Package ‘grabsampling’

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Title  Probability of Detection for Grab Sample Selection
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Description  Functions for obtaining the probability of detection, for grab samples selection by using two different methods such as systematic or random based on two-state Markov chain model. For detection probability calculation, we used results from Bhat, U. and Lal, R. (1988) <doi:10.2307/1427041>.
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AOQL_grab_A

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  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
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**

```r
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)
```

---

**Description**

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

**Usage**

```r
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, $\lambda$ 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 $\lambda P_a$. 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

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

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

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

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
**compare_plans_oc**

**Description**

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

**Value**

Probability of detection or non detection vs limiting fraction curves

**Examples**

```r
c1 <- 0
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)
```
correlation_grab

Usage

```r
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

```r
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)
```

---

**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

$$d_g = \frac{dp(1 - p(1 - d))^{r-1}}{p_d}$$

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
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

```r
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

```r
  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

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

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,

\[ p_d = P(X > m) = 1 - P_{\text{distribution}}(X \leq m | \mu, \sigma) \]

and acceptance probability in t selected samples is given by

\[ P_a = P_{\text{binomial}}(X \leq c | t, p_d) \].

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 \( \mu_y \), standard deviation \( \sigma_y \) (see Mehta et al (2006)) where \( E(Y) = mE(X) \) and \( V(Y) = mV(X) + \text{cov}(X_i, X_j) \) for all \( i \neq j = 1 \cdots r \).

The parameters \( \mu_y \) and \( \sigma_y \) of the grab sample unit Y is given by,

\[ \mu_y = \log_{10} \left( E[Y] \right) - \frac{\sigma_y^2}{2 \log_e(10)} \]

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

Value

Probability of acceptance

References


Examples

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

**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**

```r
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
prob_detect

References


See Also

prob_detect_single_grab, correlation_grab

Examples

```r
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

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

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

**Value**

Probability of detection in all selected grab samples

**See Also**

`prob_contaminant`

**Examples**

```r
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)
```

---

**Description**

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

**Usage**

```r
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

\[ p_d = 1 - (1 - p)(1 - p(1 - d))^{r-1} \]
**prob_detect_single_grab**

**Value**

Probability of detection in a grab sample

**Examples**

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