# Package 'mixingsimulation'

January 19, 2022

**Type** Package

**Title** Microbiological Risk Assessment of Powder Mixing Process by Simulation Results

**Version** 0.0.1

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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)

**Encoding** UTF-8

**LazyData** true

**Imports** ggplot2, ggthemes, gridExtra, magrittr, plyr, purrr, reshape2, stats, VGAM

**Suggests** testthat

**RoxygenNote** 7.1.2

**Depends** R (>= 4.0)

**Maintainer** Mayooran Thevaraja <mayooran@eng.jfn.ac.lk>

**Language** en-US

## R topics documented:

compare_mixing_detectability *Graphical comparison of mixing plans based on estimated detectability in the mixing process.*

## Description

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

## Usage

```
compare_mixing_detectability(
  mulower,
  muupper,
  sigma,
  alpha_in,
  k,
  l,
  rate,
  distribution,
  UDL,
  n_sim
)
```

## Arguments

| | |
|---|---|
| mulower | the lower value of the mean concentration ($\mu$) for use in the graphical display's x-axis. |
| muupper | the upper value of the mean concentration ($\mu$) 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 |
| rate | concentration parameter changing rate in each of the 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" or "Poisson lognormal-Type A" or "Poisson lognormal-Type B" |
| UDL | the upper decision limit of the expected total CFUs, which can be found from a stabilising point when the mean is about standard deviation |
| n_sim | number of simulations |

## Details

Let $N'$ be the number of CFUs in the mixed sample, which is produced by a contribution of $k$ primary samples mixing, $N' = \sum N_i$, and let $l$ be the number of revolutions in the mixing. This function provides a graphical display to compare mixing plans based on the estimated average detectability in the mixing process with different input variables, such as number of revolutions, type of distribution and number of primary samples.

The detectability is given by the following formula,

$$detectability = 1 - (1 - p_d)^k;$$

where $p_d$ is the average probability of detection after $l$ number of revolutions in each mixing plan. The probability of detection at every stage of the mixing process can be estimated by employing function sim_single_pd_stages. However, if we want to estimate detectability values in each revolution of the mixing process of each plan, we have to utilise function sim_single_detectability. We can flexibly change the mixing parameters of this function, which depends on what purpose the comparison is needed for.

## Value

Estimates the detectability-based graphical display for a comparison of mixing plans.

## References


- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.
- McCallum DA (2005) A conceptual guide to detection probability for point counts and other count-based survey methods. USDA Forest Service General Technical Report PSW-GTR-191, pp 754-761.


## See Also

sim_single_detectability

## Examples

```
## Not run:
mulower <- 0
muupper <- 200
sigma <- 0.8
alpha_in <- 0.01
k <- c(30,30)
l <- c(500,25000)
rate <- 0.01
distribution <- c("Poisson lognormal-Type B","Poisson lognormal-Type B")
UDL <- 138
n_sim <- 20000
compare_mixing_detectability(mulower, muupper, sigma, alpha_in, k, l, rate, distribution, UDL, n_sim)
## End(Not run)
```

`compare_mixing_stages` *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_stages(mu, sigma, alpha_in, k, l, rate, distribution, n_sim)
```

## Arguments

| | |
|---|---|
| `mu` | the average number of CFUs ($\mu$) 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 |
| `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"` 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 $\alpha$. 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(30,50,75)
rate <- 0.01
distribution <- c("Poisson lognormal-Type B","Poisson lognormal-Type B","Poisson lognormal-Type B")
n_sim <- 20000
plot1 <- compare_mixing_stages(mu, sigma, alpha_in, k , l = 50,rate, distribution,n_sim) +
ggplot2::theme(legend.text = ggplot2::element_text(size = 5),
legend.title = ggplot2::element_text(size = 5),
legend.key.size = ggplot2::unit(2, 'mm')) + ggplot2::xlim(0,300)
plot2 <- compare_mixing_stages(mu, sigma, alpha_in, k , l = 500, rate, distribution, n_sim) +
ggplot2::theme(legend.text = ggplot2::element_text(size = 5),
legend.title = ggplot2::element_text(size = 5),
legend.key.size = ggplot2::unit(2, 'mm')) + ggplot2::xlim(0,300)
plot3 <- compare_mixing_stages(mu, sigma, alpha_in, k, l = 5000,rate , distribution,n_sim) +
```

```
ggplot2::theme(legend.text = ggplot2::element_text(size = 5),
legend.title = ggplot2::element_text(size = 5),
legend.key.size = ggplot2::unit(2, 'mm')) + ggplot2::xlim(0,300)
plot4 <- compare_mixing_stages(mu, sigma , alpha_in , k , l = 25000, rate , distribution ,n_sim) +
ggplot2::theme(legend.text = ggplot2::element_text(size = 5),
legend.title = ggplot2::element_text(size = 5),
legend.key.size = ggplot2::unit(2, 'mm')) + ggplot2::xlim(0,300)
gridExtra::grid.arrange(plot1, plot2, plot3, plot4, ncol = 2, nrow = 2)
```

---

`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 ($\mu$) 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_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

```
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_detectability` *The estimated average detectability value in the multiple mixing plans.*

---

## Description

This function estimates the detectability in the mixing process after a specific number of revolutions for different mixing schemes.

## Usage

```
sim_multiple_detectability(
  mu,
  sigma,
  alpha_in,
  k,
  l,
  rate,
```

```
  distribution,
  UDL,
  n_sim
)
```

## Arguments

| | |
|---|---|
| mu | the average number of CFUs ($\mu$) 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 |
| 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" or "Poisson lognormal-Type A" or "Poisson lognormal-Type B" |
| UDL | the upper decision limit of the expected total CFUs, which can be found from stabilising point when the mean is about standard deviation |
| 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 estimates the detectability value after a specific number of revolutions in each mixing scheme. However, we need to apply function sim_single_detectability if we want to estimate individual detectability values at each stage of the mixing process.

## Value

The detectability in the mixing process after a specific number of revolutions.

## References


- Nauta, M.J., 2005. Microbiological risk assessment models for partitioning and mixing during food handling. International Journal of Food Microbiology 100, 311-322.
- McCallum DA (2005) A conceptual guide to detection probability for point counts and other count-based survey methods. USDA Forest Service General Technical Report PSW-GTR-191, pp 754-761.


## See Also

sim_single_detectability

### Examples

```
mu <- 100
sigma <- 0.8
alpha_in <- 0.01
k <- c(30,75)
l <- 25000
rate <- 0.01
distribution <- c("Poisson lognormal-Type B","Poisson lognormal-Type B")
UDL <- 138
n_sim <- 20000
sim_multiple_detectability(mu, sigma , alpha_in, k, l, rate, distribution, UDL, n_sim)
```

---

`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, rate, distribution, n_sim)
```

### Arguments

| | |
|---|---|
| `mu` | the average number of CFUs ($\mu$) 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 |
| `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"` 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

```
rate <- 0.01
l <- 25000
mu <- 100
sigma <- 0.8
alpha_in <- 0.01
k <- c(30,75)
distribution <- c("Poisson lognormal-Type B","Poisson lognormal-Type B")
n_sim <- 20000
colMeans(sim_multiple_stages(mu, sigma, alpha_in, k, l, rate, 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.

## Usage

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

## Arguments

| | |
|---|---|
| `mu` | the average number of CFUs ($\mu$) 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 |
| `rate` | concentration parameter changing rate in each of the 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"` 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 <- 5000
rate <- 0.001
distribution <-  "Poisson lognormal-Type B"
n_sim <- 20000
sim_pois_stages(mu, sigma , alpha_in, k, l, rate, 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 ($\mu$) 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 | if we need to get all simulated $N'$, use summary = 3; otherwise, if we use summary = 1 or summary = 2 or summary = 4, the function provides the mean value of the simulated $N'$ or generated CFUs in each primary sample or mean and variance values of the simulated $N'$, respectively ( default summary = 1). |

## 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 = "Poisson lognormal-Type B", n_sim)
```

---

# sim_single_detectability

*The estimated detectability in the single mixing scheme.*

---

## Description

This function provides an estimated detectability value in the mixing process of the single mixing scheme.

## Usage

```
sim_single_detectability(
  mu,
  sigma,
  alpha_in,
  k,
  l,
  rate,
  distribution,
  UDL,
  n_sim
)
```

## Arguments

| | |
|---|---|
| mu | the average number of CFUs ($\mu$) 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 |
| 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" or "Poisson lognormal-Type A" or "Poisson lognormal-Type B" |
| UDL | the upper decision limit of the expected total CFUs, which can be found from stabilising point when the mean is about standard deviation |
| 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 an estimated detectability in the mixing process of the single mixing scheme. To more details, please refer the details section of compare_mixing_detectability.

## Value

the estimated detectability 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.
- McCallum DA (2005) A conceptual guide to detection probability for point counts and other count-based survey methods. USDA Forest Service General Technical Report PSW-GTR-191, pp 754-761.


## See Also

sim_single

## Examples

```
mu <- 100
sigma <- 0.8
alpha_in <- 0.01
k <- 30
l <- 25000
rate <- 0.01
distribution <-  "Poisson lognormal-Type B"
UDL <- 138
n_sim <- 20000
sim_single_detectability(mu, sigma , alpha_in, k, l, rate, distribution, UDL, n_sim)
```

`sim_single_pd_stages` *The estimated value of detection probability at each stage of the mixing process.*

## Description

This function gives a probability of detection at each stage of the mixing process.

## Usage

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

## Arguments

| | |
|---|---|
| `mu` | the average number of CFUs ($\mu$) 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 |
| `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"` or `"Poisson lognormal-Type A"` or `"Poisson lognormal-Type B"` |
| `UDL` | the upper decision limit of the expected total CFUs, which can be found from stabilising point when the mean is about standard deviation |
| `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. It can be determined by how many of the simulated samples exceed the upper limit set for the CFUs at each stage of the mixing process.

The probability of detection ($p_d$) can be estimated from following formula,

$$p_d = \frac{\text{number of simulated samples which are greater than UDL}}{\text{number of simulations}};$$

where the upper decision limit (UDL) can be found from a stabilising point in the graphical display of the expected total number of CFUs versus the number of revolutions when the mean is about standard deviation.

## 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
rate <- 0.01
distribution <-  "Poisson lognormal-Type B"
UDL <- 138
n_sim <- 20000
no.revolutions <-c(1:l)
Prob_df <- data.frame(no.revolutions,
sim_single_pd_stages(mu,sigma,alpha_in,k,l,rate,distribution,UDL,n_sim))
colnames(Prob_df) <- c("no.revolutions","P_d")
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 = P_d))+
  # ggplot2::geom_line(ggplot2::aes(x = log10(mean), y = P_d))+
 ggplot2::geom_line( ggplot2::aes(x = no.revolutions,y = cum_mean),color = "red",size = .75)+
  ggplot2::xlab(expression("Number of revolutions"))+
  ggplot2::ylab(expression("Probability of detection"))+
  ggplot2::theme_classic()+
  ggplot2::ggtitle(label = "Probability of detection versus number of revolutions")+
  ggplot2::theme(plot.title = ggplot2::element_text(hjust = 0.5))+
  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,
```

```
  rate,
  distribution,
  n_sim,
  summary = 1
)
```

## Arguments

| | |
|---|---|
| mu | the average number of CFUs ($\mu$) 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 |
| 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" 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_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 <- 25000
rate <- 0.01
```

```
distribution <-  "Poisson lognormal-Type B"
n_sim <- 20000
no.revolutions <-c(1:l)
Prob_df <-
data.frame(no.revolutions,sim_single_stages(mu,sigma,alpha_in,k,l,rate,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 CFU"))+
ggplot2::theme_classic()+
ggplot2::ggtitle(label = "Expected total number of CFU versus number of revolutions")+
ggplot2::theme(plot.title = ggplot2::element_text(hjust = 0.5))+
ggthemes::scale_colour_colorblind()
print(plot_example)
```

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