Package ‘mixingsimulation’

March 23, 2021

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

R topics documented:

compare_mixing_stages *The graphical comparison between different mixing schemes by the simulation results in the mixing process's multiple stages with varying mixing parameters.*

Description

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

Usage

```
compare_mixing_stages(mu, sigma, alpha_in, k, l, rate, 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 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
rate	concentration parameter changing rate in the each revolutions
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 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 following either uniform distribution with parameter $1/k$ or joint distribution of $w_1, w_2, \cdots w_k$ follows Dirichlet distribution with concentration parameter α. 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 based on the beta algorithm, and the following steps formulate it.

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

and $w_1 = x_1$;

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 $Lognormal(\mu, \sigma)$

The powder mixing process can be defined as breaking clusters stage by stage. Usually, it will be occurring systematically in the standard powder mixtures. For this package development, we assume that mixing parameters also systematically changing with a fixed rate in 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 to the dependent random variable sum's distribution, we have chosen simulation techniques for this modelling.

Let l be the number of stages or revolution of the mixture, also we 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 that increasing at every stage of the mixing, which is possible to be 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 <- c(100,100,100)
sigma <- 0.8
alpha_in <- 1
k <- c(10,30,50)
l <- 800
rate <- 0.01
distribution <- c("Lognormal-Type B","Lognormal-Type B","Lognormal-Type B")
n_sim <- 20000
compare_mixing_stages(mu, sigma, alpha_in, k, l, rate, distribution, n_sim)
```

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sim_multiple *The total number of colony-forming units in the mixed sample by the simulation results in the multiple mixing plan with varying mixing parameters.*

Description

This function calculates the resulting 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 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 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"`
`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 $N' = \sum N_i$. To more details, please refer the details section of compare_mixing_stages.

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_stages

Examples

```
mu <- c(100,100)
sigma <- 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_multiple_stages — *The total number of colony-forming units in the mixed sample by the simulation results in the multiple mixing plan with multiple stages of the mixing process.*

Description

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

Usage

```
sim_multiple_stages(mu, sigma, alpha_in, k, l, rate, 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 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
`rate`	concentration parameter changing rate in the each revolutions
`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. 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 of the mixing process and assume systematically breaking clusters at every stage of the mixing. Therefore it can be assumed the concentration parameter also systematically changing with the concentration of the contribution.

Value

Estimates the total number of CFU 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

```
rate <- 0.01
l <- 800
mu <- c(100,100,100)
sigma <- 0.8
alpha_in <- 0.01
k <- c(10,20,30)
distribution <- c("Lognormal-Type B","Lognormal-Type B","Lognormal-Type B")
n_sim <- 20000
colMeans(sim_multiple_stages(mu, sigma, alpha_in, k, l, rate, distribution, n_sim))
```

---

sim_single — *The total 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 total 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 = TRUE)
```

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 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"`
`n_sim`	number of simulations
`summary`	if we need to get all simulated N', use `summary = FALSE` otherwise function provides mean value of the simulated N' (default `summary = TRUE`).

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_stages. (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

compare_mixing_stages

Examples

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

`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 CFU after each stage of the mixing process.

Usage

```
sim_single_stages(mu, sigma, alpha_in, k, l, rate, 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 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
`rate`	concentration parameter changing rate in the each revolutions
`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 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 CFU after each stages of the mixing process. To more details, please refer the details section of compare_mixing_stages.

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 <- 500
rate <- 0.01
distribution <-  "Lognormal-Type B"
n_sim <- 20000
no.stages <-c(1:l)
Prob_df <- data.frame(no.stages,sim_single_stages(mu,sigma,alpha_in,k,l,rate,distribution,n_sim))
colnames(Prob_df) <- c("no.stages","CFU")
plot_example <- ggplot2::ggplot(Prob_df) + ggplot2::geom_line(ggplot2::aes(x = no.stages, y = CFU))+
ggplot2::xlab(expression("Number of stages"))+ ggplot2::ylab(expression("Total number of CFU"))+
ggplot2::theme_classic()+ ggplot2::ggtitle(label = "Number of CFU versus number of stages")+
ggplot2::theme(plot.title = ggplot2::element_text(hjust = 0.5))+
ggthemes::scale_colour_colorblind()
print(plot_example)
```

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