Package 'RCMsize'

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Type Package

Title Sample Size Calculation in Reversible Catalytic Models

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Description Sample size and confidence interval calculations in reversible catalytic models, with applications in malaria research. Further details can be found in the paper by Sepúlveda and Drakeley (2015, <doi:10.1186/s12936-015-0661-z>).

License GPL (>= 3)

Encoding UTF-8

Imports binom, stats

RoxygenNote 7.3.2

VignetteBuilder knitr

Suggests knitr, rmarkdown, tools

URL https://CRAN.R-project.org/package=RCMsize

BugReports https://github.com/marciagraca/RCMsize/issues

NeedsCompilation no

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IC_SCR *Confidence Interval for the Seroconversion Rate (SCR)*

Description

Calculates the confidence interval for the seroconversion rate (SCR) using the confidence interval of seroprevalence.

Usage

```
IC_SCR(SP_interval, SRR, ages, A_max, limits = c(0, 1))
```

Arguments

SP_interval	A vector with the lower and upper limits of seroprevalence.
SRR	Seroreversion rate.
ages	Vector with the proportions of different ages in the population (age structure).
A_max	Maximum age considered in the population.
limits	Lower and upper limits for the calculation of SCR.

Value

A vector with the lower and upper limits for the seroconversion rate SCR.

Examples

```
A_max <- 80
age_distribution <- rep(1 / A_max, A_max)
IC_SCR(c(0.1, 0.2), 0.01, age_distribution, A_max, limits = c(0, 1))
```

IC_SP *Confidence Interval for Seroprevalence*

Description

Calculates the confidence interval for a seroprevalence estimate with a specified confidence level.

Usage

```
IC_SP(SP, n, conf.level = 0.95, method = "asymptotic")
```

Arguments

SP	Seroprevalence estimate.
n	Sample size.
conf.level	Confidence level (default is 0.95).
method	Method for calculating the confidence interval (default is "asymptotic"). Available methods: c("asymptotic","exact","ac","wilson","logit","cloglog")

Value

A vector with the lower and upper limits of the confidence interval.

References

The methods available in this function are some of the available in the binom package. For more information, see https://CRAN.R-project.org/package=binom

Examples

```
IC_SP(0.25, 100, conf.level = 0.95, method = "asymptotic")
```

IC_SP_Waldcc *Confidence Interval for Seroprevalence with Continuity Correction (Wald Method)*

Description

Calculates the confidence interval for seroprevalence using the Wald method with continuity correction.

Usage

```
IC_SP_Waldcc(SP, n, conf.level = 0.95)
```

Arguments

SP	Seroprevalence estimate.
n	Sample size.
conf.level	Confidence level (default is 0.95).

Value

A vector with the lower and upper limits of the confidence interval.

Examples

```
IC_SP_Waldcc(0.25, 100, conf.level = 0.95)
```

prob_seropositive *Calculation of Seropositivity Probability*

Description

This function calculates the probability of seropositivity based on the age and the seroconversion and seroreversion rates, using a reversible catalytic model.

Usage

```
prob_seropositive(SCR, SRR, t)
```

Arguments

SCR	Seroconversion Rate
SRR	Seroreversion Rate.
t	Age for which we want to calculate the probability of seropositivity.

Value

The probability of seropositivity for age ‘t‘.

References

For more information on the reversible catalytic model, see https://link.springer.com/article/10.1186/s12936-015-0661-z

Examples

```
prob_seropositive(0.03, 0.01, 45)
```

sample_s *Sample Size Calculation*

Description

Estimates the required sample size so that the confidence interval width for SCR does not exceed a specified limit.

Usage

```
sample_s(
  SCR,
  RL,
  SRR,
  ages,
  A_max,
  limits,
  max_iter = 10000,
  conf.level = 0.95,
  method = "asymptotic"
)
```

Arguments

SCR	Seroconversion rate.
RL	Desired relative width.
SRR	Seroreversion rate.
ages	Vector with the proportions of different ages in the population (age structure).
A_max	Maximum age considered in the population.
limits	Lower and upper limits for the calculation of SCR.
max_iter	Maximum number of iterations.
conf.level	Confidence level (default is 0.95).
method	Method for calculating the confidence interval. Available methods: "waldcc" and the methods in IC_SP documentation.

Details

Disclaimer: The sample size function may not produce accurate values for scenarios involving extremely low SCR (e.g., elimination scenarios). Users are advised to exercise caution and consider the results critically when applying this function to such cases.

Value

A list with the required sample size, the confidence interval for seroprevalence, and the confidence interval for SCR.

Examples

```
A_max <- 80
age_distribution <- rep(1 / A_max, A_max)
sample_s(0.03, 1, 0.01, age_distribution, A_max, limits = c(0, 1))
```

`seroprevalence` *Seroprevalence Calculation*

Description

Calculates the seroprevalence considering an age distribution and a reversible catalytic model.

Usage

```
seroprevalence(ages, A_max, SCR, SRR)
```

Arguments

`ages`	Vector with the proportions of different ages in the population (age structure).
`A_max`	Maximum age considered in the population.
`SCR`	Seroconversion rate.
`SRR`	Seroreversion rate.

Value

The total seroprevalence weighted by the age distribution.

Examples

```
A_max <- 80
age_distribution <- rep(1 / A_max, A_max)
seroprevalence(age_distribution, A_max, 0.03, 0.01)
```

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