

Package ‘mixingsimulation’

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Type Package

Title Simulation for powder mixing process

Version 0.0.0

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

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

Description This package develops for simulating powder mixing process for microbial risk assessment in the bulk material production process.

License GPL (>= 2)

Encoding UTF-8

LazyData true

Imports ggplot2, ggthemes, plyr, reshape2, stats

Suggests testthat

RoxygenNote 7.1.1

Depends R (>= 4.0)

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Language en-US

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compare_mixing	<i>The graphical comparison between different mixing schemes with varying parameters of mixing by simulation results.</i>
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Description

This function provides the graphical displays for a different set of mixing plans for comparison purpose. (to be finished later on)

Usage

```
compare_mixing(n_iter, mu, sigma, b, k, distribution)
```

Arguments

n_iter	number of iterations
mu	average number of colony-forming units in mixed sample which is in logarithmic scale if we use a lognormal distribution
sigma	log standard deviation of the colony-forming units in the mixed sample
b	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"

Details

Let N' be the number of colony-forming units in the mixed sample which is produced by mixing of k primary samples and $N' = \sum N_i$ and N_i be the number of colony-forming units in the i^{th} primary sample; where $i = 1, 2, \dots, k$. Following Nauta (2005), contribution weight of contamination by each primary sample can be defined by the random variable y_i which is possible to be following either uniform distribution with parameter k or joint distribution of y_1, y_2, \dots, y_k follows Dirichlet distribution with concentration parameter b . Based on the literature, Dirichlet distribution can be formulated by beta or gamma algorithm which are revealed the same results; see Nauta (2005). This function is developed by based on gamma algorithm, it is formulated the following steps.

$$y_i = \frac{x_i}{\sum_{j=1}^k x_j} \quad \forall i = 1, 2, \dots, k$$

; where x_i follows $gamma(b, 1)$ and also $\sum y_i$ must be equal to one.

- Case 1 (Poisson-Type A): N_i follows $Poisson(\mu/k)$
- Case 2 (Poisson-Type B): N_i follows $Poisson(\mu * y_i)$
- 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 $Binomial(M_i, y_i)$; where M_i follows $Lognormal(\mu, \sigma)$

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_multiple](#), [sim_single](#)

Examples

```
n_iter <- 2000000
mu <- c(log(100),log(100),log(100))
sigma <- c(0.8,0.8,0.8)
b <- c(0.1,1,10)
k <- c(30,30,30)
distribution <- c("Lognormal-Type B","Lognormal-Type B","Lognormal-Type B")
compare_mixing (n_iter, mu, sigma, b, k, distribution )
```

sim_multiple	<i>The total number of colony-forming units in the mixed sample by simulation result (in the multiple mixing plan).</i>
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Description

This function calculates the resulting total number of colony forming units in the mixed sample in the multiple mixing plans. (to be finished later on)

Usage

```
sim_multiple(n_iter, mu, sigma, b, k, distribution)
```

Arguments

n_iter	number of iterations
mu	average number of colony-forming units in mixed sample which is in logarithmic scale if we use a lognormal distribution
sigma	log standard deviation of the colony-forming units in the mixed sample
b	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"

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](#). (to be finished later on)

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](#)

Examples

```
n_iter <- 200000
mu <- c(20,30,50,60)
sigma <- c(0.8,0.8,0.8,0.8)
b <- c(0.1,0.1,0.1,0.1)
k <- c(10,10,10,10)
distribution <- c("Poisson-Type A","Poisson-Type A","Poisson-Type A","Poisson-Type A")
head(sim_multiple( n_iter, mu, sigma, b, k, distribution))
```

sim_single	<i>The total number of colony-forming units in the mixed sample by simulation result (in the single mixing plan).</i>
------------	---

Description

This function calculates the resulting total number of colony forming units in the mixed sample in the single mixing plan. (to be finished later on)

Usage

```
sim_single(n_iter, mu, sigma, b, k, distribution, summary = FALSE)
```

Arguments

n_iter	number of iterations
mu	average number of colony-forming units in mixed sample which is in logarithmic scale if we use a lognormal distribution
sigma	log standard deviation of the colony-forming units in the mixed sample
b	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"
summary	if we need to get the mean and standard deviation of simulated N' , use summary = TRUE (default summary =FALSE).

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](#). (to be finished later on)

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

[sim_multiple](#), [compare_mixing](#)

Examples

```
n_iter <- 200000
mu <- 100
sigma <- 0.8
b <- 0.1
k <- 10
sim_single( n_iter, mu, sigma, b, k, distribution = "Poisson-Type A", summary = TRUE)
```

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