Package 'CropBreeding'

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Type Package

Title Stability Analysis in Crop Breeding

Version 0.1.0

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Description

Provides tools for crop breeding analysis including Genetic Coefficient of Variation (GCV),
Phenotypic Coefficient of Variation (PCV), heritability, genetic advance calculations, stability
analysis using the Eberhart-Russell model, two-way ANOVA for genotype-
environment interactions,
and Additive Main Effects and Multiplicative Interaction (AMMI) analysis. These tools are developed
for crop breeding research and stability evaluation under various environmental conditions.
The methods are based on established statistical and biometrical principles.
Refer to Eberhart and Rus-
sell (1966) <doi:10.2135/cropsci1966.0011183X000600010011x> for stability parameters,
Fisher (1935) ``The Design of Experiments'' <ISBN:9780198522294>, Falconer (1996) ``Introduction to Quantitative Genetics''
<ISBN:9780582243026>, and Singh and Chaudhary (1985) ``Biometrical Methods in Quantitative Genetic Analysis''
<ISBN:9788122433764> for foundational methodologies.

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Imports stats, dplyr, metan, rlang

RoxygenNote 7.3.2

NeedsCompilation no

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breeding_metrics   *Breeding Metrics Calculation*

Description

This function calculates key breeding metrics such as genotypic variance, environmental variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), heritability, and genetic advance (GA). These metrics are critical for assessing genotype performance and genetic potential in crop breeding experiments.

Usage

```
breeding_metrics(data, genotype_col, trait_col, replication_col)
```

Arguments

data	A data frame containing the dataset with required columns.
genotype_col	Character. Name of the genotype column.
trait_col	Character. Name of the trait column.
replication_col	
	Character. Name of the replication column.

Value

A list containing:

- 'ANOVA': The summary of the ANOVA table.

- 'GenotypicVariance': Genotypic variance, which measures the genetic variability among genotypes.

- 'EnvironmentalVariance': Environmental variance, which reflects the variability due to environmental factors.

- 'PhenotypicVariance': Phenotypic variance, the sum of genotypic and environmental variances.

- 'GCV': Genotypic coefficient of variation, expressed as a percentage of the mean.

- 'PCV': Phenotypic coefficient of variation, expressed as a percentage of the mean.

- 'Heritability': Broad-sense heritability, the proportion of phenotypic variance attributable to genetic variance.

- 'GeneticAdvance': Genetic advance under selection, a measure of genetic improvement.

- 'GAPercentage': Genetic advance as a percentage of the mean, indicating the relative genetic improvement.

References

Falconer, D. S. (1996). "Introduction to Quantitative Genetics". ISBN: 9780582243026. Singh, R. K., & Chaudhary, B. D. (1985). "Biometrical Methods in Quantitative Genetic Analysis". ISBN: 9788122433764.

Examples

```
set.seed(123)
data <- data.frame(
  Genotype = rep(c("G1", "G2", "G3"), each = 10),
  Replication = rep(1:10, times = 3),
  Trait = c(rnorm(10, 50, 5), rnorm(10, 55, 5), rnorm(10, 60, 5))
)
result <- breeding_metrics(data, "Genotype", "Trait", "Replication")
print(result)
```

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gxe_analysis_multiple	*Two-Way ANOVA for Genotype x Environment Interaction with Multiple Traits*

Description

This function performs a two-way ANOVA to analyze genotype and environment interactions for multiple traits, including replication effects. It provides separate ANOVA results for each specified trait in the dataset.

Usage

```
gxe_analysis_multiple(
  data,
  genotype_col,
  environment_col,
  replication_col,
  trait_cols
)
```

Arguments

data	A data frame containing the dataset with required columns.
genotype_col	Character. Name of the genotype column.
environment_col	Character. Name of the environment column.
replication_col	Character. Name of the replication column.
trait_cols	A vector of trait column names to analyze.

Value

A list containing ANOVA results for each trait.

References

Fisher, R. A. (1935). "The Design of Experiments". ISBN: 9780198522294.

Examples

```
set.seed(123)
data <- data.frame(
  Genotype = rep(c("G1", "G2", "G3"), each = 12),
  Environment = rep(c("E1", "E2", "E3", "E4"), times = 9),
  Replication = rep(c("R1", "R2", "R3"), times = 12),
  Trait1 = c(rnorm(36, 50, 5)),
  Trait2 = c(rnorm(36, 150, 10)),
  Trait3 = c(rnorm(36, 250, 15))
)
anova_results <- gxe_analysis_multiple(
  data = data,
  genotype_col = "Genotype",
  environment_col = "Environment",
  replication_col = "Replication",
  trait_cols = c("Trait1", "Trait2", "Trait3")
)
print(anova_results$Trait1)
```

```
perform_ammi_single_trait
```
Perform AMMI Analysis for a Single Trait

Description

This function performs Additive Main Effects and Multiplicative Interaction (AMMI) analysis for a single trait to evaluate genotype x environment interactions. It generates biplots and PC1 vs. Trait visualizations without relying on predictions.

Usage

```
perform_ammi_single_trait(data, env_col, gen_col, rep_col, trait_col)
```

Arguments

data	A data frame containing the dataset with required columns.
env_col	Character. Name of the environment column.
gen_col	Character. Name of the genotype column.
rep_col	Character. Name of the replication column.
trait_col	Character. Name of the trait column to be analyzed.

Value

A list containing:

- 'analysis': The AMMI analysis results.
- 'biplot': The biplot (PC1 vs PC2).
- 'pc1_plot': The PC1 vs Trait plot.

Examples

```
set.seed(123)
data <- data.frame(
  GEN = rep(c("G1", "G2", "G3", "G4"), each = 12),
  ENV = rep(c("E1", "E2", "E3"), each = 4, times = 4),
  REP = rep(1:3, times = 16),
  Y = c(rnorm(12, 50, 5), rnorm(12, 55, 5), rnorm(12, 60, 5), rnorm(12, 65, 5))
)
results <- perform_ammi_single_trait(data, "ENV", "GEN", "REP", "Y")
```

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stability_analysis	*Stability Analysis using Eberhart-Russell Model*

Description

This function performs stability analysis for multiple traits across different environments using Eberhart and Russell's regression model provided by the 'metan' package. It computes ANOVA tables and regression parameters for assessing genotype stability.

Usage

```
stability_analysis(
  data,
  genotype_col,
  environment_col,
  replication_col,
  trait_cols
)
```

Arguments

data	A data frame containing the dataset with required columns.
genotype_col	Character. Name of the genotype column.
environment_col	
	Character. Name of the environment column.
replication_col	
	Character. Name of the replication column.
trait_cols	A vector of trait column names (response variables).

Value

A list containing results for each trait:

- 'anova': The ANOVA table for each trait.
- 'regression': Regression parameters for stability analysis.

References

Eberhart, S. A., & Russell, W. A. (1966). "Stability Parameters for Comparing Varieties". Crop Science, 6(1), 36–40. doi:10.2135/cropsci1966.0011183X000600010011x

Examples

```
if (!requireNamespace("metan", quietly = TRUE)) {
  install.packages("metan")
}
library(metan)

# Simulated dataset
set.seed(123)
data <- data.frame(
  Genotype = rep(c("G1", "G2", "G3"), each = 12),
  Environment = rep(c("E1", "E2", "E3", "E4"), times = 9),
  Replication = rep(1:3, times = 12),
  Trait1 = c(rnorm(36, 50, 5)),
  Trait2 = c(rnorm(36, 150, 10)),
  Trait3 = c(rnorm(36, 250, 15))
)

results <- stability_analysis(
  data = data,
  genotype_col = "Genotype",
  environment_col = "Environment",
  replication_col = "Replication",
  trait_cols = c("Trait1", "Trait2", "Trait3")
)

print(results$Trait1$anova)
print(results$Trait1$regression)
```

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