

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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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)

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AQL_LQL_heterogeneous *AQL and LQL estimations for given dilution schemes when diluted samples are collected from a heterogeneous batch.*

Description

[AQL_LQL_heterogeneous](#) provides estimated AQL and LQL values for given dilution schemes when samples are collected from a heterogeneous batch.

Usage

```
AQL_LQL_heterogeneous(c,mu_low,mu_high,sd,a,b,f,u,USL,n,type,alpha,beta,OC,n_sim)
```

Arguments

c	acceptance number
mu_low	the lower value of the mean microbial count(μ) for use in the graphical display's x-axis.
mu_high	the upper value of the mean microbial count(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 microbial count.
b	upper domain of the number of microbial count.
f	final dilution factor.
u	amount put on the plate.

USL	upper specification limit.
n	number of samples which are used for inspection.
type	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
alpha	producer's risk
beta	consumer's risk
OC	if we need AQL and LQL displayed with the OC curve, set OC = "TRUE"; otherwise, the output only provides the estimated values.
n_sim	number of simulations (large simulations provide more precise estimations).

Details

[AQL_LQL_heterogeneous](#) provides estimated AQL and LQL values for given dilution schemes when samples are collected from a heterogeneous batch. Acceptable Quality Level (AQL) is the acceptable or good quality level at which the probability of acceptance is kept at a high level, which is associated with the producer's risk. Conversely, the limiting Quality Level (LQL) refers to the rejectable or poor quality level at which the probability of acceptance is kept at a low level, which is associated with the consumer's risk.

Value

AQL and LQL when diluted samples are collected from a heterogeneous batch.

Examples

```
c <- 2
mu_low <- 4
mu_high <- 9
sd <- 0.2
a <- 0
b <- 300
f <- 0.01
u <- 0.1
USL <- 1000
alpha <- 0.05
beta <- 0.10
n <- 5
AQL_LQL_heterogeneous(c, mu_low, mu_high, sd, a, b, f, u, USL, n, type = "theory",
  alpha, beta, OC= "TRUE")
AQL_LQL_heterogeneous(c, mu_low, mu_high, sd, a, b, f, u, USL, n, type = "theory",
  alpha, beta, OC= "FALSE")
```

AQL_LQL_homogeneous	<i>AQL and LQL estimations for given dilution schemes when diluted samples are collected from a homogeneous batch.</i>
---------------------	--

Description

[AQL_LQL_homogeneous](#) provides estimated AQL and LQL values for given dilution schemes when samples are collected from a homogeneous batch.

Usage

```
AQL_LQL_homogeneous(c, lambda_low, lambda_high, a, b, f, u, USL, n, type, alpha, beta, OC, n_sim)
```

Arguments

c	acceptance number
lambda_low	the lower value of the expected microbial count(λ) for use in the graphical display's x-axis.
lambda_high	the upper value of the expected microbial count(λ) for use in the graphical display's x-axis.
a	lower domain of the number of microbial count.
b	upper domain of the number of microbial count.
f	final dilution factor.
u	amount put on the plate.
USL	upper specification limit.
n	number of samples which are used for inspection.
type	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
alpha	producer's risk
beta	consumer's risk
OC	if we need AQL and LQL displayed with the OC curve, set OC = "TRUE"; otherwise, the output only provides the estimated values.
n_sim	number of simulations (large simulations provide more precise estimations).

Details

[AQL_LQL_homogeneous](#) provides estimated AQL and LQL values for given dilution schemes when samples are collected from a homogeneous batch. Acceptable Quality Level (AQL) is the acceptable or good quality level at which the probability of acceptance is kept at a high level, which is associated with the producer's risk. Conversely, the limiting Quality Level (LQL) refers to the rejectable or poor quality level at which the probability of acceptance is kept at a low level, which is associated with the consumer's risk.

Value

AQL and LQL when diluted samples are collected from a homogeneous batch.

Examples

```
c <- 2
n <- 5
lambda_low <- 2
lambda_high <- 5000
a <- 0
b <- 300
f <- 0.01
u <- 0.1
USL <- 1000
alpha <- 0.05
beta <- 0.10
```

```
AQL_LQL_homogeneous(c, lambda_low, lambda_high, a, b, f, u, USL, n, type = "theory",
                     alpha, beta, OC = "FALSE")
AQL_LQL_homogeneous(c, lambda_low, lambda_high, a, b, f, u, USL, n, type = "theory",
                     alpha, beta, OC = "TRUE")
```

compare_plans_dilution_1_pd_betabinom

Comparison based on probability of detection curves for different dilution schemes in the first dilution stage testing.

Description

[compare_plans_dilution_1_pd_betabinom](#) provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage testing.

Usage

```
compare_plans_dilution_1_pd_betabinom(S, V0, V1, Clim_lower, Clim_upper, alpha, beta)
```

Arguments

S	amount of sample (in grams) used for diluted solution preparation
V0	dilution volume in the first dilution stage testing.
V1	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
Clim_lower	an lower value of the number of colonies counted on the two dishes retained from two successive dilutions for comparison purposes.
Clim_upper	an upper value of the number of colonies counted on the two dishes retained from two successive dilutions for comparison purposes.
alpha	non-negative parameters of the beta distribution.
beta	non-negative parameters of the beta distribution.

Details

[compare_plans_dilution_1_pd_betabinom](#) provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage testing.

Value

Comparison based on probability of detection curves for different dilution schemes in the first dilution stage testing.

Examples

```
S <- c(1,10,20)
V0 <- 100
V1 <- 1
Clim_lower <- 0
Clim_upper <- 50
alpha <- 1
beta <- 5
compare_plans_dilution_1_pd_betabinom(S, V0,V1, Clim_lower, Clim_upper, alpha, beta)
```

compare_plans_dilution_1_pd_binom

Comparison based on probability of detection curves for different dilution schemes in the first dilution stage testing.

Description

[compare_plans_dilution_1_pd_binom](#) provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage testing.

Usage

```
compare_plans_dilution_1_pd_binom (S, V0, V1, Clim_lower, Clim_upper)
```

Arguments

S	amount of sample (in grams) used for diluted solution preparation
V0	dilution volume in the first dilution stage testing.
V1	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
Clim_lower	an lower value of the number of colonies counted on the two dishes retained from two successive dilutions for comparison purposes.
Clim_upper	an upper value of the number of colonies counted on the two dishes retained from two successive dilutions for comparison purposes.

Details

[compare_plans_dilution_1_pd_binom](#) provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage testing.

Value

Comparison based on probability of detection curves for different dilution schemes in the first dilution stage testing.

Examples

```
S <- c(1,10,20)
V0 <- 100
V1 <- 1
Clim_lower <- 1
Clim_upper <- 1000
compare_plans_dilution_1_pd_binom (S, V0,V1, Clim_lower, Clim_upper)
```

compare_plans_dilution_2_pd_betabinom

Comparison based on probability of detection curves for different dilution schemes in the first dilution stage.

Description

`compare_plans_dilution_2_pd_betabinom` provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage.

Usage

```
compare_plans_dilution_2_pd_betabinom(S, V0, V1, V2, V3, n_sim, Clim_lower, Clim_upper, alpha, beta)
```

Arguments

S	amount of sample (in grams) used for diluted solution preparation
V0	dilution volume in the first dilution stage testing.
V1	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
V2	dilution volume in the first dilution stage testing.
V3	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
n_sim	number of simulations (large simulations provide a more precise estimation).
Clim_lower	an lower value of the number of colonies counted on the two dishes retained from two successive dilutions for comparison purposes.
Clim_upper	an upper value of the number of colonies counted on the two dishes retained from two successive dilutions for comparison purposes.
alpha	non-negative parameters of the beta distribution.
beta	non-negative parameters of the beta distribution.

Details

`compare_plans_dilution_2_pd_betabinom` provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage.

Value

Comparison based on probability of detection curves for different dilution schemes in the first dilution stage.

Examples

```
S <- c(1,10,20)
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
Clim_lower <- 0
```

```

Clim_upper <- 1000
n_sim <- 20000
alpha <- 1
beta <- 5
compare_plans_dilution_2_pd_betabinom(S, V0, V1, V2, V3, n_sim, Clim_lower, Clim_upper, alpha, beta)

```

```
compare_plans_dilution_2_pd_binom
```

Comparison based on probability of detection curves for different dilution schemes in the first dilution stage.

Description

[compare_plans_dilution_2_pd_binom](#) provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage.

Usage

```
compare_plans_dilution_2_pd_binom(S, V0, V1, V2, V3, n_sim, Clim_lower, Clim_upper)
```

Arguments

S	amount of sample (in grams) used for diluted solution preparation
V0	dilution volume in the first dilution stage testing.
V1	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
V2	dilution volume in the first dilution stage testing.
V3	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
n_sim	number of simulations (large simulations provide a more precise estimation).
Clim_lower	an lower value of the number of colonies counted on the two dishes retained from two successive dilutions for comparison purposes.
Clim_upper	an upper value of the number of colonies counted on the two dishes retained from two successive dilutions for comparison purposes.

Details

[compare_plans_dilution_2_pd_binom](#) provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage.

Value

Comparison based on probability of detection curves for different dilution schemes in the first dilution stage.

Examples

```

S <- c(1,10,20)
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
Clim_lower <- 1
Clim_upper <- 1000
n_sim <- 20000
compare_plans_dilution_2_pd_binom(S, V0, V1, V2, V3, n_sim, Clim_lower, Clim_upper)

```

cv_heterogeneous	<i>coefficient of variation estimation when diluted sample collected from a heterogeneous batch.</i>
------------------	--

Description

These functions provides coefficient of variation in the original sample when diluted samples collected from a heterogeneous batch.

Usage

```

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

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

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

```

Arguments

mu	the mean microbial count (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 microbial count (μ) for use in the graphical display's x-axis (on the log scale).
mu_high	the upper value of the mean microbial count (μ) for use in the graphical display's x-axis (on the log scale).

Details

These functions provides coefficient of variation in the original sample when diluted samples collected from a heterogeneous batch.

Value

coefficient of variation when sample collected from a heterogeneous batch.

Examples

```
mu_low <- -5
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 <- 500
cv_curves_heterogeneous(mu_low, mu_high, sd, a, b, f, u, USL, n_sim)
```

cv_homogeneous	<i>coefficient of variation estimation when diluted sample collected from a homogeneous batch.</i>
----------------	--

Description

These functions provides coefficient of variation in the original sample when diluted samples collected from a homogeneous batch.

Usage

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

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

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

Arguments

lambda	the expected microbial count (λ).
a	lower domain of the number of microbial count.
b	upper domain of the number of microbial count.
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 microbial count (λ) for use in the graphical display's x-axis.
lambda_high	the upper value of the expected microbial count (λ) for use in the graphical display's x-axis.

Details

These functions provides coefficient of variation in the original sample when diluted samples collected from a homogeneous batch.

Value

coefficient of variation when the diluted sample collected from a homogeneous batch.

Examples

```
lambda_low <- 1000
lambda_high <- 8000
a <- 0
b <- 300
f <- c(0.01, 0.1)
u <- c(0.1, 0.1)
USL <- 1000
n_sim <- 500
cv_curves_homogeneous(lambda_low, lambda_high, a, b, f, u, USL, n_sim)
```

dilutionrisk	<i>Probability estimations and graphical displays in modelling and assessment of risk based on aerobic plate count (APC) on diluted testing</i>
--------------	---

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 log-normal 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	<i>Comparison based on OC curves for different dilution schemes when the diluted samples collected from a heterogeneous batch.</i>
-------------------------	--

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, type, n_sim)
```

Arguments

c	acceptance number
mu_low	the lower value of the mean microbial count(μ) for use in the graphical display's x-axis.
mu_high	the upper value of the mean microbial count(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.
type	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
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
OC_curves_heterogeneous(c, mu_low, mu_high, sd, a, b, f, u, USL, n)
```

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, type, n_sim)
```

Arguments

<code>c</code>	acceptance number
<code>lambda_low</code>	the lower value of the expected microbial count(λ) for use in the graphical display's x-axis.
<code>lambda_high</code>	the upper value of the expected microbial 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>f</code>	final dilution factor.
<code>u</code>	amount put on the plate.
<code>USL</code>	upper specification limit.
<code>n</code>	number of samples which are used for inspection.
<code>type</code>	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
<code>n_sim</code>	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 <- 1
lambda_high <- 5000
a <- 0
b <- 300
f <- c(0.01, 0.1)
u <- c(0.1, 0.1)
USL <- 1000
n <- 5
OC_curves_homogeneous(c, lambda_low, lambda_high, a, b, f, u, USL, n)
```

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, type, n_sim)
```

Arguments

mu_low	the lower value of the mean microbial count (μ) for use in the graphical display's x-axis (on the log scale).
mu_high	the upper value of the mean microbial count (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.
type	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
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
pd_curves_heterogeneous(mu_low, mu_high, sd, a, b, f, u, USL)
```

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, type, n_sim)
```

Arguments

lambda_low	the lower value of the expected microbial count (λ) for use in the graphical display's x-axis.
lambda_high	the upper value of the expected microbial count (λ) for use in the graphical display's x-axis.
a	lower domain of the number of microbial count.
b	upper domain of the number of microbial count.
f	final dilution factor.
u	amount put on the plate.
USL	upper specification limit.
type	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
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
pd_curves_homogeneous(lambda_low, lambda_high, a, b, f, u, USL)
```

pd_validation_heterogeneous

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

Description

[pd_validation_heterogeneous](#) provides the probability of detection curves for validate the results when samples collected from a heterogeneous batch.

Usage

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

Arguments

mu_low	the lower value of the mean microbial count (μ) for use in the graphical display's x-axis (on the log scale).
mu_high	the upper value of the mean microbial count (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 samples collected from a heterogeneous batch (this section will be updated later on).

Value

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

Examples

```
mu_low <- 1
mu_high <- 12
sd <- 0.2
a <- 0
b <- 300
f <- 0.01
u <- 0.1
USL <- 1000
n_sim <- 50000
pd_validation_heterogeneous(mu_low, mu_high, sd, a, b, f, u, USL, n_sim)
```

pd_validation_homogeneous

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

Description

`pd_validation_homogeneous` provides the probability of detection curves for validate the results when samples collected from a homogeneous batch.

Usage

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

Arguments

<code>lambda_low</code>	the lower value of the expected microbial count (λ) for use in the graphical display's x-axis.
<code>lambda_high</code>	the upper value of the expected microbial count (λ) for use in the graphical display's x-axis.
<code>a</code>	lower domain of the number of microbial count.
<code>b</code>	upper domain of the number of microbial count.
<code>f</code>	final dilution factor.
<code>u</code>	amount put on the plate.
<code>USL</code>	upper specification limit.
<code>n_sim</code>	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 <- 0.01
u <- 0.1
USL <- 1000
n_sim <- 50000
pd_validation_homogeneous(lambda_low, lambda_high, a, b, f, u, USL, n_sim = 500)
pd_validation_homogeneous(lambda_low, lambda_high, a, b, f, u, USL, n_sim = 50000)
```

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, type, n_sim)
```

Arguments

c	acceptance number
mu	the mean microbial count (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.
type	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
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
prob_acceptance_heterogeneous(c, mu, sd, a, b, f, u, USL, n)
```

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, type, n_sim)
```

Arguments

c	acceptance number
mu	the mean microbial count (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.
type	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
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)
u <- c(0.1, 0.1)
USL <- 1000
n <- 5
prob_acceptance_heterogeneous_multiple (c, mu, sd, a, b, f, u, USL, n)
```

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, type, 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.
type	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
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 <- 0.01
u <- 0.1
USL <- 1000
n <- 5
prob_acceptance_homogeneous(c, lambda, a, b, f, u, USL, n)
```

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, type, n_sim)
```

Arguments

<code>c</code>	acceptance number
<code>lambda</code>	the expected microbial count (λ).
<code>a</code>	lower domain of the number of microbial count.
<code>b</code>	upper domain of the number of microbial count.
<code>f</code>	final dilution factor.
<code>u</code>	amount put on the plate.
<code>USL</code>	upper specification limit.
<code>n</code>	number of samples which are used for inspection.
<code>type</code>	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
<code>n_sim</code>	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)
u <- c(0.1, 0.1)
USL <- 1000
n <- 5
prob_acceptance_homogeneous_multiple(c, lambda, a, b, f, u, USL, n)
```

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, type, n_sim)
```

Arguments

<code>mu</code>	the mean microbial count (on the log scale).
<code>sd</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>f</code>	final dilution factor.
<code>u</code>	amount put on the plate.
<code>USL</code>	upper specification limit.
<code>type</code>	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
<code>n_sim</code>	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
prob_detection_heterogeneous(mu, sd, a, b, f, u, USL)
```

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, type, n_sim)
```

Arguments

<code>mu</code>	the mean microbial count (on the log scale).
<code>sd</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>f</code>	vector of final dilution factor.
<code>u</code>	vector of amount put on the plate.
<code>USL</code>	upper specification limit.
<code>type</code>	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
<code>n_sim</code>	number of simulations (large simulations provide a more precise estimation).

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)
u <- c(0.1, 0.1)
USL <- 1000
prob_detection_heterogeneous_multiple(mu, sd, a, b, f, u, USL)
```

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, type, n_sim)
```

Arguments

<code>lambda</code>	the expected microbial count (λ).
<code>a</code>	lower domain of the number of microbial count.
<code>b</code>	upper domain of the number of microbial count.
<code>f</code>	final dilution factor.
<code>u</code>	amount put on the plate.
<code>USL</code>	upper specification limit.
<code>type</code>	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
<code>n_sim</code>	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)
prob_detection_homogeneous(lambda, a, b, f, u, USL, type = "simulation", 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, type, n_sim)
```

Arguments

<code>lambda</code>	the expected microbial count (λ).
<code>a</code>	lower domain of the number of microbial count.
<code>b</code>	upper domain of the number of microbial count.
<code>f</code>	final dilution factor.
<code>u</code>	amount put on the plate.
<code>USL</code>	upper specification limit.
<code>type</code>	what type of the results you would like to consider such as "theory" or "simulation" (default "theory").
<code>n_sim</code>	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)
```

prob_detect_dilution_1_betabinom

Probability of detection for a dilution scheme in the first dilution stage testing.

Description

`prob_detect_dilution_1_betabinom` provides the probability of detection for a dilution scheme in the first dilution stage testing.

Usage

```
prob_detect_dilution_1_betabinom(S, V0, V1, C_cfu, alpha, beta)
```

Arguments

S	amount of sample (in grams) used for diluted solution preparation
V0	dilution volume in the first dilution stage testing.
V1	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
C_cfu	number of colonies counted on the two dishes retained from two successive dilutions.
alpha	non-negative parameters of the beta distribution.
beta	non-negative parameters of the beta distribution.

Details

`prob_detect_dilution_1_betabinom` provides the probability of detection for a dilution scheme in the first dilution stage testing.

Value

Probability of detection for a dilution scheme in the first dilution stage testing.

Examples

```
S <- 25
C_cfu <- 25
V0 <- 100
V1 <- 1
alpha <- 1
beta <- 5
prob_detect_dilution_1_betabinom(S, V0, V1, C_cfu, alpha, beta)
```

prob_detect_dilution_1_binom

Probability of detection for a dilution scheme in the first dilution stage testing.

Description

`prob_detect_dilution_1_binom` provides the probability of detection for a dilution scheme in the first dilution stage testing.

Usage

```
prob_detect_dilution_1_binom(S, V0, V1, C_cfu)
```

Arguments

S	amount of sample (in grams) used for diluted solution preparation
V0	dilution volume in the first dilution stage testing.
V1	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
C_cfu	number of colonies counted on the two dishes retained from two successive dilutions.

Details

`prob_detect_dilution_1_binom` provides the probability of detection for a dilution scheme in the first dilution stage testing.

Value

Probability of detection for a dilution scheme in the first dilution stage testing.

Examples

```
S <- c(1,10,20)
C_cfu <- 25
V0 <- 100
V1 <- 1
prob_detect_dilution_1_binom(S, V0, V1, C_cfu )
```

prob_detect_dilution_2_betabinom

Probability of detection for a dilution scheme in the second dilution stage testing.

Description

[prob_detect_dilution_2_betabinom](#) provides the probability of detection for a dilution scheme in the second dilution stage testing.

Usage

```
prob_detect_dilution_2_betabinom(S, V0,V1,V2,V3,C_cfu, n_sim, alpha, beta)
```

Arguments

S	amount of sample (in grams) used for diluted solution preparation
V0	dilution volume in the first dilution stage testing.
V1	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
V2	dilution volume in the first dilution stage testing.
V3	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
C_cfu	number of colonies counted on the two dishes retained from two successive dilutions.
n_sim	number of simulations (large simulations provide a more precise estimation).
alpha	non-negative parameters of the beta distribution.
beta	non-negative parameters of the beta distribution.

Details

[prob_detect_dilution_2_betabinom](#) provides the probability of detection for a dilution scheme in the second dilution stage testing.

Value

Probability of detection for a dilution scheme in the second dilution stage testing.

Examples

```
S <- 20
C_cfu <- 25
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
C_cfu <- 25
n_sim <- 25000
alpha <- 1
beta <- 5
prob_detect_dilution_2_betabinom(S, V0,V1,V2,V3,C_cfu, n_sim, alpha, beta)
```

prob_detect_dilution_2_binom

Probability of detection for a dilution scheme in the second dilution stage testing.

Description

`prob_detect_dilution_2_binom` provides the probability of detection for a dilution scheme in the second dilution stage testing.

Usage

```
prob_detect_dilution_2_binom(S, V0,V1,V2,V3,C_cfu, n_sim)
```

Arguments

S	amount of sample (in grams) used for diluted solution preparation
V0	dilution volume in the first dilution stage testing.
V1	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
V2	dilution volume in the first dilution stage testing.
V3	the volume of the diluted solution used for testing (which is equal to the plated amount in this study)
C_cfu	number of colonies counted on the two dishes retained from two successive dilutions.
n_sim	number of simulations (large simulations provide a more precise estimation).

Details

`prob_detect_dilution_2_binom` provides the probability of detection for a dilution scheme in the second dilution stage testing.

Value

Probability of detection for a dilution scheme in the second dilution stage testing.

Examples

```
S <- 20
C_cfu <- 25
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
C_cfu <- 25
n_sim <- 25000
prob_detect_dilution_2_binom(S, V0,V1,V2,V3,C_cfu, 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, mu, sd, a, b)
```

Arguments

n	number of observations. If <code>length(n) > 1</code> then the length is taken to be the number required.
mu	the mean microbial count (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 microbial count).
b	upper truncation points (upper domain of the number of microbial count).

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 microbial count (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 microbial count (μ) for use in the graphical display's x-axis (on the log scale).
mu_high	the upper value of the mean microbial count (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 microbial count (λ).
a	lower domain of the number of microbial count.
b	upper domain of the number of microbial count.
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 microbial count (λ) for use in the graphical display's x-axis.
lambda_high	the upper value of the expected microbial 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 <- 1
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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