Package 'DiallelAnalysisR'

August 1, 2020

Type Package

Title Diallel Analysis with R

Version 0.3.0

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Description Performs Diallel Analysis with R using Griffing's and Hayman's approaches. Four different Methods (1: Method-I (Parents + F1's + reciprocals); 2: Method-II (Parents and one set of F1's); 3: Method-III (One set of F1's and reciprocals); 4: Method-IV (One set of F1's only)) and two Models (1: Fixed Effects Model; 2: Random Effects Model) can be applied using Griffing's approach.

Depends R (>= 3.5.0)

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Encoding UTF-8

LazyData true

VignetteBuilder knitr

RoxygenNote 7.1.1

URL `https://github.com/myaseen208/DiallelAnalysisR`
`https://CRAN.R-project.org/package=DiallelAnalysisR`
`https://myaseen208.github.io/DiallelAnalysisR/`

BugReports `https://github.com/myaseen208/DiallelAnalysisR/issues`

Note Department of Mathematics and Statistics, University of Agriculture Faisalabad, Faisalabad-Pakistan.

Imports ggplot2, stats

Suggests knitr, rmarkdown, testthat

NeedsCompilation no

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Repository CRAN

Date/Publication 2020-08-01 10:52:05 UTC

R topics documented:

`Griffing` *Diallel Analysis using Griffing Approach*

Description

`Griffing` is used for performing Diallel Analysis using Griffing's Approach.

Usage

```
Griffing(y, Rep, Cross1, Cross2, data, Method, Model)
```

Arguments

`y`	Numeric Response Vector
`Rep`	Replicate as factor
`Cross1`	Cross 1 as factor
`Cross2`	Cross 2 as factor
`data`	A `data.frame`
`Method`	Method for Diallel Analysis using Griffing's approach. It can take **1**, **2**, **3**, or **4** as argument depending on the method being used. 1. Method-I (Parents + F_1's + reciprocals); 2. Method-II (Parents and one set of F_1's); 3. Method-III (One set of F_1's and reciprocals); 4. Method-IV (One set of F_1's only).
`Model`	Model for Diallel Analysis using Griffing's approach. It can take **1** or **2** as arguments depending on the model being used. 1. Fixed Effects Model; 2. Random Effects Model.

Details

Diallel Analysis using Griffing's approach.

Value

Means	Means
ANOVA	Analysis of Variance (ANOVA) table
Genetic.Components	Genetic Components
Effects	Effects of Crosses
StdErr	Standard Errors of Crosses

Author(s)

Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9(4)**, 463–493.
2. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

`Hayman` , `GriffingData1` , `GriffingData2` , `GriffingData3` , `GriffingData4`

Examples

```
#-------------------------------------------------------------
## Diallel Analysis with Griffing's Aproach Method 1 & Model 1
#-------------------------------------------------------------
Griffing1Data1 <-
 Griffing(
     y      = Yield
   , Rep    = Rep
   , Cross1 = Cross1
   , Cross2 = Cross2
   , data   = GriffingData1
   , Method = 1
   , Model  = 1
 )
names(Griffing1Data1)
Griffing1Data1
Griffing1Data1Means <- Griffing1Data1$Means
Griffing1Data1ANOVA <- Griffing1Data1$ANOVA
Griffing1Data1Genetic.Components <- Griffing1Data1$Genetic.Components
Griffing1Data1Effects <- Griffing1Data1$Effects
Griffing1Data1StdErr <- as.matrix(Griffing1Data1$StdErr)


#--------------------------------------------------------------
## Diallel Analysis with Griffing's Aproach Method 1 & Model 2
#--------------------------------------------------------------
```

```
Griffing2Data1 <-
 Griffing(
     y      = Yield
   , Rep    = Rep
   , Cross1 = Cross1
   , Cross2 = Cross2
   , data   = GriffingData1
   , Method = 1
   , Model  = 2
 )
names(Griffing2Data1)
Griffing2Data1
Griffing2Data1Means <- Griffing2Data1$Means
Griffing2Data1ANOVA <- Griffing2Data1$ANOVA
Griffing2Data1Genetic.Components <- Griffing2Data1$Genetic.Components


#----------------------------------------------------------------
## Diallel Analysis with Griffing's Aproach Method 2 & Model 1
#----------------------------------------------------------------
Griffing1Data2 <-
 Griffing(
     y      = Yield
   , Rep    = Rep
   , Cross1 = Cross1
   , Cross2 = Cross2
   , data   = GriffingData2
   , Method = 2
   , Model  = 1
 )
names(Griffing1Data2)
Griffing1Data2
Griffing1Data2Means <- Griffing1Data2$Means
Griffing1Data2ANOVA <- Griffing1Data2$ANOVA
Griffing1Data2Genetic.Components <- Griffing1Data2$Genetic.Components
Griffing1Data2Effects <- Griffing1Data2$Effects
Griffing1Data2StdErr <- as.matrix(Griffing1Data2$StdErr)


#----------------------------------------------------------------
## Diallel Analysis with Griffing's Aproach Method 2 & Model 2
#----------------------------------------------------------------
Griffing2Data2 <-
 Griffing(
     y      = Yield
   , Rep    = Rep
   , Cross1 = Cross1
   , Cross2 = Cross2
   , data   = GriffingData2
   , Method = 2
   , Model  = 2
 )
names(Griffing2Data2)
```

```
Griffing2Data2
Griffing2Data2Means <- Griffing2Data2$Means
Griffing2Data2ANOVA <- Griffing2Data2$ANOVA
Griffing2Data2Genetic.Components <- Griffing2Data2$Genetic.Components


#-------------------------------------------------------------
## Diallel Analysis with Griffing's Aproach Method 3 & Model 1
#-------------------------------------------------------------
Griffing1Data3 <-
 Griffing(
     y      = Yield
   , Rep    = Rep
   , Cross1 = Cross1
   , Cross2 = Cross2
   , data   = GriffingData3
   , Method = 3
   , Model  = 1
 )
names(Griffing1Data3)
Griffing1Data3
Griffing1Data3Means <- Griffing1Data3$Means
Griffing1Data3ANOVA <- Griffing1Data3$ANOVA
Griffing1Data3Genetic.Components <- Griffing1Data3$Genetic.Components
Griffing1Data3Effects <- Griffing1Data3$Effects
Griffing1Data3StdErr <- as.matrix(Griffing1Data3$StdErr)


#-------------------------------------------------------------
## Diallel Analysis with Griffing's Aproach Method 3 & Model 2
#-------------------------------------------------------------
Griffing2Data3 <-
 Griffing(
     y       = Yield
   , Rep     = Rep
   , Cross1  = Cross1
   , Cross2  = Cross2
   , data    = GriffingData3
   , Method  = 3
   , Model   = 2
 )
names(Griffing2Data3)
Griffing2Data3
Griffing2Data3Means <- Griffing2Data3$Means
Griffing2Data3ANOVA <- Griffing2Data3$ANOVA
Griffing2Data3Genetic.Components <- Griffing2Data3$Genetic.Components


#-------------------------------------------------------------
## Diallel Analysis with Griffing's Aproach Method 4 & Model 1
#-------------------------------------------------------------
Griffing1Data4 <-
 Griffing(
```

```
      y       = Yield
    , Rep     = Rep
    , Cross1  = Cross1
    , Cross2  = Cross2
    , data    = GriffingData4
    , Method  = 4
    , Model   = 1
 )
names(Griffing1Data4)
Griffing1Data4
Griffing1Data4Means <- Griffing1Data4$Means
Griffing1Data4ANOVA <- Griffing1Data4$ANOVA
Griffing1Data4Genetic.Components <- Griffing1Data4$Genetic.Components
Griffing1Data4Effects <- Griffing1Data4$Effects
Griffing1Data4StdErr <- as.matrix(Griffing1Data4$StdErr)


#-------------------------------------------------------------
## Diallel Analysis with Griffing's Aproach Method 4 & Model 2
#-------------------------------------------------------------
Griffing2Data4 <-
 Griffing(
      y       = Yield
    , Rep     = Rep
    , Cross1  = Cross1
    , Cross2  = Cross2
    , data    = GriffingData4
    , Method  = 4
    , Model   = 2
 )
names(Griffing2Data4)
Griffing2Data4
Griffing2Data4Means <- Griffing2Data4$Means
Griffing2Data4ANOVA <- Griffing2Data4$ANOVA
Griffing2Data4Genetic.Components <- Griffing2Data4$Genetic.Components
```

`GriffingData1` *Data for Diallel Analysis using Griffing Approach Method 1*

Description

`Griffing` is used for performing Diallel Analysis using Griffing's Approach.

Usage

```
data(GriffingData1)
```

Format

A `data.frame` with 256 rows and 4 variables.

Details

- Cross1 Cross 1
- Cross2 Cross 2
- Rep Replicate
- Yield Yield Response

Author(s)

Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9(4)**, 463–493.
2. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

`Griffing` , `GriffingData2` , `GriffingData3` , `GriffingData4`

Examples

```
data(GriffingData1)
```

`GriffingData2` *Data for Diallel Analysis using Griffing Approach Method 2*

Description

`Griffing` is used for performing Diallel Analysis using Griffing's Approach.

Usage

```
data(GriffingData2)
```

Format

A `data.frame` with 144 rows and 4 variables.

Details

- Cross1 Cross 1
- Cross2 Cross 2
- Rep Replicate
- Yield Yield Response

Author(s)

Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9(4)**, 463–493.
2. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

`Griffing` , `GriffingData1` , `GriffingData3` , `GriffingData4`

Examples

```
data(GriffingData2)
```

`GriffingData3` *Data for Diallel Analysis using Griffing Approach Method 3*

Description

`Griffing` is used for performing Diallel Analysis using Griffing's Approach.

Usage

```
data(GriffingData3)
```

Format

A `data.frame` with 224 rows and 4 variables.

Details

- Cross1 Cross 1
- Cross2 Cross 2
- Rep Replicate
- Yield Yield Response

Author(s)

Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9(4)**, 463–493.
2. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

`Griffing` , `GriffingData1` , `GriffingData2` , `GriffingData4`

Examples

```
data(GriffingData3)
```

`GriffingData4` *Data for Diallel Analysis using Griffing Approach Method 4*

Description

`Griffing` is used for performing Diallel Analysis using Griffing's Approach.

Usage

```
data(GriffingData4)
```

Format

A `data.frame` with 112 rows and 4 variables.

Details

- Cross1 Cross 1
- Cross2 Cross 2
- Rep Replicate
- Yield Yield Response

Author(s)

Muhammad Yaseen (`<myaseen208@gmail.com>`)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9(4)**, 463–493.
2. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

`Griffing` , `GriffingData1` , `GriffingData2` , `GriffingData3`

Examples

```
data(GriffingData4)
```

`Hayman` *Diallel Analysis using Hayman Approach*

Description

`Hayman` is used for performing Diallel Analysis using Hayman's Approach.

Usage

```
Hayman(y, Rep, Cross1, Cross2, data)
```

Arguments

`y`	Numeric Response Vector
`Rep`	Replicate as factor
`Cross1`	Cross 1 as factor
`Cross2`	Cross 2 as factor
`data`	A `data.frame`

Details

Diallel Analysis using Haymans's approach.

Value

Means Means

ANOVA Analysis of Variance (ANOVA) table

Genetic.Components Genetic Components

Effects Effects of Crosses

StdErr Standard Errors of Crosses

Author(s)

Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Hayman, B. I. (1954 a) The Theory and Analysis of Diallel Crosses. *Genetics*, **39**, 789–809.
2. Hayman, B. I. (1954 b) The Analysis of Variance of Diallel Tables. *Biometrics*, **10**, 235–244.
3. Hayman, B. I. (1957) Interaction, Heterosis and Diallel Crosses. *Genetics*, **42**, 336–355.
4. Singh, R. K. and Chaudhary, B. D. (2004) *Biometrical Methods in Quantitative Genetic Analysis*. New Delhi: Kalyani.

See Also

`Griffing`, `HaymanData`

Examples

```
#-----------------------------------------
## Diallel Analysis with Haymans's Aproach
#-----------------------------------------

Hayman1Data <-
 Hayman(
     y      = Yield
   , Rep    = Rep
   , Cross1 = Cross1
   , Cross2 = Cross2
   , data   = HaymanData
   )

Hayman1Data
names(Hayman1Data)

Hayman1DataMeans <- Hayman1Data$Means
Hayman1DataANOVA <- Hayman1Data$ANOVA
Hayman1DataWr.Vr.Table <- Hayman1Data$Wr.Vr.Table

Hayman1DataComponents.of.Variation <- Hayman1Data$Components.of.Variation
Hayman1DataOther.Parameters <- Hayman1Data$Other.Parameters
Hayman1DataFr <- Hayman1Data$Fr

#----------------
# Wr-Vr Graph
#----------------
VOLO     <- Hayman1Data$VOLO
In.Value <- Hayman1Data$In.Value
a        <- Hayman1Data$a
b        <- Hayman1Data$b
Wr.Vr    <- Hayman1Data$Wr.Vr.Table


library(ggplot2)
ggplot(data=data.frame(x=c(0, max(In.Value, Wr.Vr$Vr, Wr.Vr$Wr, Wr.Vr$Wrei))), aes(x)) +
  stat_function(fun=function(x) {sqrt(x*VOLO)}, color="blue") +
  geom_hline(yintercept = 0) +
```

```
geom_vline(xintercept = 0) +
geom_abline(intercept = a, slope = b) +
geom_abline(intercept = mean(Wr.Vr$Wr)-mean(Wr.Vr$Vr), slope = 1) +
geom_segment(aes(
    x     = mean(Wr.Vr$Vr)
  , y     = min(0, mean(Wr.Vr$Wr))
  , xend  = mean(Wr.Vr$Vr)
  , yend  = max(0, mean(Wr.Vr$Wr))
)
, color = "green"
) +
geom_segment(aes(
    x     = min(0, mean(Wr.Vr$Vr))
  , y     = mean(Wr.Vr$Wr)
  , xend  = max(0, mean(Wr.Vr$Vr))
  , yend  = mean(Wr.Vr$Wr)
)
, color = "green"
)  +
lims(x=c(min(0, Wr.Vr$Vr, Wr.Vr$Wrei), max(Wr.Vr$Vr, Wr.Vr$Wrei)),
     y=c(min(0, Wr.Vr$Wr, Wr.Vr$Wrei), max(Wr.Vr$Wr, Wr.Vr$Wri))
) +
labs(
       x = expression(V[r])
     , y = expression(W[r])
     , title = expression(paste(W[r]-V[r] , " Graph"))
     ) +
theme_bw()
```

`HaymanData` *Data for Diallel Analysis using Hayman's Approach*

Description

`Griffing` is used for performing Diallel Analysis using Hayman's Approach.

Usage

```
data(HaymanData)
```

Format

A `data.frame` with 256 rows and 4 variables.

Details

- Cross1 Cross 1
- Cross2 Cross 2
- Rep Replicate
- Yield Yield Response

Author(s)

Muhammad Yaseen (<`myaseen208@gmail.com`>)

References

1. Griffing, B. (1956) Concept of General and Specific Combining Ability in relation to Diallel Crossing Systems. *Australian Journal of Biological Sciences*, **9(4)**, 463–493.
2. Test

Examples

```
data(HaymanData)
```

`PartialDiallel` *Analysis for Partial Diallel*

Description

Analysis of Partial Diallel

Usage

```
PartialDiallel(y, Rep, Cross1, Cross2, data)
```

Arguments

`y`	Numeric Response Vector
`Rep`	Replicate as factor
`Cross1`	Cross 1 as factor
`Cross2`	Cross 2 as factor
`data`	A `data.frame`

Value

Means Means

ANOVA Analysis of Variance (ANOVA) table

Genetic.Components Genetic Components

General General

Specific Specific

Author(s)

1. Pedro A. M. Barbosa (<`pedro.barbosa@usp.br`>)
2. Muhammad Yaseen (<`myaseen208@gmail.com`>)

See Also

PartialDiallelData , Griffing , Hayman , GriffingData1 , GriffingData2 , GriffingData3 , GriffingData4

Examples

```
data(PartialDiallelData)
fm1 <-
  PartialDiallel(
      y      = y
    , Rep    = Rep
    , Cross1 = Cross1
    , Cross2 = Cross2
    , data   = PartialDiallelData
  )

fm1
```

`PartialDiallelData` *Data for Partial Diallel Analysis*

Description

Data for Partial Diallel Analysis

Usage

```
data(PartialDiallelData)
```

Details

- Cross1 Cross 1
- Cross2 Cross 2
- Rep Replicate
- Yield Yield Response

See Also

PartialDiallel , Griffing , Hayman , GriffingData1 , GriffingData2 , GriffingData3 , GriffingData4

Examples

```
data(PartialDiallelData)
```

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