Package ‘dilutionrisk’

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Type Package

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

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

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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.

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Maintainer Mayooran Thevaraja <mayooran@eng.jfn.ac.lk>

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`dilutionrisk` *Probability estimations and graphical displays in modelling and assessment of risk based on aerobic plate count (APC) on diluted testing*

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.

Details

This package aims to develop probability estimations and graphical displays in the modelling and assessing risk based on aerobic plate count (APC) on diluted testing. Mainly focuses on the risk assessment based on bounded distributions such as truncated Poisson and truncated Poisson lognormal distributions to model homogeneous and heterogeneous scenarios, respectively. Also, this package attempts to develop truncated Poisson lognormal distributions theory with validation by simulation-based results (this part will be updated later on).

`OC_curves_heterogeneous` *Comparison based on OC curves for different dilution schemes when the diluted samples collected from a heterogeneous batch.*

Description

`OC_curves_heterogeneous` provides the operating characteristic(OC) curves when samples collected from a heterogeneous batch.

Usage

```
OC_curves_heterogeneous(c, mu_low, mu_high, sd, a, b, f, u, USL, n, n_sim)
```

Arguments

`c`	acceptance number
`mu_low`	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
`mu_high`	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
`sd`	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.
f	final dilution factor.
u	amount put on the plate.
USL	upper specification limit.
n	number of samples which are used for inspection.
n_sim	number of simulations (large simulations provide more precise estimations).

Details

OC_curves_heterogeneous provides OC curves for different dilution schemes when the diluted samples collected from a heterogeneous batch (this section will be updated later on).

Value

OC curves when samples collected from a heterogeneous batch.

Examples

```
c <- 2
mu_low <- 4
mu_high <- 9
sd <- 0.2
a <- 0
b <- 300
f <- c(0.01,0.1)
u <- c(0.1,0.1)
USL <- 1000
n <- 5
n_sim <- 50000
OC_curves_heterogeneous(c, mu_low, mu_high, sd, a, b, f, u, USL, n, n_sim)
```

OC_curves_homogeneous *Comparison based on OC curves for different dilution schemes when diluted samples collected from a homogeneous batch.*

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, f, u, USL, n, n_sim)
```

Arguments

c	acceptance number
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.
f	final dilution factor.
u	amount put on the plate.
USL	upper specification limit.
n	number of samples which are used for inspection.
n_sim	number of simulations (large simulations provide more precise estimations).

Details

OC_curves_homogeneous provides OC curves for different dilution schemes when samples collected from a homogeneous batch (this section will be updated later on).

Value

OC curves when diluted samples collected from a homogeneous batch.

Examples

```
c <- 2
lambda_low <- 0
lambda_high <- 5000
a <- 0
b <- 300
f <- c(0.01,0.1)
u <- c(0.1,0.1)
USL <- 1000
n <- 5
n_sim <- 50000
OC_curves_homogeneous(c, lambda_low, lambda_high, a, b, f, u, USL, n, n_sim)
```

---

pd_curves_heterogeneous

Comparison based on probability of detection curves for different dilution schemes when the diluted samples collected from a heterogeneous batch.

Description

pd_curves_heterogeneous provides the probability of detection curves when samples collected from a heterogeneous batch.

Usage

```
pd_curves_heterogeneous(mu_low, mu_high, sd, a, b, f, u, USL, n_sim)
```

Arguments

`mu_low`	the lower value of the mean concentration (μ) for use in the graphical display's x-axis (on the log scale).
`mu_high`	the upper value of the mean concentration (μ) for use in the graphical display's x-axis (on the log scale).
`sd`	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.
`f`	final dilution factor.
`u`	amount put on the plate.
`USL`	upper specification limit.
`n_sim`	number of simulations (large simulations provide more precise estimations).

Details

`pd_curves_heterogeneous` provides probability of detection curves for different dilution schemes when the diluted samples collected from a heterogeneous batch (this section will be updated later on).

Value

Probability of detection curves when samples collected from a heterogeneous batch.

Examples

```
mu_low <- 0
mu_high <- 10
sd <- 0.2
a <- 0
b <- 300
f <- c(0.01,0.1)
u <- c(0.1,0.1)
USL <- 1000
n_sim <- 50000
pd_curves_heterogeneous(mu_low, mu_high, sd, a, b, f, u, USL, n_sim)
```

`pd_curves_homogeneous` *Comparison based on probability of detection curves for different dilution schemes when diluted samples collected from a homogeneous batch.*

Description

`pd_curves_homogeneous` provides the probability of detection curves when samples collected from a homogeneous batch.

Usage

```
pd_curves_homogeneous(lambda_low, lambda_high, a, b, f, u, 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.
`f`	final dilution factor.
`u`	amount put on the plate.
`USL`	upper specification limit.
`n_sim`	number of simulations (large simulations provide more precise estimations).

Details

`pd_curves_homogeneous` provides probability of detection curves for different dilution schemes when samples collected from a homogeneous batch (this section will be updated later on).

Value

Probability of detection curves when diluted samples collected from a homogeneous batch.

Examples

```
lambda_low <- 0
lambda_high <- 5000
a <- 0
b <- 300
f <- c(0.01,0.1)
u <- c(0.1,0.1)
USL <- 1000
n_sim <- 50000
pd_curves_homogeneous(lambda_low, lambda_high, a, b, f, u, USL, n_sim)
```

---

prob_acceptance_heterogeneous

Probability of acceptance estimation when diluted sample collected from a heterogeneous batch.

Description

`prob_acceptance_heterogeneous` provides a probability of acceptance in the original sample when samples collected from a heterogeneous batch.

Usage

```
prob_acceptance_heterogeneous(c, mu, sd, a, b, f, u, USL, n, n_sim)
```

Arguments

c	acceptance number
mu	the mean concentration (on the log scale).
sd	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.
f	final dilution factor.
u	amount put on the plate.
USL	upper specification limit.
n	number of samples which are used for inspection.
n_sim	number of simulations (large simulations provide a more precise estimation).

Details

prob_detection_heterogeneous provides a probability of acceptance when diluted sample collected from a heterogeneous batch (this section will be updated later on).

Value

Probability of acceptance when sample collected from a heterogeneous batch.

Examples

```
c <- 2
mu <- 7
sd <- 0.2
a <- 0
b <- 300
f <- 0.01
u <- 0.1
USL <- 1000
n <- 5
n_sim <- 50000
prob_acceptance_heterogeneous(c, mu, sd, a, b, f, u, USL, n, n_sim)
```

---

prob_acceptance_heterogeneous_multiple

Probability of acceptance estimation when diluted samples are collected from a heterogeneous batch.

Description

prob_acceptance_heterogeneous_multiple provides a probability of acceptance in the original sample when samples collected from a heterogeneous batch.

Usage

```
prob_acceptance_heterogeneous_multiple (c, mu, sd, a, b, f, u, USL, n, n_sim)
```

Arguments

c	acceptance number
mu	the mean concentration (on the log scale).
sd	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.
f	final dilution factor.
u	amount put on the plate.
USL	upper specification limit.
n	number of samples which are used for inspection.
n_sim	number of simulations (large simulations provide more precise estimations).

Details

prob_acceptance_heterogeneous_multiple provides a probability of acceptance when diluted samples are collected from a heterogeneous batch (this section will be updated later on).

Value

Probability of acceptance when samples collected from a heterogeneous batch.

Examples

```
c <- 2
mu <- 7
sd <- 0.2
a <- 0
b <- 300
f <- c(0.01,0.1,1)
u <- c(0.1,0.1,0.1)
USL <- 1000
n <- 5
n_sim <- 50000
prob_acceptance_heterogeneous_multiple (c, mu, sd, a, b, f, u, USL, n, n_sim)
```

---

prob_acceptance_homogeneous

Probability of acceptance estimation when diluted sample collected from a homogeneous batch.

Description

prob_acceptance_homogeneous provides a probability of acceptance in the original sample when samples collected from a homogeneous batch.

Usage

```
prob_acceptance_homogeneous(c, lambda, a, b, f, u, 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.
f	final dilution factor.
u	amount put on the plate.
USL	upper specification limit.
n	number of samples which are used for inspection.
n_sim	number of simulations (large simulations provide a more precise estimation).

Details

prob_detection_homogeneous provides a probability of acceptance when samples collected from a homogeneous batch (this section will be updated later on).

Value

Probability of acceptance when the diluted sample collected from a homogeneous batch.

Examples

```
c <- 2
lambda <- 2000
a <- 0
b <- 300
f <- 0.001
u <- 0.1
USL <- 1000
n <- 5
n_sim <- 50000
prob_acceptance_homogeneous(c, lambda, a, b, f, u, USL, n, n_sim)
```

---

prob_acceptance_homogeneous_multiple

Probability of acceptance estimation for multiple dilution schemes when diluted samples are collected from a homogeneous batch.

Description

prob_acceptance_homogeneous_multiple provides a probability of acceptance for multiple dilution schemes in the original sample when samples collected from a homogeneous batch

Usage

```
prob_acceptance_homogeneous_multiple(c, lambda, a, b, f, u, 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.
f	final dilution factor.
u	amount put on the plate.
USL	upper specification limit.
n	number of samples which are used for inspection.
n_sim	number of simulations (large simulations provide more precise estimations).

Details

prob_detection_homogeneous_multiple provides a probability of acceptance for multiple dilution schemes in the original sample when samples collected from a homogeneous batch (this section will be updated later on).

Value

Probability of acceptance when diluted samples are collected from a homogeneous batch.

Examples

```
c <- 2
lambda <- 1000
a <- 0
b <- 300
f <- c(0.01,0.1,1)
u <- c(0.1,0.1,0.1)
USL <- 1000
n <- 5
n_sim <- 50000
prob_acceptance_homogeneous_multiple(c, lambda, a, b, f, u, USL, n, n_sim)
```

---

prob_detection_heterogeneous

Probability of detection estimation when diluted sample collected from a heterogeneous batch.

Description

prob_detection_heterogeneous provides a probability of detection in the original sample when samples collected from a heterogeneous batch.

Usage

```
prob_detection_heterogeneous(mu, sd, a, b, f, u, USL, n_sim)
```

Arguments

`mu`	the mean concentration (on the log scale).
`sd`	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.
`f`	final dilution factor.
`u`	amount put on the plate.
`USL`	upper specification limit.
`n_sim`	number of simulations (large simulations provide a 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. In the heterogeneous case, we employed truncated Poisson lognormal distribution to model (this section will be updated later on).

Value

Probability of detection when sample collected from a heterogeneous batch.

Examples

```
mu <- 2
sd <- 0.2
a <- 0
b <- 300
f <- 0.01
u <- 0.1
USL <- 1000
n_sim <- 50000
prob_detection_heterogeneous(mu, sd, a, b, f, u, USL, n_sim)
```

`prob_detection_heterogeneous_multiple`

Probability of detection estimation for multiple dilution schemes when diluted samples are collected from a heterogeneous batch.

Description

`prob_detection_heterogeneous_multiple` provides a probability of detection for multiple dilution schemes in the original sample when samples collected from a heterogeneous batch.

Usage

```
prob_detection_heterogeneous_multiple(mu, sd, a, b, f, u, USL, n_sim)
```

Arguments

mu	the mean concentration (on the log scale).
sd	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.
f	vector of final dilution factor.
u	vector of amount put on the plate.
USL	upper specification limit.
n_sim	number of simulations (large simulations provide more precise estimations).

Details

prob_detection_heterogeneous_multiple provides a probability of detection when diluted samples are collected from a heterogeneous batch. 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. In the heterogeneous case, we employed truncated Poisson lognormal distribution to the model. (this section will be updated later on).

Value

Probability of detection when samples collected from a heterogeneous batch.

Examples

```
mu <- 7
sd <- 0.2
a <- 0
b <- 300
f <- c(0.01,0.1,1)
u <- c(0.1,0.1,0.1)
USL <- 1000
n_sim <- 50000
prob_detection_heterogeneous_multiple(mu, sd, a, b, f, u, USL, n_sim)
```

---

prob_detection_homogeneous

Probability of detection estimation when diluted sample collected from a homogeneous batch.

Description

prob_detection_homogeneous provides a probability of detection in the original sample when samples collected from a homogeneous batch.

Usage

```
prob_detection_homogeneous(lambda, a, b, f, u, USL, n_sim)
```

Arguments

lambda	the expected cell count (λ).
a	lower domain of the number of cell counts.
b	upper domain of the number of cell counts.
f	final dilution factor.
u	amount put on the plate.
USL	upper specification limit.
n_sim	number of simulations (large simulations provide a 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. In the homogeneous case, we employed truncated Poisson distribution to model (this section will be updated later on).

Value

Probability of detection when the diluted sample collected from a homogeneous batch.

Examples

```
lambda <- 2000
a <- 0
b <- 300
f <- 0.01
u <- 0.1
USL <- 1000
n_sim <- 50000
prob_detection_homogeneous(lambda, a, b, f, u, USL, n_sim)
```

---

prob_detection_homogeneous_multiple

Probability of detection estimation for multiple dilution schemes when diluted samples are collected from a homogeneous batch.

Description

prob_detection_homogeneous_multiple provides a probability of detection for multiple dilution schemes in the original sample when samples collected from a homogeneous batch.

Usage

```
prob_detection_homogeneous_multiple(lambda, a, b, f, u, USL, n_sim)
```

Arguments

lambda	the expected cell count (λ).
a	lower domain of the number of cell counts.
b	upper domain of the number of cell counts.
f	final dilution factor.
u	amount put on the plate.
USL	upper specification limit.
n_sim	number of simulations (large simulations provide more precise estimations).

Details

prob_detection_homogeneous_multiple 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. In the homogeneous case, we employed truncated Poisson distribution to model (this section will be updated later on).

Value

Probability of detection when diluted samples are collected from a homogeneous batch.

Examples

```
lambda <- 1000
a <- 0
b <- 300
f <- c(0.01,0.1,1)
u <- c(0.1,0.1,0.1)
USL <- 1000
n_sim <- 50000
prob_detection_homogeneous_multiple(lambda, a, b, f, u, USL, n_sim)
```

---

rtrunpoilog *Generates random deviates from truncated Poisson lognormal distribution.*

Description

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

Usage

```
rtrunpoilog(n, mu, sd, a, b)
```

Arguments

`n`	number of observations. If length(n) > 1 then the length is taken to be the number required.
`mu`	the mean concentration (on the log scale).
`sd`	the standard deviation of the normal distribution (on the log scale).
`a`	lower truncation points (lower domain of the number of cell counts).
`b`	upper truncation points (upper domain of the number of cell counts).

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
mu <-  0
sd <-  1
a <- 0
b <- 300
rtrunpoilog(n, mu, sd, a, b)
```

`true_concentration_heterogeneous`

True concentration level estimation when diluted sample collected from a heterogeneous batch.

Description

These functions provides true concentration level in the original sample when diluted samples collected from a heterogeneous batch.

Usage

```
true_concentration_heterogeneous(mu, sd, a, b, f, u, USL, n_sim)

true_concentration_heterogeneous_multiple(mu, sd, a, b, f, u, USL, n_sim)

true_concentration_curves_heterogeneous(mu_low, mu_high, sd, a, b, f, u, USL, n_sim)
```

Arguments

mu	the mean concentration (on the log scale).
sd	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.
f	final dilution factor.
u	amount put on the plate.
USL	upper specification limit.
n_sim	number of simulations (large simulations provide a more precise estimation).
mu_low	the lower value of the mean concentration (μ) for use in the graphical display's x-axis (on the log scale).
mu_high	the upper value of the mean concentration (μ) for use in the graphical display's x-axis (on the log scale).

Details

Let Y be the count of microorganisms and C be the true concentration level (in counts per ml). When diluted sample collected from heterogeneous (non-homogeneous) batch, Y can be modelled by Poisson lognormal distribution with parameter μ, σ. Let X be the count of microorganisms on a plate, and it can be modelled by truncated Poisson lognormal distribution with parameters μ_d, σ, a, b. Also, λ_d can be written in terms of μ, f and u. It is given by

$$\mu_d = \mu + \log(f) + \log(u)$$

And the true concentration level is given by

$$C = \frac{X}{f * u}$$

where f is final dilution factor and u is amount of diluted sample on plate. Based on the literatures, we used $\sigma = 0.2$ in these dilution process; see Gonzales-Barron et al. (2013, p. 370) and Schothorst et al. (2009).

Value

true concentration level when sample collected from a heterogeneous batch.

References

- Gonzales-Barron, U.A., Pilão Cadavez, V.A., Butler, F., 2013. Statistical approaches for the design of sampling plans for microbiological monitoring of foods, in: Mathematical and Statistical Methods in Food Science and Technology. Wiley, Chichester, UK, pp.363–384.
- Schothorst, M. van, Zwietering, M.H., Ross, T., Buchanan, R.L., Cole, M.B., 2009. Relating microbiological criteria to food safety objectives and performance objectives. Food Control 20, 967–979.

Examples

```
mu_low <- 0
mu_high <- 10
sd <- 0.2
a <- 0
b <- 300
f <- c(0.01,0.1)
u <- c(0.1,0.1)
USL <- 1000
n_sim <- 5000
true_concentration_curves_heterogeneous(mu_low, mu_high, sd, a, b, f, u, USL, n_sim)
```

`true_concentration_homogeneous`

True concentration level estimation when diluted sample collected from a homogeneous batch.

Description

These functions provides true concentration level in the original sample when diluted samples collected from a homogeneous batch.

Usage

```
true_concentration_homogeneous(lambda, a, b, f, u, USL, n_sim)

true_concentration_homogeneous_multiple(lambda, a, b, f, u, USL, n_sim)

true_concentration_curves_homogeneous(lambda_low, lambda_high, a, b, f, u, USL, n_sim)
```

Arguments

`lambda`	the expected cell count (λ).
`a`	lower domain of the number of cell counts.
`b`	upper domain of the number of cell counts.
`f`	final dilution factor.
`u`	amount put on the plate.
`USL`	upper specification limit.
`n_sim`	number of simulations (large simulations provide a more precise estimation).
`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.

Details

Let Y be the count of microorganisms and C be the true concentration level (in counts per ml). When diluted sample collected from homogeneous batch, Y can be modelled by Poisson distribution with parameter λ. Let X be the count of microorganisms on a plate, and it can be modelled by truncated Poisson distribution with parameters λ_d, a, b. Also, λ_d can be written in terms of λ, f and u. It is given by

$$\lambda_d = \lambda * f * u$$

And the true concentration level is given by

$$C = \frac{X}{f * u}$$

Value

true concentration level when the diluted sample collected from a homogeneous batch.

Examples

```
lambda_low <- 0
lambda_high <- 5000
a <- 0
b <- 300
f <- c(0.01,0.1)
u <- c(0.1,0.1)
USL <- 1000
n_sim <- 50000
true_concentration_curves_homogeneous(lambda_low, lambda_high, a, b, f, u, USL, n_sim)
```

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