Package 'PharmPow'

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Type Package

Title Pharmacometric Power calculations for mixed study designs

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Description This package contains functions performing power calculations for mixed (sparse/dense sampled) pharmacokinetic study designs. The input data for these functions is tailored for NONMEM .phi files.

Imports scatterplot3d

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PharmPow-package   *Pharmacometric Power calculations for mixed study designs*

Description

This package contains functions performing power calculation for mixed (sparse/dense sampled) pharmacokinetic study designs. The input data for these functions is taylored for NONMEM .phi files.

Details

Package:	PharmPow
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Version:	1.0
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PharmPow_parallel PharmPow_crossover fig_PharmPow_parallel fig_PharmPow_crossover

Author(s)

Frank Kloprogge & Joel Tarning

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fig_PharmPow_crossover

Figure for Pharmacometric power calculations for mixed crossover study designs

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Description

This funcion enables the figure customisation for power calculations of a mixed crossover study design

Usage

```
fig_PharmPow_crossover(data, power = 80,
                       colorabove = "black", colorbelow = "red",
                       designAlab = "Number of patients sampling design A",
                       designBlab = "Number of patients sampling design B",
                       zaxeslab = "power (%)",
                       axessize = 1, labsize = 1)
```

Arguments

`data`	The .csv file containing the numerical results from power calculations for a crossover design can be defined here
`power`	The target power for the study designs can be defined here (default is 80%)
`colorabove`	The color for designs above the set target can be defined here (default is black)
`colorbelow`	The color for designs below the set target can be defined here (default is red)
`designAlab`	The label for design A can be defined here (default is "Number of patients sampling design A"")
`designBlab`	The label for design B can be defined here (default is "Number of patients sampling design B")
`zaxeslab`	The label for z-axes can be defined here (default is "power (%)")
`axessize`	The relative size of the axes can be defined here (default is 1.0)
`labsize`	The relative size of the labels can be defined here (default is 1.0)

Author(s)

Frank Kloprogge & Joel Tarning

Examples

```
# Customised figure for a crossover study design
fig_PharmPow_crossover(data=system.file("extdata","Cross_results.csv",
                                  package="PharmPow"),
                    power = 80,
                    colorabove = "green", colorbelow = "red",
                    designAlab = "Number of patients with design A",
                    designBlab = "Number of patients with design B",
                    zaxeslab = "power (percent)",
                    axessize = 1.2, labsize = 1.2)
```

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fig_PharmPow_parallel *Figure for Pharmacometric power calculations for mixed parallel study designs*

Description

This funcion enables the figure customisation for power calculations of a mixed parallel study design

Usage

```
fig_PharmPow_parallel(data, power = 80,
                    colorabove = "black", colorbelow = "red",
                    designAlab = "Number of patients sampling design A",
                    designBlab = "Number of patients sampling design B",
                    zaxeslab = "power (%)",
                    axessize = 1, labsize = 1)
```

Arguments

`data`	The .csv file containing the numerical results from power calculations for a parallel design can be defined here
`power`	The target power for the study designs can be defined here (default is 80%)
`colorabove`	The color for designs above the set target can be defined here (default is black)
`colorbelow`	The color for designs below the set target can be defined here (default is red)
`designAlab`	The label for design A can be defined here (default is "Number of patients sampling design A"")
`designBlab`	The label for design B can be defined here (default is "Number of patients sampling design B")
`zaxeslab`	The label for z-axes can be defined here (default is "power (%)")
`axessize`	The relative size of the axes can be defined here (default is 1.0)
`labsize`	The relative size of the labels can be defined here (default is 1.0)

Author(s)

Frank Kloprogge & Joel Tarning

Examples

```
# Customised figure for a parallel study design
fig_PharmPow_parallel(data=system.file("extdata","Parallel_results.csv",
                                  package="PharmPow"),
                  power = 80,
                  colorabove = "green", colorbelow = "red",
                  designAlab = "Number of patients with design A",
                  designBlab = "Number of patients with design B",
                  zaxeslab = "power (percent)",
                  axessize = 1.2, labsize = 1.2)
```

PharmPow_crossover	*Pharmacometric power calculations for mixed crossover study designs*

Description

This function performs power calculations for mixed crossover study designs. The input data for these functions is taylored for NONMEM .phi files.

Usage

```
PharmPow_crossover(datafullA, datareducedA, datafullB, datareducedB,
                  maxIDsA = 200, maxIDsB = 200, nresamples = 10000,
                  power = 80,
                  designAlab = "Number of patients sampling design A",
                  designBlab = "Number of patients sampling design B")
```

Arguments

datafullA	The (NONMEM).phi file from the full model fitted on design A can be defined here
datareducedA	The (NONMEM).phi file from the reduced model fitted on design A can be defined here
datafullB	The (NONMEM).phi file from the full model fitted on design B can be defined here
datareducedB	The (NONMEM).phi file from the reduced model fitted on design B can be defined here
maxIDsA	The maximum number of ID's for design A can be defined here (default is 200)
maxIDsB	The maximum number of ID's for design B can be defined here (default is 200)
nresamples	The number of resamples (different study designs) can be defined here (default is 10000)
power	The target power for the study designs can be defined here (default is 80%)
designAlab	The label for design A can be defined here (default is "Number of patients sampling design A"")
designBlab	The label for design B can be defined here (default is "Number of patients sampling design B")

Author(s)

Frank Kloprogge & Joel Tarning

Examples

```
# Power calculations for a mixed study design (for design C & D)
## Not run: PharmPow_crossover(datafullA=system.file("extdata","designC_full",
                                        package="PharmPow"),
                      datareducedA=system.file("extdata","designC_red",
                                            package="PharmPow"),
                      datafullB=system.file("extdata","designD_full",
                                        package="PharmPow"),
                      datareducedB=system.file("extdata","designD_red",
                                            package="PharmPow"))

## End(Not run)
```

PharmPow_parallel	*Pharmacometric power calculations for mixed parallel study designs*

Description

This function performs power calculations for mixed parallel study designs. The input data for these functions is taylored for NONMEM .phi files.

Usage

```
PharmPow_parallel(datafullA, datareducedA, datastratifyA, stratifyA,
                  datafullB, datareducedB, datastratifyB, stratifyB,
                  maxIDsA = 200, maxIDsB = 200, nresamples = 10000,
                  power = 80,
                  designAlab = "Number of patients sampling design A",
                  designBlab = "Number of patients sampling design B")
```

Arguments

`datafullA`	The (NONMEM).phi file from the full model fitted on design A can be defined here
`datareducedA`	The (NONMEM).phi file from the reduced model fitted on design A can be defined here
`datastratifyA`	The (NONMEM TABLE) file containing the covariate to stratify design A for can be defined here
`stratifyA`	The covariate to stratify design A for can be defined here
`datafullB`	The (NONMEM).phi file from the full model fitted on design B can be defined here
`datareducedB`	The (NONMEM).phi file from the reduced model fitted on design B can be defined here
`datastratifyB`	The (NONMEM TABLE) file containing the covariate to stratify design B for can be defined here
`stratifyB`	The covariate to stratify design B for can be defined here
`maxIDsA`	The maximum number of ID's for design A can be defined here (default is 200)
`maxIDsB`	The maximum number of ID's for design B can be defined here (default is 200)
`nresamples`	The number of resamples (different study designs) can be defined here (default is 10000)
`power`	The target power for the study designs can be defined here (default is 80%)
`designAlab`	The label for design A can be defined here (default is "Number of patients sampling design A""")
`designBlab`	The label for design B can be defined here (default is "Number of patients sampling design B")

Author(s)

Frank Kloprogge & Joel Tarning

Examples

```
# Power calculations for a mixed study design (for design A & B)
## Not run: PharmPow_parallel(datafullA=system.file("extdata","designA_full",
                                          package="PharmPow"),
                    datareducedA=system.file("extdata","designA_red",
                                          package="PharmPow"),
```

```
                              datastratifyA=system.file("extdata","designA_stratify",
                                                  package="PharmPow"),
                         stratifyA="PREG",
                         datafullB=system.file("extdata","designB_full",
                                                  package="PharmPow"),
                         datareducedB=system.file("extdata","designB_red",
                                                  package="PharmPow"),
                         datastratifyB=system.file("extdata","designB_stratify",
                                                  package="PharmPow"),
                         stratifyB="PREG")

## End(Not run)
```

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