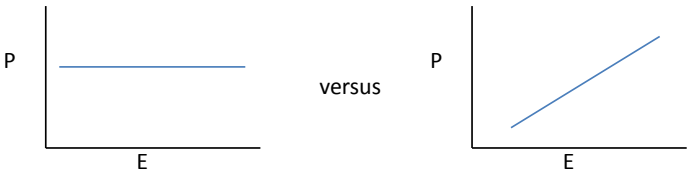
Response to selection

Piter Bijma
Animal Breeding and Genomics Centre
Wageningen University

Response to selection

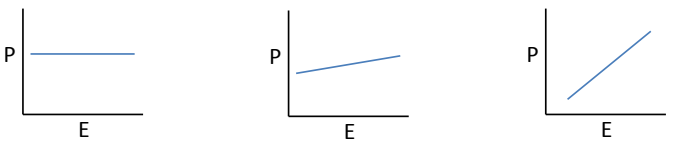
- Interest is in:
- Response in mean level of trait in each environment
- Response in environmental sensitivity

Environmental Sensitivity

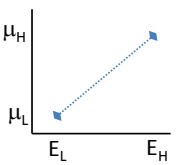


Environmental Sensitivity ("plasticity")

- Change of mean trait value of a genotype with a change in environment



Not sensitive | A bit sensitive | Very sensitive



A measure of sensitivity: $s = \mu_H - \mu_L$

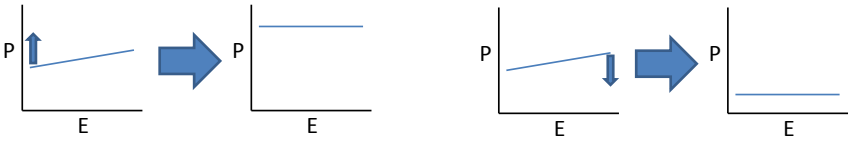
Scaled response in sensitivity: $s^* = \frac{\mu_H^* - \mu_L^*}{\mu_H - \mu_L}$ (WL38.5)

s* = relative response in the difference
s* > 1 → increase in sensitivity due to selection
s* < 1 → decrease in sensitivity due to selection

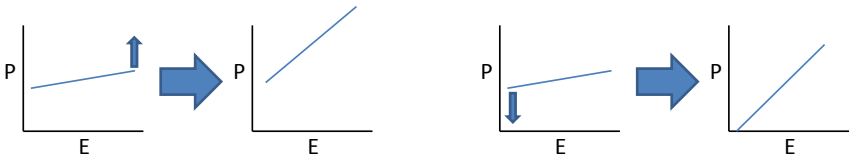
If E is quantitative (i.e. a value): $s = \frac{\mu_H - \mu_L}{E_H - E_L}$ = Slope of the reaction norm

Trends observed in response

- Jinks-Connoly rule
  - Antagonist selection reduces sensitivity



  - Synergistic selection increases sensitivity



  - A trend, not an absolute truth
  - Falconer's rule:
    - Sensitivity is less after antagonistic than after synergistic selection: holds more general

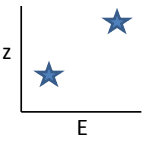
Conclusion

With GxE-interaction,

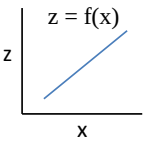
the environment and direction of selection matter for the change in environmental sensitivity

Models for GxE-interaction:

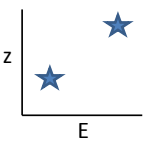
Character state model
(multitrait model)



Reaction norm model
(random regression model)



Character State Model (Via and Lande)



- Multitrait approach (Falconer)
  - Population is split into discrete environments
  - Phenotype and genotype in each environment "is" a trait.
  - The different traits (environments) may have different genetic means, genetic (co)variances, and there is a **genetic correlation** between traits in different environments
  - Vector of breeding values in each environment: $\mathbf{g}_i' = [g_{1,i}, g_{2,i}, \ldots, g_{m,i}]$
  - *i* = individual, *m* = no. of environments
- Applicable when you can split the environment into discrete classes
  - Captures *all* the GxE-interaction between these environments, in contrast to the reaction norm model.
  - Examples: purebreds vs crossbreds, temperate vs tropical climates, location, herd

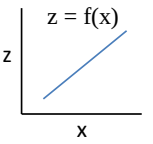
Character state model: example

Yield of dairy cows in New Zealand vs. Austalia

Two traits:
- Milk-yield in Australia
- Milk-yield in New Zealand

Key parameter:
Genetic correlation between both traits (r_g)
$r_g < 1 \rightarrow$ GxE-interaction

Reaction norm model



- Trait expression is on a continuous environmental scale (x)
  - BV and genetic parameters change gradually along the environmental scale
  - At different locations on the environmental scale, traits may have different means and (co)variances, and there is a genetic correlation between trait expression at different points of the environmental scale
- Applicable when you have a continuous environmental variable that explains (part of) the GxE interaction
  - Temperature, average herd milk yield, HYS effect, Pasture contamination
- Note: Captures only the part of the GxE-interaction due to the environmental variable (the x-axis).
- Advantage RN-model:
  - Explicit model for environmental sensitivity (slope)
  - Prediction in other (non-recorded) environments.

Reaction norm model: basics

- Breeding value is a function of the environment → g(x)
  - For example $g_i(x) = g_{0,i} + g_{1,i}x + g_{2,i}x^2 + g_{3,i}x^3 + ...$
  - $g_i(x)$ = breeding values of individual i for environment x
  - x = value of the environment
  - $g_{0,i}$, $g_{1,i}$, $g_{2,i}$ are breeding values of individual *i*
  - Vector notation: $g_i(x) = g_{0,i} + g_{1,i}x + g_{2,i}x^2 + ... = \begin{bmatrix} g_{0,i} & g_{1,i} & g_{2,i} & \cdots \end{bmatrix} \begin{bmatrix} 1 \\ x \\ x^2 \\ \vdots \end{bmatrix} = \mathbf{g}_i'\mathbf{x}$
- Phenotype
  - Analogy of P = G + E → P(x) = g(x) + e
  - Expected phenotype given the genotype: E[P(x) | g(x)] = g(x)
    - Expected phenotype equals breeding value, E [e] = 0
    - Breeding value predicts the phenotype

Reaction norm model: example

Growth rate (GR) and worm egg pasture contamination (PC)

Idea: - Sheep grow slower when pasture contamination is higher
- But not all sheep are equally sensitive to PC (=GxE)

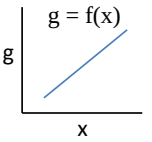
Linear reaction norm: $Y_{i,flock} = HYS + g_{0,i} + g_{1,i}\, PC_{flock} + e$

$g_{0,i}$ = breeding value for level
$g_{1,i}$ = breeding value for slope (with respect to PC)

$\mathbf{g}_i = \begin{bmatrix} g_{0,i} \\ g_{1,i} \end{bmatrix}$ $\mathbf{x} = \begin{bmatrix} 1 \\ PC_{flock} \end{bmatrix}$ Breeding value: $g_i(PC) = \mathbf{g}_i'\mathbf{x} = \begin{bmatrix} g_{0,1} & g_{1,i} \end{bmatrix} \begin{bmatrix} 1 \\ PC_{flock} \end{bmatrix} = g_{0,1} + g_{1,i}PC_{flock}$

The linear reaction norm

Breeding value: $g_i(x) = g_{0,i} + g_{1,i}\, x$



Two BV → Three genetic parameters:

- Genetic variance in level: var(g_0)
- Genetic variance in slope: var(g_1)
- Genetic correlation between level and slope: (r_{g01})

Q: What does the correlation between level and slope mean?

The correlation between level and slope

Linear reaction norm: $g_i(x) = g_{0,i} + g_{1,i}x$

Genetic correlation level-slope: $r_{g01} = corr(g_0, g_1)$

r_{g01} indicates whether animals that have better breeding values for level are also more ($r_{g01}>0$) or less ($r_{g01}<0$) environmentally sensitive

Indicates whether selection for level
will increase or decrease environmental sensitivity

However:

RN: Meaning of the correlation between level and slope

- **Message:** Correlation depends on the location of the intercept on the environmental scale (*i.e.* where x = 0).
  - General RN: $g(x) = g_0 + g_1 x$, where g_0 and g_1 are correlated with $r_{g,01}$
- Problem: Can we shift the intercept so that $r_{g,01}$ becomes zero?
  - Note: intercept is value of g(x) at x = 0. Hence, find x where g(x) is independent of g_1, and put the intercept there.
  - $Cov[g(x),g_1] = Cov(g_0+g_1x, g_1) = 0$

$$x = -r_{g_{01}} \frac{\sigma_{g_0}}{\sigma_{g_1}}$$

$r_{g,01} > 0 \rightarrow$ shift intercept to the left (down)
$r_{g,01} < 0 \rightarrow$ shift intercept to the right (up)

Conclusion: In itself, the correlation between level and slope is meaningless
Suggested convention: define the intercept in the mean environment

Modelling response to selection

Selection Index Theory

- How to predict response to selection?
  - Selection is usually on an index of EBV
  - But we don't have "genetic parameters" of EBV
  - However, EBV are predicted from phenotypes
- Hence, to predict response, we can mimic selection on EBV by selection on phenotypes
  - Villanueva, B., N. R. Wray, et al. (1993) Anim. Prod. 57: 1-13.
- Method: regress true breeding values on phenotypes

Selection index: response to selection (R)

- Selection is on an index: $I = b_1P_1 + b_2P_2 + .. + b_nP_n = \mathbf{b}'\mathbf{p}$
  - **p** are phenotypes, **b** are weights.
  - We can use any **b** or find the optimum **b**.
- Interest is in response to selection in multiple traits
  - $\mathbf{g}' = [g_1, g_2, ..., g_m]$, a vector of breeding values
- Regression of **g** on I yields an expression for response:
  - Approximate normality is assumed

$$R = \begin{bmatrix} \Delta\bar{g}_1 \\ \Delta\bar{g}_2 \\ \vdots \\ \Delta\bar{g}_m \end{bmatrix} = \mathbf{G}'\mathbf{b}\,\frac{i}{\sigma_I}$$

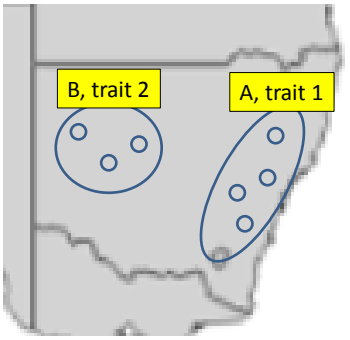
$\mathbf{G} = \mathrm{cov}(\mathbf{p}, \mathbf{g})$ Phenotypes in rows, breeding values in columns

σ_I = standard deviation of the index

i = selection intensity

Response to Selection
in the
Character-state Model

Multi-environment selection with GxE



Selection may occur in multiple flocks
- GxE between flocks
- Mixing of flocks: exchange of rams

Full model is tedious → Illustration for 2-flock system

Character State Model: Response to Selection

- Analogy of the multitrait model
  - Two environments, A and B
    - Two traits, trait 1 expressed in A, trait 2 expressed in B
    - Each individual has a BV for **both** traits, **but** only one of those BV is expressed
  - Two groups of individuals: individuals in A, and individuals in B
    - Different (genetic) means between groups: $\bar{g}_{1,A}$, $\bar{g}_{2,A}$, $\bar{g}_{1,B}$, $\bar{g}_{2,B}$
- Response to selection: 2 steps
  - Step 1: Calculate genetic level of selected parents for both traits in each environment
  - Step 2: Follow the flow of individuals/genes between environments
    - Contribution of each environment to selected individuals
    - Contribution of selected individuals to each environment (mixing)

Step 1: Genetic selection differential per environment

- Selection of individuals that are in Environment A
  - Selection criterion for environment A → $I_A = b_{i,A}P_{i,A} + b_{j,A}P_{j,A} + ..$
  - Intensity of selection for environment A → i_A
  - Covariances between P_A and true breeding values g_1 and g_2 → $\mathbf{G}_A$
  - Response in both traits → vector $\Delta\bar{\mathbf{g}}_A$

Genetic selection differential: $$\Delta\bar{\mathbf{g}}_A = \begin{bmatrix} \Delta\bar{g}_{A,1} \\ \Delta\bar{g}_{A,2} \end{bmatrix} = \mathbf{G}_A'\mathbf{b}_A \frac{i_A}{\sigma_{I_A}}$$

For environment B, the equation is analogous

Step 1: Genetic mean of selected in each environment

Genetic mean of selected indiv. in environment A:

$$\bar{\mathbf{g}}_{A,selected} = \begin{bmatrix} \bar{g}_{1,A,selected} \\ \bar{g}_{2,A,selected} \end{bmatrix} = \begin{bmatrix} \bar{g}_{1,A} \\ \bar{g}_{2,A} \end{bmatrix} + \begin{bmatrix} \Delta\bar{g}_{1,A} \\ \Delta\bar{g}_{2,A} \end{bmatrix}$$

Genetic mean of selected indiv. in environment B:

$$\bar{\mathbf{g}}_{B,selected} = \begin{bmatrix} \bar{g}_{1,B,selected} \\ \bar{g}_{2,B,selected} \end{bmatrix} = \begin{bmatrix} \bar{g}_{1,B} \\ \bar{g}_{2,B} \end{bmatrix} + \begin{bmatrix} \Delta\bar{g}_{1,B} \\ \Delta\bar{g}_{2,B} \end{bmatrix}$$

Step 2: Flow of animals → genetic mean next generation

Breeding value offspring is mean of its parents:

$$\bar{\mathbf{g}}_{A,t+1} = f_{A\to A}\,\bar{\mathbf{g}}_{A,selected} + f_{B\to A}\,\bar{\mathbf{g}}_{B,selected}$$

$$\begin{bmatrix} \bar{g}_{A,1,t+1} \\ \bar{g}_{A,2,t+1} \end{bmatrix} = f_{A\to A}\begin{bmatrix} \bar{g}_{A,1,selected} \\ \bar{g}_{A,2,selected} \end{bmatrix} + f_{B\to A}\begin{bmatrix} \bar{g}_{B,1,selected} \\ \bar{g}_{B,2,selected} \end{bmatrix}$$

$$f_{A\to A} + f_{B\to A} = 1$$

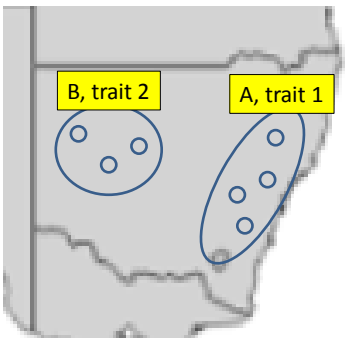
$f_{A\to A}$ = contribution of selected from A to offspring in A

$f_{B\to A}$ = contribution of selected from B to offspring in A

Simplest example: correlated response

- Mass selection in environment A, no selection in B
  - E.g. breeding nucleus and production environment
  - Flow of animals: $f_{B\to A} = 0$, $f_{B\to B} = 0$, $f_{A\to A} = 1$, $f_{A\to B} = 1$

Multi-environment selection with GxE



Selection in environment A

Producers in B get their rams from A

→ Response in both A and B

Simplest example: correlated response

- Mass selection in environment A, no selection in B
  - E.g. breeding nucleus and production environment
  - Flow of animals: $f_{B\to A} = 0$, $f_{B\to B} = 0$, $f_{A\to A} = 1$, $f_{A\to B} = 1$
  - Interest in response in both environments: two traits
    - Suppose starting level is equal (say zero)

$$\begin{bmatrix} \bar{g}_{A,1,t+1} \\ \bar{g}_{A,2,t+1} \end{bmatrix} = f_{A\to A}\begin{bmatrix} \bar{g}_{A,1,selected} \\ \bar{g}_{A,2,selected} \end{bmatrix} + f_{B\to A}\begin{bmatrix} \bar{g}_{B,1,selected} \\ \bar{g}_{B,2,selected} \end{bmatrix} = 1\times\begin{bmatrix} \bar{g}_{A,1,selected} \\ \bar{g}_{A,2,selected} \end{bmatrix} + 0$$

$$\begin{bmatrix} \bar{g}_{1,A,selected} \\ \bar{g}_{2,A,selected} \end{bmatrix} = \begin{bmatrix} \bar{g}_{1,A} \\ \bar{g}_{2,A} \end{bmatrix} + \begin{bmatrix} \Delta\bar{g}_{1,A} \\ \Delta\bar{g}_{2,A} \end{bmatrix}$$

Hence: We need selection differentials for both traits due to selection in environment A

Simplest application: correlated response

Selection differentials: $\begin{bmatrix} \Delta\bar{g}_{A,1} \\ \Delta\bar{g}_{A,2} \end{bmatrix} = \mathbf{G}'_A\mathbf{b}_A\frac{i_A}{\sigma_{I_A}}$

Mass selection in environment A

Selection criterion: $I = P_1$ (=1 x P_1)

$\mathbf{b} = 1$; $\sigma_I = \sigma_{P,1}$

$$\begin{bmatrix} \Delta\bar{g}_{A,1} \\ \Delta\bar{g}_{A,2} \end{bmatrix} = \begin{bmatrix} Cov(P_1, g_1) \\ Cov(P_1, g_2) \end{bmatrix}[1]\frac{i}{\sigma_{P,1}}$$

$$= \begin{bmatrix} \sigma^2_{A,1} \\ r_g\sigma_{A,1}\sigma_{A,2} \end{bmatrix}\frac{i}{\sigma_{P,1}}$$

$$= \begin{bmatrix} ih_1\sigma_{A,1} \\ ih_1 r_g\sigma_{A,2} \end{bmatrix}$$ (see e.g. Falconer & Mackaybook)

Response in BV in environment B is the same ($f_{A\to B} = 1$, $f_{B\to B} = 0$)

Simplest example: correlated response

- $h^2_1 = 0.30$, $h^2_2 = 0.25$, $\sigma^2_{P,1} = 1$, $\sigma^2_{P,2} = 1.33$, $r_g = 0.84$, selected proportion in env. A = 20% → $i_1 = 1.4$

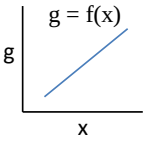
$$\begin{bmatrix} \Delta\bar{g}_{A,1} \\ \Delta\bar{g}_{A,2} \end{bmatrix} = \begin{bmatrix} i_1 h_1 \sigma_{A,1} \\ i_1 h_1 r_g \sigma_{A,2} \end{bmatrix} = \begin{bmatrix} 1.4 \times \sqrt{0.3} \times \sqrt{0.3 \times 1} \\ 1.4 \times \sqrt{0.3} \times 0.84 \times \sqrt{0.25 \times 1.33} \end{bmatrix} = \begin{bmatrix} 0.42 \\ 0.37 \end{bmatrix} = \begin{bmatrix} \Delta\bar{g}_{B,1} \\ \Delta\bar{g}_{B,2} \end{bmatrix}$$

Expressed

Question:
What does this mean for environmental sensitivity / plasticity?

Assignment 1: GxE in sheep breeding

- Breeding program for meat sheep (body weight)
  - Two flocks, one in each environment (H_{igh} and L_{ow})
  - Both environments have a breeding program, there is exchange of animals
  - Phenotypic means: $\mu_H = 60$kg, $\mu_L = 50$kg
  - In generation 0, both breeds are a random sample from a single breed imported from elsewhere
  - In each environment:
    - 50% of the selected parents come from the environment itself (e.g. the dams)
    - 50% come from the other environment (e.g. the sires)
  - Mass selection in both environments
    - Selected proportions in both sexes: $p_H = 20\%$, $p_L = 50\%$
    - $h^2_H = 0.4$; $h^2_L = 0.2$; $r_g = 0.7$; $\sigma_{P,H} = 6$kg, $\sigma_{P,L} = 5$kg,
  - Calculate the change of phenotypic means for 10 generations (e.g use Excel)
    - Consequences for environmental sensitivity?
    - Can you achieve zero change in environmental sensitivity? (using mass selection)
  - See Excelsheet “sheepbreeding GxE.xlsx”



$$g_i(x) = g_{0,1} + g_{1,i}\, x$$

Response to Selection in the Reaction Norm Model

$$R(x) = \Delta\bar{g}_i(x) = \Delta\bar{g}_{0,1} + \Delta\bar{g}_{1,i}\, x$$

Reaction norm model: response to sel.

- Response is in the average parameters of the RN (mean values of the g's)
- $\Delta\bar{g}_0, \Delta\bar{g}_1, \Delta\bar{g}_2, \Delta\bar{g}_3, \ldots$
- Response in the g's depends on the environment of selection
- Observed <u>phenotypic</u> response depends on the environment in which the offspring perform

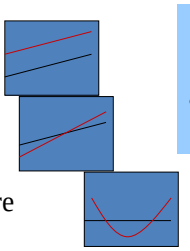
$$\Delta\bar{g}(x_{off}) = \Delta\bar{g}_0 + \Delta\bar{g}_1 x_{off} + \Delta\bar{g}_2 x_{off}^2 + \Delta\bar{g}_3 x_{off}^3 + \ldots\ldots$$

$$E[\Delta\bar{P}(x_{off})] = \Delta\bar{g}(x_{off})$$

$\Delta\bar{g}_0 \rightarrow$ change in level

$\Delta\bar{g}_1 \rightarrow$ change in slope

$\Delta\bar{g}_{\geq 2} \rightarrow$ change in curvature



Δg(x) depends on the changes in level, slope, quadratic, etc., and on the environment in which performance is expressed

Reaction norm model: response to sel.

- Mass selection in a single environment x_s
  - Selection is for phenotype $P(x_s)$
  - Hence, the "index" is: $I = P(x_s) = g_0 + g_1 x_s + g_2 x_s^2 + \ldots + e$
  - Hence, the index weights are: $\mathbf{b}' = (1 \quad x_s \quad x_s^2 \quad \cdots)$
    - I ignore e here, as it does not correlate with g
  - Response is in the average genetic coefficients of the reaction norm: $\Delta\bar{\mathbf{g}}' = (\Delta\bar{g}_0 \quad \Delta\bar{g}_1 \quad \Delta\bar{g}_2 \quad \cdots)$

$$\Delta\bar{\mathbf{g}} = \begin{bmatrix} \Delta\bar{g}_0 \\ \Delta\bar{g}_1 \\ \vdots \\ \Delta\bar{g}_n \end{bmatrix} = \mathbf{G}'\mathbf{b}\frac{i}{\sigma_I} \qquad \text{where } \sigma_I = \sigma_{P(x_S)}$$ the phenotypic standard deviation in the selection environment

Hence, selection on a reaction norm trait can be interpreted as index selection, the weights (**b**) being the powers of the environmental variable (x)

Reaction norm model: response to sel.

- Response to selection

$$\Delta\bar{\mathbf{g}} = \begin{bmatrix} \Delta\bar{g}_0 \\ \Delta\bar{g}_1 \\ \vdots \\ \Delta\bar{g}_n \end{bmatrix} = \mathbf{G}'\mathbf{b}\frac{i}{\sigma_I} \qquad \text{with} \qquad \mathbf{G} = \text{cov}(\mathbf{g},\mathbf{g}) = \text{var}(\mathbf{g}) = \begin{bmatrix} \sigma^2_{g_0} & \sigma_{g_0,g_1} & \cdots & \sigma_{g_0,g_n} \\ \sigma_{g_0,g_1} & \sigma^2_{g_1} & & \vdots \\ \vdots & & \ddots & \vdots \\ \sigma_{g_0,g_n} & \cdots & \cdots & \sigma^2_{g_n} \end{bmatrix}$$

and $\mathbf{b} = \begin{bmatrix} 1 \\ x_s \\ x_s^2 \\ \vdots \\ x_s^n \end{bmatrix}$ where x_s is the <u>selection</u> environment.

Reaction norm: Example

- Linear reaction norm for milk yield, mass selection
  - Environmental variable (x) = mean milk yield in an environment
    - E.g. HYS = Finlay Wilkinson-regression
  - $g(x)=g_0 + g_1x$
    - $Var(g_0) = 550^2$; $Var(g_1) = 0.05$
    - Meta-population mean milk yield = 7000kg
    - Genetic correlation **mean** milk yield and slope = -0.2

Q: How does the mean RN before selection look like?
- where to put the intercept?
- what is the mean slope?

Reaction norm: Example

- Linear reaction norm for milk yield, mass selection
  - Environmental variable = mean milk yield in an environment
    - E.g. HYS = Finlay Wilkinson-regression
  - $g(x)=g_0 + g_1x$
    - $Var(g_0) = 550^2$; $Var(g_1) = 0.05$, $Corr(g_0,g_1) = -0.2$
    - Meta-population mean milk yield = 7000kg
  - Two environments
    - Selection environment 9000kg,

$$I = P(x_s) = g_0 + g_1(9000 - 7000) + e = (1 \quad 2000)\begin{pmatrix} g_0 \\ g_1 \end{pmatrix} + e$$

      - $\mathbf{b}'$ =(1, 2000)
      - $Var(P_s) = 1308^2\ kg^2$ (assumed given here)
      - Selected proportion = 20% → i = 1.4
    - Production environment 8000kg
      - x_{off}' =(1, 1000)

Reaction norm: Example

$$\Delta\bar{\mathbf{g}} = \begin{bmatrix} \Delta\bar{g}_0 \\ \Delta\bar{g}_1 \\ \vdots \\ \Delta\bar{g}_n \end{bmatrix} = \mathbf{G}'\mathbf{b}\frac{i}{\sigma_I} \quad \Rightarrow \quad \Delta\bar{\mathbf{g}} = \begin{bmatrix} \Delta\bar{g}_0 \\ \Delta\bar{g}_1 \end{bmatrix} = \begin{bmatrix} \sigma^2_{g_0} & \sigma_{g_0 g_1} \\ \sigma_{g_0 g_1} & \sigma^2_{g_1} \end{bmatrix} \begin{bmatrix} 1 \\ x_s \end{bmatrix} \frac{i}{\sigma_{P,\mathbf{x}_s}}$$

$$\begin{bmatrix} \Delta\bar{g}_0 \\ \Delta\bar{g}_1 \end{bmatrix} = \begin{bmatrix} 550^2 & -24.5 \\ -24.5 & 0.05 \end{bmatrix} \begin{bmatrix} 1 \\ 2000 \end{bmatrix} \frac{1.4}{1308} = \begin{bmatrix} +271 \\ +0.081 \end{bmatrix} \quad \Rightarrow$$

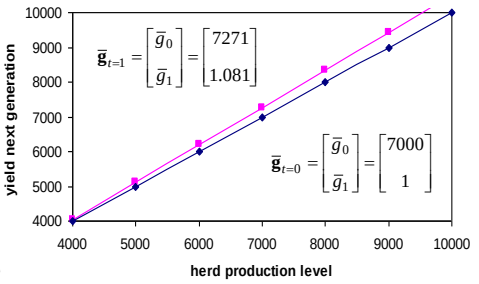
$$\Delta g(x_{off}) = \Delta\bar{\mathbf{g}}'\mathbf{x}_{off} = \begin{bmatrix} 271 & 0.081 \end{bmatrix} \begin{bmatrix} 1 \\ 1000 \end{bmatrix} = 352kg$$

$$\Delta g(x_s) = \Delta\bar{\mathbf{g}}'\mathbf{x}_s = \begin{bmatrix} 271 & 0.081 \end{bmatrix} \begin{bmatrix} 1 \\ 2000 \end{bmatrix} = 433kg$$

- An increase in level (+271)
- An increase in slope (+0.081)

⇒ More response in better environments
Increased sensitivity
Despite r_{g01} = -0.2

The Result:



R(x<3654) is negative

Due to selection in a good environment,
herds with good environments gain more,
and environmental sensitivity increases.

Question: what are the consequences
of simultaneous improvements in genetic merit and nutrition
for environmental sensitivity
of our livestock breeds?

Assignment 2: Selection for milk yield when GxE is modelled as a linear RN

- See word document: “Single trait selection on a linear reaction norm trait.docx”
- See R-code: “univariate reaction norm milk yield.R”
- Investigate:
  - Consequences of selection for environmental sensitivity
  - Effect of the selection environment