Package 'uneqmixr'

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Type Package

Title Modelling the Quantity of Material Sampled in the Risk Assessment

Version 0.0.1

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URL https://github.com/Mayooran1987/uneqmixr

BugReports https://github.com/Mayooran1987/uneqmixr/issues

Description This package allows practitioners to get probability estimations and graphical displays in the risk assessment. This study mainly focuses on the risk assessment when aggregating unequal incremental samples in the production process.

License GPL (>= 2)

Encoding UTF-8

LazyData true

Imports extraDistr, ggplot2, ggthemes, reshape2, stats

Suggests spelling, testthat

RoxygenNote 7.2.3

Depends R (>= 4.0)

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Language en-US

R topics documented:

`AOQL_scenarios` *Construction of AOQ curve and calculate AOQL value based on average microbial counts*

Description

`AOQL_scenarios` provides the Average Outgoing Quality (AOQ) curve and calculates Average Outgoing Quality Level (AOQL) value based on expected microbial counts in each scenario.

Usage

```
AOQL_scenarios(c,llim, sd, m1, m2, scenario, n, type, K, n_sim)
```

Arguments

`c`	acceptance number
`llim`	the upper limit for graphing the arithmetic mean of cell count
`sd`	standard deviation on the log10 scale (default value 0.8).
`m1`	the vector of the first set of incremental samples (with equal/unequal weights).
`m2`	the vector of the second set of incremental samples (with equal/unequal weights).
`scenario`	what scenario we have considered such as `"1"`or `"2"`or `"3"`
`n`	number of aggregate samples which are used for inspection.
`type`	what type of the results you would like to consider such as "theory" or "simulation".
`K`	dispersion parameter of the Poisson gamma distribution (default value 0.25)
`n_sim`	number of simulations (large simulations provide more precise estimation).

Details

Since p_a is the probability of acceptance, λ is the arithmetic mean of cell count and the outgoing contaminated arithmetic mean of cell count of incremental samples is given by AOQ as the product λp_a. The quantity $AOQL$ is defined as the maximum proportion of outgoing contaminated incremental samples and is given by

$$AOQL = \max_{\lambda \geq 0} \lambda p_a$$

Value

AOQ curve and AOQL value based on expected microbial counts in each scenario.

See Also

scenario_1_pa, scenario_2_pa, scenario_3_pa

Examples

```
c <- 0
llim <- 0.02
sd <- 0.8
m1 <- c(10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10)
m2 <- c(15,5,5,5,10,5,10,5,15,10,5,10,5,25,10,5,10,5,5,10,5,15,10,
5,5,20,5,10,5,10,20,5,10,30,5,20,5,10,5,10,20,15,10,15,10,
10,5,10,15,5)
n <- 10
AOQL_scenarios(c,llim, sd, m1, m2, scenario = "1", n, type = "theory")
```

`compare_ex_var_scenario_1`

Graphical displays of expectation or variance of different sampling schemes under scenario 1.

Description

`compare_ex_var_scenario_1` provides graphical displays based on expectation or variance under scenario 1 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
compare_ex_var_scenario_1(mulow, muhigh, sd, m1, m2, measure)
```

Arguments

`mulow`	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
`muhigh`	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
`sd`	standard deviation on the log10 scale (default value 0.8).

m1	the vector of the first set of incremental samples (with equal/unequal weights).
m2	the vector of the second set of incremental samples (with equal/unequal weights).
measure	what type of measure you would like to consider for the graph, such as "expectation" or "variance".

Details

compare_ex_var_scenario_1 provides graphical displays based on expectation or variance under scenario 1 of modelling the quantity of material sampled in the risk assessment study. Under this scenario (a lot with homogeneous contaminations), we employed Poisson distribution to the model number of micro-organisms in the incremental samples. (this section will be updated later on)

Value

Graphical displays based on expectation or variance under lot with homogeneous contaminations.

Examples

```
mulow <- -1
muhigh <- 1
sd <- 0.8
m1 <- c(10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10)
m2 <- c(15,5,5,5,10,5,10,5,15,10,5,10,5,25,10,5,10,5,5,10,5,15,10,
5,5,20,5,10,5,10,20,5,10,30,5,20,5,10,5,10,20,15,10,15,10,
10,5,10,15,5)
compare_ex_var_scenario_1(mulow, muhigh, sd = 0.8, m1, m2, measure = "variance")
compare_ex_var_scenario_1(mulow, muhigh, sd = 0.8, m1, m2, measure =  "expectation")
```

---

compare_ex_var_scenario_2

Graphical displays of expectation or variance of different sampling schemes under scenario 2.

Description

compare_ex_var_scenario_2 provides graphical displays based on expectation or variance under scenario 2 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
compare_ex_var_scenario_2(mulow, muhigh, sd, m1, m2, measure)
```

Arguments

mulow	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
muhigh	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
sd	standard deviation on the log10 scale (default value 0.8).

m1	the vector of the first set of incremental samples (with equal/unequal weights).
m2	the vector of the second set of incremental samples (with equal/unequal weights).
measure	what type of measure you would like to consider for the graph, such as "expectation" or "variance".

Details

compare_ex_var_scenario_2 provides graphical displays based on expectation or variance under scenario 2 of modelling the quantity of material sampled in the risk assessment study. Under this scenario (a lot with homogeneous contaminations), we employed Poisson lognormal distribution to the model number of micro-organisms in the incremental samples. (this section will be updated later on)

Value

Graphical displays based on expectation or variance when lot with heterogeneous and high-level contamination.

Examples

```
mulow <- -2
muhigh <- 2
m1 <- c(10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10)
m2 <- c(15,5,5,5,10,5,10,5,15,10,5,10,5,25,10,5,10,5,5,10,5,15,10,
5,5,20,5,10,5,10,20,5,10,30,5,20,5,10,5,10,20,15,10,15,10,
10,5,10,15,5)
compare_ex_var_scenario_2(mulow, muhigh, sd = 0.8, m1, m2, measure = "variance")
compare_ex_var_scenario_2(mulow, muhigh, sd = 0.8, m1, m2, measure =  "expectation")
```

---

compare_ex_var_scenario_3

Graphical displays of expectation or variance of different sampling schemes under scenario 3.

Description

compare_ex_var_scenario_3 provides graphical displays based on expectation or variance under scenario 3 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
compare_ex_var_scenario_3(mulow, muhigh, sd, m1, m2, K, measure)
```

Arguments

mulow	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
muhigh	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.

sd	standard deviation on the log10 scale (default value 0.8).
m1	the vector of the first set of incremental samples (with equal/unequal weights).
m2	the vector of the second set of incremental samples (with equal/unequal weights).
K	shape parameter (default value 0.25).
measure	what type of measure you would like to consider for the graph, such as "expectation" or "variance".

Details

compare_ex_var_scenario_3 provides a probability of acceptance under scenario 3 of modelling the quantity of material sampled in the risk assessment study. Under this scenario (a lot with homogeneous contaminations), we employed Poisson gamma distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu + log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Graphical displays based on expectation or variance when lot with heterogeneous and low-level contamination.

Examples

```
mulow <- 0
muhigh <- 2
m1 <- c(10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10)
m2 <- c(15,5,5,5,10,5,10,5,15,10,5,10,5,25,10,5,10,5,5,10,5,15,10,
5,5,20,5,10,5,10,20,5,10,30,5,20,5,10,5,10,20,15,10,15,10,
10,5,10,15,5)
K <- 0.05
compare_ex_var_scenario_3(mulow, muhigh, sd = 0.8, m1, m2, K, measure = "variance")
compare_ex_var_scenario_3(mulow, muhigh, sd = 0.8, m1, m2, K, measure =  "expectation")
```

---

compare_prevalence_scenario_4

Graphical displays of prevalence before inspection of different sampling schemes under scenario 4.

Description

compare_prevalence_scenario_4 provides graphical displays based on prevalence before inspection under scenario 4 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
compare_prevalence_scenario_4(mulow, muhigh, sd, m1, m2, l, type, n_sim)
```

Arguments

mulow	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
muhigh	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
sd	standard deviation on the log10 scale (default value 0.8).
m1	the vector of the first set of incremental samples (with equal/unequal weights).
m2	the vector of the second set of incremental samples (with equal/unequal weights).
l	the number of lots in the production process.
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

compare_prevalence_scenario_4 provides graphical displays based on prevalence before inspection under scenario 4 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

Graphical displays based on prevalence before inspection when lot with homogeneous contamination and contamination levels fluctuate from lot to lot by using theoretical or simulation-based results.

Examples

```
mulow <- -6
muhigh <- 1
m1 <- c(10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10)
m2 <- c(15,5,5,5,10,5,10,5,15,10,5,10,5,25,10,5,10,5,5,10,5,15,10,
5,5,20,5,10,5,10,20,5,10,30,5,20,5,10,5,10,20,15,10,15,10,
10,5,10,15,5)
l <- 5000
compare_prevalence_scenario_4(mulow, muhigh, sd = 0.8, m1, m2, l, type = "theory")
```

---

compare_prevalence_scenario_5

Graphical displays of prevalence before inspection of different sampling schemes under scenario 5.

Description

compare_prevalence_scenario_5 provides graphical displays based on prevalence before inspection under scenario 5 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
compare_prevalence_scenario_5(mulow, muhigh, sd, m1, m2, l, type, n_sim)
```

Arguments

mulow	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
muhigh	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
sd	standard deviation on the log10 scale (default value 0.8).
m1	the vector of the first set of incremental samples (with equal/unequal weights).
m2	the vector of the second set of incremental samples (with equal/unequal weights).
l	the number of lots in the production process.
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

compare_prevalence_scenario_5 provides graphical displays based on prevalence before inspection under scenario 5 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

Graphical displays based on prevalence before inspection when lot with heterogeneous contamination and contamination levels fluctuate from lot to lot by using theoretical or simulation-based results.

Examples

```
mulow <- -6
muhigh <- 1
m1 <- c(10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10)
m2 <- c(15,5,5,5,10,5,10,5,15,10,5,10,5,25,10,5,10,5,5,10,5,15,10,
5,5,20,5,10,5,10,20,5,10,30,5,20,5,10,5,10,20,15,10,15,10,
10,5,10,15,5)
l <- 2000
compare_prevalence_scenario_5(mulow, muhigh, sd = 0.8, m1, m2, l,
type = "theory")
```

`Ex_var_scenario_1` *Expected value or variance estimation of microorganism in the aggregate sample under scenario 1.*

Description

`Ex_var_scenario_1` provides the expected value or variance of the number of microorganisms in the aggregate sample under scenario 1 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
Ex_var_scenario_1(mu, sd = 0.8, m, type, measure, n_sim)
```

Arguments

`mu`	the the mean concentration (μ).
`sd`	standard deviation on the log10 scale (default value 0.8).
`m`	the vector of incremental samples (with equal/unequal weights).
`type`	what type of the results you would like to consider such as "theory" or "simulation".
`measure`	what type of measure you would like to consider for the graph, such as "expectation" or "variance".
`n_sim`	number of simulations (large simulations provide more precise estimation).

Details

`Ex_var_scenario_1` provides the expected value or variance of the number of microorganisms in the aggregate sample under scenario 1 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

expected value or variance of the number of microorganisms in the aggregate sample.

Examples

```
mu <- 2
sd <- 0.8
m <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
Ex_var_scenario_1(mu, sd = 0.8, m, type = "theory",  measure = "expectation")
Ex_var_scenario_1(mu, sd = 0.8, m, type = "simulation",  measure = "expectation", n_sim = 2000000)
Ex_var_scenario_1(mu, sd = 0.8, m, type = "theory",  measure = "variance")
Ex_var_scenario_1(mu, sd = 0.8, m, type = "simulation",  measure = "variance", n_sim = 2000000)
```

`Ex_var_scenario_2` *Expected value or variance estimation of microorganism in the aggregate sample under scenario 2.*

Description

`Ex_var_scenario_2` provides the expected value or variance of the number of microorganisms in the aggregate sample under scenario 2 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
Ex_var_scenario_2(mu, sd = 0.8, m, type, measure, n_sim)
```

Arguments

`mu`	the the mean concentration (μ).
`sd`	standard deviation on the log10 scale (default value 0.8).
`m`	the vector of incremental samples (with equal/unequal weights).
`type`	what type of the results you would like to consider such as "theory" or "simulation".
`measure`	what type of measure you would like to consider for the graph, such as "expectation" or "variance".
`n_sim`	number of simulations (large simulations provide more precise estimation).

Details

`Ex_var_scenario_2` provides the expected value or variance of the number of microorganisms in the aggregate sample under scenario 2 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

expected value or variance of the number of microorganisms in the aggregate sample.

Examples

```
mu <- 2
sd <- 0.8
m <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
Ex_var_scenario_2(mu, sd = 0.8, m, type = "theory",  measure = "expectation")
Ex_var_scenario_2(mu, sd = 0.8, m, type = "simulation",  measure = "expectation", n_sim = 2000000)
Ex_var_scenario_2(mu, sd = 0.8, m, type = "theory",  measure = "variance")
Ex_var_scenario_2(mu, sd = 0.8, m, type = "simulation",  measure = "variance", n_sim = 2000000)
```

`Ex_var_scenario_3` *Expected value or variance estimation of microorganism in the aggregate sample under scenario 3.*

Description

`Ex_var_scenario_3` provides the expected value or variance of the number of microorganisms in the aggregate sample under scenario 3 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
Ex_var_scenario_3 (mu, sd, m, K, type, measure, n_sim)
```

Arguments

`mu`	the the mean concentration (μ).
`sd`	standard deviation on the log10 scale (default value 0.8).
`m`	the vector of incremental samples (with equal/unequal weights).
`K`	shape parameter (default value 0.25).
`type`	what type of the results you would like to consider such as "theory" or "simulation".
`measure`	what type of measure you would like to consider for the graph, such as "expectation" or "variance".
`n_sim`	number of simulations (large simulations provide more precise estimation).

Details

`Ex_var_scenario_3` provides the expected value or variance of the number of microorganisms in the aggregate sample under scenario 3 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

expected value or variance of the number of microorganisms in the aggregate sample.

Examples

```
mu <- 2
sd <- 0.8
m <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
K <- 0.25
Ex_var_scenario_3(mu, sd = 0.8, m, K, type = "theory",  measure = "expectation")
Ex_var_scenario_3(mu, sd = 0.8, m, K, type = "simulation",  measure = "expectation",
 n_sim = 2000000)
Ex_var_scenario_3(mu, sd = 0.8, m, K, type = "theory",  measure = "variance")
Ex_var_scenario_3(mu, sd = 0.8, m, K, type = "simulation",  measure = "variance",
 n_sim = 2000000)
```

scenario_1_OC *Construction of Operating Characteristic (OC) curve under lot with homogeneous contaminations based on simulations results.*

Description

scenario_1_OC provides the Operating Characteristic (OC) curves under scenario 1 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_1_OC(c, mulow, muhigh, sd, m1, m2, n, type, n_sim)
```

Arguments

c	acceptance number
mulow	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
muhigh	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
sd	standard deviation on the log10 scale (default value 0.8).
m1	the vector of the first set of incremental samples (with equal/unequal weights).
m2	the vector of the second set of incremental samples (with equal/unequal weights).
n	number of aggregate samples which are used for inspection.
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_1_OC provides the Operating Characteristic (OC) curves under scenario 1 of modelling the quantity of material sampled in the risk assessment study. The purpose of this function used for compares two different sets of sampling schemes when lot with homogeneous contaminations. Nevertheless, each sampling scheme's total quantity (weight of aggregate sample (say M)) must be equal. The probability of acceptance is plotted against mean log10 concentration and expected cell counts. We employed Poisson distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu+log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Operating Characteristic (OC) curves when lot with homogeneous contaminations.

See Also

scenario_1_pd

Examples

```
c <- 0
mulow <- -6
muhigh <- 0
sd <- 0.8
m1 <- c(10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10)
m2 <- c(15,5,5,5,10,5,10,5,15,10,5,10,5,25,10,5,10,5,5,10,5,15,10,
5,5,20,5,10,5,10,20,5,10,30,5,20,5,10,5,10,20,15,10,15,10,
10,5,10,15,5)
n <- 10
scenario_1_OC(c, mulow, muhigh, sd = 0.8, m1, m2, n, type = "theory")
```

---

scenario_1_pa — *Probability of acceptance estimation when lot with homogeneous contaminations.*

Description

scenario_1_pa provides a probability of acceptance under scenario 1 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_1_pa(c, mu, sd, m, n, type, n_sim)
```

Arguments

c	acceptance number
mu	the the mean concentration (μ).
sd	standard deviation on the log10 scale (default value 0.8).
m	the vector of incremental samples (with equal/unequal weights).
n	number of aggregate samples which are used for inspection.
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_1_pa provides a probability of acceptance under scenario 1 of modelling the quantity of material sampled in the risk assessment study. Under this scenario (a lot with homogeneous contaminations), we employed Poisson distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu + log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Probability of acceptance under lot with homogeneous contaminations.

Examples

```
c <- 0
mu <- -3
sd <- 0.8
m <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
n <- 10
scenario_1_pa(c, mu, sd = 0.8, m, n, type = "theory")
scenario_1_pa(c, mu, sd = 0.8, m, n, type = "simulation", n_sim = 1000000)
```

`scenario_1_pd` *Probability of detection estimation when lot with homogeneous contaminations.*

Description

`scenario_1_pd` provides a probability of detection under scenario 1 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_1_pd(mu, sd, m, type, n_sim)
```

Arguments

`mu`	the the mean concentration (μ).
`sd`	standard deviation on the log10 scale (default value 0.8).
`m`	the vector of incremental samples (with equal/unequal weights).
`type`	what type of the results you would like to consider such as "theory" or "simulation".
`n_sim`	number of simulations (large simulations provide more precise estimation).

Details

`scenario_1_pd` provides a probability of detection under scenario 1 of modelling the quantity of material sampled in the risk assessment study. Under this scenario (lot with homogeneous contaminations), we employed Poisson distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu + log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Probability of detection when lot with homogeneous contaminants by using theoretical or simulation-based results.

Examples

```
mu <- -3
sd <- 0.8
m <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
scenario_1_pd(mu, sd = 0.8, m, type = "theory")
scenario_1_pd(mu, sd = 0.8, m, type = "simulation", n_sim = 1000000)
```

---

scenario_1_pd_curve — *Construction of probability of detection curves under lot with homogeneous contaminations based on simulations results.*

Description

scenario_1_pd_curve provides the probability of detection curves under scenario 1 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_1_pd_curve(mulow, muhigh, sd, m1, m2, type, n_sim)
```

Arguments

mulow	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
muhigh	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
sd	standard deviation on the log10 scale (default value 0.8).
m1	the vector of the first set of incremental samples (with equal/unequal weights).
m2	the vector of the second set of incremental samples (with equal/unequal weights).
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_1_pd_curve provides the probability of detection curves under scenario 1 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

probability of detection curves when lot with homogeneous contaminations.

See Also

scenario_1_pd

Examples

```
mulow <- -6
muhigh <- 0
sd <- 0.8
m1 <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
m2 <- c(10,15,15,20,20,15,15,15,15,20,10,10,20,20,10,20,10,15,15,20,20,15,
15,15,15,20,10,10,20,20,10,20)
scenario_1_pd_curve(mulow, muhigh, sd = 0.8, m1, m2, type = "theory")
scenario_1_pd_curve(mulow, muhigh, sd = 0.8, m1, m2, type = "simulation", n_sim = 1000000)
```

---

scenario_2_OC — *Construction of Operating Characteristic (OC) curve under lot with heterogeneous and high-level contamination.*

Description

scenario_2_OC provides the Operating Characteristic (OC) curves under scenario 2 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_2_OC(c, mulow, muhigh, sd, m1, m2, n, type, n_sim)
```

Arguments

c	acceptance number
mulow	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
muhigh	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
sd	standard deviation on the log10 scale (default value 0.8).
m1	the vector of the first set of incremental samples (with equal/unequal weights).
m2	the vector of the second set of incremental samples (with equal/unequal weights).
n	number of aggregate samples which are used for inspection.
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_2_OC provides the Operating Characteristic (OC) curves under scenario 2 of modelling the quantity of material sampled in the risk assessment study. The purpose of this function used for compares two different sets of sampling schemes when lot with heterogeneous and high-level contamination. Nevertheless, each sampling scheme's total quantity (weight of aggregate sample (say M)) must be equal. The probability of acceptance is plotted against mean log10 concentration and expected cell counts. We employed Poisson lognormal distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu+log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Operating Characteristic (OC) curves when lot with heterogeneous and high-level contamination.

See Also

scenario_2_pd

Examples

```
c <- 0
mulow <- -10
muhigh <- 0
sd <- 0.8
m1 <- c(10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10)
m2 <- c(15,5,5,5,10,5,10,5,15,10,5,10,5,25,10,5,10,5,5,10,5,15,10,
5,5,20,5,10,5,10,20,5,10,30,5,20,5,10,5,10,20,15,10,15,10,
10,5,10,15,5)
n <- 10
scenario_2_OC(c, mulow, muhigh, sd = 0.8, m1, m2, n, type = "theory")
```

`scenario_2_pa` *Probability of acceptance estimation when lot with heterogeneous and high-level contamination.*

Description

`scenario_2_pa` provides a probability of acceptance under scenario 2 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_2_pa(c, mu, sd, m, n, type, n_sim)
```

Arguments

c	acceptance number
mu	the the mean concentration (μ).
sd	standard deviation on the log10 scale (default value 0.8).
m	the vector of incremental samples (with equal/unequal weights).
n	number of aggregate samples which are used for inspection.
type	what type of the results you would like to consider such as "theory" or "simulation".But,not yet established for this scenario at this time.
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_2_pa provides a probability of acceptance under scenario 2 of modelling the quantity of material sampled in the risk assessment study. Under this scenario (a lot with heterogeneous, high-level contamination), we employed Poisson lognormal distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu + log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Probability of acceptance when lot with heterogeneous and high-level contamination.

Examples

```
c <- 0
mu <- -6
sd <- 0.8
m <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
n <- 10
scenario_2_pa(c, mu, sd, m, n, type = "theory")
scenario_2_pa(c, mu, sd, m, n, type = "simulation", n_sim = 200000)
```

---

scenario_2_pd — *Probability of detection estimation when lot with heterogeneous and high-level contamination.*

Description

scenario_2_pd provides a probability of detection under scenario 2 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_2_pd(mu, sd, m, type, n_sim)
```

Arguments

mu	the the mean concentration (μ).
sd	standard deviation on the log10 scale (default value 0.8).
m	the vector of incremental samples (with equal/unequal weights).
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_2_pd provides a probability of detection under scenario 2 of modelling the quantity of material sampled in the risk assessment study. Under this scenario (a lot with heterogeneous, high-level contamination), we employed Poisson lognormal distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu + log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Probability of detection when lot with heterogeneous and high-level contamination by using theoretical or simulation-based results.

Examples

```
mu <- -3
sd <- 0.8
m <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
scenario_2_pd(mu, sd = 0.8, m, type = "theory")
scenario_2_pd(mu, sd = 0.8, m, type = "simulation", n_sim = 2000000)
```

`scenario_2_pd_curve` *Construction of probability of detection curves curve under lot with heterogeneous and high-level contamination.*

Description

`scenario_2_pd_curve` provides the probability of detection curves under scenario 2 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_2_pd_curve(mulow, muhigh, sd, m1, m2, type, n_sim)
```

Arguments

`mulow`	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
`muhigh`	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
`sd`	standard deviation on the log10 scale (default value 0.8).
`m1`	the vector of the first set of incremental samples (with equal/unequal weights).
`m2`	the vector of the second set of incremental samples (with equal/unequal weights).
`type`	what type of the results you would like to consider such as "theory" or "simulation".
`n_sim`	number of simulations (large simulations provide more precise estimation).

Details

`scenario_2_pd_curve` provides the probability of detection curves under scenario 2 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

probability of detection curves when lot with heterogeneous and high-level contamination.

See Also

scenario_2_pd

Examples

```
mulow <- -10
muhigh <- 0
sd <- 0.8
m1 <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
m2 <- c(10,15,15,20,20,15,15,15,15,20,10,10,20,20,10,20,10,15,15,20,20,15,
15,15,15,20,10,10,20,20,10,20)
scenario_2_pd_curve(mulow, muhigh, sd = 0.8, m1, m2, type = "theory")
scenario_2_pd_curve(mulow, muhigh, sd = 0.8, m1, m2, type = "simulation", n_sim = 100000)
```

`scenario_3_OC` *Construction of Operating Characteristic (OC) curve under lot with heterogeneous and low-level contamination.*

Description

`scenario_3_OC` provides the Operating Characteristic (OC) curves under scenario 3 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_3_OC(c, mulow, muhigh, sd, m1, m2, K, n, type, n_sim)
```

Arguments

c	acceptance number
mulow	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
muhigh	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
sd	standard deviation on the log10 scale (default value 0.8).
m1	the vector of the first set of incremental samples (with equal/unequal weights).
m2	the vector of the second set of incremental samples (with equal/unequal weights).
K	shape parameter (default value 0.25).
n	number of aggregate samples which are used for inspection.
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_3_OC provides the Operating Characteristic (OC) curves under scenario 3 of modelling the quantity of material sampled in the risk assessment study. The purpose of this function used for compares two different sets of sampling schemes when lot with heterogeneous and low-level contamination. Nevertheless, each sampling scheme's total quantity (weight of aggregate sample (say M)) must be equal. We employed Poisson gamma distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu + log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Operating Characteristic (OC) curves when lot with heterogeneous and low-level contamination.

See Also

scenario_3_pd

Examples

```
c <- 0
mulow <- -5
muhigh <- 2
sd <- 0.8
m1 <- c(10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,10,
10,10,10,10,10,10,10,10,10,10)
m2 <- c(15,5,5,5,10,5,10,5,15,10,5,10,5,25,10,5,10,5,5,10,5,15,10,
5,5,20,5,10,5,10,20,5,10,30,5,20,5,10,5,10,20,15,10,15,10,
10,5,10,15,5)
K <- 0.05
n <- 10
scenario_3_OC(c, mulow, muhigh, sd, m1, m2, K, n, type = "theory")
```

---

scenario_3_pa *Probability of acceptance estimation when lot with heterogeneous and low-level contamination.*

Description

scenario_3_pa provides a probability of acceptance under scenario 3 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_3_pa(c, mu, sd, m, K,  n, type, n_sim)
```

Arguments

c	acceptance number
mu	the the mean concentration (μ).
sd	standard deviation on the log10 scale (default value 0.8).

m	the vector of incremental samples (with equal/unequal weights).
K	shape parameter (default value 0.25).
n	number of aggregate samples which are used for inspection.
type	what type of the results you would like to consider such as "theory" or "simulation".But,not yet established for this scenario at this time.
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_3_pa provides a probability of acceptance under scenario 3 of modelling the quantity of material sampled in the risk assessment study. Under this scenario (a lot with heterogeneous, low-level contamination), we employed Poisson gamma distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu + log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Probability of acceptance when lot with heterogeneous and low-level contamination.

Examples

```
c <- 0
mu <- -3
sd <- 0.8
m <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
K <- 0.25
n <- 10
scenario_3_pa(c, mu, sd = 0.8, m, K, n, type = "theory")
scenario_3_pa(c, mu, sd = 0.8, m, K, n, type = "simulation", n_sim = 1000000)
```

---

scenario_3_pd *Probability of detection estimation when lot with heterogeneous and low-level contamination.*

Description

scenario_3_pd provides a probability of detection under scenario 3 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_3_pd(mu, sd, m, K, type, n_sim)
```

Arguments

`mu`	the the mean concentration (μ).
`sd`	standard deviation on the log10 scale (default value 0.8).
`m`	the vector of incremental samples(with equal/unequal weights).
`K`	shape parameter (default value 0.25).
`type`	what type of the results you would like to consider such as "theory" or "simulation".
`n_sim`	number of simulations (large simulations provide more precise estimation).

Details

`scenario_3_pd` provides a probability of detection under scenario 3 of modelling the quantity of material sampled in the risk assessment study. Under this scenario (a lot with heterogeneous, low-level contamination), we employed Poisson gamma distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu + log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Probability of detection when lot with heterogeneous and low-level contamination by using theoretical or simulations based results.

Examples

```
mu <- -3
sd <- 0.8
m <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
K <- 0.05
scenario_3_pd(mu, sd = 0.8, m, K, type = "theory")
scenario_3_pd(mu, sd = 0.8, m, K, type = "simulation", n_sim = 1000000)
```

`scenario_3_pd_curve` *Construction of Operating Characteristic (OC) curve under lot with heterogeneous and low-level contamination.*

Description

`scenario_3_pd_curve` provides the probability of detection curves under scenario 3 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_3_pd_curve(mulow, muhigh, sd, m1, m2, K, type, n_sim)
```

Arguments

mulow	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
muhigh	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
sd	standard deviation on the log10 scale (default value 0.8).
m1	the vector of the first set of incremental samples (with equal/unequal weights).
m2	the vector of the second set of incremental samples (with equal/unequal weights).
K	shape parameter (default value 0.25).
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_3_pd_curve provides the probability of detection curves under scenario 3 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

probability of detection curves when lot with heterogeneous and low-level contamination.

See Also

scenario_3_pd

Examples

```
mulow <- -5
muhigh <- 2
sd <- 0.8
m1 <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
m2 <- c(10,15,15,20,20,15,15,15,15,20,10,10,20,20,10,20,10,15,15,20,20,15,
15,15,15,20,10,10,20,20,10,20)
K <- 0.05
scenario_3_pd_curve(mulow, muhigh, sd, m1, m2, K, type = "theory")
```

---

scenario_4_pd — *Probability of detection estimation when lot with homogeneous contaminations and concentration levels fluctuating from sublot to sublot.*

Description

scenario_4_pd provides a probability of detection under scenario 4 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_4_pd(mu, sd_b, sd_w, m, type, n_sim)
```

Arguments

mu	the the mean concentration (μ).
sd_b	standard deviation of concentration level between sublots on the log10 scale (default value 0.8).
sd_w	standard deviation of concentration level within sublot on the log10 scale (default value 0.8).
m	the vector of incremental samples (with equal/unequal weights).
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_4_pd provides a probability of detection under scenario 4 of modelling the quantity of material sampled in the risk assessment study. Under this scenario (lot with homogeneous contaminations), we employed Poisson distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu+log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Probability of detection when lot with homogeneous contaminants by using theoretical or simulation-based results.

Examples

```
m1 <- c(5,5,5,5,5,5,5,5,5,5)
m2 <- c(5,5,5,5,5,5,5,5,5,5)
m3 <- c(5,5,5,5,5,5,5,5,5,5)
m4 <- c(5,5,5,5,5,5,5,5,5,5)
mu <- -3
sd_b <- 0.2
sd_w <- 0.8
m <- list(m1,m2,m3,m4)
scenario_4_pd(mu, sd_b, sd_w = 0.8, m, type = "theory")
scenario_4_pd(mu, sd_b, sd_w = 0.8, m, type = "simulation", n_sim = 20000)
```

---

scenario_4_pd_curve *Construction of probability of detection curves under lot with homogeneous contaminations and concentration levels fluctuating from sublot to sublot based on simulations results.*

Description

scenario_4_pd_curve provides the probability of detection curves under scenario 4 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_4_pd_curve(mulow, muhigh, sd_b, sd_w = 0.8, m11, m22, type, n_sim)
```

Arguments

mulow	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
muhigh	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
sd_b	standard deviation of concentration level between sublots on the log10 scale (default value 0.8).
sd_w	standard deviation of concentration level within sublot on the log10 scale (default value 0.8).
m11	the vector of the first set of incremental samples (with equal/unequal weights).
m22	the vector of the second set of incremental samples (with equal/unequal weights).
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_4_pd_curve provides the probability of detection curves under scenario 4 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

probability of detection curves when lot with homogeneous contaminations.

See Also

scenario_1_pd

Examples

```
m1 <- c(10,10,10,10,10,10,10,10,10,10)
m2 <- c(10,10,10,10,10,10,10,10,10,10)
m3 <- c(10,10,10,10,10,10,10,10,10,10)
m4 <- c(10,10,10,10,10,10,10,10,10,10)
m5 <- c(10,10,10,10,10,10,10,10,10,10)
m11 <- list(m1,m2,m3,m4,m5)
m_1 <- c(15, 5, 5, 5, 10, 5, 10, 5, 15, 10)
m_2 <- c(5, 10, 5, 25, 10, 5, 10, 5, 5, 10)
m_3 <- c(5, 15, 10, 5, 5, 20, 5, 10, 5, 10)
m_4 <- c(20, 5, 10, 30, 5, 20, 5, 10, 5, 10)
m_5 <- c(20, 15, 10, 15, 10, 10, 5, 10, 15, 5)
m22 <- list(m_1,m_2,m_3,m_4,m_5)
mulow <- -5
muhigh <- -1
sd_b <- 0.2
sd_w <- 0.8
scenario_4_pd_curve(mulow, muhigh, sd_b, sd_w = 0.8, m11, m22, type = "theory")
scenario_4_pd_curve(mulow, muhigh, sd_b, sd_w = 0.8, m11, m22, type = "simulation", n_sim = 1000000)
```

scenario_4_prevalence *Prevalence estimation before inspection when lot with homogeneous contamination and contamination levels fluctuate from lot to lot.*

Description

scenario_4_prevalence provides a prevalence before inspection under scenario 4 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_4_prevalence(mu, sd, m, l, type, n_sim)
```

Arguments

mu	the the mean concentration (μ).
sd	standard deviation on the log10 scale (default value 0.8).
m	the vector of incremental samples (with equal/unequal weights).
l	the number of lots in the production process.
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_1_pd provides a prevalence before inspection under scenario 4 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

Prevalence estimation before inspection when lot with homogeneous contamination and contamination levels fluctuate from lot to lot by using theoretical or simulation-based results.

Examples

```
mu <- -3
sd <- 0.8
m <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
l <- 5000
scenario_4_prevalence(mu, sd, m, l, type = "theory")
```

scenario_5_pd — *Probability of detection estimation when lot with heterogeneous contamination and concentration levels fluctuating from sublot to sublot.*

Description

scenario_2_pd provides a probability of detection under scenario 2 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_5_pd(mu, sd_b, sd_w, m, type, n_sim)
```

Arguments

mu	the the mean concentration (μ).
sd_b	standard deviation of concentration level between sublots on the log10 scale (default value 0.8).
sd_w	standard deviation of concentration level within sublot on the log10 scale (default value 0.8).
m	the vector of incremental samples (with equal/unequal weights).
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_2_pd provides a probability of detection under scenario 2 of modelling the quantity of material sampled in the risk assessment study. Under this scenario (a lot with heterogeneous, high-level contamination), we employed Poisson lognormal distribution to the model number of micro-organisms in the incremental samples. Based on the food safety literature, the expected cell count is given by $\lambda = 10^{\mu + log(10)\sigma^2/2}$. (this section will be updated later on)

Value

Probability of detection when lot with heterogeneous and high-level contamination by using theoretical or simulation-based results.

Examples

```
m1 <- c(5,5,5,5,5,5,5,5,5,5)
m2 <- c(5,5,5,5,5,5,5,5,5,5)
m3 <- c(5,5,5,5,5,5,5,5,5,5)
m4 <- c(5,5,5,5,5,5,5,5,5,5)
mu <- -3
m <- list(m1,m2,m3,m4)
sd_b <- 0.2
sd_w <- 0.8
scenario_5_pd(mu, sd_b, sd_w = 0.8, m, type = "theory")
scenario_5_pd(mu, sd_b, sd_w = 0.8, m, type = "simulation", n_sim = 20000)
```

`scenario_5_pd_curve` *Construction of probability of detection curves under lot with heterogeneous contamination and concentration levels fluctuating from sublot to sublot.*

Description

scenario_5_pd_curve provides the probability of detection curves under scenario 5 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_5_pd_curve(mulow, muhigh, sd_b, sd_w, m11, m22, type, n_sim)
```

Arguments

mulow	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
muhigh	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
sd_b	standard deviation of concentration level between sublots on the log10 scale (default value 0.8).
sd_w	standard deviation of concentration level within sublot on the log10 scale (default value 0.8).
m11	the vector of the first set of incremental samples (with equal/unequal weights).
m22	the vector of the second set of incremental samples (with equal/unequal weights).
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_5_pd_curve provides the probability of detection curves under scenario 5 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

probability of detection curves when lot with heterogeneous and high-level contamination.

See Also

scenario_5_pd

Examples

```
m1 <- c(10,10,10,10,10,10,10,10,10,10)
m2 <- c(10,10,10,10,10,10,10,10,10,10)
m3 <- c(10,10,10,10,10,10,10,10,10,10)
m4 <- c(10,10,10,10,10,10,10,10,10,10)
m5 <- c(10,10,10,10,10,10,10,10,10,10)
m11 <- list(m1,m2,m3,m4,m5)
m_1 <- c(15, 5, 5, 5, 10, 5, 10, 5, 15, 10)
m_2 <- c(5, 10, 5, 25, 10, 5, 10, 5, 5, 10)
m_3 <- c(5, 15, 10, 5, 5, 20, 5, 10, 5, 10)
m_4 <- c(20, 5, 10, 30, 5, 20, 5, 10, 5, 10)
m_5 <- c(20, 15, 10, 15, 10, 10, 5, 10, 15, 5)
m22 <- list(m_1,m_2,m_3,m_4,m_5)
mulow <- -8
muhigh <- -1
sd_b <- 0.2
sd_w <- 0.8
scenario_5_pd_curve(mulow, muhigh, sd_b, sd_w, m11, m22, type = "theory")
scenario_5_pd_curve(mulow, muhigh, sd_b, sd_w, m11, m22, type = "simulation", n_sim = 1000000)
```

---

scenario_5_prevalence *Prevalence estimation before inspection when lot with heterogeneous contamination and contamination levels fluctuate from lot to lot.*

Description

scenario_5_prevalence provides a prevalence before inspection under scenario 5 of modelling the quantity of material sampled in the risk assessment study.

Usage

```
scenario_5_prevalence(mu, sd, m, l, type, n_sim)
```

Arguments

mu	the the mean concentration (μ).
sd	standard deviation on the log10 scale (default value 0.8).
m	the vector of incremental samples (with equal/unequal weights).
l	the number of lots in the production process.
type	what type of the results you would like to consider such as "theory" or "simulation".
n_sim	number of simulations (large simulations provide more precise estimation).

Details

scenario_5_prevalence provides a prevalence before inspection under scenario 5 of modelling the quantity of material sampled in the risk assessment study. (this section will be updated later on)

Value

Prevalence estimation before inspection when lot with heterogeneous contamination and contamination levels fluctuate from lot to lot by using theoretical or simulation-based results.

Examples

```
mu <- -3
sd <- 0.8
m <- c(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)
l <- 5000
scenario_5_prevalence(mu, sd, m, l, type = "theory")
```

`uneqmixr`	*Probability estimations and graphical displays in modelling the quantity of material sampled in the risk assessment.*

Description

This package aims to develop for getting probability estimations and graphical displays in the study associated with modelling the quantity of material sampled in the risk assessment.

Details

This package aims to develop probability estimations and graphical displays in modelling the quantity of material sampled in the risk assessment. This study mainly focuses on the risk assessment when aggregating unequal incremental samples in the production process. It mainly focuses on the risk assessment based on compound Poisson mixture distributions to model in five different scenarios.

The following scenarios are considered for this study:

1. Scenario 1— lots with homogeneous contamination;
2. Scenario 2— lots with heterogeneous, high-level contamination;
3. Scenario 3— lots with heterogeneous, low-level contamination;
4. Scenario 4 — lots with homogeneous contamination and concentration levels fluctuating from sub lots; and
5. Scenario 5—lots with heterogeneous contamination and concentration levels fluctuating from sub-lots.

This package allows practitioners to get probability estimations and graphical displays based on this study. Also, this package can be used to validate the derived results in this study by simulation.

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