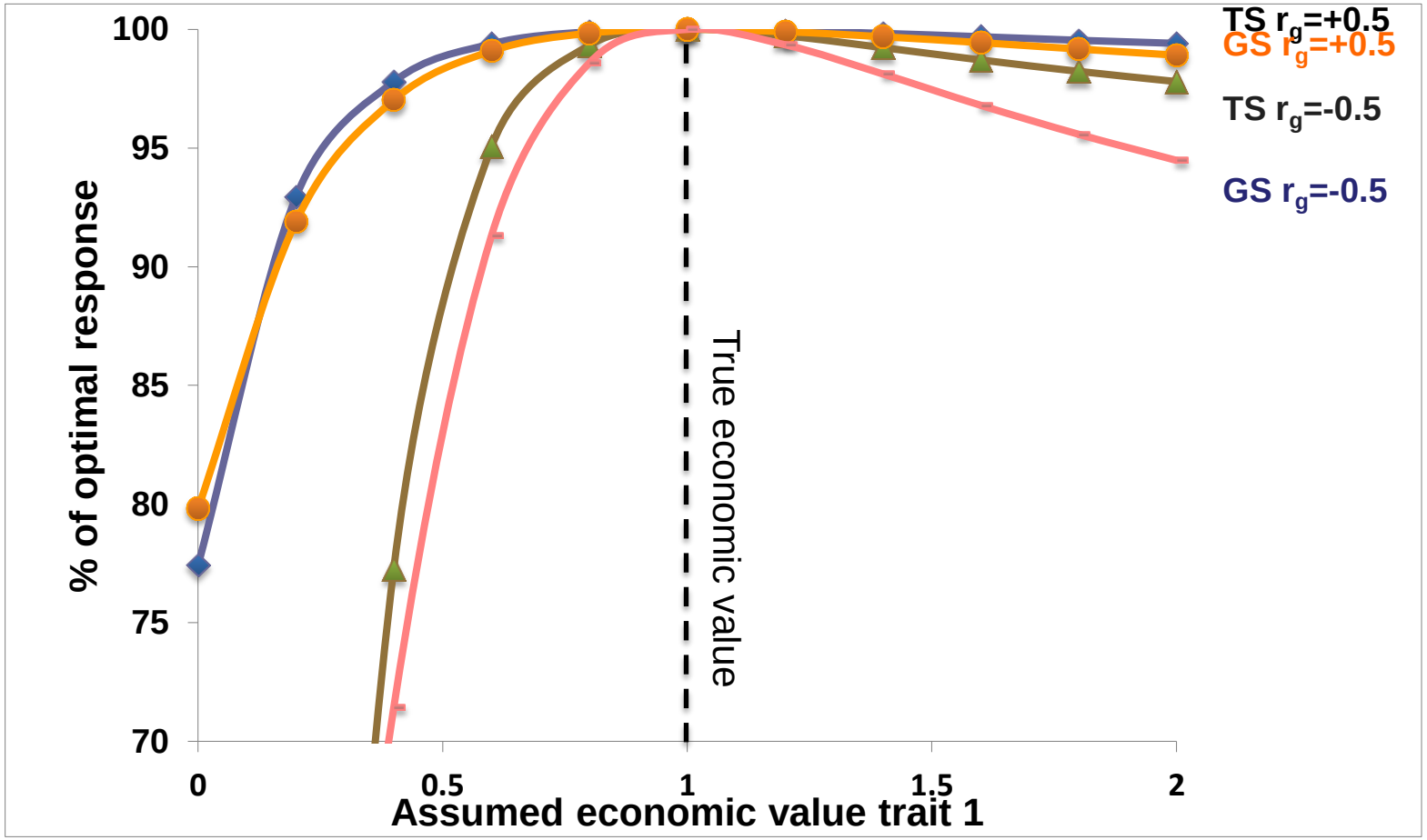


True economic values = 1 for both traits

Lost Responses from Uncertainty about Economic Values

TS = traditional selection $r_1 = 0.64$ $r_2 = 0.43$

GS = genomic selection $r_1 = 0.90$ $r_2 = 0.90$



True economic values = 1 for both traits

Breeding Goals and Phenotyping Programs for Multi-Trait Improvement in the Genomics Era

1) Impact of errors in economic values with genomic selection

- Importance of having accurate economic values is greater with genomic selection
- Impact of using suboptimal indexes is greater with genomic selection

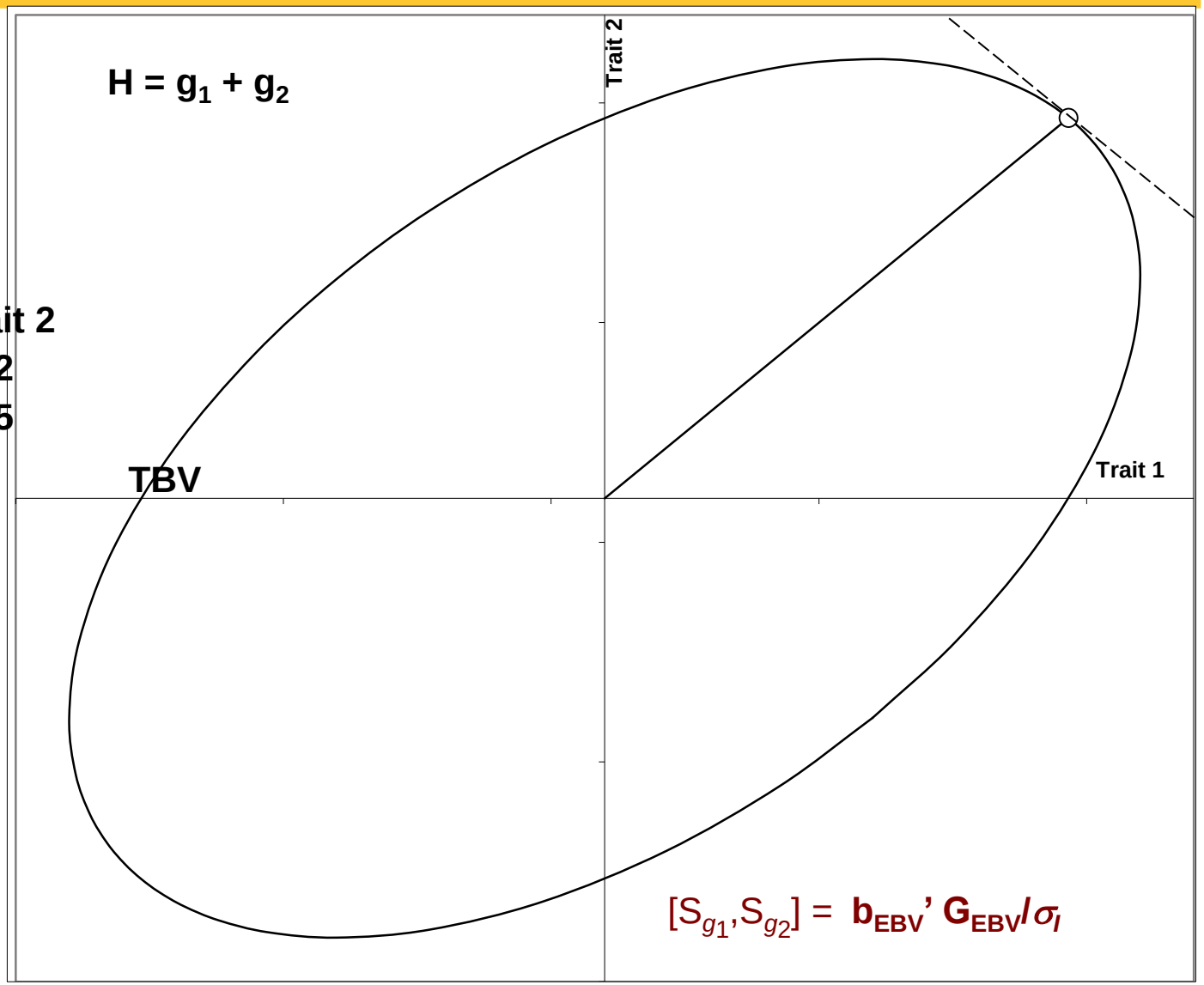
Use of Genomics to Shape Artificial Evolution

$v_1 = v_2 = 1$

$\sigma_{g1} = \sigma_{g2}$

$r_g = r_p = 0.5$

	Trait 1	Trait 2
r_{EBV} TS	0.55	0.22
r_{EBV} GS	0.75	0.75



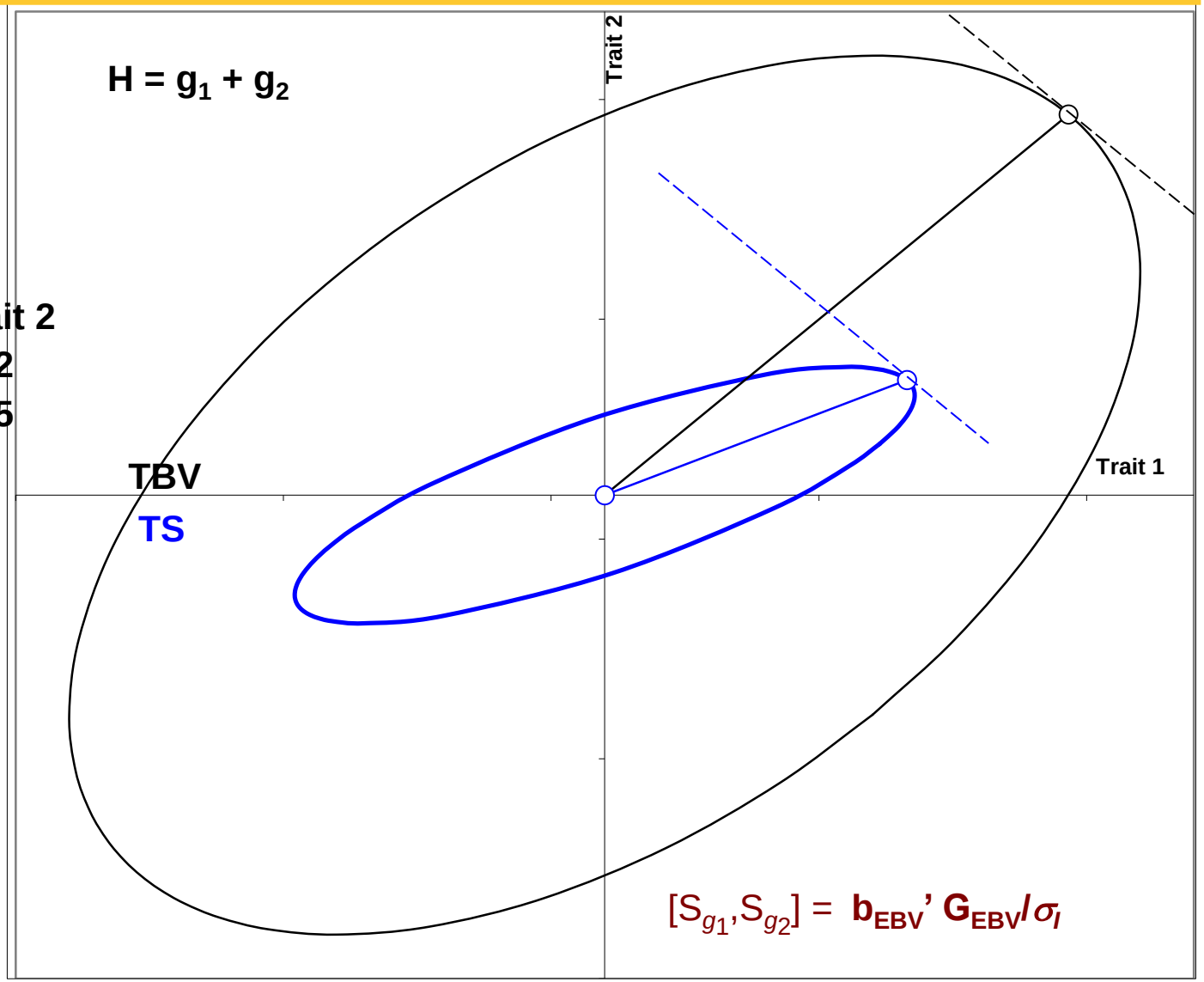
Use of Genomics to Shape Artificial Evolution

$v_1 = v_2 = 1$

$\sigma_{g1} = \sigma_{g2}$

$r_g = r_p = 0.5$

	Trait 1	Trait 2
r_{EBV} TS	0.55	0.22
r_{EBV} GS	0.75	0.75
		TBV
		TS



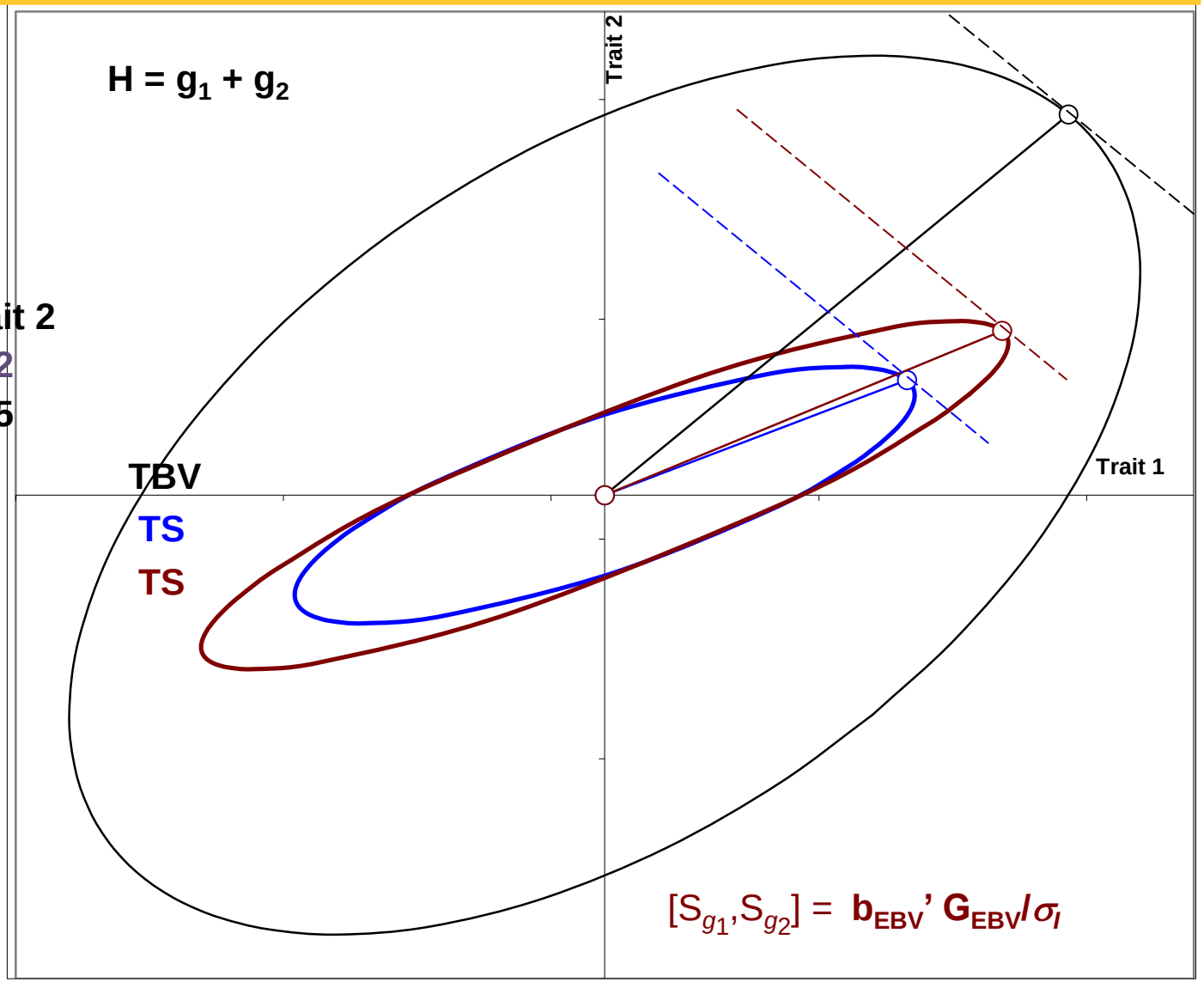
Use of Genomics to Shape Artificial Evolution

$v_1 = v_2 = 1$

$\sigma_{g1} = \sigma_{g2}$

$r_g = r_p = 0.5$

	Trait 1	Trait 2
r_{EBV} TS	0.55	0.22
r_{EBV} GS	0.75	0.75



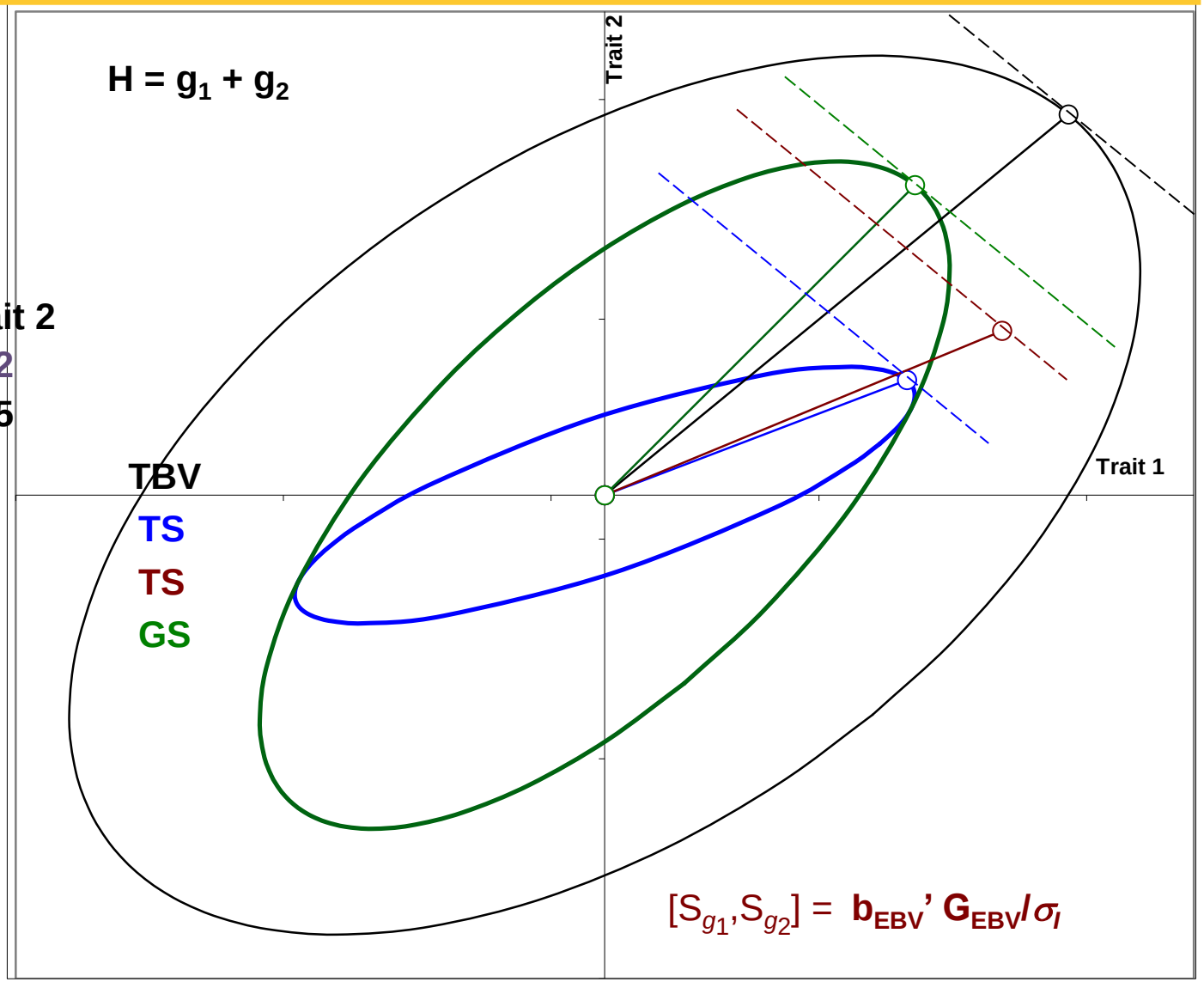
Use of Genomics to Shape Artificial Evolution

$v_1 = v_2 = 1$

$\sigma_{g1} = \sigma_{g2}$

$r_g = r_p = 0.5$

	Trait 1	Trait 2
r_{EBV} TS	0.55	0.22
r_{EBV} GS	0.75	0.75



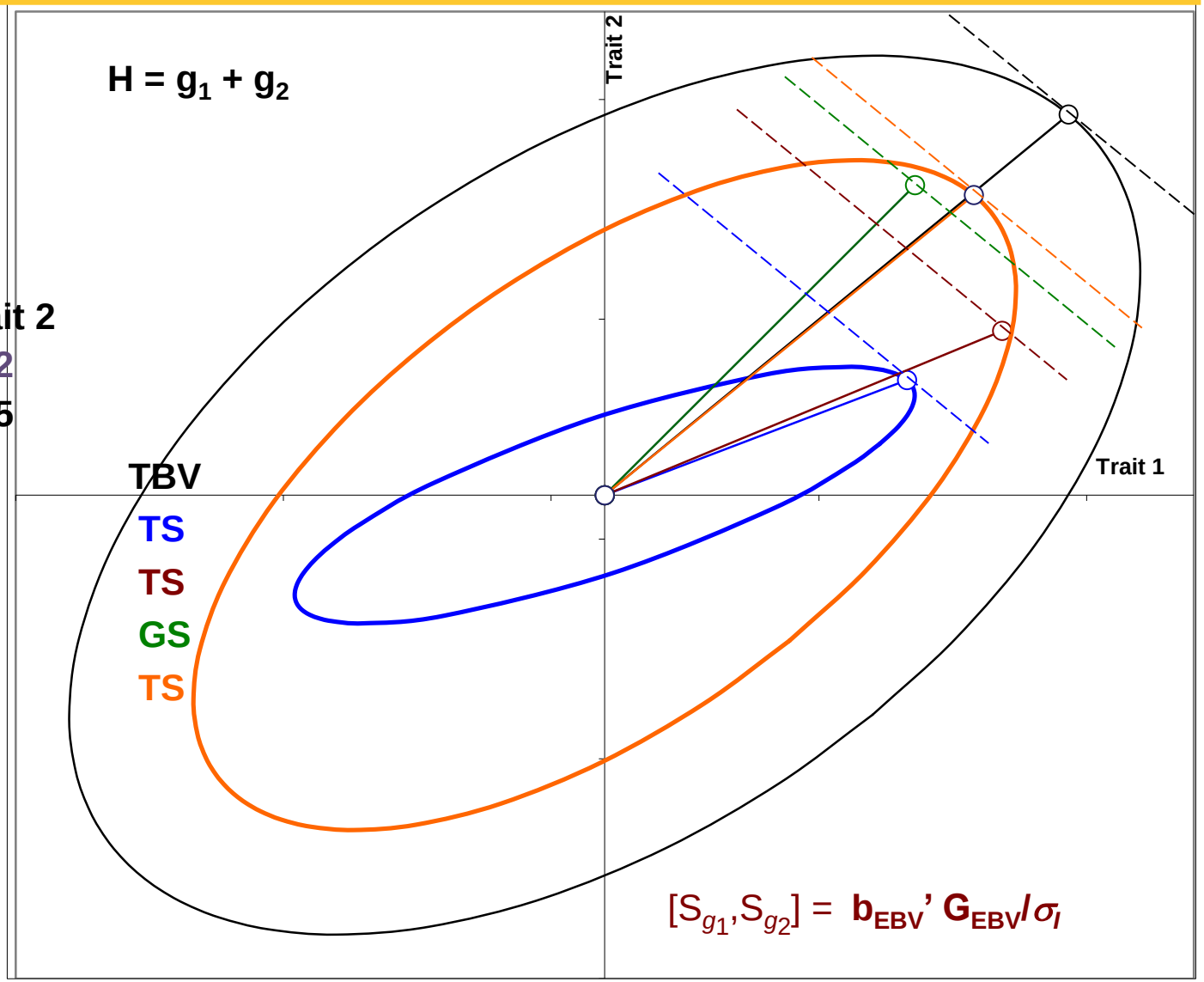
Use of Genomics to Shape Artificial Evolution

$v_1 = v_2 = 1$

$\sigma_{g1} = \sigma_{g2}$

$r_g = r_p = 0.5$

	Trait 1	Trait 2
r_{EBV} TS	0.55	0.22
r_{EBV} GS	0.75	0.75
		TBV
		TS
		GS
		TS
		TS



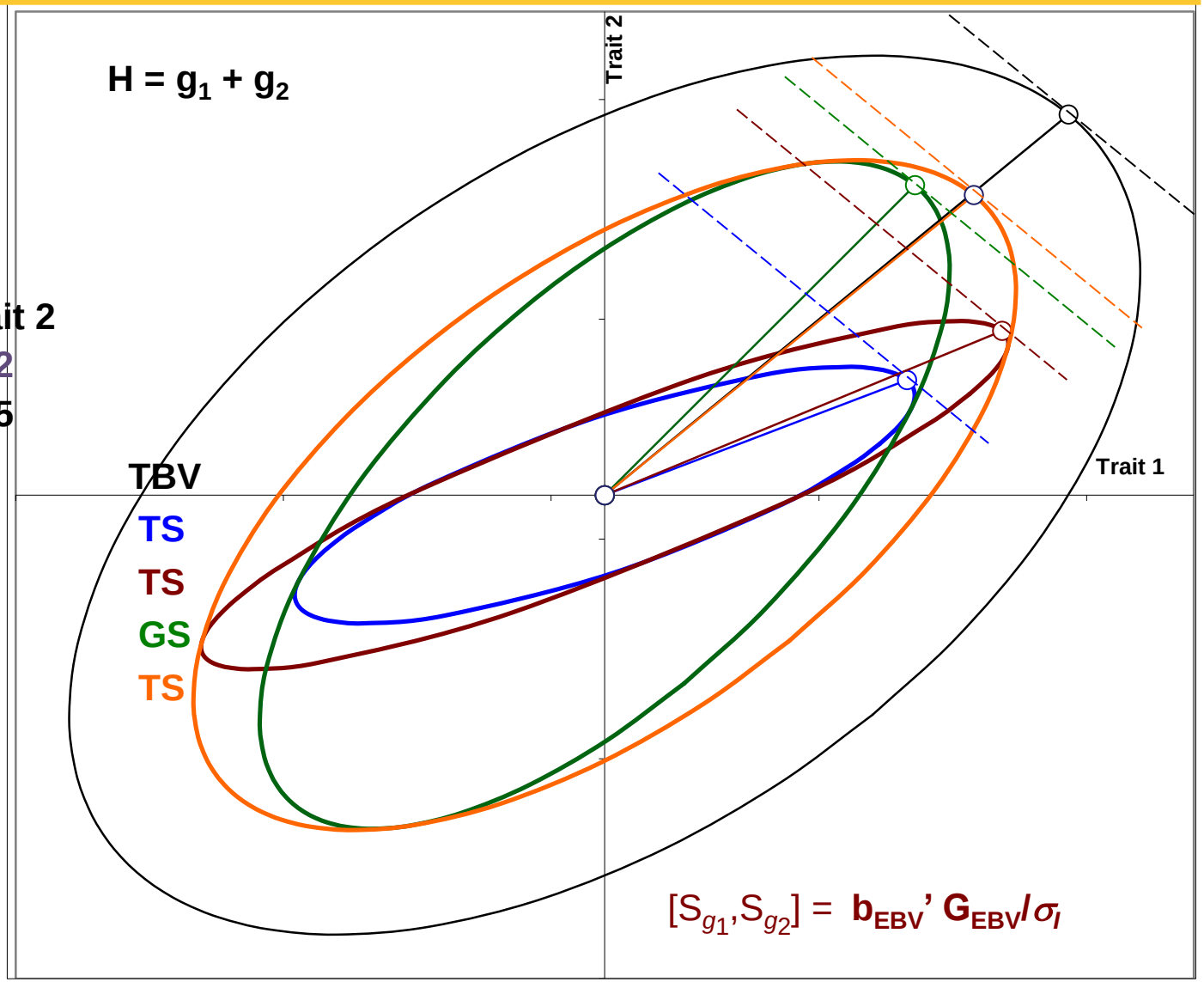
Use of Genomics to Shape Artificial Evolution

$v_1 = v_2 = 1$

$\sigma_{g1} = \sigma_{g2}$

$r_g = r_p = 0.5$

	Trait 1	Trait 2
r_{EBV} TS	0.55	0.22
r_{EBV} GS	0.75	0.75



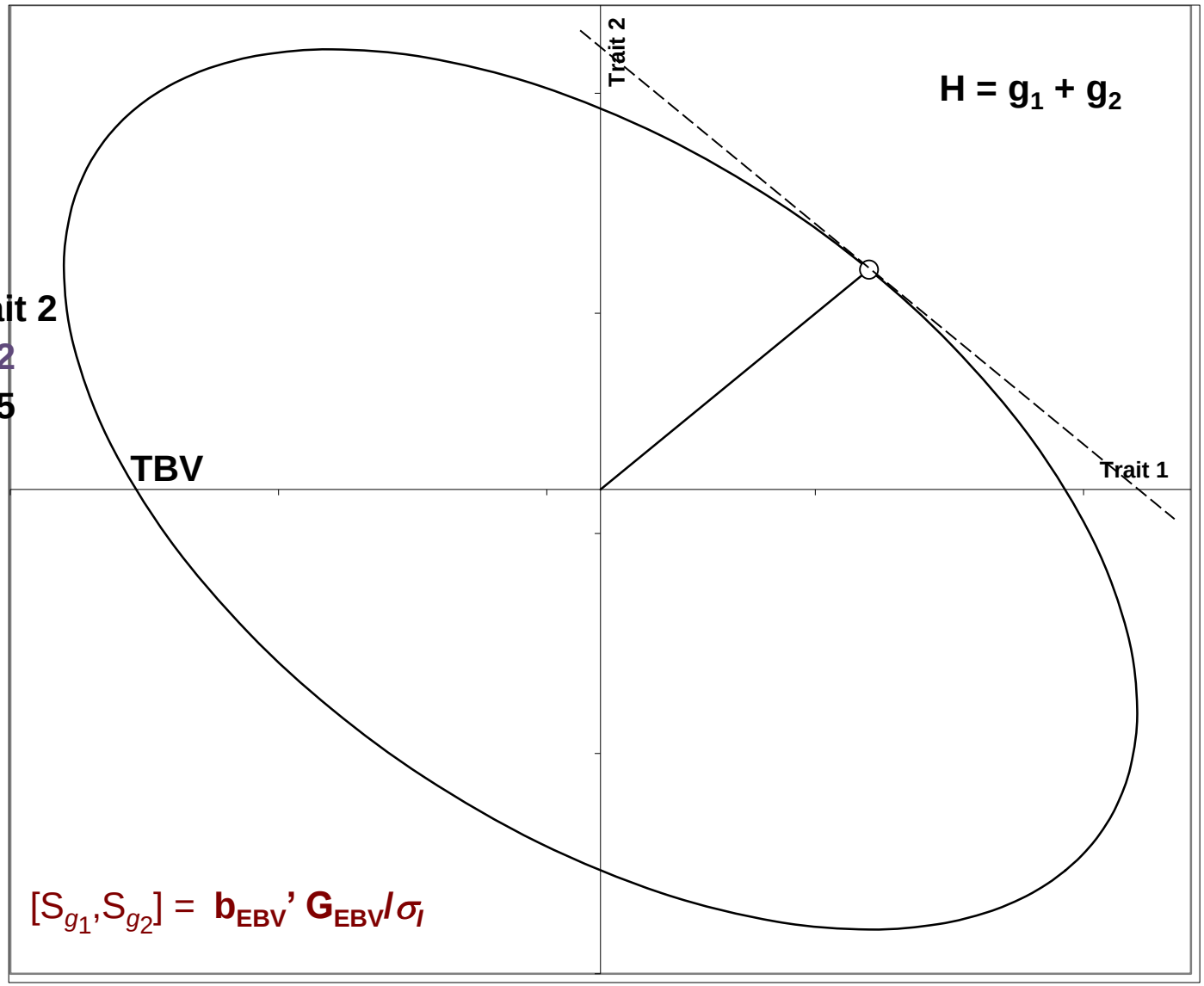
Use of Genomics to Shape Artificial Evolution

$v_1 = v_2 = 1$

$\sigma_{g1} = \sigma_{g2}$

$r_g = r_p = -0.5$

	Trait 1	Trait 2
r_{EBV} TS	0.55	0.22
r_{EBV} GS	0.75	0.75



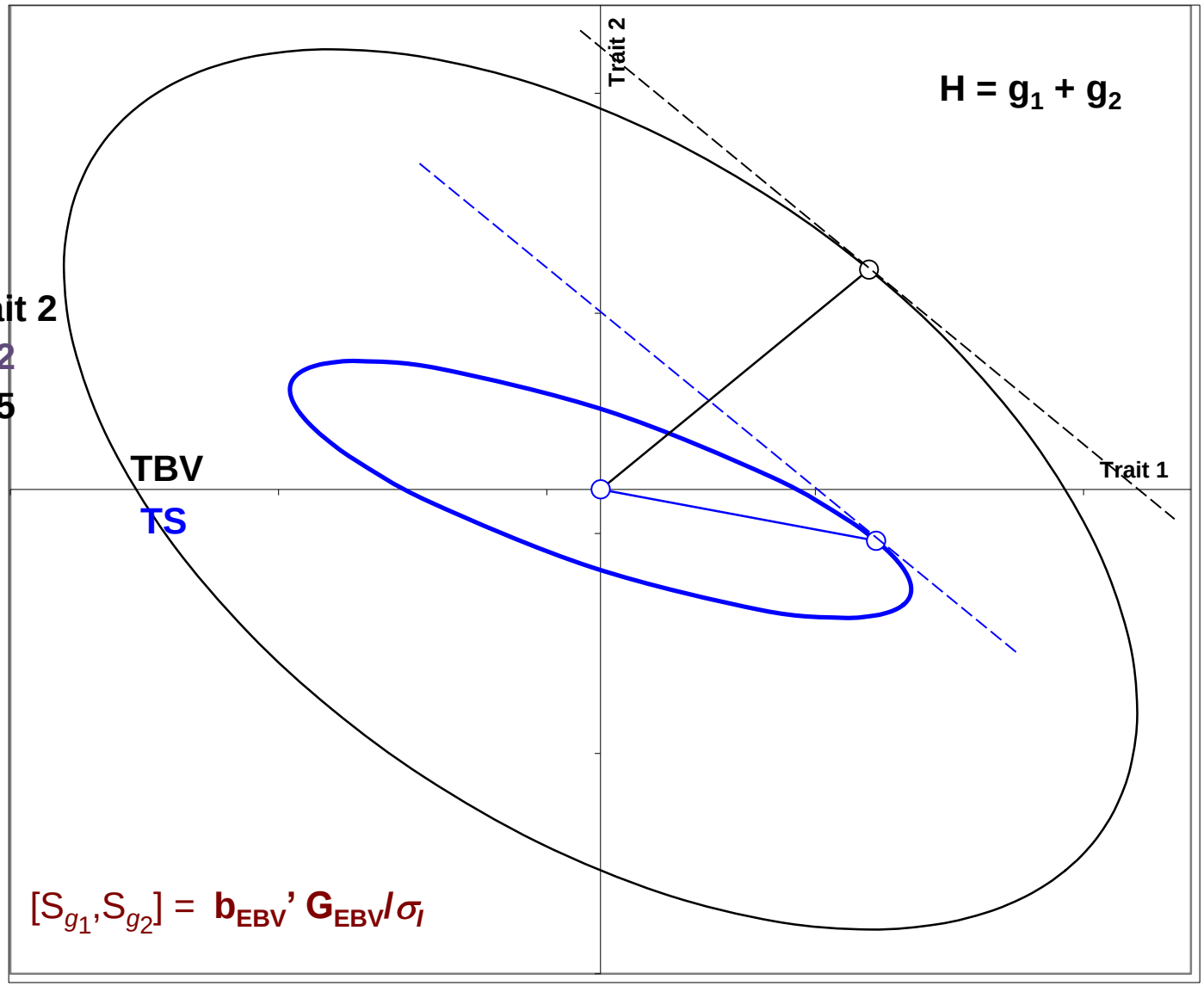
Use of Genomics to Shape Artificial Evolution

$v_1 = v_2 = 1$

$\sigma_{g1} = \sigma_{g2}$

$r_g = r_p = -0.5$

	Trait 1	Trait 2
r_{EBV} TS	0.55	0.22
r_{EBV} GS	0.75	0.75
		TBV
		TS



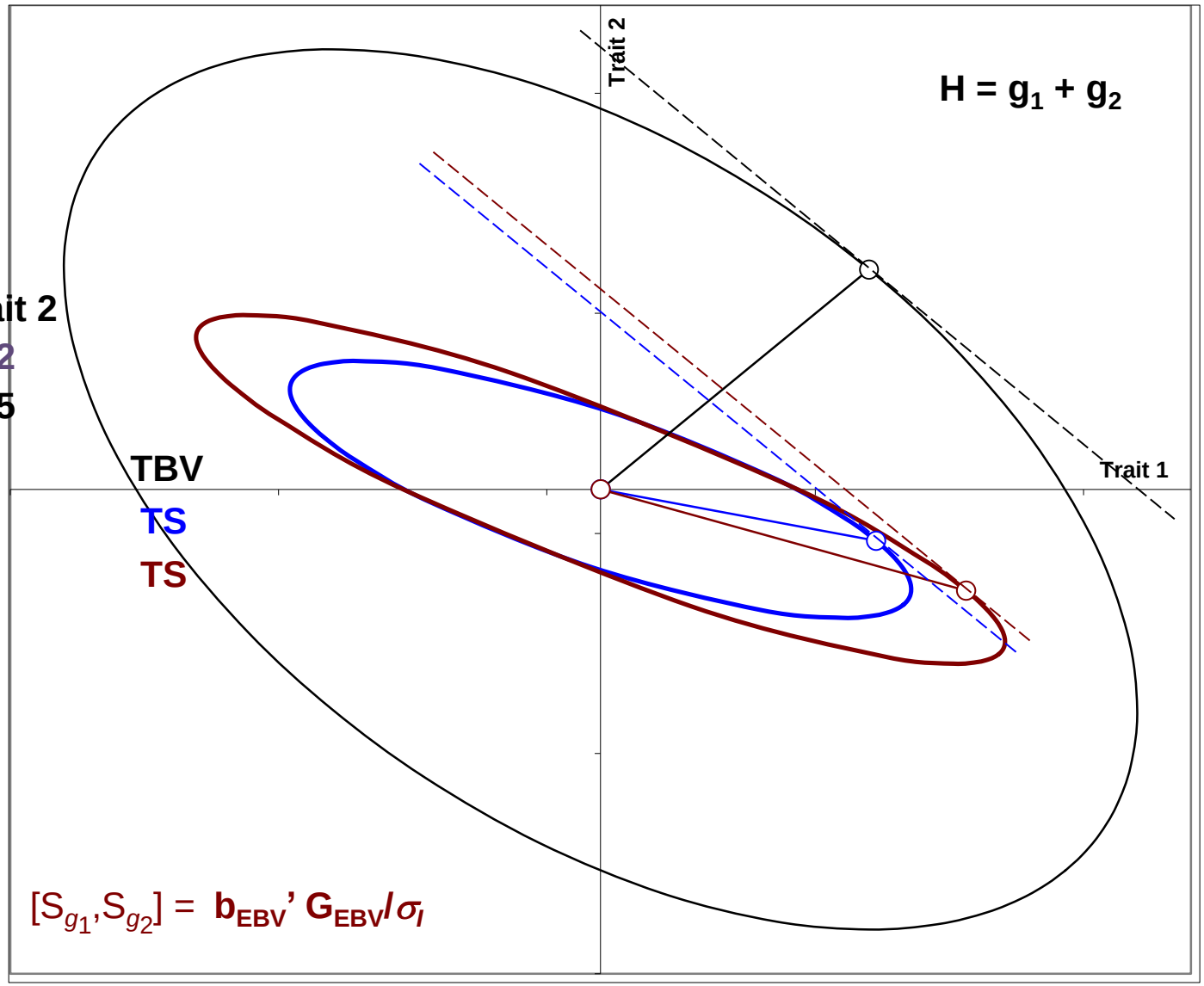
Use of Genomics to Shape Artificial Evolution

$v_1 = v_2 = 1$

$\sigma_{g1} = \sigma_{g2}$

$r_g = r_p = -0.5$

	Trait 1	Trait 2
r_{EBV} TS	0.55	0.22
r_{EBV} GS	0.75	0.75



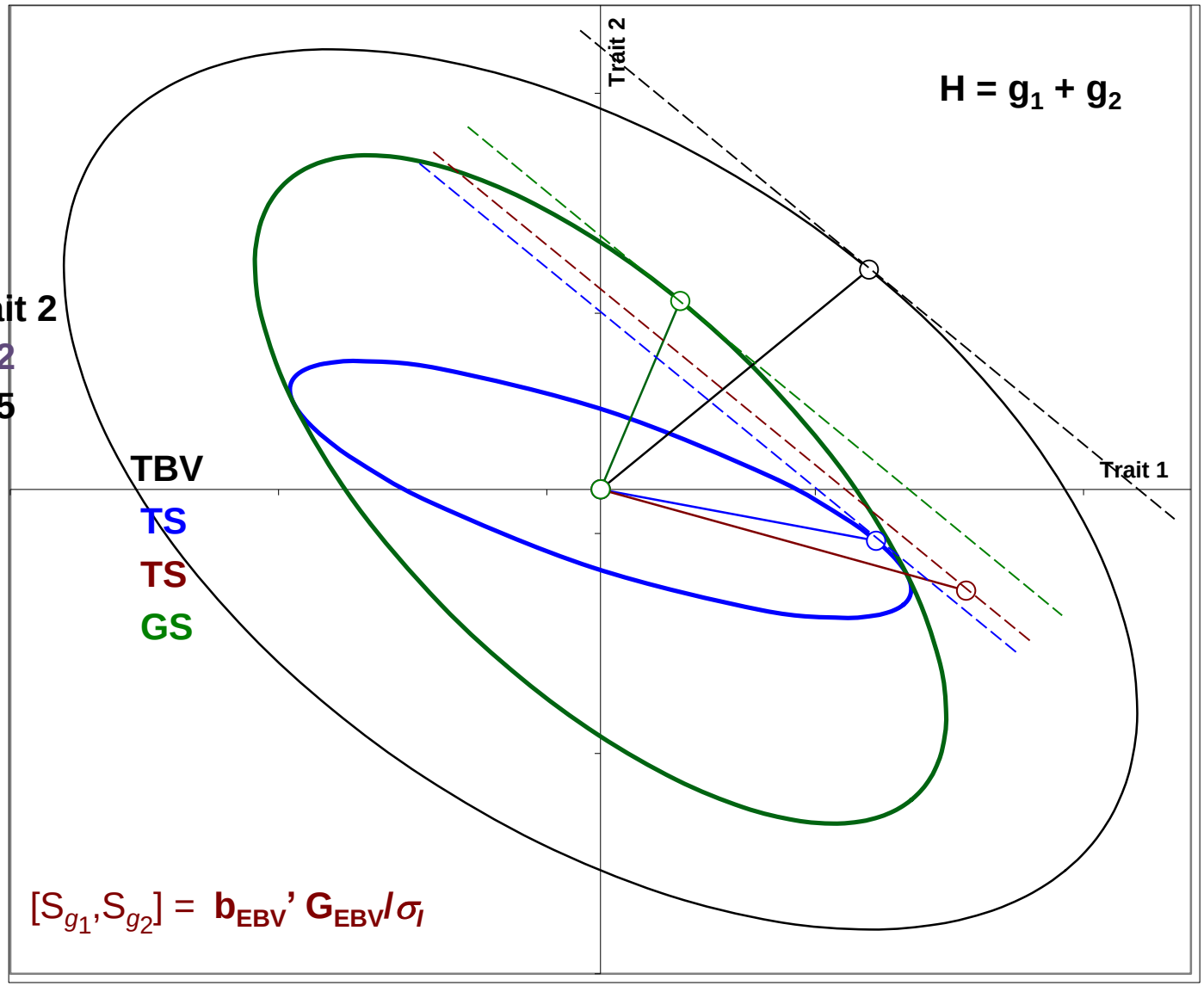
Use of Genomics to Shape Artificial Evolution

$v_1 = v_2 = 1$

$\sigma_{g1} = \sigma_{g2}$

$r_g = r_p = -0.5$

	Trait 1	Trait 2
r_{EBV} TS	0.55	0.22
r_{EBV} GS	0.75	0.75



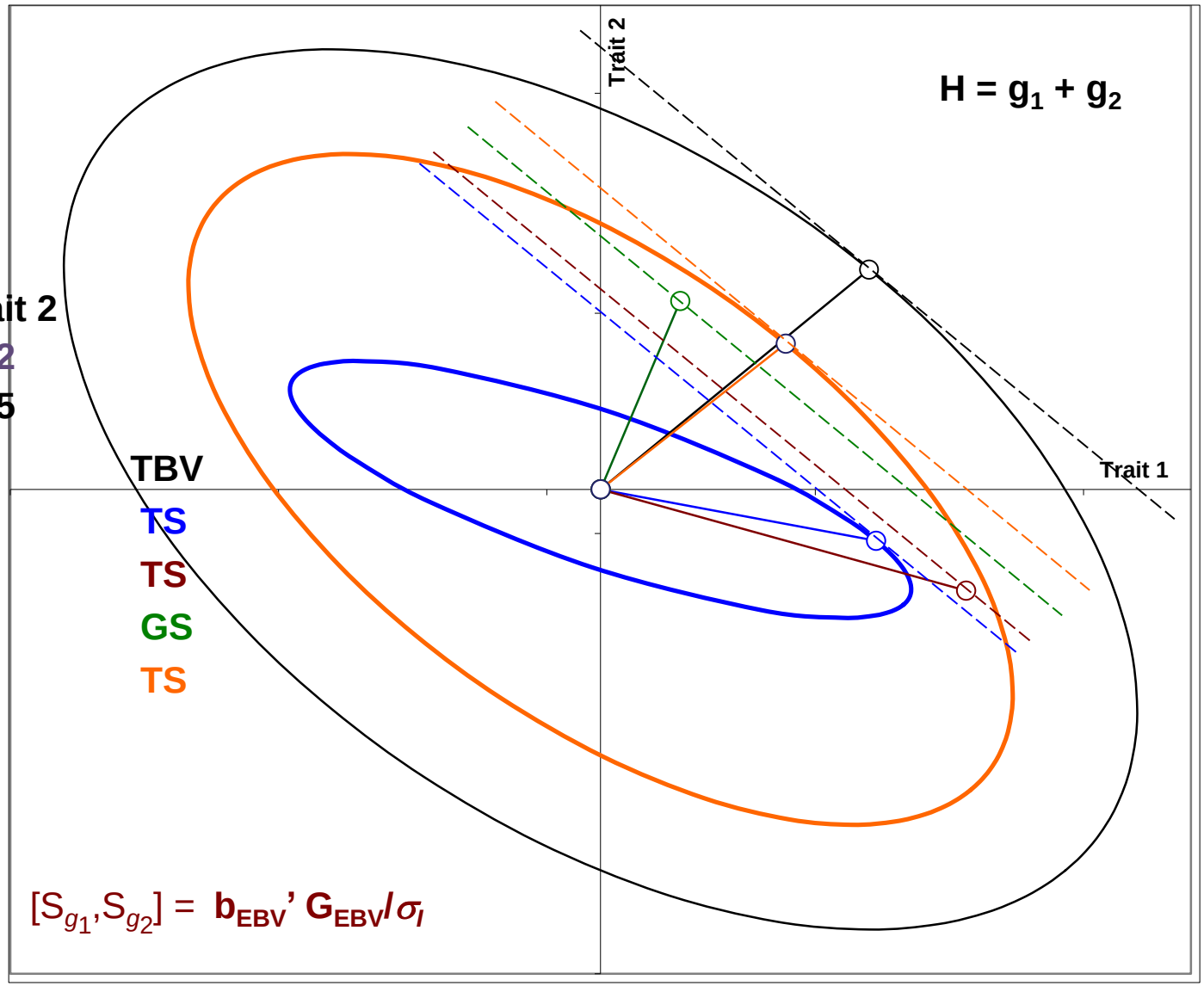
Use of Genomics to Shape Artificial Evolution

$v_1 = v_2 = 1$

$\sigma_{g1} = \sigma_{g2}$

$r_g = r_p = -0.5$

	Trait 1	Trait 2
r_{EBV} TS	0.55	0.22
r_{EBV} GS	0.75	0.75



Impact of Genomics on Response to Selection

Availability and accuracy of GEBV		r_g = r_p	Responses to selection			% increase in H
trait 1	trait 2		Trait 1	Trait 2	H	
-	-		0.56	0.26	0.83	
0.75	-		0.74	0.37	1.12	35.1
-	0.75	**0.5**	0.58	0.71	1.28	55.4
0.75	0.75		0.69	0.68	1.37	66.1
-	**0.60**		**0.56**	**0.55**	**1.12**	**35.1**

Accuracy of GEBV for trait 2 to achieve same response in H as having a GEBV for trait 1 with accuracy 0.75.

Using ST EBVs in a multi trait index

The index weights are $b = var(\hat{\mathbf{a}})^{-1} cov(\hat{\mathbf{a}},\mathbf{a}).\mathbf{v}$.

where **a** are the true breeding values of the traits.

var(**â**) is an n by n matrix with

diagonals = $r_i \cdot \sigma_{ai}^2$ where $\sigma_{ai}^2 = G(i,i)$

and

off-diagonals = $r_i.r_j.\ \sigma_{aij} + 4r_ir_j.(\ \sigma_{pij} - ¼\sigma_{aij})/n$

Why are index weights different from economic weights?

Example: Protein Yield $6.00/kg; Feed Intake -$4.00/kg

Feed Intake not measured and not in Breed Obj:

economic value PY = $6.00 + 0.5 .(-$4.00) =$4.00

Genetic regression

Note: MTEBV, Feed Intake $0.5*ST_EBV_{Protein}$

multiple trait BLUP EBVs

Mt BLUP Index $= 6.MT_EBV_{Protein} - 4.MT_EBV_{FeedIntake}$

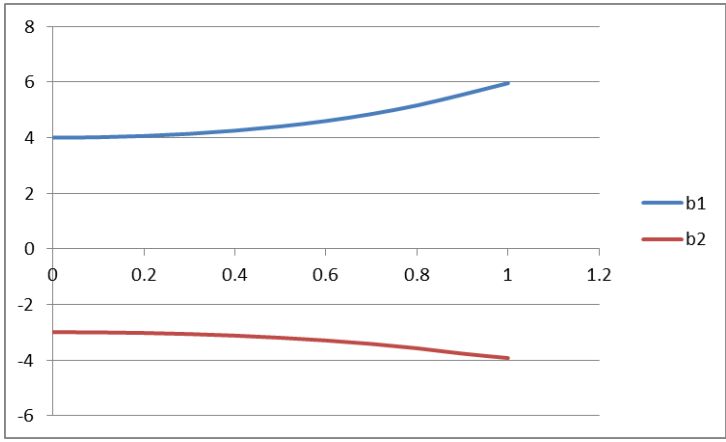
$= 4.MT_EBV_{Protein}$

But not Index $= 6.ST_EBV_{Protein}$

Index weights for single trait EBVs depending on EBV accuracies

economic values 6 and -4 and a genetic regression of 0.5

EBVAccT1	EBVAccT2	IndWGhtT1	IndWghtT2
0.90	0.00	4.00	NA
0.90	0.50	4.40	-2.93
0.90	0.70	4.83	-3.12
0.90	0.90	5.50	-3.42
0.95	0.95	5.73	-3.69
0.99	0.99	5.96	-3.95
0.999	0.999	5.99	-3.99



Explaining the Index weights for ST_EBVs

In an index of ST_EBVs an index weight for a trait (say trait 1):

b1 EV1 + b2 EV2

where:

$b1 \sim r^2_{ST_EBV1} / r^2_{MT_EBV1}$

$b2 \sim (1- r^2_{ST_EBV2})^* \text{cov}(A_1,A_2)/\text{var}(A_1)$

genetic regression

Index weights adjust for correlated response not accounted for by the non-perfect accuracy of a correlated trait

Effect of using incorrect (econ) weights on Selection Response

Case	Weight Used	Wght T1	Wght T2	$Resp T1	$Resp T2	Tot $Resp	Rel Resp
1	EV	1.00	2.00	0.36	0.61	0.96	96.5%
	IW	1.77	1.76	0.42	0.58	1.00	

STEBV accuracies 0.9 and 0.5 and a genetic correlation of 0.5.

Effect of using incorrect (econ) weights on Selection Response

Case	Weight Used	Wght T1	Wght T2	$Resp T1	$Resp T2	Tot $Resp	Rel Resp
1	EV	1.00	2.00	0.36	0.61	0.96	96.5%
	IW	1.77	1.76	0.42	0.58	1.00	
2	EV	1.00	1.00	0.41	0.29	0.71	99.2%
	IW	1.38	0.92	0.43	0.28	0.71	

STEBV accuracies 0.9 and 0.5 and a genetic correlation of 0.5.

Effect of using incorrect (econ) weights on Selection Response

Case	Weight Used	Wght T1	Wght T2	$Resp T1	$Resp T2	Tot $Resp	Rel Resp
1	EV	1.00	2.00	0.36	0.61	0.96	96.5%
	IW	1.77	1.76	0.42	0.58	1.00	
2	EV	1.00	1.00	0.41	0.29	0.71	99.2%
	IW	1.38	0.92	0.43	0.28	0.71	
3	EV	1.00	-1.00	0.37	-0.08	0.29	99.2%
	IW	0.60	-0.75	0.34	-0.05	0.29	

STEBV accuracies 0.9 and 0.5 and a genetic correlation of 0.5.

Effect of using incorrect (econ) weights on Selection Response

Case	Weight Used	Wght T1	Wght T2	$Resp T1	$Resp T2	Tot $Resp	Rel Resp
1	EV	1.00	2.00	0.36	0.61	0.96	96.5%
	IW	1.77	1.76	0.42	0.58	1.00	
2	EV	1.00	1.00	0.41	0.29	0.71	99.2%
	IW	1.38	0.92	0.43	0.28	0.71	
3	EV	1.00	-1.00	0.37	-0.08	0.29	99.2%
	IW	0.60	-0.75	0.34	-0.05	0.29	
4	EV	1.00	-1.25	0.34	-0.06	0.28	96.5%
	IW	0.50	-0.96	0.25	0.04	0.29	

STEBV accuracies 0.9 and 0.5 and a genetic correlation of 0.5.

Effect of using incorrect (econ) weights on Selection Response

Case	Weight Used	Wght T1	Wght T2	$Resp T1	$Resp T2	Tot $Resp	Rel Resp
1	EV	1.00	2.00	0.36	0.61	0.96	96.5%
	IW	1.77	1.76	0.42	0.58	1.00	
2	EV	1.00	1.00	0.41	0.29	0.71	99.2%
	IW	1.38	0.92	0.43	0.28	0.71	
3	EV	1.00	-1.00	0.37	-0.08	0.29	99.2%
	IW	0.60	-0.75	0.34	-0.05	0.29	
4	EV	1.00	-1.25	0.34	-0.06	0.28	96.5%
	IW	0.50	-0.96	0.25	0.04	0.29	
5	EV	1.00	-1.50	0.30	-0.02	0.28	91.9%
	IW	0.40	-1.17	0.15	0.16	0.31	

STEBV accuracies 0.9 and 0.5 and a genetic correlation of 0.5.

Effect of using incorrect (econ) weights on Selection Response

Case	Weight Used	Wght T1	Wght T2	$Resp T1	$Resp T2	Tot $Resp	Rel Resp
1	EV	1.00	2.00	0.36	0.61	0.96	96.5%
	IW	1.77	1.76	0.42	0.58	1.00	
2	EV	1.00	1.00	0.41	0.29	0.71	99.2%
	IW	1.38	0.92	0.43	0.28	0.71	
3	EV	1.00	-1.00	0.37	-0.08	0.29	99.2%
	IW	0.60	-0.75	0.34	-0.05	0.29	
4	EV	1.00	-1.25	0.34	-0.06	0.28	96.5%
	IW	0.50	-0.96	0.25	0.04	0.29	
5	EV	1.00	-1.50	0.30	-0.02	0.28	91.9%
	IW	0.40	-1.17	0.15	0.16	0.31	
6	EV	1.00	-2.00	0.24	0.08	0.32	82.5%
	IW	0.21	-1.59	-0.02	0.41	0.39	

STEBV accuracies 0.9 and 0.5 and a genetic correlation of 0.5.

une

Using ST EBVs Summary

- When using ST EBVs in an index:

- index weights are economic weights but adjusted for correlated changes in other traits as far as those are not accounted for by their EBVs

- Additional weight is given to traits that are well measured,
- Includes value of response other breeding objective traits not well measured

- not making this adjustment ignores the value of some correlated changes

- Although the overall response is likely to be not affected very much (less than 5%), the weight and response for Production would be higher and the weight and response for Fertility or Fitness would be considerably lower compared to an optimal index

Summary ST EBVs in index

- When using ST EBVs, best approach is to use index weights, not straight economic weights

- But Index Weights can cause some practical problems

  - Some weights maybe hard to explain

  - Different bulls might need different weights

  - Do not publish weights? Then not easy to calculate your own index