

Package ‘dilutionrisk’

July 27, 2022

Type Package

Title Modelling and assessment of risk based on aerobic plate count (APC) on diluted testing

Version 0.0.1

Authors Mayooraan Thevaraja [aut, cre], Kondaswamy Govindaraju [aut], Mark Bebbington [aut]

URL <https://github.com/Mayooraan1987/dilutionrisk>

BugReports <https://github.com/Mayooraan1987/dilutionrisk/issues>

Description This package aims to develop for getting probability estimations and graphical displays in the study associated with Modelling and assessment of risk based on aerobic plate count (APC) on diluted testing.

License GPL (>= 2)

Encoding UTF-8

LazyData true

Imports extraDistr, ggplot2, ggthemes, reshape2, stats

Suggests spelling, testthat, covr

RoxygenNote 7.2.1

Depends R (>= 4.0)

Maintainer Mayooraan Thevaraja <mayooraan@eng.jfn.ac.lk>

Language en-US

Config/testthat/edition 3

R topics documented:

OC_curves_heterogeneous	2
OC_curves_homogeneous	3
pd_curves_heterogeneous	4
pd_curves_homogeneous	5
prob_acceptance_heterogeneous	6
prob_acceptance_homogeneous	7
prob_detection_heterogeneous	8
prob_detection_homogeneous	9
rtrunpoilog	10
Index	11

OC_curves_heterogeneous

Comparison based on OC curves for different dilution schemes when the diluted sample has heterogeneous contaminants.

Description

[OC_curves_heterogeneous](#) provides the operating characteristic(OC) curves when diluted sample has heterogeneous contaminants.

Usage

```
OC_curves_heterogeneous(c, meanlog_low, meanlog_high, sdlog, a, b, FDF, USL, n, n_sim)
```

Arguments

c	acceptance number
meanlog_low	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
meanlog_high	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
sdlog	the standard deviation of the normal distribution (on the log scale).
a	lower domain of the number of cell counts.
b	upper domain of the number of cell counts.
FDF	final dilution factor.
USL	upper specification limit.
n	number of samples which are used for inspection.
n_sim	number of simulations (large simulations provide more precise estimation).

Details

[OC_curves_heterogeneous](#) provides OC curves for different dilution schemes when the diluted sample has heterogeneous contaminants (this section will be updated later on).

Value

OC curves when the diluted sample has heterogeneous contaminants.

Examples

```
c <- 0
meanlog_low <- -6
meanlog_high <- 3
sdlog <- 0.8
a <- 0
b <- 300
FDF <- 0.001
USL <- c(1000, 2000)
n <- 5
n_sim <- 1000
OC_curves_heterogeneous(c, meanlog_low, meanlog_high, sdlog, a, b, FDF, USL, n, n_sim)
```

OC_curves_homogeneous *Comparison based on OC curves for different dilution schemes when the diluted sample has homogeneous contaminants.*

Description

`OC_curves_homogeneous` provides the operating characteristic(OC) curves when diluted sample has homogeneous contaminants.

Usage

```
OC_curves_homogeneous(c, lambda_low, lambda_high, a, b, FDF, USL, n, n_sim)
```

Arguments

<code>c</code>	acceptance number
<code>lambda_low</code>	the lower value of the expected cell count (λ) for use in the graphical display's x-axis.
<code>lambda_high</code>	the upper value of the expected cell count (λ) for use in the graphical display's x-axis.
<code>a</code>	lower domain of the number of cell counts.
<code>b</code>	upper domain of the number of cell counts.
<code>FDF</code>	final dilution factor.
<code>USL</code>	upper specification limit.
<code>n</code>	number of samples which are used for inspection.
<code>n_sim</code>	number of simulations (large simulations provide more precise estimation).

Details

`OC_curves_homogeneous` provides OC curves for different dilution schemes when the diluted sample has homogeneous contaminants (this section will be updated later on).

Value

OC curves when the diluted sample has homogeneous contaminants.

Examples

```
c <- 0
lambda_low <- 0
lambda_high <- 5
a <- 0
b <- 300
FDF <- 0.001
USL <- c(1000, 2000)
n <- 5
n_sim <- 1000
OC_curves_homogeneous(c, lambda_low, lambda_high, a, b, FDF, USL, n, n_sim)
```

pd_curves_heterogeneous

comparison based on probability of detection curves for different dilution schemes when the diluted sample has heterogeneous contaminants.

Description

`pd_curves_heterogeneous` provides the probability of detection curves when the diluted sample has heterogeneous contaminants.

Usage

```
pd_curves_heterogeneous(meanlog_low, meanlog_high, sdlog, a, b, FDF, USL, n_sim)
```

Arguments

<code>meanlog_low</code>	the lower value of the mean concentration (μ) for use in the graphical display's x-axis (on the log scale).
<code>meanlog_high</code>	the upper value of the mean concentration (μ) for use in the graphical display's x-axis (on the log scale).
<code>sdlog</code>	the standard deviation of the normal distribution (on the log scale).
<code>a</code>	lower domain of the number of cell counts.
<code>b</code>	upper domain of the number of cell counts.
<code>FDF</code>	final dilution factor.
<code>USL</code>	upper specification limit.
<code>n_sim</code>	number of simulations (large simulations provide more precise estimation).

Details

`pd_curves_heterogeneous` provides probability of detection curves for different dilution schemes when the diluted sample has heterogeneous contaminants (this section will be updated later on).

Value

Probability of detection curves when the diluted sample has heterogeneous contaminants.

Examples

```
meanlog_low <- -5
meanlog_high <- 5
sdlog <- 0.8
a <- 0
b <- 300
FDF <- 0.001
USL <- c(1000, 2000)
n_sim <- 1000
pd_curves_heterogeneous(meanlog_low, meanlog_high, sdlog, a, b, FDF, USL, n_sim)
```

pd_curves_homogeneous *comparison based on probability of detection curves for different dilution schemes when the diluted sample has homogeneous contaminants.*

Description

[pd_curves_homogeneous](#) provides the probability of detection curves when the diluted sample has homogeneous contaminants.

Usage

```
pd_curves_homogeneous(lambda_low, lambda_high, a, b, FDF, USL, n_sim)
```

Arguments

lambda_low	the lower value of the expected cell count (λ) for use in the graphical display's x-axis.
lambda_high	the upper value of the expected cell count (λ) for use in the graphical display's x-axis.
a	lower domain of the number of cell counts.
b	upper domain of the number of cell counts.
FDF	final dilution factor.
USL	upper specification limit.
n_sim	number of simulations (large simulations provide more precise estimation).

Details

[pd_curves_homogeneous](#) provides probability of detection curves for different dilution schemes when the diluted sample has homogeneous contaminants (this section will be updated later on).

Value

Probability of detection curves when the diluted sample has homogeneous contaminants.

Examples

```
lambda_low <- 0
lambda_high <- 10
a <- 0
b <- 300
FDF <- 0.001
USL <- c(1000, 2000)
n_sim <- 1000
pd_curves_homogeneous(lambda_low, lambda_high, a, b, FDF, USL, n_sim)
```

prob_acceptance_heterogeneous

Probability of acceptance estimation when diluted sample has heterogeneous contaminations.

Description

[prob_acceptance_heterogeneous](#) provides a probability of acceptance in the original sample when heterogeneous contamination.

Usage

```
prob_acceptance_heterogeneous(c, meanlog, sdlog, a, b, FDF, USL, n, n_sim)
```

Arguments

c	acceptance number
meanlog	the mean concentration (on the log scale).
sdlog	the standard deviation of the normal distribution (on the log scale).
a	lower domain of the number of cell counts.
b	upper domain of the number of cell counts.
FDF	final dilution factor.
USL	upper specification limit.
n	number of samples which are used for inspection.
n_sim	number of simulations (large simulations provide more precise estimation).

Details

[prob_detection_heterogeneous](#) provides a probability of acceptance when the diluted sample has heterogeneous contaminants (this section will be updated later on).

Value

Probability of acceptance when the diluted sample has heterogeneous contaminants.

Examples

```
c <- 0
meanlog <- -2
sdlog <- 0.8
a <- 0
b <- 300
FDF <- 0.001
USL <- 1000
n <- 5
n_sim <- 10000
prob_acceptance_heterogeneous(c, meanlog, sdlog, a, b, FDF, USL, n, n_sim)
```

prob_acceptance_homogeneous

Probability of acceptance estimation when diluted sample has homogeneous contaminations.

Description

[prob_acceptance_homogeneous](#) provides a probability of acceptance in the original sample when homogeneous contamination.

Usage

```
prob_acceptance_homogeneous(c, lambda, a, b, FDF, USL, n, n_sim)
```

Arguments

c	acceptance number
lambda	the expected cell count (λ).
a	lower domain of the number of cell counts.
b	upper domain of the number of cell counts.
FDF	final dilution factor.
USL	upper specification limit.
n	number of samples which are used for inspection.
n_sim	number of simulations (large simulations provide more precise estimation).

Details

[prob_detection_homogeneous](#) provides a probability of acceptance when the diluted sample has homogeneous contaminants (this section will be updated later on).

Value

Probability of acceptance when the diluted sample has homogeneous contaminants.

Examples

```
c <- 0
lambda <- 10
a <- 0
b <- 300
FDF <- 0.001
USL <- 1000
n <- 5
n_sim <- 10000
prob_acceptance_homogeneous(c, lambda, a, b, FDF, USL, n, n_sim)
```

prob_detection_heterogeneous

Probability of detection estimation when diluted sample has heterogeneous contaminations.

Description

`prob_detection_heterogeneous` provides a probability of detection in the original sample when heterogeneous contamination.

Usage

```
prob_detection_heterogeneous(meanlog, sdlog, a, b, FDF, USL, n_sim)
```

Arguments

meanlog	the mean concentration (on the log scale).
sdlog	the standard deviation of the normal distribution (on the log scale).
a	lower domain of the number of cell counts.
b	upper domain of the number of cell counts. lower and upper truncation points ($a < x \leq b$).
FDF	final dilution factor.
USL	upper specification limit.
n_sim	number of simulations (large simulations provide more precise estimation).

Details

`prob_detection_heterogeneous` provides a probability of detection when the diluted sample has heterogeneous contaminants. We define the random variable X_i is the number of colonies on the i^{th} plate. In practice, the acceptance for countable numbers of colonies on a plate must be between 30 and 300. Therefore, we can utilise bounded distributions to model the number of colonies on a plate. heterogeneous case, we employed truncated Poisson lognormal distribution to model (this section will be updated later on).

Value

Probability of detection when the diluted sample has heterogeneous contaminants.

Examples

```
meanlog <- 2
sdlog <- 0.8
a <- 0
b <- 300
FDF <- 0.001
USL <- 1000
n_sim <- 10000
prob_detection_heterogeneous(meanlog, sdlog, a, b, FDF, USL, n_sim)
```

`prob_detection_homogeneous`*Probability of detection estimation when diluted sample has homogeneous contaminations.*

Description

`prob_detection_homogeneous` provides a probability of detection in the original sample when homogeneous contamination.

Usage

```
prob_detection_homogeneous(lambda, a, b, FDF, USL, n_sim)
```

Arguments

<code>lambda</code>	the expected cell count (λ).
<code>a</code>	lower domain of the number of cell counts.
<code>b</code>	upper domain of the number of cell counts.
<code>FDF</code>	final dilution factor.
<code>USL</code>	upper specification limit.
<code>n_sim</code>	number of simulations (large simulations provide more precise estimation).

Details

`prob_detection_homogeneous` provides a probability of detection when the diluted sample has homogeneous contaminants. We define the random variable X_i is the number of colonies on the i^{th} plate. In practice, the acceptance for countable numbers of colonies on a plate must be between 30 and 300. Therefore, we can utilise bounded distributions to model the number of colonies on a plate. homogeneous case, we employed truncated Poisson lognormal distribution to model (this section will be updated later on).

Value

Probability of detection when the diluted sample has homogeneous contaminants.

Examples

```
lambda <- 2
a <- 0
b <- 300
FDF <- 0.001
USL <- 1000
n_sim <- 10000
prob_detection_homogeneous(lambda, a, b, FDF, USL, n_sim)
```

rtrunpoilog	<i>Generates random deviates from truncated poisson lognormal distribution.</i>
-------------	---

Description

`rtrunpoilog` provides generated random numbers from truncated poisson lognormal distribution with given parameters.

Usage

```
rtrunpoilog(n, meanlog, sdlog, a, b)
```

Arguments

n	number of observations. If <code>length(n) > 1</code> then the length is taken to be the number required.
meanlog	the mean concentration (on the log scale).
sdlog	the standard deviation of the normal distribution (on the log scale).
a	lower truncation points.
b	upper truncation points ($a < x \leq b$).

Details

`rtrunpoilog` provides generated random numbers from truncated poisson lognormal distribution with given parameters. (this section will be updated later on).

Value

`rtrunpoilog` generates random numbers from truncated poisson lognormal distribution.

Examples

```
n <- 100
meanlog <- 0
sdlog <- 1
a <- 0
b <- 300
rtrunpoilog(n, meanlog, sdlog, a, b)
```

Index

OC_curves_heterogeneous, [2](#), [2](#)
OC_curves_homogeneous, [3](#), [3](#)

pd_curves_heterogeneous, [4](#), [4](#)
pd_curves_homogeneous, [5](#), [5](#)
prob_acceptance_heterogeneous, [6](#), [6](#)
prob_acceptance_homogeneous, [7](#), [7](#)
prob_detection_heterogeneous, [6](#), [8](#), [8](#)
prob_detection_homogeneous, [7](#), [9](#), [9](#)

rtrunpoilog, [10](#), [10](#)