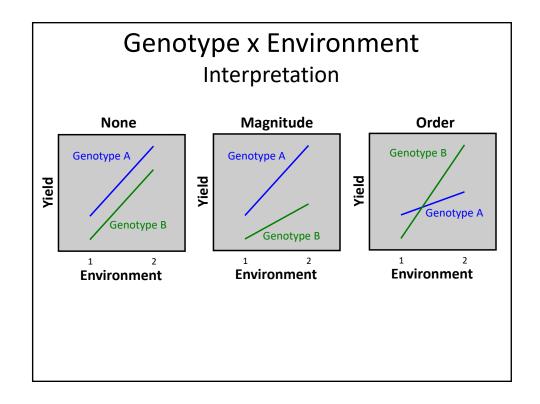
Genotype by Environment Interactions Common Approaches to Stability Analysis

- 1. Genotype considered stable if its variance over environments is small.
- 2. Genotype considered stable if its mean response to environments is parallel to the mean of all genotypes.
- 3. Genotype considered stable if the residual MS from regression on the environmental index is small.

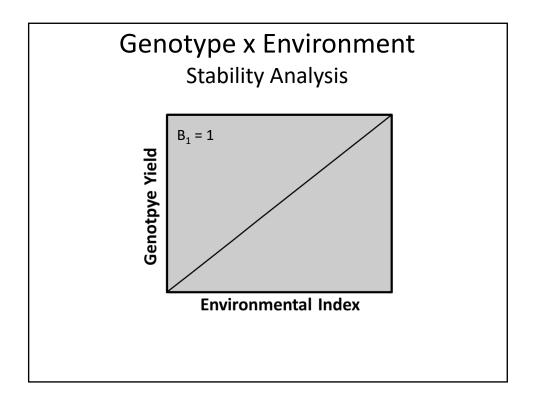


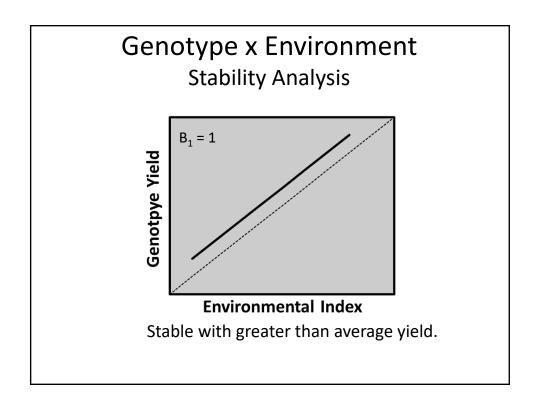
Genotype x Environment Spearman Rank Correlation

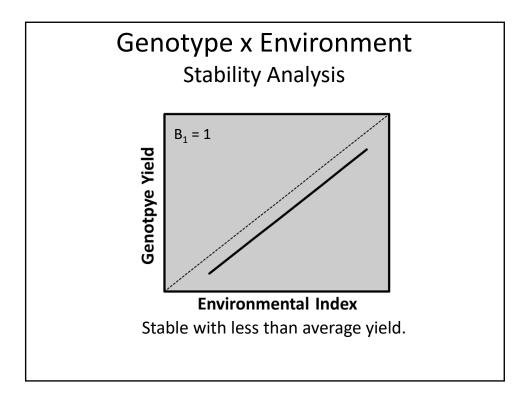
$$r_{s} = 1 - \frac{6\sum_{i=1}^{n} d_{i}^{2}}{n^{3} - n}$$

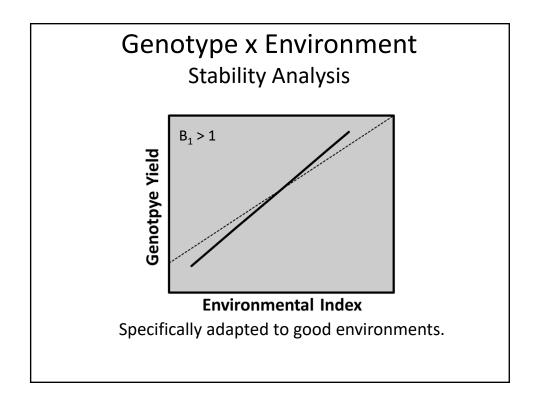
Example - Oat Variety Trial

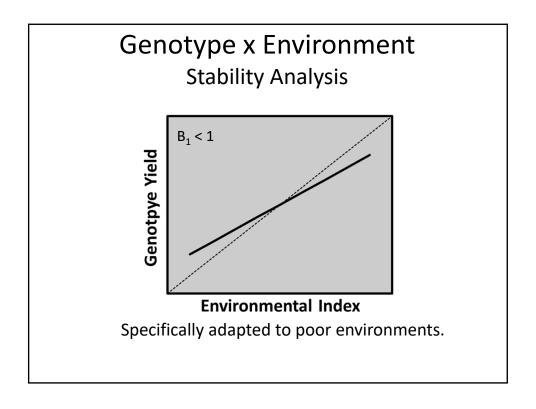
Spearman Correlation Coefficients, N = 10 Prob > r under HO: Rho=0						
	Env1	Env2	Env3	Env4	Env5	Env6
Ames	1.000	0.609	0.109	0.554	0.468	0.644
1985		0.061	0.763	0.095	0.172	0.044
Kanahwa	0.609	1.000	0.164	0.292	0.449	0.620
1985	0.061		0.650	0.411	0.192	0.055
Washington	0.109	0.164	1.000	0.370	0.660	0.200
1985	0.763	0.650		0.291	0.037	0.579
Ames	0.554	0.292	0.370	1.000	0.492	0.644
1986	0.095	0.411	0.291		0.148	0.044
Kanahwa	0.468	0.449	0.660	0.492	1.000	0.515
1986	0.172	0.192	0.037	0.148		0.127
Washington	0.644	0.620	0.200	0.644	0.515	1.000
1986	0.044	0.055	0.579	0.044	0.127	

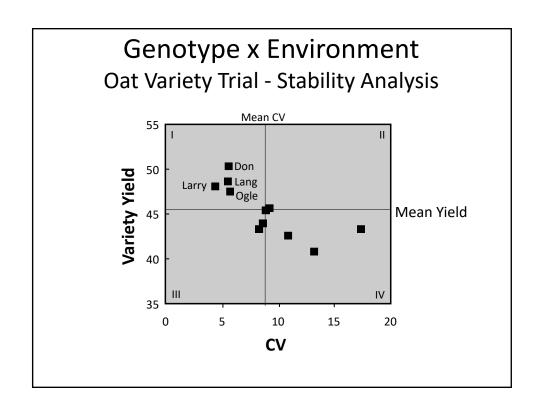












Combined Experiments Meta Analysis

Model:

$$Y_{ij} = B_0 + B_1 X_{ij} + s_i + b_i X_{ij} + e_{ij}$$

Where:

 Y_{ij} = predicted value for j^{th} level of X in study i

 B_0 = intercept for all studies

 B_1 = overall slope for Y regressed on X

X_{ii} = jth level of X in study i

s_i = random effect of study i

 b_i = random effect of study i on the regression

of Y on X in study i

 e_{ii} = residual error

Combined Experiments Meta Analysis

Proc Mixed Code:

```
PROC MIXED;
CLASS Study;
MODEL Y = X / SOLUTION;
RANDOM intercept X / TYPE=UN
SUBJECT=Study SOLUTION;
RUN;
```

St-Pierre, 2001.