Package 'fam.recrisk'

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Type Package

Title Familial Recurrence Risk

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Description Given vectors of family sizes and number of affecteds per family, calcu-
lates the risk of disease recurrence in an unaffected person, conditional on a family hav-
ing at least k affected members. Methods also model heterogeneity of disease risk across fami-
lies by fitting a mixture model, allowing for high and low risk families.

License GPL (>= 2)

LazyLoad yes

Depends R (>= 3.2.0), stats, utils

NeedsCompilation no

Author Schaid Daniel [aut],
Jason Sinnwell [aut, cre]

Maintainer Jason Sinnwell <sinnwell.jason@mayo.edu>

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R topics documented:

| fam.recrisk | *Familial risk of recurrent disease* |

Description

Given vectors of family sizes and number of affecteds per family, calculates the risk of disease recurrence

Usage

```
fam.recrisk(s, a, k)
```

Arguments

s	vector of sizes of families
a	vector of number of affected members per family; same length as vector s
k	number of affecteds to condition on; the ascertainment criterion, e.g., at least k affecteds

Details

Estimate risk of disease for a person with at least k affected relatives, where k can be specified in order to determine how risk varies with k. Estimates are based on a truncated binomial distribution where families with less than k affected relatives are truncated from the sample. If the sample of families in not a random sample from a population, the prevalence will be biased, and merely represent the frequency of disease in the sample.

Value

A list with the following values

phat	disease recurrence risk
prev	estimate of disease prevalence
var.phat	variance of phat
var.prev	variance of prev
covar	covariance between phat and prev

Author(s)

Schaid DJ, Sinnwell JP.

References

Schaid DJ, McDonnell SK, Thibodeau SN. Familial recurrence risk with varying amount of family history. Under review at Genetic Epidemiology, 2018.

Examples

```
s <- c(4,  8,  6,  6,  10, 8,  7,  8,  5,  6,  10, 4,  4,  8,  6,  8,  4,  5,  9,
       9,  5,  4,  4,  7,  3,  3,  9,  5,  3,  3,  4,  6,  8,  3,  5,  8,  6,  8, 9,  3)

a <- c(3, 4, 2, 5, 4, 5, 3, 4, 3, 3, 8, 2, 0, 3, 4, 5, 2, 3, 4, 2, 1, 1,
       1, 1, 1, 0, 0, 0, 0, 0, 1, 0, 2, 0, 0, 1, 0, 2, 3, 0)
fam.recrisk(s,a,1)
```

---

recrisk.mixture	*Recurrence Risk based on a mixure of low and high risk families*

Description

Recurrence risk assuming a mixture of low and high risk families based on a mixture of truncated binomial densities

Usage

```
recrisk.mixture(s, a, k, max.iter=1e4, eps=1e-6)
```

Arguments

s	vector of sizes of families
a	vector of number of affected members per family; same length as vector s
k	number of affecteds to condition on; the ascertainment criterion, e.g., at least k affecteds
max.iter	maximum number of EM iterations
eps	EM stop criterion value

Details

Model heterogeneity of risk across families by a mixture of truncated binomial distributions, assuming two groups: high and low risk.

Value

A list with the following values

recrisk.high	disease recurrence risk for high-risk group
recrisk.low	disease recurrence risk for low-risk group
prob.high.group	
	the mixture probability that a familiy is in the high-risk group (a scalar value)
prob.fam.high	a vector of posterior probabilities that families are in the high-risk group (same length as vector s)
iter	Number of EM iterations

Author(s)

Schaid DJ, Sinnwell JP.

References

Schaid DJ, McDonnell SK, Thibodeau SN. Familial recurrence risk with varying amount of family history. Under review at Genetic Epidemiology, 2018.

Examples

```
s <- c(4,  8,  6,  6,  10, 8,  7,  8,  5,  6,  10, 4,  4,  8,  6,  8,  4,  5,  9,
       9,  5,  4,  4,  7,  3,  3,  9,  5,  3,  3,  4,  6,  8,  3,  5,  8,  6,  8,  9,  3)
a <- c(3, 4, 2, 5, 4, 5, 3, 4, 3, 3, 8, 2, 0, 3, 4, 5, 2, 3, 4, 2, 1, 1,
       1, 1, 1, 0, 0, 0, 0, 0, 1, 0, 2, 0, 0, 1, 0, 2, 3, 0)
recrisk.mixture(s,a,k=1)
```

---

recrisk.ratio	*Recurrence risk ratio of familial recurrence risk*

Description

Estimate the recurrence risk ratio of familial recurrence risk divided by population prevalence, based on results returned from fam.recrisk

Usage

```
recrisk.ratio(fit)
```

Arguments

fit   list returned from fam.recrisk

Details

The recurrence risk is based on a truncated binomial density, and the prevalence is the frequency of disease in the sample. If the sample of families in not a random sample from a population, the prevalence will be biased, and merely represent the frequency of disease in the sample.

Value

A list with the following values

rr   ratio of recurrence risk divided by population prevalence

var.rr   variance of rr

Author(s)

Schaid DJ, Sinnwell JP.

References

Schaid DJ, McDonnell SK, Thibodeau SN. Familial recurrence risk with varying amount of family history. Under review at Genetic Epidemiology, 2018.

Examples

```
s <- c(4,  8,  6,  6,  10, 8,  7,  8,  5,  6,  10, 4,  4,  8,  6,  8,  4,  5,  9,
       9,  5,  4,  4,  7,  3,  3,  9,  5,  3,  3,  4,  6,  8,  3,  5,  8,  6,  8, 9,  3)
a <- c(3, 4, 2, 5, 4, 5, 3, 4, 3, 3, 8, 2, 0, 3, 4, 5, 2, 3, 4, 2, 1, 1,
       1, 1, 1, 0, 0, 0, 0, 0, 1, 0, 2, 0, 0, 1, 0, 2, 3, 0)
fit <- fam.recrisk(s,a,1)
recrisk.ratio(fit)
```

---

recrisk.single.ascertain

Familial recurrence risk assuming single proband

Description

Estimate familial recurrence risk, assuming there is a single identified proband in a family

Usage

```
recrisk.single.ascertain(s, a)
```

Arguments

s	vector of sizes of families
a	vector of number of affected members

Details

When affected subjects (i.e., probands) attend a clinic independent of their family size and independent of their family history, and if the family history provided by probands is complete (i.e., reporting of family history does not depend on the number of affected members), then we can view the probands and their families as sampled under complete ascertainment. This function estimates the disease recurrence risk when there is a single identified proband per family.

Value

A list with the following values

phat	disease recurrence risk
var.phat	variance of phat

Author(s)

Schaid DJ, Sinnwell JP.

References

Schaid DJ, McDonnell SK, Thibodeau SN. Familial recurrence risk with varying amount of family history. Under review at Genetic Epidemiology, 2018.

Examples

```
s <- c(4,  8,  6,  6,  10, 8,  7,  8,  5,  6,  10, 4,  4,  8,  6,  8,  4,  5,  9,
       9,  5,  4,  4,  7,  3,  3,  9,  5,  3,  3,  4,  6,  8,  3,  5,  8,  6,  8, 9,  3)
a <- c(3, 4, 2, 5, 4, 5, 3, 4, 3, 3, 8, 2, 0, 3, 4, 5, 2, 3, 4, 2, 1, 1,
       1, 1, 1, 0, 0, 0, 0, 0, 1, 0, 2, 0, 0, 1, 0, 2, 3, 0)
recrisk.single.ascertain(s,a)
```

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