Package 'mixingsimulation'

October 30, 2021

Type Package

Title Simulation results for the powder mixing process

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 for simulating the 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, VGAM

Suggests testthat

RoxygenNote 7.1.2

Depends R (>= 4.0)

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Language en-US

R topics documented:

compare_mixing_prevalence *Graphical comparison of mixing plans based on estimated average prevalence in the mixing process.*

Description

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

Usage

```
compare_mixing_prevalence(
  mulower,
  muupper,
  sigma,
  alpha_in,
  k,
  l,
  rate,
  distribution,
  UL,
  n_sim
)
```

Arguments

mulower	the lower value of the mean concentration (μ), which is desired to use in the graphical display's x-axis.
muupper	the upper value of the mean concentration (μ), which is desired to use in the graphical display's x-axis.
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"
UL	the upper limit value of the expected total CFU, 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 revolutions in the mixing process. This function provides a graphical display to compares mixing plans based on estimated average prevalence in the mixing process with different input variables such as number of revolutions, type of distribution and number of primary samples.

The prevalence is given by the following formula,

$$Prevalence = 1 - (1 - p_d)^l;$$

where p_d is the probability of detection in each stage of the mixing process, for the comparison purpose, we have applied average prevalence 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 prevalence values in each revolution of the mixing process of each plan, we have to utilise function sim_single_prevalence_stages. We can flexibly change the mixing parameters of this function which is depending on what purpose of the comparison is needed.

Value

estimated average prevalence based graphical display to the 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.

See Also

sim_single_prevalence_stages

Examples

```
mulower <- 50
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")
UL <- 138
n_sim <- 2000
compare_mixing_prevalence(mulower, muupper, sigma, alpha_in, k, l, rate, distribution, UL, n_sim)
```

`compare_mixing_stages` *Graphical comparison of mixing plans based on cumulative distribution of expected total CFU in the mixing process.*

Description

This function provides a graphical display to compare mixing plans based on the cumulative distribution of expected total CFU 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 colony-forming units (μ) in the mixed sample, which is in 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 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 $Lognormal(\mu, \sigma)$
- 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 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 <- 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")
n_sim <- 20000
compare_mixing_stages(mu, sigma, alpha_in, k, l, rate, 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 colony-forming units (μ) in the mixed sample, which is in 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

```
sigma <- 0.8
alpha <- c(0.1,5)
k <- c(30,30)
distribution <-  c("Poisson lognormal-Type B","Poisson lognormal-Type B")
n_sim <- 200000
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("density"))+
  ggplot2::theme_classic()+ ggplot2::xlab(expression("Expected total number of CFU"))+
 ggplot2::theme(plot.title = ggplot2::element_text(hjust = 0.5), legend.position = c(0.75,0.75))+
  ggplot2::ggtitle(label = f_spr(n_sim))+ ggthemes::scale_colour_colorblind()
  plot_example
```

---

sim_multiple_prevalence_stages

The estimated average prevalence value in the multiple mixing plans.

Description

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

Usage

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

Arguments

mu	the average number of colony-forming units (μ) in the mixed sample, which is in 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"
UL	the upper limit value of the expected total CFU, 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 estimates the average prevalence value after a specific number of revolutions in each mixing scheme. However, we need to apply function sim_single_prevalence_stages if we want to estimate individual prevalence values at each stage of the mixing process.

Value

the average prevalence 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.

See Also

sim_single_prevalence_stages

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")
UL <- 138
n_sim <- 20000
sim_multiple_prevalence_stages(mu, sigma , alpha_in, k, l, rate, distribution, UL, n_sim)
```

`sim_multiple_stages` *The expected total number of colony-forming units 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 colony-forming units 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 colony-forming units (μ) in the mixed sample, which is in 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 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

the expected 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 <- 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_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 colony-forming units (μ) in the mixed sample, which is in 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`, 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 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_pd_stages *The estimated value of detection probability at each stage of the mixing process.*

Description

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

Usage

```
sim_single_pd_stages(mu, sigma, alpha_in, k, l, rate, distribution, UL, 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/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"
UL	the upper limit value of the expected total CFU, 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 probability of detection in the each stage of the mixing process. It can be determined by how many of the simulated samples exceed the upper limit set for the CFU at each stage of the mixing process.

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

$$p_d = \frac{\text{number of simulated samples which are greater than the upper-limit value}}{\text{number of simulations}};$$

where upper limit value can be found from stabilising point in the graphical display of the expected total number of CFU versus number of revolutions when the mean is about standard deviation.

Value

the probability of detection in the 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"
UL <- 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,UL,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_prevalence_stages` *The estimated prevalence value at each stage of the mixing process of the single mixing scheme.*

Description

This function provides an estimated prevalence value at each stage of the mixing process of the single mixing scheme.

Usage

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

Arguments

`mu`	the average number of colony-forming units (μ) in the mixed sample, which is in 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"`
`UL`	the upper limit value of the expected total CFU, 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 prevalence in each stage of the mixing process. To more details, please refer the details section of compare_mixing_prevalence.

Value

the estimated prevalence 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

Examples

```
mu <- 100
sigma <- 0.8
alpha_in <- 0.01
k <- 30
l <- 25000
rate <- 0.01
distribution <-  "Poisson lognormal-Type B"
UL <- 138
n_sim <- 2000
mean(sim_single_prevalence_stages(mu, sigma , alpha_in, k, l, rate, distribution, UL, 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,
  summary = 1
)
```

Arguments

mu	the average number of colony-forming units (μ) in the mixed sample, which is in 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 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 <- 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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