

BeSTMod2_SplitPlotDesign.R

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#####
## BeSTMod2_SplitPlotDesign.R
## Author : Miranda Mortlock
## For      BeST module 2
## You need R and RStudio installed on your computer
## Split plot design
## Code to assist randomising this design
## Customise for your experiment
##
## For a number of treatments (more than 2 treatments)
## and randomised with blocking
## This is a restriction in the design,
## We have Main-plots and sub-plots
## Two sized units across the site
## Randomising using R code
##
#####

## Remember all lines with a hash
## are comments to help you

# Need this package
library(agricolae)

# We will use the design.split function
## This structure command gives the function:
## str(design.split)

## I have copied the function here for you to see,
## The hash at the start of the line makes it a comment
## This generates split plot design.
## "Random" uses the methods of number generation in R. The seed is
## by set.seed(seed, kinds).

## design.split(trt1, trt2,r=NULL, design=c("rcbd","crd","lsd"),serie = 2,
##             seed = 0, kinds = "Super-Duper", first=TRUE)

## str(design.split)
## looking at the function behind the split plot

## function (trt1, trt2, r = NULL, design = c("rcbd", "crd", "lsd"), serie = 2, seed = 0,
## kinds = "Super-Duper", first = TRUE)
#####
### To change for your own design - CHANGE these two lines

# trt1      Treatments in Main Plots
```

```

# trt2      Treatments in Subplots
# r         Replications or blocks
# design    Experimental design
# serie     number plot, 1: 11,12; 2: 101,102; 3: 1001,1002
# seed      seed
# kinds     method for to randomize
# first     TRUE or FALSE - randomize rep 1

#####
### Consider we have Tillage and Nitrogen within
### With 3 blocks
#####
## Here you set your two factors:

t1 <- c("Ploughing", "No-till")
t2 <- c("Nitrogen0", "Nitrogen1","Nitrogen2")
outSplit <- design.split(t1,t2,r=3,serie=2,seed=45,kinds ="Super-Duper") #seed=45

# To print the design to the Console

outSplit

```

```

## $parameters
## $parameters$design
## [1] "split"
##
## $parameters[[2]]
## [1] TRUE
##
## $parameters$trt1
## [1] "Ploughing" "No-till"
##
## $parameters$applied
## [1] "rcbd"
##
## $parameters$r
## [1] 3
##
## $parameters$serie
## [1] 2
##
## $parameters$seed
## [1] 45
##
## $parameters$kinds
## [1] "Super-Duper"
##
##
## $book
##   plots  plots  block      t1      t2
## 1   101     1     1  No-till Nitrogen2
## 2   101     2     1  No-till Nitrogen0

```

```

## 3  101    3    1  No-till Nitrogen1
## 4  102    1    1  Ploughing Nitrogen1
## 5  102    2    1  Ploughing Nitrogen2
## 6  102    3    1  Ploughing Nitrogen0
## 7  103    1    2  No-till Nitrogen1
## 8  103    2    2  No-till Nitrogen0
## 9  103    3    2  No-till Nitrogen2
## 10 104    1    2  Ploughing Nitrogen2
## 11 104    2    2  Ploughing Nitrogen1
## 12 104    3    2  Ploughing Nitrogen0
## 13 105    1    3  Ploughing Nitrogen0
## 14 105    2    3  Ploughing Nitrogen1
## 15 105    3    3  Ploughing Nitrogen2
## 16 106    1    3  No-till Nitrogen1
## 17 106    2    3  No-till Nitrogen0
## 18 106    3    3  No-till Nitrogen2

```

```
## the following gives the design output
```

```
SplitPlotbook<-outSplit$book  # field book
```

```
write.csv(SplitPlotbook,"Splitplotbook.csv",row.names=FALSE) # write to a csv file
```

```
## you now have the randomisation as a *.csv file
```

```
##### Saved as a csv file
```

```
## Next steps:
```

```
## 1 the randomisation (eg from this output)
```

```
## 2 the plot layout as in the glass house or field
```

```
## 3 your data sheet in a separate worksheet
```

```
## 4 metadata - the description of your variables and treatments
```

```
## 5 save this file and back it up
```