

# Package ‘GGtools’

October 17, 2017

**Title** software and data for analyses in genetics of gene expression

**Version** 5.12.1

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

**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

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

**License** Artistic-2.0

**biocViews** Genetics, GeneExpression, GeneticVariability, SNP

**LazyLoad** yes

**Collate** AllClasses.R AllGenerics.R eqtlTests.R managers.R topFeats.R gwSnpTests.R snpsCisToGenes.R relocate.R topSnps.R snplocsDefault.R transutils.R vcfutils.R eqtlEstimates.R alleq.R meta.R eqME.R meta.all.R best.trans.eQTLs.R meta.transScores.R summInfra.R bindmaf.R fdr.all.cis.R pifdr.R getFDR.R cisConfig.R thinclass.R harvest.R scoredist.R binqq.R gffprocess.R cisEqTools.R modutils.R seqinfo.R pureSensSoft.R cisa.R scan.R basicappraise.R Eqappr.R

**NeedsCompilation** no

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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  
 Collate: AllClasses.R AllGenerics.R eqtlTests.R managers.R topFeats.R gwSnpTests.R snpsCisToGenes.R relocate.R  
 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)**

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

**See Also**

[getSS](#) for acquiring containers for integrative data on genetics of expression.

**Examples**

```

## 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

```

```
t1 = gwSnpTests(genesym("CPNE1")~male, c20)
# get best hits
topSnps(t1)

## End(Not run)
```

---

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 <a href="#">CisConfig-class</a>
...	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**

```

## 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)
system.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 = 1*(overlapsAny(eqr, gwastagger) | ans$snp
  ans$isgwashit = isgwashit
}
ans
}
extraProps(cc) = eprops
set.seed(1234)
system.time(f2 <- cisScores( cc ))
#
#
inflammFilter # to make more restrictive predicate for prediction

## End(Not run)

```

---

appraise

*appraisal for eQTL prediction models*


---

**Description**

appraisal for eQTL prediction models

**Usage**

```
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 performed
reduceToSNP	logical telling whether ranges should be reduced to unique SNP and FDR re-computed
prefix	character atom used to prefix objects saved and folder for result objects
folder	folder name suffix
discfmlas_in	named list of model formulae
txlist	named list of functions that are used to bin certain quantitative features of SNP
cutts	numeric vector of thresholds for tabulation and discrete calibration
names2check	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 probabilities
savePinfer	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	<i>mcwBestCis instances, integrative analysis output containers generated by GGtools vignette</i>
----	---

---

**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
.. .. ..@ metadata : list()
.. ..@ 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: NULL
.. .. ..@ metadata : list()
.. ..@ strand :Formal class 'Rle' [package "IRanges"] with 4 slots
.. .. ..@ values : Factor w/ 3 levels "+","-","*": 3
.. .. ..@ lengths : int 50
.. .. ..@ elementMetadata: NULL
.. .. ..@ metadata : list()
.. ..@ elementMetadata:Formal class 'DataFrame' [package "IRanges"] with 6 slots
```

```

.. .. .. @ rownames : NULL
.. .. .. @ nrows : int 50
.. .. .. @ listData :List of 6
.. .. .. ..$ score : num [1:50] 36.5 16.8 16.7 14.8 9.8 ...
.. .. .. ..$ snpid : chr [1:50] "rs6037097" "rs3810504" "rs13043344" "rs13044229" ...
.. .. .. ..$ snploc : int [1:50] 25347221 62678549 544417 61738288 46369894 56551001
38879237 12177765 57565943 15056960 ...
.. .. .. ..$ radiusUsed: num [1:50] 1e+06 1e+06 1e+06 1e+06 1e+06 1e+06 1e+06 1e+06 1e+06
1e+06 ...
.. .. .. ..$ nsnp : int [1:50] 1387 783 2382 766 2157 2238 1658 2459 1675 1868 ...
.. .. .. ..$ fdr : num [1:50] 0 0 0 0.25 0.717 ...
.. .. .. @ elementType : chr "ANY"
.. .. .. @ elementMetadata: NULL
.. .. .. @ metadata : list()
.. .. @ seqinfo :Formal class 'Seqinfo' [package "GenomicRanges"] with 4 slots
.. .. @ seqnames : chr "20"
.. .. @ seqlengths : int NA
.. .. @ is_circular: logi NA
.. .. @ genome : chr NA
.. .. @ metadata : list()
.. @ allperm : num [1:100] 15.8 13.9 13.8 13.2 13 ...
.. @ extra : NULL
.. @ chromUsed: chr "20"
.. @ theCall : language best.cis.eQTLs(smpack = "GGdata", rhs = ~male, folderstem = "db2", radius
= 1e+06, chrnames = "20", geneApply = mclapply, snpnopk = snplocsDefault(), ...
.. @ smFilter :function (x)
.. ..- attr(*, "srcref")=Class 'srcref' atomic [1:8] 413 8 413 50 8 50 4 4
.. ..- attr(*, "srcfile")=Classes 'srcfilecopy', 'srcfile' <environment: 0xf5c0cc0>
.. @ nperm : num 2
.. @ globalMap:<environment: 0xf5c0538>
.. @ testCount: int 83969

```

## Details

As created in GGtools.Rnw vignette code, with sharply curtailed searches

## Examples

```

data(b1)
b1

```

---

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,
  chrnames = as.character(1:22),
  smchrpref = "", gchrpref = "", schrpref = "ch",
  geneApply = lapply, geneannopk = "illuminaHumanv1.db",
  snpannopk = 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,
  chrnames = as.character(1:22),
  smchrpref = "", gchrpref = "", schrpref = "ch",
  geneApply = lapply, geneannopk = "illuminaHumanv1.db",
  snpannopk = 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,
  chrnames = as.character(1:22), smchrpref = "", gchrpref = "",
  schrpref = "ch", geneApply = lapply, geneannopk = "illuminaHumanv1.db",
  snpannopk = 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, chrnames = as.character(1:22), smchrpref = "",
  gchrpref = "", schrpref = "ch", geneApply = lapply,
  geneannopk = "illuminaHumanv1.db",
  snpannopk = 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 <code>getSS</code> can be applied to extract <code>smlSet-class</code> instances
smpackvec	vector of character strings naming packages that can be used as <code>smpack</code> values in a series of <code>best.cis.eQTLs</code> calls, one per population for meta-analysis
rhs	R model formula, with no dependent variable, that will be used with <code>snp.rhs.tests</code> to adjust GWAS tests for each expression probe
rhslist	a list of model formulae to be used as <code>rhs</code> in a series of <code>best.cis.eQTLs</code> 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 <code>radius</code> 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 <code>chrnames</code> into appropriate tokens for indexing <code>smlSet</code> elements as collected from the package named by parameter <code>smpack</code>
gchrpref	prefix to convert <code>chrnames</code> into appropriate tokens for obtaining gene metadata; in future this may need to be a string transformation function
schrpref	prefix to convert <code>chrnames</code> into appropriate tokens for use with <code>snplocs</code> for the SNP location information package identified in <code>snpannopk</code> parameter below
geneApply	an <code>lapply</code> like function, defaults to <code>lapply</code>
geneannopk	character string, name of a <code>*.db</code> annotation package that annotates probe identifiers; or see <code>getCisMap</code> for additional possibilities concerning FDb.* complex token values for newer annotation formats
snpannopk	character string, name of <code>SNPlocs.Hsapiens.dbSNP.*</code> package for obtaining; global function <code>snplocsDefault()</code> can be used to get a nominally current package name
smFilter	function accepting and returning an <code>smlSet-class</code> instance
SMFilterList	list of functions, one element per <code>smlSet</code> package used in meta analysis, accepting and returning an <code>smlSet-class</code> instance
minchisq	threshold on test statistic value that must be met to include records on SNPs in the <code>All.cis.eQTLs</code> report
nperm	number of permutations to be used for plug-in FDR computation

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 <a href="#">mcwBestCis</a> 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 <a href="#">mcwBestCis</a>
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 <a href="#">mcwBestCis</a> 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 <a href="#">getSS</a> ; see Details
exFilterList	for metaanalytic applications, a list of functions in correspondence with the elements of <a href="#">smpackvec</a> to be passed to <a href="#">getSS</a> ; see Details
getDFFITS	logical; a component storing max DFFITS value for each gene will be retained if this argument TRUE
...	not used
SSgen	function to be used to create smlSet instance for testing – in general, <a href="#">GG-Base::getSS</a> 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 <a href="#">SSgen</a> 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](#)

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

**Examples**

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

## End(Not run)
```

---

best.trans.eQTLs	<i>collect strongest trans SNP-gene associations in a buffer of size K genes per SNP</i>
------------------	--

---

**Description**

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

**Usage**

```
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 <a href="#">smlSet-class</a> instances can be generated using <a href="#">getSS</a>
rhs	passed to <a href="#">snp.rhs.tests</a> for covariate or stratification adjustments; for permutation analysis, covariates should be handled via <a href="#">regressOut</a>
genechrnum	character vector of chromosome identifiers for genes, typically as <code>.character(1:22)</code> 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 <a href="#">ffrowapply</a> 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 smlSet instance

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 <code>snplocs</code> calls
exFilter	function returning an <code>smlSet</code> instance, operating on expression component prior to <code>smFilter</code> application and eQTL testing
smFilter	function returning an <code>smlSet</code> instance, operating on the full <code>smlSet</code>
geneApply	lapply-like function, typically <code>mclapply</code> or the like
SSgen	function to be used to create <code>smlSet</code> instance for testing – in general, <code>GG-Base::getSS</code> has been used to pull the <code>ExpressionSet</code> and <code>Snpmatrix</code> data from a named package, but in some cases a specialize task is needed to create the desired <code>smlSet</code> . Whatever is passed to <code>SSgen</code> must return an <code>smlSet</code> instance.

**Value**

instance of `transManager-class`

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

**Examples**

```
## Not run:
if (.Platform$OS.type != "windows") { # ff overwrites failing 5.IX.12
  nsFilter2 = 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)
  tt1o = tt1[ order(tt1[,"sumchisq"], decreasing=TRUE), ][1:10,]
  tt1o
}

## End(Not run)
```

---

bindmaf

*bind testing metadata to a best.cis.eQTLs result*

---

**Description**

bind testing metadata to a best.cis.eQTLs result

**Usage**

```
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 <code>getSS</code> for metaanalysis across populations or tissues)
smchr	the chromosome name as used in the names of the <code>smlist</code> output for the <code>getSS</code> result
obj	an instance of <code>mcwBestCis-class</code> generated using the package named in <code>smpack</code>
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 <code>smlSet</code> instances generated with the <code>smpackvec</code> spec.
SSgen	function to be used to create <code>smlSet</code> instance for testing – in general, <code>GGBase::getSS</code> has been used to pull the <code>ExpressionSet</code> and <code>Snpmatrix</code> data from a named package, but in some cases a specialize task is needed to create the desired <code>smlSet</code> . Whatever is passed to <code>SSgen</code> must return an <code>smlSet</code> 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**

```
## 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 <a href="#">gffprocess</a>
tiling	output of <a href="#">simpleTiling</a>
addHitTest	logical, telling whether to add a column on coincidence of SNP with the <a href="#">gwastagger</a> ranges
addcc878	logical, telling whether to add a column on coincidence of SNP with the <a href="#">hmm878</a> ranges, using the inferred chromatin state as factor level

**Note**

assumes unix utilities zcat, paste and bgzip are available

**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 (gff3, tiling)
{
  require(foreach)
  require(Rsamtools)
  stopifnot(is(tiling, "GRanges"))
  basen = gsub(".gff3.gz", "", gff3)
  th = headerTabix(gff3)
  orderedChr = th$seqnames
  lgr = foreach(i = 1:length(tiling)) %dopar% {
    gc()
    cat(i)
    lk = try(import.gff3(gff3, which = tiling[i]))
    if (inherits(lk, "try-error"))
      lk = NULL
    if (!is.null(lk))
      lk = as.data.table(as.data.frame(lk))
    lk
  }
  bad = sapply(lgr, is.null)
  if (any(bad))
    lgr = lgr[-which(bad)]
  ans = do.call(rbind, lgr)
  ans$snlocs = as.numeric(ans$snlocs)
  ans$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)
```

```

print(date())
ans$fdr = pifdr(ans$score, c(ans$permScore_1, ans$permScore_2,
  ans$permScore_3))
print(date())
obn = paste0(basen, "_dt")
assign(obn, ans)
save(list = obn, file = paste0(obn, ".rda"))
gwfdr = ans$fdr
gwch = ans$seqnames
gwsnp = ans$snp
gwprobeid = ans$probeid
sgwfdr = split(gwfdr, gwch)
sgwfdr = unlist(sgwfdr[orderedChr])
nn = tempfile()
fdrt = file(nn, "w")
writelines(c(c(" ", " ", " "), paste("; gwfdr=", round(sgwfdr,
  6), sep = "")), con = fdrt)
close(fdrt)
chkb = system(paste0("zcat ", gff3, " | paste -d ' ' - ",
  nn, " | bgzip > ", gsub(".gff3", "wmlf.gff3", gff3)))
if (!(chkb == 0))
  warning(paste("final system zcat-paste-bgzip returned non-zero: chkb=",
    chkb))
invisible(chkb)
}

```

---

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 <a href="#">SummarizedExperiment-class</a>
vcf.tf	instance of <a href="#">TabixFile</a> , referring to a tabix-indexed, bgzipped VCF file
rhs	formula 'right hand side' for adjustments to be made as <a href="#">snp.rhs.tests</a> 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 <a href="#">GenomeInfoDb</a> structures



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 <a href="http://www.biostars.org/p/117155/#117270">http://www.biostars.org/p/117155/#117270</a>
doEsts	logical, if TRUE, will run <code>snp.rhs.estimate</code> s 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](mailto: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$popcode=="CEU")], 1:2)
set.seed(4321)
litc = cisAssoc(lgeue, tf20, nperm=2, lbmaf=.05, cisradius=50000)
litc2 = cisAssoc(lgeue, tf20, nperm=2, lbmaf=.05, cisradius=50000, doEsts=TRUE)
summary(litc$chisq)
litc$pifdr = pifdr(litc$chisq, c(litc$permScore_1, litc$permScore_2))
litc[which(litc$pifdr < .01)]
```

---

CisConfig-class	<i>Class "CisConfig"</i>
-----------------	--------------------------

---

### Description

Object specifying configuration of cis-eQTL search, to be used with `All.cis`

### Objects from the Class

Objects can be created by calls of the form `new("CisConfig")`. Use replacement methods to update the fields.

**Slots**

- smpack:** 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
- schrpref:** 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.
- MEpvot:** 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"): ...  
**snpannopk** signature(x = "CisConfig"): ...  
**snpannopk<-** 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

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

## 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 <a href="#">getSS</a> can be applied to generate <a href="#">smlSet-class</a> 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 <a href="#">clipPCs</a>
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 <a href="#">SnpMatrix</a> 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	<i>Class "cisRun"</i>
--------------	-----------------------

---

**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**

Class "[GRanges](#)", directly. Class "[GenomicRanges](#)", by class "GRanges", distance 2. Class "[Vector](#)", by class "GRanges", distance 3. Class "[GenomicRangesORmissing](#)", by class "GRanges", distance 3. Class "[GenomicRangesORGRangesList](#)", by class "GRanges", distance 3.

Class "[Annotated](#)", by class "GRanges", distance 4.

**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	<i>given a collection of All.cis outputs (cisRun instances) compute FDRs for various filterings</i>
-------------	---

---

**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

**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**

```
## 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, maf=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$snp, sep=":"))
  atk = paste(atts$genes, atts$bestsnp, sep=":")
  tmp = lapply(1:length(tmp), function(x) tmp[[x]][ match( atk, kl[[x]], nomatch=0 ) ])
  curans = do.call(c, lapply(tmp, as, "GRanges"))
  newword = match( atk, paste(names(curans), curans$snp, sep=":"))
  newfdr = atts$fdr[newword]
  curans$fdr = 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", maf=.02, hidists=25000, targetname="gwise")
# SNPwise scores, all
cf2 = collectFiltered("f1.rda", maf=.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", maf=.02, hidists=25000, targetname="swise2",
  filterFun = cis.FDR.filter.SNPcentric )

## End(Not run) # end dontrun
```

---

concatCis	<i>combine a list of cisRun instances to a single instance</i>
-----------	--

---

**Description**

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

**Usage**

```
concatCis(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**

```
## Not run:
example(All.cis)
concatCis(f1, f1)

## End(Not run)
```

---

EqAppr-class	<i>Class "EqAppr"</i>
--------------	-----------------------

---

**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

**calfig** 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)
- ylimin** ylim setting for rendering
- xlimin** 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**

```
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 )
}
```

---

 eqsens\_dt

*support for sensitivity analyses related to eQTL enumerations*


---

**Description**

support for sensitivity analyses related to eQTL enumerations

**Usage**

```
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)
filtgen.maf.dist (maf.dist, validate.tab = function(tab) all(c("mindist",
  "MAF", "score") %in% colnames(tab)))
update_fdr_filt(tab, filt = function(x) x, by = c("pairs", "snps",
  "probes")[1])
plotsens(eqsout, ylab = "count of eQTL at given FDR",
  title = "cis radius in bp")
```

**Arguments**

dtab	data.table instance as generated by converting a <a href="#">cisScores</a> 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.

by	character atom describing the level of aggregation for sensitivity analysis. eQTL searches generally involve cartesian products of sets of SNPs and sets of genes, and if all elements of these products are of interest, set by to "pairs". For sensitivity analysis in which per-SNP associations are measured by choosing the maximum association statistic for all genes cis to the SNP, set by to "snps". For per-gene associations, with scores maximized over all SNPs cis to genes, use "probes".
targfdrs	numeric vector of FDR levels for which enumerations are performed.
parmlist	list of numeric vectors giving thresholds for use in filtering tests using <code>filtgen</code>
maf.dist	numeric vector of length two giving thresholding values for MAF and cis distance for filtering association tests
validate.tab	function of one argument, assumed to be a <code>data.table</code> instance, that can be used to check whether filtering conditions are feasible before attempting to filter; should return TRUE if they are, FALSE otherwise.
tab	<code>data.table</code> instance as generated by converting a <code>cisScores</code>
filt	function of one argument that operates on a <code>data.table</code> instance to reduce the rows to a desired set; parameters of filtering task are established in the environment of <code>filt</code>
eqsout	matrix as output by <code>eqsens_dt</code>
ylab	text string to be used to label Y axis on the left
title	text string to label top of plot
renameChisq	Some utilities fail to generate 'score' for observed association statistic, but report as 'chisq'. If TRUE and such a column name is found in <code>dtab</code> , <code>setnames</code> will be run to rename to 'score'.

## Details

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 `pi_fdr`) 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>

**Examples**

```
## Not run:
example(cisScores) # would generate f1
names(f1) = NULL
eqsens_dt( data.table(as(f1, "data.frame")) )

## End(Not run)
```

---

eqtlTests	<i>compute association statistics between all probes and SNP in an smlSet instance</i>
-----------	--

---

**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**

```
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 = "fooe", geneApply = lapply,
  shortfac = 10000,
  checkValid = TRUE, useUncertain = TRUE,
  glmfamily = "gaussian")
```

**Arguments**

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

```
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 = system.time(e1 <- eqtlTests( hm, ~male ))
time.lapply
e1
# best chisq(1) for CPNE1
topFeats(probeId(cptag), e1)
setwd(curd)
```

---

eqtlTests.me

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

---

**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 <a href="#">smlSet-class</a>
rhs	formula for adjustment of tests for covariates or stratification, see <a href="#">snp.rhs.tests</a>
runname	tag used to distinguish emitted files
targdir	folder where ff archives will reside
pvot	setting for pvOutputThreshold in <a href="#">Matrix_eQTL_engine</a>
geneApply	lapply-like function for iteration over genes, <a href="#">mclapply</a> 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 <a href="#">snp.rhs.tests</a> that imputed real-valued B allele counts may be present among genotype data
glmfamily	family specification for <a href="#">snp.rhs.tests</a>
scoretx	function to be applied to MatrixEQTL statistics. Defaults to abs, for signless association testing
matrixEQTL.engine.control	list of parameters passed to <a href="#">Matrix_eQTL_engine</a>
snpSlicedData.control	list of parameters used to define <a href="#">SlicedData-class</a> instances
geneSlicedData.control	list of parameters used to define <a href="#">SlicedData-class</a> instances
covarSlicedData.control	list of parameters used to define <a href="#">SlicedData-class</a> instances
covariates_file_name	if covariates are to be used with MatrixEQTL testing engine, they reside in this file. <a href="#">regressOut</a> can be used to avoid this if plug-in FDR are to be used

**Details**

provisional interface

**Value**

see [eqtlTests](#)

**Note**

intended for simple comparisons

**References**

Shabalin et al Bioinformatics (OUP) 2012

**Examples**

```
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(feats = "probeId", mgr = "eqtlTestsManager"): extract highest scores for SNP associated with given probeId  
**topFeats** signature(feats = "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**

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

---

 ex

*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



```

.. .. .. .. ..$ : int [1:3] 1 0 0
.. .. .. .. ..$ : int [1:3] 1 1 0
..@ assayData :<environment: 0x10bf12948>
..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. ..@ varMetadata :'data.frame': 7 obs. of 1 variable:
.. .. ..$ labelDescription: chr [1:7] "hapmap family id" "hapmap person id" "id of mother of this
person" "id of father of this person" ...
.. ..@ data :'data.frame': 90 obs. of 7 variables:
.. .. ..$ famid : int [1:90] 1341 1341 1341 1340 1340 1340 1340 1341 1341 ...
.. .. ..$ persid : int [1:90] 14 2 13 9 10 2 11 1 11 1 ...
.. .. ..$ mothid : int [1:90] 0 14 0 0 0 12 0 10 0 12 ...
.. .. ..$ fathid : int [1:90] 0 13 0 0 0 11 0 9 0 11 ...
.. .. ..$ sampid : Factor w/ 90 levels "NA06985","NA06991",...: 1 2 3 4 5 6 7 8 9 10 ...
.. .. ..$ isFounder: logi [1:90] TRUE FALSE TRUE TRUE TRUE TRUE FALSE ...
.. .. ..$ male : logi [1:90] FALSE FALSE TRUE TRUE FALSE FALSE ...
.. ..@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"
.. ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. ..@ .Data:List of 1
.. .. .. ..$ : int [1:3] 1 1 0
..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. ..@ varMetadata :'data.frame': 0 obs. of 1 variable:
.. .. ..$ labelDescription: chr(0)
.. ..@ data :'data.frame': 47293 obs. of 0 variables
.. ..@ dimLabels : chr [1:2] "featureNames" "featureColumns"
.. ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. ..@ .Data:List of 1
.. .. .. ..$ : int [1:3] 1 1 0
..@ annotation : chr "illuminaHumanv1.db"
..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. ..@ varMetadata :'data.frame': 0 obs. of 1 variable:
.. .. ..$ labelDescription: chr(0)
.. ..@ data :'data.frame': 90 obs. of 0 variables
.. ..@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"
.. ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. ..@ .Data:List of 1
.. .. .. ..$ : int [1:3] 1 1 0
..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. ..@ .Data:List of 4
.. .. ..$ : int [1:3] 2 14 0
.. .. ..$ : int [1:3] 2 13 7
.. .. ..$ : int [1:3] 1 3 0
.. .. ..$ : int [1:3] 1 0 0

```

## Details

Expression data harvested in 2007 from GENEVAR

[ftp://ftp.sanger.ac.uk/pub/genevar/CEU\\_parents\\_norm\\_march2007.zip](ftp://ftp.sanger.ac.uk/pub/genevar/CEU_parents_norm_march2007.zip)

## Examples

```
data(eset) # yields ExpressionSet instance called ex
```

---

getCisMap	<i>create, using Bioconductor annotation resources, a structure that enumerates SNP in the vicinity of ('cis' to) genes</i>
-----------	---

---

### 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 <code>revmap([dbpk]CHR)</code>
schr	the token to be used to acquire locations for SNP on a specified chromosome, using <code>snplocs</code>
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".
snpannopk	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.

**Examples**

```
## 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**

```
gffprocess(basename = "fullyri100k", n_in = 44, headpatt = "_1A", tmpForSort = "/freshdata/tmp")
```

**Arguments**

basename	basename of the resulting .gff3.gz(.tbi) file
n_in	number of gff3 files to be processed – used for consistency check against length(dir(patt="gff3"))
headpatt	pattern to identify file for the 'top' gff3 to be used as the contents are concatenated
tmpForSort	name of a folder that unix sort will use as a temporary directory

**Details**

The purpose of this utility is to exploit unix shell tools to unify a collection of gff3 files generated using link{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	<i>execute a series of tests for association between genotype and expression</i>
------------	--

---

### Description

execute a series of tests for association between genotype and expression

### Usage

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

### Arguments

sym	instance of <code>probeId</code> or <code>genesym</code>
sms	instance of <code>smlSet-class</code>
x	instance of <code>gwSnpScreenResult</code>
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, snplocsDefault())

## End(Not run)
```

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",...: 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 ...
.. .. ..$ itemRgb: chr [1:571339] "#F5F5F5" "#F5F5F5" "#0ABEFE" "#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

Ernst J, Kellis M. Discovery and characterization of chromatin states for systematic annotation of the human genome. *Nat Biotechnol.* 2010 Aug;28(8):817-25.

Ernst J, Kheradpour P, Mikkelsen TS, Shores N, Ward LD, Epstein CB, Zhang X, Wang L, Issner R, Coyne M et al. Mapping and analysis of chromatin state dynamics in nine human cell types. *Nature.* 2011 May 5;473(7345):43-9.

## 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)
```

---

qqhex

*obtain qqplot coordinates for the specific case of comparing a given distribution to that of multiple realizations from a permutation distribution, and bin these coordinates using hexbin, useful for very large samples*

---

## Description

obtain qqplot coordinates for the specific case of comparing a given distribution to that of multiple realizations from a permutation distribution, and bin these coordinates using hexbin, useful for very large samples

**Usage**

```

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, p3, 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 <a href="#">data.table</a> instance with association scores and scores obtained under permutation along with FDR, as returned by <a href="#">cgff2dt</a> or <a href="#">ciseqByCluster</a>
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 <a href="#">binhex()</a> , output of <a href="#">qqhex</a>
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 <a href="#">par</a>
...	not currently used

**Value**

for [qqhex](#), a list with elements

hb	output of <a href="#">hexbin</a>
thrs	vector of input thrs
scothrs	vector of observed statistics corresponding to FDRs in thrs

**Examples**

```

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

---

### 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(..., MAF1b = 0.01, npc = 10, radius = 250000, nperm = 1,
  innerFilt = function(x) x, outerFilt = function(x) x)

meta.richNull(..., MAF1b=.01, npc=10, radius=250000,
  nperm=1, innerFilt=function(x)x, outerFilt=function(x)x)
#
# internally:
#
# bigfilt = function(z)
#   outerFilt(MAFfilter(clipPCs(permEx(innerFilt(z))), 1:npc), lower=MAF1b))
#
```

### Arguments

...	should provide bindings for smpack and chrnames, which will be used to obtain gene/probe locations; see <a href="#">getSS</a> for information on smpack settings. meta.richNull allows a vector of smpack values bound to smpackvec
MAF1b	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 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	<i>enumerate samples available in a VCF file</i>
------------	--

---

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

---

### 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: ", ...)
```

**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	<i>Summarize information from a collection of eQTL searches for sensitivity assessment</i>
----------	--

---

**Description**

Summarize information from a collection of eQTL searches for sensitivity assessment

**Usage**

```
sensanal(object, fdrbound)
```

**Arguments**

object	instance of <a href="#">sensiCisInput-class</a>
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 visualization.

**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))
}
```

---

snplocsDefault

*name the default SNPlocs.Hsapiens.dbSNP.\* package*

---

## Description

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

## Usage

```
snplocsDefault()
```

## Details

allows centralized specification of SNPlocs resource package

## Value

a character string, see example

## Examples

```
snplocsDefault()
```

---

`strMultiPop`*serialization of a table from Stranger's multipopulation eQTL report*

---

**Description**

serialization of a table from Stranger's multipopulation eQTL report

**Usage**

```
data(strMultiPop)
```

**Format**

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

`rsid` a factor with levels rs...

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

`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**

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

---

TransConfig-class      *Class "TransConfig"*

---

### 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.



**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")
```

---

transeqByCluster	<i>convenience functions for trans-eQTL testing</i>
------------------	---

---

**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,
  snpchr = c("chr21", "chr22"),
  exchr = 1:22, baseconf,
  targname = "transrun_", nperm = 1, inseed = 1234, ...)

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

```

**Arguments**

cl	cluster instance as defined by the parallel package makeCluster API
snpchr	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
exchr	enumeration of chromosomes harboring expression measures to be checked for trans association with SNPs
baseconf	an instance of <a href="#">TransConfig-class</a>
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	<i>Class "transManager"</i>
--------------------	-----------------------------

---

**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	<i>obtain the top trans associations for each SNP in an smlSet</i>
-------------	--

---

**Description**

obtain the top trans associations for each SNP in an smlSet

**Usage**

```
transScores( tconfig )
```

```
transScores.legacy(smpack, snpchr = "chr1", rhs, K = 20, targdirpref = "tsco", geneApply = lapply,
  chrnames = 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,
  SSgen=GGBase::getSS)
```

```
meta.transScores (smpackvec = c("GGdata", "hmyriB36"),
  snpchr = "22", rhsList=list(~1, ~1), K = 20, targdirpref = "mtsco",
  geneApply = lapply, chrnames = 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),
  SSgen = GGBase::getSS)
```

**Arguments**

tconfig	instance of <a href="#">TransConfig-class</a>
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 <a href="#">eqtlTests</a> )
geneApply	passed to <a href="#">eqtlTests</a>
chrnames	names of chromosomes harboring genes that will be tested for association with genotype
geneRanges	list of <a href="#">GRanges-class</a> instances containing chromosomal coordinate defined regions occupied by genes, with regions partitioned by chromosomes, and list element names as given in chrnames above
snpRanges	list of <a href="#">GRanges-class</a> 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 <a href="#">getSS</a>
probesToKeep	passed to <a href="#">getSS</a>
batchsize	defines batch size for <a href="#">ffrowapply</a>
genegran	passed to <a href="#">eqtlTests</a>
shortfac	passed to <a href="#">eqtlTests</a>
wrapperEndo	a function accepting and returning an <code>smlSet</code> 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 <code>snplocs</code> for the SNP location information package identified in <code>snpnopack</code> parameter below
geneannopk	character string naming a Bioconductor <code>.db</code> expression chip annotation package
snpnopack	character string naming a Bioconductor <code>SNPlocs.*</code> SNP metadata package
exFilter	function to transform <code>ExpressionSet</code> component of retrieved <code>smlSet</code> , to reduce probe sets in use, for example
smFilter	function to transform <code>smlSet</code> instance before use; filter can affect genotypes in <code>smList(x)[[1]]</code> , for example
exFilterList	list of functions serving as <code>exFilters</code> for each of the elements of <code>smpackvec</code>
SMFilterList	list of functions servicing as <code>wrapperEndos</code> for each of the elements of <code>smpackvec</code>
SSgen	function to be used to create <code>smlSet</code> instance for testing – in general, <code>GG-Base::getSS</code> has been used to pull the <code>ExpressionSet</code> and <code>SnpMatrix</code> data from a named package, but in some cases a specialize task is needed to create the desired <code>smlSet</code> . Whatever is passed to <code>SSgen</code> must return an <code>smlSet</code> instance.

**Value**

a list with elements

scores	an $S$ by $K$ <code>ff</code> matrix where $S$ is number of SNPs, $K$ is number of best features to be retained, with element <code>s,k</code> the $k$ th largest score statistic among association tests computed for SNP <code>s</code>
inds	an $S$ by $K$ <code>ff</code> matrix with <code>s,k</code> element telling which element of <code>guniv</code> (see below) is the gene giving the $k$ th 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**

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

## End(Not run)
```

---

transTab	<i>tabulate results of transScores run</i>
----------	--

---

**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	<i>generate a SnpMatrix instance on the basis of a VCF (4.0) file</i>
--------	---

---

**Description**

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

**Usage**

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

**Arguments**

tbxfi	instance of <a href="#">TabixFile-class</a>
...	not used
gr	instance of <a href="#">GRanges-class</a>
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 [SnpMatrix-class](#)

**Author(s)**

VJ Carey <stvjc@channing.harvard.edu>

**References**

[http://www.1000genomes.org/wiki/doku.php?id=1000\\_genomes:analysis:vcf4.0](http://www.1000genomes.org/wiki/doku.php?id=1000_genomes:analysis:vcf4.0)

**Examples**

```
# SRC: ftp://ftp.1000genomes.ebi.ac.uk/vol1/ftp/pilot_data/release/2010_07/exon/CEU.exon.2010_03.genotypes.
vref = system.file("vcf/CEU.exon.2010_09.genotypes.vcf.gz", package="GGtools")
gg = GenomicRanges::GRanges(seqnames="1", IRanges::IRanges(10e6,20e6))
vcf2sm(Rsamtools::TabixFile(vref), gr=gg, nmetacol=9L)
```

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