Package 'gpmap'

February 16, 2021

Type Package

Title Analysing and Plotting Genotype-Phenotype Maps

Version 0.1.2

Date 2021-01-28

Author Arne B. Gjuvsland <arne.gjuvsland@nmbu.no> and Yunpeng Wang <yunpeng.wng@gmail.com>

Maintainer Arne B. Gjuvsland <arne.gjuvsland@nmbu.no>

Depends isotone, plyr, ggplot2, foreach

Description Tools for studying genotype-phenotype maps for bi-allelic loci underlying quantitative phenotypes. The 0.1 version is released in connection with the publication of Gjuvsland et al (2013) and implements basic line plots and the monotonicity measures for GP maps presented in the paper. Reference: Gjuvsland AB, Wang Y, Plahte E and Omholt SW (2013) Monotonicity is a key feature of genotype-phenotype maps. Frontier in Genetics 4:216 <doi:10.3389/fgene.2013.00216>.

License GPL-3

LazyLoad yes

NeedsCompilation no

Repository CRAN

Date/Publication 2021-02-16 00:10:02 UTC

R topics documented:

---

gpmap-package *Tools for analysing and plotting genotype-phenotype maps*

Description

The **gpmap** package deals with genotype-phenotype maps for biallelic loci underlying quantitative phenotypes. The package provides a class gpmaps, analysis functions and basic lineplots. The package is designed for studying the properties of GP maps without reference to any particular population, i.e. the physiological (Cheverud & Routman, 1995) or functional (Hansen, 2001) properties of the GP map. This is opposed to statistical effects underlying most of quantitative genetics, where the GP-map is analysed togehter with genotype frequencies in a given population (e.g. Lynch & Walsh, 1998).

In version 0.1 which is released as part of the publication of Gjuvsland *et al.* (2013) we have implemented functionality for studying monotonicity Gjuvsland *et al.* (2011) of GP maps. The package utilizes the **isotone** package for monotone regression, and the **foreach** package for parallel computation.

The package consists of the following high-level functions : `enumerate_genotypes`, `generate_gpmap`, `degree_of_monotonicity`, `decompose_monotone` and `plot.gpmap`

Author(s)

Arne B. Gjuvsland <arne.gjuvsland@nmbu.no> and Yunpeng Wang <yunpeng.wng@gmail.com>

References

Cheverud JM & Routman EJ (1995) Epistasis and Its Controbution to Genetic Variance Components. Genetics 139:1455-1461 [link]

Gjuvsland AB, Vik JO, Woolliams JA, Omholt SW (2011) Order-preserving principles underlying genotype-phenotype maps ensure high additive proportions of genetic variance. Journal of Evolutionary Biology 24(10):2269-2279 [link]

Gjuvsland AB, Wang Y, Plahte E and Omholt SW (2013) Monotonicity is a key feature of genotype-phenotype maps. Front. Genet. 4:216. doi: 10.3389/fgene.2013.00216 [link]

Hansen T & Wagner GP (2001) Modeling genetic Architecture: A Multilinear Theory of gene Interaction. Theoretical Population Biology 59:61-86 [link]

Leeuw J, Hornik K and Mair P (2009) Isotone Optimization in R: Pool-Adjacent-Violators Algorithm (PAVA) and Active Set Methods. Journal of Statistical Software 32(5) [link]

Lynch M & Walsh B (1998) Genetics and Analysis of Quantitative Traits, Sunderland, MA: Sinauer Associates

`decompose_monotone` *Decompose genotype-phenotype map(s) using monotone regression*

Description

Functions for decomposing genotype-phenotype (GP) maps with N biallelic loci using monotone regression from the `isotone` package.

Usage

```
decompose_monotone(gpmap)
decompose_monotone_single(gpmap)
```

Arguments

`gpmap`	A `gpmap` object

Details

`decompose_monotone` works for any `gpmap` object (`values` is $(3^N)xK$ matrix of genotypic values) and calls the internal function `decompose_monotone_single` for each column. `decompose_monotone_single` takes a `gpmap` object with a single set of genotypic values ($K = 1$), loops through all 2^N possible combinations of plusalleles, calls `monotone_regression` and identifies the best fit. The code uses the `foreach` package and will run in parallel if a *parallel backend* is registered (see `foreach` documentation).

Value

The input `gpmap` is returned with two added elements

`monoR2`	The coefficient of determination of the monotone regression
`values.mono`	A matrix of genotypic values for the monotone component of genotype-phenotype map(s)

Author(s)

Arne B. Gjuvsland <arne.gjuvsland@nmbu.no> and Yunpeng Wang <yunpeng.wng@gmail.com>

References

Leeuw J, Hornik K and Mair P (2009) Isotone Optimization in R: Pool-Adjacent-Violators Algorithm (PAVA) and Active Set Methods. Journal of Statistical Software 32(5) [link]

Gjuvsland AB, Wang Y, Plahte E and Omholt SW (2013) Monotonicity is a key feature of genotype-phenotype maps. Front. Genet. 4:216. doi: 10.3389/fgene.2013.00216 [link]

Examples

```
data(GPmaps)

#Additive GP map is monotone so monoR2=1 and values.mono=values
decompose_monotone(A)

#Pure AxA epistasis map
decompose_monotone(AA)

#two-locus example in Cheverud & Routman (1995)
decompose_monotone(mouseweight)

#decompose four random 3-locus GP maps
set.seed(0)
randomGP <- rnorm(3^2*4)
dim(randomGP) <- c(9,4)
decompose_monotone(generate_gpmap(randomGP))
```

`degree_of_monotonicity` *Degree of monotonicity of GP map*

Description

Functions for computing degree of monotonicity m for `gpmap` objects.

Usage

```
degree_of_monotonicity(gpmap)
degree_of_monotonicity_single(gpmap)
```

Arguments

gpmap	A `gpmap` object

Details

`degree_of_monotonicity` works for any `gpmap` object (`values` is $(3^N)xK$ matrix of genotypic values) and calls the internal function `degree_of_monotonicity_single` for each column. `degree_of_monotonicity_sin` computes substitution effect, locus weights and per-locus and overall degree of monotonicity as described in Gjuvsland *et al.* (2013).

Value

`degree_of_monotonicity` returns the input `gpmap` with the following added fields:

`degree.monotonicity`
: Overall degree of monotonicity for the K GP maps

`degree.monotonicity.locus`
: Data frame with per locus degree of monotonicity for the K GP maps

`locus.weight`
: Data frame with locus weigths

Author(s)

Arne B. Gjuvsland <arne.gjuvsland@nmbu.no> and Yunpeng Wang <yunpeng.wng@gmail.com>

References

Gjuvsland AB, Wang Y, Plahte E and Omholt SW (2013) Monotonicity is a key feature of genotype-phenotype maps. Front. Genet. 4:216. doi: 10.3389/fgene.2013.00216 [link]

Examples

```
data(GPmaps)

#Additive GP map is monotone
degree_of_monotonicity(A)

#Pure AxA epistasis map
degree_of_monotonicity(AA)

#two-locus example in Cheverud & Routman (1995)
degree_of_monotonicity(mouseweight)
```

---

enumerate_genotypes *Function for enumerating genotypes for N biallelic loci*

Description

Function for enumerating all 3^N genotypes for N biallelic loci. Optional specification of names of loci and alleles. genotypes. Generates a data frame of multilocus genotypes in the sequence used for objects of class `gpmap`.

Usage

```
enumerate_genotypes(nloci=1, locinames=NULL, allelenames=NULL)
```

Arguments

`nloci`
: The number of loci N

`locinames`
: An optional character vector with N names of loci

`allelenames`
: An optional character object specifying allele names

Details

Unless specified locinames default to "Locus 1", "Locus 2",..,"Locus N".

If `allelenames` is not specified then the alleles will be named "1" and "2".

Value

Returns a data frame with locinames as colnames, and with 3^N rows specifying all possible genotypes in the sequence used for all GP maps in the package (the same sequence as used in Gjuvsland *et al.*(2011)), where the genotype at the first locus varies fastest, then the second locus, and so on:

```
  Locus_1 Locus_2
1      11      11
2      12      11
3      22      11
4      11      12
5      12      12
6      22      12
7      11      22
8      12      22
9      22      22
```

Author(s)

Arne B. Gjuvsland <arne.gjuvsland@nmbu.no> and Yunpeng Wang <yunpeng.wng@gmail.com>

References

Gjuvsland AB, Vik JO, Woolliams JA, Omholt SW (2011) Order-preserving principles underlying genotype-phenotype maps ensure high additive proportions of genetic variance. Journal of Evolutionary Biology 24(10):2269-2279 [link]

Examples

```
#genotypes for a single locus
enumerate_genotypes()

#genotypes for two loci "A" and "B", with alleles named "H" and "L"
enumerate_genotypes(2,c("A","B"),c("H","L"))

#genotypes for the two-locus example in Cheverud & Routman (1995)
enumerate_genotypes(2,c("D7Mit17","D1Mit7"),rbind(c('A1','A2'),c('B1','B2')))
```

`generate_gpmap` *Function for creating genotype-phenotype (GP) maps*

Description

Function for creating a `gpmap` object representing a genotype-phenotype (GP) map for N biallelic loci or more generally K such maps, from a matrix of genotypic values.

Usage

```
generate_gpmap(y, locinames = NULL, allelenames = NULL, mapnames = NULL)
```

Arguments

`y`	A $(3^N \times K)$ matrix or numeric with each column specifying the 3^N genotypic values for K GP maps
`locinames`	An optional character vector with N names of loci
`allelenames`	An optional character object specifying allele names
`mapnames`	An optional character vector with K names of GP maps / phenotypes

Details

Arguments `locinames` and `allelenames` are passed on to `enumerate_genotypes`, and the genotypic values in `y` should be given in the same sequence as the sequence of genotypes returned by `enumerate_genotypes`. If `mapnames` is not specified then the GP maps will be named "GPmap_1", "GPmap_2",..,"GPmap_K".

Value

The function returns an object of class `gpmap` containing the following components

`values`	The vector or matrix of genotypic values
`nloci`	The number of loci in the map
`genotypes`	Data frame with enumeration of genotypes
`locinames`	Character vector with names for all loci
`mapname`	The name(s) of the GP map

Author(s)

Arne B. Gjuvsland <arne.gjuvsland@nmbu.no> and Yunpeng Wang <yunpeng.wng@gmail.com>

References

Gjuvsland AB, Vik JO, Woolliams JA, Omholt SW (2011) Order-preserving principles underlying genotype-phenotype maps ensure high additive proportions of genetic variance. Journal of Evolutionary Biology 24(10):2269-2279 [link]

Examples

```
#inter- and intra-locus additive GPmap with two loci
generate_gpmap(c(-2,1,0,-1,0,1,0,1,2),mapnames="Additive")

#two-locus GP map with AxA epistasis for loci named A and B
generate_gpmap(c(-1,0,1,0,0,0,1,0,-1),locinames=c("A","B"),mapnames="AxA")

#random GP map with 3 loci
set.seed(0)
generate_gpmap(rnorm(27))
```

GPmaps *Dataset containing example GP maps*

Description

Example GP maps with two loci including: The orthogonal GP maps `A`, `D`, `AA`, `AD`, `DA` and `DD` used in decomposition of genetic variance (Zeng *et al.* 2005). The GP map `mouseweight` for body weight studied by Cheverud *et al.* (1995).

Usage

```
data(GPmaps)
```

Format

Objects of class `gpmap`

References

Cheverud JM & Routman EJ (1995) Epistasis and Its Controbution to Genetic Variance Components. Genetics 139:1455-1461 [link]

Zeng ZB, Wang T, Zou W. (2005). Modelling quantitative trait loci and interpretation of models. Genetics 169: 1711-1725. [link]

---

monotone_regression *Perform monotone regression on a genotype-phenotype (GP) map*

Description

The function uses `partial_genotype_order` and `activeSet` from the isotone package to do monotone regression (Leeuw *et al.*, 2009) on a GP map.

Usage

```
monotone_regression(gpmap, plusallele)
```

Arguments

gpmap	An object of class gpmap
plusallele	An N vector of allele indexes (1 or 2)

Details

Element *i* in plusallele specifies the ordering of the genotypes at locus *i*, if the element is 1 then 11 < 12 < 22 and conversely if it is 2 then 22 < 12 < 11. monotone_regression calls partial_genotype_order to obtain the partial ordering of genotypic values for the given plusalleles. This partial ordering is then used together with the GP map itself as input to the activeSet function from the package isotone.

Value

monotone_regression returns the output from activeSet directly.

Author(s)

Arne B. Gjuvsland <arne.gjuvsland@nmbu.no> and Yunpeng Wang <yunpeng.wng@gmail.com>

References

Leeuw J, Hornik K and Mair P (2009) Isotone Optimization in R: Pool-Adjacent-Violators Algorithm (PAVA) and Active Set Methods. Journal of Statistical Software 32(5) [link]

Gjuvsland AB, Wang Y, Plahte E and Omholt SW (2013) Monotonicity is a key feature of genotype-phenotype maps. Front. Genet. 4:216. doi: 10.3389/fgene.2013.00216 [link]

Examples

```
data(GPmaps)

#Additive GP map is monotone
monotone_regression(A,c(2,2))

#Pure AxA epistasis map
monotone_regression(AA,c(2,2))

#two-locus example in Cheverud & Routman (1995)
monotone_regression(mouseweight,c(1,1))
```

---

partial_genotype_order

Generate partial ordering of genotype space based from allele content of genotypes

---

Description

Generate the strict partial order on genotype space specified in eq. (13) in Gjuvsland *et al.* (2011). For a genotype space with N biallelic loci a minimal description of this partial order is given by $2N * 3^{(N-1)}$ inequalities.

Usage

```
partial_genotype_order(plusallele)
```

Arguments

`plusallele`	A N-vector with indexes (1 or 2) for the +allele for each locus

Details

In short a partial order on a set is a binary relation defining a parwise ordering of some pairs of elements in the set, for a formal definiton see https://en.wikipedia.org/wiki/Partial_order. In the partial order on the set of genotypes defined in Gjuvsland et al. (2011) the comparable pairs of genotypes are equal at every locus except one, while all other pairs of genotypes are incomparable. This partial ordering of genotype space is implicit in the regression on gene content (the number of alleles with a given index in each genotype) used for decomposition of tne genotypic value in quantitative genetics (see e.g. Lynch and Walsh page 65).

Value

Returns a $(2N * 3^{(N-1)}) \times 2$ matrix of genotype indexes. The genotype indexes refer to row number in the genotype sequence set up in `enumerate_genotypes`. Each row vector in the matrix contains the genotype indexes of one comparable pairs, and if the first index is k and the second is l then genotype[k] < genotype[l].

Author(s)

Arne B. Gjuvsland <arne.gjuvsland@nmbu.no> and Yunpeng Wang <yunpeng.wng@gmail.com>

References

Gjuvsland AB, Vik JO, Woolliams JA, Omholt SW (2011) Order-preserving principles underlying genotype-phenotype maps ensure high additive proportions of genetic variance. Journal of Evolutionary Biology 24(10):2269-2279 [link]

Lynch M & Walsh B (1998) Genetics and Analysis of Quantitative Traits, Sunderland, MA: Sinauer Associates

plot.gpmap *Functions for creating lineplots of genotype-phenotype (GP) maps*

Description

Function for creating lineplots for genotype-phenotype (GP) map (an object of class gpmap) with 1-3 biallelic loci.

Usage

```
## S3 method for class 'gpmap'
plot(x, show=1, decomposed=FALSE, ...)
```

Arguments

x	A gpmap object
show	Which map (only used if >1 map in gpmap object) to plot
decomposed	Decomposition into monotone and non-monotone component plotted if TRUE
...	ignored

Author(s)

Arne B. Gjuvsland <arne.gjuvsland@nmbu.no> and Yunpeng Wang <yunpeng.wng@gmail.com>

Examples

```
data(GPmaps)

#plot additive gpmap
plot(A)

#plot decomposition of GPmap from Cheverud & Routman (1995)
decomp <- decompose_monotone(mouseweight)
plot(decomp, decomposed=TRUE)
```

print.gpmap *Print function for gpmap objects*

Description

Print a summary of a genotype-phenotype (GP) map (an object of class gpmap) with 1-3 N biallelic loci.

Usage

```
## S3 method for class 'gpmap'
print(x, ...)
```

Arguments

x	A gpmap object
...	ignored

Details

Prints name(s) of GP map(s) and loci, a summary of genotypic values. Monotonicity measures are printed if available.

Author(s)

Arne B. Gjuvsland <arne.gjuvsland@nmbu.no> and Yunpeng Wang <yunpeng.wng@gmail.com>

Examples

```
data(GPmaps)
print(A)
```

Index