

# Package ‘populationPDXdesign’

May 9, 2026

**Type** Package

**Title** Designing Population PDX Studies

**Version** 1.0.3

**Date** 2018-08-08

**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)

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**Depends** R (>= 3.0.0)

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

**Suggests** testthat

**RoxygenNote** 6.0.1

**NeedsCompilation** no

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**Repository** CRAN

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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	<i>Function to return the mode of a vector of values</i>
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**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	<i>Function to calculate the number of false calls for a design for a go-no go threshold</i>
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**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 particular 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	<i>Function to calculate the number of missed calls for a design for a go-no go threshold</i>
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**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

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

**Author(s)**

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plotFalsepositive	<i>A function to visualise the false positive rate as a function of PDXn and PDXr</i>
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**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
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**Value**

a graphic visualisation

**Author(s)**

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

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**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

**Author(s)**

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populationPDXdesignApp  
*Function* populationPDXdesignApp

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**Description**

Runs the 'shiny' app.

**Usage**

```
populationPDXdesignApp()
```

**Author(s)**

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**Examples**

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

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server	<i>'shiny' app server function</i>
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**Description**

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

**Usage**

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

**Arguments**

input	input
output	output
session	session

**Author(s)**

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ui	<i>'shiny' app user interface function</i>
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**Description**

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

**Usage**

```
ui()
```

**Author(s)**

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

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### Description

This is an internal function. Please use cautiously if calling directly. Simulations are used to mimic population PDX studies by inputting 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

### Author(s)

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