Package ‘GGtools’

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Title software and data for analyses in genetics of gene expression

Version 5.10.1

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Description software and data for analyses in genetics of gene expression and/or DNA methylation

Suggests GGdata, illuminaHumanv1.db, SNPlocs.Hsapiens.dbSNP144.GRCh37, multtest, aod, rmeta

Depends R (>= 2.14), GGBase (>= 3.19.7), data.table, parallel, Homo.sapiens

Imports methods, utils, stats, BiocGenerics, snpStats, ff, Rsamtools, AnnotationDbi, Biobase, bit, VariantAnnotation, hexbin, rtracklayer, Gviz, stats4, S4Vectors (>= 0.9.25), IRanges, GenomeInfoDb, GenomicRanges, iterators, Biostrings, ROCR, biglm, ggplot2, reshape2

Enhances MatrixEQTL, foreach, doParallel, gwascat

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License Artistic-2.0

biocViews Genetics, GeneExpression, GeneticVariability, SNP

LazyLoad yes


NeedsCompilation no

R topics documented:

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**GGtools-package**  
*software and data for analyses in genetics of gene expression*

**Description**  
*software and data for analyses in genetics of gene expression*
Details

Package: GGtools
Version: 4.2.26
Suggests: GGdata, illuminaHumanv1.db
Depends: R (>= 2.14), GGBase (>= 3.16.1)
Imports: methods, snpStats, ff, IRanges, GenomicRanges, AnnotationDbi, Biobase, Rsamtools, bit, VariantAnnotation
License: Artistic-2.0
LazyLoad: yes
Packaged: 2012-01-18 03:39:51 UTC; stvjc
Built: R 2.15.0; ; 2012-02-06 17:22:52 UTC; unix

Index:

- best.cis.eQTLs: collect genewise best scoring eQTL
- eqtlTests: compute association statistics between all probes and SNP in an smlSet instance
- eqtlTestsManager-class: Class "eqtlTestsManager"
- ex: ExpressionSet instance for illustrating integrative smlSet container
- getCisMap: create, using Bioconductor annotation resources, a structure that enumerates SNP in the vicinity of ("cis" to) genes
- gwSnpTests: execute a series of tests for association between genotype and expression
- strMultPop: serialization of a table from Stranger's multipopulation eQTL report
- hg19.si.df: data frame representation of seqinfo for Homo.sapiens at hg19 build

The package depends on GGBase, which includes additional infrastructure for integrative data structures and data filtering.

Author(s)

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See Also

getSS for acquiring containers for integrative data on genetics of expression.

Examples

```r
## Not run:
# acquire chromosome 20 genotypes and all expression data for
# 90 CEU samples as published at Wellcome Trust GENEVAR and
# HapMap phase II
c20 = getSS("GGtools", "20")
# perform a focused eQTL search
```
All.cis

functions that compute score tests for all SNP cis to genes, with flexible filtering

Description

function that computes score tests for all SNP cis to genes, with flexible filtering

Usage

cisScores( config = new("CisConfig"), ... )
All.cis( config = new("CisConfig"), ... )
addgwhit(ans, traitFilter=force, vname="isgwashit")
add878(ans)
inflammFilter(gwtagger)

Arguments

config instance of class CisConfig-class
... passed to eqtlTests
ans cisRun-like entity to which additional annotation will be bound by addgwhit or add878
gwtagger GRanges like gwastagger in gwascat data elements
traitFilter function that returns a gwastagger-like GRanges, see inflammFilter
vname name to be used for new data.table column added by addgwhit

Details

cisScores (All.cis) returns score statistics for associations of all SNP cis to genes, in a GRanges instance, with range names given by probes; metadata supplied SNP location, name, and score
cisAssoc targets SummarizedExperiment instances for molecular phenotype measures and VCF for variant data
addgwhit and add878 will use GWAS hit information or ChromHMM labeling to annotation ranges

Value

for cisScores: instance of cisRun-class
for cisAssoc: a GRanges with information on observed and permuted test scores per locus/feature pair

Author(s)

VJ Carey <stvjc@channing.harvard.edu>
Examples

```r
## Not run:
cc = new("CisConfig")
chrnames(cc) = "21"
genome(cc) = "hg19"
lkp = try(library(parallel))
if (!inherits(lkp, "try-error")) {
    nc = min(10, detectCores())
options(mc.cores=nc)
geneApply(cc) = mclapply
}
estimates(cc) = FALSE
set.seed(1234)
unix.time(f1 <- cisScores( cc ))
#
# demonstrate adding annotation on chromatin state and gwas status
#
eprops = function(ans) {
#
# only adds fields to values() of the input
#
data(hmm878)
ac = as.character
eqr = GRanges(ac(seqnames(ans)), IRanges(ans$snplocs, width=1))
fo = findOverlaps(eqr, hmm878)
chromcat878 = factor(rep("none", length(ans)), levels=c(unique(hmm878$name), "none"))
chromcat878[ queryHits(fo) ] = factor(hmm878$name[subjectHits(fo)])
ans$chromcat878 = chromcat878

if (require(gwascat)) {
data(gwastagger)
isgwashit = i*(overlapsAny(eqr, gwastagger) | ans$snp
    ans$isgwashit = isgwashit
}
ans
}
extraProps(cc) = eprops
set.seed(1234)
unix.time(f2 <- cisScores( cc ))
#
# inflammFilter # to make more restrictive predicate for prediction

## End(Not run)
```

---

**appraise**  
**appraisal for eQTL prediction models**

**Description**

appraise for eQTL prediction models
Usage

```r
appraise(dtab,
  discretize = TRUE,
  reduceToSNP = TRUE,
  prefix,
  folder = paste0(prefix, ",_APPROUT"),
  discfmlas_in = GGtools:::.discfmlas.demo,
txlist = list(
    distcats = function(x) {
      cut(x$mindist, c(-1, seq(0, 200001, 50000)))
    },
    fdrcats = function(x) {
      fdrfac = cut(x$fdr, c(-.01, .05, .1,.25, .5, 1.01))
      relevel(fdrfac, "[0.5,1.01]")
    },
    mafcats = function(x) {
      maffac = cut(x$MAF,c(-0.01,.05, .1,.25, .51))
      relevel(maffac, "[-0.01,0.05]")
    },
    caddcats = function(x){
      cut(x$PHRED, c(-.01, 5, seq(10, 30, 10 ), 60))
    },
    cutts = c(-0.01,seq(0.015,.12,.015),.15),
    names2check= GGtools:::.standardNames, maxit=30,
    savePinfer=FALSE)
# bindgwava( gwavadt, eqdt )
```

Arguments

dtab data.table instance as created by transforming cisRun to GRanges and then to data.table, and then adding CADD PHRED scores if available. If CADD PHRED scores are not available, the default formulas should not be used.
discretize logical telling whether binning to factors defined in txlist should be performedreduceToSNP logical telling whether ranges should be reduced to unique SNP and FDR recomputedprefix character atom used to prefix objects saved and folder for result objectsfolder folder name suffixdiscfmlas_in named list of model formulatxlist named list of functions that are used to bin certain quantitative features of SNPCutts numeric vector of thresholds for tabulation and discrete calibrationnames2check if NULL, ignored; if a character vector, function will fail unless all(names2check %in% names(dtab)maxit numeric passed to bigglm as control parameter for maximum number of iterations to use in modeling gwas hit probabilitiessavePinfer logical specifying whether the inferred probabilities of GWAS involvement are retained

Details

The appraise function wraps many tasks used to appraise eQTL collections in terms of predictive capacity. Details will be provided.
Value

A folder is opened and objects are written representing the test set (data.table on SNPs on even chromosomes), the coefficients of predictive models built on training set (SNPs on odd chromosomes), coefficients of linear regressions of binary test outcomes for calibrating the model on test data, and ROC AUC measures.

bindgwava uses simple data.table operations with match to add three columns to eqdt, gwava_tss, gwava_unmat, and gwava_regi

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

---

b1  
mcwBestCis instances, integrative analysis output containers generated by GGtools vignette

Description

integrative analysis output containers generated by GGtools vignette

Usage

data(b1)

Format

The format is:
Formal class 'mcwBestCis' [package "GGtools"] with 9 slots
.. @ scoregr :Formal class 'GRanges' [package "GenomicRanges"] with 6 slots
  .. .. @ seqnames :Formal class 'Rle' [package "IRanges"] with 4 slots
  .. .. .. .. @ values : Factor w/ 1 level "20": 1
  .. .. .. .. @ lengths : int 50
  .. .. .. .. @ elementMetadata: NULL
  .. .. .. @ ranges :Formal class 'IRanges' [package "IRanges"] with 6 slots
  .. .. .. .. .. @ start : int [1:50] 24280834 61665697 352356 61679079 45286150 55187941 38766161 10871477 56570242 13304639 ...
  .. .. .. .. .. @ width : int [1:50] 2090785 2005619 2021461 2001901 2129211 2007692 2038197 2035767 2012068 2013675 ...
  .. .. .. .. .. @ NAMES : chr [1:50] "GI_34147330-S" "hmm26961-S" "GI_17149835-I" "GI_31077201-S" ...
  .. .. .. .. .. @ elementType : chr "integer"
  .. .. .. .. .. @ elementMetadata: list()
  .. .. .. @ strand :Formal class 'Rle' [package "IRanges"] with 4 slots
  .. .. .. .. @ values : Factor w/ 3 levels "+","-","." : 3
  .. .. .. .. @ lengths : int 50
  .. .. .. .. @ elementMetadata: NULL
  .. .. .. @ elementMetadata:Formal class 'DataFrame' [package "IRanges"] with 6 slots
  .. .. .. .. @ elementMetadata: list()
best.cis.eQTLs

collect genewise best scoring eQTL

description

collect genewise best scoring eQTL
Usage

best.cis.eQTLs(smpack = "GGdata", rhs = ~1,
folderstem = "cisScratch", radius = 50000,
shortfac = 100,
chrmnames = as.character(1:22),
smchrpref = "", gchrpref = "", schrpref = "ch",
geneApply = lapply, geneannopk = "illuminaHumanv1.db",
snpnannopk = snplocsDefault(),
smFilter = function(x) nsFilter(MAFfilter(x, lower = 0.05), var.cutoff = 0.97), nperm = 2,
useME=FALSE, excludeRadius=NULL, exFilter=function(x)x,
keepMapCache=FALSE, getDFFITS=FALSE, SSgen = GGBase::getSS)

All.cis.eQTLs(maxfdr = 0.05, inbestcis = NULL, smpack = "GGdata",
rhs = ~1, folderstem = "cisScratch", radius = 50000,
shortfac = 100,
chrmnames = as.character(1:22),
smchrpref = "", gchrpref = "", schrpref = "ch",
geneApply = lapply, geneannopk = "illuminaHumanv1.db",
snpnannopk = snplocsDefault(),
smFilter4cis = function(x) nsFilter(MAFfilter(clipPCs(x,
1:10), lower = 0.05), var.cutoff = 0.85),
smFilter4all = function(x) MAFfilter(clipPCs(x,
1:10), lower = 0.05),
nperm = 2, excludeRadius=NULL, exFilter=function(x)x,
SSgen = GGBase::getSS)

meta.best.cis.eQTLs(smpackvec = c("GGdata", "hmyriB36"), rhslist = list(~1,
~1), folderstem = "cisScratch", radius = 50000, shortfac = 100,
chrmnames = as.character(1:22), smchrpref = "", gchrpref = "", schrpref = "ch",
geneApply = lapply, geneannopk = "illuminaHumanv1.db",
snpnannopk = snplocsDefault(), SMFilterList = list(
function(x) nsFilter(MAFfilter(x, lower = 0.05), var.cutoff = 0.97),
function(x) nsFilter(MAFfilter(x, lower = 0.05), var.cutoff = 0.97) ),
exFilterList = list(function(x)x, function(x)x),
nperm = 2, excludeRadius=NULL)

meta.All.cis.eQTLs(minchisq, smpackvec = c("GGdata", "hmyriB36"),
rhslist = list(~1, ~1), folderstem = "cisScratch",
radius = 50000, shortfac=100, chrmnames = as.character(1:22), smchrpref = "",
gchrpref = "", schrpref = "ch", geneApply = lapply, geneannopk = "illuminaHumanv1.db",
snpnannopk = snplocsDefault(),
SMFilterList = list(function(x) nsFilter(MAFfilter(x,
lower = 0.05), var.cutoff = 0.97), function(x)
nsFilter(MAFfilter(x, lower = 0.05), var.cutoff = 0.97));
exFilterList = list(function(x) x, function(x)
x),
nperm = 2)

chromsUsed(x)
fdr(x)
fullreport(x, type, ...)
getAll(x)
getBest(x)
getCall(x)

Arguments

smpack character string naming a package to which getSS can be applied to extract smlSet-class instances
smpackvec vector of character strings naming packages that can be used as smpack values in a series of best.cis.eQTLs calls, one per population for meta-analysis
rhs R model formula, with no dependent variable, that will be used with snp.rhs.tests to adjust GWAS tests for each expression probe
rhslist a list of model formulae to be used as rhs in a series of best.cis.eQTLs calls, one per population for meta-analysis
folderstem prefix of the folder name to be used to hold ff archives of test results
radius coding extent of each gene will be extended in both directions by radius bases, and only SNP within these limits are used for selecting best hits for the gene
shortfac a numeric that will scale up the chi-squared statistic before it is converted to short integer for storage in ff array
chrnames character vector of chromosome identifiers, to be manipulated for certain query resolutions by the following parameters
smchrpref prefix to convert chrnames into appropriate tokens for indexing smlSet elements as collected from the package named by parameter smpack
gchrpref prefix to convert chrnames into appropriate tokens for obtaining gene metadata; in future this may need to be a string transformation function
schrpref prefix to convert chrnames into appropriate tokens for use with snplocs for the SNP location information package identified in snpannopack parameter below
geneApply an lapply like function, defaults to lapply
geneannopk character string, name of a *.db annotation package that annotates probe identifiers; or see getCisMap for additional possibilities concerning FDb.* complex token values for newer annotation formats
snpannopk character string, name of SNPlocs.Hsapiens.dbSNP.* package for obtaining; global function snplocsDefault() can be used to get a nominally current package name
smFilter function accepting and returning an smlSet-class instance
SMFilterList list of functions, one element per smlSet package used in meta analysis, accepting and returning an smlSet-class instance
minchisq threshold on test statistic value that must be met to include records on SNPs in the All.cis.eQTLs report
nperm number of permutations to be used for plug-in FDR computation
best.cis.eQTLs

useME logical; if TRUE, use the rudimentary interface to the MatrixEQTL package from A. Shabalin on CRAN.

maxfdr Used in All.cis.eQTLs. The process of identifying “best” cis eQTL per probe leads to a probe-specific FDR. In All.cis.eQTLs we enumerate all probes and all SNP with FDR at most maxfdr, not just the best scoring SNP per probe.

inbestcis Used in All.cis.eQTLs. An instance of mcwBestCis that can be used to speed up the extraction of All.cis eQTL.

smFilter4cis Used in All.cis.eQTLs. A function accepting and returning an smlSet instance. When inbestcis parameter is NULL, this filter will be used for identifying the best SNP per probe.

smFilter4all Used in All.cis.eQTLs. A function accepting and returning an smlSet instance. This filter will be used for identifying the best SNP per probe. This filter should not affect the number of probes.

x instance of mcwBestCis

type character, either ‘data.frame’ or ‘GRanges’

excludeRadius numeric, defaulting to NULL; if non-null, defines radius around gene region that is excluded for cis SNP scoring; must be less than radius

keepMapCache logical, if TRUE, returned mcwBestCis object will include an environment loaded with chromosome-specific lists of maps from genes to cis SNP names; if FALSE, the mapCache environment returned will be empty – NB, this feature has been found to add too much volume to returned objects and is suspended...

exFilter this function is passed to getSS; see Details

exFilterList for metaanalytic applications, a list of functions in correspondence with the elements of snpvec to be passed to getSS; see Details

getDFFITS logical; a component storing max DFFITS value for each gene will be retained if this argument TRUE

SSgen function to be used to create smlSet instance for testing – in general, GGBase::getSS has been used to pull the ExpressionSet and SnpMatrix data from a named package, but in some cases a specialize task is needed to create the desired smlSet. Whatever is passed to SSgen must return an smlSet instance.

Details
geneApply can be set to parallel::mclapply, for example, in a multicore context.
mcwBestCis stands for ‘multi-chromosome-wide best cis’ eQTL report container.

It is possible that the filtering processes should be broken into genotype filtering and expression probe filtering.
fdr(x) will return a numeric vector of plug-in FDR estimates corresponding to probe:association tests as ordered in the fullreport of a *Cis container. More metadata should be attached to the output of this function.
exFilter may seem redundant with smFilter, but its existence allows simpler management of multitissue expression archives (which may have several records per individual) with germ line genotype data (which will have only one record per individual). In this setting, use exFilter to select records for the tissue of interest; this will occur early in the smlSet generation process.

Value

an instance of mcwBestCis
best.trans.eQTLs

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

**Examples**

```r
class("mcwBestCis")
## Not run:
best.cis.eQTLs(chrnames="20")
## End(Not run)
```

---

**best.trans.eQTLs**

*collect strongest trans SNP-gene associations in a buffer of size K genes per SNP*

**Description**

collect strongest trans SNP-gene associations in a buffer of size K genes per SNP

**Usage**

```r
best.trans.eQTLs(smpack, rhs, genechrnum, snpchrnum, K = 20, 
targdirpref = "tsco", batchsize = 200, radius = 2e+06, genequeryprefix = "", 
snploadprefix = "chr", snplocprefix = "chr", geneannopk, snpannopk, 
exFilter = function(x) x, smFilter = function(x) x, 
geneApply = lapply, SSgen = GGBase::getSS)
```

**Arguments**

- `smpack` character string naming a package from which `sm1Set-class` instances can be generated using `getSS`
- `rhs` passed to `snp.rhs.tests` for covariate or stratification adjustments; for permutation analysis, covariates should be handled via `regressOut`
- `genechrnum` character vector of chromosome identifiers for genes, typically `as.character(1:22)` for somatic genes in human studies
- `snpchrnum` specific chromosome identifier for all SNP to be analyzed
- `K` the size of the buffer: scores will be recorded for the most strongly associated K genes for each SNP
- `targdirpref` character string where buffer data will be held in ff archives
- `batchsize` passed to `ffrowapply` as scores are filtered from comprehensive testing to fill the buffer
- `radius` numeric: for same-chromosome tests, tests will not be performed for SNP-gene combinations with base-pair proximity smaller than radius
- `genequeryprefix` string: used when the numeric chromosome identifier requires a prefix like ‘chr’ for annotation query resolution on gene location
- `snploadprefix` string: used when the package identified in `smpack` requires a prefix to the `snpchrnum` token for `getSS` retrieval of `sm1Set` instance
**bindmaf**

bind testing metadata to a best.cis.eQTLs result

### Description

bind testing metadata to a best.cis.eQTLs result

---

**snplocprefix**  
string: used when the numeric chromosome identifier requires a prefix like ‘chr’ for annotation query resolution on SNP location

**geneannopk**  
package to be used for CHRLOC and CHRLOCEND queries for genes

**snpannopk**  
package to be used to resolve snplocs calls

**exFilter**  
function returning an smlSet instance, operating on expression component prior to smFilter application and eQTL testing

**smFilter**  
function returning an smlSet instance, operating on the full smlSet

**geneApply**  
lapply-like function, typically mclapply or the like

**SSgen**  
function to be used to create smlSet instance for testing – in general, GGBase::getSS has been used to pull the ExpressionSet and SnpMatrix data from a named package, but in some cases a specialize task is needed to create the desired smlSet. Whatever is passed to SSgen must return an smlSet instance.

---

**Value**

instance of **transManager-class**

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

**Examples**

```r
## Not run:
if (.Platform$OS.type != "windows") {  # ff overwrites failing 5.IX.12
sfilter2 = function(sms, var.cutoff=.5) {
  alliq = apply(exprs(sms),1,IQR)
  qs = quantile(alliq, var.cutoff, na.rm=TRUE)
  sms[ which(alliq > qs), ]
}

thefilt = function(x) GTFfilter( nsFilter2 (clipPCs(x, 1:10), var.cutoff=.95 ), lower=.05 )

tfile = tempfile()
tfold = dir.create(tfile)
t1 = best.trans.eQTLs( "GGdata", ~1, as.character(20:22), "22",  
geneannopk="illuminaHumanv1.db", snpannopk= snplocsDefault(),  
smfilter=thefilt, snploadprefix="", snplocprefix="ch", targdirpref=tfile)

tt1 = transTab(t1)

ttlo = tt1[ order(tt1[,"sumchisq"], decreasing=TRUE), ][1:10,]

ttlo

## End(Not run)
```
Usage

```r
meta.bindmaf(smpackvec=c("GGdata", "hmyriB36"),
             smchr="20", obj, usemaxMAF=FALSE, SSgen=GGBase::getSS)
```

Arguments

- **smpackvec**: a vector of candidate package names (potential `smpack` arguments to `getSS` for metaanalysis across populations or tissues
- **smchr**: the chromosome name as used in the names of the `smList` output for the `getSS` result
- **obj**: an instance of `mcwBestCis-class` generated using the package named in `smpack`
- **usemaxMAF**: if TRUE, label a SNP with maximum MAF observed across populations, otherwise compute the MAF for the combined genotypes across populations represented by the various `smList` instances generated with the `smpackvec` spec.
- **SSgen**: function to be used to create `smList` instance for testing – in general, `GGBase::getSS` has been used to pull the ExpressionSet and SnpMatrix data from a named package, but in some cases a specialize task is needed to create the desired `smList`. Whatever is passed to `SSgen` must return an `smList` instance.

Details

computes the MAF of most highly associated SNP per gene, and distance between that SNP and the transcription limits of the gene, assigning 0 for this if the SNP lies within the transcription limits

Value

a GRanges instance

Note

This will be used to stratify the permuted scores.

Examples

```r
## Not run:
b1 = best.cis.eQTLs(chr="20") # sharply filtered
b1b = bindmaf(obj=b1)
## End(Not run)
```

cgff2dt

`translate the GFF3 from a ciseqByCluster/processgff output into a serialized data.table instance, compute genome-wide plug-in FDR, and update the GFF3 with this FDR`

Description

translate the GFF3 from a ciseqByCluster/processgff output into a serialized data.table instance, compute genome-wide plug-in FDR, and update the GFF3 with this FDR
Usage

cgff2dt(gff3, tiling, addHitTest = TRUE, addcc878 = TRUE)

Arguments

gff3 character string naming a tabix-indexed, bgzipped output of \texttt{gffprocess}
tiling output of \texttt{simpleTiling}
addHitTest logical, telling whether to add a column on coincidence of SNP with the \texttt{gwastagger}
ranges
addcc878 logical, telling whether to add a column on coincidence of SNP with the \texttt{hmm878}
ranges, using the inferred chromatin state as factor level

Note

assumes unix utilities zcat, paste and bgzip are available

Examples

```r
##---- Should be DIRECTLY executable !! ----
##-- ==> Define data, use random, 
##--or do help(data=index) for the standard data sets.
## The function is currently defined as
## function (gff3, tiling)
##
## require(foreach)
## require(Rsamtools)
## stopifnot(is(tiling, "GRanges"))
## basen = gsub(".gff3.gz", ",", gff3)
## th = headerTabix(gff3)
## orderedChr = th$seqnames
## lgr = foreach(i = 1:length(tiling)) %dopar% {
## gc()
## cat(i)
## lk = try(import.gff3(gff3, which = tiling[i]))
## if (inherits(lk, "try-error"))
## lk = NULL
## if (!is.null(lk))
## lk = as.data.table(as.data.frame(lk))
## lk
## }
## bad = sapply(lgr, is.null)
## if (any(bad))
## lgr = lgr[-which(bad)]
## ans = do.call(rbind, lgr)
## ans$snplocs = as.numeric(ans$snplocs)
## ans$ests = as.numeric(ans$ests)
## ans$se = as.numeric(ans$se)
## ans$oldfdr = as.numeric(ans$fdr)
## ans$MAF = as.numeric(ans$MAF)
## ans$dist.mid = as.numeric(ans$dist.mid)
## nperm = length(grep("permS", names(ans)))
## pnames = paste("permScore_", 1:nperm, sep = "")
## for (i in 1:nperm) ans[[pnames[i]]] = as.numeric(ans[[pnames[i]]])
## ans$mindist = as.numeric(ans$mindist)
```
cisAssoc

test for variant-expression associations in cis, using VCF

Description

test for variant-expression associations in cis, using VCF and SummarizedExperiment representations

Usage

cisAssoc(summex, vcf.tf, rhs = ~1,
        nperm = 3, cisradius = 50000,
        genome = "hg19", assayind = 1, lbmaf = 1e-06,
        dropUnivHet = TRUE, doEsts=FALSE)

data(lgeu) # obtains an example SummarizedExperiment

Arguments

summex instance of SummarizedExperiment-class
vcf.tf instance of TabixFile, referring to a tabix-indexed, bgzipped VCF file
rhs formula 'right hand side' for adjustments to be made as snp.rhs.tests is run on each expression vector
nperm number of permutations to be used for plug-in FDR computation
cisradius distance in bp around each gene body to be searched for SNP association
genome tag suitable for use in GenomeInfoDb structures
CisConfig-class

assayind  index of assays (summex) to use for expression data retrieval
lbmaf    lower bound on MAF of SNP to use
dropUnivHet logical, if TRUE, will check for columns of SnpMatrix instance that possess no values other than "NA" and "A/B". See http://www.biostars.org/p/117155/#117270
doEsts   logical, if TRUE, will run snp.rhs.estimates and report beta and standard error

Details

snp.rhs.tests is the workhorse for statistical modeling. VCF content is transformed to the byte-code (which allows for uncertain imputation) and used in fast testing.

Value

a GRanges-class instance with mcols including chisq, permScore...

Note

seqlevelsStyle for summex and vcf.tf content must agree

Author(s)

VJ Carey <stvjd@channing.harvard.edu>

Examples

data(lgeu) # small excerpt from GEUVADIS FPKM
tf20 = TabixFile(system.file("vcf/c20exch.vcf.gz", package="GGtools"))
if (require(VariantAnnotation)) scanVcfHeader(tf20)
lgeue = clipPCs(lgeu[,which(lgeu$popcode=="CEU")], 1:2)
set.seed(4321)
litc = cisAssoc(lgeue, tf20, nperm=2, lbmaf=.05, cisradius=50000)
litc2 = cisAssoc(lgeue, tf20, nperm=2, lbmaf=.05, cisradius=50000, doEsts=TRUE)
litc$pifdr = pifdr(litc$chisq, c(litc$permScore_1, litc$permScore_2))
litc[which(litc$pifdr < .01)]
Slots

snapack: character string identifying package holding the expression and genotype data; see getSS
genome: character string identifying genome build in use
rhs: Object of class "formula" right hand side for calls to snp.rhs.tests
nperm: Object of class "integer" number of permutations for plug in FDR
folderStem: Object of class "character" string used for scratch space folders, relative to current folder
radius: Object of class "integer" radius of search
shortfac: Object of class "integer" scores are scaled up by this factor so that precision can be retained in short integer representation
chrnames: Object of class "character" string identifying chromosome label used in gene annotation retrieval – typically length 1
smchrpref: Object of class "character" prefix to be attached to chromosome label in chrnames to pick out the element of smlSet-class instance used in testing
gchrpref: Object of class "character" prefix on chrnames token to be used for gene location retrievals
schchrpref: Object of class "character" prefix on chrnames token to be used with SNPlocs package for retrieval of SNP locations
geneApply: Object of class "function" iterator over genes, could be lapply or mclapply
geneannopk: Object of class "character" Bioconductor annotation package for gene locations, typically for expression array
snpannopk: Object of class "character" Bioconductor dbSNP annotation package
smFilter: Object of class "function" function to be applied to smlSet instance that yields an smlSet instance with required contents; could apply MAF restriction for example by calling MAFfilter
exFilter: Object of class "function" function that is run right after smlSet is materialized, permitting replacement or filtering of expression data, when, for example, the ExpressionSet includes multiple tissue types
keepMapCache: Object of class "logical" for enhancing processing of gene-SNP cis mapping with a global cache
SSgen: Object of class "function" function that accepts name of an expression+SnpMatrix package (as generated by externalize), a chromosome tag (chrnames prefixed by smchrpref), and a function, and returns an smlSet instance
excludeRadius: Object of class "integerOrNULL" which will determine what interval about the gene is excluded for cis testing; 0 should exclude all within-gene SNP, but needs testing
estimates: Object of class "logical" if TRUE, estimates and standard errors (expanded and reduced in storage as a short int, using shortfac) are generated and retained
extraprops: Object of class "function" this function is applied to the cisScores output before it is returned, to bind additional metadata to the ranges if desired. Defaults to function(x)x.
useME: Object of class "logical" if TRUE, use the statistics generated by Matrix_eQTL_engine for association testing.
MEpval: Object of class "numeric" used if useME slot is set to TRUE: p-value output threshold for retaining association test statistic generated by Matrix_eQTL_engine; defaults to 0.5. Higher values lead to higher volumes and longer times to completion.
Methods

chrnames signature(x = "CisConfig"): ...
chrnames<- signature(object = "CisConfig", value = "character"): ...
estimates signature(x = "CisConfig"): ...
estimates<- signature(object = "CisConfig", value = "logical"): ...
excludeRadius signature(x = "CisConfig"): ...
excludeRadius<- signature(object = "CisConfig", value = "integer"): ...
exFilter signature(x = "CisConfig"): ...
exFilter<- signature(object = "CisConfig", value = "function"): ...
gchrpref signature(x = "CisConfig"): ...
gchrpref<- signature(object = "CisConfig", value = "character"): ...
geneannopk signature(x = "CisConfig"): ...
geneannopk<- signature(object = "CisConfig", value = "character"): ...
geneApply signature(x = "CisConfig"): ...
geneApply<- signature(object = "CisConfig", value = "function"): ...
initialize signature(.Object = "CisConfig"): ...
keepMapCache signature(x = "CisConfig"): ...
keepMapCache<- signature(object = "CisConfig", value = "logical"): ...
radius signature(x = "CisConfig"): ...
radius<- signature(object = "CisConfig", value = "integer"): ...
rhs signature(x = "CisConfig"): ...
rhs<- signature(object = "CisConfig", value = "function"): ...
schrpref signature(x = "CisConfig"): ...
schrpref<- signature(object = "CisConfig", value = "character"): ...
shortfac signature(x = "CisConfig"): ...
shortfac<- signature(object = "CisConfig", value = "integer"): ...
show signature(object = "CisConfig"): ...
smchrpref signature(x = "CisConfig"): ...
smchrpref<- signature(object = "CisConfig", value = "character"): ...
smFilter signature(x = "CisConfig"): ...
smFilter<- signature(object = "CisConfig", value = "function"): ...
sspannopk signature(x = "CisConfig"): ...
sspannopk<- signature(object = "CisConfig", value = "character"): ...
SSgen signature(x = "CisConfig"): ...
SSgen<- signature(object = "CisConfig", value = "function"): ...

Examples

showClass("CisConfig")
ciseqByCluster  

end-to-end cluster-based cis-eQTL search, and allied utilities

Description

description of function

Usage

ciseqByCluster(cl, pack = "yri1kgv", outprefix = "yrirun", finaltag = "partyri100k", chromsToRun = 1:22, targetfolder = "/freshdata/YRI_3", radius = 100000L, nperm = 3L, ncoresPerNode = 8, numPCtoFilter = 10, lowerMAF = 0.02, geneannopk = "lumiHumanAll.db", snpannopk = "SNPlocs.Hsapiens.dbSNP144.GRCh37", smchrpref = "chr", tmpForSort = "/tmp", numtiles = 200, postProcCores = 12, reqlist = NULL)

Arguments

cl     instance of S3 cluster class from parallel package
pack   character string naming package to which getSS can be applied to generate sm1Set-class instances
outprefix character string used to prefix names of output GFF3 files
finaltag character string used to prefix names of final amalgamated GFF3 and data.table instances
chromsToRun numeric tags of chromosomes to be analyzed
targetfolder character string naming folder where GFF3 will be deposited
radius extent of search around gene model in bp
nperm number of permutations for plug-in FDR computation (usually a small integer)ncoresPerNode number of cores for multicore testing: chromosomes map to nodes, genes map to cores
numPCtoFilter number of PCs to be removed through clipPCs
lowerMAF lower bound on MAF of SNP to be included for testing
geneannopk character string naming Bioconductor package with annotation for expression probe identifiers
snpannopk character string naming Bioconductor package with annotation for SNP locations
smchrpref character prefix converting chromsToRun elements to basenames of rda files harboring SnpMatrix instances
tmpForSort the assembly of final resources employs unix sort, and substantial temporary space can be required; this parameter tells where the temp files will reside
numtiles number of tiles into which the genome in use will be sliced for parallel processing in final assembly
postProcCores numeric establishing number of cores to use for final assembly of annotated output
reqlist rescue request, see Details section
**Details**

purpose is to maximize throughput of cis-eQTL testing in a two-level concurrent computing environment, where a cluster as defined in package parallel has nodes to which half-chromosomes will be dispatched; each node is assumed to be multicore and genes are mapped to cores during the iteration process.

the reqlist parameter consists of a list of elements (chromosome name, subchromosome token, and handler) to be used for completing a partial run

**Value**

a set of GFF3 files encoding all cis associations with location and various metadata

**See Also**

gffprocess, cgff2dt

**Examples**

#none yet

---

**cisRun-class**  
*Class “cisRun”*

**Description**

manage results of All.cis eQTL analysis

**Objects from the Class**

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

**Slots**

- `seqnames`: Object of class "Rle"  
- `ranges`: Object of class "IRanges" – will document the range searched for each probe/gene – therefore the values returned are addresses of gene extent minus/plus radius at each end  
- `strand`: Object of class "Rle"  
- `elementMetadata`: Object of class "DataFrame"  
- `seqinfo`: Object of class "Seqinfo"  
- `metadata`: Object of class "list"  

**Extends**

Methods
No methods defined with class "cisRun" in the signature.

Note
intent is to simplify output of cis eQTL testing in a GRanges instance

Author(s)
VJ Carey <stvjc@channing.harvard.edu>

Examples
showClass("cisRun")

collectBest given a collection of All.cis outputs (cisRun instances) compute FDRs for various filterings

Description
given a collection of All.cis outputs (cisRun instances) compute FDRs for various filterings

Usage
collectBest(fns,
  targetname = "harvest",
  mafs = c(0.01, 0.02, 0.025, 0.03333, 0.05, 0.075, 0.1),
  hidists = c(10000, 25000, 50000, 75000, 1e+05, 250000), interimSaves=FALSE)

collectFiltered( fns, targetname="harvest",
  mafs = c(.01, .02, .025, .03333, .05, .075, .1),
  hidists = c(10000, 25000, 50000, 75000, 100000, 250000),
  filterFun = cis.FDR.filter.best, filtApplier=lapply,
  interimSaves=FALSE)

Arguments
  fns names of .rda with the cisRun outputs
  targetname basename of rda file to be emitted
  mafs lower bounds on MAF for filtering
  hidists upper bounds on cis radius for filtering
  filterFun function like GGtools::cis.FDR.filter.best
  filtApplier function like lapply
  interimSaves logical, if TRUE save list at each maf/dist transition

Details
pifdr is repeatedly used to generate conditional plugin FDR for different filtering criteria
collectBest

Value

A list of lists is written to disk incrementally, as the job can be long running.

Note

This is the workhorse of sensitivity analysis. Permits counting of genes with eQTL at selected FDR for various criteria on cis radius and MAF.

Examples

```r
## Not run:
# contents of fns are two chromosomes of cis runs for CEU
fns = dir(system.file("rdas", package="GGtools"), full=TRUE)
cc = collectBest(fns, mafs=c(.01, .05), hidists=c(10000, 50000))
sapply(cc, sapply, function(x) sum(x$fdr <= 0.01))
# this tells us which to keep
kp = cc[["0.05"]][["50000"]]
kp = kp[kp$fdr <= 0.01,]
# the hits are in the table above; the following function
# retrieves the initial scores giving rise to the filtered hits
pullHits = function(fns, atts) {
  tmp = lapply(fns, function(x) get(load(x))
  kl = lapply(tmp, function(x) paste(names(x), x$snp, sep=":"))
  attk = paste(atts$genes, atts$bestsnp, sep=":")
  tmp = lapply(1:length(tmp), function(x) tmp[[x]][[x]][match( attk, kl[[x]], nomatch=0 )])
  curans = do.call(c, lapply(tmp, as, "GRanges"))
  neword = match( attk, paste(names(curans), curans$snp, sep=":"))
  newfdr = atts$fdr[neword]
  curans$newfdr = newfdr
  curans
}
pullHits( fns, kp )
# after executing code in example for All.cis (protected by dontrun)
# and running save(f1, file="f1.rda"), the following will work
# genewise max score
cf1 = collectFiltered("f1.rda", mafs=.02, hidists=25000, targetname="gwise")
# SNPwise scores, all
cf2 = collectFiltered("f1.rda", mafs=.02, hidists=25000, targetname="swise",
  filterFun = cis.FDR.filter.SNPcentric.complete )
# SNPwise scores, best per SNP when SNP is cis to multiple genes
cf3 = collectFiltered("f1.rda", mafs=.02, hidists=25000, targetname="swise2",
  filterFun = cis.FDR.filter.SNPcentric )
## End(Not run) # end dontrun
```
**concatCis**

*combine a list of cisRun instances to a single instance*

**Description**

combine a list of cisRun instances to a single instance, with ad hoc metadata combination

**Usage**

```r
catCis(crl)
```

**Arguments**

- `crl`: list of instances of `cisRun-class`

**Details**

the metadata for the output is a list with elements `call` and `config` as required, derived from first element of the input; the `extras` component holds the metadata elements of the remaining input list elements

**Value**

a cisRun instance

**Examples**

```r
## Not run:
example(All.cis)
catCis(f1, f1)
## End(Not run)
```

---

**EqAppr-class**

*Class* "EqAppr"

**Description**

Manage the appraisal of an eQTL search

**Objects from the Class**

Objects can be created by calls of the form `new("EqAppr", ...)`, or via `buildEqAppr()`

**Slots**

- `meta`: Object of class "ApprMeta" basic descriptive information about source analysis
- `sens`: Object of class "ApprSens" outputs of sensitivity analysis
- `pruned`: Object of class "ApprRes" outputs of appraisal for LD-pruned predictions
- `unpruned`: Object of class "ApprRes" outputs of general appraisal without LD pruning
Methods

callfig signature(x = "EqAppr", ind = "character"): Additional arguments can be specified:

  ind  index or name of model to be plotted
  hfudgetxt  distance to move rendered fractions relative to bin x coordinate
  tickend  maximum value at which axis tick mark will be plotted
  tickgap  axis will have ticks at seq(0, tickend, tickgap)
  ylim  ylim setting for rendering
  xlim  xlim setting for rendering
  fraccex  cex setting for fraction rendering
  fuselast  if data are sparse in entries of high predicted probability, you can fuse the nearby
cells up to the end – pick fuselast=2 for final 2 cells, 3 for final 3 and so on

getModnames signature(x = "EqAppr"): obtain the list of strings used to name different appraisal models

getPruned signature(x = "EqAppr"): get the ApprRes instance corresponding to the LD-
pruned loci

getUnpruned signature(x = "EqAppr"): get the ApprRes instance for all loci in use

getSens signature(x = "EqAppr"): get sensitivity analysis results

show signature(object = "EqAppr"): concise report

Examples

showClass("EqAppr")

eqBox  descriptive plot of expression against genotype for cisAssoc results

Description

descriptive plot of expression against genotype for cisAssoc results

Usage

eqBox(gene, snp, se, tf, radius=1e6, genome="hg19", ...)
eqDesc(gene, snp, se, tf, radius=1e6, genome="hg19", ...)

Arguments

gene  identifier of gene in SummarizedExperiment se, must be present in rownames(se)
snp  identifier of variant in VCF referenced by tf
se  SummarizedExperiment instance
tf  TabixFile reference for a VCF file that has been bgzipped and tabix-indexed
radius  in order to limit the VCF import, we filter variants to those within a radius
around the selected gene – it is assumed that the selected snp will exist in that
region (we can’t extract SNP by name from vcf...)
genome  a simple genome identifier tag
...  (not used with eqDesc) will embellish plot; xlab and ylab already taken care of
Details

The chromosome names in the VCF and the seqlevelsStyle of the Summarized Experiment must match.

Value

eqBox produces a boxplot for all categories (including NA) of genotype. eqDesc tabulates the genotype calls in categories.

Examples

```r
if (require(VariantAnnotation)) {
  data(lgeu)
  lgeue = lgeu[, which(lgeu$popcode == "CEU")]
  tf20 = TabixFile(system.file("vcf/c20exch.vcf.gz", package="GGtools"))
  eqBox("ENSG00000126005.10", "rs2425038", lgeue, tf20)
}
```

Description

support for sensitivity analyses related to eQTL enumerations

Usage

```r
eqsens_dt(dtab, filtgen = filtgen.maf.dist, by = c("pairs", "snps", "probes")[1],
          targfdrs = c(0.05, 0.01, 0.005),
          parmslist = list(mafs = c(0.025, 0.05, 0.075, 0.1, 0.125),
                           dists = c(1000, 5000, 10000, 25000, 50000, 1e+05)),
          renameChisq = TRUE)
```

Arguments

dtab data.table instance as generated by converting a cisScores GRanges. In general it will need to have column names score, MAF, mindist, and columns with names permScore_1, ....
filtgen a function that generates a closure. The function returned by filtgen will be a function of one argument that filters an input data.table. The environment of the returned function will possess bindings used to define the filtering operation. filtgen.maf.dist, documented here, is a working example.
The objective is to generate data for tabulation or visualization of sensitivity analyses, and the scope of sensitivity analysis can be established in various ways. This software is mostly intended as a framework.

Value

`eqsens_dt` returns a data.frame instance with enumerations of eQTL at various FDR thresholds for various settings of tuning parameters

`update_fdr_filt` revises (using `pifdr`) the `fdr` field of an input data.table instance using variable `score` as observed value, and permuted values furnished by the variables named with `permScore` as leading substring

Note

To do: allow filtering on the number of permutations to be used in FDR calculation.

Author(s)

VJ Carey <stvjc@channing.harvard.edu>
eqtlTests

compute association statistics between all probes and SNP in an smlSet instance

description
compute association statistics (or point estimates and standard errors) between all probes and SNP in an smlSet instance, using out-of-memory storage; the basic test statistics are generated by the snp.rhs.tests function of the snpStats package

usage

```r
eqtlTests(smlSet, rhs = ~1 - 1, runname = "foo", targdir = "foo", geneApply = lapply, shortfac = 100, checkValid = TRUE, useUncertain = TRUE, glmfamily = "gaussian", doFFSUMM = FALSE)
eqtlEstimates(smlSet, rhs = ~1 - 1, runname = "foo", targdir = "foo", geneApply = lapply, shortfac = 10000, checkValid = TRUE, useUncertain = TRUE, glmfamily = "gaussian")
```

arguments

- **smlSet**: instance of *smlSet*
- **rhs**: fragment of a standard formula, minus a dependent variable (i.e., starts with tilde); bindings will be sought in pData(smlSet)
- **runname**: string used to identify output ff files
- **targdir**: string naming the folder where ff outputs will reside
- **geneApply**: analog to lapply to drive iteration over probes
- **shortfac**: ff contents will be multiplied by this quantity and stored as short integers
- **checkValid**: logical, will apply validObject to smlSet if TRUE
- **useUncertain**: logical, passed as uncertain parameter to snp.rhs.tests to specify whether uncertain genotypes will be used (as 'dosage' in GLM fitting)
- **glmfamily**: family specification for snp.rhs.tests
- **doFFSUMM**: logical indicating whether ff archives will be retained for col.summary outputs for SNPs
Details

The purpose of the `eqtlTests` function is to allow very substantial eQTL search processes to occur with R. For several million SNP and tens of thousands of probes, the storage of test results requires attention to parsimony. The storage occurs out of memory, using the ff package, and employs short integers to represent chi squared statistics. These are scaled up prior to storage, and will be scaled down prior to use.

`eqtlEstimates` will use compact storage for both the point estimates and standard errors of association estimated under an additive genetic model.

Note: `snp.rhs.estimates` will emit a warning whenever the parameters are not estimable. These warnings are suppressed by temporary setting of `options()[`'warn']` to zero.

Value

returns an instance of `eqtlTestsManager`

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Examples

```r
hm2ceuSMS = getSS("GGtools", c("20"), renameChrs=c("chr20"))
library(illuminaHumanv1.db)
cptag = get("CPNE1", revmap(illuminaHumanv1SYMBOL))
indc = which(featureNames(hm2ceuSMS) == cptag[1])
#
# get a set of additional genes on chr20
all20 = get("20", revmap(illuminaHumanv1CHR))
g20 = unique(c(all20[1:10], cptag))
#
hm = hm2ceuSMS[probeId(g20),] # reduce problem
td = tempdir()
curd = getwd()
setwd(td)
time.lapply = unix.time(e1 <- eqtlTests( hm, ~male ))
time.lapply
e1
# best chisq(1) for CPNE1
topFeats(probeId(cptag), e1)
setwd(curd)
```

Description

use MatrixEQTL computations and statistics as a back end to GGtools eqtlTests
Usage

eqtlTests.me(smlSet, rhs = ~1, runname = "20",
        targdir = "cisScratch.me", pvot = 0.5, geneApply = lapply,
        shortfac = 100, checkValid = TRUE, useUncertain = TRUE,
        glmfamily = "gaussian", scoretx = abs,
        matrixEQTL.engine.control =
            list(output_file_name = "/dev/null",
                useModel = modelLINEAR,
                errorCovariance = numeric(),
                verbose = FALSE,
                pvalue.hist = FALSE),
        snpSlicedData.control = .slicedDataDefaults,
        geneSlicedData.control = .slicedDataDefaults,
        covarSlicedData.control = .slicedDataDefaults,
        covariates_file_name = character())

Arguments

smlSet instance of smlSet-class
rhs formula for adjustment of tests for covariates or stratification, see snp.rhs.tests
runname tag used to distinguish emitted files
targdir folder where ff archives will reside
pvot setting for pvOutputThreshold in Matrix_eQTL_engine
geneApply lapply-like function for iteration over genes, mclapply is suitable when in multicore environments
shortfac scaling factor to increase precision when test results are stored as short ints in ff
checkValid logical to check validity of input smlSet
useUncertain logical informing snp.rhs.tests that imputed real-valued B allele counts may be present among genotype data
glmfamily family specification for snp.rhs.tests
scoretx function to be applied to MatrixEQTL statistics. Defaults to abs, for signless association testing
matrixEQTL.engine.control list of parameters passed to Matrix_eQTL_engine
snpSlicedData.control list of parameters used to define SlicedData-class instances
geneSlicedData.control list of parameters used to define SlicedData-class instances
covarSlicedData.control list of parameters used to define SlicedData-class instances
covariates_file_name if covariates are to be used with MatrixEQTL testing engine, they reside in this file. regressOut can be used to avoid this if plug-in FDR are to be used

Details

provisional interface
**eqtlTestsManager-class**

Value

see eqtlTests

Note

intended for simple comparisons

References

Shabalin et al Bioinformatics (OUP) 2012

Examples

```r
if (require(MatrixEqTL)) {
  g22 = nsfilter( chrFilter( getSS("GGdata", "22"), "22" ), var.cutoff = .8 )
  m22 = eqtlTests.me(g22)
}
```

---

**eqtlTestsManager-class**

*Class* "eqtlTestsManager"

Description

manage out-of-memory elements of an eQTL search

Objects from the Class

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

Slots

- `fffile`: Object of class "ff_matrix" chisquared statistics stored as short ints in ff out of memory file
- `call`: Object of class "call" audit of creation call
- `sess`: Object of class "ANY" session info structure at time of creation
- `exdate`: Object of class "ANY" date at time of creation
- `shortfac`: Object of class "numeric" number by which chisq stats are multiplied to allow recovery of precision
- `geneanno`: Object of class "character" string naming annotation package relevant for probe identifier translation
- `df`: Object of class "numeric" degrees of freedom of chisq stats
- `summaryList`: Object of class "list" list of genotype statistical summaries
Methods

- `signature(x = "eqtlTestsManager", i = "ANY", j = "ANY", drop = "ANY")`: extract chisq statistics properly rescaled from short int to double
- `show signature(object = "eqtlTestsManager")`: concise report
- `topFeats signature(feat = "probeId", mgr = "eqtlTestsManager")`: extract highest scores for SNP associated with given probeId
- `topFeats signature(feat = "rsid", mgr = "eqtlTestsManager")`: extract highest scores for probes associated with given SNP

Note

instances are created by `eqtlTests`

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Examples

```r
showClass("eqtlTestsManager")
```

---

ExpressionSet instance for illustrating integrative smlSet container

Description

ExpressionSet instance for illustrating integrative smlSet container

Usage

data(eset)

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData ..Formal class 'MIAME' [package "Biobase"] with 13 slots .. ..@ name : chr "" .. ..@ lab : chr "" .. ..@ contact : chr "" .. ..@ title : chr "" .. ..@ abstract : chr "" .. ..@ url : chr "" .. ..@ pubMedIds : chr "" .. ..@ samples : list() .. ..@ hybridizations : list() .. ..@ normControls : list() .. ..@ preprocessing : list() .. ..@ other : list() .. ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. .. ..@ .Data:List of 2
Details

Expression data harvested in 2007 from GENEV AR

Examples

data(eset) # yields ExpressionSet instance called ex
getCisMap create, using Bioconductor annotation resources, a structure that enumerates SNP in the vicinity of (‘cis’ to) genes

Description
create a structure that enumerates SNP in the vicinity of (‘cis’ to) genes

Usage
getCisMap(radius = 50000, gchr = "20", schr = "ch20", geneannopk = "illuminaHumanv1.db", snpannopk = snplocsDefault(), as.GRangesList = FALSE, excludeRadius=NULL)

Arguments
radius How far, in bases, up or down stream from the asserted coding region limits to include SNP
gchr the token to be used to acquire locations for probes on a specified chromosome, using revmap([dbpk]CHR)
schr the token to be used to acquire locations for SNP on a specified chromosome, using snplocs
geneannopk character string naming a Bioconductor .db expression chip annotation package; or a complex string with first part naming a Bioconductor FDb.* annotation package, colon separator, and a second string naming the getter hook that when called returns a GRanges with names corresponding to features and ranges corresponding to feature extents. For example "FDb.InfiniumMethylation.hg19:get27k" is valid. Note that in this case, gchr must have prefix "chr".
snpnopk character string naming a Bioconductor SNPlocs.* SNP metadata package
as.GRangesList logical telling whether a GRangesList should be returned
excludeRadius numeric or NULL: radius of interval around gene extent from which SNP will be excluded, required to be less than radius

Details
This is a utility that the developer would rather not export. The complexity of harmonizing queries among probe and SNP annotation resources leads to a somewhat fragile product. Users who have their own gene ranges and SNP locations can examine the namelist component of the output of the default call to see what is expected for the *.cis.eQTLs function. For the set of chromosomes to be analyzed, there will be a list of chromosome specific namelist-like lists.

Value
Instance of cisMap class, which will retain SNP location, gene range, and radius information for auditing.
gffprocess

Examples

```r
## Not run:
getCisMap()

## End(Not run)
```

gffprocess  transform a collection of gff3 into a single tabix-indexed gff3

Description

process a collection of gff3 into a single tabix-indexed gff3 using unix utilities to minimize memory requirements

Usage

```r
gffprocess(basename = "fullyri100k", n_in = 44, headpatt = ".1A", tmpForSort = "/freshdata/tmp")
```

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>basename</td>
<td>basename of the resulting .gff3.gz(tbi) file</td>
</tr>
<tr>
<td>n_in</td>
<td>number of gff3 files to be processed – used for consistency check against length(dir(patt=&quot;gff3&quot;))</td>
</tr>
<tr>
<td>headpatt</td>
<td>pattern to identify file for the 'top' gff3 to be used as the contents are concatenated</td>
</tr>
<tr>
<td>tmpForSort</td>
<td>name of a folder that unix sort will use as a temporary directory</td>
</tr>
</tbody>
</table>

Details

The purpose of this utility is to exploit unix shell tools to unify a collection of gff3 files generated using `All.cis`. The use case is cluster-based per-chromosome (or split chromosome) cis-testing generating a large number of GRanges that are transformed to gff3 to allow targeted interrogation.

Value

Used for side effects. Will fail if any unix utility call via `system()` returns nonzero value. Returns NULL otherwise.

Author(s)

VJ Carey <stvjc@channing.harvard.edu>
gwSnpTests

execute a series of tests for association between genotype and expression

Description
execute a series of tests for association between genotype and expression

Usage
gwSnpTests(sym, sms, ...)
topSnps(x, n=10)

Arguments
sym instance of probeId or genesym
sms instance of smlSet-class
x instance of gwSnpScreenResult
n integer, number of test results to be reported, sorted decreasing from the most significant
... not used

Details
The plot method for gwSnpScreenResult instances takes a second argument, the name of a Bioconductor SNPlocs package.

Value
an instance of the gwSnpScreenResult class, to be examined by topSnps

Note
The most basic application yields one d.f. chi-squared statistics based on score tests.

Author(s)
VJ Carey <stvjc@channing.harvard.edu>

Examples
s20 = getSS("GGtools", "20")
t1 = gwSnpTests(genesym("CPNE1")-male, s20)
topSnps(t1)
## Not run:
plot(t1, snplocDefault())
## End(Not run)
Description

labeled GRanges with ChromHMM chromatin states for GM12878

Usage

data(hmm878)

Format

The format is:
Formal class 'GRanges' [package "GenomicRanges"] with 6 slots
.. ..@ seqnames : Formal class 'Rle' [package "IRanges"] with 4 slots
.. .. ..@ values : Factor w/ 23 levels "chr1","chr2",...: 1 2 3 4 5 6 7 8 9 10 ...
.. .. ..@ lengths : int [1:23] 54467 46499 37617 25155 30071 34846 29420 24506 24123 27263 ...
.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
.. ..@ ranges : Formal class 'IRanges' [package "IRanges"] with 6 slots
.. .. ..@ start : int [1:571339] 10001 10601 11138 11738 11938 12138 14538 20338 22138 22938 ...
.. .. ..@ width : int [1:571339] 600 537 600 200 200 2400 5800 1800 800 4000 ...
.. .. ..@ NAMES : NULL
.. .. ..@ elementType : chr "integer"
.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
.. .. @ strand : Formal class 'Rle' [package "IRanges"] with 4 slots
.. .. ..@ values : Factor w/ 3 levels "+","-","*": 3
.. .. ..@ lengths : int 571339
.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
.. .. @ elementMetadata: Formal class "DataFrame" [package "IRanges"] with 6 slots
.. .. ..@ rownames : NULL
.. .. ..@ nrows : int 571339
.. .. ..@ listData : List of 4
.. .. .. ..$ name : chr [1:571339] "15_Repetitive/CNV" "13_Heterochrom/lo" "8_Insulator" "11_Weak_Txn"
.. .. .. ..@ score : num [1:571339] 0 0 0 0 0 0 0 0 0 0 ...
.. .. .. ..$ itemRgb : chr [1:571339] "#F5F5F5" "#F5F5F5" "#F5F5F5" "#99FF66" "#99FF66" ...
.. .. .. ..$ thick : Formal class 'IRanges' [package "IRanges"] with 6 slots
.. .. .. .. ..@ start : int [1:571339] 10001 10601 11138 11738 11938 12138 14538 20338 22138 22938 ...
.. .. .. .. ..@ width : int [1:571339] 600 537 600 200 200 2400 5800 1800 800 4000 ...
.. .. .. .. ..@ NAMES : NULL
.. .. .. .. ..@ elementType : chr "integer"
.. .. .. .. ..@ elementMetadata: NULL
.. .. .. .. ..@ metadata : list()
.. .. .. ..@ elementType : chr "ANY"
.. .. .. ..@ elementMetadata: NULL
metadata: list()

seqinfo: Formal class 'Seqinfo' [package "GenomicRanges"] with 4 slots

.. .. ..@ seqnames: chr [1:23] "chr1" "chr2" "chr3" "chr4" ...

.. .. ..@ seqlengths: int [1:23] 249250621 243199373 198022430 191154276 180915260 171115067 159138663 146364022 141213431 135534747 ...

.. .. ..@ is_circular: logi [1:23] FALSE FALSE FALSE FALSE FALSE FALSE ...

.. .. ..@ genome: chr [1:23] "hg19" "hg19" "hg19" "hg19" ...

.. @ metadata: List of 1

..$ url: chr "http://genome.ucsc.edu/cgi-bin/hgFileUi?g=wgEncodeBroadHmm&db=hg19"

Details

acquired using rtracklayer import from the bed file given at metadata(hmm878)["url"]

Source

see details

References


Examples

data(hmm878)
table(hmm878$name)

pifdr

utility for computing plug-in FDR

Description

utility for computing plug-in FDR

Usage

pifdr( obs, perms, legacy=FALSE, trimToUnit = TRUE, ... )

Arguments

obs observed association scores
perms vector of association scores under permutation; length should be integer multiple of length(obs)
legacy logical, if TRUE, use the approximate version of pifdr() available before 12/30/2013, with additional arguments if desired
trimToUnit logical, if TRUE, values greater than 1 are replaced by 1. Such values can occur, for example, with relatively small sample sizes.
...
extra arguments passed if legacy is TRUE
Details
Revised 12/30/13 to employ hist() to rapidly bin the permuted values.

Use legacy=TRUE to obtain the approximate implementation, for which the following remarks held:
“As currently implemented the algorithm is quadratic in length(obs). While it is possible to get a unique FDR value for every element of obs, an approximate approach yields practically identical precision and by default this will be used for obs with length 2000 or more. In this case, approx is used with rule=2 to interpolate from the grid-based FDR estimates back to the data values.”
Additional parameters npts and applier may be supplied if legacy is set to TRUE.

npts defined the number of points spanning the range of obs to be used for a lossy grid-based computation only used if length(obs)>npts.
applier is to be an sapply-like function.

Value
vector of plug-in FDR estimates congruent to obs

References
Hastie Tibshirani and Friedman Elements of Statistical Learning ch 18.7

Examples
set.seed(1234)
op = par(no.readonly=TRUE)
par(mfrow=c(2,2))
X = c(rchisq(30000,1),rchisq(300,10))
Y = rchisq(30300*3,1)
qqplot(Y, X, xlab="null", ylab="observed")
hist(pp <- pifdr(X,Y), xlab="plug-in FDR", main=" ")
library(multtest)
rawp = 1-pchisq(X, 1)
MT <- mt.rawp2adjp(rawp)
MT2 = MT[[1]][order(MT[[2]]),]
plot(MT2[,"BH"], pp, xlab="BH FDR", ylab="plug-in FDR")
par(op)
Usage

```r
binnedQQ(dt, nxbins=20,
    ylim=c(0,76), xlim=c(0,30), end45=5, thrs=c(0,.001,.005,.01,.05),
    tempmar = c(6,4,4,5), ...)
qqhex(sco, p1, p2, fdr, nxbins = 20, thrs = c(0, 0.001, 0.005, 0.01, 0.05))
binqq(qqob, ylim = c(0, 76), xlim = c(0, 30), end45=5, ...)
```

Arguments

dt  a `data.table` instance with association scores and scores obtained under permutation along with FDR, as returned by `cgff2dt` or `ciseqByCluster`
sco  numeric vector of observed statistics
p1  realization of null distribution for sco, independent of p2 and p3
p2  realization of null distribution for sco, independent of p1 and p3
p3  realization of null distribution for sco, independent of p1 and p2
fdr  vector of FDR associated with elements of sco
nxbins  number of bins to be used for samples from the null distribution
thrs  vector of thresholds in FDR to be used for ruling the plot
qqob  for binhex(), output of qqhex
ylim  vertical limits of rendering
xlim  horizontal limits of rendering
end45  a segment is drawn from (0,0) to (end45,end45) to depict the line of identity
tempmar  numerical vector with 4 elements serving as a temporary setting of the mar parameter of `par`
...
  not currently used

Value

for qqhex, a list with elements

hb  output of `hexbin`
thrs  vector of input thrs
scothrs  vector of observed statistics corresponding to FDRs in thrs

Examples

```r
opar = par(no.readonly=TRUE)
set.seed(123)
x = c(rchisq(9000,1), rchisq(1000,12))
nn = lapply(1:3, function(x) rchisq(10000,1))
fd = pifdr(x, unlist(nn))
qqh = qqhex(x, nn[[1]], nn[[2]], nn[[3]], fd)
par(mar=c(4,4,4,7))
binqq(qqh,xlim=c(0,10), ylim=c(0,20))
mtext(4, "FDR")
par(opar)
```
richNull

bind metadata concerning SNP allele frequency and other aspects of optimized cis-eQTL association to an mcwBestCis instance

Description

bind metadata concerning SNP allele frequency and other aspects of optimized cis-eQTL association to an mcwBestCis instance, to allow conditional FDR computation

Usage

richNull(..., MAFlb = 0.01, npc = 10, radius = 250000, nperm = 1, innerFilt = function(x) x, outerFilt = function(x) x)

meta.richNull(..., MAFlb = 0.01, npc = 10, radius = 250000, nperm = 1, innerFilt = function(x) x, outerFilt = function(x) x)

# internally:
#
# bigfilt = function(z)
# outerFilt(MAFilter(clipPCs(permEx(innerFilt(z)), 1:npc), 1:npc), lower=MAFlb))
#

Arguments

... should provide bindings for smpack and chrnames, which will be used to obtain gene/probe locations; see \texttt{getSS} for information on smpack settings.
meta.richNull allows a vector of smpack values bound to \texttt{smpackvec}

MAFlb lower bound on SNP MAF for null distribution evaluation

npc number of expression principal components to be removed

radius radius used for testing

nperm This establishes how many permutations of expression against genotype will be performed for this process.

innerFilt function immediately applied to generated smlSet instances

outerFilt function applied to generated smlSet instances after clipPCs and MAFilter are applied in that order

Details

The purpose of \texttt{richNull} is to obtain realizations from the permutation distribution of cis-eQTL association statistics, binding information on the characteristics of the optimal results with the scores. This allows us to use conditioning with the realizations from the permutation distribution.

Value

richNull returns a list of nperm mcwBestCis instances with additional metadata bound in

Author(s)

Vince Carey <stvjc@channing.harvard.edu>
sampsInVCF  enumerate samples available in a VCF file

Description

enumerate samples available in a VCF file

Usage

sampsInVCF(tf)

Arguments

tf instance of TabixFile referring to a tabix-indexed VCF

Value

vector of available sample identifiers

Note

This package exports TabixFile for the sake of the example below.

Examples

tf = TabixFile(system.file("vcf/CEU.exon.2010_09.genotypes.vcf.gz", package="GGtools"))
sampsInVCF(tf)

scoresCis  visualize a gene model with cis-eQTL association scores (-log FDR by default) on the basis of a ciseqByCluster data.table output

Description

visualize a gene model with cis-eQTL association scores (-log FDR by default) on the basis of a ciseqByCluster data.table output

Usage

scoresCis(sym = "ORMDL3", cisRun,  
cisannopk = "lumiHumanAll.db", radius = 1e+05, pad = 1000,  
txScore = function(x) -log10(x + (1e-05)), ylim = c(0, 4),  
genometag = "hg19", plot.it = TRUE, laxistag = "-log10 FDR: ", ...)


sensanal

Arguments

  sym         gene symbol to be resolved into probe id using cisannopk
  cisRun      data.table output of ciseqByCluster
  cisannopk   Annotation resource, often a ChipDb instance
  radius      radius to be added to gene model for display, should typically agree with that
               used in the search
  pad         some extra space
  txScore     function that will transform fdr for rendering
  ylim        vertical limits for fdr display
  genometag   coordinates from this build of genome
  plot.it     logical dictating whether plotTracks will be run
  laxistag    token used to tell what units are used on vertical axis
  ...         not used

Value

  a list of Gviz tracks, invisibly returned

See Also

  The Bioconductor workflow on cloud-enabled cis-eQTL analysis.

---

sensanal                        Summarize information from a collection of eQTL searches for sensitivity assessment

Description

  Summarize information from a collection of eQTL searches for sensitivity assessment

Usage

  sensanal(object, fdrbound)

Arguments

  object        instance of sensiCisInput-class
  fdrbound      numeric upper bound on FDR for declarations of eQTL yield

Details

  Sensitivity analysis for cis-eQTL search involves checking effects of scope of search, allele
  frequency filtering, and adjustment for expression heterogeneity on eQTL declarations. In this
  version, we focus on collections of outputs of best.cis.eQTLs, to which the values of tuning parameters
  are bound. These collections are identified in a sensiCisInput-class instance, and the sensanal
  function processes these outputs into a sensiCisOutput-class instance for tabulation and visual-
  ization.
Value

a `sensiCisOutput-class` instance

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

---

`sensiCisInput-class`  
Class "sensiCisInput"

Description

Manage references to collections of cis-eQTL searches for sensitivity analysis.

Objects from the Class

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

Slots

cisMgrFiles: Object of class "character": a vector of filenames, each file is an instance of class `mcwBestCis-class`

cisMgrProperties: Object of class "list" one vector with named elements per element of cisMgrFiles, with components rad, excl, maf, nperm, npc; see details below.

probeannopk: Object of class "character", identifying a bioconductor probe annotation package that can be used to map probe identifiers to other vocabularies or feature value sets

Methods

`sensanal` signature(object = "sensiCisInput", fdrbound = "numeric"): generates an instance of `sensiCisOutput-class` with summarization of sensitivities

`show` signature(object = "sensiCisInput"): concise rendering

Note

This version of sensitivity analysis support is rudimentary and involves manual construction of metadata that should be extractable from analysis outputs. The radius of the cis search (and radius of excluded interior if used) are identified as elements named rad and excl in the cisMgrProperties vectors; additional elements maf, nperm, and npc define the lower bound for minor allele frequency, number of permutations for plug-in FDR computation, and number of principal components removed to adjust for expression heterogeneity in the associated cis-eQTL search.

Examples

`showClass("sensiCisInput")`
sensiCisOutput-class

Class "sensiCisOutput"

Description
This class helps to manage the results from a collection of cis-eQTL searches.

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

Slots
- `byGene`: Object of class "GRanges", organized to provide ranges for genes and their best associated cis SNP
- `bySNP`: Object of class "GRanges" organized to provide easy access to genomic coordinates of SNP found to be most strongly associated with a gene in cis
- `tabAtFDRB`: Object of class "ANY" a flattened table that defines tuning parameters and eQTL yield for a collection of searches
- `input`: Object of class "sensiCisInput": object that describes the files and parameter settings used for the sensitivity analysis
- `thecall`: Object of class "call": the call generating this instance
- `fdrbound`: Object of class "numeric": gives the upper bound on FDR for declaring an eQTL
- `sessionInfo`: Object of class "ANY": describes state of system in which the object was made.

Methods
- `show` signature(object = "sensiCisOutput"): concise rendering with hints

Author(s)
VJ Carey <stvjc@channing.harvard.edu>

Examples
- `showClass("sensiCisOutput")`

---

simpleTiling

create a GRanges with a tiling of the human genome

Description
create a GRanges with a tiling of the human genome

Usage
- `simpleTiling(ntile)`
Arguments
ntile

Examples
### Should be DIRECTLY executable !! ----
###-- ==> Define data, use random,  
###--or do help(data=index) for the standard data sets.

## The function is currently defined as
function (ntile)
{
  require(Homo.sapiens)
  hsi = seqinfo(Homo.sapiens)[paste0("chr", 1:22), ]
  GenomicRanges::unlist(tileGenome(hsi, ntile = 100))
}

tsnplocsDefault

snplocsDefault

name the default SNPlocs.Hsapiens.dbSNP.* package

Description
generate a string naming the default SNPlocs.Hsapiens.dbSNP.* package for use with GGtools

Usage
tsnplocsDefault()

Details
allows centralized specification of SNPlocs resource package

Value
a character string, see example

Examples
tsnplocsDefault()
**strMultPop**

serialization of a table from Stranger’s multipopulation eQTL report

**Description**

serialization of a table from Stranger’s multipopulation eQTL report

**Usage**

```r
data(strMultPop)
```

**Format**

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

- `rsid` a factor with levels...
- `genesym` a factor with levels 37865 39692 ABC1 ABCD2 ABHD4 ACAS2 ...
- `illv1pid` 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**

```r
data(strMultPop)
strMultPop[1:2,]
```
TransConfig-class

Description

Instances from this class can be input to the transScores function to control a trans-eQTL search.

Objects from the Class

Instances from this class can be input to the transScores function to control a trans-eQTL search. Objects can be created by calls of the form `new("TransConfig")`.

Slots

- **snpchr**: Object of class "character" identifies the name of the chromosome harboring SNP that will all be used (subject to filtering by smFilter function) in transcriptome-wide searches for associated transcripts.
- **gbufsize**: Object of class "integer", scores for the top gbufsize genes are retained as the search proceeds.
- **batchsize**: Object of class "integer" used in processing ff-based archives for association scores.
- **smpack**: Object of class "character", tells the name of the installed package used for retrieval of expression-genotype data using `getSS`.
- **rhs**: Object of class "formula", formula used in `snp.rhs.tests`; typically not used. If plug-in FDR is desired, adjustments should be executed in a regressOut call.
- **folderStem**: Object of class "character", name of a folder where interim results are sequestered.
- **radius**: Object of class "integer", defines region around SNP within which genes are considered 'cis' so tests are not conducted.
- **shortfac**: Object of class "integer" see documentation for CisConfig-class.
- **chrnames**: Object of class "character" see documentation for CisConfig-class.
- **smchrpref**: Object of class "character" see documentation for CisConfig-class.
- **gchrpref**: Object of class "character" see documentation for CisConfig-class.
- **schrpref**: Object of class "character" see documentation for CisConfig-class.
- **geneApply**: Object of class "function" see documentation for CisConfig-class.
- **geneannopk**: Object of class "character" see documentation for CisConfig-class.
- **snpannopk**: Object of class "character" see documentation for CisConfig-class.
- **smFilter**: Object of class "function" see documentation for CisConfig-class.
- **exFilter**: Object of class "function" see documentation for CisConfig-class.
- **keepMapCache**: Object of class "logical" see documentation for CisConfig-class.
- **SSgen**: Object of class "function" see documentation for CisConfig-class.
- **excludeRadius**: Object of class "integerOrNULL" see documentation for CisConfig-class.
- **estimates**: Object of class "logical" see documentation for CisConfig-class.

Extends

Class "CisConfig", directly.
transeqByCluster

Methods

- **batchsize** signature(x = "TransConfig"): ...
- **batchsize**: signature(object = "TransConfig", value = "integer"): ...
- **gbufsize** signature(x = "TransConfig"): ...
- **gbufsize**: signature(object = "TransConfig", value = "integer"): ...
- **show** signature(object = "TransConfig"): ...
- **snpchr** signature(x = "TransConfig"): ...
- **snpchr**: signature(object = "TransConfig", value = "character"): ...

Examples

showClass("TransConfig")

---

**Description**

Convenience functions for trans-eQTL testing, one assuming a parallel-based cluster instance is available, one assuming a chromosome’s SNPs will all be candidates for testing

**Usage**

```
transeqByCluster(cl, 
snpchrs = c("chr21", "chr22"), 
exchrs = 1:22, baseconf, 
targname = "transrun_", nperm = 1, inseed = 1234, ...) 
```

```
transeqByChrom(snpchr = "chr22", 
exchrs = 1:22, baseconf, targname = "transrun_", 
nperm = 1, inseed = 1234, ...) 
```

**Arguments**

- **cl** cluster instance as defined by the parallel package makeCluster API
- **snpchrs** character vector of tokens to be used to enumerate chromosomes harboring SNP for testing
- **snpchr** character atom, for transeqByChrom, the chromosome on which testing will be conducted
- **exchrs** enumeration of chromosomes harboring expression measures to be checked for trans association with SNPs
- **baseconf** an instance of **TransConfig-class**
- **targname** folder where scratch results are computed
- **nperm** number of permutations to be used for plug-in FDR
- **inseed** seed to be set before permutations are attempted, in conjunction with RNGkind("L’Ecuyer-CMRG")
- **...** not used
Details

the TransConfig-class instance determines most of the details of the testing procedure

Value

a data.frame with test results as chisq, and permScore* with scores obtained after permuting expression against genotype

transManager-class

Class "transManager"

Description

simple container for manager of transScores output

Objects from the Class

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

Slots

base: Object of class "list" includes ff references for scores and indices of genes corresponding to scores, and other metadata about the run

Methods

show signature(object = "transManager"): simple reporter

See Also

transTab

Examples

showClass("transManager")

transScores

obtain the top trans associations for each SNP in an smlSet

Description

obtain the top trans associations for each SNP in an smlSet
transScores

Usage

transScores( tconfig )

transScores.legacy(smpack, snpchr = "chr1", rhs, K = 20, targdirpref = "tsco", geneApply = lapply, chrnmes = paste("chr", as.character(1:22), sep = ""), geneRanges = NULL, snpRanges = NULL, radius = 2e+06, renameChrs = NULL, probesToKeep = NULL, batchsize = 200, genegran = 50, shortfac = 10, wrapperEndo = NULL, geneannopk = "illuminaHumanv1.db", snpannopk = snplocsDefault(), gchrpref = "", schrpref = "ch", exfilter=function(x)x, smFilter=function(x)x, SSmgen=GGBase::getSS)

meta.transScores (smpackvec = c("GGdata", "hmyriB36"), snpchr = "22", rhsList=list(~1, ~1), K = 20, targdirpref = "mtsco", geneApply = lapply, chrnmes = as.character(21:22), radius = 2e+06, renameChrs=NULL, probesToKeep=NULL, batchsize=200, genegran=50, shortfac=10, wrapperEndo=NULL, geneannopk = "illuminaHumanv1.db", snpannopk = snplocsDefault(), gchrpref = "", schrpref="ch", exFilterList= list(function(x)x, function(x)x), SMFilterList = list(function(x)x, function(x)x), SSSgen = GGBase::getSS)

Arguments

- tconfig: instance of TransConfig-class
- smpack: name of package holding eset.rda providing 'ex' ExpressionSet when loaded, and holding SnpMatrix instances in inst/parts
- smpackvec: vector of names of package holding eset.rda providing 'ex' ExpressionSet when loaded, and holding SnpMatrix instances in inst/parts
- snpchr: name or vector of chromosome names of SNPs of interest
- rhs: right hand side of snp.rhs.tests model for which expression is left hand side, e.g., covariates other than genotype
- rhsList: list of right hand side of snp.rhs.tests model for which expression is left hand side, e.g., covariates other than genotype, one per element of smpackvec
- K: number of most highly associated features to be retained
- targdirpref: prefix of target folder name (passed to eqtlTests)
- geneApply: passed to eqtlTests
- chrnmes: names of chromosomes harboring genes that will be tested for association with genotype
- geneRanges: list of GRanges-class instances containing chromosomal coordinate defined regions occupied by genes, with regions partitioned by chromosomes, and list element names as given in chrnmes above
- snpRanges: list of GRanges-class instances with SNP addresses
- radius: radius within which an association is considered cis and therefore the corresponding test statistic is set to zero
renameChrs passed to getSS
probesToKeep passed to getSS
batchsize defines batch size for ffrowapply
genegran passed to eqtlTests
shortfac passed to eqtlTests

wrapperEndo a function accepting and returning an smlSet instance, evaluated before numerical analysis of associations, which will be executed on the output of this function
gchrpref prefix to convert chrnames into appropriate tokens for obtaining gene metadata; in future this may need to be a string transformation function
schrpref prefix to convert chrnames into appropriate tokens for use with snplocs for the SNP location information package identified in snpnanopack parameter below
geneannopk character string naming a Bioconductor db expression chip annotation package
snpnanopk character string naming a Bioconductor SNPlocs.* SNP metadata package
exFilter function to transform ExpressionSet component of retrieved smlSet, to reduce probe sets in use, for example
smFilter function to transform smlSet instance before use; filter can affect genotypes in smList(x)[[1]], for example
exFilterList list of functions serving as exFilters for each of the elements of smpackvec
SMFilterList list of functions servicing as wrapperEndos for each of the elements of smpackvec
SSgen function to be used to create smlSet instance for testing – in general, GGBase::getSS has been used to pull the ExpressionSet and SnpMatrix data from a named package, but in some cases a specialize task is needed to create the desired smlSet. Whatever is passed to SSgen must return an smlSet instance.

Value

a list with elements

scores an S by K ff matrix where S is number of SNPs, K is number of best features to be retained, with element s,k the kth largest score statistic among association tests computed for SNP s

inds an S by K ff matrix with s,k element telling which element of guniv (see below) is the gene giving the kth largest score statistic for association

guniv the vector of gene identifiers defining the universe of genes tested

snpnames vector of SNP identifiers
call the call used to create the result

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Examples

```r
## Not run:
library(GGdata)
# need to define the geneRanges and snpRanges ...
transScores("GGdata", "20", renameChrs="chr20", chrnames="chr21")

## End(Not run)
```
transTab

**Description**

Tabulate results of transScores run

**Usage**

```
transTab(x, snps2keep, ...)
```

**Arguments**

- `x`: a transManager instance.
- `snps2keep`: character vector used for filtering SNPs whose scores will be retained; intersection with SNPs named in `x` will be used.
- `...`: not used

**Value**

Data frame instance

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

vcf2sm

**Description**

Generate a SnpMatrix instance on the basis of a VCF (4.0) file.

**Usage**

```
vcf2sm(tbxfi, ..., gr, nmetacol)
```

**Arguments**

- `tbxfi`: instance of `TabixFile-class`
- `...`: not used
- `gr`: instance of `GRanges-class`
- `nmetacol`: numeric: tells number of columns used in each record as locus-level metadata

**Details**

This function is relevant only for diallelic SNP. If any base call is denoted ‘.’, the associated genotype is set to missing (raw 0), even if the nonmissing call is ALT, implying at least one ALT.
Value

an instance of \texttt{SnpMatrix-class}

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

References


Examples

```r
vref = system.file("vcf/CEU.exon.2010_09.genotypes.vcf.gz", package="GGtools")
gg = GenomicRanges::GRanges(seqnames="1", IRanges::IRanges(1e6,20e6))
vcf2sm(Rsamtools::TabixFile(vref), gr=gg, nmetacol=9L)
```
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