Package ‘BMRV’

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Type Package
Title Bayesian models for rare variant association detection
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Description This package provides two methods for detecting the association between rare variants and continuous traits. One of them detects interaction effect and can be applied to twin studies. The other incorporates genotype uncertainty information.
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Description

This package provides two methods for detecting the association between rare variants and continuous traits. One of them detects interaction effect and can be applied to twin studies. The other incorporates genotype uncertainty information.

Details
blvcm

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References

Examples

data(blvcm_data)
temp <- blvcm(blvcm_data$pheno_data, blvcm_data$geno_data, iter = 20000, model = 3)

blvcm Bayesian latent variable collapsing model (BLVCM)

Description
The function implements BLVCM using Gibbs sampling method.

Usage
blvcm(pheno, geno, model = 3, iter = 30000, burnin = 500, var = -1, lambda = -1, cov = 0)

Arguments
pheno N x 3 Phenotypic data matrix (trait, family number, zyg), where N is the number of subjects. Please see the example data for more details. For faster convergence, it is recommended that phenotype should be standardized.
geno N x K Genotypic data matrix, where N is the number of subjects and K is the number of rare variants. The value can be 0 or 1. A missing genotype is represented by -9, which will be imputed by BLVCM based on HWE.
model Twin model: 1 for ACE model, 2 for AE model, 3 for independent subjects
iter The number of MCMC iterations
burnin The number of burn-in.
blvcm_data

var

variance hyperparameter of priors for beta and gamma. The default value is 25.

lambda

threshold lambda for hypothesis test. The default value is 0.2.

cov

covariate matrix

Value

BF_main

The Bayes factor of the main effect

BF_int

The Bayes factor of the interaction effect

post_odds_beta

The posterior odds of beta

post_odds_gamma

The posterior odds of gamma

com_a

The inverse of the posterior mean of the precision for additive genetic component

com_c

The inverse of the posterior mean of the precision for shared environmental component

mean_mu

The posterior mean of intercept

mean_beta

The posterior mean of beta

mean_gamma

The posterior mean of gamma

Author(s)

Liang He

References


Examples

data(blvcm_data)
blvcm(blvcm$pheno_data, blvcm$geno_data, iter=20000, burnin=1000, model=3)

Usage

data(blvcm_data)

Format

The format is: List of 2 $ pheno_data: num [1:600, 1:3] -0.0813 -1.0135 0.4363 0.7927 0.9597 ...

...- attr(*, "dimnames")=List of 2 ...

$ : NULL ...

$ : chr [1:3] "pheno" "fam" "zyg" $ geno_data: int [1:600, 1:40] 0 0 0 0 0 0 0 0 0 0 ...
Examples

data(blvcm_data)
## maybe str(blvcm_data) ; plot(blvcm_data) ...

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hbmr

Hierarchical Bayesian multiple regression model incorporating genotype uncertainty (HBMR)

Description

The function implements HBMR using Gibbs sampling method.

Usage

hbmr(pheno, geno, qi, iter = 10000L, burnin = 500L, gq = -1L, imp = -1L, cov = 0L, maf = -1L, rivinfo = FALSE, pa = -1L, pb = -1L)

Arguments

- **pheno**: Phenotypic vector (N x 1). For faster convergence, it is recommended that phenotype should be standardized.
- **geno**: N x K Genotypic data matrix, where N is the number of subjects and K is the number of rare variants. Genotypic value is only for dominant coding, i.e. 0 or 1. Plug in 0 for imputed genotypes.
- **qi**: N x K Genotypic quality matrix, where N is the number of subjects and K is the number of rare variants. If the genotype is sequenced, this must be an integer >=1 and its GQ score in VCF file. If the genotype is imputed, this must be a value <1, and is its expected genotypic value.
- **iter**: Number of MCMC iterations
- **burnin**: Number of burn-in
- **gq**: cutoff for GQ score (lambda_Q). If not specified, default value is 20. See the reference for more details.
- **imp**: cutoff for imputed genotype (lambda_I). If not specified, default value is 0.1. See the reference for more details.
- **cov**: N x M covariate data matrix, where N is the number of subjects and K is the number of covariates.
- **maf**: Minor allele frequency information vector (K by 1).
- **rivinfo**: 0 or 1. Default is 0. Indicator of showing estimated RV effect size and sdt error.
- **pa**: The hyper-parameter a in the gamma distribution of Bayesian shrinkage prior. The default value is 1.3.
- **pb**: The hyper-parameter b in the gamma distribution of Bayesian shrinkage prior. The default value is 0.04.
Value

- **BF**: The Bayes factor of delta=1 vs. delta=0
- **BF_RB**: The BF estimated by using Rao-Blackwellization theorem
- **mean**: The mean of the posterior of beta_0
- **var**: The inverse of the mean of posterior of precision 1/sigma
- **est_geno**: The number of genotypes whose uncertainty are considered in estimation
- **rv_mean_es**: The means of the posterior of gamma for the K RVs
- **rv_sd_es**: The standard deviations of the posterior of gamma for the K RVs
- **mean_cov**: The means of the posterior of for the M covariates

Author(s)

- Liang He

References


Examples

```r
data(hbmr_data)
hbmr(hbmr_data$pheno_data, hbmr_data$geno_data, hbmr_data$qual_data, iter=10000, burnin=1000)
```

---

**hbmr_data**

*Example data for HBMR*

Usage

```r
data(hbmr_data)
```

Format

The format is: List of 3

- `$ pheno_data`: num [1:600] -0.255 0.398 2.982 1.361 -0.165...
- `$ geno_data`: num [1:600, 1:50] 1 0 0 0 0 0 0 0 0 0...
- `$ qual_data`: num [1:600, 1:50] 5 5 99 99 99 99 99 99 99 99...

Examples

```r
data(hbmr_data)
## maybe str(hbmr_data); plot(hbmr_data) ...
```
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