Package ‘VariABEL’

July 12, 2016

Type  Package
Title  Testing of Genotypic Variance Heterogeneity to Detect Potentially Interacting SNP
Version  0.9-2.1
Date  2013-11-07
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Depends  R (>= 2.13.0)
Imports  methods
Suggests  GenABEL, DatABEL
Description  Presence of interaction between a SNP and another SNP (or another factor) can result in heterogeneity of variance between the genotypes of an interacting SNP. Detecting such heterogeneity gives prior knowledge for constructing a genetic model underlying complex trait.
License  GPL (>= 2)
NeedsCompilation  yes
Repository  CRAN
Date/Publication  2016-07-12 07:39:13

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**Description**

The presence of a significant difference of genotypic variances points to possible presence of interaction between a tested SNP and a factor (or set of factors). This function tests for that.

**Usage**

```r
var_test_gwaa(formula, genodata, phenodata, genodata_info=NULL,
               testname="svlm", analysis_type="AAvsABvsBB")
```

**Arguments**

- **formula**: Regression model used for analysis. In the first stage linear regression is run to exclude the main SNP effect. In this stage adjustment for covariates is performed.
- **genodata**: The genotypes data in GenABEL format or as DatABEL object.
- **phenodata**: The phenotypes data in format of data.frame object.
- **genodata_info**: The file with SNP information (name, position). Used if genotype data is a DatABEL object.
- **testname**: Name of the variance heterogeneity test to perform. "svlm" (for imputed genotype data), "Levene", and "Bartlett" test are supported. Note that "svlm" test only additive genetic model and the parameter analysis_type is ignored.
- **analysis_type**: Type of analysis to perform. AAVsABvsBB - each genotypic group is tested against other two, AAVsABBandBB - group AA tested against AB and BB, ABvsAAandAB - AB against AA and BB, BBvsAAandAB - BB against AA and AB. Only available for typed SNPs. Note that the input parameter analysis_type is ignored if testname="svlm"

**Details**

The function `var_test_gwaa` tests for difference in genotypic variances. This difference points to the presence of possible interaction between the tested SNP and some factor. In the case of the `svlm` test the analysis consists of two stages: first the regular GWA is done where regression analysis is performed with covariates specified in the input parameter `formula`, in the second stage the regression analysis is performed with using residuals from the first stage and a SNP as a covariate.

**Value**

The output is a data.frame object. The table contains the chi^2 of the variance heterogeneity test (the name is chisq) the effects and standard errors of all covariates included into the regression model, main SNP effect (the names are snp_eff and snp_se). In the case of the `svlm` test the columns `snp_eff_dispertion` and `snp_se_dispertion` contain effect of a SNP on the squared values of the trait.
Author(s)
Maksim Struchalin

References
Struchalin et al., An R package VariABEL for genome-wide searching of potentially interacting loci by testing genotypic variance heterogeneity. Submitted.

Examples
```r
if (require(GenABEL)) {
  data(srdta)
  result1 <- var_test_gwaa(bt ~ qt1 + qt2,
                           genodata=gdata(srdta),
                           phenodata=pdata(srdta))

  # If there is covariates are needed:
  result2 <- var_test_gwaa("bt",
                           genodata=gdata(srdta),
                           phenodata=pdata(srdta))
}
```
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