Package 'populationPDXdesign'

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Type Package

Title Designing Population PDX Studies

Version 1.0.3

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Description Run simulations to assess the impact of various designs features
and the underlying biological behaviour on the outcome of a Patient Derived
Xenograft (PDX) population study. This project can either be deployed to a
server as a 'shiny' app or installed locally as a package and run the app
using the command 'populationPDXdesignApp()'.

License GPL (>= 3)

Depends R (>= 3.0.0)

Imports devtools, ggplot2, plyr, roxygen2, shiny, shinycssloaders

Suggests testthat

RoxygenNote 6.0.1

NeedsCompilation no

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R topics documented:

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callsInSingleExperiment

Simulation of a single population PDX experiment

Description

This is an internal function. Please use cautiously if calling directly. Samples some animals and classify as responders or non-responders based on number of models studied (PDXn), number of mice measured per model (PDXr), the classification accuracy (C_Acc) and the underlying biological response rate (Biol_RR). Example usage: `callsInSingleExperiment(PDXn=8, PDXr=3, C_Acc=0.95, Biol_RR=30)`

Usage

```
callsInSingleExperiment(PDXn, PDXr, C_Acc, Biol_RR)
```

Arguments

PDXn	number of PDX models studied
PDXr	number of mice measured per PDX model
C_Acc	classification accuracy
Biol_RR	underlying biological response rate for this treatment

Value

dataframe with three columns:

- PDXModel is a string that indicates the model id

- PDXclassification is a numeric value that indicates the true biological classification of that PDX - 0 equal non-responder and 1 equal responder

- StudyResult is a numeric value that indicates the classification of the PDX model after sampling - 0 equal non-responder and 1 equal responder

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getMode *Function to return the mode of a vector of values*

Description

This is an internal function. Please use cautiously if calling directly. Returns the mode from numeric vector. Example usage: getMode(c(0,1,1))

Usage

```
getMode(v)
```

Arguments

v   vector of numeric values

Value

a numeric value

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noFalseCalls *Function to calculate the number of false calls for a design for a go-no go threshold*

Description

This is an internal function. Please use cautiously if calling directly. Returns the number of false calls from a simulation study exploring the impact of varying PDXn and PDXr for an underlying Biol_RR for a particularly go-no go threshold. A false call can only arise in the situation where the underlying Biol_RR is below the go-no go threshold. Example usage: noFalseCalls(ImpactVarying_PDXn_PDXr_BRR, GoNoGoThreshold=30)

Usage

```
noFalseCalls(dataset, GoNoGoThreshold)
```

Arguments

dataset   dataset obtained as output from the 'varying_PDXn_PDXr' function

GoNoGoThreshold

                 go-no go threshold

Value

vector with three elements:

- numeric value indicating the number of experiments simulated

- numeric value indicating the number of experiments which were above the go-no go threshold

- numeric value indicating the FPR

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noMissedCalls	*Function to calculate the number of missed calls for a design for a go-no go threshold*

Description

This is an internal function. Please use cautiously if calling directly. Returns the number of missed calls from a simulation study exploring the impact of varying PDXn and PDXr for an underlying Biol_RR for a particularly go-no go threshold. A missed call can only arise in the situation where the underlying Biol_RR exceeds the go-no go threshold. Example usage: noMissedCalls(ImpactVarying_PDXn_PDXr_BRR, GoNoGoThreshold=30)

Usage

```
noMissedCalls(dataset, GoNoGoThreshold)
```

Arguments

dataset   dataset obtained as output from the 'varying_PDXn_PDXr' function
GoNoGoThreshold
                   go-no go threshold

Value

vector with three elements:

- numeric value indicating the number of experiments simulated

- numeric value indicating the number of experiments which were below the go-no go threshold

- numeric value indicating the percent of missed calls

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outcomeInSingleExperiment

Function to summarise the results for a single simulation representing one experiment

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Description

This is an internal function. Please use cautiously if calling directly. From a simulation of a single experiment, the estimated response rate is determined and captured with the meta data (e.g. PDXn, PDXr) for that experiment. Example usage: `outcomeInSingleExperiment(df=outcomeInSingleExperiment_1, PDXn=8, PDXr=3, C_Acc=0.95, Biol_RR=30)`

Usage

```
outcomeInSingleExperiment(df, PDXn, PDXr, C_Acc, Biol_RR)
```

Arguments

df	data frame from callsInSingleExperiment
PDXn	PDXn
PDXr	PDXr
C_Acc	the classification accuracy (numeric value between 0 and 1)
Biol_RR	Biol_RR

Value

a vector with 8 values that captures the input design and the estimated response rate for that design from a single simulation

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outcomeMultipleExperiments

Function to run simulations to mimic population PDX studies for a defined scenario

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Description

This is an internal function. Please use cautiously if calling directly. Simulations are used to mimic population PDX studies for specified values of PDXn, PDXr, Biol_RR and C_Acc. Example usage: `outcomeMultipleExperiments(PDXn=8, PDXr=3, C_Acc=0.95, Biol_RR=30, iterations=500)`

Usage

```
outcomeMultipleExperiments(PDXn, PDXr, C_Acc, Biol_RR, iterations)
```

Arguments

PDXn	PDXn
PDXr	PDXr
C_Acc	the classification accuracy (numeric value between 0 and 1)
Biol_RR	Biol_RR
iterations	no of experiments to simulated

Value

a dataframe where each row represents the results from a simulation mimicking an individual experiment for a particular design with meta data returned to describe the experimental design

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plotFalsepositive	*A function to visualise the false postive rate as a function of PDXn and PDXr*

Description

This is an internal function. Please use cautiously if calling directly. A visualisation of the false positive rate behaviour from the simulations

Usage

```
plotFalsepositive(data)
```

Arguments

data	data frame with four columns which indicate the PDXn, PDXr, Biol_RR and the FPR for a specified go-no go threshold

Value

a graphic visualisation

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plotSensitivity *A function to visualise the sensitivity as a function of PDXn and PDXr*

Description

This is an internal function. Please use cautiously if calling directly. A visualisation of the sensitivity from the simulations

Usage

```
plotSensitivity(data)
```

Arguments

data   data frame with four columns which indicate the PDXn, PDXr, Biol_RR and the
            MissedCalls for a specified go-no go threshold

Value

a graphic visualisation

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populationPDXdesignApp

Function populationPDXdesignApp

Description

Runs the 'shiny' app.

Usage

```
populationPDXdesignApp()
```

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Examples

```
if (interactive()) {
populationPDXdesignApp()
}
```

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server	*'shiny' app server function*

Description

This is an internal function. Please use cautiously if calling directly

Usage

```
server(input, output, session)
```

Arguments

`input`	input
`output`	output
`session`	session

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ui	*'shiny' app user interface function*

Description

This is an internal function. Please use cautiously if calling directly.

Usage

```
ui()
```

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varyingPDXnPDXrBiolRR *Function to run simulations to mimic population PDX studies for variety of experimental and biological scenarios*

Description

This is an internal function. Please use cautiously if calling directly. Simulations are used to mimic population PDX studies by inputing a variety of experimental factors (PDXn and PDXr) and biological factors (Biol_RR and C_Acc). Example usage: `varyingPDXnPDXrBiolRR(PDXn_range=c(8,10,12), PDXr_range=c(1,3,5), Biol_RR_range=c(30,40,50), C_Acc=0.95, iterations=500)`

Usage

```
varyingPDXnPDXrBiolRR(PDXn_range, PDXr_range, Biol_RR_range, C_Acc, iterations)
```

Arguments

`PDXn_range`	a vector of PDXn values to study
`PDXr_range`	a vector of PDXr values to study
`Biol_RR_range`	a vector of values between 0 and 100 to indicate the Biol_RR to study
`C_Acc`	the classification accuracy (numeric value between 0 and 1)
`iterations`	iterations

Value

a dataframe where each row represents the results from a simulation mimicking an individual experiment for a particular design with meta data returned to describe the experimental design

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