

# Package ‘PoPdesign’

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**Type** Package

**Title** Posterior Predictive (PoP) Design for Phase I Clinical Trials

**Version** 1.0.4

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**Depends** R (>= 3.5.0)

**Imports** Iso, knitr, magick

**Description** The primary goal of phase I clinical trials is to find the maximum tolerated dose (MTD). To reach this objective, we introduce a new design for phase I clinical trials, the posterior predictive (PoP) design. The PoP design is an innovative model-assisted design that is as simply as the conventional algorithmic designs as its decision rules can be pre-tabulated prior to the onset of trial, but is of more flexibility of selecting diverse target toxicity rates and cohort sizes. The PoP design has desirable properties, such as coherence and consistency. Moreover, the PoP design provides better empirical performance than the BOIN and Key-board design with respect to high average probabilities of choosing the MTD and slightly lower risk of treating patients at subtherapeutic or overly toxic doses.

**License** GPL-2

**Encoding** UTF-8

**RoxygenNote** 7.2.3

**VignetteBuilder** knitr

**Suggests** rmarkdown

**NeedsCompilation** no

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get.boundary.pop	<i>Generate the dose escalation and de-escalation boundaries for single-agent trials.</i>
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## Description

Use this function to generate the dose escalation and deescalation boundaries for single-agent trials.

## Usage

```
get.boundary.pop(target, n.cohort, cohortsize, cutoff, K, cutoff_e)
```

## Arguments

target	the target DLT rate
n.cohort	the total number of cohorts
cohortsize	the cohort size
cutoff	the cutoff for the predictive Bayes Factor (PrBF). Users can specify either a value or a function for cutoff. If $\text{PrBF} < \text{cutoff}$ , we assign the next cohort of patients to an adjacent dose based on observed DLT. Otherwise, the evidence is in favor of $H_{0j}$ and we need to retain the current dose.
K	number of dose levels. It is required when argument cutoff is a function that requires K.
cutoff_e	the cutoff for the dose exclusion rule. If $\text{PrBF}_{0,1} < E(n_j)$ , the evidence is in favor of $H_{1j}$ . If $\hat{\pi}_j < \phi$ , the current dose is deemed as subtherapeutic and we exclude the current dose and lower doses; If $\hat{\pi}_j > \phi$ , the current dose is overly toxic and we exclude the current dose and higher doses.

## Details

We assume that there are  $J$  pre-specified dose levels of the drug of interest. Let  $d_1, d_2, \dots, d_J$  denote these dose levels. The dose-limiting toxicity (DLT) is assessed as a binary outcome, experiencing toxicity or not. The true dose toxicity is monotonically increasing as the dose level increases. Let  $\phi$  be the target toxicity rate and  $\pi_j$  be the true dose-toxicity of dose level  $d_j$ , for  $j = 1, 2, \dots, J$ .

We formulate our hypothesis as:

$$H_{0j} : \pi_j = \phi$$

$$H_{1j} : \pi_j \neq \phi$$

$H_{0j}$  indicates that  $d_j$  is the desired MTD so that we should stay;  $H_{1j}$  reflects the current dose is either below or above the MTD so that we should transit to a lower or upper dose level. Whether



```
summary(bound) # get the descriptive summary of the boundary
plot(bound)    # plot the flowchart of the design along with decision boundaries
```

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get.oc.pop                      *Operating characteristics for single-agent trials*

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## Description

Generate the operating characteristics of the PoP design by simulating trials.

## Usage

```
get.oc.pop(target,n.cohort,cohortsizes,titration,skeleton,n.trial,cutoff,cutoff_e,
            risk.cutoff,earlyterm,start,seed)
```

## Arguments

target	the target DLT rate
n.cohort	the total number of cohorts
cohortsizes	the cohort size
titration	default is TRUE. Set titration=TRUE to perform dose escalation with cohort size = 1 to accelerate dose escalation at the beginning of the trial.
skeleton	a vector containing the true toxicity probabilities of the investigational dose levels.
n.trial	the total number of trials to be simulated
cutoff	the cutoff for the predictive Bayes Factor (PrBF). Users can specify either a value or a function for cutoff. If $PrBF < cutoff$ , we assign the next cohort of patients to an adjacent dose based on observed DLT. Otherwise, the evidence is in favor of $H_{0j}$ and we need to retain the current dose.
cutoff_e	the cutoff for the dose exclusion rule. If $PrBF_{0,1} < E(n_j)$ , the evidence is in favor of $H_{1j}$ . If $\hat{\pi}_j < \phi$ , the current dose is deemed as subtherapeutic and we exclude the current dose and lower doses; If $\hat{\pi}_j > \phi$ , the current dose is overly toxic and we exclude the current dose and higher doses.
risk.cutoff	the cutoff to eliminate an over/under toxic dose. We recommend the default value of (risk.cutoff=0.8) for general use.
earlyterm	the early termination parameter.
start	specify the starting dose level. Default value is 1.
seed	the seed for random number generation. Default is 123.

## Details

TBD

**Value**

get.oc.pop() returns the operating characteristics of the PoP design as a list, including:

- (1) selection percentage at each dose level (\$sel.pct),
- (2) the number of patients treated at each dose level (\$num.p),
- (3) the number of toxicities observed at each dose level (\$num.tox),
- (4) the average number of toxicities,
- (5) the average number of patients,
- (6) the percentage of early stopping without selecting the MTD (\$early),
- (7) risk of underdosing 80% or more of patients (\$risk.under),
- (8) risk of overdosing 80% or more of patients (\$risk.over)

**References**

Brunk, H., Barlow, R. E., Bartholomew, D. J. & Bremner, J. M (1972, ISBN-13: 978-0471049708).

**Examples**

```
## get the operating characteristics for single-agent trials
oc <- get.oc.pop(target=0.3,n.cohort=10,cohortsize=3,titration=TRUE,
                cutoff=2.5,cutoff_e=5/24,
                skeleton=c(0.3,0.4,0.5,0.6),n.trial=1000,
                risk.cutoff=0.8,earlyterm=TRUE,start=1, seed=123)

summary(oc) # summarize design operating characteristics
plot(oc)
```

---

plot.pop

*Plot the flowchart and simulation results for PoP designs*

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**Description**

Plot the objects returned by other functions, including (1) flowchart of PoP design; (2) operating characteristics of the design, including selection percentage and the number of patients treated at each dose; (3) the estimate of toxicity probability for each dose and corresponding 95% credible interval

**Usage**

```
## S3 method for class 'pop'
plot(x, ...)
```

**Arguments**

x                    the object returned by other functions  
 ...                  ignored arguments

**Value**

plot() returns a figure or a series of figures depending on the object entered

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print.pop	<i>Generate descriptive summary for objects returned by other functions</i>
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**Description**

Generate descriptive summary for objects returned by other functions.

**Usage**

```
## S3 method for class 'pop'
print(x, ...)
```

**Arguments**

x                    the object returned by other functions  
 ...                  ignored arguments

**Details**

print() prints the objects returned by other functions.

**Value**

print() prints the objects returned by other functions.

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select.mtd.pop	<i>Maximum tolerated dose (MTD) selection for single-agent trials</i>
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**Description**

Select the maximum tolerated dose (MTD) when the single-agent trial is completed

**Usage**

```
select.mtd.pop(target, n.pts, n.tox)
```

**Arguments**

target	the target DLT rate
n.pts	a vector containing the number of patients treated at each dose level
n.tox	a vector containing the number of patients who experienced dose-limiting toxicity at each dose level

**Value**

select.mtd.pop() returns (1) selected MTD (\$MTD), (2) isotonic estimate of the DLT probability at each dose and associated

**References**

Brunk, H., Barlow, R. E., Bartholomew, D. J. & Bremner, J. M (1972, ISBN-13: 978-0471049708).

**Examples**

```
### select the MTD for PoP trial
n <- c(4, 4, 16, 8, 0)
y <- c(0, 0, 5, 5, 0)
selmtd <- select.mtd.pop(target=0.3,n.pts=n, n.tox=y)
summary(selmtd)
plot(selmtd)
```

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summary.pop	<i>Generate descriptive summary for objects returned by other functions in PoPdesign</i>
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**Description**

Generate descriptive summary for objects returned by other functions.

**Usage**

```
## S3 method for class 'pop'
summary(object, ...)
```

**Arguments**

object	the object returned by other functions.
...	ignored arguments

**Value**

summary() prints the objects returned by other functions.

**Examples**

```
## summarize the results returned by get.boundary.pop()
bound <- get.boundary.pop(n.cohort = 10, cohortsize = 3, target=0.3,
                          cutoff=exp(1), K=3,cutoff_e=exp(-1))
summary(bound)

## summarize the results returned by get.oc.pop()
oc <- get.oc.pop(target=0.3,n.cohort=10,cohortsize=3,titration=TRUE,
                 cutoff=TRUE,cutoff_e=exp(-1),skeleton=c(0.3,0.4,0.5,0.6),n.trial=1000,
                 risk.cutoff=0.8,earlyterm=TRUE,start=1)
summary(oc)

### summarize the results returned by select.mtd.pop()
n <- c(3, 3, 15, 9, 0)
y <- c(0, 0, 4, 4, 0)
selmtd <- select.mtd.pop(target=0.3,n.pts=n, n.tox=y)
summary(selmtd)
```

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