Lecture 08: G x E: Genotype-by-environment interactions: Standard methods

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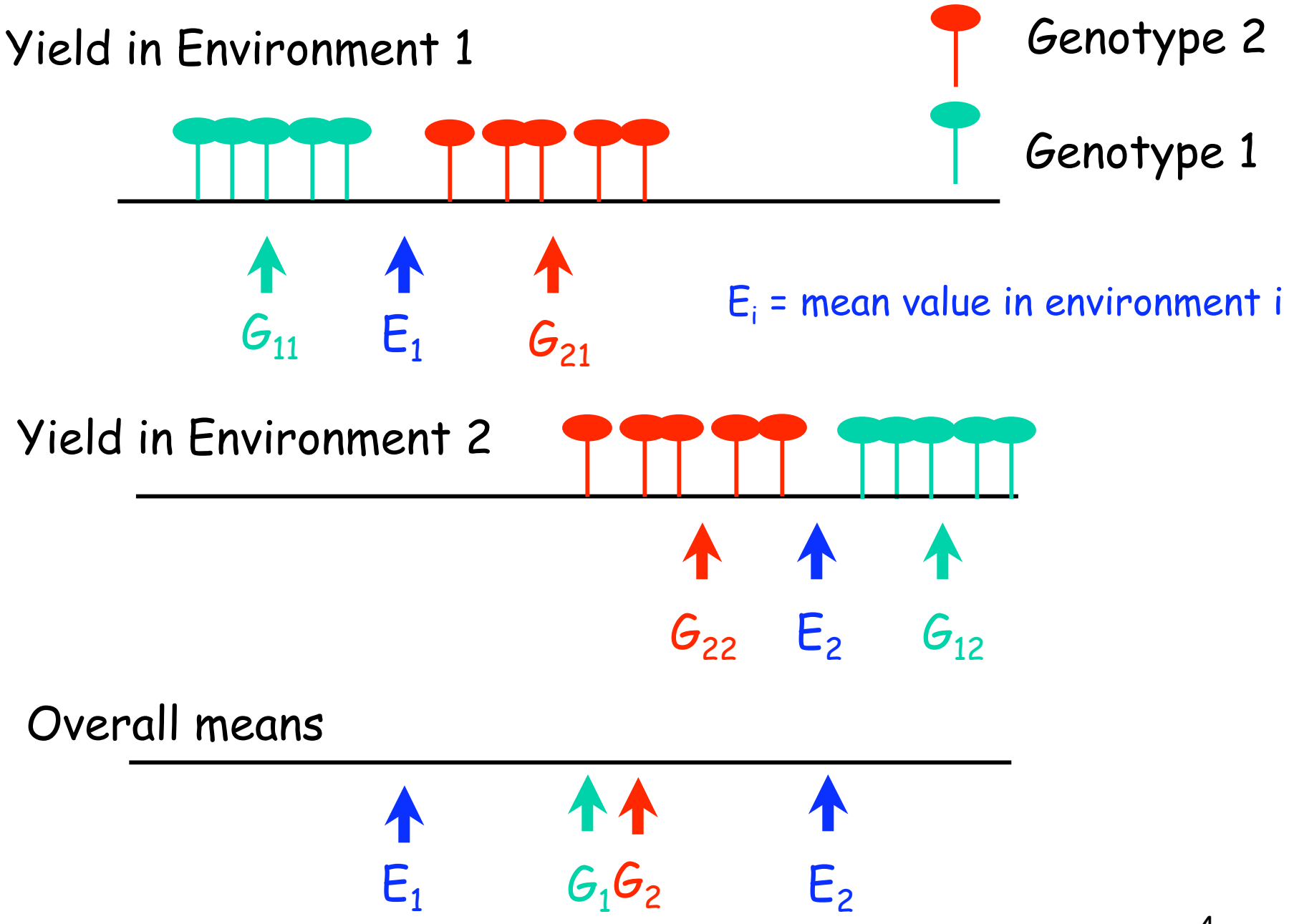
G x E

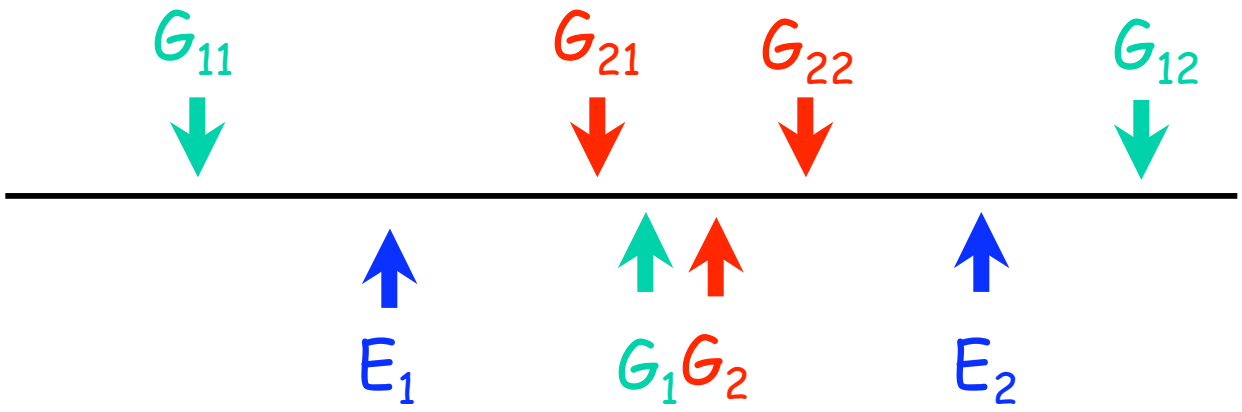
- Introduction to G x E
  - Basics of G x E
  - G x E is a correlated characters problem
  - Finlay-Wilkinson regressions
- SVD-based methods
  - The singular value decomposition (SVD)
  - AMMI models
- Factorial regressions

Genotypes vs. individuals

- Much of the G x E theory is developed for plant breeders who are using pure (= fully inbred) lines, so that every individual has the same genotype
- The same basic approaches can be used by taking family members as the replicates for outbred species. Here the "genotype" over the family members is some composite value.


Yield in Environment 1
Genotype 2
Genotype 1
G_{11}
E_1
G_{21}
E_i = mean value in environment i
Yield in Environment 2
G_{22}
E_2
G_{12}
Overall means
E_1
G_1G_2
E_2

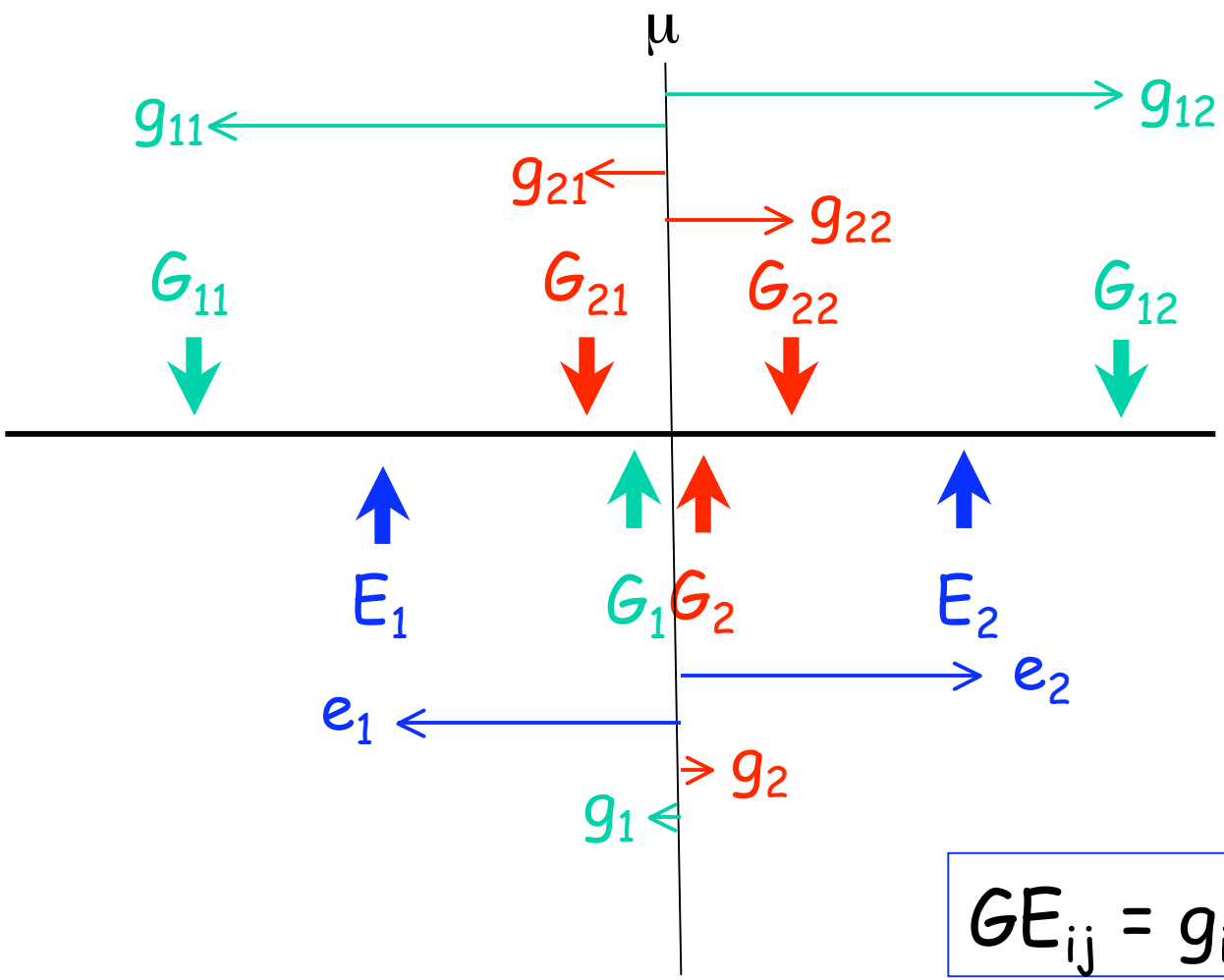
G_{ij} = mean of genotype i in environment j



Under base model of Quantitative Genetics,

$G_{ij} = \mu + G_i + E_j$

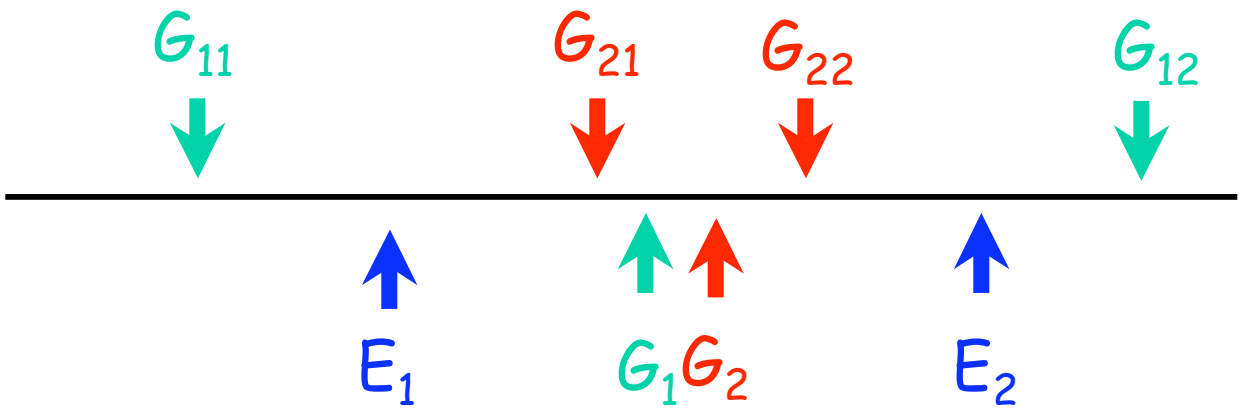
When G x E present, there is an interaction between a particular genotype and a particular environment so that G_{ij} is no longer additive, $G_{ij} = \mu + G_i + E_j + GE_{ij}$



$$GE_{ij} = g_{ij} - g_i - e_j$$

Components measured as deviations from the mean μ

Which genotype is the best?



Depends: If the genotypes are grown in both environments, G_2 has a higher mean

If the genotypes are only grown in environment 1, G_2 has a higher mean

If the genotypes are only grown in environment 2, G_1 has a higher mean

G x E: Both a problem and an opportunity

- A line with little G x E has stability across environments.
- However, a line with high G x E may outperform all others in specific environments.
- G x E implies the opportunity to fine-tune specific lines to specific environments
- High $\sigma^2(GE)$ implies high G x E in at least some lines in the sample.

G x E is Both a Challenge and an Opportunity

		Mean Performance: High	Mean Performance: Low
Amount of G x E	High	Potential for locally-adapted lines	Potential for locally-adapted lines
	Low	Ideal. Potential for widely adaptive lines	Undersirable

High G x E = potential for locally-adapted lines

High G x E = poor stability across environments

G x E can be generated by either differences in the additive variance over environments or by lack of perfect genetic correlation among environments

For two environments, Robertson (1959) showed that the G x E interaction variance can be partitioned into theses two sources,

$$\sigma^2_{G\times E} = \frac{(\sigma_{A_1} - \sigma_{A_2})^2}{2} + \sigma_{A_1}\,\sigma_{A_2}(1 - r_A) \qquad (38.1a)$$

where $\sigma^2_{A_i}$ is the additive variance in environment i and r_A is the additive genetic correlation across environments. Cockerham (1963) and Itoh and Yamada (1990) extended Robertson's decomposition to n_e environments,

$$\sigma^2_{G\times E} = \frac{1}{n_e - 1}\sum_{j}^{n_e}\left(\sigma_{A_j} - \overline{\sigma}_A\right)^2 + \frac{2}{n_e(n_e-1)}\sum_{i<j}^{n_e}\sigma_{A_i}\sigma_{A_j}[1 - r_A(i,j)] \qquad (38.1b)$$

Here $\overline{\sigma}_A$ is the average of the square root of the genetic variances over all environments, and $r_A(i,j)$ is the correlation between environments i and j.

Major vs. minor environments

- An identical genotype will display slightly different traits values even over apparently identical environments due to micro-environmental variation and developmental noise
- However, macro-environments (such as different locations or different years <such as a wet vs. a dry year>) can show substantial variation, and genotypes (pure lines) may differentially perform over such macro-environments (G x E).
- Problem: The mean environment of a location may be somewhat predictable (e.g., corn in the tropics vs. temperate North American), but year-to-year variation at the same location is essentially unpredictable.
- Decompose G x E into components
  - $G \times E_{locations} + G \times E_{years} + G \times E_{years \times locations}$
  - Ideal: strong G x E over locations, high stability over years.

Where to select?

- Suppose can only select in one environment when G x E is present
  - Selection with G x E is a correlated traits problem
  - Direct response = change when selected in that environment
  - Correlated response = change when selected in another environment
- Is it better to select in the better, or in the poorer, environment?
  - Hammond's conjecture: Best to select in the poor environment. Support mixed

Jinks-Connolly Rule

- Antagonistic selection
  - Select in opposite direction from environmental effect
    - Up-select in an environment with reduced trait value
- Synergistic selection
  - Select in same direction as environmental effect
    - Up-select in an environment with increased trait value
- Jink and Connolly (1973) suggested that
  - Antagonistic selection reduces environmental sensitivity (i.e., improves stability)
  - Synergistic selection increases sensitivity (decreases stability)
  - While not always true, this is often true, and hence is a trend (rather than a rule)
- Falconer's (1990) generalization is that
  - sensitivity is less after antagonistic selection than after synergistic selection

Estimating the GE term

- While GE can be estimated directly from the mean in a cell (i.e., G_i in E_j), we can usually get more information (and a better estimate) by considering the entire design and exploiting structure in the GE terms
- This approach also allows us to potentially predict the GE terms in specific environments
- Basic idea: replace GE_{ij} by $\alpha_i\gamma_j$ or more generally by $\Sigma_k \alpha_{ki}\gamma_{kj}$ These are called biadditive or bilinear models. This (at first sight) seems more complicated. Why do this?
- With n_G genotypes and n_E environments, we have
  - $n_G\, n_E$ GE terms (assuming no missing values)
  - $n_G + n_E$ α_i and γ_i unique terms
  - $k(n_G + n_E)$ unique terms in $\Sigma_k \alpha_{ki}\gamma_{kj}$.
- Suppose 50 genotypes in 10 environments
  - 500 GE_{ij} terms, 60 unique α_i and γ_i terms, and (for k=3), 180 unique α_{ki} and γ_{ki} terms.

Finlay-Wilkinson Regression

Also called a joint regression or regression on an environmental index.

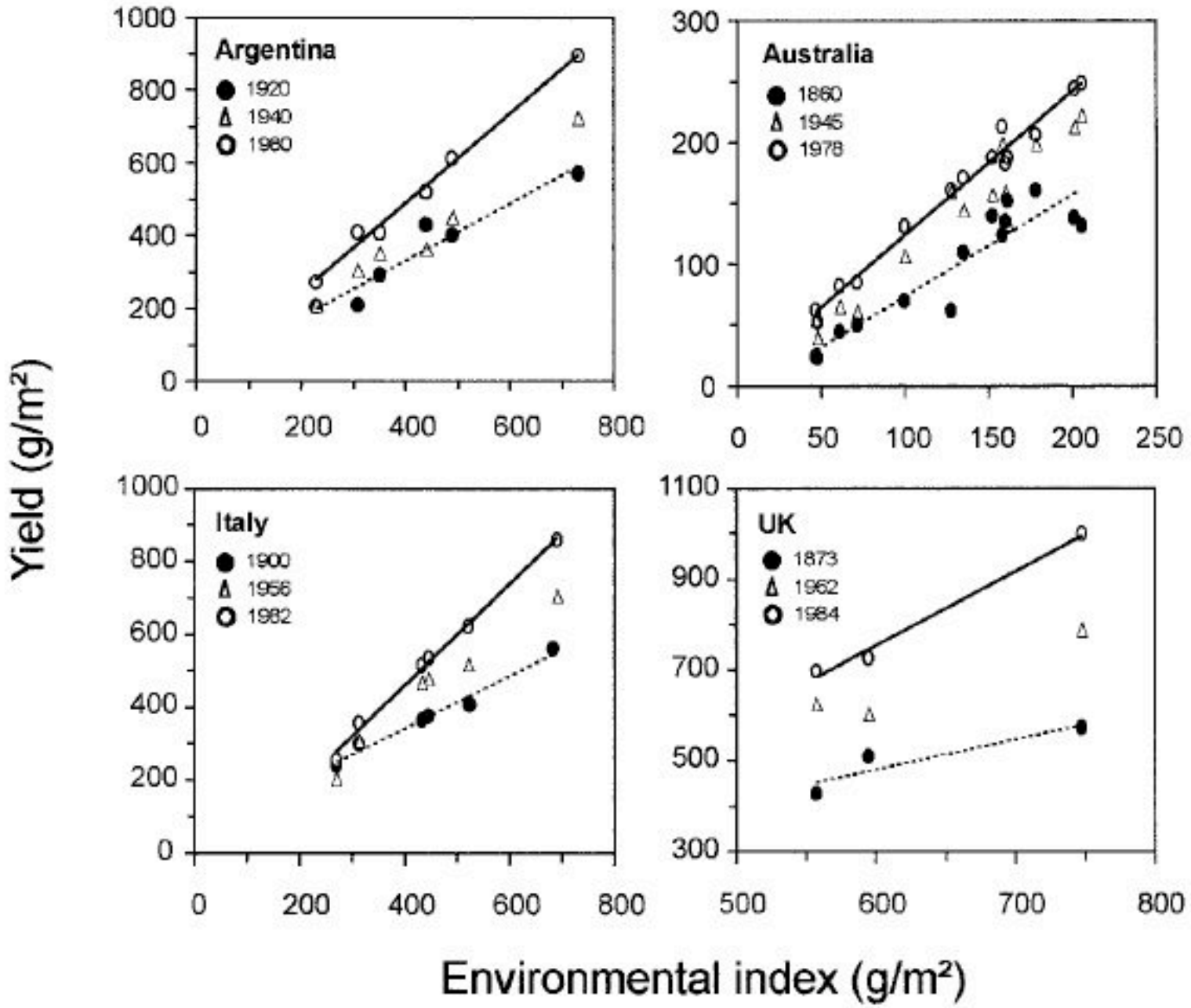
Let $\mu + G_i$ be the mean of the ith genotype over all the environments, and $\mu + E_j$ be the average yield of all genotypes in environment j

$$\mu_{ij} = \mu + G_i + E_j(1 + \beta_i) + \delta_{ij}$$

The FW regression estimates GE_{ij} by the regression $GE_{ij} = \beta_i E_j + \delta_{ij}$. The regression coefficient is obtained for each genotype from the slope of the regression of the G_{ij} over the E_j. δ_{ij} is the residual (lack of fit). If $\sigma^2(GE) >> \sigma^2(\delta)$, then the regression accounts for most of the variation in GE.

Application

- Yield in lines of wheat over different environments was examined by Calderini and Slafer (1999). The lines they examined where lines from different eras of breeding (for four different countries)
- Newer lines had larger values, but also had higher slopes (large β_i values), indicating less stability over mean environmental conditions than see in older lines



Regression slope for each genotype is β_i

β and Stability

$$\mu_{ij} = \mu + G_i + E_j(1 + \beta_i) + \delta_{ij}$$

- Since predicted GE_{ij} term is $\beta_i E_j$, β_i measures the sensitivity of genotype i over the sampled environments
  - Positive β implies sign of GE = sign of E
    - Good environment = extra gain from positive GE
    - Poorer environment = extra loss from negative GE
  - Negative β implies sign of GE opposite of sign of E
    - Performs better in poorer environments
  - Large |β| implies a higher sensitivity over environments
  - $\beta_i = -1$ implies $\mu_{ij} = \mu + G_i + \delta_{ij}$ (no dependence on Ej)

Types of Stability

$$\mu_{ij} = \mu + G_i + E_j(1 + \beta_i) + \delta_{ij}$$

- Type I stability (β_i = -1):
  - Genotypic value is constant over environments
- Type II stability (β_i = 0):
  - No *G* x E, but this also implies that genotypic value changes over environments
- Type III stability ($\sigma^2(\delta)$ small):
  - The FW regression accounts for most of *G* x E

SVD approaches

- In Finlay-Wilkinson, the GE_{ij} term was estimated by $\beta_i E_j$, where E_j was observed. We could also have used $\gamma_j G_i$, where γ_j is the regression of genotype values over the j-th environment. Again G_i is observable.
- Singular-value decomposition (SVD) approaches consider a more general approach, approximating GE_{ij} by $\Sigma_k \alpha_{ki}\gamma_{kj}$ where the α_{ki} and γ_{kj} are determined by the first k terms in the SVD of the matrix of GE terms.
- The SVD is a way to obtain the best approximation of a full matrix by some matrix of lower dimension

The Singular-Value Decomposition (SVD)

An $n \times p$ matrix $\mathbf{A}$ can always be decomposed as the product of three matrices: an $n \times p$ diagonal matrix $\boldsymbol{\Lambda}$ and two unitary matrices, $\mathbf{U}$ which is $n \times n$ and $\mathbf{V}$ which is $p \times p$. The resulting **singular value decomposition** (**SVD**) of $\mathbf{A}$ is given by

$$\mathbf{A}_{n\times p} = \mathbf{U}_{n\times n}\boldsymbol{\Lambda}_{n\times p}\mathbf{V}^T_{p\times p} \tag{39.16a}$$

We have indicated the dimensionality of each matrix to allow the reader to verify that each matrix multiplication conforms. The diagonal elements $\lambda_1, \cdots, \lambda_s$ of $\boldsymbol{\Lambda}$ correspond to the **singular values** of $\mathbf{A}$ and are ordered by decreasing magnitude. Returning to the unitary matrices $\mathbf{U}$ and $\mathbf{V}$, we can write each as a row vector of column vectors,

$$\mathbf{U} = (\mathbf{u}_1, \cdots, \mathbf{u}_i, \cdots \mathbf{u}_n), \qquad \mathbf{V} = (\mathbf{v}_1, \cdots, \mathbf{v}_i, \cdots \mathbf{v}_p) \tag{39.16b}$$

where $\mathbf{u}_i$ and $\mathbf{v}_i$ are n and p-dimensional column vectors (often called the **left** and **right singular vectors**, respectively). Since both $\mathbf{U}$ and $\mathbf{V}$ are unitary, by definition (Appendix 4) each column vector has length one and are mutually orthogonal (i.e., if $i \neq j$, $\mathbf{u}_i\mathbf{u}_j^T = \mathbf{v}_i\mathbf{v}_j^T = 0$). Since $\boldsymbol{\Lambda}$ is diagonal, it immediately follows from matrix multiplication that we can write any element in $\mathbf{A}$ as

$$A_{ij} = \sum_{k=1}^{s} \lambda_k \, u_{ik} \, v_{kj} \tag{39.16c}$$

where λ_k is the kth singular value and $s \leq \min(p, n)$ is the number of non-zero singular values.

The importance of the singular value decomposition in the analysis of G×E arises from the **Eckart-Young theorem** (1938), which relates the best approximation of a matrix by some lower-rank (say k) matrix with the SVD. Define as our measure of goodness of fit between a matrix $\mathbf{A}$ and a lower rank approximation $\widehat{\mathbf{A}}$ as the sum of squared differences over all elements,

$$\sum_{ij}(A_{ij} - \hat{A}_{ij})^2$$

Eckart and Young show that the best fitting approximation $\widehat{\mathbf{A}}$ of rank $m < s$ is given from the first m terms of the singular value decomposition (the **rank-m SVD**),

$$\hat{A}_{ij} = \sum_{k=1}^{m} \lambda_k \, u_{ik} \, v_{kj} \tag{39.17a}$$

For example, the best rank-2 approximation for the G×E interaction is given by

$$GE_{ij} \simeq \lambda_1 \, u_{i1} \, v_{j1} + \lambda_2 \, u_{i2} \, v_{j2} \tag{39.17b}$$

where λ_i is the ith singular value of the **GE** matrix, $\mathbf{u}$ and $\mathbf{v}$ are the associated singular vectors (see Example 39.3). The fraction of total variation of a matrix accounted for by taking the first m terms in its SVD is

$$\sum_{k=1}^{m} \lambda_k^2 / \sum_{ij} A_{ij}^2 = \frac{\lambda_1^2 + \cdots + \lambda_m^2}{\lambda_1^2 + \cdots + \lambda_s^2}$$

A data set for soybeans grown in New York (Gauch 1992) gives the GE matrix as

$$\mathbf{GE} = \begin{pmatrix} 57 & 176 & -233 \\ -36 & -196 & 233 \\ -45 & -324 & 369 \\ -66 & 178 & -112 \\ 89 & 165 & -254 \end{pmatrix}$$

Where GE_{ij} = value for Genotype i in envir. j

In **R**, the compact SVD (Equation 39.16d) of a matrix X is given by **`svd(X)`**, returning the SVD of $\mathbf{GE}$ as

$$\begin{pmatrix} 0.40 & 0.21 & 0.18 \\ -0.41 & 0.00 & 0.91 \\ -0.66 & 0.12 & -0.30 \\ 0.26 & -0.83 & 0.11 \\ 0.41 & 0.50 & 0.19 \end{pmatrix} \begin{pmatrix} 746.10 & 0 & 0 \\ 0 & 131.36 & 0 \\ 0 & 0 & 0.53 \end{pmatrix} \begin{pmatrix} 0.12 & 0.64 & -0.76 \\ 0.81 & -0.51 & -0.30 \\ 0.58 & 0.58 & 0.58 \end{pmatrix}$$

The first singular value accounts for $746.10^2/(743.26^2 + 131.36^2 + 0.53^2) = 97.0\%$ of the total variation of $\mathbf{GE}$, while the second singular value accounts for 3.0%, so that together they account for essentially all of the total variation. The rank-1 SVD approximation of $\mathbf{GE}$ is given by setting all of the diagonal elements of $\boldsymbol{\Lambda}$ except the first entry to zero,

$$\mathbf{GE}_1 = \begin{pmatrix} 0.40 & 0.21 & 0.18 \\ -0.41 & 0.00 & 0.91 \\ -0.66 & 0.12 & -0.30 \\ 0.26 & -0.83 & 0.11 \\ 0.41 & 0.50 & 0.19 \end{pmatrix} \begin{pmatrix} 746.10 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} 0.12 & 0.64 & -0.76 \\ 0.81 & -0.51 & -0.30 \\ 0.58 & 0.58 & 0.58 \end{pmatrix}$$

Similarly, the rank-2 SVD is given by setting all but the first two singular values to zero,

$$\mathbf{GE}_2 = \begin{pmatrix} 0.40 & 0.21 & 0.18 \\ -0.41 & 0.00 & 0.91 \\ -0.66 & 0.12 & -0.30 \\ 0.26 & -0.83 & 0.11 \\ 0.41 & 0.50 & 0.19 \end{pmatrix} \begin{pmatrix} 746.10 & 0 & 0 \\ 0 & 131.36 & 0 \\ 0 & 0 & 0 \end{pmatrix} \begin{pmatrix} 0.12 & 0.64 & -0.76 \\ 0.81 & -0.51 & -0.30 \\ 0.58 & 0.58 & 0.58 \end{pmatrix}$$

For example, the rank-1 SVD approximation for GE_{32} is $g_{31}\lambda_1 e_{12}$ = 746.10*(-0.66)*0.64 = -315

While the rank-2 SVD approximation is $g_{31}\lambda_2 e_{12} + g_{32}\lambda_2 e_{22}$ = 746.10*(-0.66)*0.64 + 131.36* 0.12*(-0.51) = -323

Actual value is -324

Generally, the rank-2 SVD approximation for GE_{ij} is $g_{i1}\lambda_1 e_{1j} + g_{i2}\lambda_2 e_{2j}$

AMMI models

Additive main effects, multiplicative interaction (AMMI) models use the first m terms in the SVD of GE:

$$GE_{ij} = \sum_{k=1}^{m} \lambda_k \, \gamma_{ki} \, \eta_{kj} + \delta_{ij}$$

Giving

$$\mu_{ij} = \mu + G_i + E_j + \sum_{k=1}^{m} \lambda_k \, \gamma_{ki} \, \eta_{kj} + \delta_{ij}$$

AMMI is actually a *family* of models, with $AMMI_m$ denoting AMMI with the first m SVD terms

AMMI models

$$\mu_{ij} = \mu + G_i + E_j + \sum_{k=1}^{m} \lambda_k \gamma_{ki} \eta_{kj} + \delta_{ij}$$

Fit main effects

Fit principal components to the interaction term (SVD is a generalization of PC methods)

$$\longrightarrow \quad GE_{ij} = \sum_{k=1}^{m} \lambda_k \gamma_{ki} \eta_{kj} + \delta_{ij}$$

Why do AMMI?

- One can plot the SVD terms (γ_{ki}, η_{kj}) to visualize interactions
  - Called biplots (see online notes Chapter 33 for details)
- AMMI can better estimate mean values of GE_{ij} than just using the cell value (the observed mean of Genotype i in Environment j)
- AMMI can predict GE values for genotype-environment combination not measured
- A ***huge*** amount more on AMMI in the online notes (Chapter 33)!

Modifications of the Basic AMMI Family of Models

A variety of modifications of Equation 39.19 appear in the literature. Two common variations are the **sites regression model**, or **SREG** (Crossa and Cornelius 1997) wherein the genetic main effect (G_i) is absorbed into the interaction terms and hence the regression main effects are only over sites (E_j),

$$\mu_{ij} = \mu + E_j + \sum_{k=1}^{m} \lambda_k \gamma_{ki} \eta_{kj} + \delta_{ij} \tag{39.20a}$$

and the **shifted multiplicative model**, or **SHMM**, Crossa and Cornelius 1997) where *both* the environment and genetic main effects are absorbed into the interaction terms,

$$\mu_{ij} = \mu + \sum_{k=1}^{m} \lambda_k \gamma_{ki} \eta_{kj} + \delta_{ij} \tag{39.20b}$$

As with AMMI, these models are usually subscripted to indicate the number of multiplicative terms included, so that SREG_3 is Equation 39.20a with $m = 3$ terms. As we will shortly see, these variants can prove useful for joint visualization of both genetic main effects plus GE interactions. Other variants have also been proposed, again based on which terms are kept as main effects versus being absorbed into a general interaction term, see Cornelius and Crossa (1999) for details.

Factorial Regressions

- While AMMI models attempt to extract information about how G x E interactions are related across sets of genotypes and environments, factorial regressions incorporate direct measures of environmental factors in an attempt to account for the observed pattern of G x E.
- The power of this approach is that if we can determine which genotypes are more (or less) sensitive to which environmental features, the breeder may be able to more finely tailor a line to a particular environment without necessarily requiring trials in the target environment.

Suppose we have a series of *m* measured values from the environments of interest (such as average rainfall, maximum temperature, etc.) Let x_{kj} denote the value of the k-th environmental variable in environment j

Factorial regressions then model the GE term as the sensitivity ζ_{ki} of environmental value k to genotype i, (this is a regression slope to be estimated from the data)

$$GE_{ij} = \sum_{k=1}^{m} \zeta_{ki}\, x_{kj} + \delta_{ij}$$

Note that the Finlay-Wilkinson regression is a special case where m = 1 and x_j is the mean trait value (over all genotypes) in that environment.

Model	Interpretation
Finlay-Wilkinson $GE_{ij} = \beta_i(E_j - \mu) + \delta_{ij}$	$\beta_i =$ sensitivity of genotype i to the average effect E_j of the environment.
AMMI $GE_{ij} = \sum_{k=1}^{m} \lambda_k \gamma_{ki} \eta_{kj} + \delta_{ij}$	First m terms of the SVD of the $\mathbf{GE}$ matrix λ_k^2 is the amount of variation explained by axis k $\gamma_{ki} =$ sensitivity of genotype i to environmental axis k $\eta_{kj} =$ value of environment j on the kth environmental axis
Factorial Regression $GE_{ij} = \sum_{k=1}^{m} \zeta_{ki} x_{kj} + \delta_{ij}$	Modeling G x E using m measured environmental factors $x_{kj} =$ value of kth environmental factor in environment j $\zeta_{ki} =$ sensitivity of genotype i to kth environmental factor
Reduced rank Factorial Regression $GE_{ij} = \sum_{k=1}^{m} \zeta_{ki} (\sum_p c_{kp} x_{pj}) + \delta_{ij}$	Modeling G x E based on a reduced dimensional set of the observed environmental factors by constructing m combinations (axes) of these effects. $c_{kp} =$ loading of pth environmental factor on axis k. $\zeta_{ki} =$ sensitivity of genotype i to kth environmental combination (axis)
AMMI using Reduced rank Factorial Regression $GE_{ij} = \sum_{k}^{m} \lambda_k \gamma_{ki} (\sum_p c_{kp} x_{pj}) + \delta_{ij}$	The environmental axes η_{kj} under AMMI are replaced by the environmental axes generated by linear combinations of measured environmental factors generated by a reduced rank factorial regression, with $\eta_{kj} = \sum_p c_{kp} x_{pj}$.