

Package ‘RVsharing’

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Type Package

Title Bureau

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Description Computes estimates of the probability of related individuals sharing a rare variant.

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Depends R (>= 2.15.2), methods, kinship2

Imports

Suggests

Enhances

Collate AllGenerics.R AllClasses.R functions.R methods-pedigree.R methods-trio.R
approx2_functions.R compute_kinship_prop_coef.R ped2trio.R PFU.R
rare_variant_sharing_v3.R rare_variant_sharing_approx2_v2.R
rare_variant_sharing_weighted_v2.R zzz.R

LazyLoad yes

biocViews

Local Variables

time-stamp-pattern ``8/Date: %3a %3b %2d %02H:%02M:%02S %Z %:y\{ }n"

End

R topics documented:

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GeneDrop-method	<i>Gene Dropping method</i>
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Description

Foo!

Usage

```
## S4 method for signature 'Trio,numeric'  
GeneDrop(trio,geno.vec)
```

Arguments

- trio A Trio object.
- geno.vec A named genotype vector.

Details

Foo.

Value

A numeric genotype vector.

Author(s)

Samuel G. Younkin <syounkin@jhsph.edu>

ped.list	<i>Example pedigrees</i>
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Description

List of example pedigree objects

Usage

```
ped.list
```

RVsharing

Probability of sharing a rare variant among relatives

Description

Computing probability that a rare variant is shared by a set of subjects in a pedigree using equation (1) of Bureau et al.

Usage

```
RVsharing(data, dad.id, mom.id)
```

Arguments

<code>data</code>	a pedigree object or character/numeric vector of subject IDs
<code>dad.id</code>	if data is a vector, character or numeric vector of father IDs. Founders' parents should be coded to NA or 0
<code>mom.id</code>	if data is a vector, character or numeric vector of mother IDs. Founders' parents should be coded to NA or 0

Details

The function RV sharing computes the probability that all final descendants in the pedigree share a rare variant given that a rare variant has been detected in any one of these final descendants. For now, there can only be one lineage of branching individuals (intermediate ancestors) with more than one child each. Multiple marriages can only involve one of the top founders. Branching individuals can have only one spouse. All final descendants must share a common ancestor or couple of ancestors, otherwise an erroneous response may be obtained.

The function recursively processes branching individuals (intermediate ancestors) from the lowest one in the pedigree to the one who is a top founder, applying the formulas in Bureau et al. to compute the terms of $P[C1 = \dots = Cn = 1]$ and $P[C1 = \dots = Cn = 0]$ involving each branching individual.

Value

<code>p.share</code>	probability that all final descendants in the pedigree share a rare variant given that a rare variant has been detected in any one of these final descendants
<code>iancestors</code>	Vector of the IDs of branching individuals (intermediate ancestors): subjects who are ancestors to final descendants through two or more of their children and have ancestors above them in the pedigree. The only exception is that one of the top founders is designated as the last branching individual.
<code>desfounders</code>	List of vectors. Each final descendant has a vector in the list containing the distances to the founders above him.
<code>id</code>	vector of subject IDs passed as argument
<code>dad.id</code>	vector of father IDs passed as argument
<code>mom.id</code>	vector of mother IDs passed as argument

Author(s)

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References

Bureau, A et al. Sharing of rare variants by affected relatives: building evidence for causal variants based on exact sharing probabilities. Submitted.

Examples

```
data(ped.list)
plot(ped.list[[1]])
RVsharing(ped.list[[1]])
```

Trio-class

Trio Class

Description

Foo!

Author(s)

Samuel G. Younkin <syounkin@jhsph.edu>

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