Package: Boptbd (via r-universe)

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Title Bayesian Optimal Block Designs

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Depends R (>= 3.4.0), MASS, Matrix, igraph, tcltk

Description Computes Bayesian A- and D-optimal block designs under the linear mixed effects model settings using block/array exchange algorithm of Debusho, Gemechu and Haines (2018) <doi:10.1080/03610918.2018.1429617> where the interest is in a comparison of all possible elementary treatment contrasts. The package also provides an optional method of using the graphical user interface (GUI) R package 'tcltk' to ensure that it is user friendly.

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Contents

`Boptbd` *Bayesain optimal block designs*

Description

The function `Boptbd` is used to compute Bayesian A- or D-optimal block designs under the linear mixed effects model settings using array/block exchange algorithm of Debusho, Gemechu and Haines (2018).

Usage

```
Boptbd(trt.N, blk.N, alpha, beta, nrep, brep, itr.cvrgval, Optcrit = "", ...)

## Default S3 method:
Boptbd(trt.N, blk.N, alpha, beta, nrep, brep, itr.cvrgval, Optcrit = "", ...)
## S3 method for class 'Boptbd'
print(x, ...)
## S3 method for class 'Boptbd'
summary(object, ...)
```

Arguments

`trt.N`	integer, specifying number of treatments, `v`.
`blk.N`	integer, specifying number of blocks, `b`.
`alpha`	numeric, representing the shape parameter of beta distribution.
`beta`	numeric, representing the shape parameter of beta distribution.
`nrep`	integer, specifying number of replications of the optimization procedure.
`brep`	integer, specifying number of Monte Carlo samples from a prior beta distribution.
`itr.cvrgval`	integer, specifying number of iterations required for convergence during the block exchange procedure.
`Optcrit`	character, specifying the optimality criteria to be used. `Optcrit` takes the letter `"A"` and `"D"` for Bayesian `A-` and `D-`optimal block designs, respectively.
`x`	the object to be printed.
`object`	an object of class `"Boptbd"`.
`...`	not used.

Details

`Boptbd` computes Bayesian optimal block designs where the interest is in a comparison of all possible elementary treatment contrasts. Under the linear mixed effects model setting, where the block effects are assumed to be random, the treatment information matrix (C-matrix) is dependent on the unknown parameter `rho` (ratio of unknown variance components of random error and block effects). A Bayesian optimal design extends the locally optimal approach by specifying a prior distribution for the parameter `rho`. `Boptbd` function computes Bayesian `A-` and `D-`optimal block designs via calling of two sub-functions `Baoptbd` and `Bdoptbd`, respectively. Each function requires an initial connected block designs generated using the function `intcbd`.

The minimum value of `trt.N` and `blk.N` is 3 and `trt.N` should be less than or equal to `blk.N - 1`.

`Boptbd` perform the block exchange procedure through deletion and addition of candidate block at a time and selects a design with best block exchange with respect to the optimality criterion value. It uses the steps of Bueno Filho and Gilmour (2007) for numerical evaluation of the Bayesian criterion values.

`nrep` takes a value of greater than or equal to 2. However, to ensure optimality of the resultant design, the `nrep` should be greater than or equal to 10 and in addition, as `trt.N` and `blk.N` increase, to ensure optimality of resultant design, it is advised to further increase the value of `nrep` up to greater than or equal to 100. `brep` takes a value of greater than or equal to 2. As `brep` value increase, the execution time to generate Bayesian optimal design increase.

`itr.cvrgval` number of iterations during exchange procedure. It takes a value between 2 and `blk.N`. It is used to speedup the computer search time by setting how long should the user should wait for the exchange process to obtain any different (if any) design than the one that was produced as the result of the preceding exchange of the current array in the initial design with candidate array. This is mainly effective if `blk.N` is very large. For example `itr.cvrgval = 2`, means the exchange procedure will jump to the next block test if the exchange of the two preceding blocks with candidate block results with the same efficient designs. The function will not give error message if the users set `itr.cvrgval > blk.N` and it will automatically set `itr.cvrgval = blk.N`. The smaller the `itr.cvrgval` means the faster the exchange procedure is, but this will reduce the chance of getting optimal block design and users are advised to set `itr.cvrgval` closer to `blk.N`.

Value

Returns the resultant Bayesian A- or D-optimal block design with its corresponding score value and parametric combination saved in excel file in a temporary directory. In addition, the function `Boptbd` displays the graphical layout of the resultant Bayesian optimal block designs. Specifically:

`call`	the method call.
`v`	number of treatments.
`b`	number of blocks
`alpha`	alpha value.
`beta`	beta value.
`nrep`	number of replications of the optimization procedure.
`itr.cvrgval`	number of iterations required for convergence during the exchange procedure.
`Optcrit`	optimality criteria.
`brep`	umber of Monte Carlo samples from a prior beta distribution.
`OptdesF`	a `2 x b` obtained Bayesain optimal block design.
`Optcrtsv`	score value of the optimality criteria `'Optcrit'` of the resultant Bayesian optimal block design `'OptdesF'`.
`file_loc`, `file_loc2`	location where the summary of the resultant Bayesian optimal block design is saved in .csv format.

`equireplicate`	logical value indicating whether the resultant Bayesian optimal block design is equireplicate or not.
`vtrtrep`	vector of treatment replication of the resultant Bayesian optimal block design.
`Cmat`	the C-matrix or treatment information matrix of the Bayesian optimal block design.

The graphical layout of the resultant Bayesain optimal block design.

NB: The function "Boptbd" also saves the summary of the resultant Bayesian optimal block design in .csv format in a temporary directory. Furthermore, this function reports only one final optimal block design, however, there is a possibility of more than one optimal block designs for a given parametric combination. The function `graphoptBbd` can be used to view and rearrange the graphical layout of the resultant optimal block design on `tcltk` window. Alternative to the function `Boptbd`, a GUI tcltk window can be used to generate Bayesain optimal block designs, see `mmenuBbd` and `fixparBbd`.

Author(s)

Dibaba Bayisa Gemechu, Legesse Kassa Debusho, and Linda Haines

References

Bueno Filho, J. S. de S., Gilmour, S. G. and Rosa, G. J. M. (2006). Design of microarray experiments for genetical genomics studies. Genetics, 174, 945-957

Debusho, L. K., Gemechu, D. B. and Haines, L. (2018). Algorithmic construction of optimal block designs for two-colour cDNA microarray experiments using the linear mixed effects model. *Communications in Statistics - Simulation and Computation, https://doi.org/10.1080/03610918.2018.1429617*.

Gemechu D. B., Debusho L. K. and Haines L. M. (2014). A-optimal designs for two-colour cDNA microarray experiments using the linear mixed effects model. *Peer-reviewed Proceedings of the Annual Conference of the South African Statistical Association for 2014 (SASA 2014), Rhodes University, Grahamstown, South Africa*. pp 33-40, ISBN: 978-1-86822-659-7.

See Also

`mmenuBbd`, `fixparBbd`, `intcbd`

Examples

```
 ##To obtain Bayesian A-optimal block design for the following treatment combintions:
 trt.N <- 3 #Number of treatments
 blk.N <- 3 #Number of blocks
 alpha <- 0.1 #alpha value
 beta <- 0.1 #beta value
 nrep <- 5  #Number of replications
brep <- 5  #Number of Monte Carlo samples from a prior beta distribution, Beta(0.1, 0.1)
 itr.cvrgval <- 6 #Number of iterations required during the exchange procedure
 Optcrit <- "A"   #Optimality criteria

Baoptbd_example <- Boptbd(trt.N = 3, blk.N = 3, alpha = 0.1, beta = 0.1, nrep = 5, brep = 5,
                          itr.cvrgval = 6, Optcrit = "A")
```

```
summary(Baoptbd_example)
```

`Boptbd-internal` *Internal function*

Description

This function is for internal usage only

Usage

```
## Computes Bayesian A-optimal block designs
## using block/array exchange algorithm
Baoptbd(trt.N, blk.N, alpha, beta, nrep, brep, itr.cvrgval)

## Computes Bayesian D-optimal  block designs
## using block/array exchange algorithm
Bdoptbd(trt.N, blk.N, alpha, beta, nrep, brep, itr.cvrgval)
```

Arguments

`trt.N`	integer, specifying number of treatments, v.
`blk.N`	integer, specifying number of arrays, b.
`alpha`	numeric, representing shape parameter of beta distribution.
`beta`	numeric, representing shape parameter of beta distribution.
`nrep`	integer, specifying number of replications of the optimization procedure.
`brep`	integer, specifying number of Monte Carlo samples from a prior beta distribution, Beta(alpha, beta).
`itr.cvrgval`	integer, specifying number of iterations required for convergence during the exchange procedure. See `Boptbd` documentation for details.

Details

These functions are handled via a generic function `Boptbd`. Please refer to the `Boptbd` documentation for details.

Author(s)

Dibaba Bayisa Gemechu, Legesse Kassa Debusho, and Linda Haines

References

Debusho, L. K., Gemechu, D. B. and Haines, L. (2018). Algorithmic construction of optimal block designs for two-colour cDNA microarray experiments using the linear mixed effects model. *Communications in Statistics - Simulation and Computation, https://doi.org/10.1080/03610918.2018.1429617*.

Gemechu D. B., Debusho L. K. and Haines L. M. (2014). A-optimal designs for two-colour cDNA microarray experiments using the linear mixed effects model. *Peer-reviewed Proceedings of the Annual Conference of the South African Statistical Association for 2014 (SASA 2014), Rhodes University, Grahamstown, South Africa*. pp 33-40, ISBN: 978-1-86822-659-7.

See Also

`Boptbd`

`cmatbd` *Computes the treatment information matrix*

Description

The function `cmatbd` computes the information matrix (C-matrix) for treatment effects under either the linear fixed effects model or the linear mixed effects model setting for a given block design of size 2.

Usage

```
cmatbd(trt.N, blk.N, theta, des)
```

Arguments

`trt.N`	integer, specifying number of treatments, `v`.
`blk.N`	integer, specifying number of blocks, `b`.
`theta`	numeric, representing function of the ratio of random block variance and random error variance. It takes any value between 0 and 1, inclusive.
`des`	matrix, a `2 x b` block design with `b` blocks of size `k = 2` and `v` treatments.

Value

Returns a `v x v` treatment information matrix (C-matrix).

Author(s)

Dibaba Bayisa Gemechu, Legesse Kassa Debusho, and Linda Haines

References

Debusho, L. K., Gemechu, D. B. and Haines, L. (2018). Algorithmic construction of optimal block designs for two-colour cDNA microarray experiments using the linear mixed effects model. *Communications in Statistics - Simulation and Computation, https://doi.org/10.1080/03610918.2018.1429617*.

Gemechu D. B., Debusho L. K. and Haines L. M. (2014). A-optimal designs for two-colour cDNA microarray experiments using the linear mixed effects model. *Peer-reviewed Proceedings of the Annual Conference of the South African Statistical Association for 2014 (SASA 2014), Rhodes University, Grahamstown, South Africa*. pp 33-40, ISBN: 978-1-86822-659-7.

See Also

`Boptbd`, `fixparBbd`, `intcbd`

Examples

```
##Information matrix

     trt.N <- 3

     blk.N <- 3

     theta <- 0.2

     des <- intcbd(trt.N = 4, blk.N = 3)

     cmatbd(trt.N, blk.N, theta, des)
```

`fixparBbd` *Sets parametric values*

Description

The function `fixparbd` creates a `tcltk` widow that allows users to set or fix values for the parametric combinations to compute Bayesian optimal block designs.

Usage

```
fixparBbd(Optcrit)
```

Arguments

`Optcrit`	character, specifying the optimality criteria to be used. `Optcrit` takes the letter `"A"` and `"D"` for Bayesian `A-` and `D-` optimal block designs, respectively.

Details

`fixparBbd` creates a pop-up tcltk window that allows users to set the parametric combinations to compute optimal or near-optimal block designs. The parameters include the number of treatments, number blocks, alpha and betha value, number of replications of the optimization procedure `nrep`, number of Monte Carlo samples `brep` and number of iterations required during exchange procedure `itr.cvrgval`. Furthermore, on this window, the checkbox options that allow the users to choose whether or not they need to have the graphical layout of the resultant Bayesian optimal block design and to print the summary of the resultant Bayesian optimal design on R-console directly are available.

After setting all the required parametric combinations and selecting the algorithm of interest, clicking on the search button on the set parametric combinations tcltk window, similar to the results that can be obtained when using the function `Boptbd`, the summary of the resultant Bayesian optimal block design is also saved in a temporary directory in .csv format and it will also be displayed on R console with graphical layout of the resultant Bayesian optimal block designs.

Value

The `fixparBbd` function creates a pop-up tcltk window that allows users to set the parametric combinations to compute Bayesian optimal block designs.

Author(s)

Dibaba Bayisa Gemechu, Legesse Kassa Debusho, and Linda Haines

See Also

`Boptbd`, `mmenuBbd`, `tcltk`, `TkWidgets`

`graphoptBbd` *Creates the graphical layout of resultant optimal design*

Description

The function `graphoptBbd` creates the graphical layout of resultant Bayesian A-, or D-optimal block design on a separate pop-up GUI tcltk window.

Usage

```
graphoptBbd(trt.N, blk.N, alpha, beta, OptdesF, Optcrit)
```

Arguments

`trt.N`	integer, specifying number of treatments, `v`.
`blk.N`	integer, specifying number of blocks, `b`.
`alpha`	numeric, representing parameter of beta distribution.
`beta`	numeric, representing parameter of beta distribution.

`OptdesF`	matrix, a `2 x b` obtained Bayesian optimal block design.
`Optcrit`	character specifying the optimality criteria to be used. Thus, `Optcrit` takes the letter `"A"` and `"D"` for Bayesian `A-` and `D`-optimal block designs, respectively.

Details

Detail discussions concerning the constructions of a graphs can be found in `igraph` R package.

Value

Returns the graphical layout of the resultant Bayesian optimal block design '`OptdesF`' on a separate pop-up window. Furthermore, the function saves the graphical layout of the resultant Bayesain optimal block design in .pdf format in a temporary directory.

Note

When closing a pop-up window for graphical layout of the resultant designs (Graph plot), if the window is closed by clicking on the red button with "X" sign (top-right), the warning message "Warning message: In `rm(list = cmd, envir = .tkplot.env)`: object 'tkp ...' not found" will occur in R-console irrespective of what command is executed next. To resolve this warning message, click on "`close`" menu that is located at the top-left of the graph plot pop-up window when closing this window.

Author(s)

Dibaba Bayisa Gemechu, Legesse Kassa Debusho, and Linda Haines

See Also

`igraph`

Examples

```
##To create the graphical layout of the D-optimal block design
##obtained using the treatment exchange algorithm for
trt.N <- 10  #Number of treatments
blk.N <- 10  #Number of blocks
alpha <- 0.1 #alpha value
beta  <- 0.1 #beta value
OptdesF <- rbind(1:10, c(2:10,1)) #Bayesian A-optimal block design (loop design)

graphoptBbd(trt.N = 10, blk.N = 10, alpha = 0.1, beta = 0.1, OptdesF, Optcrit = "A")
```

`intcbd` *Generates initial connected block design*

Description

The function `intcbd` generates a random initial connected block design for a given number of blocks `b` of size `k = 2` and the number of treatments `v`.

Usage

```
intcbd(trt.N, blk.N)
```

Arguments

`trt.N`	integer, specifying number of treatments, `v`.
`blk.N`	integer, specifying number of arrays, `b`.

Value

Returns a `2 x b` connected block design with `b` blocks of size `k = 2` and number of treatments `v`.

Author(s)

Dibaba Bayisa Gemechu, Legesse Kassa Debusho, and Linda Haines

References

Debusho, L. K., Gemechu, D. B., and Haines, L. M. (2018). Algorithmic construction of optimal block designs for two-colour cDNA microarray experiments using the linear mixed model.

Gemechu D. B., Debusho L. K. and Haines L. M. (2014). A-optimal designs for two-colour cDNA microarray experiments using the linear mixed effects model. *Peer-reviewed Proceedings of the Annual Conference of the South African Statistical Association for 2014 (SASA 2014), Rhodes University, Grahamstown, South Africa.* pp 33-40, ISBN: 978-1-86822-659-7.

See Also

`Boptbd`, `cmatbd`

Examples

```
#Initial connected block design for
trt.N <- 4 #Number of treatments
blk.N <- 4 #Number of blocks

intcbd(trt.N = 4, blk.N = 3)
```

`mmenuBbd` *Creates the main menu tcltk window*

Description

Alternative to directly using the function `Boptbd` on the R console, the function `mmenuBbd` creates the main menu tcltk window with the list of two optimality criteria (A and D) for search of Bayesian optimal block designs.

Usage

```
mmenuBbd()
```

Details

The main menu window created using the function `mmenuBbd` contains the list of two optimality criteria (the A- and D) for block designs that allows user to choose an optimality criterion of interest. The function will then call for function `fixpaBrbd` for further option regarding the setup of parametric combinations and output, see `fixparBbd` documentation.

Author(s)

Dibaba B. Gemechu, Legesse K. Debusho, and Linda M. Haines

See Also

`Boptbd`, `fixparBbd`, `tcltk`, `TkWidgets`

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