Package ‘TBA’

July 21, 2025

Type Package

Title Collection of 'shiny' Apps for Tree Breeding Analysis

Version 0.1.0

Description A collection of interactive 'shiny' applications for performing comprehensive analyses in the field of tree breeding and genetics. The package is designed to assist users in visualizing and interpreting experimental data through a user-friendly interface. Each application is launched via a simple function, and users can upload data in 'Excel' format for analysis. For more information, refer to Singh, R.K. and Chaudhary, B.D. (1977, ISBN:9788176633079).

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Encoding UTF-8

Imports shiny, ggplot2, readxl, reshape2, shinybusy

NeedsCompilation no

Suggests testthat (>= 3.0.0)

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Repository CRAN

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Contents

`ANOVA_app` *Analysis of Variance (ANOVA)*

Description

`ANOVA_app()` function opens an interactive and user friendly Shiny application that enables users to perform Analysis of Variance (ANOVA) for multi-trait experimental data based on the **Randomized Block Design (RBD)** by uploading an Excel file.

Usage

```
ANOVA_app()
```

Details

The application is designed to perform ANOVA for datasets based on the **Randomized Block Design (RBD)**.

Users can upload an Excel file (.xlsx or .xls) containing data for multiple traits. After uploading the file, users need to click the "Analyze" button.

Results are presented in a tabular format showing sources of variation, their respective degrees of freedom (Df), and the Mean Sum of Squares for each trait. Significance is also indicated.

The output table is downloadable in CSV format.

Value

Opens a user-friendly interactive shiny application for performing ANOVA on experimental data.

Data Format

The uploaded Excel file should be formatted as follows:

- First column: Replication
- Second column: Genotypes
- Subsequent columns: Trait values (e.g., DBH, PH, FW, SW, KW, OC)

Trait names should be concise. Example:

- DBH : Diameter at Breast Height
- PH : Plant Height
- FW : Fruit Weight
- SW : Seed Weight
- KW : Kernel Weight
- OC : Oil Content

Note: The uploaded file name should not contain spaces. For example, use `Sample_Data.xlsx` instead of `Sample Data.xlsx`.

An example Excel file is available for download using the `Download Example Data` button within the application.

The example dataset includes:

- 170 genotypes
- 3 replications for each genotype
- 6 traits: DBH, PH, FW, SW, KW, OC

References

Singh, R. K., & Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis.

Examples

```
if(interactive()) ANOVA_app()
```

`Genetic_Variability_Parameters_app`

Genetic Variability Parameters

Description

`Genetic_Variability_Parameters_app()` function opens an interactive and user friendly Shiny application that enables users to estimate genetic variability parameters for multi-trait experimental data based on the **Randomized Block Design (RBD)**.

Usage

```
Genetic_Variability_Parameters_app()
```

Details

The application is designed to calculate genetic variability parameters for datasets based on the **Randomized Block Design (RBD)**.

Users can upload an Excel file (.xlsx or .xls) containing data for multiple traits. After uploading the file, users need to click the "Analyze" button.

The results are displayed in a tabular format including the following parameters for each trait:

- Grand Mean
- Phenotypic Variance
- Genotypic Variance
- Phenotypic Coefficient of Variation (%)
- Genotypic Coefficient of Variation (%)

- Broad-Sense Heritability (%)
- Genetic Advance
- Genetic Advance as Percentage of Mean (%)
- Standard Error of Mean

The output table is downloadable in CSV format.

Value

Opens a user-friendly interactive Shiny application for calculating genetic variability parameters from experimental data.

Data Format

The uploaded Excel file should be formatted as follows:

- First column: Replication
- Second column: Genotypes
- Subsequent columns: Trait values (e.g., DBH, PH, FW, SW, KW, OC)

Trait names should be concise. Example:

- DBH : Diameter at Breast Height
- PH : Plant Height
- FW : Fruit Weight
- SW : Seed Weight
- KW : Kernel Weight
- OC : Oil Content

Note: The uploaded file name should not contain spaces. For example, use `Sample_Data.xlsx` instead of `Sample Data.xlsx`.

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The example dataset includes:

- 170 genotypes
- 3 replications for each genotype
- 6 traits: DBH, PH, FW, SW, KW, OC

References

Singh, R. K., & Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis.
Johnson, Herbert W., H. F. Robinson, and R. E. Comstock. (1955). Estimates of genetic and environmental variability in soybeans. Agronomy Journal, 47(7), 314-318.

Examples

```
if(interactive()) Genetic_Variability_Parameters_app()
```

`Genotypic_Correlation_app`

Genotypic Correlation

Description

`Genotypic_Correlation_app()` function opens an interactive and user-friendly Shiny application that enables users to compute genotypic correlation coefficients among multiple traits from experimental data.

Usage

```
Genotypic_Correlation_app()
```

Details

The application is designed to perform genotypic correlation analysis across multiple traits using experimental data.

Users can upload an Excel file (.xlsx or .xls) containing observations for several genotypes and traits. After uploading the file, users need to click the "Analyze" button.

The output is presented as a matrix showing the genotypic correlation coefficients between traits. A significance indication is provided along with an option to visualize the matrix as a heatmap plot.

The correlation table can be downloaded in CSV format, and the heatmap plot as an image in JPEG and PNG format

Note: The analysis is based on the Randomized Block Design (RBD).

Value

Opens a user-friendly interactive Shiny application for performing genotypic correlation analysis.

Data Format

The uploaded Excel file should be formatted as follows:

- First column: Replication
- Second column: Genotypes
- Subsequent columns: Trait values (e.g., DBH, PH, FW, SW, KW, OC)

Trait names should be concise. Example:

- DBH : Diameter at Breast Height
- PH : Plant Height
- FW : Fruit Weight
- SW : Seed Weight
- KW : Kernel Weight

- OC : Oil Content

Note: The uploaded file name should not contain spaces. For example, use `Sample_Data.xlsx` instead of `Sample Data.xlsx`.

An example Excel file is available for download using the `Download Example Data` button within the application.

The example dataset includes:

- 170 genotypes
- 3 replications for each genotype
- 6 traits: DBH, PH, FW, SW, KW, OC

References

Singh, R. K., & Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis.
Dewey, D. R., & Lu, K. H. (1959). A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production.Agronomy Journal, 51(9), 515-518.
Rajarajan, K., & K. Ganesamurthy(2014). Genetic diversity of sorghum [Sorghum bicolor (L.)] germplasm for drought tolerance. Range Management and Agroforestry, 35(2), 256-262.

Examples

```
if(interactive()) Genotypic_Correlation_app()
```

`Genotypic_Path_app` *Genotypic Path*

Description

`Genotypic_Path_app()` function opens an interactive and user-friendly Shiny application that enables users to perform genotypic path analysis.

Usage

```
Genotypic_Path_app()
```

Details

The application is designed to perform genotypic path analysis using experimental data.

Users can upload an Excel file (.xlsx or .xls) containing observations for several genotypes and traits. After uploading the file users should click the "Analyze" button.

The output includes:

- A table displaying direct and indirect effects of independent traits on the dependent trait.
- Residual effect value.

The result table can be downloaded in CSV format.

Note: The analysis is based on the Randomized Block Design (RBD).

Value

Opens a user-friendly interactive Shiny application for performing genotypic path analysis.

Data Format

The uploaded Excel file should be formatted as follows:

- First column: Replication
- Second column: Genotypes
- Subsequent columns: Trait values (e.g., DBH, PH, FW, SW, KW, OC)
- **Important:** The last column must be the dependent trait for path analysis. For example, if OC (Oil Content) is the dependent trait , it must be in the last column.

Trait names should be concise. Example:

- DBH : Diameter at Breast Height
- PH : Plant Height
- FW : Fruit Weight
- SW : Seed Weight
- KW : Kernel Weight
- OC : Oil Content

Note: The uploaded file name should not contain spaces. For example, use `Sample_Data.xlsx` instead of `Sample Data.xlsx`.

An example Excel file is available for download using the `Download Example Data` button within the application.

The example dataset includes:

- 170 genotypes
- 3 replications for each genotype
- 6 traits: 5 independent traits (DBH, PH, FW, SW, KW) and 1 dependent trait: OC

References

Singh, R. K., & Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis. Dewey, D. R., & Lu, K. H. (1959). A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production.Agronomy Journal, 51(9), 515-518.

Examples

```
if(interactive()) Genotypic_Path_app()
```

`Phenotypic_Correlation_app`

Phenotypic Correlation

Description

`Phenotypic_Correlation_app()` function opens an interactive and user-friendly Shiny application that enables users to compute phenotypic correlation coefficients among multiple traits experimental data.

Usage

```
Phenotypic_Correlation_app()
```

Details

The application is designed to perform phenotypic correlation analysis across multiple traits using experimental data.

Users can upload an Excel file (.xlsx or .xls) containing observations for several genotypes and traits. After uploading the file, users need to click the "Analyze" button.

The output is presented as a matrix showing the phenotypic correlation coefficients between traits. A significance indication is provided along with an option to visualize the matrix as a heatmap plot.

The correlation table can be downloaded in CSV format, and the heatmap plot as an image in JPEG and PNG format.

Note: The analysis is based on the Randomized Block Design (RBD).

Value

Opens a user-friendly interactive Shiny application for performing phenotypic correlation analysis.

Data Format

The uploaded Excel file should be formatted as follows:

- First column: Replication
- Second column: Genotypes
- Subsequent columns: Trait values (e.g., DBH, PH, FW, SW, KW, OC)

Trait names should be concise. Example:

- DBH : Diameter at Breast Height
- PH : Plant Height
- FW : Fruit Weight
- SW : Seed Weight
- KW : Kernel Weight

- OC : Oil Content

Note: The uploaded file name should not contain spaces. For example, use `Sample_Data.xlsx` instead of `Sample Data.xlsx`.

An example Excel file is available for download using the `Download Example Data` button within the application.

The example dataset includes:

- 170 genotypes
- 3 replications for each genotype
- 6 traits: DBH, PH, FW, SW, KW, OC

References

Singh, R. K., & Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis.
Dewey, D. R., & Lu, K. H. (1959). A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production.Agronomy Journal, 51(9), 515-518.
Rajarajan, K., & K. Ganesamurthy(2014). Genetic diversity of sorghum [Sorghum bicolor (L.)] germplasm for drought tolerance. Range Management and Agroforestry, 35(2), 256-262.

Examples

```
if(interactive()) Phenotypic_Correlation_app()
```

`Phenotypic_Path_app` *Phenotypic Path*

Description

`Phenotypic_Path_app()` function opens an interactive and user-friendly Shiny application that enables users to perform phenotypic path analysis.

Usage

```
Phenotypic_Path_app()
```

Details

The application is designed to perform phenotypic path analysis using experimental data.

Users can upload an Excel file (.xlsx or .xls) containing observations for several genotypes and traits. After uploading the file users should click the "Analyze" button.

The output includes:

- A table displaying direct and indirect effects of independent traits on the dependent trait.
- Residual effect value.

The result table can be downloaded in CSV format.

Note: The analysis is based on the Randomized Block Design (RBD).

Value

Opens a user-friendly interactive Shiny application for performing phenotypic path analysis.

Data Format

The uploaded Excel file should be formatted as follows:

- First column: Replication
- Second column: Genotypes
- Subsequent columns: Trait values (e.g., DBH, PH, FW, SW, KW, OC)
- **Important:** The last column must be the dependent trait for path analysis. For example, if OC (Oil Content) is the dependent trait , it must be in the last column.

Trait names should be concise. Example:

- DBH : Diameter at Breast Height
- PH : Plant Height
- FW : Fruit Weight
- SW : Seed Weight
- KW : Kernel Weight
- OC : Oil Content

Note: The uploaded file name should not contain spaces. For example, use `Sample_Data.xlsx` instead of `Sample Data.xlsx`.

An example Excel file is available for download using the `Download Example Data` button within the application.

The example dataset includes:

- 170 genotypes
- 3 replications for each genotype
- 6 traits: 5 independent traits (DBH, PH, FW, SW, KW) and 1 dependent trait: OC

References

Singh, R. K., & Chaudhary, B. D. (1977). Biometrical Methods in Quantitative Genetic Analysis.
Dewey, D. R., & Lu, K. H. (1959). A Correlation and Path-Coefficient Analysis of Components of Crested Wheatgrass Seed Production.Agronomy Journal, 51(9), 515-518.

Examples

```
if(interactive()) Phenotypic_Path_app()
```

Index