# Package 'dilutionrisk'

April 12, 2023

**Type** Package

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

**Version** 0.0.1

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

**URL** https://github.com/Mayooran1987/dilutionrisk

**BugReports** https://github.com/Mayooran1987/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, Rcpp, stats, poilog

**LinkingTo** Rcpp

**Suggests** spelling,
testthat (>= 3.0.0),
covr

**RoxygenNote** 7.2.3

**Depends** R (>= 4.0)

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

**Language** en-US

**Config/testthat/edition** 3

## R topics documented:

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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($\mu$) for use in the graphical display's x-axis. |
| mu_high | the upper value of the mean microbial count($\mu$) 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` *AQL and LQL estimations for given dilution schemes when diluted samples are collected from a homogeneous batch.*

---

## 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($\lambda$) for use in the graphical display's x-axis. |
| `lambda_high` | the upper value of the expected microbial count($\lambda$) 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_pln`

*Comparison based on beta binomial distribution-based probability of detection curves for different dilution schemes in the first dilution stage.*

---

## Description

`compare_plans_dilution_1_pd_betabinom_pln` provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.

## Usage

```
compare_plans_dilution_1_pd_betabinom_pln(S, sd, V0, V1, mu_lower, mu_upper, alpha, beta)
```

## Arguments

| | |
|---|---|
| `S` | amount of sample (in grams) used for diluted solution preparation |
| `sd` | the standard deviation of the normal distribution (on the log scale). |
| `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) |
| `mu_lower` | the lower value of the mean microbial count($\mu$) for use in the graphical display's x-axis. |
| `mu_upper` | the upper value of the mean microbial count($\mu$) for use in the graphical display's x-axis. |
| `alpha` | non-negative parameters of the beta distribution. |
| `beta` | non-negative parameters of the beta distribution. |

## Details

compare_plans_dilution_1_pd_betabinom_pln provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution. (This section will be updated later on.)

## Value

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

## Examples

```
S <- c(25,125,250)
sd <- 0.8
V0 <- 100
V1 <- 1
mu_lower <- -8
mu_upper <- 8
alpha <- 1
beta <- 5
compare_plans_dilution_1_pd_betabinom_pln(S, sd, V0, V1, mu_lower, mu_upper, alpha, beta)
```

---

# compare_plans_dilution_1_pd_betabinom_pois

*Comparison based on beta binomial distribution-based probability of detection curves for different dilution schemes in the first dilution stage.*

---

## Description

compare_plans_dilution_1_pd_betabinom_pois provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson distribution.

## Usage

```
compare_plans_dilution_1_pd_betabinom_pois(S, V0, V1, lambda_lower, lambda_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) |
| lambda_lower | an lower value of the expected number of microorganisms count per gram. |
| lambda_upper | an upper value of the expected number of microorganisms count per gram. |
| alpha | non-negative parameters of the beta distribution. |
| beta | non-negative parameters of the beta distribution. |

## Details

compare_plans_dilution_1_pd_betabinom_pois provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson distribution.(This section will be updated later on.)

## Value

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

## Examples

```
S <- c(25,125,250)
V0 <- 100
V1 <- 1
lambda_lower <- 0
lambda_upper <- 40
alpha <- 1
beta <- 5
compare_plans_dilution_1_pd_betabinom_pois(S, V0, V1, lambda_lower, lambda_upper, alpha, beta)
```

---

# compare_plans_dilution_1_pd_binom_pln

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

---

## Description

compare_plans_dilution_1_pd_binom_pln provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.

## Usage

```
compare_plans_dilution_1_pd_binom_pln(S, sd, V0, V1, mu_lower, mu_upper)
```

## Arguments

| | |
|---|---|
| S | amount of sample (in grams) used for diluted solution preparation |
| sd | the standard deviation of the normal distribution (on the log scale). |
| 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) |
| mu_lower | the lower value of the mean microbial count($\mu$) for use in the graphical display's x-axis. |
| mu_upper | the upper value of the mean microbial count($\mu$) for use in the graphical display's x-axis. |

## Details

compare_plans_dilution_1_pd_binom_pln provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.(This section will be updated later on.)

## Value

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

## Examples

```
S <- c(25,125,250)
sd <- 0.8
V0 <- 100
V1 <- 1
mu_lower <- -4
mu_upper <- -1
compare_plans_dilution_1_pd_binom_pln(S, sd, V0, V1, mu_lower, mu_upper)
```

---

# compare_plans_dilution_1_pd_binom_pois

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

---

## Description

compare_plans_dilution_1_pd_binom_pois provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson distribution.

## Usage

```
compare_plans_dilution_1_pd_binom_pois (S, V0, V1, lambda_lower, lambda_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) |
| lambda_lower | an lower value of the expected number of microorganisms count per gram. |
| lambda_upper | an upper value of the expected number of microorganisms count per gram. |

## Details

compare_plans_dilution_1_pd_binom_pois provides graphical displays of the probability of the detection curves for dilution schemes in the first dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson distribution.(This section will be updated later on.)

## Value

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

## Examples

```
S <- c(25,125,250)
V0 <- 100
V1 <- 1
lambda_lower <- 0
lambda_upper <- 30
compare_plans_dilution_1_pd_binom_pois (S, V0, V1, lambda_lower, lambda_upper)
```

---

`compare_plans_dilution_2_pd_betabinom_pln`

*Comparison based on beta binomial distribution-based probability of detection curves for different dilution schemes in the second dilution stage.*

---

## Description

`compare_plans_dilution_2_pd_betabinom_pln` provides graphical displays of the probability of the detection curves for dilution schemes in the second dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.

## Usage

```
compare_plans_dilution_2_pd_betabinom_pln (S,sd, V0, V1, V2, V3, n_sim, mu_lower, mu_upper, alpha,
```

## Arguments

| | |
|---|---|
| `S` | amount of sample (in grams) used for diluted solution preparation |
| `sd` | the standard deviation of the normal distribution (on the log scale). |
| `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). |
| `mu_lower` | the lower value of the mean microbial count($\mu$) for use in the graphical display's x-axis. |
| `mu_upper` | the upper value of the mean microbial count($\mu$) for use in the graphical display's x-axis. |
| `alpha` | non-negative parameters of the beta distribution. |
| `beta` | non-negative parameters of the beta distribution. |

## Details

compare_plans_dilution_2_pd_betabinom_pln provides graphical displays of the probability of the detection curves for dilution schemes in the second dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.(This section will be updated later on.)

## Value

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

## Examples

```
S <- c(25,125,250)
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
n_sim <- 20000
mu_lower <- -3
mu_upper <- -1
alpha <- 1
beta <- 5
compare_plans_dilution_2_pd_betabinom_pln (S,sd, V0, V1, V2, V3, n_sim, mu_lower, mu_upper, alpha, beta)
```

---

# compare_plans_dilution_2_pd_betabinom_pois

*Comparison based on beta binomial distribution-based probability of detection curves for different dilution schemes in the second dilution stage.*

---

## Description

compare_plans_dilution_2_pd_betabinom_pois provides graphical displays of the probability of the detection curves for dilution schemes in the second dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson distribution.

## Usage

```
compare_plans_dilution_2_pd_betabinom_pois(S, V0, V1, V2, V3, n_sim, lambda_lower, lambda_upper, al
```

## 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). |
| lambda_lower | an lower value of the expected number of microorganisms count per gram. |
| lambda_upper | an upper value of the expected number of microorganisms count per gram |
| alpha | non-negative parameters of the beta distribution. |
| beta | non-negative parameters of the beta distribution. |

## Details

compare_plans_dilution_2_pd_betabinom_pois provides graphical displays of the probability of the detection curves for dilution schemes in the second dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson distribution.(This section will be updated later on.)

## Value

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

## Examples

```
S <- c(25,125,250)
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
n_sim <- 20000
lambda_lower <- 0
lambda_upper <- 50
alpha <- 1
beta <- 5
compare_plans_dilution_2_pd_betabinom_pois(S, V0, V1, V2, V3, n_sim, lambda_lower, lambda_upper, alpha, beta)
```

---

# compare_plans_dilution_2_pd_binom_pln

*Comparison based on binomial distribution-based probability of detection curves for different dilution schemes in the second dilution stage.*

---

## Description

compare_plans_dilution_2_pd_binom_pln provides graphical displays of the probability of the detection curves for dilution schemes in the second dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.

## Usage

```
compare_plans_dilution_2_pd_binom_pln(S, sd,V0, V1, V2, V3, n_sim, mu_lower, mu_upper)
```

### Arguments

| | |
|---|---|
| S | amount of sample (in grams) used for diluted solution preparation |
| sd | the standard deviation of the normal distribution (on the log scale). |
| 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). |
| mu_lower | the lower value of the mean microbial count($\mu$) for use in the graphical display's x-axis. |
| mu_upper | the upper value of the mean microbial count($\mu$) for use in the graphical display's x-axis. |

### Details

compare_plans_dilution_2_pd_binom_pln provides graphical displays of the probability of the detection curves for dilution schemes in the second dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.(This section will be updated later on.)

### Value

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

### Examples

```
S <- c(25,125,250)
sd <- 0.8
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
n_sim <- 20000
mu_lower <- -3
mu_upper <- 6
compare_plans_dilution_2_pd_binom_pln(S, sd,V0, V1, V2, V3, n_sim, mu_lower, mu_upper)
```

---

## compare_plans_dilution_2_pd_binom_pois

*Comparison based on binomial distribution-based probability of detection curves for different dilution schemes in the second dilution stage.*

---

### Description

compare_plans_dilution_2_pd_binom_pois provides graphical displays of the probability of the detection curves for dilution schemes in the second dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson distribution.

## Usage

```
compare_plans_dilution_2_pd_binom_pois(S, V0, V1, V2, V3, n_sim, lambda_lower, lambda_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). |
| lambda_lower | an lower value of the expected number of microorganisms count per gram. |
| lambda_upper | an upper value of the expected number of microorganisms count per gram. |

## Details

compare_plans_dilution_2_pd_binom_pois provides graphical displays of the probability of the detection curves for dilution schemes in the second dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson distribution. (This section will be updated later on.)

## Value

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

## Examples

```
S <- c(25,125,250)
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
n_sim <- 20000
lambda_lower <- 1
lambda_upper <- 30
compare_plans_dilution_2_pd_binom_pois(S, V0, V1, V2, V3, n_sim, lambda_lower, lambda_upper)
```

---

# cv_heterogeneous *coefficient of variation estimation when diluted sample collected from a heterogeneous batch.*

---

## 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 ($\mu$) for use in the graphical display's x-axis (on the log scale). |
| mu_high | the upper value of the mean microbial count ($\mu$) 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 *coefficient of variation estimation when diluted sample collected from a homogeneous batch.*

## 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 ($\lambda$). |
| 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 ($\lambda$) for use in the graphical display's x-axis. |
| lambda_high | the upper value of the expected microbial count ($\lambda$) 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` *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, type, n_sim)
```

## Arguments

| | |
|---|---|
| `c` | acceptance number |
| `mu_low` | the lower value of the mean microbial count($\mu$) for use in the graphical display's x-axis. |
| `mu_high` | the upper value of the mean microbial count($\mu$) 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

| | |
|---|---|
| c | acceptance number |
| lambda_low | the lower value of the expected microbial count($\lambda$) for use in the graphical display's x-axis. |
| lambda_high | the upper value of the expected microbial count($\lambda$) 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. |
| 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_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 ($\mu$) for use in the graphical display's x-axis (on the log scale). |
| mu_high | the upper value of the mean microbial count ($\mu$) 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 ($\lambda$) for use in the graphical display's x-axis. |
| lambda_high | the upper value of the expected microbial count ($\lambda$) 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 ($\mu$) for use in the graphical display's x-axis (on the log scale). |
| mu_high | the upper value of the mean microbial count ($\mu$) 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

| | |
|---|---|
| lambda_low | the lower value of the expected microbial count ($\lambda$) for use in the graphical display's x-axis. |
| lambda_high | the upper value of the expected microbial count ($\lambda$) 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_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 <- 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 ($\lambda$). |
| 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

| | |
|---|---|
| c | acceptance number |
| lambda | the expected microbial count ($\lambda$). |
| 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"). |
| 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)
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

| | |
|---|---|
| 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. |
| 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 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

| | |
|---|---|
| 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 | vector of final dilution factor. |
| u | vector of 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 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

| | |
|---|---|
| lambda | the expected microbial count ($\lambda$). |
| 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 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

| | |
|---|---|
| lambda | the expected microbial count ($\lambda$). |
| 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

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_pln

*Beta binomial distribution-based probability of detection for a dilution scheme in the first dilution stage testing.*

---

### Description

prob_detect_dilution_1_betabinom_pln provides a probability of detection for a dilution scheme in the first dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.

### Usage

```
prob_detect_dilution_1_betabinom_pln(S, mu, sd, V0, V1, alpha, beta)
```

### Arguments

| | |
|---|---|
| S | amount of sample (in grams) used for diluted solution preparation |
| mu | the mean microbial count (on the log scale). |
| sd | the standard deviation of the normal distribution (on the log scale). |
| 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) |
| alpha | non-negative parameters of the beta distribution. |
| beta | non-negative parameters of the beta distribution. |

### Details

prob_detect_dilution_1_betabinom_pln provides a probability of detection for a dilution scheme in the first dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.(This section will be updated later on.)

### Value

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

### Examples

```
S <- 25
mu <- -1
sd <- 0.8
V0 <- 100
V1 <- 1
alpha <- 1
beta <- 5
prob_detect_dilution_1_betabinom_pln(S, mu, sd, V0, V1, alpha, beta)
```

---

## prob_detect_dilution_1_betabinom_pois

*Beta binomial distribution-based probability of detection for a dilution scheme in the first dilution stage testing.*

---

### Description

prob_detect_dilution_1_betabinom_pois provides a probability of detection for a dilution scheme in the first dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson distribution.

### Usage

```
prob_detect_dilution_1_betabinom_pois(S, lambda, V0, V1, alpha, beta)
```

### Arguments

| | |
|---|---|
| S | amount of sample (in grams) used for diluted solution preparation |
| lambda | the expected number of microorganisms count per gram |
| 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) |
| alpha | non-negative parameters of the beta distribution. |
| beta | non-negative parameters of the beta distribution. |

### Details

prob_detect_dilution_1_betabinom_pois provides a probability of detection for a dilution scheme in the first dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson distribution.(This section will be updated later on.)

### Value

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

### Examples

```
S <- 25
lambda  <- 10
V0 <- 100
V1 <- 1
alpha <- 1
beta <- 5
prob_detect_dilution_1_betabinom_pois(S, lambda, V0, V1, alpha, beta)
```

---

## prob_detect_dilution_1_binom_pln

*Binomial distribution-based probability of detection for a dilution scheme in the first dilution stage testing.*

---

### Description

prob_detect_dilution_1_binom_pln provides a probability of detection for a dilution scheme in the first dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.

### Usage

```
prob_detect_dilution_1_binom_pln(S,mu,sd, V0, V1)
```

### Arguments

| | |
|---|---|
| S | amount of sample (in grams) used for diluted solution preparation |
| mu | the mean microbial count (on the log scale). |
| sd | the standard deviation of the normal distribution (on the log scale). |
| 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) |

### Details

prob_detect_dilution_1_binom_pln provides a probability of detection for a dilution scheme in the first dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.(This section will be updated later on.)

### Value

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

### Examples

```
S <- c(1,10,20)
mu  <- 25
sd <- 0.8
V0 <- 100
V1 <- 1
prob_detect_dilution_1_binom_pln(S,mu,sd, V0, V1)
```

---

## prob_detect_dilution_1_binom_pois

*Binomial distribution-based probability of detection for a dilution scheme in the first dilution stage testing.*

---

### Description

prob_detect_dilution_1_binom_pois provides a probability of detection for a dilution scheme in the first dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson distribution.

### Usage

```
prob_detect_dilution_1_binom_pois(S,lambda, V0, V1)
```

### Arguments

| | |
|---|---|
| S | amount of sample (in grams) used for diluted solution preparation |
| lambda | the expected number of microorganisms count per gram |
| 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) |

### Details

prob_detect_dilution_1_binom_pois provides a probability of detection for a dilution scheme in the first dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson distribution.(This section will be updated later on.)

### Value

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

## Examples

```
S <- c(1,10,20)
lambda  <- 10
V0 <- 100
V1 <- 1
prob_detect_dilution_1_binom_pois(S,lambda, V0, V1)
```

---

`prob_detect_dilution_2_betabinom_pln`
*Beta binomial distribution-based probability of detection for a dilution scheme in the second dilution stage testing.*

---

## Description

`prob_detect_dilution_2_betabinom_pln` provides a probability of detection for a dilution scheme in the second dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.

## Usage

```
prob_detect_dilution_2_betabinom_pln(S,mu,sd, V0, V1, V2, V3, n_sim, alpha, beta)
```

## Arguments

| | |
|---|---|
| `S` | amount of sample (in grams) used for diluted solution preparation |
| `mu` | the mean microbial count (on the log scale). |
| `sd` | the standard deviation of the normal distribution (on the log scale). |
| `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). |
| `alpha` | non-negative parameters of the beta distribution. |
| `beta` | non-negative parameters of the beta distribution. |

## Details

`prob_detect_dilution_2_betabinom_pln` provides a probability of detection for a dilution scheme in the second dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution. (This section will be updated later on.)

## Value

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

## Examples

```
S <- 20
mu <- -1
sd <- 0.8
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
n_sim <- 25000
alpha <- 1
beta <- 5
prob_detect_dilution_2_betabinom_pln(S,mu,sd, V0, V1, V2, V3, n_sim, alpha, beta)
```

---

# prob_detect_dilution_2_betabinom_pois

*Beta binomial distribution-based probability of detection for a dilution scheme in the second dilution stage testing.*

---

## Description

prob_detect_dilution_2_betabinom_pois provides a probability of detection for a dilution scheme in the second dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson distribution.

## Usage

```
prob_detect_dilution_2_betabinom_pois(S, lambda, V0, V1, V2, V3, n_sim, alpha, beta)
```

## Arguments

| | |
|---|---|
| S | amount of sample (in grams) used for diluted solution preparation |
| lambda | the expected number of microorganisms count per gram |
| 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). |
| alpha | non-negative parameters of the beta distribution. |
| beta | non-negative parameters of the beta distribution. |

## Details

prob_detect_dilution_2_betabinom_pois provides a probability of detection for a dilution scheme in the second dilution stage based on the beta binomial distribution, while the count of microorganisms is modelled by Poisson distribution.(This section will be updated later on.)

## Value

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

## Examples

```
S <- 20
lambda  <- 10
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
n_sim <- 25000
alpha <- 1
beta <- 5
prob_detect_dilution_2_betabinom_pois(S, lambda, V0, V1, V2, V3, n_sim, alpha, beta)
```

---

`prob_detect_dilution_2_binom_pln` *Binomial distribution-based probability of detection for a dilution scheme in the second dilution stage testing.*

---

## Description

prob_detect_dilution_2_binom_pln provides a probability of detection for a dilution scheme in the second dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.

## Usage

```
prob_detect_dilution_2_binom_pln (S,mu,sd, V0, V1, V2, V3, n_sim)
```

## Arguments

| | |
|---|---|
| S | amount of sample (in grams) used for diluted solution preparation |
| mu | the mean microbial count (on the log scale). |
| sd | the standard deviation of the normal distribution (on the log scale). |
| 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). |

## Details

prob_detect_dilution_2_binom_pln provides a probability of detection for a dilution scheme in the second dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson lognormal distribution.(This section will be updated later on.)

## Value

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

## Examples

```
S <- 20
mu  <- 25
sd <- 0.8
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
n_sim <- 25000
prob_detect_dilution_2_binom_pln (S,mu,sd, V0, V1, V2, V3, n_sim)
```

---

`prob_detect_dilution_2_binom_pois`
*Binomial distribution-based probability of detection for a dilution scheme in the second dilution stage testing.*

---

## Description

`prob_detect_dilution_2_binom_pois` provides a probability of detection for a dilution scheme in the second dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson distribution.

## Usage

```
prob_detect_dilution_2_binom_pois(S,lambda, V0, V1, V2, V3, n_sim)
```

## Arguments

| | |
|---|---|
| `S` | amount of sample (in grams) used for diluted solution preparation |
| `lambda` | the expected number of microorganisms count per gram |
| `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). |

## Details

`prob_detect_dilution_2_binom_pois` provides a probability of detection for a dilution scheme in the second dilution stage based on the binomial distribution, while the count of microorganisms is modelled by Poisson distribution.(This section will be updated later on.)

## Value

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

## Examples

```
S <- 20
lambda  <- 10
V0 <- 100
V1 <- 1
V2 <- 10
V3 <- 1
n_sim <- 25000
prob_detect_dilution_2_binom_pois(S,lambda, V0, V1, V2, V3, 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 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 ($\mu$) for use in the graphical display's x-axis (on the log scale). |
| `mu_high` | the upper value of the mean microbial count ($\mu$) 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 $\mu, \sigma$. Let X be the count of microorganisms

on a plate, and it can be modelled by truncated Poisson lognormal distribution with parameters $\mu_d, \sigma, a, b$. Also, $\lambda_d$ can be written in terms of $\mu$,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 ($\lambda$). |
| 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 ($\lambda$) for use in the graphical display's x-axis. |
| lambda_high | the upper value of the expected microbial count ($\lambda$) 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 $\lambda$. Let X be the count of microorganisms on a plate, and it can be modelled by truncated Poisson distribution with parameters $\lambda_d, a, b$. Also, $\lambda_d$ can be written in terms of $\lambda$,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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