Package 'gwasQxE'

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Type Package

Title Genome-wide association study to detect QTL-by-Environment interactions (QxE) effect

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Author Eiji Yamamoto

Maintainer Eiji Yamamoto <yame.repos@gmail.com>

Description GWAS functions to detect QTL-by-Environment interactions (QxE) effect.

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R topics documented:

`gwasQxE` *Genome-wide association study to detect QTL-by-Environment interaction (QxE) effect*

Description

This function detects QxE effect by comparing linear mixed models with assumption that a QTL has same effect in different environments and the QTL has QxE effect. This function test only additive effect. For dominant effect, see 'gwasQxEd'.

Usage

```
gwasQxE(geno,
        pheno,
        trait,
        Env,
        n.PC,
        Fixed,
        n.core,
        scale.pheno.by.trial)
```

Arguments

geno	Data frame with the marker names in the first column. The second and third columns contain the chromosome and map position (either bp or cM), respectively. Columns four and higher contain the marker scores for each line, coded as (-1,0,1) = (aa,Aa,AA). Missing (NA) values are not allowed. The column names must match the line names in the "pheno" data frame.
pheno	Data frame where the first column is the line name (line_name) and the second colum is information on trials. The remaining columns include environments, phenotypic values, and fixed covariate(s).
trait	The name of the column that is used as phenotypic values.
Env	The name of the column that is used as environmental covariate.
n.PC	Number of principal components to be include as fixed effects.
Fixed	The name(s) of the column(s) that should be included as fixed effect(s).
n.core	Number of cores to be used for the calculation.
scale.pheno.by.trial	Whether the phenotypic values are scaled for each trial or not. Default is TRUE.

Value

Returns a data frame where the columns are the marker name, chromosome, position, -log10(p) for additive main effect (P.ame), all QTL effects (P.all), and QxE terms (P.int), additive effect (Add), additive effect in each environment (effect@~~), Wald test score for the additive effects (wald@~~), and minor allele frequency (MAF).

Author(s)

Eiji Yamamoto

See Also

gwasQxEd

gwasQxEd *Genome-wide association study to detect QTL-by-Environment interaction (QxE) effect with dominant effect*

Description

This function detects QxE effect by comparing linear mixed models with assumption that a QTL has same effect in different environments and the QTL has QxE effect. Unlike gwasQxE, this function test dominant effect. For additive effect, see 'gwasQxE'.

Usage

```
gwasQxEd(geno,
         pheno,
         trait,
         Env,
         n.PC,
         Fixed,
         n.core,
         scale.pheno.by.trial)
```

Arguments

geno	Data frame with the marker names in the first column. The second and third columns contain the chromosome and map position (either bp or cM), respectively. Columns four and higher contain the marker scores for each line, coded as (-1,0,1) = (aa,Aa,AA). Missing (NA) values are not allowed. The column names must match the line names in the "pheno" data frame.
pheno	Data frame where the first column is the line name (line_name) and the second colum is information on trials. The remaining columns include environments, phenotypic values, and fixed covariate(s).
trait	The name of the column that is used as phenotypic values.
Env	The name of the column that is used as environmental covariate.
n.PC	Number of principal components to be include as fixed effects.
Fixed	The name(s) of the column(s) that should be included as fixed effect(s).
n.core	Number of cores to be used for the calculation.
scale.pheno.by.trial	Whether the phenotypic values are scaled for each trial or not. Default is TRUE.

Value

Returns a data frame where the columns are the marker name, chromosome, position, -log10(p) for additive main effect (P.ame), all QTL effects (P.all), and QxE terms (P.int), additive effect (Add), dominance effect (Dom), additive and dominance effects in each environment (effect.add@~~ and effect.dom@~~), Wald test score (wald@~~), minor allele frequency (MAF), and minor genotype count (MGC).

Author(s)

Eiji Yamamoto

See Also

gwasQxE

`gwasQxEd_all` *Comparison of power to detect QTL-by-Environment interactions (QxE) between the linear mixed models with dominant effect terms.*

Description

This function calculate -log10(p) from the linear mixed models that consist of various combinations of fixed genetic effect and background random genetic effect terms.

Usage

```
gwasQxEd_all(geno,
             pheno,
             trait,
             Env,
             n.PC,
             Fixed,
             n.core,
             scale.pheno.by.trial = TRUE)
```

Arguments

`geno`	Data frame with the marker names in the first column. The second and third columns contain the chromosome and map position (either bp or cM), respectively. Columns four and higher contain the marker scores for each line, coded as (-1,0,1) = (aa,Aa,AA). Missing (NA) values are not allowed. The column names must match the line names in the "pheno" data frame.
`pheno`	Data frame where the first column is the line name (line_name) and the second colum is information on trials. The remaining columns include environments, phenotypic values, and fixed covariate(s).
`trait`	The name of the column that is used as phenotypic values.
`Env`	The name of the column that is used as environmental covariate.
`n.PC`	Number of principal components to be include as fixed effects.
`Fixed`	The name(s) of the column(s) that should be included as fixed effect(s).
`n.core`	Number of cores to be used for the calculation.
`scale.pheno.by.trial`	Whether the phenotypic values are scaled for each trial or not. Default is TRUE.

Details

This function performs GWAS using all the linear mixed models presented in the reference manuscript. The main objective of this function is a comparison of power between the linear mixed models. The best combination of the liner mixed models to detect QxE was selected based on results from this function and has been implemented in the another function "gwasQxEd".

Value

A data frame where the first to the third columns are the marker name, chromosome and position, respectively. The subsequent colmuns are -log10(p) values for each linear mixed model.

Author(s)

Eiji Yamamoto

See Also

gwasQxE_all

`gwasQxE_all` *Comparison of power to detect QTL-by-Environment interactions (QxE) between the linear mixed models.*

Description

This function calculate -log10(p) from the linear mixed models that consist of various combinations of fixed genetic effect and background random genetic effect terms.

Usage

```
gwasQxE_all(geno,
            pheno,
            trait,
            Env,
            n.PC,
            Fixed,
            n.core,
            scale.pheno.by.trial = TRUE)
```

Arguments

`geno`	Data frame with the marker names in the first column. The second and third columns contain the chromosome and map position (either bp or cM), respectively. Columns four and higher contain the marker scores for each line, coded as (-1,0,1) = (aa,Aa,AA). Missing (NA) values are not allowed. The column names must match the line names in the "pheno" data frame.
`pheno`	Data frame where the first column is the line name (line_name) and the second colum is information on trials. The remaining columns include environments, phenotypic values, and fixed covariate(s).
`trait`	The name of the column that is used as phenotypic values.
`Env`	The name of the column that is used as environmental covariate.
`n.PC`	Number of principal components to be include as fixed effects.
`Fixed`	The name(s) of the column(s) that should be included as fixed effect(s).
`n.core`	Number of cores to be used for the calculation.
`scale.pheno.by.trial`	Whether the phenotypic values are scaled for each trial or not. Default is TRUE.

Details

This function performs GWAS using all the linear mixed models presented in the reference manuscript. The main objective of this function is a comparison of power between the linear mixed models. The best combination of the liner mixed models to detect QxE was selected based on results from this function and has been implemented in the another function "gwasQxE".

Value

A data frame where the first to the third columns are the marker name, chromosome and position, respectively. The subsequent colmuns are -log10(p) values for each linear mixed model.

Author(s)

Eiji Yamamoto

See Also

gwasQxEd_all

`simPhenoQxE` *Generator of simulated phenotypic values*

Description

This function generates simulated phenotypic values using genotype data in the argument 'geno'.

Usage

```
simPhenoQxE(geno,
            n.qtl,
            seed,
            q.Effs,
            Env,
            w_ratio,
            PVE.qtl,
            h2,
            domEff = FALSE)
```

Arguments

`geno`	Data frame with the marker names in the first column. The second and third columns contain the chromosome and map position (either bp or cM), respectively. Columns four and higher contain the marker scores for each line, coded as (-1,0,1) = (aa,Aa,AA). Missing (NA) values are not allowed.
`n.qtl`	Number of major QTLs in the simulated phenotype.
`seed`	Random number generator state.
`q.Effs`	Effect size of the major QTLs for each experimental trials. Namely, the number of elements in q.Effs must be equal to total number of experimental trials in the simulated phenotype.

Env	Identifier of environmental conditions for each q.Effs value. The number of elements in Env must be equal to the number of elements in q.Effs.
w_ratio	Ratio of contribution of background random effects. This must contain three values. First to third for not-specific-to-environments, genotype-by-environment, and genotype-by-trial effects, respectively.
PVE.qtl	Proportion of variance explained by each major QTL in total phenotypic values (namely, not specific to environments or trials).
h2	Heritability for total phenotypic values (namely, not specific to environments or trials).
domEff	If TRUE, the major QTLs include dominant effects. The dominant effect is coded as (1,3,2) = (aa,Aa,AA). Default FALSE.

Value

$pheno is data frame with the line names in the first column. The second and third columns contain identifier for environments and experimental trials, respectively. The fourth column is the simulated phenotypic values. $simQTLs is the marker names of the simulated major QTLs. $realized_PVE.qtl is the realized PVE of each major QTL. $realized_h2 is the realized h2. $PVE.each contains realized PVE of the major QTLs in each trial.

Author(s)

Eiji Yamamoto

See Also

gwasQxE

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