R SCIPT FOR ESTIMATION OF HERITABILITY, GENETIC ADVANCE, CORRELATION COEFFICIENT

Here is a comprehensive R script and explanation for estimating **heritability (broad sense), genetic advance, and correlation coefficient** in a breeding dataset, along with clear instructions and formulas.

1. Preparing Your Data

Suppose you have a data frame (`mydata`) with measurements for various genotypes over replications, structured like this:

Genotype	Rep	Trait1	Trait2	...
G1	1	21.5	13.2	...
G1	2	20.7	14.1	...
...	...	...	...	...

You will estimate parameters *for a single trait at a time* (repeat as needed).

2. Required R Packages

```
install.packages("agricolae")       # For ANOVA
install.packages("variability")      # For genetic parameters (optional but simplifies calc
```

3. Analysis and Calculation in R

A. Heritability and Genetic Advance

Manual Calculation Using ANOVA

```
library(agricolae)

# Example: replace "Trait1" with your trait of interest
model <- aov(Trait1 ~ Genotype + Rep, data = mydata)
anova_tab <- summary(model)

# Extracting mean squares
ms_gen <- anova_tab[[^1]]["Genotype", "Mean Sq"]
ms_error <- anova_tab[[^1]]["Residuals", "Mean Sq"]
n_rep <- length(unique(mydata$Rep))

# Genetic and phenotypic variance
```

```
var_gen <- (ms_gen - ms_error) / n_rep
var_pheno <- var_gen + ms_error

# Broad-sense heritability (in percentage)
h2 <- (var_gen / var_pheno) * 100

# Genetic advance
mean_trait <- mean(mydata$Trait1)
GA <- 2.056 * sqrt(var_pheno) * h2 / 100   # 2.056: ~selection differential for 5% select

cat(sprintf("Heritability: %.2f%%\nGenetic Advance: %.2f\n", h2, GA))
```

Using the variability Package

```
# Data columns start at the trait columns
library(variability)
var_res <- gen.var(mydata[, 3:ncol(mydata)], mydata$Genotype, mydata$Rep)
print(var_res)
```

This function gives genotypic variance, phenotypic variance, heritability, and genetic advance for all traits at once.

B. Correlation Coefficient

To get phenotypic and genotypic correlations:

```
library(variability)

# Genotypic and phenotypic correlation coefficients (for all pairs)
pheno.corr(mydata[, 3:ncol(mydata)], mydata$Genotype, mydata$Rep) # Phenotypic
geno.corr(mydata[, 3:ncol(mydata)], mydata$Genotype, mydata$Rep)  # Genotypic
```

You can also use `cor()` for simple Pearson correlations ignoring genotypic structure.

4. Table Example: R Output

Parameter	Value
Genetic variance	2.32
Phenotypic variance	5.17
Heritability (%)	44.9
Genetic advance	1.92
Genotypic corr.	0.73
Phenotypic corr.	0.64

(Actual results will depend on your data.)

5. Formulas Used

- **Genotypic Variance:** $\sigma_g^2 = \frac{MS_{genotype} - MS_{error}}{r}$
- **Phenotypic Variance:** $\sigma_p^2 = \sigma_g^2 + MS_{error}$
- **Heritability (broad sense, %):** $h^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$
- **Genetic Advance:** $GA = K \times \sqrt{\sigma_p^2} \times h^2$

  where K is the selection differential (2.056 for 5% selection intensity).

You can easily adapt and expand this script for multiple traits or datasets.
Make sure to load your data and change the column names as needed. The `variability` package is especially useful for quick and accurate estimation of all genetic parameters and correlation coefficients at once[1] [2].

Let me know if you want help working this script with your actual dataset!

<div align="center">❆</div>

1. https://cran.r-project.org/web/packages/variability/variability.pdf
2. https://www.youtube.com/watch?v=FbQihMqwFXw