

Package ‘uneqmixr’

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Type Package

Title Modelling the Quantity of Material Sampled in the Risk Assessment

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

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

Description This package allows general 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

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AOQL_scenarios	<i>Construction of AOQ curve and calculate AOQL value based on average microbial counts</i>
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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, m, 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).
m	the vector 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(5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,  
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,  
5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5,5)  
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"  
n <- 10  
AOQL_scenarios(c,llim, sd, m = m1, scenario, n, type = "theory")  
AOQL_scenarios(c,llim, sd, m = m2, scenario, 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

<code>mulow</code>	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
<code>muhigh</code>	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
<code>sd</code>	standard deviation on the log10 scale (default value 0.8).
<code>m1</code>	the vector of the first set of incremental samples (with equal/unequal weights).
<code>m2</code>	the vector of the second set of incremental samples (with equal/unequal weights).
<code>measure</code>	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)

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

```
mulow <- -1  
muhigh <- 1  
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)  
m2 <- c(10,15,15,20,20,15,15,15,15,20,10,10,20,20,10,20,10,15,15,20,20,15,  
15,15,20,10,10,20,20,10,20)  
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")
```

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

`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.

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

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".

`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)

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

```
mulow <- 0  
muhigh <- 2  
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)  
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  
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")
```

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

`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.

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

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).

[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)

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)  
l <- 5000  
scenario_5_prevalence(mu, sd, m, l, type = "simulation", n_sim = 20000)
```

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