Package 'mixingsimulation'

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Type Package

Title Microbiological Risk Assessment of Powder Mixing Process by Simulation Results

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

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

Description This package develops to study microbiological risk assessment of mixing primary samples in the powdered products using simulation results.

License GPL (>= 2)

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LazyData true

Imports DescTools, ggplot2, ggthemes, gridExtra, magrittr, plyr, purrr, reshape2, stats

Suggests testthat

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Depends R (>= 4.0)

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Language en-US

R topics documented:

`compare_mixing_1` *Graphical comparison of mixing plans based on the estimated cumulative moving average (CMA) of detection probability at each revolution.*

Description

This function provides a graphical display to compare mixing plans based on the estimated cumulative moving average (CMA) of detection probability at each revolution of the mixing process.

Usage

```
compare_mixing_1(mu, sigma, alpha_in, k, l, r, distribution, UDL, n_sim)
```

Arguments

`mu`	the average number of CFUs (μ) in the mixed sample, which is in a logarithmic scale if we use a Lognormal / Poisson lognormal distribution
`sigma`	the standard deviation of the colony-forming units (CFUs) in the mixed sample on the logarithmic scale (default value 0.8)
`alpha_in`	concentration parameter at the initial stage
`k`	number of small portions / primary samples
`l`	number of revolutions / stages
`r`	the rate of the concentration parameter changes at each mixing stage
`distribution`	what suitable distribution type we have employed for simulation such as `"Poisson-Type A"` or `"Poisson-Type B"` or `"Lognormal-Type A"` or `"Lognormal-Type B"` or `"Poisson lognormal-Type A"` or `"Poisson lognormal-Type B"`
`UDL`	the upper decision limit, which depends on the type of microorganisms and testing regulations.
`n_sim`	number of simulations

Value

graphical display of estimated cumulative moving average (CMA) of detection probability at each revolution in the mixing.

References

- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.

See Also

sim_single_pd_stages

Examples

```
mu <- 100
sigma <- 0.8
alpha_in <- 0.01
k <- c(10,30,60)
l <- 25000
r <- 0.01
distribution <-  "Poisson lognormal-Type B"
UDL <- 0
n_sim <- 2000
compare_mixing_1(mu,sigma , alpha_in, k, l, r, distribution, UDL, n_sim)
```

`compare_mixing_2` *Graphical comparison of mixing plans based on estimated probability of detection at the end of the mixing with different revolutions*

Description

This function provides a graphical display to compare mixing plans using a different number of revolutions based on the estimated probability of detection at the end of mixing.

Usage

```
compare_mixing_2(
  mulower,
  muupper,
  sigma,
  alpha_in,
  k,
  l,
  r,
  distribution,
  UDL,
  n_sim
)
```

Arguments

`mulower`	the lower value of the mean concentration (μ) for use in the graphical display's x-axis.
`muupper`	the upper value of the mean concentration (μ) for use in the graphical display's x-axis.
`sigma`	the standard deviation of the colony-forming units (CFUs) in the mixed sample on the logarithmic scale (default value 0.8)
`alpha_in`	concentration parameter at the initial stage
`k`	number of small portions / primary samples
`l`	number of revolutions / stages
`r`	the rate of the concentration parameter changes at each mixing stage

distribution	what suitable distribution type we have employed for simulation such as "Poisson-Type A" or "Poisson-Type B" or "Lognormal-Type A" or "Lognormal-Type B" or "Poisson lognormal-Type A" or "Poisson lognormal-Type B"
UDL	the upper decision limit, which depends on the type of microorganisms and testing regulations.
n_sim	number of simulations

Value

graphical display compares mixing plans using a different number of revolutions based on the estimated probability of detection at the end of the mixing.

References

- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.

See Also

sim_single_pd_stages

Examples

```
mulower <- 0.1
muupper <- 200
sigma <- 0.8
alpha_in <- 0.01
k <- 30
l <- c(500,5000)
r <- 0.01
distribution <-  "Poisson lognormal-Type B"
UDL <- 0
n_sim <- 2000
compare_mixing_2(mulower, muupper, sigma , alpha_in, k, l, r, distribution, UDL, n_sim)
```

---

compare_mixing_3 *Graphical comparison of mixing plans based on cumulative distribution of expected total CFUs in the mixing process.*

Description

This function provides a graphical display to compare mixing plans based on the cumulative distribution of expected total CFUs in the mixing process using different mixing parameters, such as type of distribution and number of primary samples.

Usage

```
compare_mixing_3(mu, sigma, alpha_in, k, l, r, distribution, n_sim)
```

Arguments

mu	the average number of CFUs (μ) in the mixed sample, which is in a logarithmic scale if we use a Lognormal / Poisson lognormal distribution
sigma	the standard deviation of the colony-forming units in the mixed sample on the logarithmic scale (default value 0.8)
alpha_in	concentration parameter at the initial stage
k	number of small portions / primary samples
l	number of revolutions / stages
r	the rate of the concentration parameter changes at each mixing stage
distribution	what suitable distribution type we have employed for simulation such as "Poisson-Type A" or "Poisson-Type B" or "Lognormal-Type A" or "Lognormal-Type B" or "Poisson lognormal-Type A" or "Poisson lognormal-Type B"
n_sim	number of simulations

Details

Let N' be the number of CFUs in the mixed sample, which is produced by the mixing of k primary samples and $N' = \sum N_i$ and let N_i be the number of CFUs in the i^{th} primary sample; where $i = 1, 2, ...k$.

For this package development, we have employed the notations 'Type-A' and 'Type-B' to indicate the type of distributions, which are applied in the previous literature as 'fair' and 'beta', respectively; see Nauta (2005).

Following Nauta (2005), the contribution weight of contamination by each primary sample can be defined by the random variable w_i, which is possible to be followed by either uniform distribution with parameter $1/k$ or the joint distribution of $w_1, w_2, \cdots w_k$ follows a Dirichlet distribution with concentration parameter α. From the previous literature, a Dirichlet distribution can be formulated by beta or gamma algorithms, which have revealed the same results; see Nauta (2005).

This function is developed based on the beta algorithm and the following steps formulate it.

$$w_i = x_i \prod_{j=1}^{i-1} 1 - x_j \quad \forall i = 2, 3, \cdots k, \qquad w_1 = x_1$$

;

where x_i follows $Beta(\alpha, \alpha(k-i))$ and also $\sum w_i$ must be equal to one.

- Case 1 (Poisson-Type A): N_i follows $Poisson(\mu/k)$
- Case 2 (Poisson-Type B): N_i follows $Poisson(\mu w_i)$
- Case 3 (Lognormal-Type A): N_i follows $Binomial(M_i, 1/k)$; where M_i follows $Lognormal(\mu, \sigma)$
- Case 4 (Lognormal-Type B): N_i follows $Binomial(M_i, w_i)$; where M_i follows $Lognormal(\mu, \sigma)$
- Case 5 (Poisson lognormal-Type A): N_i follows $Binomial(M_i, 1/k)$; where M_i follows $Poissonlognormal(\mu, \sigma)$
- Case 6 (Poisson lognormal-Type B): N_i follows $Binomial(M_i, w_i)$; where M_i follows $Poissonlognormal(\mu, \sigma)$

The powder-mixing process can be defined as breaking clusters stage-by-stage. Usually, it occurs systematically in the standard powder mixtures. For this package development, we assume that mixing parameters also systematically change with a fixed rate at each stage of the mixing. The mixing parameter can be defined as revolutions instead of the mixing stage in general. Due to the

lack of theoretical results for the dependent random variable sum's distribution, we have chosen simulation techniques for this modelling.

Let l be the number of stages or revolutions of the mixture, and we also assumed a fixed concentration parameter value at the initial phase of the mixing process. Based on the literature in this area, the concentration parameter can be assumed to increase at every stage of the mixing, which is possible to do systematically.

Therefore, this function exhibits the graphical display with different quantities of primary sample mixing as a large unit.

Value

Graphical comparison between different mixing schemes.

References

- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.

See Also

sim_single, sim_single_stages, sim_multiple_stages

Examples

```
mu <- 100
sigma <- 0.8
alpha_in <- 0.01
k <- c(10,30,60)
r <- 0.01
distribution <- c("Poisson lognormal-Type B","Poisson lognormal-Type B","Poisson lognormal-Type B")
n_sim <- 20000
plot1 <- compare_mixing_3(mu, sigma, alpha_in, k , l = 50,r, distribution,n_sim) +
ggplot2::theme(legend.text = ggplot2::element_text(size = 7.5),
legend.title = ggplot2::element_text(size = 7.5),
legend.key.size = ggplot2::unit(4, 'mm')) + ggplot2::xlim(0,300)
plot2 <- compare_mixing_3(mu, sigma, alpha_in, k , l = 500, r, distribution, n_sim) +
ggplot2::theme,
legend.title = ggplot2::element_text(size = 7.5),
legend.key.size = ggplot2::unit(4, 'mm')) + ggplot2::xlim(0,300)
plot3 <- compare_mixing_3(mu, sigma, alpha_in, k, l = 5000,r , distribution,n_sim) +
ggplot2::theme(legend.text = ggplot2::element_text(size = 7.5),
legend.title = ggplot2::element_text(size = 7.5),
legend.key.size = ggplot2::unit(4, 'mm')) + ggplot2::xlim(0,300)
plot4 <- compare_mixing_3(mu, sigma , alpha_in , k , l = 25000, r , distribution ,n_sim) +
ggplot2::theme(legend.text = ggplot2::element_text(size = 7.5),
legend.title = ggplot2::element_text(size = 7.5),
legend.key.size = ggplot2::unit(4, 'mm')) + ggplot2::xlim(0,300)
gridExtra::grid.arrange(plot1, plot2, plot3, plot4, ncol = 2, nrow = 2)
```

`mixing_usl` *Graphical display to find out upper stabilizing limit (USL).*

Description

This function provides a graphical display to find out upper stabilizing limit (USL). Based on the cumulative mean at each stage of the mixing, the cumulative mean persists in the same value after a particular number of stages. Therefore, the upper stabilizing limit (USL) is defined as a stabilizing point in the graphical display of the expected total number of CFUs versus the number of revolutions when the cumulative mean remains stable.

Usage

```
mixing_usl(mu, sigma, alpha_in, k, l, r, distribution, n_sim)
```

Arguments

`mu`	the average number of CFUs (μ) in the mixed sample, which is in a logarithmic scale if we use a Lognormal / Poisson lognormal distribution
`sigma`	the standard deviation of the colony-forming units in the mixed sample on the logarithmic scale (default value 0.8)
`alpha_in`	concentration parameter at the initial stage
`k`	number of small portions / primary samples
`l`	number of revolutions / stages
`r`	the rate of the concentration parameter changes at each mixing stage
`distribution`	what suitable distribution type we have employed for simulation such as "Poisson-Type A" or "Poisson-Type B" or "Lognormal-Type A" or "Lognormal-Type B" or "Poisson lognormal-Type A" or "Poisson lognormal-Type B"
`n_sim`	number of simulations

Value

graphical display to find out upper stabilizing limit (USL).

References

- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.

See Also

sim_single_stages

Examples

```
mu <- 100
sigma <- 0.8
alpha_in <- 0.01
k <- 30
l <- 25000
r <- 0.01
distribution <-  "Poisson lognormal-Type B"
n_sim <- 2000
mixing_usl(mu, sigma, alpha_in, k, l, r, distribution, n_sim)
```

`sim_multiple` *The expected total number of colony-forming units in the mixed sample in the multiple mixing schemes at the single stage of the mixing process.*

Description

This function calculates the resulting expected total number of colony-forming units in the mixed sample in the multiple mixing plans at the single stage of the mixing process.

Usage

```
sim_multiple(mu, sigma, alpha, k, distribution, n_sim)
```

Arguments

`mu`	the average number of CFUs (μ) in the mixed sample, which is in a logarithmic scale if we use a Lognormal / Poisson lognormal distribution
`sigma`	the standard deviation of the colony-forming units in the mixed sample on the logarithmic scale (default value 0.8)
`alpha`	concentration parameter
`k`	number of small portions / primary samples
`distribution`	what suitable distribution type we have employed for simulation such as `"Poisson-Type A"` or `"Poisson-Type B"` or `"Lognormal-Type A"` or `"Lognormal-Type B"` or `"Poisson lognormal-Type A"` or `"Poisson lognormal-Type B"`
`n_sim`	number of simulations

Details

Let N' be the number of colony-forming units in the mixed sample which is produced by contribution of k primary samples mixing and $N' = \sum N_i$. This function provides the simulated resulting of the expected total number of colony-forming units in the mixed sample in the multiple mixing plans at the single stage of the mixing process. To more details, please refer the details section of compare_mixing_3.

Value

total number of colony forming units in the multiple mixing scheme

References

- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.

See Also

sim_single, compare_mixing_3

Examples

```
set.seed(1350)
sigma <- 0.8
alpha <- c(0.1,5)
k <- c(30,30)
distribution <-  c("Poisson lognormal-Type B","Poisson lognormal-Type B")
n_sim <- 20000
f_spr <- function(n_sim) {
  sprintf("Simulation results (no.simulations = %.0f)", n_sim)
}
f_spri <- function(alpha, distribution) {
  sprintf("mixing plan (alpha = %.1f, %s)", alpha, distribution)
}
mu <- seq(100, 200, 0.1)
sim.sum3 <- matrix(NA, nrow = length(mu), ncol = length(distribution))
for(i in 1:nrow(sim.sum3)){
  sim.sum3[i,] <-  colMeans(sim_multiple(mu[i], sigma, alpha, k, distribution, n_sim))
}
result <- data.frame(mu, sim.sum3)
colnames(result) <- c("mu", f_spri(alpha, distribution))
melten.Prob <- reshape2::melt(result, id = "mu", variable.name = "mixing_scheme",
                              value.name = "Total_CFU")
plot_example <-
ggplot2::ggplot(melten.Prob, ggplot2::aes(Total_CFU, group = mixing_scheme,colour = mixing_scheme))+
  ggplot2::geom_line(stat="density",ggplot2::aes(x = Total_CFU))+
  ggplot2::ylab(expression("pmf"))+
 ggplot2::theme_classic()+ ggplot2::xlab(expression("Total number of CFU in the mixed sample"))+
 ggplot2::theme(plot.title = ggplot2::element_text(hjust = 0.5), legend.position = c(0.75,0.75))+
  ggthemes::scale_colour_colorblind()
  plot_example
```

---

sim_multiple_stages *The expected total number of CFUs in the mixed sample in the multiple mixing schemes at each stage of the mixing process.*

Description

This function calculates the resulting expected total number of CFUs in the mixed sample in the multiple mixing plans at each stage of the mixing process.

Usage

```
sim_multiple_stages(mu, sigma, alpha_in, k, l, r, distribution, n_sim)
```

Arguments

mu	the average number of CFUs (μ) in the mixed sample, which is in a logarithmic scale if we use a Lognormal / Poisson lognormal distribution
sigma	the standard deviation of the colony-forming units in the mixed sample on the logarithmic scale (default value 0.8)
alpha_in	concentration parameter at the initial stage
k	number of small portions / primary samples
l	number of revolutions / stages
r	the rate of the concentration parameter changes at each mixing stage
distribution	what suitable distribution type we have employed for simulation such as "Poisson-Type A" or "Poisson-Type B" or "Lognormal-Type A" or "Lognormal-Type B" or "Poisson lognormal-Type A" or "Poisson lognormal-Type B"
n_sim	number of simulations

Details

Let N' be the number of CFUs in the mixed sample, which is produced by the mixing of k primary samples and $N' = \sum N_i$ and let N_i be the number of CFUs. For this package development, we have employed the notations 'Type-A' and 'Type-B' to indicate the type of distributions, which are applied in the previous literature as 'fair' and 'beta', respectively; see Nauta (2005).

This package will consider stage-by-stage the mixing process and assumes systematically breaking clusters at every stage of the mixing. Therefore, it can be assumed the concentration parameter also systematically changes with the concentration of the contribution.

Value

The expected total number of CFUs in each revolution / stage.

References

- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.

See Also

sim_single

Examples

```
mu <- 100
sigma <- 0.8
alpha_in <- 0.01
k <- c(30,60)
l <- 25000
r <- 0.01
distribution <- c("Poisson lognormal-Type B","Poisson lognormal-Type B")
n_sim <- 2000
colMeans(sim_multiple_stages(mu, sigma, alpha_in, k, l, r, distribution, n_sim))
```

`sim_pois_stages` *A graphical display of the mean and variance changes at each mixing stage.*

Description

This function creates a graphical display of the mean and variance changes at each mixing stage. To the comparison purpose, estimated cumulative moving average (CMA) of mean and variance are

Usage

```
sim_pois_stages(mu, sigma, alpha_in, k, l, r, distribution, n_sim)
```

Arguments

`mu`	the average number of CFUs (μ) in the mixed sample, which is in a logarithmic scale if we use a Lognormal / Poisson lognormal distribution
`sigma`	the standard deviation of the colony-forming units in the mixed sample on the logarithmic scale (default value 0.8)
`alpha_in`	concentration parameter at the initial stage
`k`	number of small portions / primary samples
`l`	number of revolutions / stages
`r`	the rate of the concentration parameter changes at each mixing stage
`distribution`	what suitable distribution type we have employed for simulation such as `"Poisson-Type A"` or `"Poisson-Type B"` or `"Lognormal-Type A"` or `"Lognormal-Type B"` or `"Poisson lognormal-Type A"` or `"Poisson lognormal-Type B"`
`n_sim`	number of simulations

Details

Let N' be the number of colony-forming units in the mixed sample which is produced by mixing of k primary samples and $N' = \sum N_i$. This function produces a graphical display of the mean and variance changes at each mixing stage. It is helpful to identify the optimal number of revolutions of the mixture, which is a point of mixing that initiates Poisson-like homogeneity.

Value

Mean and variance changes at each mixing stage.

Examples

```
mu <- 100
sigma <- 0.8
alpha_in <- 0.01
k <- 30
l <- 2500
r <- 0.001
distribution <-  "Poisson lognormal-Type B"
n_sim <- 2000
sim_pois_stages(mu, sigma , alpha_in, k, l, r, distribution, n_sim)
```

`sim_single` *The generated number of colony-forming units in the mixed sample by the simulation results in the single mixing plan with a single stage of the mixing.*

Description

This function calculates the resulting generated number of colony forming units in the mixed sample in the single mixing plan with single stage of the mixing.

Usage

```
sim_single(mu, sigma, alpha, k, distribution, n_sim, summary = 1)
```

Arguments

`mu`	the average number of CFUs (μ) in the mixed sample, which is in a logarithmic scale if we use a Lognormal / Poisson lognormal distribution
`sigma`	the standard deviation of the colony-forming units in the mixed sample on the logarithmic scale (default value 0.8)
`alpha`	concentration parameter
`k`	number of small portions / primary samples
`distribution`	what suitable distribution type we have employed for simulation such as `"Poisson-Type A"` or `"Poisson-Type B"` or `"Lognormal-Type A"` or `"Lognormal-Type B"` or `"Poisson lognormal-Type A"` or `"Poisson lognormal-Type B"`
`n_sim`	number of simulations
`summary`	need to select one number from the list 1 to 5 which depends on what simulated observations are needed (default 1). If `summary = 1`, the function provides the expected total number of the simulated N' after `n_sim` simulations are run. If `summary = 2`, the function provides generated CFUs in each primary sample after `n_sim` simulations are run. If `summary = 3`, the function provides the expected total number of the simulated N' at each simulation run. If `summary = 4`, the function provides the mean and variance values of the simulated samples. If `summary = 5`, the function provides all simulated observations in the `n_sim * k` matrix.

Details

Let N' be the number of colony-forming units in the mixed sample which is produced by mixing of k primary samples and $N' = \sum N_i$. To more details, please refer the details section of compare_mixing_3.

Value

total number of colony forming units in the single mixing plan

References

- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.

See Also

compare_mixing_3

Examples

```
mu <- 100
sigma <- 0.8
alpha <- 0.1
k <- 30
n_sim <- 20000
sim_single(mu, sigma, alpha, k, distribution = "Poisson lognormal-Type B", n_sim, summary = 2)
```

`sim_single_pd` *The estimated value of detection probability at a single stage (or revolution) of the mixing process.*

Description

This function gives a probability of detection at a single stage (or revolution) of the mixing process.

Usage

```
sim_single_pd(mu, sigma, alpha, k, distribution, UDL, n_sim)
```

Arguments

`mu`	the average number of CFUs (μ) in the mixed sample, which is in a logarithmic scale if we use a Lognormal / Poisson lognormal distribution
`sigma`	the standard deviation of the colony-forming units in the mixed sample on the logarithmic scale (default value 0.8)
`alpha`	concentration parameter
`k`	number of small portions / primary samples
`distribution`	what suitable distribution type we have employed for simulation such as `"Poisson-Type A"` or `"Poisson-Type B"` or `"Lognormal-Type A"` or `"Lognormal-Type B"` or `"Poisson lognormal-Type A"` or `"Poisson lognormal-Type B"`
`UDL`	the upper decision limit, which depends on the type of microorganisms and testing regulations.
`n_sim`	number of simulations

Details

Let N' be the number of CFUs in the mixed sample, which is produced by the contribution of k primary samples mixing, $N' = \sum N_i$ and let l be the number of stages in the mixing process. This function provides the probability of detection at each stage of the mixing process. The probability of detection can be determined by how many primary samples contain CFUs greater than UDL out of the number of primary samples engaged at each mixing stage.

Therefore, the probability of detection (p_d) can be estimated from following formula,

$$p_d = \frac{\text{Number of simulated primary samples which contain CFUs greater than UDL}}{\text{Number of primary samples}};$$

where the upper decision limit (UDL) depends on microorganisms and testing regulations. For example, UDL should be equal to 0 for testing Salmonella in milk powder sample if we consider 25g primary sample.

Value

The probability of detection at each stage of the mixing process.

References

- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.

See Also

sim_single_stages

Examples

```
mu <- 100
sigma <- 0.8
alpha <- 0.1
k <- 30
distribution <-  "Poisson lognormal-Type B"
UDL <- 0
n_sim <- 2000
sim_single_pd(mu, sigma , alpha , k, distribution, UDL, n_sim)
```

---

sim_single_pd_stages *The estimated value of detection probability at each stage (or revolution) of the mixing process.*

Description

This function gives a probability of detection at each stage (or revolution) of the mixing process.

Usage

```
sim_single_pd_stages(mu, sigma, alpha_in, k, l, r, distribution, UDL, n_sim)
```

Arguments

mu	the average number of CFUs (μ) in the mixed sample, which is in a logarithmic scale if we use a Lognormal / Poisson lognormal distribution
sigma	the standard deviation of the colony-forming units in the mixed sample on the logarithmic scale (default value 0.8)
alpha_in	concentration parameter at the initial stage
k	number of small portions / primary samples
l	number of revolutions /stages
r	the rate of the concentration parameter changes at each mixing stage

distribution	what suitable distribution type we have employed for simulation such as "Poisson-Type A" or "Poisson-Type B" or "Lognormal-Type A" or "Lognormal-Type B" or "Poisson lognormal-Type A" or "Poisson lognormal-Type B"
UDL	the upper decision limit, which depends on the type of microorganisms and testing regulations.
n_sim	number of simulations

Details

Let N' be the number of CFUs in the mixed sample, which is produced by the contribution of k primary samples mixing, $N' = \sum N_i$ and let l be the number of stages in the mixing process. This function provides probability of detection at each stage of the mixing process. At each stage (or revolution), the probability of detection (p_d) can be estimated by using function sim_single_pd.

Value

The probability of detection at each stage of the mixing process.

References

- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.

See Also

sim_single_stages

Examples

```
mu <- 100
sigma <- 0.8
alpha_in <- 0.01
k <- 30
l <- 25000
r <- 0.01
distribution <- "Poisson lognormal-Type B"
UDL <- 0
n_sim <- 2000
no.revolutions <- c(1:l)
cummean <- function(x){cumsum(x)/seq_along(x)}
cum_mean <- cummean(Prob_df[,2])
Prob_df <- data.frame(no.revolutions,
sim_single_pd_stages(mu,sigma,alpha_in,k,l,r,distribution,UDL,n_sim))
colnames(Prob_df) <- c("stages","prob.detection")
plot_example <- ggplot2::ggplot(Prob_df) +
# ggplot2::geom_point(ggplot2::aes(x = stages, y = prob.detection)) +
ggplot2::geom_line(ggplot2::aes(x = stages, y = cummean(prob.detection))) +
# ggplot2::stat_smooth(geom = "smooth", method = "gam", mapping = ggplot2::aes(x = stages,
#   y = prob.detection), se = FALSE, n = 1000) +
ggplot2::ylab(expression("cumulative moving average of prob. detection" ~~ (bar(P[d[l]])))) +
ggplot2::theme_classic() + ggplot2::xlab(expression("No. of revolutions")) +
ggplot2::theme(plot.title = ggplot2::element_text(hjust = 0.5), legend.position = c(0.75,0.25)) +
# ggplot2::ggtitle(label = f_spr(n_sim))+
ggthemes::scale_colour_colorblind()
print(plot_example)
```

`sim_single_stages` *The total number of colony-forming units in the mixed sample by the simulation results in the single mixing plan with l number of stages.*

Description

This function gives a simulated number of CFUs after each stage of the mixing process.

Usage

```
sim_single_stages(
  mu,
  sigma,
  alpha_in,
  k,
  l,
  r,
  distribution,
  n_sim,
  summary = 1
)
```

Arguments

`mu`	the average number of CFUs (μ) in the mixed sample, which is in a logarithmic scale if we use a Lognormal / Poisson lognormal distribution
`sigma`	the standard deviation of the colony-forming units in the mixed sample on the logarithmic scale (default value 0.8)
`alpha_in`	concentration parameter at the initial stage
`k`	number of small portions / primary samples
`l`	number of revolutions / stages
`r`	the rate of the concentration parameter changes at each mixing stage
`distribution`	what suitable distribution type we have employed for simulation such as `"Poisson-Type A"` or `"Poisson-Type B"` or `"Lognormal-Type A"` or `"Lognormal-Type B"` or `"Poisson lognormal-Type A"` or `"Poisson lognormal-Type B"`
`n_sim`	number of simulations
`summary`	if we need to get all simulated N', use `summary = 3`; otherwise, if we use `summary = 1` or `summary = 2`, the function provides the mean value of the simulated N' or generated CFUs in each primary sample, respectively (default `summary = 1`).

Details

Let N' be the number of colony-forming units in the mixed sample which is produced by contribution of k primary samples mixing, $N' = \sum N_i$ and l be the number of stages in the mixing process. This function provides simulated number of CFUs after each stages of the mixing process. To more details, please refer the details section of compare_mixing_3.

Value

average number of colony forming units in the single mixing plan with l number of stages.

References

- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.

See Also

sim_single

Examples

```
mu <- 100
sigma <- 0.8
alpha_in <- 0.01
k <- 30
l <- 25000
r <- 0.01
distribution <-  "Poisson lognormal-Type B"
n_sim <- 2000
no.revolutions <-c(1:l)
Prob_df <-
data.frame(no.revolutions,sim_single_stages(mu,sigma,alpha_in,k,l,r,distribution,n_sim))
colnames(Prob_df) <- c("no.revolutions","CFU")
cummean <- function(x){cumsum(x)/seq_along(x)}
cum_mean <- cummean(Prob_df[,2])
plot_example <- ggplot2::ggplot(Prob_df) +
ggplot2::geom_line(ggplot2::aes(x = no.revolutions, y = CFU))+
ggplot2::geom_line( ggplot2::aes(x = no.revolutions, y = cum_mean), color = "red", size = .75)+
ggplot2::xlab(expression("Number of revolutions"))+
ggplot2::ylab(expression("Expected total number of CFUs"))+
ggplot2::theme_classic()+
ggplot2::theme(plot.title = ggplot2::element_text(hjust = 0.5))+
ggthemes::scale_colour_colorblind()
print(plot_example)
```

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