Package 'augmentedRCBD'

May 16, 2018

Title Analysis of Augmented Randomised Complete Block Design

Version 0.0.0.9000

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Encoding UTF-8

LazyData true

Depends R (>= 3.0.1)

RoxygenNote 6.0.1

URL https://github.com/aravind-j/augmentedRCBD

BugReports https://github.com/aravind-j/augmentedRCBD/issues

Imports data.table,
ggplot2,
moments,
plyr,
Rdpack,
ReporteRs

RdMacros Rdpack

R topics documented:

`augmentedRCBD` *Analysis of Augmented Randomised Complete Block Design*

Description

`augmentedRCBD` is a function for analysis of variance of an augmented randomised block design (Federer, 1956; Federer, 1961) and the generation as well as comparison of the adjusted means of the treatments/genotypes.

Usage

```
augmentedRCBD(block, treatment, y, checks = NULL, method.comp = c("lsd",
  "tukey"), alpha = 0.05, group = TRUE, console = TRUE)
```

Arguments

block	Vector of blocks (as a factor).
treatment	Vector of treatments/genotypes (as a factor).
y	Numeric vector of response variable (Trait).
checks	Character vector of the checks present in treatment levels. If not specified, checks are inferred from the data on the basis of number of replications of treatments/genotypes.
method.comp	Method for comparison of treatments ("lsd" for least significant difference or "tukey" for Tukey's honest significant difference).
alpha	Type I error probability (Significance level) to be used for multiple comparisons.
group	If TRUE, genotypes will be grouped according to "method.comp".
console	If TRUE, output will be printed to console.

Details

This function borrows code from DAU.test function of agricolae package (de Mendiburu et al., 2016) as well as from Appendix VIII of Mathur et al., (2008).

Value

A list of class augmentedRCBD containing the following components:

Details	Details of the augmented design used.
Means	A data frame with the "Means", "Block", "SE", "Mix", "Max" and "Adjusted Means" for each "Treatment".
ANOVA, Treatment Adjusted	An object of class summary.aov for ANOVA table with treatments adjusted.
ANOVA, Block Adjusted	An object of class summary.aov for ANOVA table with block adjusted.
Block effects	A vector of block effects.
Treatment effects	A vector of treatment effects.
Std. Errors	A data frame of standard error of difference between various combinations along with critical difference and tukey's honest significant difference (when method.comp = "tukey") at alpha.
Overall adjusted mean	Overall adjusted mean.
CV	Coefficient of variation.
Comparisons	A data frame of pairwise comparisons of treatments. This is computed only if argument group is TRUE
Groups	A data frame with compact letter display of pairwise comparisons of treatments. Means with at least one letter common are not significantly different statistically. This is computed only if argument group is TRUE

Note

- Data should preferably be balanced i.e. all the check genotypes should be present in all the blocks. If not, a warning is issued.
- There should not be any missing values.
- The number of test genotypes can vary within a block.

References

Federer WT (1956). "Augmented (or hoonuiaku) designs." *The Hawaiian Planters' Record*, **LV(2)**, 191–208.

Federer WT (1961). "Augmented designs with one-way elimination of heterogeneity." *Biometrics*, **17**(3), 447–473.

Mathur P, Muralidharan K, Parthasarathy VA, Batugal P, Bonnot F (2008). *Data Analysis Manual for Coconut Researchers-Bioversity Technical Bulletin No. 14*. Bioversity International.

de Mendiburu F (2015). *agricolae: Statistical Procedures for Agricultural Research*. R package version 1.2-8. https://CRAN.R-project.org/package=agricolae.

See Also

DAU.test, ea1, emmeans, cld, aug.rcb

Examples

```
# Example data
blk <- c(rep(1,7),rep(2,6),rep(3,7))
trt <- c(1, 2, 3, 4, 7, 11, 12, 1, 2, 3, 4, 5, 9, 1, 2, 3, 4, 8, 6, 10)
y1 <- c(92, 79, 87, 81, 96, 89, 82, 79, 81, 81, 91, 79, 78, 83, 77, 78, 78,
        70, 75, 74)
y2 <- c(258, 224, 238, 278, 347, 300, 289, 260, 220, 237, 227, 281, 311, 250,
        240, 268, 287, 226, 395, 450)
data <- data.frame(blk, trt, y1, y2)
# Convert block and treatment to factors
data$blk <- as.factor(data$blk)
data$trt <- as.factor(data$trt)
# Results for variable y1
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
# Results for variable y2
out2 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                     alpha = 0.05, group = TRUE, console = TRUE)
```

---

describe.augmentedRCBD

Compute Descriptive Statistics from augmentedRCBD *Output*

Description

describe.augmentedRCBD computes descriptive statistics from the adjusted means in an object of class augmentedRCBD.

Usage

```
describe.augmentedRCBD(aug)
```

Arguments

aug	An object of class augmentedRCBD.

Details

describe.augmentedRCBD computes the following descriptive statistics from the adjusted means in an object of class augmentedRCBD.

- Count
- Mean
- Standard deviation
- Standard error
- Minimum
- Maximum
- Skewness statistic along with p-value from D'Agostino test of skewness (D'Agostino, 1970).
- Kurtosis statistic along with p-value from Anscombe-Glynn test of kurtosis (Anscombe and Glynn, 1983).

Value

A list with the following descriptive statistics:

Count	The number of treatments/genotypes.
Mean	The mean value.
Std.Error	The standard error.
Std.Deviation	The standard deviation.
Min	The minimum value
Max	The maximum value
Skewness(statistic)	The skewness estimator.
Skewness(p.value)	The p-value from D'Agostino test of skewness.
Kurtosis(statistic)	The kurtosis estimator.
Kurtosis(p.value)	The p-value from Anscombe-Glynn test of kurtosis.

References

D'Agostino RB (1970). "Transformation to normality of the null distribution of g_1." *Biometrika*, **57**(3), 679–681.

Anscombe FJ, Glynn WJ (1983). "Distribution of the kurtosis statistic b_2 for normal samples." *Biometrika*, **70**(1), 227–234.

See Also

augmentedRCBD

Examples

```
# Example data
blk <- c(rep(1,7),rep(2,6),rep(3,7))
trt <- c(1, 2, 3, 4, 7, 11, 12, 1, 2, 3, 4, 5, 9, 1, 2, 3, 4, 8, 6, 10)
y1 <- c(92, 79, 87, 81, 96, 89, 82, 79, 81, 81, 91, 79, 78, 83, 77, 78, 78,
        70, 75, 74)
y2 <- c(258, 224, 238, 278, 347, 300, 289, 260, 220, 237, 227, 281, 311, 250,
        240, 268, 287, 226, 395, 450)
data <- data.frame(blk, trt, y1, y2)
# Convert block and treatment to factors
data$blk <- as.factor(data$blk)
data$trt <- as.factor(data$trt)
# Results for variable y1
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
# Results for variable y2
out2 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                     alpha = 0.05, group = TRUE, console = TRUE)

# Descriptive statistics
describe.augmentedRCBD(out1)
describe.augmentedRCBD(out2)
```

---

gva.augmentedRCBD *Perform Genetic Variability Analysis on* augmentedRCBD *Output*

Description

gva.augmentedRCBD performs genetic variability analysis on an object of class augmentedRCBD.

Usage

```
gva.augmentedRCBD(aug, k = 2.063)
```

Arguments

aug	An object of class augmentedRCBD.
k	The standardized selection differential or selection intensity. Default is 2.063 for 5% selection proportion (see **Details**).

Details

gva.augmentedRCBD performs genetic variability analysis from the ANOVA results in an object of class augmentedRCBD and computes several variability estimates.

The phenotypic, genotypic and environmental variance (σ_p^2, σ_g^2 and σ_e^2) are obtained from the ANOVA tables as follows:

$$\sigma_p^2 = \text{Sum of squares of test treatments(genotypes)}$$

$$\sigma_e^2 = \text{Sum of squares of residuals(error)}$$

$$\sigma_g^2 = \sigma_p^2 - \sigma_e^2$$

Phenotypic and genotypic coefficients of variation (PCV and GCV) are estimated according to Burton (1951, 1952) as follows:

$$PCV = \frac{\sigma_p^2}{\sqrt{\overline{x}}} \times 100$$

$$GCV = \frac{\sigma_g^2}{\sqrt{\overline{x}}} \times 100$$

Where $\overline{x}$ is the mean.

The estimates of PCV and GCV are categorised according to Sivasubramanian and Madhavamenon (1978) as follows:

***CV* (%)**	**Category**
x $<$ 10	Low
10 $\leq$ x $<$ 20	Medium
$\geq$ 20	High

The broad-sense heritability (H^2) is calculated according to method of Lush (1940) as follows:

$$H^2 = \frac{\sigma_g^2}{\sigma_p^2}$$

The estimates of broad-sense heritability (H^2) are cateogrised according to Robinson (1966) as follows:

H^2	**Category**
x $<$ 30	Low
30 $\leq$ x $<$ 60	Medium
$\geq$ 60	High

Genetic advance (GA) and genetic advance as per cent of mean (GAM) are estimated and categorised according to Johnson et al., (1955) as follows:

$$GA = k \times \sigma_g \times \frac{H^2}{100}$$

Where the constant k is the standardized selection differential or selection intensity. The value of k at 5% proportion selected is 2.063. Values of k at other selected proportions are available in Appendix Table A of Falconer and Mackay (1996).

$$GAM = \frac{GA}{\overline{x}} \times 100$$

GAM	**Category**
x $<$ 10	Low
10 $\leq$ x $<$ 20	Medium
$\geq$ 20	High

Value

A list with the following descriptive statistics:

`Count` The number of treatments/genotypes.

`Mean` The mean value.

`Std.Error` The standard error.

`Std.Deviation` The standard deviation.

`Min` The minimum value

`Max` The maximum value

`Skewness(statistic)`
The skewness estimator.

`Skewness(p.value)`
The p-value from D'Agostino test of skewness.

`Kurtosis(statistic)`
The kurtosis estimator.

`Kurtosis(p.value)`
The p-value from Anscombe-Glynn test of kurtosis.

Note

Genetic variability analysis needs to be performed only if the sum of squares of "Treatment: Test" are significant.

Negative estimates of variance components if computed are not abnormal. For information on how to deal with these, refer Dudley and Moll (1969).

References

Lush JL (1940). "Intra-sire correlations or regressions of offspring on dam as a method of estimating heritability of characteristics." *Proceedings of the American Society of Animal Nutrition*, **1940**(1), 293–301.

Burton GW (1951). "Quantitative Inheritance in pearl millet (*Pennisetum glaucum*)." *Agronomy Journal*, **43**(9), 409–417.

Burton GW (1952). "Qualitative inheritance in grasses. Vol. 1." In *Proceedings of the 6th International Grassland Congress, Pennsylvania State College*, 17–23.

Johnson HW, Robinson H, Comstock R (1955). "Estimates of genetic and environmental variability in soybeans." *Agronomy journal*, **47**(7), 314–318.

Robinson H (1966). "Quantitative genetics in relation to breeding on centennial of Mendelism." *Indian Journal of Genetics and Plant Breeding*, 171.

Dudley JW, Moll RH (1969). "Interpretation and Use of Estimates of Heritability and Genetic Variances in Plant Breeding." *Crop Science*, **9**(3), 257–262.

Sivasubramanian S, Madhavamenon P (1973). "Genotypic and phenotypic variability in rice." *The Madras Agricultural Journal*, **60**(9-13), 1093–1096.

Falconer DS, Mackay TFC (1996). *Introduction to quantitative genetics*. Pearson/Prenctice Hall, New York, NY.

See Also

`augmentedRCBD`

Examples

```
# Example data
blk <- c(rep(1,7),rep(2,6),rep(3,7))
trt <- c(1, 2, 3, 4, 7, 11, 12, 1, 2, 3, 4, 5, 9, 1, 2, 3, 4, 8, 6, 10)
y1 <- c(92, 79, 87, 81, 96, 89, 82, 79, 81, 81, 91, 79, 78, 83, 77, 78, 78,
        70, 75, 74)
y2 <- c(258, 224, 238, 278, 347, 300, 289, 260, 220, 237, 227, 281, 311, 250,
        240, 268, 287, 226, 395, 450)
data <- data.frame(blk, trt, y1, y2)
# Convert block and treatment to factors
data$blk <- as.factor(data$blk)
data$trt <- as.factor(data$trt)
# Results for variable y1
out1 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                      alpha = 0.05, group = TRUE, console = TRUE)
# Results for variable y2
out2 <- augmentedRCBD(data$blk, data$trt, data$y1, method.comp = "lsd",
                     alpha = 0.05, group = TRUE, console = TRUE)

# Genetic variability analysis
gva.augmentedRCBD(out1)
gva.augmentedRCBD(out2)
```

---

print.augmentedRCBD *Prints summary of* augmentedRCBD *object*

Description

print.augmentedRCBD prints to console the summary of an object of class augmentedRCBD including the augmented design details, ANOVA (Treatment adjusted), ANOVA (Block adjusted), Treatment means, Coefficient of variation, overall adjusted mean and standard errors. The treatment/genotype groups along with the grouping method are also printed if they were computed.

Usage

```
## S3 method for class 'augmentedRCBD'
print(x, ...)
```

Arguments

x	An object of class augmentedRCBD.
...	Unused

See Also

augmentedRCBD

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