Package ‘gQTLstats’

January 14, 2017

Title gQTLstats: computationally efficient analysis for eQTL and allied studies

Version 1.6.0

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

Description computationally efficient analysis of eQTL, mQTL, dsQTL, etc.

Suggests geuvPack, geuvStore2, Rsamtools, knitr, markdown, ggbio,
    BiocStyle, Homo.sapiens, RUnit, multtest

Depends R (>= 3.1.0)

Imports methods, snpStats, BiocGenerics, S4Vectors (>= 0.9.25),
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    SummarizedExperiment, VariantAnnotation, Biobase, BatchJobs,
    gQTLBase, limma, mcgv, dplyr, AnnotationDbi, GenomicFeatures,
    ggplot2, reshape2, doParallel, foreach, ffbase, BBmisc,
    beeswarm

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

License Artistic-2.0

LazyLoad yes

VignetteBuilder knitr

BiocViews SNP, GenomeAnnotation, Genetics

NeedsCompilation no

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gQTLstats-package

Description

computationally efficient analysis of eQTL, mQTL, dsQTL, etc.

Details

The DESCRIPTION file:

Package: gQTLstats
Title: gQTLstats: computationally efficient analysis for eQTL and allied studies
Version: 1.6.0
Author: VJ Carey <stvjc@channing.harvard.edu>
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Suggests: geuvPack, geuvStore2, Rsamtools, knitr, rmarkdown, ggbio, BiocStyle, Homo.sapiens, RUnit, multtest
Depends: R (>= 3.1.0)
Imports: methods, snpStats, BiocGenerics, S4Vectors (>= 0.9.25), IRanges, GenomeInfoDb, GenomicFiles, GenomicRanges, ... limma, mgcv, dplyr, AnnotationDbi, GenomicFeatures, ggplot2, reshape2, doParallel, foreach, ffbase, BBmisc, beeswarm
Maintainer: VJ Carey <stvjc@channing.harvard.edu>
License: Artistic-2.0
LazyLoad: yes
VignetteBuilder: knitr
BiocViews: SNP, GenomeAnnotation, Genetics

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This package addresses the management of map-reduce like computations for cis-association tests between DNA variants and genomic features like gene expression measurements. It makes essential use of data structures defined in package gQTLBase.

A number of experimental functions are present in the current version of the package: prep.cisAssocNB (assembles information to assess negative binomial regression in cis association testing), storeToMaxAssocBySNP (progress towards SNP-specific FDR), table_sensobj_thresh (reporting on sensitivity analysis).

Additional experimental functions are available to support scalable trans-gQTL testing TransChunk, filteredDFwPerm, and transTable operate on output of AllAssoc.

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

Maintainer: VJ Carey <stvjc@channing.harvard.edu>

cisAssoc test for variant-expression associations in cis, using VCF

description

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

cisAssoc(summex, vcf.tf, rhs = ~1, nperm = 3, cisradius = 50000, genome = "hg19", assayind = 1, lbmaf = 1e-06, lbgtf = 1e-06, dropUnivHet = TRUE, infoFields = c("LDAF", "SVTYPE"), simpleSNV = TRUE)
cisEsts(summex, vcf.tf, rhs = ~1, nperm = 3, cisradius = 50000, genome = "hg19", assayind = 1, lbmaf = 1e-06, lbgtf = 1e-06, dropUnivHet = TRUE, infoFields = c("LDAF", "SVTYPE"), simpleSNV = TRUE)
cisCount(summex, vcf.tf, rhs = ~1, nperm = 3, cisradius = 50000, genome = "hg19", assayind = 1, lbmaf = 1e-06, lbgtf = 1e-06, dropUnivHet = TRUE, infoFields = c("LDAF", "SVTYPE"), simpleSNV = TRUE)
AllAssoc(summex, vcf.tf, variantRange, rhs = ~1, nperm = 3, genome = "hg19", assayind = 1, lbmaf = 1e-06, lbgtf = 1e-06, dropUnivHet = TRUE, infoFields = c("LDAF", "SVTYPE"))

Arguments

- **summex**: a `RangedSummarizedExperiment` object
- **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
- **assayind**: index of `assays(summex)` to use for expression data retrieval
- **lbmaf**: lower bound on MAF of SNP to retain for analysis, computed using `col.summary`
- **lbgtf**: lower bound on genotype frequency of SNP to retain for analysis
- **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
- **infoFields**: character – VCF fields to retain in vcfInfo() part of query
- **simpleSNV**: logical – will use simple computation of `isSNV` to filter variants for analysis to SNV
- **variantRange**: GRanges instance that defines the scope of the VCF to be used for testing against all features on `summex`

Details

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

Value

- `cisAssoc`: a `GRanges-class` instance with mcols including chisq, permScore...
- `cisCount`: enumerate locations in VCF that would be tested
**Note**
seqlevelsStyle for summex and vcf.tf content must agree

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

**Examples**

```r
require(GenomeInfoDb)
require(geuvPack)
require(Rsamtools)
data(geuFPKM)
lgeu = geuFPKM[, which(seqnames(geuFPKM) == "chr20"),]
seqlevelsStyle(lgeu) = "NCBI"
tf20 = TabixFile(system.file("vcf/c20exch.vcf.gz", package="gQTLstats"))
if (require(VariantAnnotation)) scanVcfHeader(tf20)
lgeue = clipPCs(lgeu[, which(lgeu$popcode == "CEU")], 1:2)
set.seed(1234)
litc = cisAssoc(lgeue[,c(162,201),], tf20, nperm=2, lbmaf=.05, cisradius=50000)
set.seed(1234)
lite = cisEsts(lgeue[,c(162,201),], tf20, nperm=2, lbmaf=.05, cisradius=50000)
summary(litc$schisq)
mysr = range(litc)
litc$pifdr = gQTLstats:::pifdr(litc$schisq, c(litc$permScore_1, litc$permScore_2))
litc[which(litc$pifdr < .01)]
lita = AllAssoc(geuFPKM[1:10,], tf20, mysr)
lita3 = AllAssoc(geuFPKM[11:20,], tf20, mysr)
#lita5 = AllAssoc(geuFPKM[21:30,], tf20, mysr)
n1 = gQTLstats:::collapseToBuf(lita, lita3)
#n1 = collapseToBuf(n1, lita5)
```

---

**clipPCs**

**transformations of expression data in smlSet instances**

**Description**
transformations of expression data in smlSet instances or assay data in RangedSummarizedExperiment

**Usage**
clipPCs(x, inds2drop, center = TRUE)

regressOut(x, rhs, ...)

**Arguments**

- **x**  
a RangedSummarizedExperiment object
- **inds2drop**  
Vector of PCs to be eliminated by setting the associated diagonal elements in the SVD to zero before recomposing the matrix of expression values. If the value 0 is present in inds2drop, the smlSet is returned unchanged, with a message.
**center**

logical, passed to `prcomp`

**rhs**

formula fragment (no dependent variable) used to form residuals in a reexpression of the expression matrix; variable bindings found in pData of an ExpressionSet or colData of a RangedSummarizedExperiment

... arguments passed to `lmFit`

**Details**

clipPCs is an operation on the n x p transposed matrix X of expression data. The singular value decomposition $X = UDV^t$ is formed, the diagonal elements of $D$ corresponding to `inds2drop` are set to zero yielding the diagonal matrix $E$, and then $Y = UEV^t$ is computed and transposed to replace the expression data.

`regressOut` obtains residuals after genewise regression of expression on the design matrix specified by the `rhs`; `lmFit` is used to compute coefficients, linear predictions and residuals.

**Value**

a `RangedSummarizedExperiment` object

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

**References**

The use of PCA-based adjustments to remove mass extraneous effects from expression matrices has been criticized in work of Oliver Stegle and Jeffrey Leek, who offer Bayesian PEER and SVA respectively as alternative solutions.

**Examples**

```r
if(require(geuvPack)){
  data(geuFPKM)
  cg = clipPCs(geuFPKM, 1:10)
  ro = regressOut(cg, ~popcode)
  ro
}
```

**directPlot**

visualize relationship between empirical and modeled FDR based on analysis of a gQTL store

**Description**

visualize relationship between empirical and modeled FDR based on analysis of a gQTL store

**Usage**

directPlot(FDRsupp)
**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>fdrsupp</td>
<td>instance of FDRsupp-class</td>
</tr>
</tbody>
</table>

**Details**

This plot is used to show the degree of fit between a smooth model relating modeled FDR to empirical FDR, and the empirical FDR themselves. It should be used in conjunction with `txsPlot`. It is possible for an implausible squiggly model to yield perfect agreement for all empirical FDR estimates. See the example.

**Examples**

```r
data(filtFDR)
directPlot(filtFDR)
```

**Description**

filter a ciseStore instance using an FDR threshold

**Usage**

```r
enumerateByFDR(store, fdrsupp, threshold = 0.05, filter=force,
               ids=NULL, trimToUnit=TRUE)
```

**Arguments**

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>store</td>
<td>instance of ciseStore-class</td>
</tr>
<tr>
<td>fdrsupp</td>
<td>instance of FDRsupp-class</td>
</tr>
<tr>
<td>threshold</td>
<td>upper bound on FDR to be included</td>
</tr>
<tr>
<td>filter</td>
<td>The FDR can be computed for any association score. To return only records satisfying a given filter, supply the filter function here. It may be desirable to carry a filter function from the storeToFDR stage, and this may be considered in future versions.</td>
</tr>
<tr>
<td>ids</td>
<td>if NULL, process all results in store, otherwise limit attention to jobs with id values in ids</td>
</tr>
<tr>
<td>trimToUnit</td>
<td>plug-in FDR estimates can sometimes lie outside [0,1] owing to sparsity or defects of extrapolation; if this parameter is TRUE, estimated FDR values outside [0,1] are moved to the nearest boundary</td>
</tr>
</tbody>
</table>

**Details**

uses `storeApply`, which will use BiocParallel infrastructure when available

**Value**

A GRanges instance with store contents to which `estFDR` is appended for each range. The `estFDR` quantity is predicted using the GAM model held in the FDRsupp instance.
Examples

```r
require(geuvStore2)
require(gQTLBase)
st = makeGeuvStore2()
data(filtFDR)
filtEnum = enumerateByFDR(st, filtFDR,
  filter=function(x)x[which(x$mindist <= 500000 & x$MAF >= 0.05)]
  names(metadata(filtEnum))
filtEnum[order(filtEnum$chisq, decreasing=TRUE)[1:2]]
```

---

eqBox2

visualization of expression or other assay measure against genotypes extracted from VCF

Description

visualization of expression or other assay measure against genotypes extracted from VCF

Usage

```r
eqBox2(gene, se, tf, snpgr, genome = "hg19", forceRs=TRUE, ...)
eqDesc2(gene, se, tf, snpgr, genome = "hg19", forceRs=TRUE)
```

Arguments

- `gene`: an element of rownames(se) from which a vector of assay values will be created
- `se`: a `RangedSummarizedExperiment` object
- `tf`: instance of class `TabixFile-class`, defining paths to a tabix-indexed VCF and index file
- `snpgr`: instance of `GRanges-class` identifying the SNP to be visualized
- `genome`: tag identifying reference genome
- `forceRs`: In the 1000 genomes VCF, there are sometimes variants identified with DELLY that are grabbed by readVcf on an SNV address. Set forceRs to TRUE to retain only variants with 'rs' in the name. Has no effect if readVcf extracts only a single variant.
- `...`: extra arguments passed to beeswarm

Details

In 1.5.4, altered to supply beeswarm data visualization in addition to boxplot. Use additional option corral="gutter" to reduce horizontal sprawl in large samples.

Examples

```r
require(Rsamtools)
require(SummarizedExperiment)
mygr = GRanges("1", IRanges(54683925, width=1))
gene = "ENSG00000231581.1"
library(geuvPack)
data(geuFPKM)
```
FDRsupp-class

#tf = gpath()
tf = TabixFile(system.file("vcf/small_1.vcf.gz", package="gQTLstats"))
eqBox2(gene, se=geuFPKM, tf, mygr )
eqDesc2(gene, se=geuFPKM, tf, mygr )

FDRsupp-class  Class "FDRsupp"

Description
Support for FDR computations with ciseStore instances

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

Slots
- tab: Object of class "data.frame" a table with association scores and plug-in FDR estimates evaluated on selected score values
- FDRfunc: Object of class "function" a function of one argument with input association score and output the corresponding FDR estimate
- FDRmodel: Object of class "gam" that was fit to elements of tab
- filterUsed: Object of class "function" a copy of the function used for filtering the store to create the FDRfunc element.
- sessinfo: sessionInfo() value at time of construction
- theCall: instance of class "call" showing call leading to construction

Methods
- getFDRfunc signature(x = "FDRsupp"): extract the FDR approximating function, a function of one (vector) argument assumed to represent association scores, evaluating to the plug-in FDR estimates corresponding to these scores
- getTab signature(x = "FDRsupp"): extract the table of association scores and empirical FDR estimates

Note
Typically the FDRfunc function is constructed using a smooth model relating the estimated FDR to association scores.

Examples
showClass("FDRsupp")
**filtFDR**

*illustration of FDRsupp class*

**Description**

*illustration of FDRsupp class*

**Usage**

```r
data("filtFDR")
```

**Format**

A FDRsupp object.

**Details**

filtFDR was constructed on geuvStore contents, filtering to MAF at least five percent and radius at most 500kbp. rawFDR uses the entire geuvStore contents, with 1Mbp radius and 1 percent MAF lower bound.

**Examples**

```r
data(filtFDR)
filtFDR
```

---

**gQTLs**

*use SummarizedExperiment to manage a collection of gQTL results of interest*

**Description**

*use SummarizedExperiment to manage a collection of gQTL results of interest*

**Usage**

```r
gQTLs(filtgr, se, tf, genome = "hg19", forceRs = TRUE, chunksize = 50)
gQTLswarm(se, ind, covar = NULL, inpch = 19, xlab, ylab, featTag="probeid", ...)
```

**Arguments**

- `filtgr`: a GRanges instance typically obtained by filtering a cisEStore instance
- `se`: SummarizedExperiment with individual level expression and sample-level data from which filtgr statistics were derived; for gQTLswarm, output of gQTLs
- `tf`: TabixFile for VCF on which filtgr statistics are based
- `genome`: tag for `readVcf`
- `forceRs`: if TRUE insist that snp ids include 'rs'
- `chunksize`: VCF processing proceeds via foreach in chunks of size chunksize
ind  index into rows of se to be used for visualization, must be length 1

covar  a character string indicating a variable in colData(se) to be used to color the
points

inpch  pch setting for dots in swarm

xlab  xlabel for beeswarm plot, defaults to snp id as recovered from rowRanges(se)$snp

ylab  ylabel for beeswarm plot, defaults to probe id as recovered from rowRanges(se)$probeid

featTag  element of mcols(rowRanges(se)) used to find ylab text, defaults to 'probeid', 'symbol' is often preferred

...  passed to beeswarm

Value

a SummarizedExperiment instance with two assays, the first is genotype the second is expression

Note

very preliminary

Examples

```r
require(Rsamtools)
tf = TabixFile(system.file("vcf/litv.vcf.gz", package="gQTLstats"))
data(sigInlit) # 33 loci with significant cis eQTL on a specific filtering
library(geuvPack)
data(geuFPKM)
require(doParallel)
registerDoSEQ()
gdem = gQTLs(sigInlit, geuFPKM, tf, genome = "hg19")
gQTLswarm(gdem, 1, "popcode")
```

---

**hmm878**

labeled GRanges with ChromHMM chromatin states for GM12878

**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"...
  .. ..@ 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
```
Details
acquired using rtracklayer import from the bed file given at metadata(hmm878)["url"]

Source
see details

References

Examples

data(hmm878)
table(hmm878$name)

manhWngr

manhattan plot with named GRanges

Description

manhattan plot with named GRanges

Usage

manhWngr(store, probeid = "ENSG00000183814.10", sym = "LIN9", fdrsupp, namedGR, slstyle = "NCBI", xlab.in, ylab.in, applyFDRfilter = TRUE, ...)

Arguments

store instance of ciseStore-class
probeid name of feature identifier to use for cis association
sym symbol for feature identifier
fdrsupp instance of FDRsupp-class
namedGR GRanges instance with 'name' in mcols element
slstyle seqlevelsStyle
xlab.in x axis label
ylab.in y axis label
applyFDRfilter if TRUE, use the filter defined in the filterUsed element of the object supplied as fdrsupp on the output
...
additional arguments for plotting

Examples

require(geuvStore2)
require(gQTLBase)
store = makeGeuvStore2()
data(hmm878)
data(filtFDR)
manhWngr(store, fdrsupp=filtFDR, namedGR=hmm878)
mixedVCFtoSnpMatrix

amalgamate called genotypes and imputed allelic dosages in VCF to SnpMatrix representation

Description
amalgamate called genotypes and imputed allelic dosages in VCF to SnpMatrix representation

Usage
mixedVCFtoSnpMatrix(vcf, preferGT = TRUE)

Arguments
vcf object inheriting from CollapsedVCF-class
preferGT logical. VCF allows loci for samples to be reported in various formats, and a given locus can have a call tagged GT and a genotype probability or likelihood representation tagged GP or GL. genotypeToSnpMatrix has an uncertain parameter that, if TRUE, will transform GP or GL content to allelic dose. Note that only the "first" dosage type appearing in the header will be transformed. Thus if GP is first in the header but a given locus is tagged only with GL, the genotype for thus locus will be recorded as NA.

Details
emulates output from genotypeToSnpMatrix

Value
list with elements genotypes and map

Author(s)
VJ Carey

See Also
genotypeToSnpMatrix

Examples
fn = system.file("vcf/polytypeSNV.vcf", package="gQTLstats")
require("VariantAnnotation")
require("snpStats")
vv = readVcf(fn, genome="hg19") # only 4th SNP will have dosage coding
mixedVCFtoSnpMatrix(vv)$genotypes@.Data
pifdr utility for computing plug-in FDR

Description
utility for computing plug-in FDR

Usage
pifdr( obs, perms, trimToUnit = TRUE, ... )

Arguments
obs observed association scores
perms vector of association scores under permutation; length should be integer multiple of length(obs)
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 ignored

Details
Revised 12/30/13 to employ hist() to rapidly bin the permuted values.

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)
create a binned QQplot for a sharded store

Description

create a binned QQplot for a sharded store with association and permutation statistics

Usage

```r
qqStore(st, ids = NULL,
        .probs = c(0, seq(0.6, 0.8, 0.2), 0.9, 0.95, 0.99, 0.999, 0.9999, 1),
        xlim.in = c(0.2, 75), lowfac = 0.5, xlab = "Permutation distribution",
        ylab = "Distribution of score statistic", countpos = 50,
        plot.it = TRUE, doab = TRUE, scoreField = "chisq",
        permField = "permScore_1", ...)
```

Arguments

- `st`: instance of `ciseStore-class`
- `ids`: optional job id vector; if NULL, all jobs used
- `.probs`: vector of probabilities for use with quantile evaluation, as provided in `ffbase`, using `storeToQuantiles`
- `xlim.in`: xlim setting for QQplot
- `lowfac`: we use a log-log plot, and the first quantile (as prescribed in `.probs`) is often close to zero; we reassign it to `lowfac*(second quantile)`
- `xlab`: label
- `ylab`: label
- `countpos`: where on the x axis will we stack the information on bin counts
- `plot.it`: logical, if FALSE, a list is returned with elements on quantile values and bin counts
- `doab`: logical prescribing drawing of line of identity
- `scoreField`: tag in store naming the statistic, typically 'chisq', can also be 'tstat' for GTEx
- `permField`: tag in store naming the field holding statistics on realizations from permutation distribution
- `...`: passed to `storeToQuantiles`

Value

invisibly returns list with elements qx, qy, counts, fracs

Examples

```r
## Not run:
library(geuvStore2)
library(gQTLBase)
gs = makeGeuvStore2()
qqStore(gs) #, ids=partialIds()[1:20])
## End(Not run)
```
**queryVCF**

*obtain SnpMatrix from VCF genotypes*

**Description**

obtain SnpMatrix from VCF genotypes

**Usage**

```r
queryVCF(gr, vcf.tf, samps, genome = "hg19", getSM = TRUE, snvOnly=TRUE)
```

**Arguments**

- `gr`: GRanges instance; SNPs lying within will be processed
- `vcf.tf`: TabixFile instance pointing to VCF
- `samps`: samples to be retained
- `genome`: tag identifying build
- `getSM`: logical; if FALSE, `genotypeToSnpMatrix` will not be run and only the output of `readVcf` is returned.
- `snvOnly`: logical, if TRUE, will confine results to SNV

**Value**

a list of length two

- `readout`: output of `readVcf`
- `sm`: output of `genotypeToSnpMatrix` run on the read result

**Examples**

```r
require(Rsamtools)
tf20 = TabixFile(system.file("vcf/c20exch.vcf.gz", package="gQTLstats"))
require(geuvPack)
data(geuFPKM)
lgeu = geuFPKM[ which(seqnames(geuFPKM)="chr20"),
    which(geuFPKM$popcode=="CEU") ]
seqlevelsStyle(lgeu) = "NCBI"
rng = rowRanges(lgeu)[232] # CPNE1
myq = queryVCF( rng, tf20, samps=colnames(lgeu), genome="hg19" )
myq
```
Description

create a plottable table for eQTL sensitivity analysis visualization

Usage

```r
senstab(x, filt = force)
## S3 method for class 'senstab'
plot(x, ...)
```

Arguments

- `x`: a list generated by a process analogous to the sensitivity survey exhibited in the example below
- `filt`: a function that operates on and returns a data.frame; typically will select rows based on values of fields 'MAF' and 'radius'
- `...`: extra arguments passed to plot

Details

`sensByProbe` is a list structure; for information on this and other elements of sensitivity analysis workflow, see extensive non-executed code in example below

Value

an instance of the S3 class 'senstab', `data.frame`

Examples

```r
## Not run:
#
# illustration of sensitivity analysis using BatchJobs
#
# assume the following content in 'parms.R' (uncommented)
# MAFS = c(.03, .04, .05, .075, .10, .125, .15)
# dists = c(5000, 7500, 10000, 15000, 20000, 
# 25000, 50000, 100000, 250000, 500000, 750000, 1000000)
# parms = expand.grid(MAFS, dists)
# library(BatchJobs) # for bigStore manip
library(gQTLstats)

# could use multilevel parallelism here
# because it is a somewhat large, fragile job, BatchJobs
# is a relevant tool for iteration. but storeToFDRByProbe is
# already using bplapply. so register 3 cores for it
# and specify 15 cpu for BatchJobs in .BatchJobs.R

senstab1 = makeRegistry("sens1", file.dir="sens1",
  packages=c("gQTLstats", "dplyr"),
  src.files="parms.R") # note parms.R
```
sens4One = function(z) {
  load("../bigStore.rda") # get a ciseStore instance
  ans = storeToFDRByProbe(bigStore, xprobs=seq(.01,.99,.01), # xprobs
    # needs to be chosen with care
    filter=function(x) x[which(x$MAF >= parms[z,1] &
      x$mindist <= parms[z,2])])
  ans = setFDRfunc(ans, span=.35) # span can be important
  list(fdrsupp=ans, parms=parms[z,])
}

batchMap(sens1, sens4One, 1:nrow(parms))
submitJobs(sens1)

# now loadResult(sens1) or the equivalent can be the input to senstab()
# as in the example to continue here:

## End(Not run)
library(gQTLstats)
data(sensByProbe)
ptab = t(sapply(sensByProbe, function(x)as.numeric(x[[2]]))
unique(ptab[,1]) # MAFs used
unique(ptab[,2]) # radii used
# here we filter away some extreme values of the design space
tab = senstab(sensByProbe, filt=function(x) {
  x[ x$radius > 10000 & x$ radius < 500000 & x$MAF > .03, ]
})
plot(tab)

---

**setFDRfunc**

*estimate and store function relating association scores to approximate plug-in FDR*

**Description**

estimate and store function relating association scores to approximate plug-in FDR

**Usage**

`setFDRfunc(FDRsupp, fudge = 1e-06, zthresh = 30, maxch = 30, ...)`

**Arguments**

- **FDRsupp** instance of `FDRsupp-class`
- **fudge** if FDR is zero, a log or logistic transform will fail; we add the small positive number fudge to avoid this
- **zthresh** for association scores greater than this value, a hard value of FDR 0 is assigned
- **maxch** the model for the functional relationship between association and FDR is subset to observations for which association chisq score is no greater than 1.1*maxch
- **...** arguments passed to `s` for the smooth model relating association score to FDR at selected quantiles of the association score distribution
storeToStats

Value

returns an updated FDRsupp-class instance

Examples

data(filtFDR)
filtFDR2 = setFDRfunc(filtFDR)

storeToStats  
extract a vector from store results as ff (out of memory reference); support statistical reductions

Description

extract a vector from store results as ff (out of memory reference); support statistical reductions

Usage

storeToQuantiles(store, field,
probs=c(seq(0,.999,.001), 1-(c(1e-4,1e-5,1e-6,1e-7))),
ids = NULL, ..., checkField = FALSE, filter=force)
storeToHist(store, getter = function(x)
as.numeric(S4Vectors::as.matrix(mcols(x)[,
grep("permScore", names(mcols(x))))]), breaks, ids =
NULL, filter = force)
storeToFDR(store, xprobs = c(seq(0, 0.999, 0.001), 1 - (c(1e-04,
1e-05, 1e-06, 1e-07))), xfield = "chisq", getter =
function(x) as.numeric(S4Vectors::as.matrix(mcols(x)[,
grep("permScore", names(mcols(x))))]))), filter = force,
.id4coln=1, ids=NULL)

Arguments

store  
instance of ciseStore-class
field  
character tag, length one, must be name of a numeric field in the result set (typically something like ‘chisq’ in the GRanges generated by cisAssoc)
xfield  
as field, for FDR computation, see Details.
ids  
job ids to be used; if NULL, process all jobs
breaks  
boundaries of histogram bins
...  
supplied to makeRegistry for a temporary registry: typically will be a vector of package names if additional packages are needed to process results
checkField  
if TRUE steps will be taken to verify that the tag to which ‘field’ evaluates is present in result in the first job
probs  
numeric vector of probabilities with values in [0,1]. See quantile.ff.
xprobs  
percentiles of the empirical distribution of the association statistic at which FDR estimates are recorded.
getter  
function of a single argument that extracts a numeric vector of association scores obtained under permutation
storeToStats

x instance of FDRsupp

filter function accepting and returning GRanges instance, executed when cisAssoc result is loaded to modify that result, defaults to no-op

.id4coln job id to be used for initial probe to determine names of fields in mcols of all jobs

Details

uses current BatchJobs configuration to parallelize extraction; reduceResults could be used for a sequential solution

Value

storeToQuantiles and storeToHist return objects analogous to those returned by stats::quantile and graphics::hist.

However, it should be noted that storeToQuantiles will use the quantile.ff of ffbase. For vectors of modest length, this can disagree with results of base::quantile by a few percent.

storeToFDR and storeToFDRByProbe return an instance of FDRsupp class

Note

uses ffbase::c.ff explicitly to concatenate outputs; there is no guarantee of order among elements

Examples

stopifnot(require(geuvStore2))
require(BatchJobs)
require(gQTLBase)
store = makeGeuvStore2()
library(doParallel)
if (.Platform$OS.type == "windows") {
  registerDoSEQ()
} else registerDoParallel(cores=max(c(detectCores()-1,1)))
smchisq = storeToFf( store, "chisq", ids=store@validJobs[1:3])
smchisq
if (.Platform$OS.type != "windows") { # avoid timeout
  qs = storeToQuantiles( store, "chisq", ids = store@validJobs[1:5],
    probs=seq(.1,.9,.1) )
  qs
  hh = storeToHist( store, ids = store@validJobs[1:5], breaks=
    c(0,qs,1e9) )
  hh$counts
  fd = storeToFDR( store, xprobs=c(seq(.05,.95,.05),.99,.999) )
tail(getTab(fd),4)
  sss = storeToFDRByProbe( store , xprobs=c(seq(.05,.95,.05),.99) )
tail(getTab(sss),4)
}
transAssoc

compute 'trans' SNP-feature associations by wrapping AllAssoc

Description

compute 'trans' SNP-feature associations by wrapping AllAssoc, retaining only the strongest associations (and similarly filtered association scores computed under permutation)

Usage

transAssoc(variantGR, exSE, vcfgen, bufsize = 10, nperm = 3, exChLen = 2 * bufsize, ...)

Arguments

- variantGR: GRanges instance establishing scope of variants to test
- exSE: SummarizedExperiment instance, all of whose features will be tested for association with all SNP
- vcfgen: a function returning a path to a tabix-indexed VCF file from which SNP genotypes will be extracted
- bufsize: Size of 'buffer' used to retain largest feature association scores encountered during the search. The scores and the names of associated genes are retained in 'scorebuf' and 'elnames' components of output GRanges
- nperm: number of permutations of features against genotypes to be performed for realizing null distribution of association scores
- exChLen: size of chunks of exSE to be tested through calls to AllAssoc; this is intended to allow control of RAM usage
- ...: arguments passed to AllAssoc

Value

a GRanges with mcols including

Examples

```r
## Not run: # requires access to 1KG S3
library(geuvPack)
data(geuFPKM)
seqlevelsStyle(geuFPKM) = "NCBI"
mysr = GRanges("20", IRanges(33000055, 33020055))
genome(mysr) = "hg19"
tt = transAssoc(mysr, geuFPKM[1:16,],
    bufsize=3, exChLen=4, vcfgen=function(x)gtpath(paste0("chr", x)) )
colnames(mcols(tt))
table(as.character(mcols(tt)$elnames))
## End(Not run)
```
Description

Instance constructor for managing trans gQTL results

Usage

TransStore(regs, paths = NULL)

Arguments

- **regs**: a list of `Registry` instances, typically one per (variant-oriented) chromosome
- **paths**: if desired, paths to folders for which `loadRegistry` succeeds, used instead of `regs`

Value

instance of `TransStore-class`

Examples

```r
## Not run:  # requires devel experimental as of april 15 2016
if (require(geuvStore2) && require(doParallel)) {
  registerDoSEQ()
  r17 = g17transRegistry()
  r18 = g18transRegistry()
  g1718 = TransStore(list(r17, r18))
  g1718
}
## End(Not run)
```

Description

Class "TransStore"

Manage collection of related trans-gQTL results in BatchJobs registries, typically one per chromosome

Objects from the Class

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

- `allRegistries`: Object of class "list" containing `Registry` instances
- `numSubmitted`: Object of class "numeric" records number of jobs submitted for each registry
- `numDone`: Object of class "numeric" records number of jobs completed for each registry
- `nloci`: Object of class "numeric" records number of loci with test results for each registry
- `jobinfos`: Object of class "list" records results of `getJobInfo` for each registry

Methods

- `describe` signature(object = "TransStore"): summarize information about a store

Examples

showClass("TransStore")

txsPlot(FDRsupp, xmax=50)

Description

visualize transformed FDR against transformed association statistics

Usage

txsPlot(FDRsupp, xmax=50)

Arguments

- `FDRsupp`: an instance of `FDRsupp-class`
- `xmax`: upper bound on xlim for display

Examples

data(filtFDR)
txsPlot(filtFDR)
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