## Purposes:

- 1. Gain experience in clustering environments due to GxE interactions
- 2. Utilize knowledge from clustering to make advancement decisions

**Keywords**: Multi-Environment Trial (MET), Variance due to GxE interactions, interactions due to heterogeneous variance, interactions due to changes in rank

## Useful R commands

- rm()
- attach()
- factor()
- lm()
- aov()
- summary()
- reshape()
- dist()
- hclust()
- plot()
- cutree()

## **Reading:**

Chapter 12: Multi Environment Trials – Types of GxE – Cluster Analysis

Chapter 8, Bernardo

Cooper and DeLacy, 1994

After a preliminary trial in which experimental lines are evaluated at the breeding station for maturity, height and other non-yield traits, a selected set of 49 experimental lines and a check cultivar were entered into a replicated multi-environment trial (MET). The experimental lines are designated 1-49 and the check is designated as line 50. Harvestable yield from two row plots were obtained from 10 locations in a single year. The lines were assigned to the field plots using a randomized complete block design, where each block is represented as one of two replicates per location. The data is found in "Multi Environment Trials Types of GxE ds5.csv". Your team needs to

- 1. Classify environments based on the phenotypic responses of these 50 genotypes.
- 2. Classify genotypes based on similar responses to the 10 environments.
- 3. Generate graphical representations of the classifications and provide an interpretation of the graphics.
- 4. Use the information to make selections for advancement.