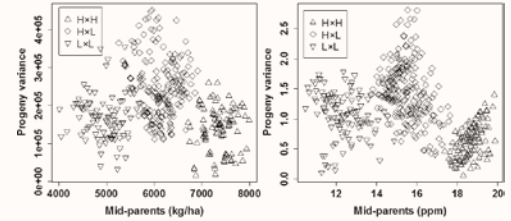


AGRY 611 QUANTITATIVE GENETICS

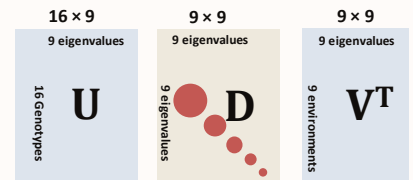
Motivation

- R scripting for genetics
- Mean and variance of populations
- Inbreeding, co-ancestry, & individual relatedness
- Changes in allele frequency & population differentiation
- Variance of gene frequency
- Heritability, selection, & genetic gain
- Indirect selection, index selection, & GxE analysis
- Gene mapping, QTL and GWAS
- Genomic predictions
 - Featured by real-world breeding perspective, industry representative, & the latest discussions and developments in the field of predictive breeding



Developing a function

```
my.sum.mean <- function (z)
{
  sum = 0
  for(i in 1:length(z))
  {
    sum = sum + z[i]
  }
  return(c(sum, sum/length(z)))
}
```



$$Z = M - P = \begin{bmatrix} -0.766 & 0.512 & -0.334 & 0.866 \\ -0.766 & 0.512 & 0.666 & -0.134 \\ 1.234 & -0.488 & -0.334 & -0.134 \end{bmatrix}$$

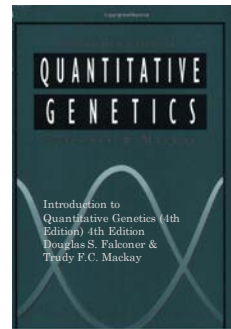
$$G = \frac{ZZ'}{2 \sum p_i(1 - p_i)}$$

Prerequisites

Sufficient knowledge of genetics, breeding science, probability, statistics, & experimental designs

Text

Douglas S. Falconer & Trudy F.C. Mackay
Introduction to Quantitative Genetics, 4th Edition



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