Package 'mixingsimulation'

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Type Package

Title Simulation for powder mixing process

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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

R topics documented:

| compare_mixing | *The graphical comparison between different mixing schemes with varying parameters of mixing by simulation results.* |

Description

This function provides the graphical displays for a different set of mixing parameters for comparison purpose of mixing schemes.

Usage

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

Arguments

mu	the average number of colony-forming units in the mixed sample, which is in logarithmic scale if we use a lognormal distribution
sigma	the standard deviation of the colony-forming units in the mixed sample on the log10 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"
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 $N' = \sum N_i$ and N_i be the number of colony-forming units in the ith primary sample; where $i = 1, 2, ...k$. Following Nauta (2005), contribution weight of contamination by each primary sample can be defined by the random variable w_i which is possible to be following either uniform distribution with paramater $1/k$ or joint distribution of $w_1, w_2, \cdots w_k$ follows Dirichlet distribution with concentration parameter $alpha$. From the previous 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.

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

; where x_i follows $gamma(alpha, 1)$ 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 $Lognormal(\mu, \sigma)$

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).

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

```
mu <- c(100,100,100)
sigma <- c(0.8,0.8,0.8)
alpha <- c(0.1,1,10)
k <- c(30,30,30)
distribution <-  c("Lognormal-Type B","Lognormal-Type B","Lognormal-Type B")
n_sim <- 20000
compare_mixing (mu, sigma, alpha, k, distribution, n_sim )
```

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sim_multiple	*The total number of colony-forming units in the mixed sample by simulation result (in the multiple mixing plan).*

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

Arguments

mu	the average number of colony-forming units in the mixed sample, which is in logarithmic scale if we use a lognormal distribution
sigma	the standard deviation of the colony-forming units in the mixed sample on the log10 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"
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 $N' = \sum N_i$. 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

```
mu <- c(100,100)
sigma <- c(0.8,0.8)
alpha <- c(0.1,10)
k <- c(10,10)
distribution <-  c("Lognormal-Type B","Lognormal-Type B")
n_sim <- 20000
n_sim_df <-data.frame(n_simulations = c(1:n_sim))
Prob_df <- cbind.data.frame(n_sim_df,sim_multiple(mu, sigma, alpha, k, distribution, n_sim))
melten.Prob <- reshape2::melt(Prob_df, id = "n_simulations", variable.name = "mixing_scheme",
value.name = "Total_CFU")
plot_example <- ggplot2::ggplot(melten.Prob) + ggplot2::geom_point(ggplot2::aes(x = n_simulations,
y = Total_CFU, group = mixing_scheme, colour = mixing_scheme))+
ggplot2::xlab(expression("Number of simulations"))+ ggplot2::theme_classic()+
ggplot2::theme(plot.title = ggplot2::element_text(hjust = 0.5),legend.position = c(0.70,0.90),
legend.box.background = ggplot2::element_rect(),legend.box.margin = ggplot2::margin(1,1,1,1))+
ggplot2::ylab(expression("Total number of CFU"))+
ggthemes::scale_colour_colorblind()
print(plot_example)
```

---

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

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

Arguments

mu	the average number of colony-forming units in the mixed sample, which is in logarithmic scale if we use a lognormal distribution
sigma	the standard deviation of the colony-forming units in the mixed sample on the log10 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"
n_sim	number of simulations
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

```
mu <- 100
sigma <- 0.8
alpha <- 0.1
k <- 10
n_sim <- 20000
sim_single(mu, sigma, alpha, k, distribution = "Poisson-Type A", n_sim, summary = TRUE)
```

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