

Package ‘eda4treeR’

February 4, 2018

Type Package

Title Experimental Design and Analysis for Tree Improvement

Version 0.2.0

Maintainer Muhammad Yaseen <myaseen208@gmail.com>

Description Provides data sets and R Codes for Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). Experimental Design and Analysis for Tree Improvement, CSIRO Publishing.

Depends R (>= 3.2.3)

Imports dplyr, dae, emmeans, ggplot2, lme4, magrittr, pbkrtest, stats, tidyverse

License GPL-3

URL <https://github.com/MYaseen208/eda4treeR>

LazyData TRUE

RoxygenNote 6.0.1

Suggests testthat

NeedsCompilation no

Author Muhammad Yaseen [aut, cre],
Sami Ullah [aut, ctb]

Repository CRAN

Date/Publication 2018-02-04 19:06:12 UTC

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DataExam2.1	<i>Data for Example 2.1 from Experimental Design & Analysis for Tree Improvement</i>
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Description

Exam2.1 is used to compare two seed lots by using single factor ANOVA.

Usage

```
data(DataExam2.1)
```

Format

A data.frame with 16 rows and 2 variables.

Seedlot Two Seedlots Seed Orchard (SO) and rutin plantation (P)

dbh Diameter at breast height

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also[Exam2.1](#)**Examples**

```
data(DataExam2.1)
```

DataExam2.2	<i>Data for Example 2.2 from Experimental Design & Analysis for Tree Improvement</i>
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Description

Exam2.2 is used to compare two seed lots by using ANOVA under RCB Design.

Usage

```
data(DataExam2.2)
```

Format

A data . frame with 16 rows and 2 variables.

Seedlot Two Seedlots Seed Orchard (SO) and routin plantation (P)

dbh Diameter at breast height

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002).*Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also[Exam2.2](#)**Examples**

```
data(DataExam2.2)
```

DataExam3.1

Data for Example 3.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam3.1 is part of data from Australian Centre for Agricultural Research (ACIAR) in Queensland, Australia (Experiment 309).

Usage

```
data(DataExam3.1)
```

Format

A data.frame with 80 rows and 6 variables.

Rep1 Replication number of different Seedlots

PlotNo Plot No of different Trees

SeedLot Seed Lot number

TreeNo Tree number of Seedlots

Ht Height in meter

Dg1 Diameter at ground level

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[Exam3.1](#)

Examples

```
data(DataExam3.1)
```

DataExam3.1.1

Data for Example 3.1.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam3.1.1 is part of data from Australian Centre for Agricultural Research (ACIAR) in Queensland, Australia (Experiment 309).

Usage

```
data(DataExam3.1.1)
```

Format

A data.frame with 10 rows and 6 variables.

Rep1 Replication number of different Seedlots

PlotNo Plot No of different Trees

SeedLot Seed Lot number

TreeNo Tree number of Seedlots

Ht Height in meter

Dg1 Diameter at ground level

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[Exam3.1.1](#)

Examples

```
data(DataExam3.1.1)
```

DataExam4.3

Data for Example 4.3 from Experimental Design & Analysis for Tree Improvement

Description

Exam4.3 presents the germination count data for 4 Pre-Treatments and 6 Seedlots.

Usage

```
data(DataExam4.3)
```

Format

A data.frame with 72 rows and 8 variables.

Row Row number of different Seedlots

Column Column number of different Trees

Replication Replication number of Treatment

Contcomp Control or Trated Plot

Pretreatment Treatment types

SeedLot Seed lot number

GerminationCount Number of germinated seeds out of 25

Percent Germination Percentage

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[Exam4.3](#)

Examples

```
data(DataExam4.3)
```

DataExam4.3.1

Data for Example 4.3.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam4.3.1 presents the germination count data for 4 Pre-Treatments and 6 Seedlots.

Usage

```
data(DataExam4.3.1)
```

Format

A data.frame with 72 rows and 8 variables.

Row Row number of different Seedlots

Column Column number of different Trees

Replication Replication number of Treatment

Contcomp Control or Trated Plot

Pretreatment Treatment types

SeedLot Seed lot number

GerminationCount Number of germinated seeds out of 25

Percent Germination Percentage

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[Exam4.3.1](#)

Examples

```
data(DataExam4.3.1)
```

DataExam4.4

Data for Example 4.4 from Experimental Design & Analysis for Tree Improvement

Description

Exam4.4 presents the height means for 4 seedlots under factorial arrangement for two levels of Fertilizer and two levels of Irrigation.

Usage

```
data(DataExam4.4)
```

Format

A data.frame with 32 rows and 5 variables.

Rep Replication number

Irrig Irrigation type

Ferti Fertilizer type

SeedDLot Seed Lot number

Height Height of the plants

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[Exam4.4](#)

Examples

```
data(DataExam4.4)
```

DataExam5.1

Data for Example 5.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam5.1 presents the height of 27 seedlots from 4 sites.

Usage

```
data(DataExam5.1)
```

Format

A data.frame with 108 rows and 4 variables.

Site Sites for the experiment

SeedLot Seed lot number

Ht Height of the plants

SiteMean Mean Height of Each Site

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[Exam5.1](#)

Examples

```
data(DataExam5.1)
```

DataExam5.2

Data for Example 5.2 from Experimental Design & Analysis for Tree Improvement

Description

Exam5.2 presents the height of 37 seedlots from 6 sites.

Usage

```
data(DataExam5.2)
```

Format

A data.frame with 108 rows and 4 variables.

Site Sites for the experiment

SeedLot Seed lot number

Ht Height of the plants

SiteMean Mean Height of Each Site

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[Exam5.2](#)

Examples

```
data(DataExam5.2)
```

DataExam6.2	<i>Data for Example 6.2 from Experimental Design & Analysis for Tree Improvement</i>
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Description

Exam 6.2 Dbh mean, Dbh varince and number of trees per plot from 3 provinces("PNG", "Sabah", "Queensland") with 4 replicationsof 48 families.

Exam 6.2 Dbh mean, Dbh varince and number of trees per plot from 3 provinces("PNG", "Sabah", "Queensland") with 4 replicationsof 48 families.

Usage

```
data(DataExam6.2)
```

Format

A data.frame with 192 rows and 7 variables.

Replication Replication number of different Families

Plot.number Plot number of differnt Trees

Family Family Numuber

Province Province of family

Dbh.mean Average Diameter at breast height of trees within plot

Dbh.variance Variance of Diameter at breast height of trees within plot

Dbh.count Number of trees within plot

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)
1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002).*Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.
1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002).*Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam6.2](#)

Examples

```

data(DataExam6.2)

data(DataExam6.2)
library(tidyverse)
library(lme4)

print("Dbh Heritability for PNG")
DataExam6.2.1<- DataExam6.2[DataExam6.2$Province=="PNG",]
fm6.3 <- lm(formula      =
  Dbh.mean      ~ Replication+Family
  ,data         = DataExam6.2.1
  #, subset
  #, weights
  #, na.action
  , method      = "qr"
  , model       = TRUE
  , x           = FALSE
  , y           = FALSE
  , qr          = TRUE
  , singular.ok = TRUE
  , contrasts    = NULL
  )
b <- anova(fm6.3)
print(b)
HM <- function(x){length(x)/sum(1/x)}
w <- HM(DataExam6.2.1$Dbh.count)
S2 <- b[["Mean Sq"]][length(b[["Mean Sq"]])]
Sigma2t <- mean(DataExam6.2.1$Dbh.variance)
sigma2m <- S2-(Sigma2t/w)
fm6.3.1<- lmer(formula=
  Dbh.mean ~ 1+Replication+(1|Family)
  ,data = DataExam6.2.1
  ,REML = TRUE
  ,control = lmerControl()
  ,start = NULL
  , verbose = 0L
  #, subset
  #, weights
  #, na.action
  #,offset
  , contrasts = NULL
  , devFunOnly = FALSE)
summary(fm6.3.1)
print(VarCorr(fm6.3.1),comp=c("Variance"))
sigma2f <- 0.2584
h2 <- (sigma2f/(0.3))/(Sigma2t+sigma2m+sigma2f)
cbind(w,Sigma2t,sigma2m,sigma2f,h2)

print("Dbh Heritability for all the Provinces")
fm6.4 <- lm(formula      =
  Dbh.mean      ~ Replication+Family

```

```

      ,data          = DataExam6.2
    #, subset
    #, weights
    #, na.action
      , method      = "qr"
      , model       = TRUE
      , x           = FALSE
      , y           = FALSE
      , qr          = TRUE
      , singular.ok = TRUE
      , contrasts    = NULL
    )
b    <- anova(fm6.4)
print(b)
HM   <- function(x){length(x)/sum(1/x)}
w    <- HM(DataExam6.2$Dbh.count)
S2   <- b[["Mean Sq"]][length(b[["Mean Sq"]])]
Sigma2t <- mean(DataExam6.2$Dbh.variance)
sigma2m <- S2-(Sigma2t/w)
fm6.4.1<- lmer(formula=
  Dbh.mean ~ 1+Replication+Province+(1|Family)
  ,data = DataExam6.2
  ,REML = TRUE
  ,control = lmerControl()
  ,start = NULL
  , verbose = 0L
  #, subset
  #, weights
  #, na.action
  #,offset
  , contrasts = NULL
  , devFunOnly = FALSE)
summary(fm6.4.1)
print(VarCorr(fm6.4.1),comp=c("Variance"))
sigma2f <- 0.3514
h2 <- (sigma2f/(0.3))/(Sigma2t+sigma2m+sigma2f)
cbind(w,Sigma2t,sigma2m,sigma2f,h2)
print("Genetic Correlation Between Dbh and Height for PNG Province")
fm6.7.1<- lmer(formula=
  Dbh.mean ~ 1+Replication+(1|Family)
  ,data = DataExam6.2.1
  ,REML = TRUE
  ,control = lmerControl()
  ,start = NULL
  , verbose = 0L
  #, subset
  #, weights
  #, na.action
  #,offset
  , contrasts = NULL
  , devFunOnly = FALSE)
summary(fm6.7.1)
print(VarCorr(fm6.7.1),comp=c("Variance"))

```

```

sigma2f[1] <- 0.2584

fm6.7.2<- lmer(formula=
  Ht.mean ~ 1+Replication+(1|Family)
  ,data = DataExam6.2.1
  ,REML = TRUE
  ,control = lmerControl()
  ,start = NULL
  , verbose = 0L
  #, subset
  #, weights
  #, na.action
  #,offset
  , contrasts = NULL
  , devFunOnly = FALSE)
summary(fm6.7.2)
print(VarCorr(fm6.7.2),comp=c("Variance"))
sigma2f[2] <- 0.2711

fm6.7.3<- lmer(formula=
  Sum.means ~ 1+Replication+(1|Family)
  ,data = DataExam6.2.1
  ,REML = TRUE
  ,control = lmerControl()
  ,start = NULL
  , verbose = 0L
  #, subset
  #, weights
  #, na.action
  #,offset
  , contrasts = NULL
  , devFunOnly = FALSE)
summary(fm6.7.3)
print(VarCorr(fm6.7.3),comp=c("Variance"))
sigma2f[3] <- 0.873
sigma2xy <- 0.5*(sigma2f[3]-sigma2f[1]-sigma2f[2])
GenCorr <- sigma2xy/sqrt(sigma2f[1]*sigma2f[2])
cbind(S2x=sigma2f[1],S2y=sigma2f[2],S2.x.plus.y=sigma2f[3],GenCorr)

```

DataExam8.1

Data for Example 8.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam8.1 presents the Diameter at breast height (Dbh) of 60 SeedLots under layout of row column design with 6 rows and 10 columns in 18 countries and 59 provinces of 18 selected countries.

Usage

```
data(DataExam8.1)
```

Format

A data.frame with 236 rows and 8 variables.

Replication There are 4 replication for the design

Row Experiment is conducted under 6 rows\

Column Experiment is conducted under 4 columns

Inoc Seedling were inoculated for 2 different time periods half for one week and half for seven weeks

Province Experiment was performed in 59 provinces of selected countries

Country Data for different seedlots was collected from 18 countries

Dbh Diameter at breast height

Country.1 Recoded Country lables

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002).*Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[Exam8.1](#)

Examples

```
data(DataExam8.1)
```

Exam2.1

Example 2.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam2.1 is used to compare two seed lots by using single factor ANOVA.

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam2.1](#)

Examples

```
data(DataExam2.1)
library(tidyverse)
fmtab2.3 <-
  lm(
    formula      = dbh ~ SeedLot
  , data         = DataExam2.1
  # , subset
  # , weights
  # , na.action
  , method      = "qr"
  , model       = TRUE
  , x           = FALSE
  , y           = FALSE
  , qr         = TRUE
  , singular.ok = TRUE
  , contrasts    = NULL
  )

anova(fmtab2.3)

DataExam2.1 %>%
  dplyr::group_by(SeedLot) %>%
  dplyr::summarize(Mean = mean(dbh), SD = sd(dbh))
```

Exam2.2

Example 2.2 from Experimental Design & Analysis for Tree Improvement

Description

Exam2.2 is used to compare two seed lots by using ANOVA under RCB Design.

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R.; Matheson, A.C.; Harwood, C.E. (2002). *Experimental design and analysis for tree improvement*. CSIRO Publishing.

See Also

[DataExam2.2](#)

Examples

```
library(tidyverse)
data(DataExam2.2)
fmtab2.5 <-
  lm(
    formula      = dbh~Blk+SeedLot
    , data       = DataExam2.2
    # , subset
    # , weights
    # , na.action
    , method     = "qr"
    , model      = TRUE
    , x          = FALSE
    , y          = FALSE
    , qr         = TRUE
    , singular.ok = TRUE
    , contrasts   = NULL
  )

anova(fmtab2.5)

DataExam2.2 %>%
  dplyr::group_by(SeedLot) %>%
  dplyr::summarize(Mean=mean(dbh), sd=sd(dbh))
```

Exam3.1

Data for Example 3.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam3.1 is part of data from Australian Centre for Agricultural Research (ACIAR) in Queensland, Australia (Experiment 309).

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam3.1](#)

Examples

```
data(DataExam3.1)
library(tidyverse)

fmtab3.3 <- lm(
  formula = Ht~Repl*SeedLot
, data = DataExam3.1
#, subset
#, weights
#, na.action
, method = "qr"
, model = TRUE
, x = FALSE
, y = FALSE
, qr = TRUE
, singular.ok = TRUE
, contrasts = NULL
)
anova(fmtab3.3)
DataExam3.1 %>%
  dplyr::group_by(SeedLot) %>%
  dplyr::summarize(Mean=mean(Ht),SD=sd(Ht))
RESFIT <- data.frame(residualvalue=residuals(fmtab3.3),fittedvalue=fitted.values(fmtab3.3))
library(ggplot2)
ggplot(RESFIT,aes(x=fittedvalue,y=residualvalue))+
  geom_point(size=2)+
  labs(x="Residual vs Fitted Values",y="")+
  theme_bw()
```

Exam3.1.1

Example 3.1.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam3.1.1 is part of data from Australian Centre for Agricultural Research (ACIAR) in Queensland, Australia (Experiment 309).

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam3.1.1](#)

Examples

```
library(tidyverse)
data(DataExam3.1.1)

fm3.8 <- lm(
  formula = Mean~Rep1+SeedLot
  , data = DataExam3.1.1
  #, subset
  #, weights
  #, na.action
  , method = "qr"
  , model = TRUE
  , x = FALSE
  , y = FALSE
  , qr = TRUE
  , singular.ok = TRUE
  , contrasts = NULL
)
anova(fm3.8)
DataExam3.1.1 %>%
  dplyr::group_by(SeedLot) %>%
  dplyr::summarize(Mean=mean(Mean))
```

Exam4.3

Example 4.3 from Experimental Design & Analysis for Tree Improvement

Description

Exam4.3 presents the germination count data for 4 Pre-Treatments and 6 Seedlots.

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam4.3](#)

Examples

```
data(DataExam4.3)
library(tidyverse)
library(ggplot2)
fm4.2 <- aov(
  formula      = Percent~Replication +Contcomp + SeedLot + Pretreatment/Contcomp+
               Contcomp /SeedLot + Pretreatment/ Contcomp/SeedLot
  , data       = DataExam4.3
  #, subset
  #, weights
  #, na.action
  , method     = "qr"
  , model      = TRUE
  , x          = FALSE
  , y          = FALSE
  , qr         = TRUE
  , singular.ok = TRUE
  , contrasts   = NULL
)
anova(fm4.2)

DataExam4.3 %>%
  dplyr::group_by(Contcomp) %>%
  dplyr::summarize(Mean=mean(Percent),n=length(Percent))
DataExam4.3 %>%
  dplyr::group_by(Contcomp,Pretreatment) %>%
  dplyr::summarize(Mean=mean(Percent),n=length(Percent))
DataExam4.3 %>%
  dplyr::group_by(SeedLot) %>%
  dplyr::summarize(Mean=mean(Percent))
DataExam4.3 %>%
  dplyr::group_by(Contcomp,SeedLot) %>%
  dplyr::summarize(Mean=mean(Percent))
DataExam4.3 %>%
  dplyr::group_by(Pretreatment,Contcomp,SeedLot) %>%
  dplyr::summarize(Mean=mean(Percent))
RESFIT <- data.frame(residualvalue=residuals(fm4.2),fittedvalue=fitted.values(fm4.2))
ggplot(RESFIT,aes(x=fittedvalue,y=residualvalue))+
  geom_point(size=2)+
  labs(x="Residual vs Fitted Values",y="")+
  theme_bw()
```

```

fm4.4 <- aov(
  formula = Percent~Replication+Pretreatment*SeedLot
  , data    = DataExam4.3
  , subset  = Contcomp=="Treated"
  #, weights
  #, na.action
  , method = "qr"
  , model = TRUE
  , x = FALSE
  , y = FALSE
  , qr = TRUE
  , singular.ok = TRUE
  , contrasts = NULL
)
anova(fm4.4)
DataExam4.3>%group_by(Pretreatment)%>%summarize(Mean=mean(Percent))
DataExam4.3>%group_by(SeedLot)%>%summarize(Mean=mean(Percent))
DataExam4.3>%group_by(Pretreatment,SeedLot)%>%summarize(Mean=mean(Percent))

```

Exam4.3.1

Example 4.3.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam4.3.1 presents the germination count data for 4 Pre-Treatments and 6 Seedlots.

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam4.3.1](#)

Examples

```

data(DataExam4.3.1)
library(tidyverse)
library(ggplot2)
fm4.4 <- aov(
  formula    = Percent~Replication+Pretreatment*SeedLot

```

```

, data      = DataExam4.3.1
#, subset
#, weights
#, na.action
, method    = "qr"
, model     = TRUE
, x         = FALSE
, y         = FALSE
, qr        = TRUE
, singular.ok = TRUE
, contrasts  = NULL
)
anova(fm4.4)

DataExam4.3.1 %>%
  dplyr::group_by(Pretreatment) %>%
  dplyr::summarize(Mean=mean(Percent))

DataExam4.3.1 %>%
  dplyr::group_by(SeedLot) %>%
  dplyr::summarize(Mean=mean(Percent))

DataExam4.3.1 %>%
  dplyr::group_by(Pretreatment, SeedLot) %>%
  dplyr::summarize(Mean=mean(Percent))

```

Exam4.4

Example 4.4 from Experimental Design & Analysis for Tree Improvement

Description

Exam4.4 presents the height means for 4 seedlots under factorial arrangement for two levels of Fertilizer and two levels of Irrigation.

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam4.4](#)

Examples

```

data(DataExam4.4)
library(tidyverse)
library(ggplot2)
library(dae)

fm4.6 <- aov(
  formula      = Height~Rep+Irrig*Ferti*SeedDLot+Error(Rep/Irrig:Ferti)
  , data       = DataExam4.4
  #, subset
  #, weights
  #, na.action
  , method     = "qr"
  , model      = TRUE
  , x          = FALSE
  , y          = FALSE
  , qr         = TRUE
  , singular.ok = TRUE
  , contrasts  = NULL
)
summary(fm4.6)

DataExam4.4 %>%
  dplyr::group_by(Irrig) %>%
  dplyr::summarize(Mean=mean(Height))

DataExam4.4 %>%
  dplyr::group_by(Ferti) %>%
  dplyr::summarize(Mean=mean(Height))

DataExam4.4 %>%
  dplyr::group_by(SeedDLot) %>%
  dplyr::summarize(Mean=mean(Height))

DataExam4.4 %>%
  dplyr::group_by(Irrig,Ferti) %>%
  dplyr::summarize(Mean=mean(Height))

DataExam4.4 %>%
  dplyr::group_by(Irrig,SeedDLot) %>%
  dplyr::summarize(Mean=mean(Height))

DataExam4.4 %>%
  dplyr::group_by(Ferti,SeedDLot) %>%
  dplyr::summarize(Mean=mean(Height))

DataExam4.4 %>%
  dplyr::group_by(Irrig,Ferti,SeedDLot) %>%
  dplyr::summarize(Mean=mean(Height))
RESFIT <- data.frame(residualvalue=residuals(fm4.6),fittedvalue=fitted.values(fm4.6))
ggplot(RESFIT,aes(x=fittedvalue,y=residualvalue))+
  geom_point(size=2)+

```

```
labs(x="Residual vs Fitted Values",y="")+
theme_bw()
```

Exam5.1

Example 5.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam5.1 presents the height of 27 seedlots from 4 sites.

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam5.1](#)

Examples

```
data(DataExam5.1)
library(tidyverse)
library(ggplot2)

fm5.4 <- lm(formula = Ht~Site*SeedLot
, data = DataExam5.1
, #, subset
, #, weights
, #, na.action
, method = "qr"
, model = TRUE
, x = FALSE
, y = FALSE
, qr = TRUE
, singular.ok = TRUE
, contrasts = NULL
)

anova(fm5.4)

DataExam5.1 %>%
```



```

dplyr::group_by(Site) %>%
dplyr::summarize(Mean=mean(Ht))

DataExam5.1 %>%
dplyr::group_by(SeedLot) %>%
dplyr::summarize(Mean=mean(Ht))

b<-anova(fm5.4)
Res          <- length(b[["Sum Sq"]])
df           <- 208
MSS         <- 1040
b[["Df"]][Res] <- df
b[["Sum Sq"]][Res] <- MSS*df
b[["Mean Sq"]][Res] <- b[["Sum Sq"]][Res]/b[["Df"]][Res]
b[["F value"]][1:Res-1] <- b[["Mean Sq"]][1:Res-1]/b[["Mean Sq"]][Res]
b[["Pr(>F)"]][Res-1] <- df(b[["F value"]][Res-1],b[["Df"]][Res-1],b[["Df"]][Res])
b

RegCoeff <- function(DataExam5.1)
{
  fm <- lm(formula = Ht ~ SiteMean
           ,data   = DataExam5.1)
           setNames(data.frame(t(coef(fm)))
           ,c("intercept", "slope"))
}
X1 <- DataExam5.1%>%group_by(Site)%>%summarize(sitemean=mean(Ht))
X2 <- filter(DataExam5.1, SeedLot=="13653")
X3 <- filter(DataExam5.1, SeedLot=="13871")
dffig5.1 <-merge(rbind(X2,X3),X1)
ggplot(dffig5.1, aes(x=sitemean, y=Ht, color=SeedLot, shape=SeedLot)) +
geom_point() +
geom_smooth(method=lm, se=FALSE, fullrange=TRUE)+
theme_classic()+
labs(y="Seedlot mean",x="Sitemean")

RegCoeff <- DataExam5.1 %>%
group_by(SeedLot) %>%
do(RegCoeff(.))

SeedLot.Mean <- DataExam5.1 %>%
group_by(SeedLot) %>%
summarize(mean(Ht))

Tab5.10 <- data.frame(RegCoeff,Mean=SeedLot.Mean$'mean(Ht)')
Tab5.10
ggplot(Tab5.10, aes(x=Mean, y=slope))+
geom_point(size=2)+
theme_bw()+
labs(x="Seed Lot Mean", y="Regression Coefficient")

```

Exam5.2

Example 5.2 from Experimental Design & Analysis for Tree Improvement

Description

Exam5.2 presents the height of 37 seedlots from 6 sites.

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam5.2](#)

Examples

```
data(DataExam5.2)
library(tidyverse)
library(ggplot2)

fm5.7 <- aov(formula = height~env*gen
, data = DataExam5.2
, subset
, weights
, na.action
, method = "qr"
, model = TRUE
, x = FALSE
, y = FALSE
, qr = TRUE
, singular.ok = TRUE
, contrasts = NULL
)

anova(fm5.7)

fm5.9 <- aov(formula = height~env*gen
, data = DataExam5.2
, subset
, weights
```

```

#, na.action
, method = "qr"
, model = TRUE
, x = FALSE
, y = FALSE
, qr = TRUE
, singular.ok = TRUE
, contrasts = NULL
)
anova(fm5.9)
b<-anova(fm5.9)
Res          <- length(b[["Sum Sq"]])
df           <- 384
MSS         <- 964
b[["Df"]][Res] <- df
b[["Sum Sq"]][Res] <- MSS*df
b[["Mean Sq"]][Res] <- b[["Sum Sq"]][Res]/b[["Df"]][Res]
b[["F value"]][1:Res-1] <- b[["Mean Sq"]][1:Res-1]/b[["Mean Sq"]][Res]
b[["Pr(>F)"]][Res-1] <- df(b[["F value"]][Res-1],b[["Df"]][Res-1],b[["Df"]][Res])
b

X1<- DataExam5.2 %>%
group_by(env) %>%
summarize(SiteMean=mean(height))

Data5.2new<-merge(DataExam5.2,X1, by.x="env",by.y="env")
RegCoeff <- function(Data5.2new)
{
fm      <- lm(formula = height ~ SiteMean
, data   = Data5.2new)
      setNames(data.frame(t(coef(fm)))
, c("intercept", "slope"))
}
RegCoeff1 <- Data5.2new %>%
group_by(gen) %>%
do(RegCoeff(.))
SeedLot.Mean <- DataExam5.2 %>%
group_by(gen) %>%
summarize(mean(height))
Tab5.14 <- data.frame(RegCoeff1,Mean=SeedLot.Mean$'mean(height)')
Tab5.14
ggplot(Tab5.14,aes(x=Mean,y=slope))+
geom_point(size=2)+
theme_bw()+
geom_text(aes(label=gen),hjust=0, vjust=0)+
labs(x="Seed Lot Mean",y="Regression Coefficient")

Code<-c("a","a","a","a","b","b","b","b","c","d","d","d","d","e","f","g",
"h","h","i","i","j","k","l","m","n","n","n","n","o","p","p","q","r",
"s","t","t","u","v")
Tab5.14$Code<-Code
ggplot(Tab5.14,aes(x=Mean,y=slope))+
geom_point(size=2)+

```

```
theme_bw()+
geom_text(aes(label=Code),hjust=-0.5, vjust=-0.5)+
labs(x="Seed Lot Mean",y="Regression Coefficient")
```

Exam8.1

Example 8.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam8.1 presents the Diameter at breast height (Dbh) of 60 SeedLots under layout of row column design with 6 rows and 10 columns in 18 countries and 59 provinces of 18 selected countries.

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam8.1](#)

Examples

```
data(DataExam8.1)
library(tidyverse)
library(ggplot2)

fm8.4 <- aov(formula      =
  Dbh ~ Inoc+Replication+Error(Replication/Inoc)+Inoc*Country*Province
  ,data      = DataExam8.1
  #, subset
  #, weights
  #, na.action
  , method   = "qr"
  , model    = TRUE
  , x        = FALSE
  , y        = FALSE
  , qr       = TRUE
  , singular.ok = TRUE
  , contrasts = NULL
)
summary(fm8.4)
DataExam8.1 %>%
```

```

dplyr:: group_by(Inoc) %>%
dplyr:: summarize(Mean=mean(Dbh))

DataExam8.1 %>%
  dplyr::group_by(Country)%>%
  dplyr::summarize(Mean=mean(Dbh))

DataExam8.1 %>%
dplyr::group_by(Country,Province)%>%
dplyr::summarize(Mean=mean(Dbh))
library(dae)
RESFit<-data.frame(fittedvalue=fitted.aovlist(fm8.4),residualvalue=proj(fm8.4)$Within[,"Residuals"])
library(ggplot2)
ggplot(RESFit,aes(x=fittedvalue,y=residualvalue))+
geom_point(size=2)+
labs(x="Residuals vs Fitted Values", y="")+
theme_bw()

fm8.6 <- aov(formula      =
Dbh ~ Inoc+Replication+Column+Replication/Row+Replication/Column+Province+Inoc/Province
,data      = DataExam8.1
#, subset
#, weights
#, na.action
, method   = "qr"
, model    = TRUE
, x        = FALSE
, y        = FALSE
, qr       = TRUE
, singular.ok = TRUE
, contrasts = NULL
)
summary(fm8.6)

```

Exam8.1.1

Example 8.1.1 from Experimental Design & Analysis for Tree Improvement

Description

Exam8.1.1 presents the Mixed Effects Analysis of Diameter at breast height (Dbh) of 60 SeedLots under layout of row column design with 6 rows and 10 columns in 18 countries and 59 provinces of 18 selected countries given in Example 8.1.

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam8.1](#)

Examples

```
data(DataExam8.1)
library(tidyverse)
library(emmeans)
library(lme4)
fm8.8<- lmer(formula=
  Dbh~1+Replication+Column+Province+(1|Replication:Row)+(1|Replication:Column)
  ,data = DataExam8.1
  ,REML = TRUE
  ,control = lmerControl()
  ,start = NULL
  , verbose = 0L
  #, subset
  #, weights
  #, na.action
  #,offset
  , contrasts = NULL
  , devFunOnly = FALSE)
anova(fm8.8)
summary(fm8.8)
anova(fm8.8, ddf = "Kenward-Roger")
emmeans::emmeans(fm8.8,specs ="Replication")
emmeans::emmeans(fm8.8,specs ="Column")
emmeans::emmeans(fm8.8,specs ="Province")
RCB1<- aov(Dbh~Province+Replication,data = DataExam8.1)
RCB<- emmeans::emmeans(RCB1,specs="Province")
Mixed<- emmeans::emmeans(fm8.8,specs ="Province")
table8.9<-data.frame(as.data.frame(summary(RCB))[c('emmean', 'SE')],
  as.data.frame(summary(Mixed))[c('emmean', 'SE')])
colnames(table8.9)<- c("RCB(Mean)", "RCB(SE)", "Mixed(Mean)", "Mixed(SE)")
print(table8.9)
```

Exam8.1.2

Example 8.1.2 from Experimental Design & Analysis for Tree Improvement

Description

Exam8.1.2 presents the Analysis of Nested Seedlot Structure of Diameter at breast height (Dbh) of 60 SeedLots under layout of row column design with 6 rows and 10 columns in 18 countries and 59 provinces of 18 selected countries given in Example 8.1.

Author(s)

1. Muhammad Yaseen (<myaseen208@gmail.com>)
2. Sami Ullah (<samiullahuos@gmail.com>)

References

1. Williams, E.R., Matheson, A.C. and Harwood, C.E. (2002). *Experimental Design and Analysis for Tree Improvement*. CSIRO Publishing.

See Also

[DataExam8.1](#)

Examples

```
data(DataExam8.1)
library(tidyverse)
library(emmeans)
fm8.11 <- aov(formula      =
  Dbh~Country*Province
  ,data      = DataExam8.1
  #, subset
  #, weights
  #, na.action
  , method   = "qr"
  , model    = TRUE
  , x        = FALSE
  , y        = FALSE
  , qr       = TRUE
  , singular.ok = TRUE
  , contrasts = NULL
  )
b<-anova(fm8.11)
  Res          <- length(b[["Sum Sq"]])
  df           <- 119
  MSS         <- 0.1951
  b[["Df"]][Res] <- df
  b[["Sum Sq"]][Res] <- MSS*df
  b[["Mean Sq"]][Res] <- b[["Sum Sq"]][Res]/b[["Df"]][Res]
  b[["F value"]][1:Res-1] <- b[["Mean Sq"]][1:Res-1]/b[["Mean Sq"]][Res]
  b[["Pr(>F)"]][Res-1] <- df(b[["F value"]][Res-1],b[["Df"]][Res-1],b[["Df"]][Res])
  b
library(emmeans)
emmeans::emmeans(fm8.11,specs = "Country")
```

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