Package 'PIST'

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Type Package

Title Prevalence with Imperfect Serological Tests

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Description This package contains all functions that allow for the simulation and analysis of serological surveys with imperfect serological tests.

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Encoding UTF-8

LazyData true

RoxygenNote 7.1.0

R topics documented:

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analyze.serosurvey   *analyze.serosurvey*

Description

analyze quantitative test measures with the likelihood-based method or one of the cutoff-based methods

Usage

```
analyze.serosurvey(
  data.serosurvey = data.serosurvey,
  mean = 4,
  scale.cases = 1,
  shape.controls = 1,
  scale.controls = 1,
  type = "likelihood",
  threshold = NULL,
  TNR = NULL,
  TPR = NULL,
  correct = FALSE
)
```

Arguments

data.serosurvey
: data of all observed quantitative test measures

mean
: the mean of the distribution of case sera

scale.cases
: the scale parameter of the distirbution of the case sera

shape.controls
: the shape parameter of the distribution of the control sera

scale.controls
: the scale parameter of the distribution of the control sera

type
: method used either 'naive' (cutoff-based) or 'likelihood'

threshold
: in case of 'naive' the threshold to assign someone a positive seroconversion status

correct
: TRUE if the estimate should be corrected for the sensitivity and specificity

Value

a vector with the estimate of the seroprevalence and the standard deviation in the estimate

AUC.ROC	*AUC.ROC*

Description

Calculates the area under the curve of a ROC curve.

Usage

```
AUC.ROC(mean)
```

Arguments

mean   the shape parameter of the distribution of case sera

Value

the area under the ROC-curve

classical.threshold	*classical.threshold*

Description

Calculates the threshold for either the maximal youden or the high specificity method

Usage

```
classical.threshold(mean, method = "youden")
```

Arguments

mean   the mean of the distribution of case sera

method   'youden' or 'specificity'

Value

a vector with the threshold value, the true positive rate and the true negative rate

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create.figure   *create.figure*

Description

Make figure with inferred prevalences for all 4 methods and various AUC-ROC values.

Usage

```
create.figure(N_tests = 1000, N = 50, means, AUC, true_prev = 0.08)
```

Arguments

N_tests	number of individuals tested in each simulation
N	number of simulations performed for each AUC value
means	the means of the titer distribution that match the AUC values
AUC	the AUC-ROC values that should be tested
true_prev	the true prevalence

Value

the figure

---

create.figure.bootstrap

create.figure

Description

Make figure with inferred prevalences for all 4 methods and various AUC-ROC values.

Usage

```
create.figure.bootstrap(N_tests = 10000, N = 200, means, AUC, true_prev = 0.08)
```

Arguments

N_tests	number of individuals tested in each simulation
N	number of simulations performed for each AUC value
means	the means of the titer distribution that match the AUC values
AUC	the AUC-ROC values that should be tested
true_prev	the true prevalence

Value

the figure

---

determine.means *determine.means*

Description

Calculate the required means for the distribution of the cases to obtain the desired AUC-ROC curves

Usage

```
determine.means(desired.AUC = c(0.7, 0.75, 0.8, 0.85, 0.9, 0.95, 0.975, 1))
```

Arguments

desired.AUC   the AUC values that should be the result of the distribution of case sera

Value

list with as first element the true AUC-ROC values and as second element the means corresponding to those AUC values

---

estimate.CC.distr *estimate.CC.distr*

Description

Simulates the sampling of controls and cases to estimate their distribution

Usage

```
estimate.CC.distr(
  true.mean,
  sample.sizes,
  name = "0.9",
  N_tests = 10000,
  N = 200,
  real.prev = 0.08
)
```

Arguments

sample.sizes	the sample size that should be tested
name	the AUC value of the tested sample sizes
N	the number of replicates
real.prev	the actual prevalence
mean	mean of the distribution of case sera

Value

a dataframe with the results of all N in silico serosurveys

---

get.st | *get.st*

Description

get.st

Usage

```
get.st(fit)
```

Arguments

fit   result of the optim function

Value

matrix with the values and upper and lower bands for the

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ll.titer | *ll.titer*

Description

Calculates the log likelihood of observing the quantitative test measures (titer.data) for a prevalence given the distribution of quantitive test measures for the controls and cases

Usage

```
ll.titer(
  prev,
  mean,
  scale.cases,
  shape.controls,
  scale.controls,
  data.serosurvey
)
```

Arguments

prev   the seroprevalence for which the loglikelihood is calculated

mean   the shape parameter of the distribution of the case sera

scale.cases   the scale parameter of the distirbution of the case sera

shape.controls the shape parameter of the distribution of the control sera

scale.controls the scale parameter of the distribution of the control sera

data.serosurvey

                the reuslts of the serosurvey

Value

loglikelihood

sim.serosurvey   *sim.serosurvey*

Description

sim.serosurvey

Usage

```
sim.serosurvey(N_tests = 10000, mean = 4, prev = 0.08)
```

Arguments

N_tests	number of individuals enrolled in the serosurvey
mean	shape parameter of the case sera
prev	the seroprevalence

Value

vector with the quantitative test values of each individual

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