

Package ‘rsalvador’

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Title rSalvador: An R Tool for the Luria-Delbruck Fluctuation Assay

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Depends R (>= 2.15.0), hypergeo, gdata

Description Like its predecessor SALVADOR, rSalvador is a software tool intended for experimentalists running fluctuation experiments in the laboratory, and for biology educators and students teaching or learning fluctuation assay in the classroom. rSalvador comprises R routines for inferring microbial mutation rates from fluctuation assay data. rSalvador can compute maximum likelihood estimates and likelihood ratio-based confidence intervals, adjusting for relative fitness, final cell population size N_t or plating efficiency when necessary. rSalvador can also be used to compare mutation rates. In addition to the usual continuous-time Lea-Coulson mutation model, rSalvador can accommodate Haldane's discrete-time mutation model. Furthermore, rSalvador can compute mutant cell distribution functions, plot log-likelihood functions and simulate fluctuation experiments.

LazyData yes

License GPL (>= 2)

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rsalvador-package *rSalvador: An R Tool for the Luria-Delbruck Fluctuation Assay.*

Description

Adapted from SALVADOR 2.3 (Zheng, 2008). An overview of the package's functionalities is given in Zheng (2015).

Details

Package: rSalvador
Type: Package
Version: 1.6
Date: 2016-08-01
License: GPL 2.0

Note

Eric H. Zheng provided technical support.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- Q. Zheng, SALVADOR 2.3: A Tool for Studying Mutation Rates, published in September 2008, available at <http://library.wolfram.com/infocenter/MathSource/7082>.
- Q. Zheng, A new practical guide to the Luria-Delbruck protocol, Mutation Research/Fundamental and Molecular Mechanisms of Metagenesis 781 (2015) 7-13.

boshoff.data *Experimental Data by Boshoff et al.*

Description

Data from 6 fluctuation experiments by Boshoff et al. (2003). The final cell population sizes N_t are: 7.2e8, 3.3e8, 1.02e9, 7.65e8, 2.1e9 and 1.9e9. According to the authors, some large mutants counts are not very reliable. Data are from Supplementary Table of Boshoff (2003).

References

- HIM Boshoff, MB Reed, CE Barry III, V Mizrahi, DnaE2 polymerase contributes to in vivo survival and the emergence of drug resistance in Mycobacterium tuberculosis, Cell 113 (2003) 183-193.

Examples

```
newton.LD(boshoff.data[[1]]) / (7.2e8)
```

```
cairns.foster.data Experimental Data from Cairns and Foster
```

Description

Well-known data, analyzed by Rosche and Foster (2000).

Details

Experiment described in detail in Cairns and Foster (1991), data first appeared in Rosche and Foster (2000) with the maximum likelihood estimate of m explicitly given.

Source

WA Rosche and PL Foster, Determining mutation rates in bacterial population, *Methods* 20: 4-17 (2000)

References

J Cairns and PL Foster, Adaptive reversion of a frameshift mutation in *Escherichia coli*, *Genetics* 128:695-701 (1991)

Examples

```
newton.LD(cairns.foster.data, show.iter=TRUE)
```

```
compare.LD Compare mutation rates with a common Nt
```

Description

This function compares the expected number of mutations per test tube (m) between two fluctuation experiments. Because a common Nt is assumed, it compares the mutation rates between the two experiments.

Usage

```
compare.LD(x1, x2, init.m0 = 0, init.m1 = 0, init.m2 = 0, phi = 1)
```

Arguments

<code>x1</code>	a data vector representing mutant counts in the first experiment.
<code>x2</code>	a data vector representing mutant counts in the second experiment.
<code>init.m0</code>	initial value for estimating a common m shared by the two experiments.
<code>init.m1</code>	initial value for estimating m for the first experiment.
<code>init.m2</code>	initial value for estimating m for the second experiment.
<code>phi</code>	the common clock parameter, often set to unity.

Value

a pair of positive real numbers: (chi-squared test statistic, p-value).

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q Zheng, Methods for comparing mutation rates using fluctuaion assay data, Mutat. Res. Fundam. Mol. Mech. Mutagen. 777 (2015) 20-22.

Examples

```
x=simu.cultures(15,1e-7,1,1,5,1e7)
y=simu.cultures(15,3e-7,1,1,5,1e7)
compare.LD(x,y)
```

confint.B0	<i>Likelihood ratio-based confidence interval for m, under the Luria-Delbruck model, accounting for variation in Nt</i>
------------	---

Description

This function computes a likelihood ratio-based confidence interval for m, taking into consideration of the variation in Nt, the cell population size immediately prior to plating. The algorithm is given in Zheng (2016), which is adapted from an algorithm given in Zheng (2011).

Usage

```
confint.B0(data, cv = 0.1, alpha = 0.05, tol = 1e-08, init.m = 5.1,
  init.lower = 0, init.upper = 0, max.iter = 30, show.iter = FALSE)
```

Arguments

data	A data vector representing the numbers of mutants in the test tubes.
cv	Coefficient of variation indicating the variation in Nt.
alpha	Significance level.
tol	Tolerance parameter to control numerical accuracy.
init.m	Initial guess for the parameter m.
init.lower	Initial guess for the lower limit of the confidence interval.
init.upper	Initial guess for the upper limit of the confidence interval.
max.iter	Maximum number of numerical iterations.
show.iter	To show the numerical iteration process.

Value

A pair of real numbers representing a confidence interval for m.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- Q. Zheng, A Bayesian two-level model for fluctuation assay, *Genetica* 139 (2011) 1409-1416.
- Q. Zheng, A second look at the final number of cells in a fluctuation experiment, *Journal of Theoretical Biology* 401 (2016) 54-61.

See Also

newton.B0, confint.LD, confint.MK, confint.LD.plating

Examples

```
confint.B0(demerec.data, cv=0.1)
```

confint.Haldane	<i>Confidence Intervals for Mutation Rates Under the Haldane Model</i>
-----------------	--

Description

It uses an algorithm described in Zheng (2007) to compute a confidence interval for μ , the probability of mutation per cell division under the Haldane model.

Usage

```
confint.Haldane(data, g, N0 = 1, alpha = 0.05, tol = 1e-06, init.mu = 0,
init.lower = 0, init.upper = 0, max.iter = 30, show.iter = FALSE)
```

Arguments

data	a vector of experimental data (non-negative integers).
g	number of generations.
N0	initial number of nonmutant cells.
alpha	level of the confidence interval.
tol	tolerance parameter to control the iteration process.
init.mu	an initial guess for μ .
init.lower	an initial guess for lower limit of μ , rarely needed.
init.upper	an initial guess for upper limit of μ , rarely needed.
max.iter	maximum number of iterations.
show.iter	to show the iteration progress.

Details

The algorithm is described in Zheng (2007).

Value

a confidence interval for the mutation rate μ .

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, (2007). On Haldane's formulation of Luria and Delbruck's mutation model, *Mathematical Biosciences* 209:500-513.

See Also

confint.LD confint.LD.plating

Examples

```
confint.Haldane(demerec.data, g=25, N0=90, show.iter=TRUE)
```

confint.LD

Likelihood Ratio-Based Confidence Interval under the Luria-Delbruck Model

Description

This function employs an algorithm described in Zheng (2005) to compute a likelihood ratio-based confidence interval for m , the expected number of mutations per test tube.

Usage

```
confint.LD(data, alpha = 0.05, phi = 1, tol = 1e-06, init.m = 0,
  init.lower = 0, init.upper = 0, max.iter = 30, show.iter = FALSE)
```

Arguments

data	a vector of numbers of mutant colonies
alpha	significance level
phi	this parameter is defined by $\phi=1-N_0/N_t$, is usually assumed to be 1.0.
tol	tolerance parameter
init.m	an initial guess for m , rarely needed
init.lower	an initial guess for lower limit of m , rarely needed
init.upper	an initial guess for upper limit of m , rarely needed
max.iter	maximum number of iterations
show.iter	to show iteration progress

Details

The algorithm is described in Zheng (2005).

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, (2005). New algorithms for Luria-Delbruck fluctuation analysis, *Mathematical Biosciences* 196:198-214 (2005).

See Also

confint.LD.plating

Examples

```
confint.LD(demerec.data, show.iter=TRUE)
```

confint.LD.plating *Confidence Intervals for m that Accounts for Plating Efficiency*

Description

This function computes likelihood ratio-based confident intervals for m that accounts for plating efficiency. The algorithm was described in Zheng (2008).

Usage

```
confint.LD.plating(data, e, alpha = 0.05, tol = 1e-06, init.m = 0,
  init.lower = 0, init.upper = 0, max.iter = 30, show.iter = FALSE)
```

Arguments

data	A vector of experimental data, all integers.
e	Plating efficiency e ($0 < e < 1$)
alpha	A 1-alpha confidence interval is to be constructed.
tol	Tolerance parameter to control the number of iterations.
init.m	An initial guess for m can be supplied, but is rarely needed.
init.lower	An initial guess for the lower limit of the confidence interval, but is rarely needed.
init.upper	An initial guess for the upper limit of the confidence interval, but is rarely needed.
max.iter	Maximum number of iterations allowed.
show.iter	To view the iteration process.

Value

A pair of positive real numbers.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng. A note on plating efficiency in fluctuation experiments, *Mathematical Biosciences*, 216:150-153 (2008).

See Also

confint.LD

confint.MK	<i>Likelihood-Based Confidence Interval under the Mandelbrot-Koch Model</i>
------------	---

Description

This function computes confidence intervals for m under the Mandelbrot-Koch model that allows for differential growth between mutants and nonmutants. A value of the relative fitness w is obtained from a fitness assay. The algorithm used is a specialization of a more general algorithm described in Zheng (2005).

Usage

```
confint.MK(data, w = 1, alpha = 0.05, tol = 1e-08, init.m = 0,
  init.lower = 0, init.upper = 0, max.iter = 30, show.iter = FALSE)
```

Arguments

<code>data</code>	A vector of experimental data (non-negative integers as mutant counts).
<code>w</code>	Relative fitness defined as (mutant growth rate)/(nonmutant growth rate).
<code>alpha</code>	The confidence coefficient is $1 - \alpha$.
<code>tol</code>	Tolerance parameter to control numerical accuracy.
<code>init.m</code>	Initial guess for the parameter m , often the default is sufficient.
<code>init.lower</code>	Initial guess for the lower limit of the confidence interval.
<code>init.upper</code>	Initial guess for the upper limit of the confidence interval.
<code>max.iter</code>	Maximum number of numerical iterations.
<code>show.iter</code>	To show the numerical iteration process.

Value

A pair of real numbers as the confidence limits.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, New algorithms for Luria-Delbruck fluctuation analysis, *Mathematical Biosciences* 196 (2005) 198-214.

See Also

confint.LD

Examples

```
confint.MK(demerec.data, w=0.75)
```

confint.profile.m	<i>Profile Likelihood Confidence Intervals for m Under the Mandelbrot-Koch Model</i>
-------------------	--

Description

This function computes profile likelihood confidence intervals for m under the Mandelbrot-Koch model (Mandelbrot 1974; Koch 1982). Here m is the expected number of mutations per culture. The Mandelbrot-Koch model allows for differential growth between mutants and nonmutants, that is, the relative fitness of mutants, w , can be different from 1.0. The adopted iterative algorithm is described in detail in Zheng (2005).

Usage

```
confint.profile.m(data, alpha = 0.05, init.low.m = -1, init.low.w = -1,
  init.up.m = -1, init.up.w = -1, init.m = -1, init.w = -1,
  max.iter = 30, tol = 1e-06, show.iter = FALSE)
```

Arguments

data	A vector containing mutant counts.
alpha	The confidence level is $1.0 - \alpha$.
init.low.m	A starting value for the lower confidence limit of m .
init.low.w	A starting value for the lower confidence limit of w .
init.up.m	A starting value for the upper confidence limit of m .
init.up.w	A starting value for the upper confidence limit of w .
init.m	A starting value for the MLE of m , needed for computing the profile likelihood CI.
init.w	A starting value for the MLE of w , needed for computing the profile likelihood CI.
max.iter	Maximum number of numerical iterations.
tol	A tolerance parameter to control the number of iterations.
show.iter	A logical variable controlling the display of numerical iterations.

Value

A pair of real numbers representing the profile confidence interval for m .

Author(s)

Qi Zheng <qzheng.@sph.tamhsc.edu>

References

- A. L. Koch, Mutation and growth rates from Luria-Delbruck fluctuation tests, *Mutation Research* 95 (1982) 129-143.
- B. Mandelbrot, A population birth-and-mutation process, I: Explicit distributions for the number of mutants in an old culture of bacteria, *J Appl Prob* 11 (1974) 437-444.
- Q. Zheng, New algorithms for Luria-Delbruck fluctuation analysis, *Mathematical Biosciences* 196 (2005) 198-214.

See Also

confint.MK, confint.profile.w

Examples

```
confint.profile.m(demerec.data)
```

`confint.profile.w` *Profile Likelihood Confidence Intervals for w (Relative Fitness) Under the Mandelbrot-Koch Model*

Description

This function computes profile likelihood confidence intervals for w under the Mandelbrot-Koch model (Mandelbrot 1974; Koch 1982), which allows for differential growth between mutants and nonmutants. That is, the relative fitness of mutants, w , can be different from 1.0. The adopted iterative algorithm is described in detail in Zheng (2005).

Usage

```
confint.profile.w(data, alpha = 0.05, init.low.m = -1, init.low.w = -1,
  init.up.m = -1, init.up.w = -1, init.m = -1, init.w = -1,
  max.iter = 30, tol = 1e-06, show.iter = FALSE)
```

Arguments

<code>data</code>	A vector containing mutant counts.
<code>alpha</code>	The confidence level is $1.0 - \alpha$.
<code>init.low.m</code>	A starting value for the lower confidence limit of m .
<code>init.low.w</code>	A starting value for the lower confidence limit of w .
<code>init.up.m</code>	A starting value for the upper confidence limit of m .
<code>init.up.w</code>	A starting value for the upper confidence limit of w .
<code>init.m</code>	A starting value for the MLE of m , needed for computing the profile likelihood CI.
<code>init.w</code>	A starting value for the MLE of w , needed for computing the profile likelihood CI.
<code>max.iter</code>	Maximum number of numerical iterations.
<code>tol</code>	A tolerance parameter to control the number of iterations.
<code>show.iter</code>	A logical variable controlling the display of numerical iterations.

Value

A pair of real numbers representing the profile confidence interval for m.

Author(s)

Qi Zheng <qzheng.@sph.tamhsc.edu>

References

- A. L. Koch, Mutation and growth rates from Luria-Delbruck fluctuation tests, *Mutation Research* 95 (1982) 129-143.
- B. Mandelbrot, A population birth-and-mutation process, I: Explicit distributions for the number of mutants in an old culture of bacteria, *J Appl Prob* 11 (1974) 437-444.
- Q. Zheng, New algorithms for Luria-Delbruck fluctuation analysis, *Mathematical Biosciences* 196 (2005) 198-214.

See Also

confint.MK, confint.profile.m

Examples

```
confint.profile.w(demerec.data)
```

crane.data

Experimental data of Crane, Thomas and Jones

Description

A pair of fluctuation experiments conducted by Crane et al. (1996). For the first experiment, $N_t=3.6e9$, and the second $N_t=3.9e9$. In both experiments, a 0.2 ml portion was plated from each of the eleven 2.0-ml cultures. Thus, plating efficiency is $e=0.1$ in both experiments.

References

- GJ Crane, SM Thomas, ME Jones, A modified Luria-Delbruck fluctuation assay for estimating and comparing mutation rates, *Mutation Research* 354 (1996) 171-182.

Examples

```
newton.LD.plating(crane.data[[1]],e=0.1)
```

demerec.data*Classic Experimental Data of Demerec*

Description

This data set came from one of the earliest fluctuation experiments performed by one of the pioneers in the field. It has been cited in the literature numerous times. $N_t=1.9e8$.

Source

M. Demerec, Production of staphylococcus strains resistant to various concentrations of penicillin, Proc. Natl. Acad. Sci. USA 31 (1945) 16-24.

Examples

```
newton.LD(demerec.data, show.iter=TRUE)
```

export.text.data*Exporting Data to an External Text File*

Description

It is sometimes desirable to save experimental data already in rSalvador to an external text file. For example, data imported by import.excel.data may later be exported as a text file so that other programs can use the data.

Usage

```
export.text.data(filename, data)
```

Arguments

filename	Name of the text file to be written.
data	A vector of experimental data to be exported.

Author(s)

Qi Zheng <qzheng@sprh.tamhsc.edu>

See Also

import.text.data

Examples

```
export.text.data('testing.txt', demerec.data)
```

fisher.LD.plating	<i>Computing Expected Fisher Information for m Under the Standard Luria-Delbruck Distribution with Partial Plating</i>
-------------------	--

Description

This function computes approximate expected Fisher information for m under the standard Luria-Delbruck distribution with partial plating. The algorithm is adapted from that given in Zheng (2002). The expected Fisher information can be utilized in determining sample size (the number of cultures) in a fluctuation experiment.

Usage

```
fisher.LD.plating(m, e, n)
```

Arguments

m	The expected number of mutations.
e	The parameter of plating efficiency ($0 < e < 1$).
n	The number of terms kept in summing an infinite series that defines the expected Fisher information.

Value

A positive real number.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, Statistical and algorithmic methods for fluctuation analysis with SALVADOR as an implementation, Mathematical Biosciences 176 (2002) 237-252.

See Also

fisher.MK

Examples

```
fisher.LD.plating(m=50.0, e=0.2, n=2000)
```

`fisher.MK`*Computing Expected Fisher Information for m Under the MK distribution*

Description

This function computes approximate expected Fisher information for m under the Mandelbrot-Koch distribution. The algorithm is adapted from that given in Zheng (2002). The expected Fisher information can be utilized in determining sample size (the number of cultures) in a fluctuation experiment.

Usage

```
fisher.MK(m, w, n)
```

Arguments

m	The expected number of mutations.
w	The parameter of relative fitness.
n	The number of terms kept in summing an infinite series that defines the expected Fisher information.

Value

A positive real number.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, Statistical and algorithmic methods for fluctuation analysis with SALVADOR as an implementation, Mathematical Biosciences 176 (2002) 237-252.

See Also

`fisher.LD.plating`

Examples

```
fisher.MK(3.0, 1.0, 2000)
```

ford.data

Data of Mycobacterium tuberculosis Mutation by Fort et al.

Description

One of several fluctuation experiments performed by Ford et al. (2011) to study Mycobacterium tuberculosis mutation rates. $Nt=1.08e9$.

References

CB Ford, PL Lin, MR Chase, RR Shah, O Iartchouk, J Galagan, N. Mohaideen, TR Ioerger, JC Sacchettini, M Lipsitch, JL Flynn, SM Fortune, Use of whole genome sequencing to estimate the mutation rate of Mycobacterium tuberculosis during latent infection, Nature Genetics 43 (2011) 482-486. See supplementary information.

Examples

```
newton.LD(ford.data)
confint.LD(ford.data) / (1.08e9)
```

foster.data

Fluctuation Experimental Data by P. Foster

Description

Data from an experiment conducted by P. Foster in 1994. The study was about a reversion of Lac- to Lac+ in the FC 40 strain of Escherichia coli. Three cultures were sampled to estimate Nt. At the $1e-6$ dilution, the three measurements were 702, 645 and 536. Therefore, $Nt=6.16e8$. The data first appeared in Zheng (2011).

References

Q. Zheng, A Bayesian two-level model for fluctuation assay, Genetica 139 (2011) 1409-1416.

Examples

```
newton.LD(foster.data)
```

golden.benchmark.LD

Maximum Likelihood Estimation of the Mutation Rate Accounting for Variation in Nt

Description

Nt is the (non-mutant) cell population size immediately prior to plating. In a fluctuation experiment comprising n tubes, the final cell population sizes are Nt(1), Nt(2), ..., Nt(n). Measuring all Nt(i) is a daunting experimental challenge. However, theoretically, when all Nt(i) are known, a maximum likelihood estimate of m can be computed. Thus, this scenario serves as a theoretical benchmark model. This function uses the golden section search method to calculate an MLE of mu (the mutation rate), incorporating the measurements of Nt(i). The likelihood function is formed using the Luria-Delbruck distribution as described by Lea and Coulson (1949).

Usage

```
golden.benchmark.LD(data, Nt, mu.low = 1e-12, mu.up = 5e-07,
                    tol = 1e-09, max.iter = 100, show.iter = FALSE)
```

Arguments

data	A vector containing the mutant counts.
Nt	A vector containing the final cell population sizes.
mu.low	A lower bound for the mutation rate.
mu.up	An upper bound for the mutation rate. Because $\exp(-m)$ will cause underflow when m exceeds 744, it is imperative to ensure that $(\max Nt(i)) * \mu.up < 700$.
tol	A parameter to control numerical accuracy.
max.iter	Maximum number of iterations allowable in the golden section search process.
show.iter	To exhibit the step-by-step golden section search process.

Value

A real number as an estimate of the mutation rate, not the expected number of mutations (m).

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

E.A. Lea, C.A. Coulson, The distribution of the numbers of mutants in bacterial populations. J Genetics 49 (1949) 264-285.

Examples

```
golden.benchmark.LD(demerec.data, rep(1.9e8, 30))
```

golden.LD.B0

*Accounting for Varying Nt Under the Luria-Delbruck Model***Description**

This function uses the B0 distribution (Zheng 2010, 2011) to account for variation in Nt, the final cell population size prior to plating. The function employs the golden section search algorithm to find a value of m that maximizes the log likelihood functions.

Usage

```
golden.LD.B0(data, cv = 0.1, m.low = 0.1, m.up = 30, tol = 1e-8,
             max.iter = 60, show.iter = FALSE)
```

Arguments

data	A vector containing the mutant count data.
cv	Known (independently estimated) coefficient of variation for Nt, final cell population size.
m.low	A lower starting value of m for the golden section search.
m.up	An upper starting value of m for the golden section search.
tol	A tolerance parameter to control numerical precision.
max.iter	Maximum number of iterations.
show.iter	A logical variable controlling the exhibition of the numerical iteration process.

Value

A positive real number as an estimate of m, the expected number of mutations per culture.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, A new discrete distribution induced by the Luria-Delbruck mutation model, *Statistics* 44 (2010) 529-540.

Q. Zheng, A Bayesian two-level model for fluctuation assay, *Genetica* 139 (2011) 1409-1416.

See Also

newton.LD, newton.LD.plating

Examples

```
golden.LD.B0(demerec.data, cv=0.064)
```

`import.excel.data` *Importing Data from an Excel File*

Description

Biologists often keep their experimental results in Excel files. In addition to the numbers of mutant cells, such files usually contain other experimental details. rSalvador requires excel files to satisfy two conditions. First, the first row of the file should be reserved as a header, and second, the first non-blank column should be reserved to keep the numbers of mutant cells that rSalvador intends to import. The parameter `col` (which has a default value of 1) can be used to choose which column of the file is to be imported.

Usage

```
import.excel.data(filename, col = 1)
```

Arguments

<code>filename</code>	the data file to be imported.
<code>col</code>	the desired column to be imported.

Value

A vector of non-negative integers.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

See Also

`import.text.data`

`import.text.data` *Importing Data from a Text File*

Description

The text data file to be imported can have several header lines at the beginning, followed by a single-column of experimental data. The parameter `jump` specifies the number of header lines.

Usage

```
import.text.data(filename, jump = 1, col = 1)
```

Arguments

<code>filename</code>	Experimental data should be listed in a single column, but the first few lines can be the experimenter's note.
<code>jump</code>	Number of lines to skip.
<code>col</code>	Which column contains data.

Value

A vector of non-negative integers imported from the text file.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

`LD.p0.est`*The Classic P0 Method of Luria and Delbruck*

Description

This is one of the two methods proposed in the classic paper of Luria and Delbruck (1943) to estimate the expected number of mutations per test tube, now commonly known as m . An important property of this method is often overlooked: the P0 method does not rely on the assumption that mutant cells and wild type cells grow at the same rate.

Usage

```
LD.p0.est (data)
```

Arguments

`data` a vector of non-negative integers representing mutant cell counts.

Value

An estimate of m , the expected number of mutations.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

S.E. Luria, M. Delbruck, Mutations of bacteria from virus sensitivity to virus resistance, *Genetics* 28 (1943) 491-511.

See Also

`newton.LD`

Examples

```
LD.p0.est (cairns.foster.data)
```

likely.average	<i>A family of Estimators of m Based on Delbruck's Concept of the Likely Average</i>
----------------	--

Description

The concept of the likely average (Luria and Delbruck 1943) spawns a family of estimators. The well-known method of Lea and Coulson (1949) is a member of that family. However, most of these estimators are given solely for their pedagogical values and historical interest.

Usage

```
likely.average(data, b = 1.24, classic = FALSE, init.m = 0, tol = 1e-09,
               max.iter = 25, use.median = TRUE, show.iter = FALSE)
```

Arguments

data	A vector of experimental data.
b	Setting b=1.24 (default) gives the Lea-Coulson estimator when the variable classic is set to False.
classic	If classic is true, the estimator depends on the number of cultures in an experiment. That was Delbruck's original idea.
init.m	An initial guess of m.
tol	Tolerance limit to control accuracy.
max.iter	Maximum number of iterations in the Newton procedure.
use.median	Either the sample median (default) or the sample mean is used in the equation.
show.iter	Show iteration history.

Value

A real number as an estimate of m.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

E. A. Lea, C. A. Coulson, The distribution of the numbers of mutants in bacterial populations. *J Genetics* 49 (1949) 264-285.

S. E. Luria, M. Delbruck, Mutations of bacteria from virus sensitivity to virus resistance. *Genetics* 28 (1943) 491-511.

See Also

newton.LD

Examples

```
likely.average(demerec.data)
```

```
log.likelihood.Haldane
```

Computing the Log-Likelihood Function Under the Haldane Model

Description

This function computes the log-likelihood function for data under the Haldane model. The algorithm is based on Zheng (2007).

Usage

```
log.likelihood.Haldane(data, g, mu, N0 = 1)
```

Arguments

data	A vector of data.
g	Number of generations.
mu	The mutation rate.
N0	Initial number of nonmutant cells.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng (2007) On Haldane's formulation of Luria and Delbruck's mutation model, *Mathematical Biosciences* 209:500-513.

See Also

log.likelihood.LD, log.likelihood.LD.plating

Examples

```
log.likelihood.Haldane(niccum.data, 25, 1e-6)
```

```
log.likelihood.LD
```

Computing the Log-Likelihood Function Under the Luria-Delbruck Model

Description

This function computes the log-likelihood function for data under the Lea-Coulson formulation of the Luria-Delbruck mutation model.

Usage

```
log.likelihood.LD(data, m, phi = 1)
```

Arguments

data	A vector of data.
m	The parameter m is regarded as the argument of the log-likelihood function.
phi	This parameter is defined as $\phi=1-N_0/N_t$.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

See Also

log.likelihood.LD.plating

Examples

```
log.likelihood.LD(demerec.data,m=8.5)
```

```
log.likelihood.LD.plating
```

Computing the Log-Likelihood Function That Adjusts for Plating Efficiency

Description

This function computes the log-likelihood function that adjusts for plating efficiency. The parameter m is regarded as the argument of the log-likelihood function.

Usage

```
log.likelihood.LD.plating(data, m, e)
```

Arguments

data	A vector of experimental data.
m	A real positive number as a given value of the parameter m.
e	plating efficiency.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

See Also

log.likelihood.LD

LRT.LD

Likelihood Ratio Test under the Luria-Delbruck Model

Description

The function computes the likelihood ratio test statistic to compare the mutation rates in two independent fluctuation experiments. Both experiments are modeled by the standard Luria-Delbruck distribution. The algorithm is described in Zheng (2016), which is a generalization of a simpler algorithm given in Zheng (2015).

Usage

```
LRT.LD(X1, X2, R = 1, phi1 = 1, phi2 = 1, init.mc = 0, init.m1 = 0,
        init.m2 = 0, tol = 1e-09, show.iter = FALSE)
```

Arguments

X1	Data from the first experiment.
X2	
R	Data from the second experiment.
phi1	"Time" parameter for the first experiment, usually set to unit.
phi2	"Time" parameter for the second experiment, usually set to unit.
init.mc	Initial guess of m under the null hypothesis – the combined model.
init.m1	Initial guess of m for the first experiment.
init.m2	Initial guess of m for the second experiment.
tol	Tolerance parameter to control numerical accuracy.
show.iter	Logical variable to control the display of the numerical iteration process.

Value

A pair of real numbers: (test statistic, p-value).

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, Methods for comparing mutation rates using fluctuation assay data, *Mutation Research/Fundamental and Molecular Mechanisms of Mutagenesis* 777 (2015) 20-22.

Q. Zheng, Comparing mutation rates under the Luria-Delbruck protocol, *Genetica* 144 (2016) 351-359.

See Also

LRT.MK, LRT.LD.plating

Examples

```
x=simu.cultures(20,1e-8,1,1,50,2e8)
y=simu.cultures(20,1e-8,1,1,50,3e8)
LRT.LD(x,y,1.5)
```

LRT.LD.plating	<i>Likelihood Ratio Test under the Classic Luria-Delbruck Model with Partial Plating</i>
----------------	--

Description

The function computes the likelihood ratio test statistics to compare the mutation rates in two independent fluctuation experiments. The algorithm is described in Zheng (2016), which is a generalization of a simpler algorithm given in Zheng (2015).

Usage

```
LRT.LD.plating(X1, X2, R = 1, e1 = 0.1, e2 = 0.1, init.mc = 0,
               init.m1 = 0, init.m2 = 0, tol = 1e-09, show.iter = FALSE)
```

Arguments

X1	Data from the first experiment.
X2	Data from the second experiment.
R	Ratio of final cell population sizes, $R=(N_t \text{ of second experiment})/(N_t \text{ of first experiment})$.
e1	Plating efficiency in the first experiment.
e2	Plating efficiency in the second experiment.
init.mc	Initial guess of m under the null hypothesis.
init.m1	Initial guess for m_1 , m of the first experiment.
init.m2	Initial guess for m_2 , m of the second experiment.
tol	Tolerance parameter to control numerical accuracy.
show.iter	Logical variable to allow for display of the numerical iteration process.

Value

A pair of real numbers: (test statistic, p-value).

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, Methods for comparing mutation rates using fluctuation assay data, *Mutation Research/Fundamental and Molecular Mechanisms of Mutagenesis* 777 (2015) 20-22.

Q. Zheng, Comparing mutation rates under the Luria-Delbruck protocol, *Genetica* 144 (2016) 351-359.

See Also

LRT.MK

Examples

```
R=0.5/2.3
LRT.LD.plating(wh.data[[1]], wh.data[[2]], R=R, e1=0.4, e2=0.4)
```

LRT.MK

*Likelihood Ratio Test under the Mandelbrot-Koch Model***Description**

The function computes the likelihood ratio test statistic that compares the mutation rates in two independent fluctuation experiments. The algorithm is described in Zheng (2016), which is a generalization of a simpler algorithm given in Zheng (2015).

Usage

```
LRT.MK(X1, X2, R = 1, w1 = 1, w2 = 1, init.mc = 0, init.m1 = 0,
       init.m2 = 0, tol = 1e-09, show.iter = FALSE)
```

Arguments

X1	Data from the first experiment.
X2	Data from the second experiment.
R	Ratio of final cell population sizes, $R=(N_t \text{ of second experiment})/(N_t \text{ of first experiment})$.
w1	Relative fitness in the first experiment.
w2	Relative experiment in the second experiment.
init.mc	Initial guess of m under the null hypothesis.
init.m1	Initial guess for m_1 , m of the first experiment.
init.m2	Initial guess for m_2 , m of the second experiment.
tol	Tolerance parameter to control numerical accuracy.
show.iter	Logical variable to allow for display of the numerical iteration process.

Value

A pair of real numbers: (test statistic, p-value).

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, Methods for comparing mutation rates using fluctuation assay data, *Mutation Research/Fundamental and Molecular Mechanisms of Mutagenesis* 777 (2015) 20-22.

Q. Zheng, Comparing mutation rates under the Luria-Delbruck protocol, *Genetica* 144 (2016) 351-359.

See Also

LRT.LD, LRT.LD.plating

Examples

```
x=simu.cultures(20,1e-8,1,1.2,50,2e8)
y=simu.cultures(20,1e-8,1,1.4,50,3e8)
LRT.MK(x,y,R=1.5,w1=1.2,w2=1.4)
```

luria.16.data

*Classic Experimental Data from Luria and Delbruck***Description**

Data taken from Luria and Delbruck (1943) and analyzed in Zheng (2008).

Details

In this experiment, each test tube had a 0.2-ml culture, but only a portion of 0.08 ml was plated. Therefore, the plating efficiency was $e=0.4$.

References

S.E. Luria, M. Delbruck, Mutations of bacteria from virus sensitivity to virus resistance, *Genetics* 28 (1943) 491-511.

Q. Zheng. A note on plating efficiency in fluctuation experiments, *Mathematical Biosciences*, 216 (2008) 150-153.

Examples

```
newton.LD.plating(luria.16.data, e=0.4, show.iter = TRUE)
```

mcmc.LD.plating

*Estimating mutation rates under the LD model (with partial plating) using an MCMC approach***Description**

This function assumes the classic Luria-Delbruck model under which relative fitness $w=1$. Plating is partial, and hence plating efficiency $e<1.0$. An MCMC method is used to simulate the posterior distribution of the logarithm of the mutation rate. A Gaussian prior distribution is assumed. For a general introduction to MCMC computing, see Albert (2007); for an application of MCMC technique in the analysis of fluctuation assay data, see Zheng (2011).

Usage

```
mcmc.LD.plating(y, Nt, e = 0.1, Iter = 100, init.mu = 2e-08,
                b0 = -15, v0 = 30, s0 = 0.8, show.simu = FALSE)
```

Arguments

<code>y</code>	A data vector containing the number of mutants in a fluctuation experiment.
<code>Nt</code>	Average final cell population size.
<code>e</code>	Plating efficiency.
<code>Iter</code>	Length of the simulated Markov chain.
<code>init.mu</code>	Initial guess of the mutation rate (not the expected number of mutations).
<code>b0</code>	Prior mean of log of the mutation rate.
<code>v0</code>	Variance in the Gaussian prior distribution.
<code>s0</code>	A tuning parameter to control acceptance rate; it is the variance of a Gaussian proposal distribution.
<code>show.simu</code>	A logical variable to control the display of the evolution of the MCMC process.

Value

`list(acc.rate,chain)` where `acc.rate` is the acceptance rate and where `chain` is the simulated Markov chain. Note that `chain` usually needs further processing, e.g., discarding a burn-in period and thinning, etc.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

J. Albert, Bayesian Computation Using R, Wiley, 2007.

Q. Zheng, A Bayesian approach for correcting for partial plating in fluctuation experiments, *Genetics Research* 93 (2011) 351-356.

See Also

`mcmc.MK.test`

Examples

```
mcmc.LD.plating(unlist(wh.data[1]),1.59e9,e=0.2,Iter=1000,s0=0.2)
```

```
mcmc.LD.plating.test
```

Comparison of mutation rates under the LD model (with partial plating) using an MCMC approach

Description

This function assumes the classic LD model, under which the relative fitness $w=1$. The classic approach to the comparison of mutation rates is the likelihood ratio test (LRT), which can be done with the LRT.MK functions, for example. The function allows for a Bayesian approach to the comparison of mutation rates. In the first experiment, the expected number of mutations per culture is $N1 \cdot \exp(b0)$, while in the second experiment that quantity is $N2 \cdot \exp(b0+b1)$. Therefore, the two mutation rates are $\exp(b0)$ and $\exp(b0+b1)$, respectively. Equality of the two mutation rates is equivalent to $b1=0$. Note that the ratio of the two mutation rates is $\mu2:\mu1=\exp(b1)$. For a general introduction to MCMC computing, see Albert (2007); for an application of MCMC technique in the analysis of fluctuation assay data, see Zheng (2011).

Usage

```
mcmc.LD.plating.test(x, y, N1, N2, e1 = 0.1, e2 = 0.1, Iter = 100,
  init.mu0 = -20, init.mu1 = 0.05, mu0 = -20.7, mu1 = 2.7,
  v0 = 30, v1 = 30, s0 = 0.5, s1 = 0.5, show.simu = FALSE)
```

Arguments

x	A data vector containing mutant counts in the first experiment.
y	A data vector containing mutant counts in the second experiment.
N1	Average final cell population size of the first experiment.
N2	Average final cell population size of the second experiment.
e1	Plating efficiency in the first experiment.
e2	Plating efficiency in the second experiment.
Iter	Number of MCMC simulation cycles.
init.mu0	Initial guess of the logarithm of the mutation rate in the first experiment.
init.mu1	Initial guess of the difference between log(second mutation rate) and log(first mutation rate).
mu0	Prior mean of log(first mutation rate)
mu1	Prior mean of log(second mutation rate) - log(first mutation rate).
v0	Prior variance of log(first mutation rate).
v1	Prior variance of mu1.
s0	Tuning parameter to control the acceptance rate of b0, the variance of a normal proposal distribution.
s1	Tuning parameter to control the acceptance rate of b1, the variance of a normal proposal distribution.
show.simu	A logic variable to control the display of the evolution of the MCMC simulation process.

Value

list(c(a1,a2), chain), where a1 and a2 are the two acceptance rates, and chain is a Iter by 2 matrix containing the simulated posterior distributions of mu0 and mu1.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

J. Albert, Bayesian Computation Using R, Wiley, 2007.

Q. Zheng, A Bayesian approach for correcting for partial plating in fluctuation experiments, Genetics Research 93 (2011) 351-356.

See Also

mcmc.MK.test

Examples

```
x=unlist(wh.data[1])
y=unlist(wh.data[2])
z=mcmc.LD.plating.test(x,y,1.15e9,2.5e8,e1=0.2,e2=0.2,Iter=100)
exp(median(z[[2]][,1]))
```

mcmc.MK	<i>Estimating mutation rates under the MK model using an MCMC approach</i>
---------	--

Description

An MCMC method is used to simulate the posterior distribution of the logarithm of the mutation rate. A Gaussian prior distribution is assumed. For a general introduction to MCMC computing, see Albert (2007); for an application of MCMC technique in the analysis of fluctuation assay data, see Zheng (2011).

Usage

```
mcmc.MK(y, Nt, w = 1, Iter = 100, init.mu = 2e-08, b0 = -15,
        v0 = 30, s0 = 0.8, show.simu = FALSE)
```

Arguments

y	A data vector containing the number of mutants in a fluctuation experiment.
Nt	Average final cell population size.
w	Relative fitness defined as (division rate of mutants)/(division rate of wide-type cells).
Iter	Length of the simulated Markov chain.
init.mu	Initial guess of the mutation rate (not the expected number of mutations).
b0	Prior mean of log of the mutation rate.
v0	Variance in the Gaussian prior distribution.
s0	A tuning parameter to control acceptance rate; it is the variance of a Gaussian proposal distribution.
show.simu	A logical variable to control the display of the evolution of the MCMC process.

Value

list(acc.rate,chain) where acc.rate is the acceptance rate and where chain is the simulated Markov chain. Note that chain usually needs further processing, e.g., discarding a burn-in period and thinning, etc.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

J. Albert, Bayesian Computation Using R, Wiley, 2007.

Q. Zheng, A Bayesian approach for correcting for partial plating in fluctuation experiments, Genetics Research 93 (2011) 351-356.

See Also

mcmc.MK.test

Examples

```
mcmc.MK(demerec.data, 1.9e8, w=1, Iter=100)
```

mcmc.MK.test	<i>Comparison of mutation rates using an MCMC approach</i>
--------------	--

Description

The classic approach to the comparison of mutation rates is the likelihood ratio test (LRT), which can be done with the LRT.MK functions, for example. The function allows for a Bayesian approach to the comparison of mutation rates. In the first experiment, the expected number of mutations per culture is $N1 \cdot \exp(b0)$, while in the second experiment that quantity is $N2 \cdot \exp(b0+b1)$. Therefore, the two mutation rates are $\exp(b0)$ and $\exp(b0+b1)$, respectively. Equality of the two mutation rates is equivalent to $b1=0$. Note that the ratio of the two mutation rates is $\mu2:\mu1=\exp(b1)$. For a general introduction to MCMC computing, see Albert (2007); for an application of MCMC technique in the analysis of fluctuation assay data, see Zheng (2011).

Usage

```
mcmc.MK.test(x, y, N1, N2, w1 = 1, w2 = 1, Iter = 100, init.mu0 = -20,
             init.mu1 = 0.05, mu0 = -20.7, mu1 = 2.7, v0 = 30, v1 = 30, s0 = 0.5,
             s1 = 0.5, show.simu = FALSE)
```

Arguments

x	A data vector containing mutant counts in the first experiment.
y	A data vector containing mutant counts in the second experiment.
N1	Average final cell population size of the first experiment.
N2	Average final cell population size of the second experiment.
w1	Relative fitness in the first experiment.

w2	Relative fitness in the second experiment.
Iter	Number of MCMC simulation cycles.
init.mu0	Initial guess of the logarithm of the mutation rate in the first experiment.
init.mu1	Initial guess of the difference between log(second mutation rate) and log(first mutation rate).
mu0	Prior mean of log(first mutation rate)
mu1	Prior mean of log(second mutation rate) - log(first mutation rate).
v0	Prior variance of log(first mutation rate).
v1	Prior variance of mu1.
s0	Tuning parameter to control the acceptance rate of b0, the variance of a normal proposal distribution.
s1	Tuning parameter to control the acceptance rate of b1, the variance of a normal proposal distribution.
show.simu	A logic variable to control the display of the evolution of the MCMC simulation process.

Value

list(c(a1,a2), chain), where a1 and a2 are the two acceptance rates, and chain is a Iter by 2 matrix containing the simulated posterior distributions of mu0 and mu1.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- J. Albert, Bayesian Computation Using R, Wiley, 2007.
- Q. Zheng, A Bayesian approach for correcting for partial plating in fluctuation experiments, Genetics Research 93 (2011) 351-356.

See Also

mcmc.MK

Examples

```
mcmc.MK.test(demerec.data, ford.data, 1.9e8, 1.08e9, 1, 1, 100)
```


newcombe.data

*Classic Experimental Data of Howard B. Newcombe***Description**

The data frame contains 8 fluctuation experiments, labeled exptA, exptB, ... , exptH. Each experiment consists of 25 cultures (0.2ml). Initial numbers of cells (N0) are: (10,10,10,10,1e4,1e4,1e4,1e4). Terminal cell population sizes (Nt) are: (3.1e8, 4.6e8, 2.5e8, 2.8e8, 4.2e8, 3.7e8, 3.2e8, 3.8e8).

References

HB Newcombe, Delayed phenotypic expression of spontaneous mutations in Escherichia Coli, Genetics 33 (1948) 447-476.

Examples

```
LD.p0.est(newcombe.data[[1]])
newton.LD(newcombe.data[[1]])
```

newton.B0

*Computing MLE of m under the Luria-Delbruck model, accounting for variation in Nt***Description**

This function computes the MLE of m by accounting for the variation in Nt, the cell population size immediately prior to plating. Let the final cell population sizes be Nt(1), Nt(2), ..., Nt(n). If the coefficient of variation (CV) of Nt(1), ..., Nt(n) is large, an MLE of m can be computed by taking into consideration of the CV for Nt. An underlying assumption is that each test tube has a different values of m, i.e., m(1), m(2), ..., m(n), which are generated by a Gamma distribution with mean m0 and coefficient of variation CV. The output of newton.B0 is an estimate of m0, computed using the Newton-Raphson algorithm. The function name reflects the fact that a gamma mixture of the Luria-Delbruck distribution is a B0 distribution (Zheng 2010). The specific algorithm is given in Zheng (2016), which is adapted from an algorithm given in Zheng (2011).

Usage

```
newton.B0(data, cv = 0.1, init.m = 0, tol = 1e-08, max.iter = 30,
  show.iter = FALSE)
```

Arguments

data	A data vector containing numbers of mutant cells in all test tubes.
cv	Coefficient of variation, believed to represent the variability in Nt.
init.m	An initial guess of m.
tol	A tolerance parameter to control convergence.
max.iter	To control the maximum number of iterations during the Newton-Raphson process.
show.iter	To exhibit the intermediate values of m during the Newton-Raphson iteration process.

Value

A positive real number.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, A new discrete distribution induced by the Luria-Delbruck mutation model, *Statistics* 44 (2010) 529-540.

Q. Zheng, A Bayesian two-level model for fluctuation assay, *Genetica* 139 (2011) 1409-1416.

Q. Zheng, A second look at the final number of cells in a fluctuation experiment, *Journal of Theoretical Biology* 401 (2016) 54-63.

See Also

newton.LD, newton.MK, newton.LD.plating

Examples

```
newton.B0(demerec.data, cv=0.1)
```

newton.Haldane

Computing MLE of the Mutation Rate Under the Haldane Model

Description

This function computes maximum likelihood estimates of μ , the probability of a mutation per cell division, under the Haldane model. The Haldane model was described by Sarkar (1991), the maximum likelihood estimate of μ is computed using a Newton-Raphson type iterative algorithm described in Zheng (2007).

Usage

```
newton.Haldane(data, g, N0 = 1, tol = 1e-08, init.mu = 0, max.iter = 30,
  show.iter = FALSE)
```

Arguments

data	a data vector, containing numbers of mutant cells in all tubes.
g	the number of generations.
N0	the number of initial cells.
tol	tolerance parameter to control convergence.
init.mu	an initial guess of μ can be supplied.
max.iter	maximum number of iterations allowed.
show.iter	exhibition of the intermediate values of m during the iteration process.

Value

A positive number.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

S. Sarkar (1991) Haldane's solution of the Luria-Delbruck distribution, *Genetics* 127, 257-261.
 Q. Zheng (2007) On Haldane's formulation of Luria and Delbruck's mutation model, *Mathematical Biosciences* 209:500-513.

See Also

newton.LD, newton.LD.plating

Examples

```
newton.Haldane(niccum.data, g=25, show.iter=TRUE)
```

newton.joint.MK	<i>Joint Estimation of m and w Under the Mandelbrot-Koch Model</i>
-----------------	--

Description

This function computes maximum likelihood estimates of m and w simultaneously under the Mandelbrot-Koch model (Mandelbrot 1974; Koch 1982). Here m is the expected number of mutations per culture, and w is relative fitness of mutants. The Mandelbrot-Koch model allows for differential growth between mutants and nonmutants. The Newton-Raphson algorithm adopted is described in detail in Zheng (2005).

Usage

```
newton.joint.MK(data, tol = 1e-08, init.m = -1, init.w = -1,
  max.iter = 30, show.iter = FALSE)
```

Arguments

data	A vector containing mutant counts.
tol	Tolerance parameter to control the number of numerical iterations.
init.m	A starting value for the m parameter, the expected number of mutations per culture.
init.w	A starting value for the w parameter, relative fitness of the mutants.
max.iter	Maximum number of Newton-Raphson iterations.
show.iter	A logical variable enabling the display of the numerical iteration process.

Value

A pair of non-negative numbers representing the maximum likelihood estimates of m and w.

Author(s)

Qi Zheng <qzheng@sph.tamhse.edu>

References

A. L. Koch, Mutation and growth rates from Luria-Delbruck fluctuation tests, *Mutation Research* 95 (1982) 129-143.

B. Mandelbrot, A population birth-and-mutation process, I: Explicit distributions for the number of mutants in an old culture of bacteria, *J Appl Prob* 11 (1974) 437-444.

Q. Zheng, New algorithms for Luria-Delbruck fluctuation analysis, *Mathematical Biosciences* 196 (2005) 198-214.

See Also

newton.MK

Examples

```
newton.joint.MK(demerec.data)
```

newton.LD

Computing MLE of m Under the Luria-Delbruck Model

Description

This function computes maximum likelihood estimates of m , the expected number of mutations per culture, using a Newton-Raphson type algorithm described in Zheng (2005).

Usage

```
newton.LD(data, phi = 1, tol = 1e-08, init.m = 0, max.iter = 30,
  show.iter = FALSE)
```

Arguments

data	a data vector, containing numbers of mutant cells in all test tubes.
phi	this parameter is defined by $1-N_0/N_t$, usually phi is taken as unity.
tol	tolerance parameter to control convergence.
init.m	an initial guess of m , it is rarely needed.
max.iter	maximum number of iterations.
show.iter	exhibition of the intermediate values of m during the iteration process.

Value

A positive number.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, New algorithms for Luria-Delbruck fluctuation analysis, Mathematical Biosciences 196 (2005) 198-214.

See Also

newton.LD.plating

Examples

```
newton.LD(demerec.data, show.iter=TRUE)
```

newton.LD.plating	<i>Computing Maximum Likelihood Estimate of m that Adjusts for Plating Efficiency</i>
-------------------	---

Description

This function computes the m.l.e. of m (the expected number of mutations) when plating efficiency is imperfect. It employs a Newton-Raphson type algorithm described in Zheng (2008).

Usage

```
newton.LD.plating(data, e, tol = 1e-08, init.m = 0, max.iter = 30,
  show.iter = FALSE)
```

Arguments

data	a vector of numbers of mutant colonies in a fluctuation experiment.
e	plating efficiency assumed to be known.
tol	tolerance parameter to control the number of iterations.
init.m	an initial guess about m can be specified, but is rarely needed.
max.iter	maximum number of iterations allowed.
show.iter	to view the iteration process.

Value

A positive number.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, A note on plating efficiency in fluctuation experiments, Mathematical Biosciences 216 (2008) 150-153.

See Also

newton.LD

Examples

```
newton.LD.plating(wh.data[[1]],e=0.4)
```

newton.MK

Computing MLE of m Under the Mandelbrot-Koch Model

Description

This function computes maximum likelihood estimate of m , the expected number of mutations per culture, under the Mandelbrot-Koch model that allows for differential growth between mutants and nonmutants (Mandelbrot 1974; Koch 1982). The relative fitness (w) is usually obtained from a fitness assay (aka competition assay). The algorithm is a simple specialization of a more general algorithm given in Zheng (2005).

Usage

```
newton.MK(data, w = 1, tol = 1e-08, init.m = 0, max.iter = 30,
  show.iter = FALSE)
```

Arguments

<code>data</code>	A data vector containing the numbers of mutant cells from a fluctuation experiment.
<code>w</code>	Relative fitness define as (growth rate of mutants)/(growth rate of nonmutnats).
<code>tol</code>	Tolerance parameter to set a desired convergence criterion.
<code>init.m</code>	An initial guess of m , it is rarely needed.
<code>max.iter</code>	A parameter to set the maximum number of iteration for the Newton-Raphson procedure.
<code>show.iter</code>	A logical variable to show the numerical iteration process.

Value

A positive number as an MLE of m .

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- A. L. Koch, Mutation and growth rates from Luria-Delbruck fluctuation tests, *Mutation Research* 95 (1982) 129-143.
- B. Mandelbrot, A population birth-and-mutation process, I: Explicit distributions for the number of mutants in an old culture of bacteria, *J Appl Prob* 11 (1974) 437-444.
- Q. Zheng, New algorithms for Luria-Delbruck fluctuation analysis, *Mathematical Biosciences* 196 (2005) 198-214.

See Also

newton.LD

Examples

```
newton.MK(demerec.data,w=1.25)
```

niccum.data	<i>An Experiment Reported by Niccum et al.</i>
-------------	--

Description

Data reported by Niccum et al. (2012).

Details

This data set is the Time 1 part of Experiment A of Niccum et al. (2012). The estimated number of viable cells is 31350000 and the plating efficiency is 0.10.

References

BA Niccum, R Poteau, GE Hamman, JC Varada, JH Dshalalow, RR Sinden, On an unbiased and consistent estimator for mutation rates, Journal of Theoretical Biology 300 (2012) 360-367.

Examples

```
newton.LD.plating(niccum.data,e=0.1)
```

plot.likelihood.Haldane	<i>Plotting the Log-Likelihood Function Under the Haldane Model</i>
-------------------------	---

Description

This function plots the log-likelihood function of data under the Haldane model. The argument of the log-likelihood function is the mutation rate mu. It is based on the algorithm described in Zheng (2007).

Usage

```
plot.likelihood.Haldane(data,g, init.mu=0, mu.low = -1, mu.up = -1,
  plot.pts = 30, lik.col = "black", mle.col = "red", title = "",
  x.lab = "Value of mu", y.lab = "Log-likelihood", show.secant = TRUE)
```

Arguments

<code>data</code>	A vector of experimental data (non-negative integers).
<code>g</code>	number of generations.
<code>init.mu</code>	a user specified initial guess of the mutation rate μ .
<code>mu.low</code>	plot.likelihood.Haldane plots the log-likelihood function for μ between <code>mu.low</code> and <code>mu.up</code> .
<code>mu.up</code>	see above.
<code>plot.pts</code>	number of points used to plot the log-likelihood functions. A larger number of points yields a smoother graph, but takes more computing time.
<code>lik.col</code>	color for the log-likelihood function.
<code>mle.col</code>	color for the vertical bar that marks the maximum likelihood estimate of m .
<code>title</code>	title to be given to the graph.
<code>x.lab</code>	x label.
<code>y.lab</code>	y label.
<code>show.secant</code>	A secant line will be drawn at the maximum of the log-likelihood function.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, On Haldane's formulation of Luria and Delbruck mutation model, Mathematical Biosciences 209 (2007) 500-513.

See Also

plot.likelihood.LD, plot.likelihood.LD.plating

Examples

```
plot.likelihood.Haldane(niccum.data,g=25)
```

plot.likelihood.LD *Plotting the Log-Likelihood Function under the Luria-Delbruck Model*

Description

This function plots the log-likelihood function of data under the Luria-Delbruck model, using the stochastic formulation first proposed by Lea and Coulson (1948). A history of the Lea-Coulson formulation is given in Zheng (1999).

Usage

```
plot.likelihood.LD(data, init.m=0, m.low = -1, m.up = -1, plot.pts = 30,
  lik.col = "black", mle.col = "red", title = "", x.lab = "Value of m",
  y.lab = "Log-likelihood", show.secant = TRUE)
```


Arguments

<code>data</code>	A vector of experimental data (non-negative integers).
<code>init.m</code>	An initial guess of <code>m</code> for computing MLE of <code>m</code> .
<code>m.low</code>	<code>plot.likelihood.LD</code> plots the log-likelihood function for <code>m</code> ranging from between <code>m.low</code> to <code>m.up</code> .
<code>m.up</code>	see above.
<code>plot.pts</code>	number of points used to plot the log-likelihood functions. A larger number of points yields a smoother graph, but takes more computing time.
<code>lik.col</code>	color for the log-likelihood function.
<code>mle.col</code>	color for the vertical bar that marks the maximum likelihood estimate of <code>m</code> .
<code>title</code>	title to be given to the graph.
<code>x.lab</code>	x label.
<code>y.lab</code>	y label.
<code>show.secant</code>	A secant line will be drawn at the maximum of the log-likelihood function.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- Q. Zheng, Progress of a half century in the study of the Luria-Delbruck distribution, *Mathematical Biosciences* 162 (1999) 1-32.
- E.A. Lea and C.A. Coulson, The distribution of the numbers of mutants in bacterial populations. *J. Genetics* 49 (1949) 264-285.

See Also

`plot.likelihood.LD.plating`

Examples

```
plot.likelihood.LD(demerec.data)
```

```
plot.likelihood.LD.plating
```

Plotting the Log-Likelihood Function that Adjusts for Plating Efficiency

Description

This functions plots the log-likelihood function that adjusts for plating efficiency. The plating efficiency `e` is assumed to be known, the parameter `m` is regarded as the argument of the log-likelihood function.

Usage

```
plot.likelihood.LD.plating(data, e, m.low = -1, m.up = -1, plot.pts = 30,
  lik.col = "black", mle.col = "red", title = "",
  x.lab = "Value of m", y.lab = "Log-likelihood", show.secant = TRUE)
```

Arguments

data	A vector of experimental data (non-negative integers).
e	Plating efficiency.
m.low	It plots the log-likelihood function for m ranging from m.low to m.up.
m.up	see above.
plot.pts	number of points used to plot the log-likelihood functions. A larger number of points yields a smoother graph, but takes more computing time.
lik.col	color for the log-likelihood function.
mle.col	color for the vertical bar that marks the maximum likelihood estimate of m.
title	title to be given to the graph.
x.lab	x label.
y.lab	y label.
show.secant	A secant line will be drawn at the maximum of the log-likelihood function.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

See Also

plot.likelihood.LD

Examples

```
plot.likelihood.LD.plating(luria.16.data, e=0.4)
```

plot.likelihood.MK *Plotting the Log-Likelihood Function under the Mandelbrot-Koch Model*

Description

This function plots the log-likelihood function under the Mandelbrot-Kock mutation model. A value for the relative fitness parameter w is often obtained via a fitness assay. The algorithm for computing the maximum likelihood estimate of m is a specialization of an algorithm given in Zheng (2005).

Usage

```
plot.likelihood.MK(data, w = 1, m.low = -1, m.up = -1, init.m = 0,
  plot.pts = 30, lik.col = "black", mle.col = "red", title = "",
  x.lab = "Value of m", y.lab = "Log-likelihood", show.secant = TRUE)
```

Arguments

<code>data</code>	A vector of experimental data.
<code>w</code>	Relative fitness.
<code>m.low</code>	The range of <code>m</code> for the plot is from <code>m.low</code> to <code>m.up</code> .
<code>m.up</code>	See above.
<code>init.m</code>	An initial guess of the parameter <code>m</code> .
<code>plot.pts</code>	Number of points used to plot the log-likelihood function.
<code>lik.col</code>	Color for the log-likelihood function.
<code>mle.col</code>	Color of the vertical line segment indicating the maximum likelihood estimate of <code>m</code> .
<code>title</code>	Plot title.
<code>x.lab</code>	Plot x-label.
<code>y.lab</code>	Plot y-label.
<code>show.secant</code>	A secant line will be drawn at the maximum of the log-likelihood function.

Value

None. A plot is created.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

Q. Zheng, New algorithms for Luria-Delbruck fluctuation analysis, *Mathematical Biosciences* 196 (2005) 198-214.

Examples

```
plot.likelihood.MK(demerec.data, w=1.2)
```

prob.B0

A Limiting Distribution Induced by the Bartlett Mutation Model

Description

This discrete distribution, as a limiting distribution induced by the Bartlett model (Bartlett 1955; Zheng 2008), was first discovered by Zheng (2010). This distribution is often denoted by $B0(A, k)$, where A and k are both positive real parameters. It was later found that this distribution can also be regarded as a continuous mixture of the Luria-Delbruck distribution, where the mixing distribution of the parameter m is a gamma distribution (Zheng 2011). Therefore, the relation between the Luria-Delbruck distribution and the $B0$ distribution is similar to that between the Poisson distribution and the negative binomial distribution.

Usage

```
prob.B0(A, k, n = 5)
```

Arguments

A	A positive real number.
k	A positive real number.
n	An non-negative integer specifying the number of probabilities to be computed.

Value

A vector containing the first n+1 probabilities.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- M.S. Bartlett, An Introduction to Stochastic Processes, Cambridge University Press, London, 1955 (pp.132-135).
- Q. Zheng, On Bartlett's formulation of the Luria-Delbruck mutation model, Mathematical Biosciences 215 (2008) 48-54.
- Q. Zheng, A new discrete distribution induced by the Luria-Delbruck mutation model, Statistics 44 (2010) 529-540.
- Q. Zheng, A Bayesian two-level model for fluctuation assay, Genetica 139 (2011) 1409-1416.

See Also

prob.LD, prob.MK

Examples

```
prob.B0(5, 0.8, 12)
```

prob.Haldane

Computing the Haldane Distribution

Description

The Haldane mutation model is described in Sarkar (1991). Under the Haldane model, cell division is synchronized. When a nonmutant cell divides, the probability is mu that one daughter cell will be a mutant cell. This function computes the Haldane distribution using an algorithm described in Zheng (2007).

Usage

```
prob.Haldane(gen, mu, n, N0)
```

Arguments

gen	number of generations.
mu	the mutation rate.
n	It calculates the first n+1 probabilities, starting from the zeroth probability.
N0	The number of initial nonmutant cells.

Value

A vector containing the first $n+1$ probabilities.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- S. Sarkar (1991) Haldane's solution of the Luria-Delbruck distribution, *Genetics* 127, 257-261.
- Q. Zheng, On Haldane's formulation of Luria and Delbruck mutation model, *Mathematical Biosciences* 209 (2007) 500-513.

See Also

prob.LD

Examples

```
prob.Haldane(12, 0.0003, 20, 1)
```

prob.LD

Computing the Luria-Delbruck Mutant Cell Distribution

Description

This function computes the Luria-Delbruck distribution function. This particular version of the Luria-Delbruck distribution was first proposed by Lea and Coulson (1949), which was not an exact form of the intended distribution. Bartlett later (see, e.g. Bartlett, 1955) modified this distribution by introducing the parameter ϕ , making the distribution exact. A historical account of this distribution was given by Zheng (1999). The algorithm for computing this distribution was given by Ma et al. (1992), although the parameter ϕ was not considered at the time.

Usage

```
prob.LD(m, phi, k)
```

Arguments

- | | |
|-----|--|
| m | expected number of mutations. |
| phi | This parameter is defined as $1-N_0/N_t$. |
| k | It computes the first $k+1$ probabilities, starting with the zeroth probability. |

Details

Most implementations did not include the clock parameter ϕ .

Value

A vector of the $k+1$ probabilities.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- M.S. Bartlett, An Introduction to Stochastic Processes, Cambridge University Press, London, 1955 (pp.132-135).
- D.E. Lea and C.A. Coulson, The distribution of the numbers of mutants in bacterial populations, J. Genetics 49 (1949) 264-285.
- W.T. Ma, G. vH. Sandri, S. Sarkar, Analysis of the Luria-Delbruck distribution using discrete convolution powers, J. Appl. Prob. 29 (1992) 255-267.
- Q. Zheng, Progress of a half century in the study of the Luria-Delbruck distribution, Mathematical Biosciences 162 (1999) 1-32.

See Also

prob.LD.plating

Examples

```
prob.LD(5.8, 1, 12)
```

prob.LD.plating	<i>Calculating the Luria-Delbruck Mutant Cell Distribution that Adjusts for Plating Efficiency</i>
-----------------	--

Description

This function computes the mutant cell distribution that adjusts for plating efficiency. Several authors contributed to the computation of this distribution, among them are Armitage (1952), Stewart (1991) and Jones (1994). Inspired by these important results, Zheng (2008) proposed a computationally feasible algorithm, which prob.LD.plating adopts.

Usage

```
prob.LD.plating(m, e, n)
```

Arguments

- | | |
|---|---|
| m | the expected number of mutations per culture. |
| e | plating efficiency ranging between 0 and 1. |
| n | the function computes the first n+1 probabilities, i.e., P0, P1, ..., Pn. |

Value

A vector of the first n+1 probabilities.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- P. Armitage, The statistical theory of bacterial populations subject to mutation, J. Royal Statistical Society, ser. B, 14:1-44, 1952.
- M. E. Jones, Luria-Delbruck fluctuation experiments; Accounting simultaneously for plating efficiency and differential growth rate, Journal of Theoretical Biology, 166: 355-363, 1994.
- F.M. Stewart, Fluctuation analysis: the effect of plating efficiency, Genetica 54: 51-55, 1991.
- Q. Zheng, A note on plating efficiency in fluctuation experiments, Mathematical Biosciences, 216:150-153, 2008.

See Also

prob.LD

Examples

```
prob.LD.plating(5.8, 0.2, 20)
```

prob.MK

Calculating the Mandelbrot-Koch Probability Distribution

Description

This mutant distribution was first proposed by Mandelbrot (1974). Kock (1982) and Stewart et al. (1990) made independent contributions. Explicit algorithm for computing the probabilities were given by Zheng (2005).

Usage

```
prob.MK(m, w = 1, n)
```

Arguments

- | | |
|---|---|
| m | Expected number of mutation per culture. |
| w | Relative fitness $w = (\text{birth rate of mutants}) / (\text{birth rate of nonmutants})$. |
| n | The first $n+1$ probabilities will be computed. |

Value

A vector of $n+1$ probabilities.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- A. L. Koch, Mutation and growth rates from Luria-Delbruck fluctuation tests, *Mutation Research* 95 (1982) 129-143.
- B. Mandelbrot, A population birth-and-mutation process, I: Explicit distributions for the number of mutants in an old culture of bacteria, *J Appl Prob* 11 (1974) 437-444.
- F. M. Stewart, D. M. Gordon, B. R. Levin, Fluctuation analysis: the probability distribution of the number of mutants under different conditions, *Genetics* 124 (1990) 175-185.
- Q. Zheng, New algorithms for Luria-Delbruck fluctuation analysis, *Mathematical Biosciences* 196 (2005) 198-214.

See Also

prob.LD, prob.Haldane

Examples

```
prob.MK(2.3, 1.5, 20)
```

```
simu.Bartlett
```

Simulating a Fluctuation Experiment Under the Bartlett Model

Description

This function simulates the dynamics of (X_t, Y_t) , where X_t is the number of nonmutant cells at time t , and where Y_t is the number of mutant cells at time t . This model was first proposed by Bartlett (1955) and further studied by Zheng (2008). The simulation algorithm is similar to that given on page 281 of Renshaw (1991).

Usage

```
simu.Bartlett(b1, b2, mu, N0, T, max.events = 1e+10, show.growth = FALSE)
```

Arguments

b1	Wild cell growth rate
b2	Mutant cell growth rate
mu	The mutation parameter "mu", giving a mutation rate of $\alpha = \mu / (b1 + \mu)$.
N0	Initial number of wild cells.
T	Terminating time.
max.events	Maximum number of simulation iterations; if exceeded, return value will be NA.
show.growth	A logical variable; if set to TRUE, cellular dynamics will be shown.

Value

A pair of non-negative integers in the form of (wild, mutant).

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- M.S. Bartlett, An Introduction to Stochastic Processes, Cambridge University Press, (1955).
- E. Renshaw, Modeling Biological Populations in Space and Time, Cambridge University Press (1991).
- Q. Zheng, On Bartlett's formulation of the Luria-Delbruck mutation model, Mathematical Biosciences 215:48-54 (2008).

See Also

simu.cultures, simu.Haldane

Examples

```
simu.Bartlett(1, 1, 5e-3, 1, 5.8, show.growth=TRUE)
```

simu.cultures

Simulating Fluctuation Experiments

Description

This function simulates the numbers of mutant cells in all cultures prior to plating. The mutation model used here was proposed by Mandelbrot (1966) and Koch (1974). Under this model, the nonmutant cell growth rate, b_1 , can differ from that of mutant cells, b_2 . The expected number of mutations is $m = \mu \cdot (N_t - N_0) / b_1$. The simulation algorithm is described in Zheng (2002).

Usage

```
simu.cultures(n, mu, b1, b2, N0, Nt)
```

Arguments

<code>n</code>	total number of tubes in an experiment.
<code>mu</code>	the mutation rate, not the expected number of mutations.
<code>b1</code>	wild-type cell growth rate.
<code>b2</code>	mutant cell growth rate.
<code>N0</code>	initial number of wild-type cells in a tube.
<code>Nt</code>	final number of wild-type cells in a tube.

Value

A vector of n non-negative integers.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- A.L. Koch, Mutation and growth rates from Luria-Delbruck fluctuation tests, *Mutation Research* 95:129-143 (1982).
- B. Mandelbrot, A population birth-and-mutation process, I: Explicit distributions for the number of mutants in an old culture of bacteria. *J. Appl. Prob.* 11:437-444 (1974).
- Q. Zheng. Statistical and algorithmic methods for fluctuation analysis with SALVADOR as an implementation. *Mathematical Biosciences*, 176:237-252 (2002).

Examples

```
simu.cultures(30, 10^-8, 1, 1, 20, 5*10^8)
```

```
simu.Haldane
```

```
Simulating a Fluctuation Experiment Under the Haldane Model
```

Description

This function simulates the numbers of mutant cells in a fluctuation experiment under the Haldane model as described in Sarkar (1991) and Zheng (2007).

Usage

```
simu.Haldane(gen, mu, culture)
```

Arguments

gen	The number of generations of cell division.
mu	The mutation rate
culture	The total number of cultures in an experiment.

Value

A vector of non-negative integers.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- S. Sarkar (1991) Haldane's solution of the Luria-Delbruck distribution, *Genetics* 127, 257-261.
- Q. Zheng (2007) On Haldane's formulation of Luria and Delbruck's mutation model, *Mathematical Biosciences* 209:500-513.

See Also

newton.LD, newton.LD.plating, simu.Kimmel.

Examples

```
simu.Haldane(9, 0.03, 22)
```

simu.Haldane2	<i>Simulating the Numbers of Mutant Cells for the Last Two Generations under the Haldane Model</i>
---------------	--

Description

This functions is the same as simu.Haldane, except that it returns the numbers of mutant cells for the last two generations.

Usage

```
simu.Haldane2(gen, mu, culture = 1)
```

Arguments

gen	The last generation.
mu	The mutation rate.
culture	The Number of cultures to be simulated.

Value

A pair of non-negative integer vectors.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

See Also

simu.Kimmel2

Examples

```
simu.Haldane2(9, 0.08, 20)
```

simu.Kimmel	<i>Simulating a Fluctuation Experiment Under a variation of the Haldane Model</i>
-------------	---

Description

This function simulates the numbers of mutant cells in a fluctuation experiment under a variation of the Haldane model. Unlike the original Haldane model, this model allows both daughter cells to be mutant cells when a nonmutant cell divides. (Each daughter cell has a probability mu to be a mutant cell.) This model was studied by Kimmel and Axelrod (1994).

Usage

```
simu.Kimmel(gen, mu, culture)
```

Arguments

gen	The number of generations.
mu	The mutation rate.
culture	The total number of cultures in an experiment.

Value

A vector of non-negative integers.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

M. Kimmel, D.E. Axelrod, 1994. Fluctuation test for two-stage mutations: application to gene amplification, Mutation Research 306, 45-60.

See Also

simu.Haldane

Examples

```
simu.Kimmel(9, 0.03, 22)
```

simu.Kimmel2	<i>Simulating the Numbers of Mutant Cells for the Last Two Generations Under the Kimmel Model</i>
--------------	---

Description

This function is the same as simu.Kimmel, except that it returns the numbers of mutant cells for the last two generations.

Usage

```
simu.Kimmel2(gen, mu, culture = 1)
```

Arguments

gen	The last generation.
mu	The mutation rate.
culture	The number of cultures to be simulated.

Value

A pair of non-negative integer vectors.

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

See Also

simu.Haldane2

Examples

```
simu.Kimmel2(9,0.08,20)
```

wh.data

Experimental Data of Werngren and Hoffner

Description

There are 13 fluctuation experiments in this data object. From each condensed culture of 2.5ml a sample of 1ml was plated, and hence the plating efficiency is $e=0.4$. Terminal cell population sizes are $c(2.3, 0.5, 1.3, 1.0, 1.6, 1.0, 1.0, 0.8, 1.2, 0.6, 0.8, 0.9, 0.9)$ times $1e8$ per ml. Thus, for example, $N_t=1.15e9$ for the first experiment.

References

J Werngren, SE Hoffner, Drug-susceptible Mycobacterium tuberculosis Beijing genotype does not develop mutation-conferred resistance to rifampin at an elevated rate, Journal of Clinical Microbiology 41 (2003) 1520-1524.

Examples

```
newton.LD.plating(wh.data[[1]],e=0.4)
```

wierdl.est

Wierdl method of accounting for variation in N_t

Description

N_t is the (non-mutant) cell population size immediately prior to plating. In a fluctuation experiment comprising n tubes, the final cell population sizes are $N_t(1)$, $N_t(2)$, ..., $N_t(n)$. The method proposed by Wierdl et al. (1996) appears to be the first to account for variation in N_t . However, this method requires the experimentalist to measure N_t for all tubes, which is a daunting experimental challenge. The Wierdl method is a generalization of the method of the median devised by Lea and Coulson (1949).

Usage

```
wierdl.est(y, Nt, init.m = 0, tol = 1e-09, max.iter = 25,
  show.iter = FALSE)
```

Arguments

<code>y</code>	A vector containing the mutant counts.
<code>Nt</code>	A vector containing the final cell population sizes.
<code>init.m</code>	An initial guess for <code>m</code> .
<code>tol</code>	Tolerance parameter to control numerical accuracy.
<code>max.iter</code>	A parameter to control the number of iterations in solving the Lea-Coulson equation.
<code>show.iter</code>	To show the iteration process.

Value

A real number as an estimate of the mutation rate, not the usual mean number of mutations (`m`).

Author(s)

Qi Zheng <qzheng@sph.tamhsc.edu>

References

- E.A. Lea, C.A. Coulson, The distribution of the numbers of mutants in bacterial populations. *J Genetics* 49 (1949) 264-285.
- M. Wierdl, C.N. Green, A. Datta, S. Jinks-Robertson, T.D. Petes, Destabilization of simple repetitive DNA sequences by transcription in yeast. *Genetics* 143 (1996) 713-721.

See Also

`newton.B0`

Examples

```
Nt=rep(1.9e8, 30); wierdl.est(demerec.data,Nt)
```

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