

Breeding Objectives

Multi-trait selection – how to implement?

- Need to combine
 - the relative economic weights
 - genetic parameters (heritabilities, correlations)

to determine the weights we put on the observed phenotypes

$$\text{Index} = b_1X_1 + b_2X_2$$

Issues with MT selection

- We have to spread our selection efforts over several traits, each of them weighted economically
- Selection for one trait gives also a correlated response for other traits

We need weights for selection criteria

- Index = $b_1X_1 + b_2X_2 + \dots + b_nX_n$

Selection index with more information sources (multiple regression)

X = vector with phenotypes (criteria)

A = aggregate genotype (single trait here)

$$\text{var}(X) = P = \text{matrix} = \begin{bmatrix} \text{var}(X_1) & \text{cov}(X_1, X_2) \\ \text{cov}(X_2, X_1) & \text{var}(X_2) \end{bmatrix}$$

$$\text{cov}(X, A) = G = \text{vector} = \begin{bmatrix} \text{cov}(x_1, A) \\ \text{cov}(x_2, A) \end{bmatrix}$$

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

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

X = vector with phenotypes (criteria)

H = aggregate genotype (multiple traits here)

$$= \mathbf{v}_1 \mathbf{A}_1 + \mathbf{v}_2 \mathbf{A}_2$$

$$\text{var}(X) = \mathbf{P} = \text{matrix} = \begin{bmatrix} \text{var}(X_1) & \text{cov}(X_1, X_2) \\ \text{cov}(X_2, X_1) & \text{var}(X_2) \end{bmatrix}$$

$$\text{cov}(X, \mathbf{A}) = \mathbf{G} = \text{matrix} = \begin{bmatrix} \text{cov}(X_1, A_1) & \text{cov}(X_1, A_2) \\ \text{cov}(X_2, A_1) & \text{cov}(X_2, A_2) \end{bmatrix}$$

$$\text{weights: } \mathbf{b} = \mathbf{P}^{-1} \mathbf{G} \mathbf{v}$$

Index weights example

	σ_p	h^2	rg	rp	a	b
FW	.4	.4			5	2
			0	0		
FD	2	.4			-1	-0.4

Heritabilities same and no correlation;

Weights are proportional to rel. economic weight

Index weights example

	σ_p	h^2	rg	rp	a	b
FW	.4	.3			5	1.5
			0	0		
FD	2	.5			-1	-0.5



More weight for traits with higher heritability

Index weights example

	σ_p	h^2	rg	rp	a	b
FW	.4	.3			5	0.53
			0.5	0		
FD	2	.5			-1	-0.31



Weights also depend on correlations

In general, weights on phenotypic information sources are not easy to 'recognize'

Selection index for Single Trait

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

$$\text{cov}(X, A) = G = \text{vector} = \begin{bmatrix} \text{cov}(x_1, A) \\ \text{cov}(x_2, A) \end{bmatrix}$$

weights: $b = P^{-1}G$ gives weight for all sources about one EBV

Selection index for multiple traits

$$H = \text{aggregate genotype} = v_1 A_1 + v_2 A_2$$

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

$$\text{cov}(X, A) = G = \text{matrix} = \begin{bmatrix} \text{cov}(x_1, A_1) & \text{cov}(x_1, A_2) \\ \text{cov}(x_2, A_1) & \text{cov}(x_2, A_2) \end{bmatrix}$$

$$\text{weights: } b = P^{-1} G v = [b_1 \quad b_2] \begin{bmatrix} v_1 \\ v_2 \end{bmatrix}$$

b_i is a subset of weights for i^{th} trait to give EBV_i

Overall weights are weighting each subset with its economic weight

Using EBV's rather than own phenotypes as selection criteria

$$\text{Index} = v_1 \text{EBV}_1 + v_2 \text{EBV}_2 + \dots + v_n \text{EBV}_n$$

weights are equal to economic values!

as genetic parameters are already accounted for in MT-BLUP generation of EBV's

Index selection is more efficient than single trait selection!

Predicting response to MT selection

- Response in dollars:

$$R = i \cdot S_{\text{Index}} = i \cdot \mathbf{0} \mathbf{b}' \mathbf{P} \mathbf{b}$$

Response for each trait

$$[R_1 \ R_2 \ \dots R_m] = i \cdot \mathbf{b}' \mathbf{G} / \mathbf{0} \mathbf{b}' \mathbf{P} \mathbf{b}$$

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?

Predicting genetic change to multiple trait selection

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

Direct response to single trait selection

$$R = i \cdot h^2 \cdot \sigma_P \quad \text{if mass selection}$$

$$R = i \cdot r_{IA} \cdot \sigma_A \quad \text{more general:}$$

r_{IA} is accuracy of selection

Direct and Correlated response to single trait selection

$$\text{Response} = i \cdot h_1 \cdot \sigma_{A1}$$

and

$$\text{Correlated Response} = i \cdot h_1 \cdot r_g \cdot \sigma_{A2}$$

single trait selection!

Combining information on two traits

selection index

$$I = b_1 X_1 + b_2 X_2$$

$$P = \text{var} \begin{pmatrix} X_1 \\ X_2 \end{pmatrix} = \begin{pmatrix} \text{var}(X_1) & \text{cov}(X_1, X_2) \\ \text{cov}(X_2, X_1) & \text{var}(X_2) \end{pmatrix} = \begin{pmatrix} \mathbf{s}_{p_1}^2 & r_p \mathbf{s}_{p_1} \mathbf{s}_{p_2} \\ r_p \mathbf{s}_{p_1} \mathbf{s}_{p_2} & \mathbf{s}_{p_2}^2 \end{pmatrix}$$

$$G = \text{cov} \begin{pmatrix} X_1 \\ X_2 \end{pmatrix}, A_1 = \begin{pmatrix} \text{cov}(X_1, A_1) \\ \text{cov}(X_2, A_1) \end{pmatrix} = \begin{pmatrix} \mathbf{s}_{A_1}^2 \\ r_g \mathbf{s}_{A_1} \mathbf{s}_{A_2} \end{pmatrix}$$

$$b = P^{-1}G = \begin{pmatrix} 115 & 21.9 \\ 21.9 & 145 \end{pmatrix}^{-1} \begin{pmatrix} 5.75 \\ 2.74 \end{pmatrix} = \begin{pmatrix} 0.6517 \\ 0.0796 \end{pmatrix}$$

Multiple Trait breeding goal

- Aggregate genotype: $H = v_1 A_1 + v_2 A_2$
- selection index $I = b_1 X_1 + b_2 X_2$

Multiple Trait breeding goal

- Aggregate genotype: $\mathbf{H} = v_1 \mathbf{g}_1 + v_2 \mathbf{g}_2$
- selection index $\mathbf{l} = b_1 \mathbf{X}_1 + b_2 \mathbf{X}_2$

$$G = \text{cov} \begin{pmatrix} X_1 \\ X_2 \end{pmatrix}, (A_1 \quad A_2) = \begin{pmatrix} \text{cov}(X_1, A_1) & \text{cov}(X_1, A_2) \\ \text{cov}(X_2, A_1) & \text{cov}(X_2, A_2) \end{pmatrix}$$

$$= \begin{pmatrix} \mathbf{s}_{g_1}^2 & r_g \mathbf{s}_{A_1} \mathbf{s}_{A_2} \\ r_g \mathbf{s}_{A_1} \mathbf{s}_{A_2} & \mathbf{s}_{A_2}^2 \end{pmatrix} = \begin{pmatrix} 5.75 & 2.74 \\ 2.74 & 14.5 \end{pmatrix}$$

$$\begin{pmatrix} b_1 \\ b_2 \end{pmatrix} = P^{-1} G a = \begin{pmatrix} 11.5 & 22.05 \\ 22.05 & 145 \end{pmatrix}^{-1} \begin{pmatrix} 5.75 & 2.74 \\ 2.74 & 14.5 \end{pmatrix} \begin{pmatrix} 1.0 \\ -0.5 \end{pmatrix} = \begin{pmatrix} 0.618 \\ -0.125 \end{pmatrix}$$

- Variance of index:

$$s_I^2 = b'Pb = 3.27 \quad \$\$$$

- Variance of the aggregate genotype

$$s_H^2 = v'Cv = 6.64 \quad \$\$ \quad C = \text{var}(A) \text{ ..of breeding values}$$

- Accuracy of Index:

$$r_{IH} = s_I / s_H = \sqrt{(b'Pb / v'Cv)}$$

- **Response to selection**

$$R = i \cdot r_{IH} \cdot S_A = i \cdot S_I \quad \text{in } \$\$$$

- **Response in each trait:**

$$\begin{aligned} dg_i &= b_{gi,l} R \\ &= i \cdot b'_i G_i / S_I \end{aligned}$$

- **Notice that sum of $dg_i \cdot v_i = R$**

See also mtindex.xls

Example

body weight $h^2_A = 0.40$ $s_p = 17$ kg

feed intake $h^2_B = 0.25$ $s_p = 2.0$ kg

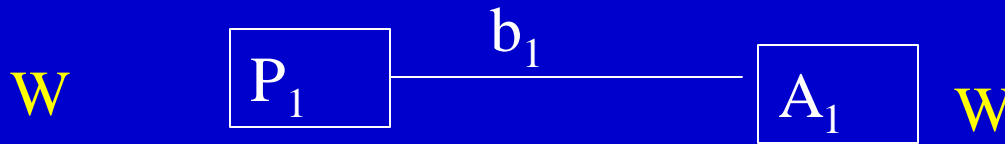
$$r_g = .50$$

$$r_p = 0.20$$

selection intensity=1.0

Criteria for selection

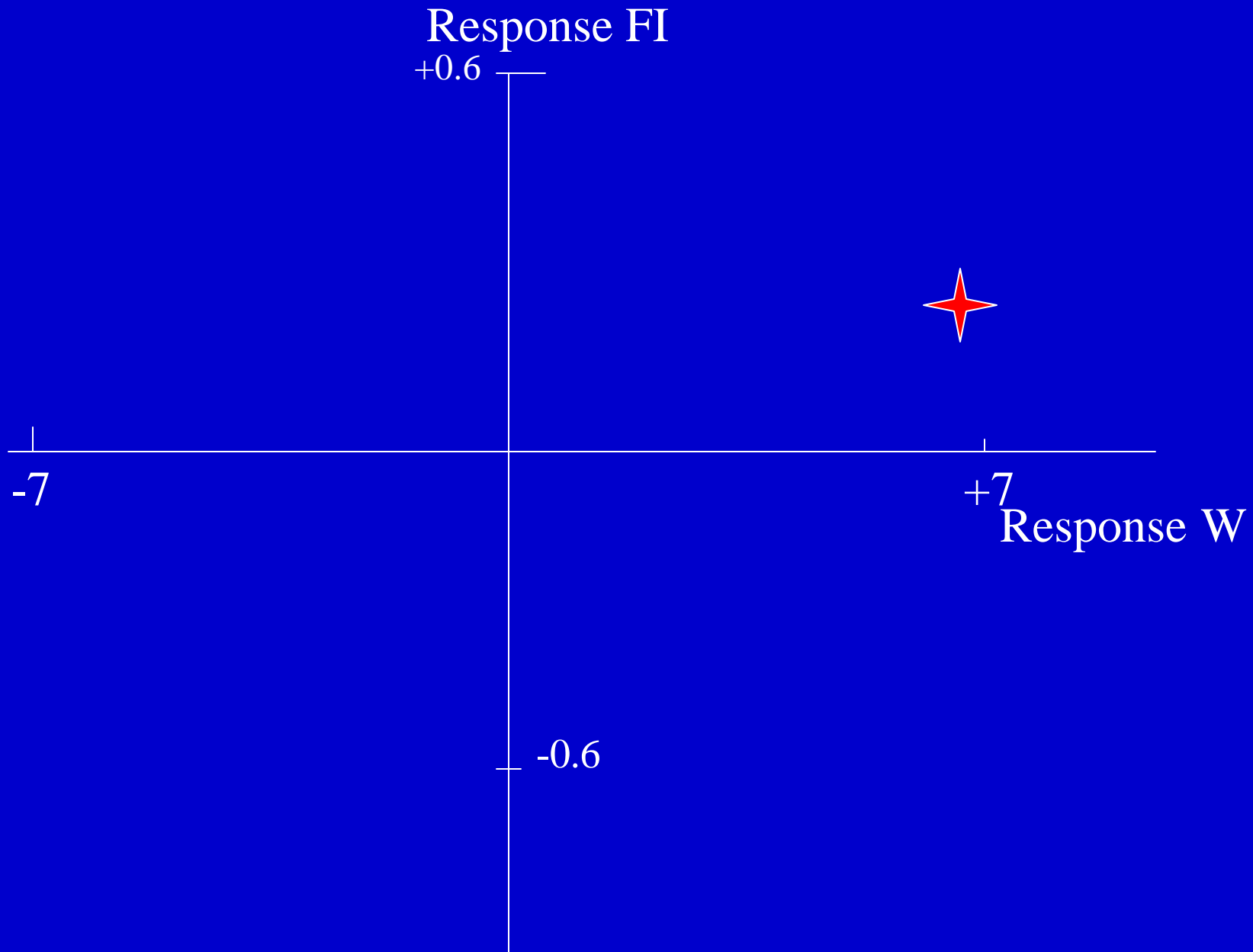
True Breeding Value

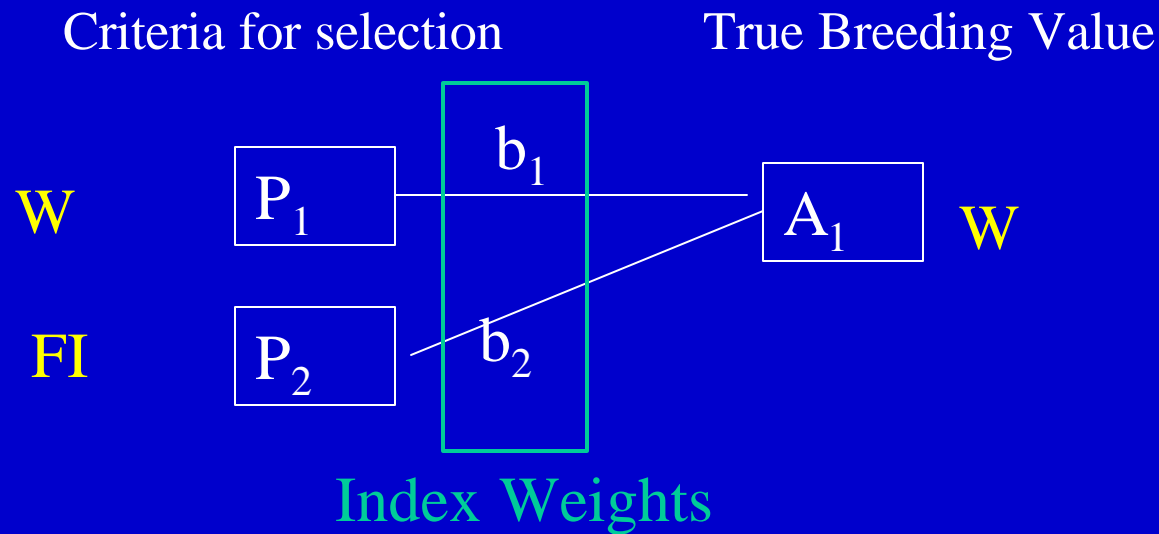


$$\text{Index} = \text{EBV} = 0.4P_W$$

$$\text{Response} = \mathbf{6.80} \text{ kg Weight}$$

$$\text{Correl. Resp.} = \mathbf{0.32} \text{ kg Feed Intake}$$

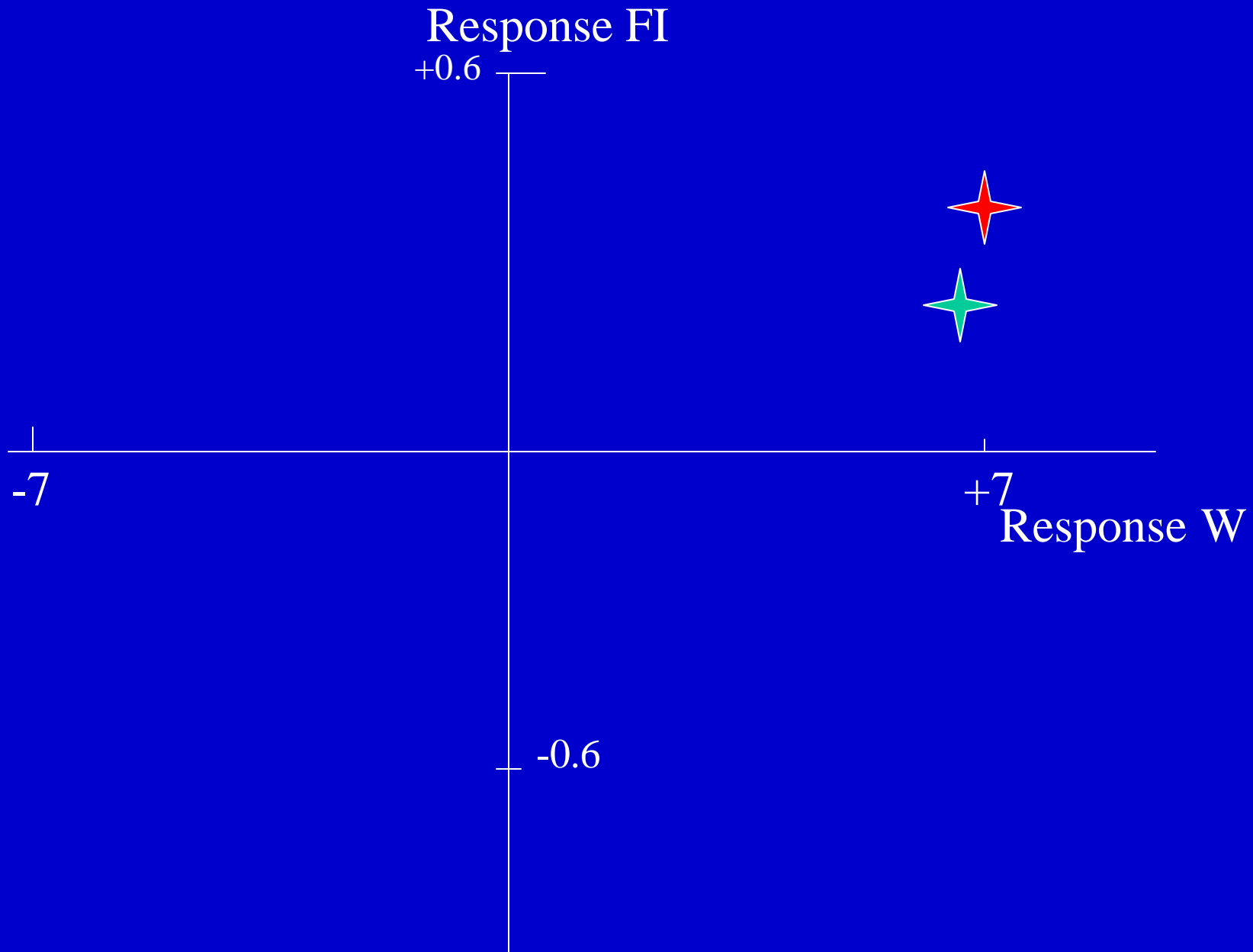


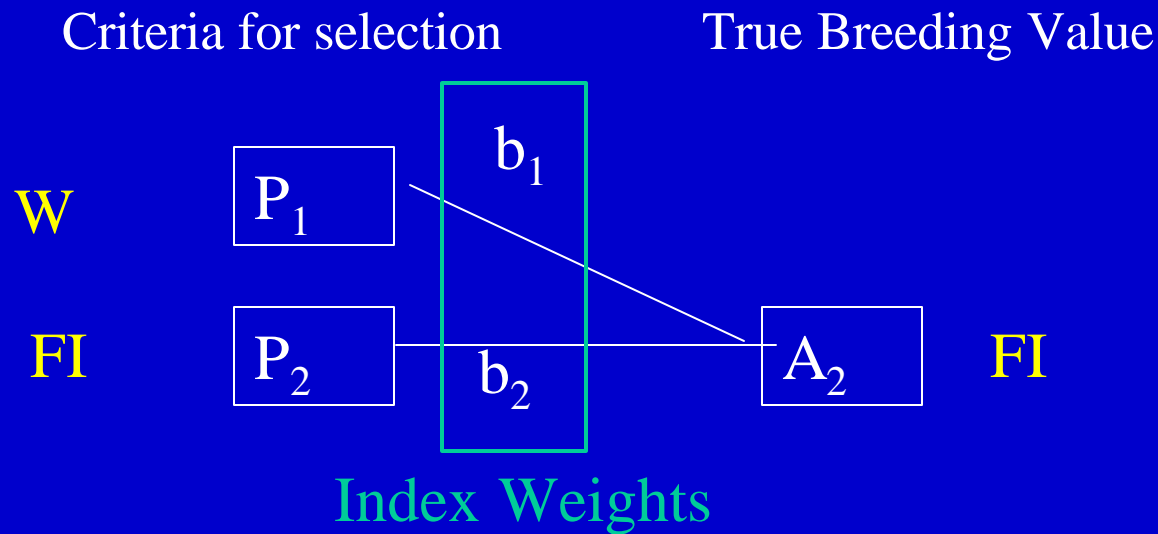


$$\text{Index} = \$EBV = 0.38P_{W+} + 0.69P_{FI}$$

$$R_W = \mathbf{6.93} \text{ kg}$$

$$R_{FI} = \mathbf{0.40} \text{ kg}$$

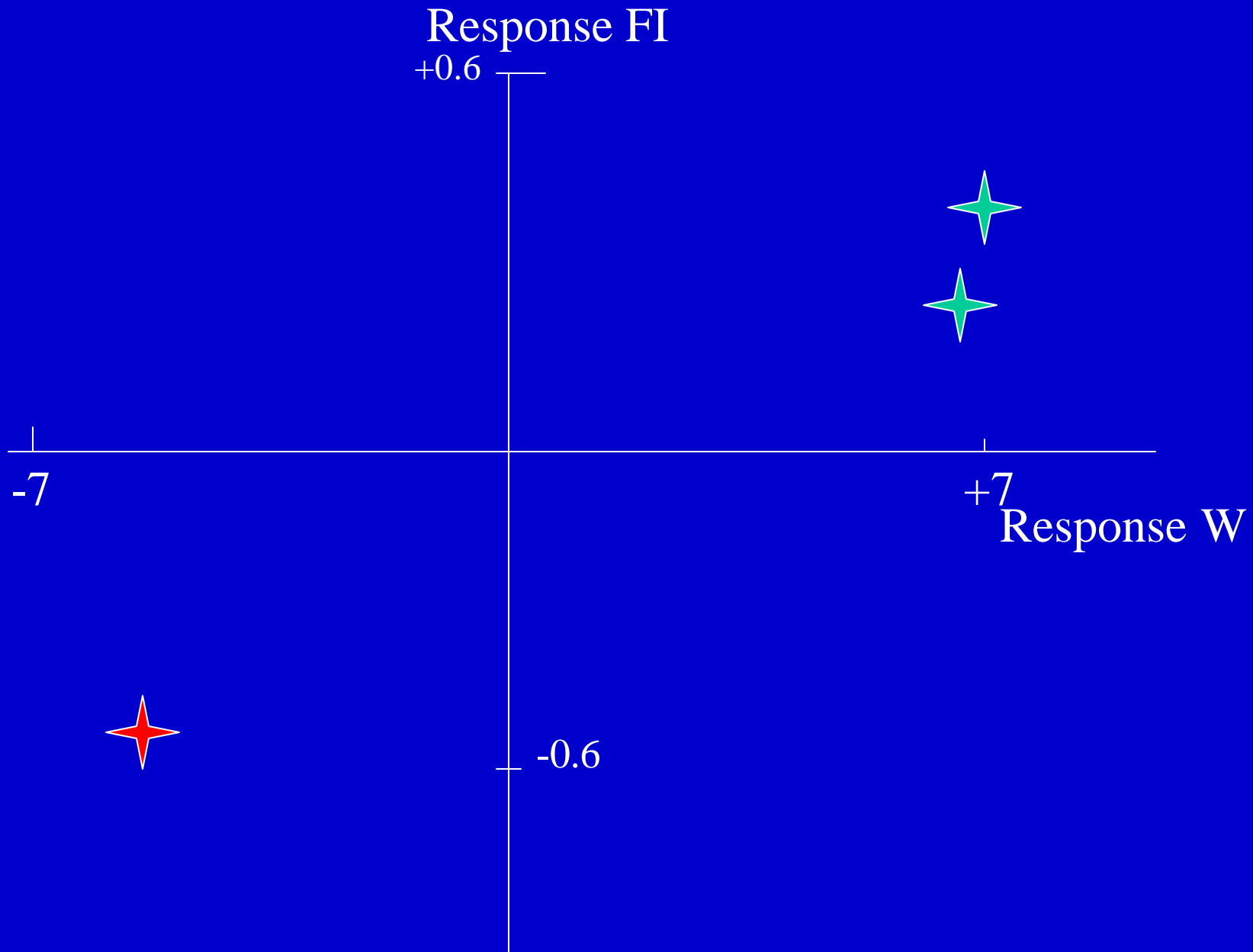


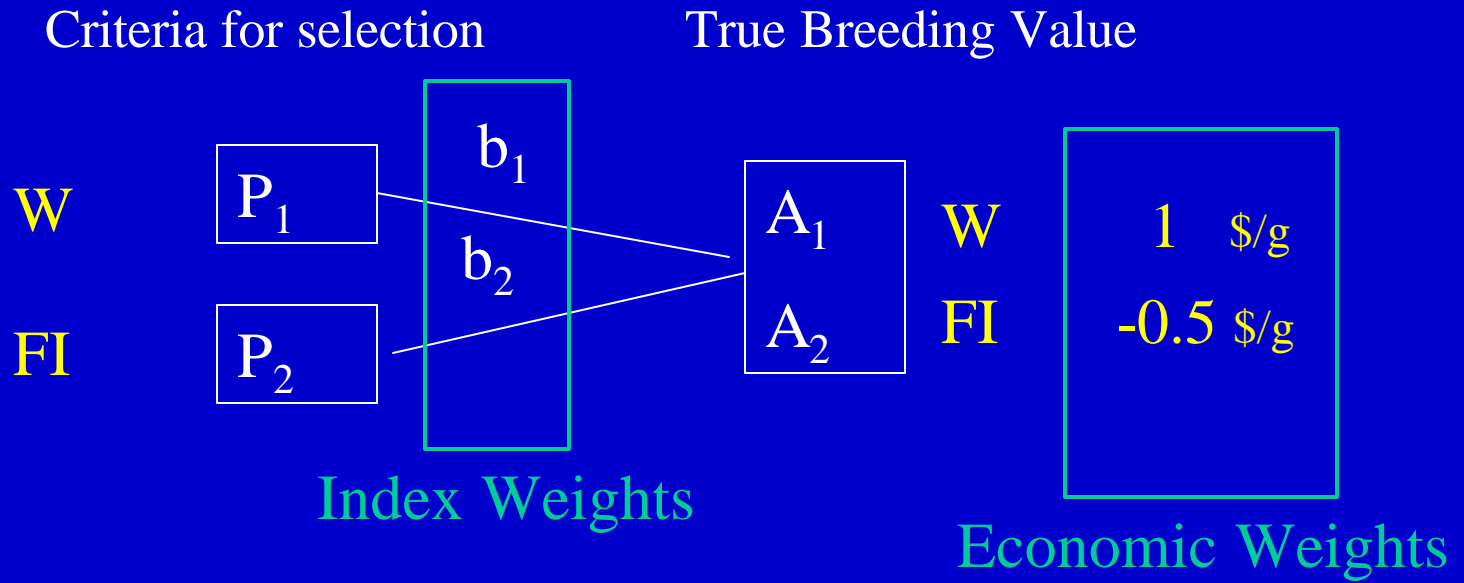


$$\text{Index} = \$EBV = -0.013P_W - 0.23P_{FI}$$

$$R_W = -5.04 \text{ kg}$$

$$R_{FI} = -0.55 \text{ kg}$$



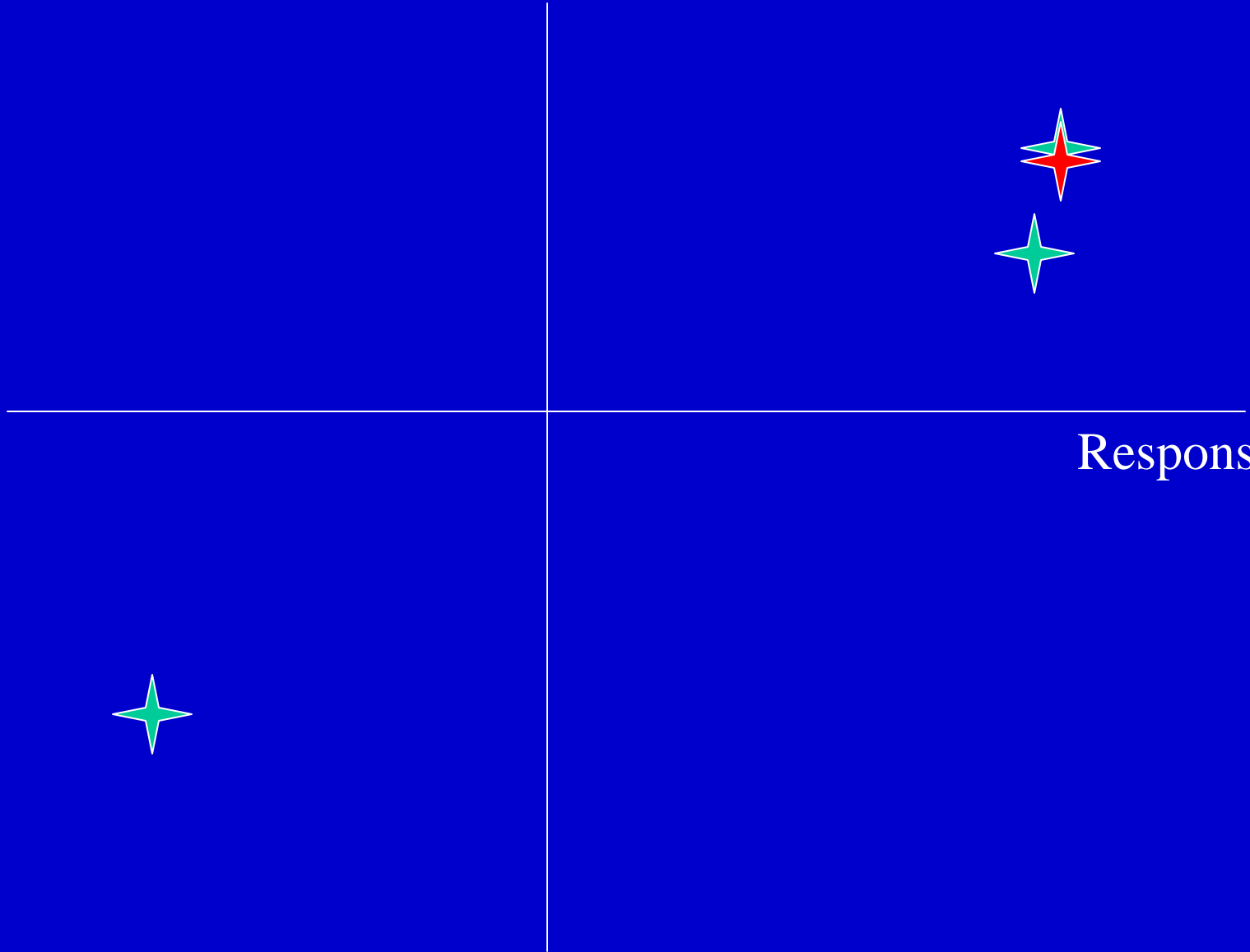


$$\text{Index} = \$EBV = 0.62P_W - 0.13P_{FI}$$

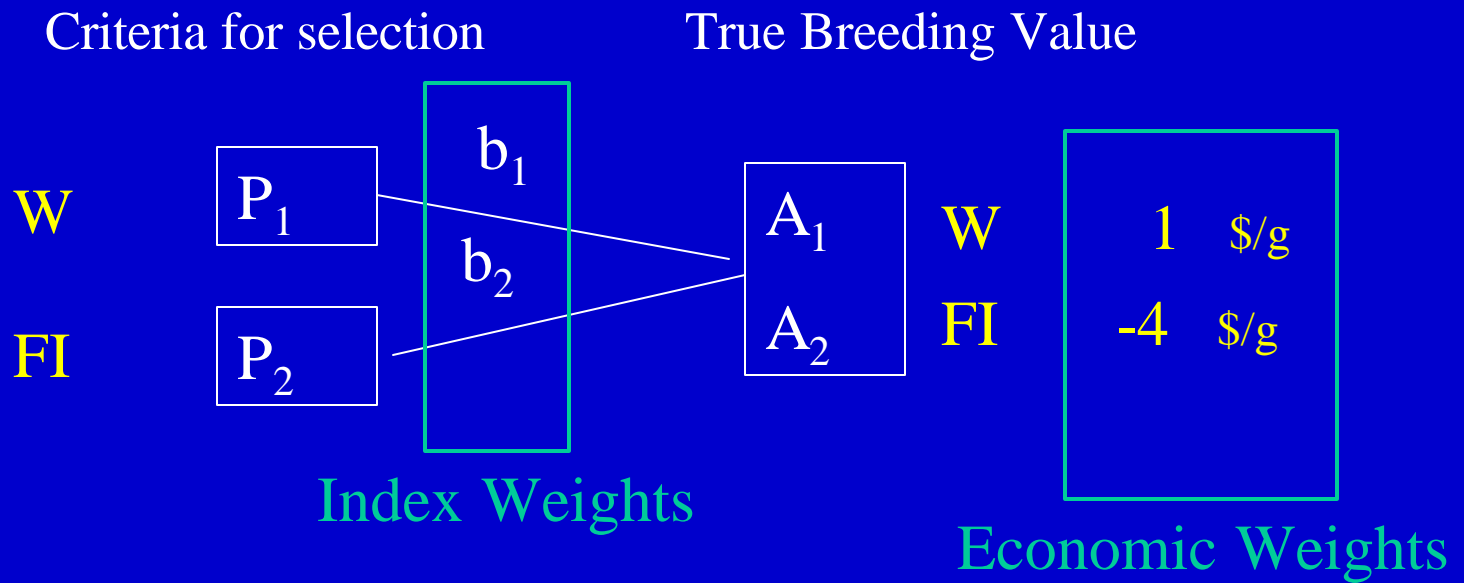
$$R_W = \mathbf{6.93} \text{ kg}$$

$$R_{FI} = \mathbf{0.39} \text{ kg}$$

Response FI



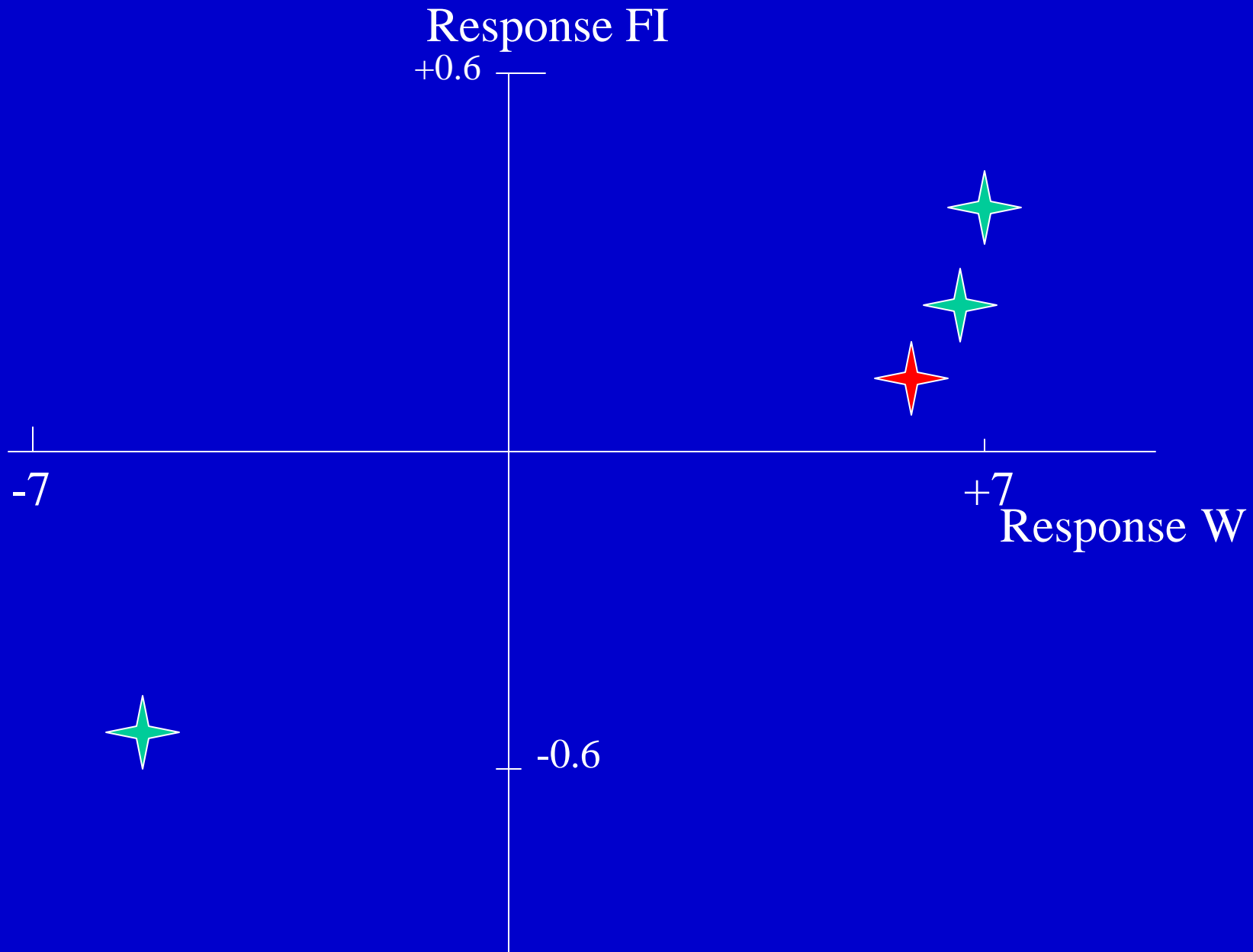
Response W

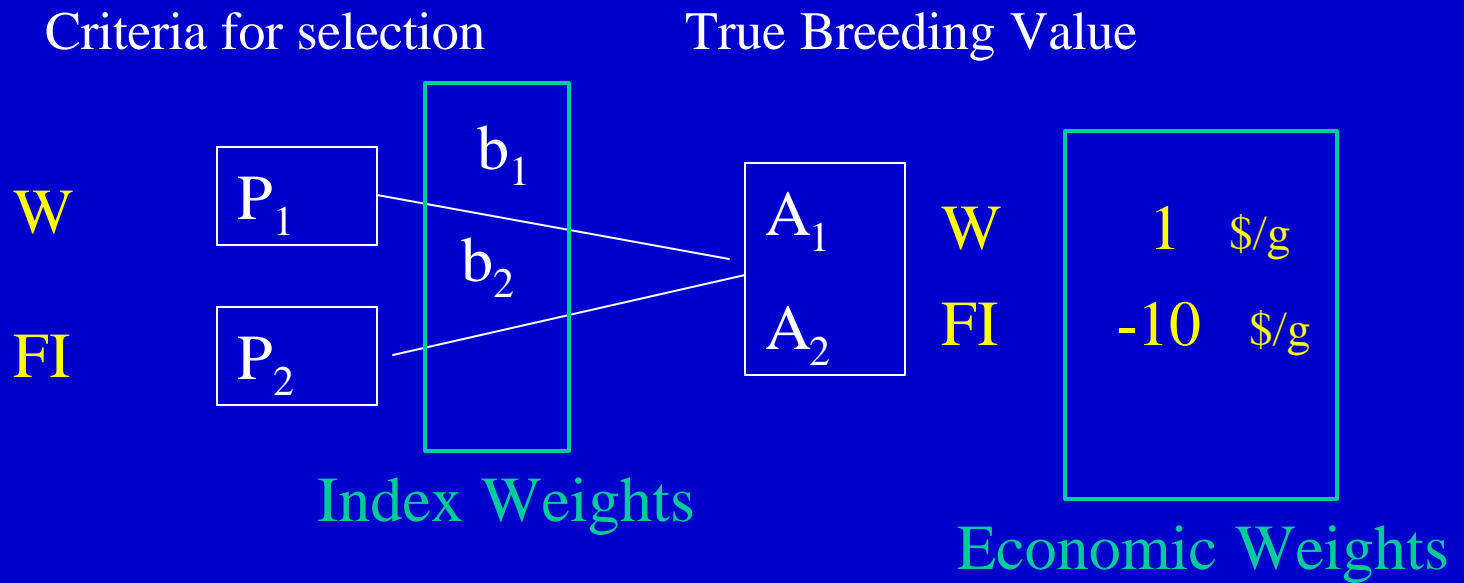


$$\text{Index} = \$EBV = 0.33P_W - 0.22P_{FI}$$

$$R_W = \mathbf{6.68} \text{ kg}$$

$$R_{FI} = \mathbf{0.28} \text{ kg}$$

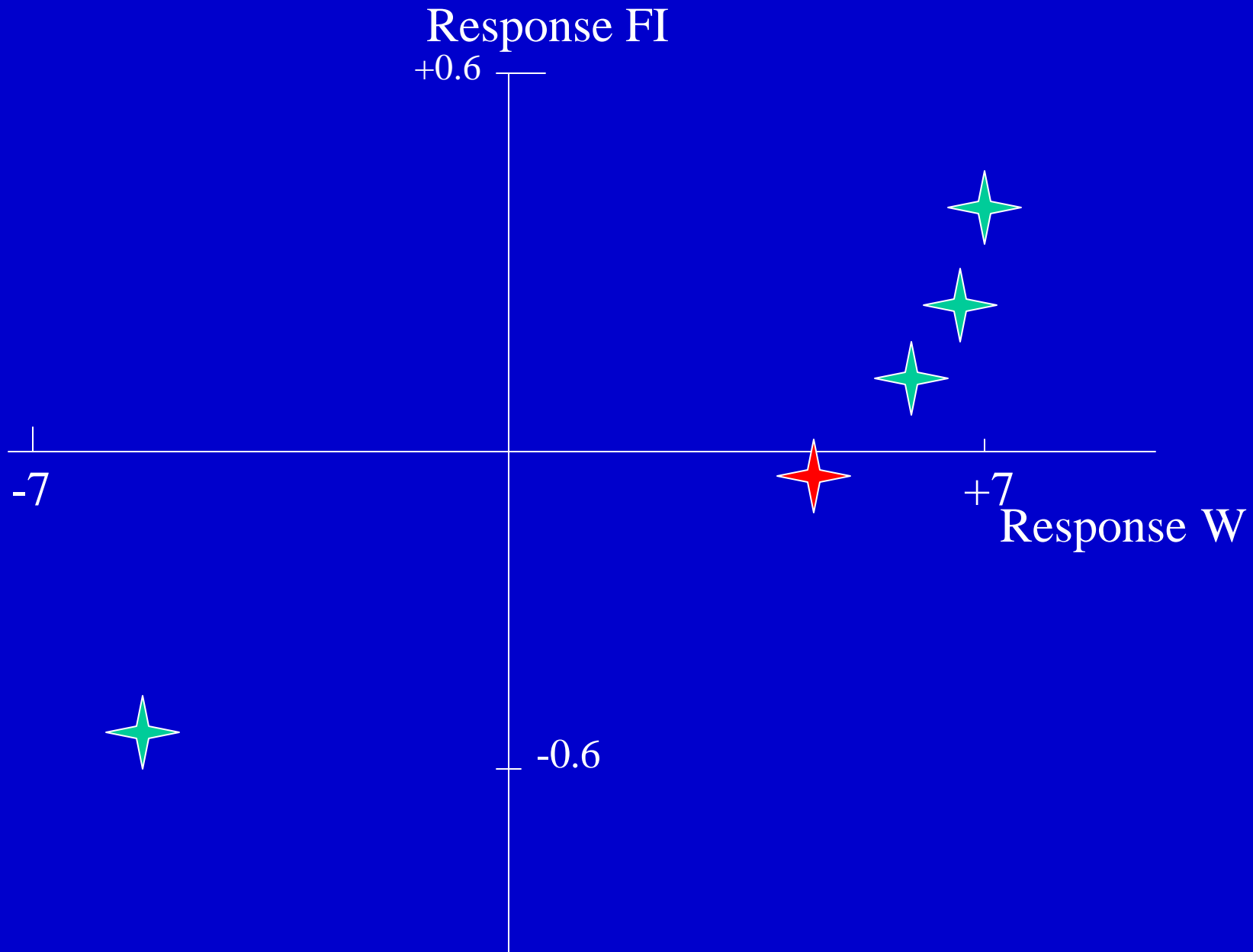


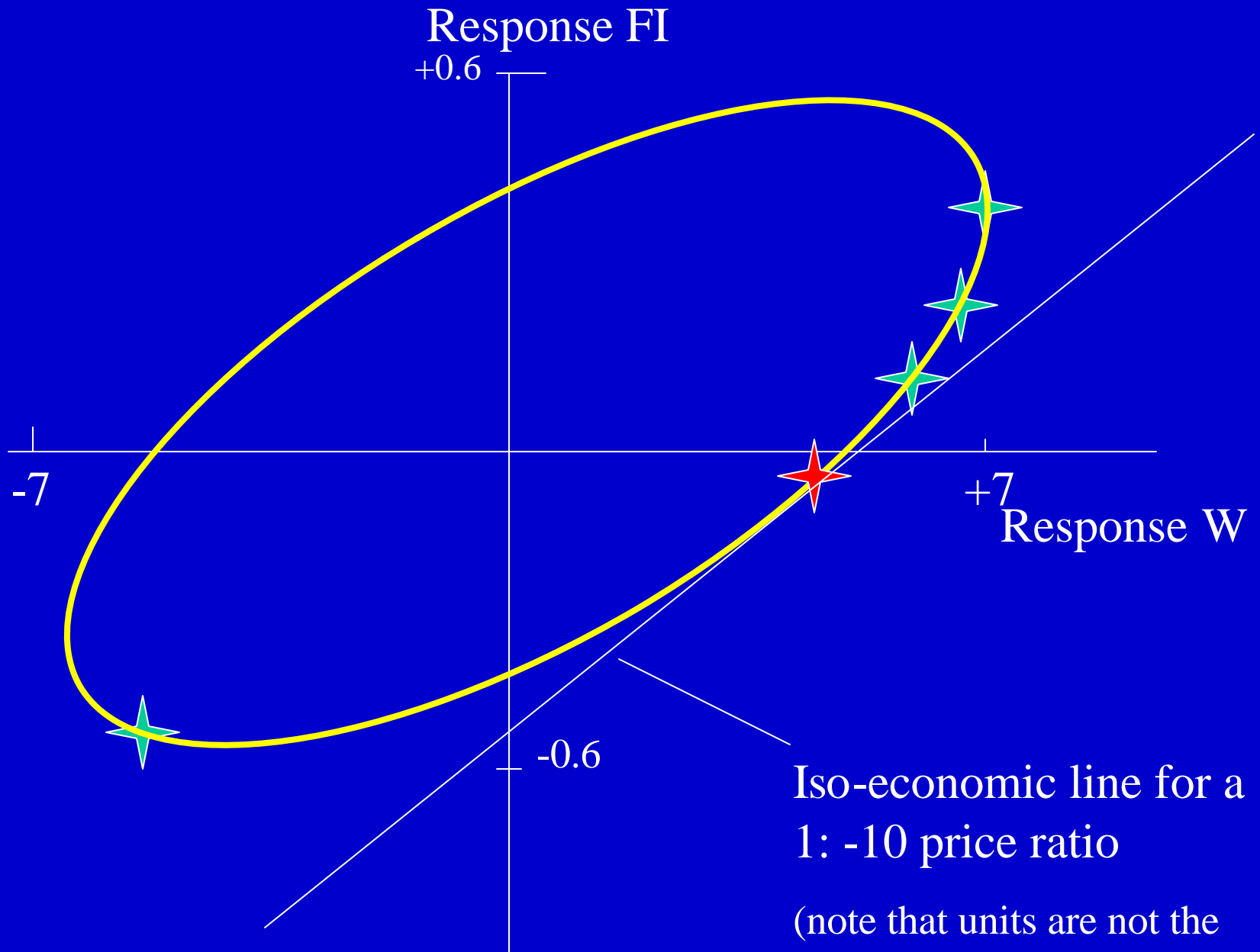


$$\text{Index} = \$EBV = 0.25P_W - 1.58P_{FI}$$

$$R_W = 4.29 \text{ kg}$$

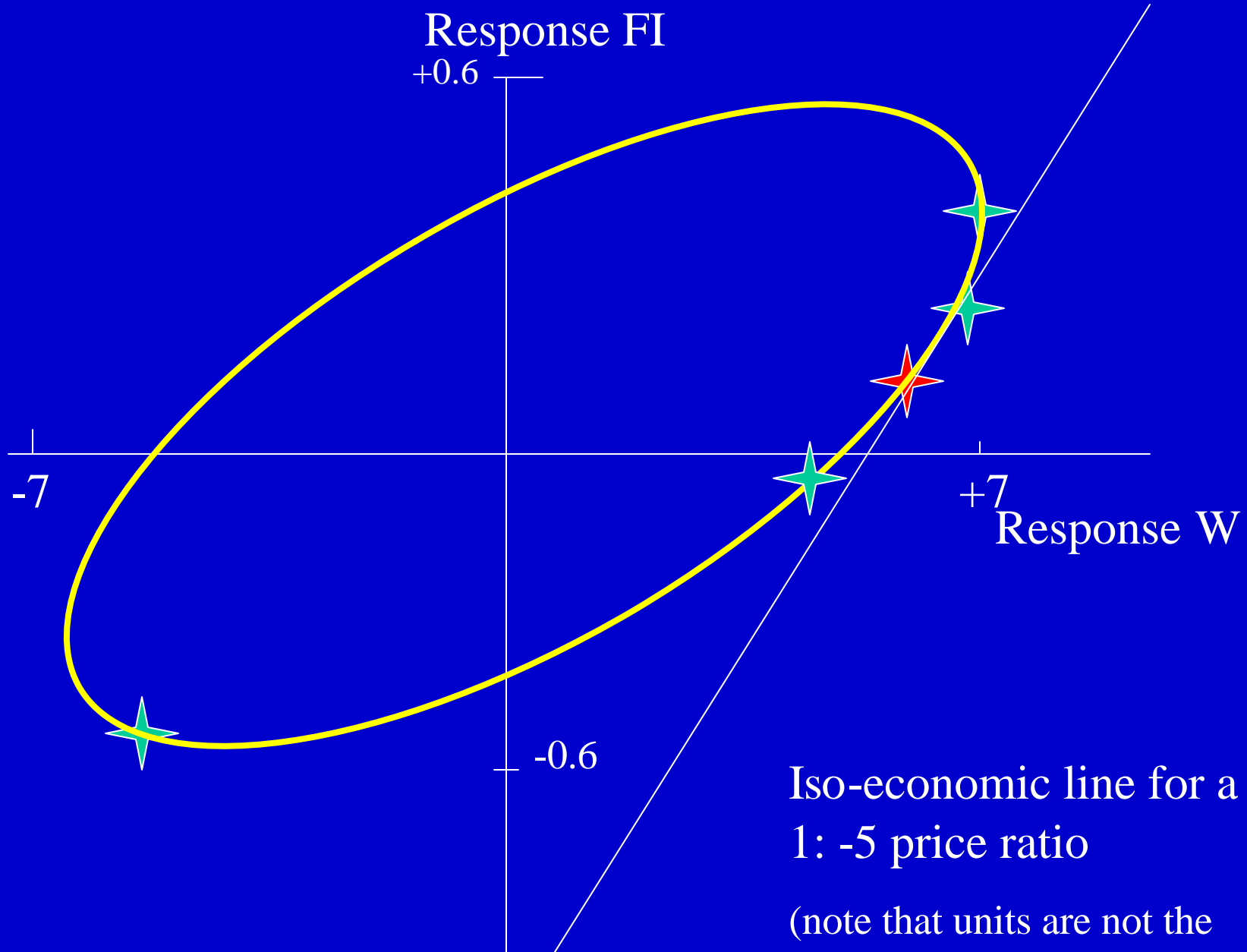
$$R_{FI} = -0.05 \text{ kg}$$



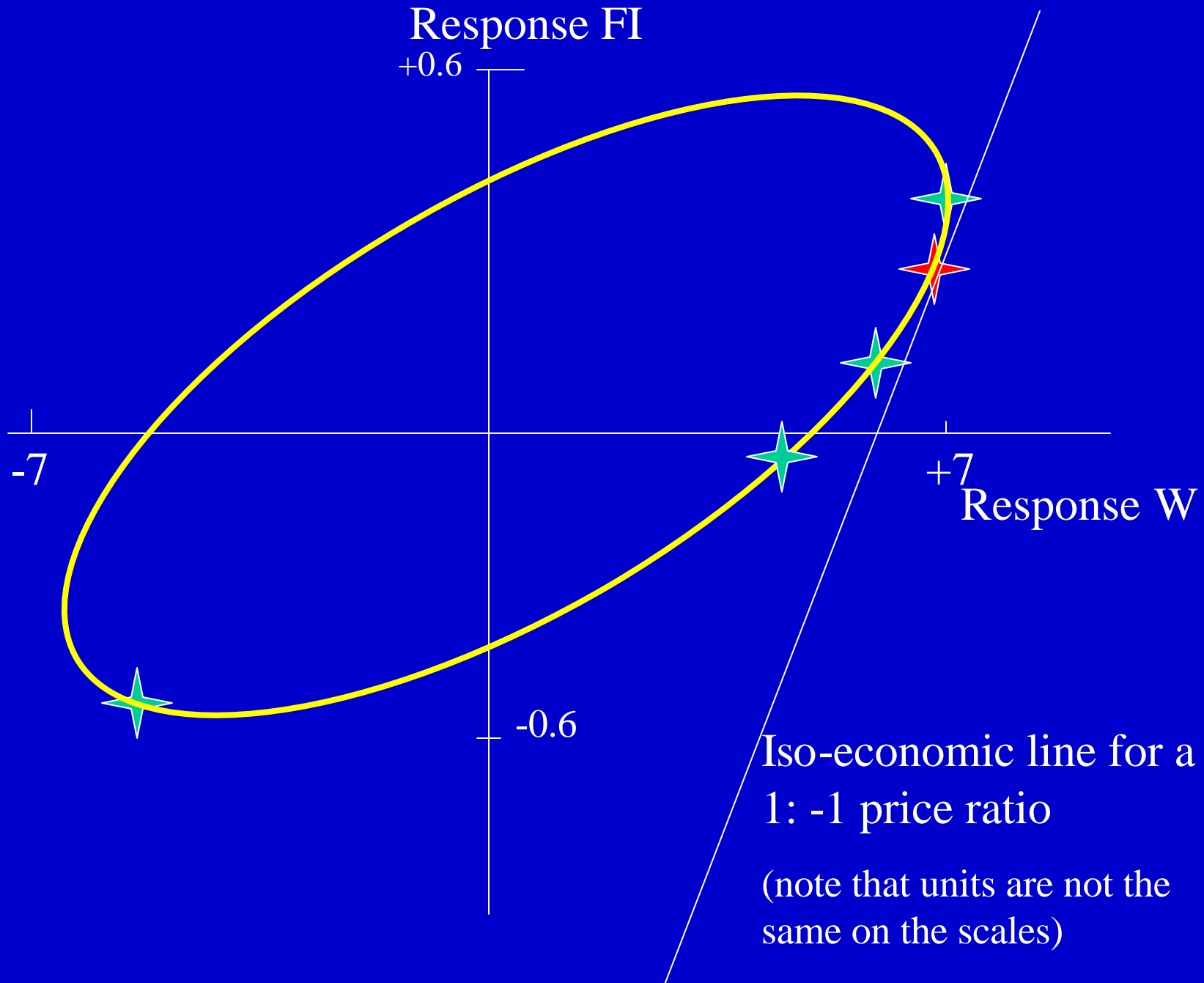


Iso-economic line for a
1: -10 price ratio

(note that units are not the
same on the scales)



Iso-economic line for a
1: -5 price ratio
(note that units are not the
same on the scales)



Predicting genetic change to multiple trait selection

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