Package 'gwerAM'

February 20, 2015

Version 1.0

Date 2011-30-05

Title Controlling the genome-wide type I error rate in association
mapping experiments

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Depends R (>= 2.10.0), MASS, Matrix

Description This package provides functions to calculate the
significance threshold for controlling the type I error rate in
mixed-model association mapping analyses.

License GPL (>= 2)

URL <http://www.r-project.org>

Repository CRAN

Date/Publication 2012-10-29 08:58:55

NeedsCompilation no

R topics documented:

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gwerAM	*Calculates signifance thresholds for mixed-model association mapping*

Description

The function *gwerAM* calculates for homozygous species significance thresholds with which the genome-wide error rate in mixed-model association mapping analyses can be controlled (Mueller et al. 2011).

Usage

```
gwerAM(A,
        Q,
        W,
        varianceA,
        varianceE,
        Nrsim=10000,
        k=c(0,1,2,5),
        alpha=c(0.05))
```

Arguments

A	Numerator relationship matrix or kinship matrix
Q	Population structure matrix with linearly independent columns
W	Matrix with molecular marker data
varianceA	Genotypic variance of the trait under consideration as inferred from QK mixed model without marker data
varianceE	Error variance of the trait under consideration as inferred from QK mixed model without marker data
Nrsim	Number of simulations; default = 10000
k	Number of allowed false positives for generalized genome-wide type I error rate (GWER_k); default = c(0,1,2,5)
alpha	vector of alpha levels; default = c(0.05)

Value

A list comprising the significance thresholds for all combinations of k and alpha is generated.

References

Mueller, B., B. Stich, and H.-P. Piepho. 2011. A general method for controlling the genome-wide Type I error rate in linkage and association mapping experiments in plants. Heredity. 106: 825-831.

Examples

```
data(maizeA)
data(maizeQ)
data(maizeW)
data(maizevarianceA)
data(maizevarianceE)

gwerAM(A=maizeA,
       Q=maizeQ[,-ncol(maizeQ)],
       W=maizeW[,1:10],
       varianceA=maizevarianceA,
       varianceE=maizevarianceE,
       Nrsim=1000,
       k=c(0,1,2,5),
       alpha=c(0.01,0.05))

## Not run:
The last column of maizeQ was removed in this example, as the
columns sum up to one and, thus, are linearly dependent and
confounded with the common intercept, whereas the columns of
Q have to be linearly independent. Note that dropping the last
column of maizeQ does not alter the model.

## End(Not run)
## Not run:
In this example, only the first ten markers were included to
reduce the computational effort. You should run it with all your markers.

## End(Not run)
```

---

maizeA   *Numerator relationship matrix required for "gwerAM()"*

Description

This matrix contains the pairwise relatedness information required for `gwerAM`.

Usage

```
data(maizeA)
```

Format

The matrix has 277 rows and columns. Each cell gives the relatedness of the corresponding pair of maize inbred lines. This information has been derived from `data(maizeW)` of 277 diverse maize inbreds which have been used in the study of Yu et al. (2006).

References

Yu, J., Pressoir, G., Briggs, W.H., Bi, I.V., Yamasaki, M., Doebley, J.F., McMullen, M.D., Gaut, B.S., Holland, J.B., Kresovich, S., and Buckler, E.S. 2006. A unified mixed-model method for association mapping accounting for multiple levels of relatedness. Nature Genetics 38: 203-208.

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maizeQ	*Population structure matrix required for "gwerAM()"*

Description

This matrix contains the population structure information required for gwerAM.

Usage

```
data(maizeQ)
```

Format

The matrix has five columns, one for each subpopulation. Each row gives the probability that the corresponding genotype belongs to the corresponding subpopulations. The data set comprises information from 277 diverse maize inbreds which have been used in the study of Yu et al. (2006).

References

Yu, J., Pressoir, G., Briggs, W.H., Bi, I.V., Yamasaki, M., Doebley, J.F., McMullen, M.D., Gaut, B.S., Holland, J.B., Kresovich, S., and Buckler, E.S. 2006. A unified mixed-model method for association mapping accounting for multiple levels of relatedness. Nature Genetics 38: 203-208.

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maizevarianceA	*Genotypic variance required for "gwerAM()"*

Description

This value is the genotypic variance of the trait days to pollen (Yu et al. 2006) of a diverse set of 277 maize inbred lines as inferred from QK mixed model analysis without marker data. This information is required for gwerAM.

Usage

```
data(maizevarianceA)
```

Format

This data set comprises only one value.

References

Yu, J., Pressoir, G., Briggs, W.H., Bi, I.V., Yamasaki, M., Doebley, J.F., McMullen, M.D., Gaut, B.S., Holland, J.B., Kresovich, S., and Buckler, E.S. 2006. A unified mixed-model method for association mapping accounting for multiple levels of relatedness. Nature Genetics 38: 203-208.

| maizevarianceE | *Error variance required for "gwerAM()"* |

Description

This value is the error variance of the trait days to pollen (Yu et al. 2006) of a diverse set of 277 maize inbred lines as inferred from QK mixed model analysis without marker data. This information is required for gwerAM.

Usage

```
data(maizevarianceE)
```

Format

This data set comprises only one value.

References

Yu, J., Pressoir, G., Briggs, W.H., Bi, I.V., Yamasaki, M., Doebley, J.F., McMullen, M.D., Gaut, B.S., Holland, J.B., Kresovich, S., and Buckler, E.S. 2006. A unified mixed-model method for association mapping accounting for multiple levels of relatedness. Nature Genetics 38: 203-208.

| maizeW | *Marker matrix required for "gwerAM()"* |

Description

This matrix contains the molecular marker information required for gwerAM.

Usage

```
data(maizeW)
```

Format

The matrix has 553 columns, one for each single nucleotide polymorphism marker. Each row gives the genotypic information for one of the 277 diverse maize inbred lines (Yu et al. 2006). Missing data is coded with NA. Multiallelic markers are coded similarly to biallelic markers with integers indicating which allele being present at each marker-genotype combination.

References

Yu, J., Pressoir, G., Briggs, W.H., Bi, I.V., Yamasaki, M., Doebley, J.F., McMullen, M.D., Gaut, B.S., Holland, J.B., Kresovich, S., and Buckler, E.S. 2006. A unified mixed-model method for association mapping accounting for multiple levels of relatedness. Nature Genetics 38: 203-208.

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