Package 'Ace'

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Title Assay-based Cross-sectional Estimation of incidence rates

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Depends R (>= 2.9.0), stats

Description The package contains functions for estimating incidence rate from assay-based cross-sectional studies

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R topics documented:

`csi.est` *Cross-sectional incidence estimation for HIV surveillance.*

Description

Estimating incidence rate from assay-based cross-sectional studies, allowing for a subpopulation that remains negative on the less-sensitive assay indefinitely.

Usage

```
csi.est(N1, N2, N3, mu = 0.5, p = 1, se.mu = 0, se.p = 0, alpha = 0.05)
```

Arguments

`N1`	Number of subjects testing negative on the sensitive test (e.g. ELISA).
`N2`	Number of subjects testing positive on the sensitive test (e.g. ELISA) but Testing negative on the less-sensitive test (e.g. BED).
`N3`	Number of subjects testing positive on the less-sensitive test (e.g. BED).
`mu`	Mean window period for the subpopulation of infected individuals that would eventually test positive on the less-sensitive test, expressed on the same time scale for which incidence rate is desired.
`p`	Proportion of subjects who would become testing positive at some point after seroconversion. `p=1` corresponds to the setting where all infected subjects will test positive on the less-sensitive test.
`se.mu`	standard error of an externally-estimated $\hat{\mu}$.
`se.p`	standard error of an externally-estimated $\hat{\mu}$.
`alpha`	specifys the coverage level (`100*(1-alpha)%`) of resulting confidence interval for incidence rate.

Details

Confidence interval is obtained via the delta method, and is symmetric on the log scale.

Value

A list with 3 elements:

`inc.est`	estimated incidence rate
`se.est`	standard error of the estimated incidence rate
`incidence.ci`	`100*(1-alpha)%` confidence interval of the incidence rate

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References

Wang R and Lagakos S. (2009). On the Use of Adjusted Cross-Sectional Estimators of HIV Incidence. *J Acquir Immune Defic Syndr*, 52(5):538-547.

Examples

```
csi.est(N1 = 5126, N2 = 77, N3 = 797, mu = 0.5, p = 1,
    se.mu = 0, se.p = 0, alpha = 0.05)
```

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csiaug.est *Augmented Cross-sectional Estimation of incidence rate*

Description

Estimating incidence rate based on augmented cross-sectional studies.

Usage

```
csiaug.est(N1,  n1,  n0,  N3,  ftime, alpha = 0.05)
```

Arguments

N1	Number of subjects in cross-sectional sample testing negative on sensitive test (e.g., ELISA); (Uninfected).
n1	Number of subjects in cross-sectional sample testing positive on sensitive test and negative on less-sensitive test (e.g., BED) AND will eventually test positive on less-sensitive test; (Recently Infected).
n0	Number of subjects in cross-sectional sample testing positive on sensitive test and negative on less-sensitive test AND will continue to test negative on less-sensitive test indefinitely; (Long-term Non-progressors).
N3	Number of subjects in cross-sectional sample testing positive on sensitive and less-sensitive; (Non-recently Infected).
ftime	$n_1 \times 2$ matrix giving interval-censored observation of forward recurrence time (time from cross-sectional sample to first positive result on less-sensitive test or end of follow-up, whichever occurs first). Times should be expressed on the same scale for which incidence rate is desired (e.g. years, in order to obtain annual incidence rate).
alpha	specifys the coverage level (`100*(1-alpha)%`) of resulting confidence interval for incidence rate.

Details

If no upper bound for `ftime` is known, do not use Inf. A finite upper bound is required. A value of 20 years is generally sufficiently large if no information is known.

Value

`parameters` A 2×4 matrix of parameter estimates (row 1) and corresponding standard errors (row 2). Parameters estimated are 1. λ, the incidence rate; 2. ϕ, the proportion of the population uninfected at the time of cross-sectional sample (1-prevalence); 3. μ, the mean time spent in the recent infection state; 4. p, proportion of infected subjects who will eventually test positive on the less-sensitive test.

`incidence.ci` A `100*(1-alpha)%` confidence interval for λ, calculated by transforming and back-transforming the `100*(1-alpha)%` confidence interval for $\log(\lambda)$ via the delta method, to ensure that the interval contains only positive values. This interval is symmetric about $\log(\hat{\lambda})$, and not about $\hat{\lambda}$.

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References

Wang R and Lagakos S. (2009). On the Use of Adjusted Cross-Sectional Estimators of HIV Incidence. *J Acquir Immune Defic Syndr*, 52(5):538-547.

Wang R and Lagakos S. (2010). Augmented Cross-Sectional Prevalence Testing for Estimating HIV Incidence. *Biometrics*, 66:864-874.

Claggett B, Lagakos S, Wang R. (2011). Augmented Cross-Sectional Studies with Abbreviated Follow-up for Estimating HIV Incidence. *Biometrics*, DOI:10.1111/j.1541-0420.2011.01632.x.

Examples

```
####Example with Simulated data

set.seed(1234)
N = 6000
phi = 0.85
lambda = 0.02
Mu = 0.5
p = 0.95
W = 52  ###max followup time
interval = 2 ### interval between follow-up visits, in weeks

pt = (p * phi * lambda * Mu) / (p * phi * lambda * Mu + (1 - p) * (1 - phi))


Ns =  rmultinom(1, N,
          c(phi, phi * p * lambda * Mu, (1 - p) * (1 - phi),
            p * (1 - phi - phi * lambda * Mu)))

t1 = runif(500000,  -5, 0)
t2 = t1 + rweibull(500000, 2.7, Mu / gamma(1 + 1 / 2.7))
frd = t2[t2 > 0]
```

```
X = sample(frd, Ns[2])

### interval censoring ####
a = floor(X * (52 / interval)) * interval
b = ceiling(X * (52 / interval)) * interval
ints = cbind(a, b)
sortints = ints[order(ints[, 1]), ]

N2 = Ns[2] + Ns[3]
n1t = sum(sortints[, 2] <= W)

################################################
## p=1; in the absence of long-term non-progressors ##
csiaug.est(N1 = Ns[1], n1 = N2, n0 = 0, N3 = Ns[4],
    ftime = rbind( sortints[1:n1t, ],
                   t(matrix(rep(c(W, 999), N2 - n1t), nrow = 2)) ) / 52,
    alpha = 0.05)

################################################
## p<1; in the presence of long-term non-progressors ##
csiaug.est(N1 = Ns[1], n1 = n1t, n0 = N2 - n1t, N3 = Ns[4],
    ftime = sortints[1:n1t, ] / 52,
    alpha = 0.05)
```

Index