

GGtools

April 19, 2009

<code>gwSnpTests</code>	<i>methods for iterating association tests (expression vs SNP) across genomes or chromosomes</i>
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Description

methods for iterating association tests (expression vs SNP) across genomes or chromosomes

Usage

```
gwSnpTests(sym, sms, cnum, ...)
```

Arguments

<code>sym</code>	genesym, probeId, or formula instance
<code>sms</code>	smlSet instance
<code>cnum</code>	chrnum instance or missing
<code>...</code>	...

Details

invokes `snpMatrix` test procedures as appropriate
`gwSnpScreen` is deprecated and simply throws a message indicating this.

Value

`gwSnpScreenResult` or `cwSnpScreenResult` instance

Author(s)

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Examples

```

if (!exists("hmceuB36.2021")) data(hmceuB36.2021)
# condense to founders only
hmFou = hmceuB36.2021[, which(hmceuB36.2021$isFounder)]
# show basic formula fit
f1 = gwSnpTests(genesym("CPNE1")~male, hmFou, chrnum(20))
f1
plot(f1)
# show how to avoid adjusted fit
f1b = gwSnpTests(genesym("CPNE1")~1-1, hmFou, chrnum(20))
# show gene set modeling on chromosome
library(GSEABase)
gs1 = GeneSet(c("CPNE1", "ADA"))
geneIdType(gs1) = SymbolIdentifier()
f2 = gwSnpTests(gs1~male, hmFou, chrnum(20))
f2
names(f2)
plot(f2[["ADA"]])
# show 'smlSet-wide' fit
f3 = gwSnpTests(gs1~male, hmFou)
f3

```

hbTestResults-class

Class "hbTestResults" holds results of tests of association of expression levels with haplotype within haplotype block

Description

Class "hbTestResults" holds results of tests of association of expression levels with haplotype within haplotype block

Objects from the Class

Objects can be created by calls of the form `new("hbTestResults", ...)`.

Slots

hscores: Object of class "list" series of haplo.stats::haplo.score results for blocks

locs: Object of class "numeric" locations at which blocks were found (mean location within each block)

chrnum: Object of class "chrnum" chromosome being analyzed

smlSetName: Object of class "character" name of the smlSet harboring data in use

rsid: Object of class "ANY" can be a dbSNP id to use as an anchor, or a number constituting absolute chromosomal location at which blocks will be sought

rad: Object of class "numeric" radius in base pairs around the rsid to be searched for blocks

ldStruc: Object of class "ANY" the result of the mapLD:::mapLD function

Methods

pvals signature(x = "hbTestResults"): extracts p-values for global score tests, one per block

locs signature(x = "hbTestResults"): extracts locations of haplotype blocks found (average SNP location within block)

hscores signature(x = "hbTestResults"): extracts `haplo.score` results as a list, for all blocks

Author(s)

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Examples

```
showClass("hbTestResults")
```

hbTests-methods

haplotype-block based tests for structured expression variation

Description

haplotype-block based tests for structured expression variation

Methods

fmla = "genesym", sms = "smlSet", cnum = "chrnum", rsid = "numeric", rad = "numeric" expression data for gene identified by `genesym` is extracted from `sms`, and genotype data within `rad` base pairs of `rsid` are obtained and processed by `mapLD` to define haplotype blocks and the SNP tagging these blocks. Score tests are then computed for the association of expression of the gene identified by `genesym` with haplotype copy number (additive model by default, but options captured by ... are passed to `haplo.score`.)

Examples

```
library(GGtools)
data(hmceuB36.2021)
hmFou = hmceuB36.2021[, hmceuB36.2021$isFounder==TRUE]
hh = hbTests(genesym("CPNE1"), hmFou, chrnum(20), 33600000, 2e4 )
hh
pvals(hh)
plot(locs(hh), -log10(pvals(hh)))
hscores(hh)[[which.min(pvals(hh))]]
```

```
hmceuB36.2021      two chromosomes of genotype data and full expression data for CEPH
CEU hapmap data
```

Description

two chromosomes of genotype data and full expression data for CEPH CEU hapmap data

Usage

```
data(hmceuB36.2021)
```

Format

The format is: Formal class 'smlSet' [package "GGBase"] with 9 slots ..@ smlEnv :<environment: 0x3902e98> ..@ annotation : chr "illuminaHumanv1.db" ..@ chromInds : num [1:2] 20 21 ..@ organism : chr "Hs" ..@ assayData :<environment: 0x3c96504> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots ..@ ...classVersion..:Formal class 'Versions' [package "Biobase"] with 1 slots

Examples

```
#data(hmceuB36.2021)
```

```
invokePhase-methods
~~ Methods for Function invokePhase in Package 'GGtools' ~~
```

Description

~~ Methods for function invokePhase in Package 'GGtools' ~~

Methods

x = "snp.matrix", cnum = "chrnum", parmstring = "character", globpname = "character", where2run = "character"
transform snp.matrix entity to phaseInput (uses tempfile()) and invokes PHASE

x = "phaseInput", cnum = "chrnum", parmstring = "character", globpname = "character", where2run = "character"
for prepared 'phaseInput' structure, invoke PHASE

Examples

```
## Not run:
data(smtest)
invokePhase(smtest, chrnum(20), "", Sys.getenv("PHASE_LOC"),
            ".", TRUE)
## End(Not run)
```

plot-methods *~~ Methods for Function plot in Package 'GGtools' ~~*

Description

~~ Methods for function plot in Package 'GGtools' ~~

Methods

x = "cwSnpScreenResult", y = "missing" shows results of chromosome-wide screen for expression-associated SNP

x = "filteredGwSnpScreenResult", y = "ANY" shows results of genome-wide screen for expression-associated SNP

x = "filteredMultiGwSnpScreenResult", y = "ANY" fails, need to pick gene at this time

snpm2mapLD *prepare input to mapLD function for haplotype block identification*

Description

prepare input to mapLD function for haplotype block identification

Usage

```
snpm2mapLD(x, chrnum, runMAP=TRUE, ...)
```

Arguments

x	snp.matrix instance
chrnum	chromosome number
runMAP	logical indicating whether or not to run mapLD
...	additional arguments to mapLD

Details

sets up a data frame suitable for mapLD, and will invoke with appropriate arguments identifying columns for alleles and other identifiers if runMAP is TRUE (default).

smtest is a small snp.matrix instance

Value

a list with element struc holding the data frame, and mapLD output if requested. Note that mapLD writes an eps file to disk *sigh*.

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```
data(smtest)
ss = snpm2mapLD(smtest, chrnum=20, runMAP=FALSE)
ss
# you could run mapLD on ss[[1]]
```

snpm2phase	<i>convert information in a snp.matrix to PHASE input format; invokePhase can run a suitably installed version of PHASE</i>
------------	---

Description

convert information in a snp.matrix to PHASE input format; invokePhase can run a suitably installed version of PHASE

Usage

```
snpm2phase(snpm, cnum, outfilename)
parsePh.out(fn)
personalHap(x)
```

Arguments

snpm	snp.matrix instance
cnum	chromosome number as chrnum instance
outfilename	character name of file to write
fn	character name of PHASE .out file to read
x	output of parsePh.out

Details

follows phase 2.1 documentation for input format
a phaseInput container class can store relevant metadata

Value

writes to a file and gives a message

Author(s)

Vince Carey <stvjc@channing.harvard.edu>

Examples

```

data(smtest)
tt = tempfile()
pin = snpm2phase(smtest, chrnum(20), tt)

class(pin)
getClass("phaseInput")
pin
readLines(tt)
unlink(tt)
pp = parsePh.out(system.file("phaseOut/cpne1_20k.out", package="GGtools"))
pp[[1]][1:3]
personalHap(pp)

```

strMultiPop

*serialization of a table from Stringer's multipopulation eQTL report***Description**

serialization of a table from Stringer's multipopulation eQTL report

Usage

```
data(strMultiPop)
```

Format

A data frame with 39649 observations on the following 12 variables.

rsid a factor with levels rs...

genesym a factor with levels 37865 39692 ABC1 ABCD2 ABHD4 ACAS2 ...

illvlpid a factor with levels GI_10047105-S GI_10092611-A GI_10190705-S GI_10567821-S
GI_10835118-S GI_10835186-S ...

snpChr a numeric vector

snpCoordB35 a numeric vector

probeMidCoorB35 a numeric vector

snp2probe a numeric vector

minuslog10p a numeric vector

adjR2 a numeric vector

assocGrad a numeric vector

permThresh a numeric vector

popSet a factor with levels CEU-CHB-JPT CEU-CHB-JPT-YRI CHB-JPT

Details

imported from the PDF(!) distributed by Stranger et al as supplement to PMID 17873874

Source

PMID 17873874 supplement

References

PMID 17873874 supplement

Examples

```
data(strMultiPop)
strMultiPop[1:2, ]
```

`topSnps-methods` *report on most significant SNP with gwSnpTests results*

Description

report on most significant SNP with gwSnpTests results

Methods

x = "cwSnpScreenResult" also takes argument n for number to report

x = "gwSnpScreenResult" also takes argument n for number to report

`GGtools-trackSet-methods`
create a browser track from a chromosome-wide SNP screen

Description

create a browser track from a chromosome-wide SNP screen

Methods

object = "cwSnpScreenResult" returns a track set with genomic coordinates for x axis and $-\log_{10}$ p-values for y axis

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