

Package: ScottKnott (via r-universe)

October 23, 2024

Type Package

Title The ScottKnott Clustering Algorithm

Version 1.3-2

Date 2023-08-30

Author Enio Jelihovschi, José Cláudio Faria and Ivan Bezerra Allaman

Maintainer Ivan Bezerra Allaman <ivanalaman@gmail.com>

Depends R (>= 4.0.0), base

Imports doBy, xtable

Suggests lme4

Description Perform the balanced (Scott and Knott, 1974) and unbalanced <doi:10.1590/1984-70332017v17n1a1> Scott & Knott algorithm.

License GPL (>= 2)

URL <https://github.com/ivanalaman/ScottKnott>,
<https://lec.pro.br/software/pac-r/scottknott>

Encoding UTF-8

LazyLoad yes

LazyData true

Repository <https://ivanalaman.r-universe.dev>

RemoteUrl <https://github.com/ivanalaman/scottknott>

RemoteRef HEAD

RemoteSha 91832327eba163c79d0e2858318bdfa530d5ea8b

Contents

ScottKnott-package	2
boxplot.SK	4
CRD1	6
CRD2	6

FE	7
LSD	7
plot.SK	8
print.SK	10
RCBD	11
SK	12
sorghum	20
SPE	21
SPET	22
SSPE	22
summary	23
xtable.SK	24

Index	25
--------------	-----------

ScottKnott-package	<i>The ScottKnott Clustering Algorithm</i>
--------------------	--

Description

The Scott & Knott clustering algorithm is a very useful clustering algorithm widely used as a multiple comparison method in the Analysis of Variance context, as for example Gates and Bilbro (1978), Bony et al. (2001), Dilson et al. (2002) and Jyotsna et al. (2003).

It was developed by Scott, A.J. and Knott, M. (Scott and Knott, 1974). All methods used up to that date as, for example, the t-test, Tukey, Duncan, Newman-Keuls procedures, have overlapping problems. By overlapping we mean the possibility of one or more treatments to be classified in more than one group, in fact, as the number of treatments reach a number of twenty or more, the number of overlappings could increase as reaching 5 or greater what makes almost impossible to the experimenter to really distinguish the real groups to which the means should belong. The Scott & Knott method does not have this problem, what is often cited as a very good quality of this procedure.

The Scott & Knott method make use of a clever algorithm of cluster analysis, where, starting from the the whole group of observed mean effects, it divides, and keep dividing the sub-groups in such a way that the intersection of any two groups formed in that manner is empty.

Using their own words ‘we study the consequences of using a well-known method of cluster analysis to partition the sample treatment means in a balanced design and show how a corresponding likelihood ratio test gives a method of judging the significance of difference among groups obtained’.

Many studies, using the method of Monte Carlo, suggest that the Scott Knott method performs very well compared to other methods due to fact that it has high power and type I error rate almost always in accordance with the nominal levels. The **ScottKnott** package performs this algorithm starting either from vectors, matrices or data.frames joined as default, a aov, aovlist, lm and lmer resulting object of previous analysis of variance. The results are given in the usual way as well as in graphical way using thermometers with diferent group colors.

In a few words, the test of Scott & Knott is a clustering algorithm used as an one of the alternatives where multiple comparizon procedures are applied with a very important and almost unique characteristic: it does not present overlapping in the results.

As of version 1.2-8, the ScottKnott package is able to analyze unbalanced data based on the article 'Adjusting the Scott-Knott cluster analyzes for unbalanced designs' by Conrado et al.

Author(s)

Enio Jelihovschi (<eniojelihovs@gmail.com>)
Jose Claudio Faria (<joseclaudio.faria@gmail.com>)
Ivan Bezerra Allaman (<ivanalaman@gmail.com>)

References

- Bony S., Pichon N., Ravel C., Durix A., Balfourier F., Guillaumin J.J. 2001. The Relationship between Mycotoxin Synthesis and Isolate Morphology in Fungal Endophytes of *Lolium perenne*. *New Phytologist*, **1521**, 125-137.
- Borges L.C., FERREIRA D.F. 2003. Poder e taxas de erro tipo I dos testes Scott-Knott, Tukey e Student-Newman-Keuls sob distribuicoes normal e nao normais dos residuos. Power and type I errors rate of Scott-Knott, Tukey and Student-Newman-Keuls tests under normal and no-normal distributions of the residues. *Rev. Mat. Estat.*, Sao Paulo, **211**: 67-83.
- Calinski T., Corsten L.C.A. 1985. Clustering Means in ANOVA by Simultaneous Testing. *Biometrics*, **411**, 39-48.
- Da Silva E.C, Ferreira D.F, Bearzoti E. 1999. Evaluation of power and type I error rates of Scott-Knott's test by the method of Monte Carlo. *Cienc. agrotec.*, Lavras, **23**, 687-696.
- Dilson A.B, David S.D., Kazimierz J., William W.K. 2002. Half-sib progeny evaluation and selection of potatoes resistant to the US8 genotype of *Phytophthora infestans* from crosses between resistant and susceptible parents. *Euphytica*, **125**, 129-138.
- Gates C.E., Bilbro J.D. 1978. Illustration of a Cluster Analysis Method for Mean Separation. *Agron J*, **70**, 462-465.
- Wilkinson, G.N, Rogers, C.E. 1973. Journal of the Royal Statistical Society. Series C (Applied Statistics), Vol. 22, No. 3, pp. 392-399.
- Jyotsna S., Zettler L.W., van Sambeek J.W., Ellersieck M.R., Starbuck C.J. 2003. Symbiotic Seed Germination and Mycorrhizae of Federally Threatened *Platanthera praeclara* Orchidaceae. *American Midland Naturalist*, **1491**, 104-120.
- Ramalho M.A.P., Ferreira DF, Oliveira AC 2000. *Experimentacao em Genetica e Melhoramento de Plantas*. Editora UFLA.
- Scott R.J., Knott M. 1974. A cluster analysis method for grouping mans in the analysis of variance. *Biometrics*, **30**, 507-512.
- Conrado, T. V., Ferreira, D. F., Scapim, C. A., and Maluf, W. R. "Adjusting the Scott-Knott cluster analyses for unbalanced designs." *Crop Breeding and Applied Biotechnology* **17.1** (2017): 1-9.

 boxplot.SK

Boxplot SK Objects

Description

S3 method to plot SK objects.

Usage

```
## S3 method for class 'SK'
boxplot(x,
        mean.type = c('line', 'point', 'none'),
        xlab      = NULL,
        mean.col  = 'gray',
        mean.pch  = 1,
        mean.lwd  = 1,
        mean.lty  = 1,
        args.legend = NULL, ...)
```

Arguments

<code>x</code>	A SK object.
<code>mean.type</code>	The type of mean must be plotted. O default is "line".
<code>xlab</code>	A label for the 'x' axis.
<code>mean.col</code>	A vector of colors for the means representation.
<code>mean.pch</code>	A vector of plotting symbols or characters. Only if type are "point".
<code>mean.lwd</code>	Line width of mean.
<code>mean.lty</code>	Line type of mean. Only if type are "line".
<code>args.legend</code>	List of additional arguments to be passed to legend; The default is NULL.
<code>...</code>	Optional plotting parameters.

Details

The `boxplot.SK` function is a S3 method to plot 'SK' objects. The difference to generic function is the Scott & Knott inference under frame and the plot of means within box.

Author(s)

Jose Claudio Faria (<joseclaudio.faria@gmail.com>
 Enio Jelihovschi (<eniojelihovs@gmail.com>
 Ivan Bezerra Allaman (<ivanalaman@gmail.com>)

References

Murrell, P. (2005) *R Graphics*. Chapman and Hall/CRC Press.

See Also[boxplot](#)**Examples**

```
##
## Examples: Completely Randomized Design (CRD)
## More details: demo(package='SK')
##

library(ScottKnott)
data(CRD1)

## From: formula
# Simple!
sk1 <- SK(y ~ x,
          data=CRD1$dfm,
          which='x')
boxplot(sk1)

# A little more elaborate!
boxplot(sk1,
        mean.lwd=1.3,
        mean.col='red')

# A little more!
boxplot(sk1,
        mean.lwd=1.3,
        mean.lty=2,
        mean.col='red',
        args.legend=list(x='bottomleft'))

# With point type!
boxplot(sk1,
        mean.type='point')

boxplot(sk1,
        mean.type='point',
        mean.pch=19,
        cex=1.5,
        mean.col='red')

# With other point
boxplot(sk1,
        mean.type='point',
        mean.pch='+',
        cex=2,
        mean.col='blue',
        args.legend=list(x='bottomleft'))
```

CRD1	<i>Completely Randomized Design (CRD)</i>
------	---

Description

A list illustrating the resources of **ScottKnott** package related to Completely Randomized Design ('CRD').

Usage

```
data(CRD1)
CRD1
```

Details

A simulated data to model a Completely Randomized Design ('CRD') of 4 factor levels and 6 repetitions.

CRD2	<i>Completely Randomized Design (CRD)</i>
------	---

Description

A list illustrating the resources of **ScottKnott** package related to Completely Randomized Design ('CRD').

Usage

```
data(CRD2)
CRD2
```

Details

A simulated data to model a Completely Randomized Design ('CRD') of 45 factor levels and 4 repetitions.

FE	<i>Factorial Experiment (FE)</i>
----	----------------------------------

Description

A list illustrating the resources of **ScottKnott** package related to Factorial Experiment ('FE').

Usage

```
data(FE)  
FE
```

Details

A simulated data to model a Factorial Experiment ('FE') with 3 factors, 2 levels per factor and 4 blocks.

LSD	<i>Latin Squares Design (LSD)</i>
-----	-----------------------------------

Description

A list illustrating the resources of **ScottKnott** package related to Latin Squares Design ('LSD').

Usage

```
data(LSD)  
LSD
```

Details

A simulated data to model a Latin Squares Design ('LSD') with 5 factor levels 5 rows and 5 columns.

plot.SK

*Plot SK objects***Description**

S3 method to plot SK objects.

Usage

```
## S3 method for class 'SK'
plot(x,
      result          = TRUE,
      replicates      = TRUE,
      pch              = 19,
      col              = NULL,
      xlab             = NULL,
      ylab             = NULL,
      xlim             = NULL,
      ylim             = NULL,
      axisx            = TRUE,
      axisy            = TRUE,
      id.lab           = NULL,
      id.las           = 1,
      yl               = TRUE,
      yl.lty           = 3,
      yl.col           = 'gray',
      dispersion       = c('none', 'mm', 'sd', 'ci', 'cip'),
      d.lty            = 1,
      d.col            = 'black',
      title            = '', ...)
```

Arguments

x	A SK object.
result	The result of the test (letters) should be visible.
replicates	The number of replicates should be visible.
pch	A vector of plotting symbols or characters.
col	A vector of colors for the means representation.
xlab	A label for the 'x' axis.
ylab	A label for the 'y' axis.
xlim	The 'x' limits of the plot.
ylim	The 'y' limits of the plot.
axisx	Axis x? If 'TRUE' you must accept the default, otherwise, you must customize.
axisy	Axis y? If 'TRUE' you must accept the default, otherwise, you must customize.

id.lab	Factor level names at 'x' axis.
id.las	Factor level names written either horizontally or vertically.
yl	Horizontal (reference) line connecting the circle to the 'y' axis.
yl.lty	Line type of 'yl'.
yl.col	Line color of 'yl'.
dispersion	Vertical line through the circle (mean value) linking the minimum to the maximum of the factor level values corresponding to that mean value. Other options are: sd (standard deviation), ci (confidence interval), cip (pooled confidence interval) and none.
d.lty	Line type of dispersion.
d.col	A vector of colors for the line type of dispersion.
title	A title for the plot.
...	Optional plotting parameters.

Details

The plot.SK function is a S3 method to plot 'Scott and Knott' objects. It generates a series of points (the means) and a vertical line showing the dispersion of the values corresponding to each group mean. The ci option is calculated utilizing each treatment variance as estimating of population variance. The cip option is calculated utilizing the means square error (MSE) as estimating of population variance.

Author(s)

Jose Claudio Faria (<joseclaudio.faria@gmail.com>
 Enio Jelihovschi (<eniojelihovs@gmail.com>
 Ivan Bezerra Allaman (<ivanalaman@gmail.com>)

References

Murrell, P. (2005) *R Graphics*. Chapman and Hall/CRC Press.

See Also

[plot](#)

Examples

```
##
## Examples: Completely Randomized Design (CRD)
## More details: demo(package='SK')
##

library(ScottKnott)
data(CRD2)

## From: formula
sk1 <- with(CRD2,
```

```
      SK(y ~ x,
         data=dfm,
         which='x'))

old.par <- par(mar=c(6, 3, 6, 2))
plot(sk1,
      id.las=2)

plot(sk1,
      yl=FALSE,
      disp='sd',
      id.las=2)

## From: aov
av <- with(CRD2,
           aov(y ~ x,
              data=dfm))
summary(av)

sk2 <- SK(x=av,
          which='x')
plot(sk2,
      disp='sd',
      yl=FALSE,
      id.las=2)

# From: lm
av_lm <- with(CRD2,
             lm(y ~ x,
               data=dfm))

sk3 <- SK(x=av_lm,
          which='x')

par(mfrow=c(2, 1))
plot(sk3,
      disp='ci',
      id.las=2,
      yl=FALSE)

plot(sk3,
      disp='cip',
      id.las=2,
      yl=FALSE)

par(mfrow=c(1, 1))
par(old.par)
```

Description

Returns (and prints) a list for objects of class SK.

Usage

```
## S3 method for class 'SK'
print(x, digits = 2L,...)
```

Arguments

x	A given object of the class SK.
digits	Minimal number of <code>_significant_</code> digits. The default is 2.
...	Further arguments (require by generic).

Author(s)

Jose Claudio Faria (<joseclaudio.faria@gmail.com>
 Enio G. Jelihovschi (<eniojelihovs@gmail.com>
 Ivan Bezerra Allaman (<ivanalaman@gmail.com>)

See Also

[SK](#)

Examples

```
data(RCBD)

sk <- with(RCBD,
           SK(y ~ blk + tra,
             data=dfm,
             which='tra'))

sk
```

RCBD

Randomized Complete Block Design (RCBD)

Description

A list illustrating the resources of **ScottKnott** package related to Randomized Complete Block Design ('RCBD').

Usage

```
data(RCBD)
RCBD
```

Details

A simulated data to model a Randomized Complete Block Design ('RCBD') of 5 factor levels, 4 blocks and 4 factor levels repetitions one in each block.

 SK

The SK Test for Single Experiments

Description

These are methods for objects of class `formula`, `lm`, `aov`, `aovlist` and `lmerMod` for single, factorial, split-plot and split-split-plot experiments.

Usage

```
SK(x, ...)

## S3 method for class 'formula'
SK(formula,
    data      = NULL,
    which     = NULL,
    f11       = NULL,
    f12       = NULL,
    error     = NULL,
    sig.level = .05,
    round     = 2,
    ...)

## S3 method for class 'lm'
SK(x,
    which     = NULL,
    f11       = NULL,
    f12       = NULL,
    error     = NULL,
    sig.level = .05,
    round     = 2,
    ...)

## S3 method for class 'aovlist'
SK(x,
    which     = NULL,
    f11       = NULL,
    f12       = NULL,
```

```

        error          = NULL,
        sig.level      = .05,
        round         = 2,
        ...)

## S3 method for class 'lmerMod'
SK(x,
    which            = NULL,
    fl1              = NULL,
    fl2              = NULL,
    error            = NULL,
    sig.level        = .05,
    round            = 2,
    ...)

```

Arguments

x, formula	A formula, lm, aov, aovlist and lmerMod class object. Objects of the formula class follow “response variable ~ predicted variable.
data	A object of the data.frame class. Use only objects of formula class.
which	The name of the treatment to be used in the comparison. The name must be inside quoting marks.
fl1	A vector of length 1 giving the level of the first factor in nesting order tested.
fl2	A vector of length 1 giving the level of the second factor in nesting order tested.
error	The error to be considered. If from experiment at split plot or split-split plot pay attention! See details!
sig.level	Level of Significance used in the SK algorithm to create the groups of means. The default value is 0.05.
round	Integer indicating the number of decimal places.
...	Potential further arguments (required by generic).

Details

The function SK returns an object of class SK containing the groups of means plus other necessary variables for summary and plot.

The generic functions `summary` and `plot` are used to obtain and print a summary and a plot of the results.

The error arguments may be used whenever the user want a specific error other than the experimental error. At the split plot and split-split plot experiment, combination of error may be specified with "/" in the sequence of the which argument. For example, a object of aovlist class, a possible combination would be `error = 'Within/blk:plot'` at case block split plot experiment with which = 'subplot:plot' argument.

Value

The function SK returns a list of the class SK with the slots:

out	A list storing the result of Scott & Knott test.
info	A list storing the descriptive statistics.
stat	A matrix with the statistics of each clustering process.
clus	A list with the groups formed in each clustering process.

Author(s)

Jose Claudio Faria (<joseclaudio.faria@gmail.com>)

Enio Jelihovschi (<eniojelihovs@gmail.com>)

Ivan Bezerra Allaman (<ivanalaman@gmail.com>)

References

Miller, R.G. (1981) *Simultaneous Statistical Inference*. Springer.

Ramalho M.A.P, Ferreira D.F and Oliveira A.C. (2000) *Experimentacao em Genetica e Melhoramento de Plantas*. Editora UFLA.

Steel, R.G., Torrie, J.H and Dickey D.A. (1997) *Principles and procedures of statistics: a biometrical approach*. Third Edition.

Yandell, B.S. (1997) *Practical Data Analysis for Designed Experiments*. Chapman and Hall.

Examples

```
##
## Examples: Randomized Complete Block Design (RCBD)
## More details: demo(package='SK')
##

## The parameters can be: formula, aov, lm, aovlist and lmerMod

data(RCBD)

## From: formula
sk1 <- with(RCBD,
            SK(y ~ blk + tra,
              data=dfm,
              which='tra'))
summary(sk1)

## From: merMod
## This class is specific of the lme4 package.
## Not run:
if(require(lme4)){
  lmer1 <- with(RCBD,
               lmer(y ~ (1|blk) + tra,
                   data=dfm))
}
```

```
    sk2 <- SK(lmer1,
              which='tra')
  summary(sk2)
}

## End(Not run)
##
## Example: Latin Squares Design (LSD)
## More details: demo(package='SK')
##

data(LSD)

## From: formula
sk3 <- with(LSD,
            SK(y ~ rows + cols + tra,
              data=dfm,
              which='tra'))
summary(sk3)

## From: aov
av1 <- with(LSD,
            aov(y ~ rows + cols + tra,
              data=dfm))

sk4 <- SK(av1,
          which='tra')
summary(sk4)

## From: lm
lm1 <- with(LSD,
            lm(y ~ rows + cols + tra,
              data=dfm))

sk5 <- SK(lm1,
          which='tra')
summary(sk5)

##
## Example: Factorial Experiment (FE)
## More details: demo(package='SK')
##

data(FE)
## From: formula
## Main factor: N
sk6 <- with(FE,
            SK(y ~ blk + N*P*K,
              data=dfm,
              which='N'))
summary(sk6)

## Nested: p1/N
```

```

# From: formula
n_sk1 <- with(FE,
              SK(y ~ blk + N*P*K,
                 data=dfm,
                 which='P:N',
                 f11=1))
summary(n_sk1)

## Nested: p2/N
# From: lm
lm2 <- with(FE,
            lm(y ~ blk + N*P*K,
               dfm))

n_sk2 <- with(FE,
              SK(lm2,
                 which='P:N',
                 f11=2))
summary(n_sk2)

## Nested: n1/P
# From: aov
av2 <- with(FE,
            aov(y ~ blk + N*P*K,
               dfm))

n_sk3 <- with(FE,
              SK(av2,
                 which='N:P',
                 f11=1))
summary(n_sk3)

# From: merMod
## Not run:
if(require(lme4)){
  lmer2 <- with(FE,
               lmer(y ~ (1|blk) + N*P*K,
                   dfm))

  n_sk4 <- with(FE,
                SK(lmer2,
                   which='N:P',
                   f11=1))
  summary(n_sk4)
}

## End(Not run)

##
## Example: Split-plot Experiment (SPET)
## More details: demo(package='SK')
##
data(SPET)

```



```

## From lm
lm3 <- with(SPET,
            lm(y ~ blk*tra + tra*year,
              dfm))

# crotgrantiana/year
sp_sk1 <- SK(lm3,
            which='tra:year',
            f11=1)
summary(sp_sk1)

# year1/tra
# It is necessary to set year error with trat error in the order of the "which" argument.
# It is necessary to inform how to combine the errors
sp_sk2 <- SK(lm3,
            which='year:tra',
            error='Residuals/blk:tra',
            f11=1)
summary(sp_sk2)

# From merMod
# Only tra
## Not run:
if(require(lme4)){
  lmer3 <- with(SPET,
              lmer(y ~ blk + (1|blk:tra) + tra*year,
                  dfm))

  # comparison only tra
  sp_sk3 <- SK(lmer3,
              which = 'tra',
              error = 'blk:tra')
  summary(sp_sk3)

  # year1/tra
  sp_sk4 <- SK(lmer3,
              which='year:tra',
              error='Residual/blk:tra',
              f11=1)
  summary(sp_sk4)
}

## End(Not run)

## Example: Split-split-plot Experiment (SSPE)
## More details: demo(package='SK')
##

data(SSPE)
## From: formula
## Main factor: P
## It is necessary to inform the appropriate error for the test

```

```

ssp_sk1 <- with(SSPE,
               SK(y ~ blk + P*SP*SSP + Error(blk/P/SP),
                  data=dfm,
                  which='P',
                  error='blk:P'))
summary(ssp_sk1)

## Main factor: SP
## It is necessary to inform the appropriate error for the test
ssp_sk2 <- with(SSPE,
               SK(y ~ blk + P*SP*SSP + Error(blk/P/SP),
                  data=dfm,
                  which='SP',
                  error='blk:P:SP'))
summary(ssp_sk2)

## Main factor: SSP
ssp_sk3 <- with(SSPE,
               SK(y ~ blk + P*SP*SSP + Error(blk/P/SP),
                  data=dfm,
                  which='SSP'))
summary(ssp_sk3)

## From: aov
## Main factor: SSP
av3 <- with(SSPE,
            aov(y ~ blk + P*SP*SSP + Error(blk/P/SP),
                data=dfm))

ssp_sk4 <- SK(av3,
              which='SSP')
summary(ssp_sk4)

## Nested: p1/SP
## It is necessary to inform the appropriate error for the test
ssp_sk5 <- SK(av3,
              which='P:SP',
              error='blk:P:SP',
              f11=1)
summary(ssp_sk5)

## Nested: p1/SSP
ssp_sk6 <- SK(av3,
              which='P:SSP',
              f11=1)
summary(ssp_sk6)

## Nested: p1/sp1/SSP
## Testing SSP inside of level one of P and level one of SP
ssp_sk7 <- SK(av3,
              which='P:SP:SSP',
              f11=1,
              f12=1)

```

```
summary(ssp_sk7)

## Nested: p2/sp1/SSP
ssp_sk8 <- SK(av3,
              which='P:SP:SSP',
              f11=2,
              f12=1)
summary(ssp_sk8)

## Nested: sp1/P
## It is necessary to inform the appropriate error for the test
ssp_sk9 <- SK(av3,
              which='SP:P',
              error='blk:P:SP/blk:P',
              f11=1)

summary(ssp_sk9)

## Nested: ssp1/SP
ssp_sk10 <- SK(av3,
               which='SSP:SP',
               error='Within/blk:P:SP',
               f11=1)
summary(ssp_sk10)

## Nested: ssp1/sp1/P
## It is necessary to inform the appropriate error for the test
ssp_sk11 <- SK(av3,
               which='SSP:SP:P',
               error='Within/blk:P:SP/blk:P',
               f11=1,
               f12=1)
summary(ssp_sk11)

## UNBALANCED DATA
## The average are adjusted by "Least-Square-Means" methodology.
## From: formula
data(CRD2)

uCRD2 <- CRD2$dfm
uCRD2[c(3, 5, 10, 44, 45), 3] <- NA

usk1 <- SK(y ~ x,
           data=uCRD2,
           which='x')
summary(usk1)

## From: lm
u1m1 <- lm(y ~ x,
           data=uCRD2)

usk2 <- SK(u1m1,
           which='x')
```

```

summary(usk2)

## Factorial Experiments
## Nested: p1/N
# From: lm

uFE <- FE$dfm
uFE[c(3, 6, 7, 20, 31, 32), 5] <- NA

u1m2 <- lm(y ~ blk + N*P*K,
           uFE)

## Nested: p1/N
usk3 <- SK(u1m2,
           data=uFE,
           which='P:N',
           f11=1)
summary(usk3)

## Nested: p2/n2/K
usk4 <- SK(u1m2,
           data=uFE,
           which='P:N:K',
           f11=2,
           f12=2)
summary(usk4)

```

sorghum

Completely Randomized Design (CRD)

Description

The experiment consists of 16 treatments (cultivars) of sorghum conducted in a balanced squared lattice design and the yield by plot (kg/plot).

Usage

```

data(sorghum)
sorghum

```

Format

An incomplete balanced block design with 4 blocks, 16 treatments, and 5 repetitions, that is, the yield of each treatment is measured 5 times. `sorghum` is a list with 4 elements. The first `'tr'` is a factor of length 80 with 16 levels describing the treatments. The second `'dm'` is data.frame describing the design matrix. Its columns are `'x'`, `'bl'` (blocks) and `'r'` repetitions. The third `'y'` is a numeric vector the yields. The fourth `'dfm'` is a data frame with four columns. The first three columns are the design matrix and the fourth is `'y'`.

Details

The experiment was conducted at EMBRAPA Milho e Sorgo (The Brazilian Agricultural Research Corporation, Corn and Sorghum section).

Source

Ramalho, M.A.P. and Ferreira, D.F. and Oliveira, A.C. (2000). Experimentacao em Genetica e Melhoramento de Plantas. Editora UFLA, Lavras, Brazil, page 167.

Examples

```
library(ScottKnott)

data(sorghum)

av <- aov(y ~ r/bl + x,
         data=sorghum$dfm)

sk <- SK(av,
        which='x',
        sig.level=0.05)

summary(sk)

plot(sk)
```

SPE

Split-plot Experiment (SPE)

Description

A list to illustrate the resources of **ScottKnott** package related to Split-plot Experiment ('SPE').

Usage

```
data(SPE)
SPE
```

Details

A simulated data to model a Split-plot Experiment ('SPE') with 3 plots, each one split 4 times and 6 repetitions per split.

SPET

Split-plot Experiment in Time (SPET)

Description

The experiment consists of 8 treatments (7 leguminous cover crops and maize) in a Randomized Complete Block Design ('RCBD') and the yield by plot (kg/plot).

Usage

```
data(SPET)
SPET
```

Source

Gomes, F.P. (1990). Curso de Estatística Experimental. 13 ed. Editora NOBEL, Piracicaba, Brazil, page 157.

SSPE

Split-split-plot Experiment (SSPE)

Description

A list to illustrate the resources of **ScottKnott** package related to Split-split-plot Experiment ('SSPE').

Usage

```
data(SSPE)
SSPE
```

Details

A simulated data to model a Split-split-plot Experiment ('SSPE') with 3 plots, each one split 3 times, each split, split again 5 times and 4 repetitions per split-split.

summary

Summary Method for SK Objects

Description

Returns (and prints) a summary list for SK objects.

Usage

```
## S3 method for class 'SK'  
summary(object,  
  ...)
```

Arguments

object A given object of the class SK.
... Potential further arguments (required by generic).

Author(s)

Jose Claudio Faria (<joseclaudio.faria@gmail.com>
Enio Jelihovschi (<eniojelihovs@gmail.com>
Ivan Bezerra Allaman (<ivanalaman@gmail.com>

References

Chambers, J.M. and Hastie, T.J. (1992) *Statistical Models in S*. Wadsworth and Brooks/Cole.

See Also

[SK](#)

Examples

```
##  
## Examples: Completely Randomized Design (CRD)  
## More details: demo(package='SK')  
##  
  
data(CRD2)  
## From: formula  
sk1 <- with(CRD2,  
  SK(y ~ x,  
    data=dfm,  
    which='x',  
    id.trim=5))  
  
summary(sk1)
```

xtable.SK	<i>xtable method for SK objects.</i>
-----------	--------------------------------------

Description

Convert an SK object to an xtable.SK object, which can then be printed as a LaTeX or HTML table. This function is an additional method to xtable function of **xtable** package.

Usage

```
## S3 method for class 'SK'  
xtable(x, ...)
```

Arguments

x	A given object of the class SK.
...	Further arguments (require by xtable::xtable).

Author(s)

Jose Claudio Faria (<joseclaudio.faria@gmail.com>
Enio G. Jelihovschi (<eniojelihovs@gmail.com>
Ivan Bezerra Allaman (<ivanalaman@gmail.com>

See Also

[xtable](#)

Examples

```
data(RCBD)  
## Not run:  
  if(require(xtable)){  
    lm1 <- with(RCBD,  
               lm(y ~ blk + tra,  
                  data=dfm))  
  
    sk1 <- SK(lm1,  
             which='tra')  
    tb <- xtable(sk1)  
    print(tb)  
  }  
  
## End(Not run)
```


Index

- * **SK**
 - print.SK, [10](#)
 - xtable.SK, [24](#)
 - * **datasets**
 - CRD1, [6](#)
 - CRD2, [6](#)
 - FE, [7](#)
 - LSD, [7](#)
 - RCBD, [11](#)
 - sorghum, [20](#)
 - SPE, [21](#)
 - SPET, [22](#)
 - SSPE, [22](#)
 - * **design**
 - ScottKnott-package, [2](#)
 - * **htest**
 - ScottKnott-package, [2](#)
 - * **package**
 - boxplot.SK, [4](#)
 - plot.SK, [8](#)
 - print.SK, [10](#)
 - ScottKnott-package, [2](#)
 - SK, [12](#)
 - summary, [23](#)
 - xtable.SK, [24](#)
 - * **tree**
 - ScottKnott-package, [2](#)
 - * **univar**
 - ScottKnott-package, [2](#)
- boxplot, [5](#)
boxplot.SK, [4](#)
- CRD1, [6](#)
CRD2, [6](#)
- FE, [7](#)
- LSD, [7](#)
- plot, [9](#)
- plot.SK, [8](#)
print.SK, [10](#)
- RCBD, [11](#)
- ScottKnott (ScottKnott-package), [2](#)
ScottKnott-package, [2](#)
SK, [11](#), [12](#), [23](#)
sorghum, [20](#)
SPE, [21](#)
SPET, [22](#)
SSPE, [22](#)
summary, [23](#)
- xtable, [24](#)
xtable.SK, [24](#)