Package 'Bureau'

May 20, 2013

Type Package

Title Bureau

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Author Alexandre Bureau, Ingo Ruczinski, Samuel G. Younkin

Maintainer Samuel G. Younkin <syounkin@jhsph.edu>

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

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Depends R (>= 3.0.0), methods, kinship2

Imports

Suggests

Enhances

Collate approx2_functions.R compute_kinship_prop_coef.R rare_variant_sharing_v3.R
rare_variant_sharing_approx2_v2.R rare_variant_sharing_weighted_v2.R zzz.R

LazyLoad yes

biocViews

R topics documented:

RVsharing	*Main function of package Bureau*

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

Arguments

`id`	vector of subject IDs, format unknown
`dad.id`	vector of father IDs, format unknown
`mom.id`	vector of mother IDs, format unknown

Details

Version 0.2 2013/02/12 Addition of a wrapper for pedigree objects Change of fdi from a logical vector to a vector of indices, to correct a problem occuring when an intermediate ancestor is before the final descendants in the ID list Restriction of currentnonfounders to the active ones when determining whether there is an intermediate ancestor Removed currentfounders that are NA when computing how many there are. At depth 0, Include previous ancestors of only the final descendants that are active Version 0.3 2013/04/08 Adding the names of the founders to the desfounders list of degrees between final descendants and founders Moving the inactivation of final descendants below an intermediate ancestor and the removal of the spouse of the intermediate ancestor after the update of the List of distance to founders of each final descendant to insure inclusion of the spouse in the list Adding desfounders, id, dad.id and mom.id to the list of returned elements for further computations with other functions

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 intermediate ancestors with more than one child each Multiple mariages can only involve one of the top founders. Intermediate ancestors can have only one spouse All final descendants must share a common ancestor or couple of ancestors, otherwise an erroneous response may be obtained Correction to the extration of the kth name : names(tmp)[k]

Value

`p.share`	no details yet
`iancestors`	no details yet
`desfounders`	no details yet
`id`	no details yet
`dad.id`	no details yet
`mom.id`	no details yet

RVsharing.weighted   *Main function of package Bureau*

Description

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

Usage

```
RVsharing.weighted(id, dad.id, mom.id,relfounders,phi)
```

Arguments

id	vector of subject IDs, format unknown
dad.id	vector of father IDs, format unknown
mom.id	vector of mother IDs, format unknown
relfounders	vector specifying the ids of the founders who are related, format unkown
phi	either a scalar giving the constant kinhsip coefficient between the founders in relfounders, or a square symmetric matrix of kinship coefficients for every pair of founders in relfounders

Details

For now, there can only be one lineage of intermediate ancestors with more than one child each Multiple mariages can only involve one of the top founders.

Intermediate ancestors can have only one spouse

All final descendants must share a common ancestor or couple of ancestors, otherwise an erroneous response may be obtained

Correction to the extration of the kth name : names(tmp)[k]

The function RVsharing.weighted computes the probability that all sequenced subjects inherit the variant from a single ancestor (num) and the probability that no sequenced subject inherited the variant from any of the founders given that a single copy of the variant is present in the founders (p0), weighted by the probability that each founder was the only one to introduce the variant.

Value

num	no details yet
p0	no details yet
iancestors	no details yet
desfounders	no details yet
id	no details yet
dad.id	no details yet
mom.id	no details yet

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