Package 'grabsampling'

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Type Package

Title Probability of detection for grab sample selection

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Authors Mayooran Thevaraja [aut, cre], Kondaswamy Govindaraju [aut], Mark Bebbington [aut]

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

URL https://github.com/Mayooran1987/grabsampling

BugReports https://github.com/Mayooran1987/grabsampling/issues

Description The goal of grabsampling package is to enable probability of detection calculation for grab samples selection by using two different methods such as systematic or random based on two-state Markov chain in bulk production process.

License GPL (>= 2)

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Suggests testthat

RoxygenNote 7.2.3

Depends R (>= 3.2)

R topics documented:

grabsampling-package *Probability of detection for grab sample selection*

Description

This package provides the probability of detection calculation for grab samples selection by various method of samplings such as systematic or random and also it is useful to generate the comparison curves. Moreover, this package calculates the probability of acceptance calculations based on suitable microbiological distributions such as Poisson gamma or Lognormal or Poisson lognormal and also provides a comparison based on OC curves with different sampling schemes. Most of the researchers have studied the uncorrelated case, but in this study, we have a high spatial correlation between contamination of primary increments. For this package development, we used default standard deviation as 0.8 and also spatial correlation not affected for composite mean for the probability of acceptance calculation. A future version will be included deeply study about variability effects in grab sample selection.

Author(s)

Mayooran Thevaraja, Kondaswamy Govindaraju, Mark Bebbington

References

- Bhat, U., & Lal, R. (1988). Number of successes in Markov trials. Advances in Applied Probability, 20(3), 677-680.
- Jongenburger, I., Besten, H.M., & Zwietering, M.H. (2015). Statistical aspects of food safety sampling. Annual review of food science and technology, 6, 479-503.
- Mussida, A., Vose, D. & Butler, F. Efficiency of the sampling plan for Cronobacter spp. assuming a Poisson lognormal distribution of the bacteria in powder infant formula and the implications of assuming a fixed within and between-lot variability, Food Control, Elsevier, 2013 , 33 , 174-185.
- Van Schothorst, M., Zwietering, M., Ross, T., Buchanan, R. & Cole, M., Relating microbiological criteria to food safety objectives and performance objectives Food Control , 2009 , 20 , 967-979.

AOQL_grab_A *Construction of AOQ curve and calculate AOQL value based on limiting fraction*

Description

AOQL_grab_A provides the AOQ curve and calculates AOQL value based on limiting fraction of contaminated increments.

Usage

```
AOQL_grab_A(c, r, t, d, N, method, plim)
```

Arguments

c	acceptance number
r	nurber of primary increments in a grab sample or grab sample size
t	number of grab samples
d	serial correlation of contamination between the primary increments
N	length of the production
method	what sampling method we have applied such as 'systematic' or 'random' selection methods
plim	the upper limit for graphing the fraction nonconforming or proportion of contaminated increments

Details

Since P_{ND} is the probability of non-detection, p is the limiting fraction of contaminated increments and the outgoing contaminated proportion of primary increments is given by AOQ as the product pP_{ND}. The quantity $AOQL$ is defined as the maximum proportion of outgoing contaminated primary increments and is given by

$$AOQL = \max_{0 \leq p \leq 1} pP_{ND}$$

Value

AOQ curve and AOQL value based on on limiting fraction

See Also

prob_detect

Examples

```
c <-  0
r <-  25
t <-  30
d <-  0.99
N <-  1e9
method <- 'systematic'
plim <- 0.30
AOQL_grab_A(c, r, t, d, N, method, plim)
```

AOQL_grab_B *Construction of AOQ curve and calculate AOQL value based on average microbial counts*

Description

AOQL_grab_B provides the AOQ curve and calculates AOQL value based on average microbial counts.

Usage

```
AOQL_grab_B(c, r, t, distribution,llim, K, m, sd)
```

Arguments

c	acceptance number
r	number of primary increments in a grab sample or grab sample size
t	number of grab samples
distribution	what suitable microbiological distribution we have used such as 'Poisson gamma' or 'Lognormal'or 'Poisson lognormal'
llim	the upper limit for graphing the arithmetic mean of cell count
K	dispersion parameter of the Poisson gamma distribution (default value 0.25)
m	microbiological limit with default value zero, generally expressed as number of microorganisms in specific sample weight
sd	standard deviation of the lognormal and Poisson-lognormal distributions on the log10 scale (default value 0.8)

Details

Since P_a is the probability of acceptance, λ is the arithmetic mean of cell count and the outgoing contaminated arithmetic mean of cell count of primary increments is given by AOQ as the product λP_a. The quantity $AOQL$ is defined as the maximum proportion of outgoing contaminated primary increments and is given by

$$AOQL = \max_{\lambda \geq 0} \lambda P_a$$

Value

AOQ curve and AOQL value based on average microbial counts

See Also

prob_accept

Examples

```
c <-  0
r <-  25
t <-  30
distribution <- 'Poisson lognormal'
llim <- 0.20
AOQL_grab_B(c, r, t, distribution, llim)
```

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compare_plans *Probability of detection or non detection versus fraction nonconforming curve*

Description

This function allows comparison of different sampling schemes, which can be systematic and random sampling of primary increments or grab sampling of blocks of primary increments. A graphical display of the probability of detection P_D or probability of non detection P_{ND} versus fraction nonconforming p for up to four selected schemes will be produced.

Usage

```
compare_plans(d, N, plim, type, c1, r1, t1, method1, c2, r2, t2, method2,
                    c3, r3, t3, method3, c4, r4, t4, method4,linetype)
```

Arguments

d	serial correlation of contamination between the primary increments
N	length of the production
plim	the upper limit for graphing the fraction nonconforming or proportion of contaminated increments
type	what type of graph we want to produce such as D or ND. compare_plans produces a graphical display of P_D or P_{ND} versus p depending on the D or ND of type
c1, c2, c3, c4	acceptance numbers
r1, r2, r3, r4	number of primary increments in a grab sample or grab sample size
t1, t2, t3, t4	number of grab samples
method1, method2, method3, method4	what sampling method we have applied such as 'systematic' or 'random' selection methods
linetype	if we want to get a different type of line for each sampling scheme, set it to FALSE otherwise graph will be produced with the same type of line (default TRUE)

Value

Probability of detection or non detection vs limiting fraction curves

Examples

```
c1 <- 0
c2 <- 0
c3 <- 0
c4 <- 0
r1 <- 1
r2 <- 10
r3 <- 30
r4 <- 75
t1 <- 750
t2 <- 75
t3 <- 25
t4 <- 10
d <- 0.99
N <- 1e9
method1 <- method2 <- method3 <- method4 <- 'systematic'
plim <- 0.10
compare_plans(d, N, plim, type ='D', c1, r1, t1, method1, c2, r2, t2, method2)
compare_plans(d, N, plim, type ='D', c1, r1, t1, method1, c2, r2, t2, method2,
                        c3, r3, t3, method3)
compare_plans(d, N, plim, type ='D', c1, r1, t1, method1, c2, r2, t2, method2,
                        c3, r3, t3, method3, c4, r4, t4, method4)
compare_plans(d, N, plim, type ='ND', c1, r1, t1, method1, c2, r2, t2, method2,
                        c3, r3, t3, method3, c4, r4, t4, method4)
```

`compare_plans_oc` *Comparison based on OC curve*

Description

This function produces overlaid Operating Characteristic (OC) curves for any three systematic/random sampling schemes for specified parameters.

Usage

```
compare_plans_oc(c1, c2, c3, r1, t1, r2, t2, r3, t3, distribution, K, m, sd)
```

Arguments

`c1, c2, c3`	acceptance numbers
`r1, r2, r3`	number of primary increments in a grab sample or grab sample size
`t1, t2, t3`	number of grab samples
`distribution`	what distribution we have used such as `'Poisson gamma'` or `'Lognormal'`or `'Poisson lognormal'`
`K`	dispersion parameter of the Poisson gamma distribution (default value 0.25)
`m`	microbiological limit with default value zero, generally expressed as number of microorganisms in specific sample weight
`sd`	standard deviation of the lognormal and Poisson-lognormal distributions on the log10 scale (default value 0.8)

Value

overlaid OC curves

See Also

prob_accept

Examples

```
c1 <- 0
c2 <- 0
c3 <- 0
r1 <- 25
r2 <- 50
r3 <- 75
t1 <- 10
t2 <- 10
t3 <- 10
distribution <- 'Poisson lognormal'
compare_plans_oc(c1, c2, c3, r1, t1, r2, t2, r3, t3, distribution)
```

`compare_plans_oc_sd` *Comparison based on OC curve with different standard deviations*

Description

This function produces overlaid Operating Characteristic (OC) curves for any three systematic/random sampling schemes for specified parameters with different standard deviation vlues.

Usage

```
compare_plans_oc_sd(c1, c2, c3, r1, t1, r2, t2, r3, t3, sd1, sd2, sd3, distribution, K, m)
```

Arguments

`c1, c2, c3`	acceptance numbers
`r1, r2, r3`	number of primary increments in a grab sample or grab sample size
`t1, t2, t3`	number of grab samples
`sd1, sd2, sd3`	standard deviations of the lognormal and Poisson-lognormal distributions on the log10 scale
`distribution`	what distribution we have used such as `'Poisson gamma'` or `'Lognormal'`or `'Poisson lognormal'`
`K`	dispersion parameter of the Poisson gamma distribution (default value 0.25)
`m`	microbiological limit with default value zero, generally expressed as number of microorganisms in specific sample weight

Value

overlaid OC curves

See Also

prob_accept

Examples

```
c1 <- 0
c2 <- 0
c3 <- 0
r1 <- 25
r2 <- 25
r3 <- 25
t1 <- 30
t2 <- 30
t3 <- 30
sd1 <- 0.2
sd2 <- 0.4
sd3 <- 0.8
distribution <- 'Poisson lognormal'
compare_plans_oc_sd(c1, c2, c3, r1, t1, r2, t2, r3, t3, sd1, sd2, sd3, distribution)
```

`correlation_grab` *Serial correlation between grab samples*

Description

This function calculates the resulting serial correlation between grab samples each having `r` primary increments with original serial correlation `d`.

Usage

```
correlation_grab(r, p, d)
```

Arguments

`r`	number of primary increments in a grab sample or grab sample size
`p`	limiting fraction or proportion of contaminated increments
`d`	serial correlation of contamination between the primary increments

Details

The serial correlation between blocks (grab samples) is given by d_g as

$$d_g = [dp(1 - p(1 - d))^{r-1}]/p_d$$

where p_d is the probability of detection in any of the block (grab sample) which is calculated by using prob_detect_single_grab.

Value

Serial correlation between grab samples

See Also

prob_detect_single_grab

Examples

```
r <-  25
p <-  0.005
d <-  0.99
correlation_grab(r, p, d)
```

oc_plan *Construction of Operating Characteristic (OC) curve*

Description

oc_plan provides the Operating Characteristic (OC) curve for known microbiological distribution such as lognormal. The probability of acceptance is plotted against mean log10 concentration.

Usage

```
oc_plan(c, r, t, distribution, K, m, sd)
```

Arguments

c	acceptance number
r	number of primary increments in a grab sample or grab sample size
t	number of grab samples
distribution	what suitable distribution we have used such as 'Poisson gamma' or 'Lognormal' or 'Poisson lognormal'
K	dispersion parameter of the Poisson gamma distribution (default value 0.25)
m	microbiological limit with default value zero, generally expressed as number of microorganisms in specific sample weight
sd	standard deviation of the lognormal and Poisson-lognormal distributions on the log10 scale (default value 0.8)

Details

Based on the food safety literature, mean concentration is given by $\lambda = 10^{\mu + log(10)\sigma^2/2}$.

Value

Operating Characteristic (OC) curve

See Also

prob_accept

Examples

```
c <-  0
r <-  25
t <-  30
distribution <- 'Poisson lognormal'
oc_plan(c, r, t, distribution)
```

`prob_accept` *Probability of acceptance for grab sampling scheme*

Description

This function calculates the overall probability of acceptance for given microbiological distribution such as lognormal.

Usage

```
prob_accept(c, r, t, mu, distribution, K, m, sd)
```

Arguments

`c`	acceptance number
`r`	number of primary increments in a grab sample or grab sample size
`t`	number of grab samples
`mu`	location parameter (mean log) of the Lognormal and Poisson-lognormal distributions on the log10 scale
`distribution`	what suitable microbiological distribution we have used such as `'Poisson gamma'` or `'Lognormal'`or `'Poisson lognormal'`
`K`	dispersion parameter of the Poisson gamma distribution (default value 0.25)
`m`	microbiological limit with default value zero, generally expressed as number of microorganisms in specific sample weight
`sd`	standard deviation of the lognormal and Poisson-lognormal distributions on the log10 scale (default value 0.8)

Details

Based on the food safety literature, for given values of `c`, `r` and `t`, the probability of detection in a primary increment is given by, $p_d = P(X > m) = 1 - P_{distribution}(X \leq m|\mu, \sigma)$ and acceptance probability in `t` selected sample is given by $P_a = P_{binomial}(X \leq c|t, p_d)$.

If Y be the sum of correlated and identically distributed lognormal random variables X, then the approximate distribution of Y is lognormal distribution with mean μ_y, standard deviation σ_y (see Mehta et al (2006)) where $E(Y) = mE(X)$ and $V(Y) = mV(X) + cov(X_i, X_j)$ for all $i \neq j = 1 \cdots r$.

The parameters μ_y and σ_y of the grab sample unit Y is given by,

$$\mu_y = \log_{10}(E[Y]) - {\sigma_y}^2/2\log_e(10)$$

(see Mussida et al (2013)). For this package development, we have used fixed σ_y value with default value 0.8.

Value

Probability of acceptance

References

- Mussida, A., Vose, D. & Butler, F. Efficiency of the sampling plan for Cronobacter spp. assuming a Poisson lognormal distribution of the bacteria in powder infant formula and the implications of assuming a fixed within and between-lot variability, Food Control, Elsevier, 2013 , 33 , 174-185.
- Mehta, N.B, Molisch, A.F, Wu, J, & Zhang, J., 'Approximating the Sum of Correlated Lognormal or, Lognormal-Rice Random Variables,' 2006 IEEE International Conference on Communications, Istanbul, 2006, pp. 1605-1610.

Examples

```
c <-  0
r <-  25
t <-  30
mu <-  -3
distribution <- 'Poisson lognormal'
prob_accept(c, r, t, mu, distribution)
```

`prob_contaminant` *Probability of contaminated sample*

Description

This function calculates the probability of exactly `l` contaminated samples out of `t` selected grab samples for given gram sample size `r` and serial correlation `d` at the process contamination level `p` for a production length of `N`.

Usage

```
prob_contaminant(l, r, t, d, p, N, method)
```

Arguments

`l`	number of contaminated in `t` selected samples
`r`	number of primary increments in a grab sample or grab sample size
`t`	number of grab samples
`d`	serial correlation of contamination between the primary increments
`p`	limiting fraction or proportion of contaminated increments
`N`	length of the production
`method`	what sampling method we have applied such as `'systematic'` or `'random'` selection methods

Details

Let S_t be the number of contaminated samples and $S_t = \sum X_t$ where $X_t = 1$ or 0 depending on the presence or absence of contamination, then $P(S_t = l)$ formula given in Bhat and Lal (1988), also we can use following recurrence relation formula,

$$P(S_t = l) = P(X_t = 1; S_{t-1} = l - 1) + P(X_t = 0; S_{t-1} = l)$$

which is given in Vellaisamy and Sankar (2001). Both methods will be produced the same results. For this package development, we directly applied formula which is from Bhat and Lal (1988).

Value

Probability of contaminated

References

- Bhat, U., & Lal, R. (1988). Number of successes in Markov trials. Advances in Applied Probability, 20(3), 677-680.
- Vellaisamy, P., Sankar, S., (2001). Sequential and systematic sampling plans for the Markov-dependent production process. Naval Research Logistics 48, 451-467.

See Also

prob_detect_single_grab, correlation_grab

Examples

```
l <-  1
r <-  25
t <-  30
d <-  0.99
p <-  0.005
N <-  1e9
method <- 'systematic'
prob_contaminant(l, r, t, d, p, N, method)
```

`prob_detect` *Probability of detection under the grab sampling method*

Description

This function gives the detection probability for `t` grab samples and given acceptance number under systematic or random sampling methods. This function is also used to calculate the detection probability for primary increments selection by setting the number of primary increments as one.

Usage

```
prob_detect(c, r, t, d, p, N, method)
```

Arguments

`c`	acceptance number
`r`	number of primary increments in a grab sample or grab sample size
`t`	number of grab samples
`d`	serial correlation of contamination between the primary increments
`p`	limiting fraction or proportion of contaminated increments
`N`	length of the production
`method`	what sampling method we have applied such as `'systematic'` or `'random'` selection methods

Details

The detection probability of entire selected grab samples is given by,

$$P_D = 1 - [P(S_t = 0) + P(S_t = 1) + \cdots + P(S_t = c)]$$

Value

Probability of detection in all seleceted grab samples

See Also

prob_contaminant

Examples

```
c <-  1
r <-  25
t <-  30
d <-  0.99
p <-  0.005
N <-  1e9
method <- 'systematic'
prob_detect(c, r, t, d, p, N, method)
```

---

prob_detect_single_grab

Probability of detection in a single grab sample

Description

This function calculates the probability of detection in a single grab sample comprising of `r` primary increments for given serial correlation `d`.

Usage

```
prob_detect_single_grab(r, p, d)
```

Arguments

`r`	number of primary increments in a grab sample or grab sample size
`p`	limiting fraction or proportion of contaminated increments
`d`	serial correlation of contamination between the primary increments

Details

The probability of detection in any of the grab sample is given by p_d as

$$p_d = 1 - (1 - p)(1 - p(1 - d))^{r-1}$$

Value

Probability of detection in a grab sample

Examples

```
r <-  25
p <-  0.005
d <-  0.99
prob_detect_single_grab(r, p, d)
```

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