

Package ‘gQTLstats’

October 9, 2015

Title gQTLstats: computationally efficient analysis for eQTL and allied studies

Version 1.0.0

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

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

Suggests geuvPack, geuvStore, Rsamtools, knitr, rmarkdown, ggbio, BiocStyle, Homo.sapiens

Depends R (>= 3.1.0)

Imports snpStats, GenomicRanges, VariantAnnotation, methods, Biobase, BatchJobs, gQTLBase, GenomeInfoDb, S4Vectors, limma, BiocGenerics, gam, dplyr, AnnotationDbi, IRanges, GenomicFeatures, ggplot2, reshape2, doParallel, foreach

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

License Artistic-2.0

LazyLoad yes

VignetteBuilder knitr

BiocViews SNP, GenomeAnnotation, Genetics

NeedsCompilation no

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gQTLstats-package	<i>gQTLstats: computationally efficient analysis for eQTL and allied studies</i>
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Description

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

Details

The DESCRIPTION file:

```

Package:      gQTLstats
Title:       gQTLstats: computationally efficient analysis for eQTL and allied studies
Version:     1.0.0
Author:      VJ Carey <stvjc@channing.harvard.edu>
Description: computationally efficient analysis of eQTL, mQTL, dsQTL, etc.
Suggests:   geuvPack, geuvStore, Rsamtools, knitr, rmarkdown, ggbio, BiocStyle, Homo.sapiens
Depends:    R (>= 3.1.0)
Imports:    snpStats, GenomicRanges, VariantAnnotation, methods, Biobase, BatchJobs, gQTLBase, GenomeInfoDb,
Maintainer: VJ Carey <stvjc@channing.harvard.edu>
License:    Artistic-2.0
LazyLoad:   yes
VignetteBuilder: knitr
BiocViews:  SNP, GenomeAnnotation, Genetics

```

Index of help topics:

```

FDRsupp-class      Class '"FDRsupp"'
cisAssoc           test for variant-expression associations in
                  cis, using VCF
clipPCs           transformations of expression data in smlSet
                  instances
directPlot        visualize relationship between empirical and
                  modeled FDR based on analysis of a gQTL store
enumerateByFDR    filter a ciseStore instance using an FDR
                  threshold
eqBox2            visualization of expression or other assay
                  measure against genotypes extracted from VCF
filtFDR           illustration of FDRsupp class

```

gQTLstats-package	gQTLstats: computationally efficient analysis for eQTL and allied studies
hmm878	labeled GRanges with ChromHMM chromatin states for GM12878
manhWngr	manhattan plot with named GRanges
queryVCF	obtain SnpMatrix from VCF genotypes
senstab	create a plottable table for eQTL sensitivity analysis visualization
setFDRfunc	estimate and store function relating association scores to approximate plug-in FDR
storeToQuantiles	extract a vector from store results as ff (out of memory reference); support statistical reductions
txsPlot	visualize transformed FDR against transformed association statistics

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

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

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

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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, infoFields = c("LDAF", "SVTYPE"))
```

Arguments

summex	instance of SummarizedExperiment-class
vcf.tf	instance of TabixFile , referring to a tabix-indexed, bgzipped VCF file
rhs	formula ‘right hand side’ for adjustments to be made as snp.rhs.tests is run on each expression vector
nperm	number of permutations to be used for plug-in FDR computation
cisradius	distance in bp around each gene body to be searched for SNP association
genome	tag suitable for use in GenomeInfoDb structures
assayind	index of assays(summex) to use for expression data retrieval
lbmaf	lower bound on MAF of SNP to use
dropUnivHet	logical, if TRUE, will check for columns of SnpMatrix instance that possess no values other than "NA" and "A/B". See http://www.biostars.org/p/117155/#117270
infoFields	character – VCF fields to retain in vcfInfo() part of query

Details

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

Value

a [GRanges-class](#) instance with mcols including chisq, permScore...

Note

seqlevelsStyle for summex and vcf.tf content must agree

Author(s)

VJ Carey <stvjd@channing.harvard.edu>

Examples

```
require(GenomeInfoDb)
require(geuvPack)
require(Rsamtools)
data(geuFPKM)
lgeu = geuFPKM[ which(seqnames(geuFPKM)=="chr20"), ]
seqlevelsStyle(lgeu) = "NCBI"
tf20 = TabixFile(system.file("vcf/c20exch.vcf.gz", package="GGtools"))
if (require(VariantAnnotation)) scanVcfHeader(tf20)
lgeue = clipPCs(lgeu[,which(lgeu$popcode=="CEU")], 1:2)
litc = cisAssoc(lgeue[c(162,201),], tf20, nperm=2, lbmaf=.05, cisradius=50000)
summary(litc$chisq)
## Not run:
litc$pifdr = gQTLstats:::pifdr(litc$chisq, c(litc$permScore_1, litc$permScore_2))
```

```

litc[which(litc$pifdr < .01)]
## End(Not run)

```

clipPCs *transformations of expression data in smlSet instances*

Description

transformations of expression data in smlSet instances or assay data in SummarizedExperiment

Usage

```

clipPCs(x, inds2drop, center = TRUE)

regressOut(x, rhs, ...)

```

Arguments

x	instance of SummarizedExperiment
inds2drop	Vector of PCs to be eliminated by setting the associated diagonal elements in the SVD to zero before recomposing the matrix of expression values. If the value 0 is present in inds2drop, the smlSet is returned unchanged, with a message.
center	logical, passed to prcomp
rhs	formula fragment (no dependent variable) used to form residuals in a reexpression of the expression matrix; variable bindings found in pData of an ExpressionSet or colData of a SummarizedExperiment
...	arguments passed to lmFit

Details

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

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

Value

an instance of [SummarizedExperiment-class](#)

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

References

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

Examples

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

directPlot	<i>visualize relationship between empirical and modeled FDR based on analysis of a gQTL store</i>
------------	---

Description

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

Usage

```
directPlot(FDRsupp)
```

Arguments

FDRsupp instance of [FDRsupp-class](#)

Details

This plot is used to show the degree of fit between a smooth model relating modeled FDR to empirical FDR, and the empirical FDR themselves. It should be used in conjunction with [txsPlot](#).

It is possible for an implausible squiggly model to yield perfect agreement for all empirical FDR estimates. See the example.

Examples

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

enumerateByFDR *filter a ciseStore instance using an FDR threshold*

Description

filter a ciseStore instance using an FDR threshold

Usage

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

Arguments

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

Details

uses [storeApply](#), which will use BiocParallel infrastructure when available

Value

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

Examples

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

eqBox2	<i>visualization of expression or other assay measure against genotypes extracted from VCF</i>
--------	--

Description

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

Usage

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

Arguments

gene	an element of rownames(se) from which a vector of assay values will be created
se	instance of class SummarizedExperiment-class
tf	instance of class TabixFile-class , defining paths to a tabix-indexed VCF and index file
snpgr	instance of GRanges-class identifying the SNP to be visualized
genome	tag identifying reference genome
...	extra arguments passed to boxplot

Examples

```
require(Rsamtools)
require(GenomicRanges)
mygr = GRanges("1", IRanges(54683925, width=1))
gene = "ENSG00000231581.1"
library(geuvPack)
data(geuFPKM)
#tf = gtpath(1)
tf = TabixFile(system.file("vcf/small_1.vcf.gz", package="gQTLstats"))
eqBox2(gene, se=geuFPKM, tf, mygr )
eqDesc2(gene, se=geuFPKM, tf, mygr )
```

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

Description

Support for FDR computations with ciseStore instances

Objects from the Class

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

Slots

tab: Object of class "data.frame" a table with association scores and plug-in FDR estimates evaluated on selected score values

FDRfunc: Object of class "function" a function of one argument with input association score and output the corresponding FDR estimate

FDRmodel: Object of class "gam" that was fit to elements of tab

filterUsed: Object of class "function" a copy of the function used for filtering the store to create the FDRfunc element.

sessinfo: `sessionInfo()` value at time of construction

theCall: instance of class "call" showing call leading to construction

Methods

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

getTab signature(`x = "FDRsupp"`): extract the table of association scores and empirical FDR estimates

Note

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

Examples

```
showClass("FDRsupp")
```

filtFDR

illustration of FDRsupp class

Description

illustration of FDRsupp class

Usage

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

Format

```

The format is: Formal class 'FDRsupp' [package "gQTLstats"] with 5 slots
..@ tab :'data.frame': 27 obs. of 4 variables:
.. ..$ assoc : num [1:27] 0.00403 0.01632 0.03726 0.06758 0.10704 ...
.. ..$ fdr : num [1:27] 0.946 0.942 0.937 0.932 0.925 ...
.. ..$ ncalls : num [1:27] 1567862 1485343 1402824 1320305 1237786 ...
.. ..$ avg.false: num [1:27] 1483742 1399124 1314093 1230747 1145307 ...
..@ FDRfunc :function (assoc)
..@ FDRmodel:List of 34
.. ..$ smooth.frame :'data.frame': 27 obs. of 1 variable:
.. .. ..$ lo(assoc, ...): smooth [1:27, 1] 0.00403 0.01632 0.03726 0.06758 0.10704 ...
.. .. ..- attr(*, "dimnames")=List of 2
.. .. .. ..$ : NULL
.. .. .. ..$ : chr "assoc"
.. .. ..- attr(*, "degree")= num 1
.. .. ..- attr(*, "span")= num 0.25
.. .. ..- attr(*, "ncols")= num 1
.. .. ..- attr(*, "call")= language gam.lo(data[["lo(assoc, ...)"]], z, w, span = 0.25, degree = 1, ncols
= 1)
.. .. ..- attr(*, "class")= chr [1:2] "smooth" "matrix"
.. ..$ coefficients : Named num [1:2] -0.1472 -0.0713
.. .. ..- attr(*, "names")= chr [1:2] "(Intercept)" "lo(assoc, ...)"
.. ..$ residuals : Named num [1:27] 0.016 -0.0246 -0.0445 -0.0186 -0.016 ...
.. .. ..- attr(*, "names")= chr [1:27] "5 .. ..$ fitted.values : Named num [1:27] 2.85 2.81 2.74 2.64
2.53 ...
.. .. ..- attr(*, "names")= chr [1:27] "5 .. ..$ effects : Named num [1:27] 14.6928 -27.7869 -0.045
-0.0191 -0.0166 ...
.. .. ..- attr(*, "names")= chr [1:27] "(Intercept)" "lo(assoc, ...)" "" "" ...
.. ..$ weights : Named num [1:27] 1 1 1 1 1 1 1 1 1 1 ...
.. .. ..- attr(*, "names")= chr [1:27] "5 .. ..$ rank : int 2
.. ..$ assign : int [1:2] 0 1
.. ..$ qr :List of 5
.. .. ..$ qr : num [1:27, 1:2] -5.196 0.192 0.192 0.192 0.192 ...
.. .. ..- attr(*, "dimnames")=List of 2
.. .. .. ..$ : chr [1:27] "5 .. .. ..$ : chr [1:2] "(Intercept)" "lo(assoc, ...)"
.. .. .. ..- attr(*, "assign")= int [1:2] 0 1
.. .. ..$ qraux: num [1:2] 1.19 1.08
.. .. ..$ rank : int 2
.. .. ..$ pivot: int [1:2] 1 2
.. .. ..$ tol : num 1e-07
.. .. ..- attr(*, "class")= chr "qr"
.. ..$ smooth : num [1:27, 1] 3 2.96 2.89 2.79 2.69 ...
.. .. ..- attr(*, "dimnames")=List of 2
.. .. .. ..$ : chr [1:27] "5 .. .. ..$ : chr "lo(assoc, ...)"
.. ..$ nl.df : Named num 10.6
.. .. ..- attr(*, "names")= chr "lo(assoc, ...)"
.. ..$ df.residual : num 14.4
.. ..$ var : num [1:27, 1] 0.454 0.291 0.183 0.278 0.315 ...

```

```

.. .. - attr(*, "dimnames")=List of 2
.. .. ..$ : chr [1:27] "5 .. .. ..$ : chr "lo(assoc, ...)"
.. ..$ additive.predictors: Named num [1:27] 2.85 2.81 2.74 2.64 2.53 ...
.. .. - attr(*, "names")= chr [1:27] "5 .. ..$ R : num [1:2, 1:2] -5.2 0 -195.4 389.8
.. .. - attr(*, "dimnames")=List of 2
.. .. ..$ : chr [1:2] "(Intercept)" "lo(assoc, ...)"
.. .. ..$ : chr [1:2] "(Intercept)" "lo(assoc, ...)"
.. ..$ rank : int 2
.. ..$ family :List of 11
.. .. ..$ family : chr "gaussian"
.. .. ..$ link : chr "identity"
.. .. ..$ linkfun :function (mu)
.. .. ..$ linkinv :function (eta)
.. .. ..$ variance :function (mu)
.. .. ..$ dev.resids:function (y, mu, wt)
.. .. ..$ aic :function (y, n, mu, wt, dev)
.. .. ..$ mu.eta :function (eta)
.. .. ..$ initialize: expression(n <- rep.int(1, nobs) if (is.null(etastart) && is.null(start) && is.null(mustart)
&& ((family$link == "inverse" && any(y == 0)) || (family$link == "log" && any(y <= 0))))
stop("cannot find valid starting values: please specify some") mustart <- y )
.. .. ..$ validmu :function (mu)
.. .. ..$ valideta :function (eta)
.. .. - attr(*, "class")= chr "family"
.. ..$ deviance : num 0.158
.. ..$ aic : num -35.1
.. ..$ null.deviance : num 1236
.. ..$ iter : int 2
.. ..$ prior.weights : num [1:27] 1 1 1 1 1 1 1 1 1 1 ...
.. ..$ y : Named num [1:27] 2.87 2.79 2.7 2.62 2.52 ...
.. .. - attr(*, "names")= chr [1:27] "5 .. ..$ df.null : int 26
.. ..$ nl.chisq : Named num 464
.. .. - attr(*, "names")= chr "lo(assoc, ...)"
.. ..$ call : language gam(formula = qlogis(fdr + fudge) ~ lo(assoc, ...), data = getTab(FDRsupp))
.. ..$ formula :Class 'formula' length 3 qlogis(fdr + fudge) ~ lo(assoc, ...)
.. .. - attr(*, ".Environment")=<environment: 0x7fc2a2b75350>
.. ..$ terms :Classes 'terms', 'formula' length 3 qlogis(fdr + fudge) ~ lo(assoc, ...)
.. .. - attr(*, "variables")= language list(qlogis(fdr + fudge), lo(assoc, ...))
.. .. - attr(*, "factors")= int [1:2, 1] 0 1
.. .. - attr(*, "dimnames")=List of 2
.. .. ..$ : chr [1:2] "qlogis(fdr + fudge)" "lo(assoc, ...)"
.. .. ..$ : chr "lo(assoc, ...)"
.. .. - attr(*, "term.labels")= chr "lo(assoc, ...)"
.. .. - attr(*, "specials")=Dotted pair list of 3
.. .. ..$ s : NULL
.. .. ..$ lo : int 2
.. .. ..$ random: NULL
.. .. - attr(*, "order")= int 1
.. .. - attr(*, "intercept")= int 1

```

```

.. .. attr(*, "response")= int 1
.. .. attr(*, ".Environment")=<environment: 0x7fc2a2b75350>
.. ..$ data : 'data.frame': 27 obs. of 4 variables:
.. ..$ assoc : num [1:27] 0.00403 0.01632 0.03726 0.06758 0.10704 ...
.. ..$ fdr : num [1:27] 0.946 0.942 0.937 0.932 0.925 ...
.. ..$ ncalls : num [1:27] 1567862 1485343 1402824 1320305 1237786 ...
.. ..$ avg.false: num [1:27] 1483742 1399124 1314093 1230747 1145307 ...
.. ..$ offset : NULL
.. ..$ control :List of 5
.. ..$ epsilon : num 1e-07
.. ..$ maxit : num 30
.. ..$ bf.epsilon: num 1e-07
.. ..$ bf.maxit : num 30
.. ..$ trace : logi FALSE
.. ..$ method : chr "glm.fit"
.. ..$ contrasts : NULL
.. ..$ xlevels : Named list()
.. .. attr(*, "class")= chr [1:3] "gam" "glm" "lm"
..@ theCall : language storeToFDR(store = prst, xprobs = c(seq(0.05, 0.95, 0.05), 0.975, 0.99,
0.995, 0.9975, 0.999, 0.9995, 0.9999, 0.99999), filter = function(x) x[which(x$MAF >= ...
..@ sessinfo:List of 6
.. ..$ R.version :List of 14
.. ..$ platform : chr "x86_64-apple-darwin13.4.0"
.. ..$ arch : chr "x86_64"
.. ..$ os : chr "darwin13.4.0"
.. ..$ system : chr "x86_64, darwin13.4.0"
.. ..$ status : chr "Under development (unstable)"
.. ..$ major : chr "3"
.. ..$ minor : chr "2.0"
.. ..$ year : chr "2014"
.. ..$ month : chr "10"
.. ..$ day : chr "14"
.. ..$ svn rev : chr "66761"
.. ..$ language : chr "R"
.. ..$ version.string: chr "R Under development (unstable) (2014-10-14 r66761)"
.. ..$ nickname : chr "Unsuferred Consequences"
.. ..$ platform : chr "x86_64-apple-darwin13.4.0 (64-bit)"
.. ..$ locale : chr "en_US.UTF-8/en_US.UTF-8/en_US.UTF-8/C/en_US.UTF-8/en_US.UTF-8"
.. ..$ basePkgs : chr [1:10] "stats4" "parallel" "stats" "graphics" ...
.. ..$ otherPkgs :List of 17
.. ..$ gQTLstats :List of 13
.. ..$ Package : chr "gQTLstats"
.. ..$ Title : chr "gQTLstats: computationally efficient analysis for eQTL and allied studies"
.. ..$ Version : chr "0.0.14"
.. ..$ Author : chr "VJ Carey <stvjc@channing.harvard.edu>"
.. ..$ Description : chr "computationally efficient analysis of eQTL, mQTL, dsQTL, etc."
.. ..$ Suggests : chr "geuvPack, geuvStore, Rsamtools, knitr, rmarkdown"
.. ..$ Depends : chr ""

```

```

... ..$ Imports : chr "snpStats, GenomicRanges, VariantAnnotation, methods, Biobase, BiocParallel,
BatchJobs, gQTLBase, GenomeInfoDb, S4Vectors, limm"| __truncated__
... ..$ Maintainer : chr "VJ Carey <stvjc@channing.harvard.edu>"
... ..$ License : chr "Artistic-2.0"
... ..$ LazyLoad : chr "yes"
... ..$ VignetteBuilder: chr "knitr"
... ..$ Built : chr "R 3.2.0; ; 2014-11-26 13:08:50 UTC; unix"
... ..- attr(*, "class")= chr "packageDescription"
... ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/gQTLstats/M
... ..$ gQTLBase :List of 14
... ..$ Package : chr "gQTLBase"
... ..$ Title : chr "gQTLBase: infrastructure for eQTL, mQTL and similar studies"
... ..$ Version : chr "0.0.7"
... ..$ Author : chr "VJ Carey <stvjc@channing.harvard.edu>"
... ..$ Description : chr "infrastructure for eQTL, mQTL and similar studies"
... ..$ Suggests : chr "geuvStore, knitr, rmarkdown, BiocStyle"
... ..$ Imports : chr "GenomicRanges, methods, BatchJobs, BiocParallel, BBmisc, S4Vectors, ff,
ffbase, BiocGenerics"
... ..$ Depends : chr ""
... ..$ Maintainer : chr "VJ Carey <stvjc@channing.harvard.edu>"
... ..$ License : chr "Artistic-2.0"
... ..$ LazyLoad : chr "yes"
... ..$ VignetteBuilder: chr "knitr"
... ..$ Packaged : chr "2014-11-23 12:40:41 UTC; stvjc"
... ..$ Built : chr "R 3.2.0; ; 2014-11-25 15:31:33 UTC; unix"
... ..- attr(*, "class")= chr "packageDescription"
... ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/gQTLBase/M
... ..$ geuvStore :List of 11
... ..$ Package : chr "geuvStore"
... ..$ Title : chr "demonstrate storage discipline for eQTL enumerations"
... ..$ Version : chr "0.2.1"
... ..$ Author : chr "VJ Carey <stvjc@channing.harvard.edu>"
... ..$ Description: chr "demonstrate storage discipline for eQTL enumerations and analyses
based on a selection of GEUVADIS results"
... ..$ Suggests : chr "Homo.sapiens"
... ..$ Depends : chr "BatchJobs, GenomicRanges"
... ..$ Maintainer : chr "VJ Carey <stvjc@channing.harvard.edu>"
... ..$ License : chr "Artistic-2.0"
... ..$ LazyLoad : chr "yes"
... ..$ Built : chr "R 3.2.0; ; 2014-11-21 17:45:10 UTC; unix"
... ..- attr(*, "class")= chr "packageDescription"
... ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/geuvStore/M
... ..$ GenomicRanges:List of 15
... ..$ Package : chr "GenomicRanges"
... ..$ Title : chr "Representation and manipulation of genomic intervals"
... ..$ Description: chr "The ability to efficiently represent and manipulate genomic annotations
and alignments is playing a central role when it com"| __truncated__
... ..$ Version : chr "1.19.14"

```

```

.. .. ..$ Author : chr "P. Aboyoun, H. Pages and M. Lawrence"
.. .. ..$ Maintainer : chr "Bioconductor Package Maintainer <maintainer@bioconductor.org>"
.. .. ..$ bioViews : chr "Genetics, Infrastructure, Sequencing, Annotation, Coverage,GenomeAnnotation"
.. .. ..$ Depends : chr "R (>= 2.10), methods, BiocGenerics (>= 0.11.3), S4Vectors (>=0.5.10),
IRanges (>= 2.1.19), GenomeInfoDb (>= 1.1.20)"
.. .. ..$ Imports : chr "utils, stats, XVector"
.. .. ..$ LinkingTo : chr "S4Vectors, IRanges"
.. .. ..$ Suggests : chr "AnnotationDbi (>= 1.21.1), AnnotationHub, BSgenome,BSgenome.Hsapiens.UCSC.hg19,
BSgenome.Scerevisiae.UCSC.sacCer2,Biostring"|__truncated__
.. .. ..$ License : chr "Artistic-2.0"
.. .. ..$ Collate : chr "utils.R phicoef.R transcript-utils.R constraint.Rstrand-utils.R range-
squeezers.R GenomicRanges-class.RGRanges-class.R Dele"|__truncated__
.. .. ..$ Packaged : chr "2014-11-22 03:21:36 UTC; biocbuild"
.. .. ..$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-23 12:10:22 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/GenomicRa
.. .. ..$ GenomeInfoDb :List of 16
.. .. ..$ Package : chr "GenomeInfoDb"
.. .. ..$ Title : chr "Utilities for manipulating chromosome and other 'seqname' identifiers"
.. .. ..$ Description : chr "Contains data and functions that define and allow translation between
different chromosome sequence naming conventions (e"|__truncated__
.. .. ..$ Version : chr "1.3.7"
.. .. ..$ Author : chr "Sonali Arora, Martin Morgan, Marc Carlson, H. Pages"
.. .. ..$ Maintainer : chr "Bioconductor Package Maintainer <maintainer@bioconductor.org>"
.. .. ..$ bioViews : chr "Genetics, DataRepresentation, Annotation, GenomeAnnotation"
.. .. ..$ Depends : chr "R (>= 3.1), methods, stats4, BiocGenerics, S4Vectors (>=0.2.0), IRanges
(>= 1.99.26)"
.. .. ..$ Imports : chr "methods, BiocGenerics, S4Vectors"
.. .. ..$ Suggests : chr "GenomicRanges, Rsamtools, GenomicAlignments, BSgenome,GenomicFeatures,
BSgenome.Scerevisiae.UCSC.sacCer2,BSgenome.Celegans."|__truncated__
.. .. ..$ License : chr "Artistic-2.0"
.. .. ..$ Collate : chr "utils.R assembly-utils.R fetchExtendedChromInfoFromUCSC.RrankSeqlevels.R
seqinfo.R seqlevelsStyle.R seqlevels-wrappers.RSeq"|__truncated__
.. .. ..$ VignetteBuilder: chr "knitr"
.. .. ..$ Video : chr "http://youtu.be/wdEjCYSXa7w"
.. .. ..$ Packaged : chr "2014-11-15 05:34:47 UTC; biocbuild"
.. .. ..$ Built : chr "R 3.2.0; ; 2014-11-16 03:48:46 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/GenomeInfo
.. .. ..$ IRanges :List of 16
.. .. ..$ Package : chr "IRanges"
.. .. ..$ Title : chr "Infrastructure for manipulating intervals on sequences"
.. .. ..$ Description : chr "The package provides efficient low-level and highly reusable S4 classes
for storing ranges of integers, RLE vectors (Run-Len"|__truncated__
.. .. ..$ Version : chr "2.1.19"
.. .. ..$ Author : chr "H. Pages, P. Aboyoun and M. Lawrence"
.. .. ..$ Maintainer : chr "Bioconductor Package Maintainer <maintainer@bioconductor.org>"
.. .. ..$ bioViews : chr "Infrastructure, DataRepresentation"

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.. .. .$. Depends : chr "R (>= 3.1.0), methods, utils, stats, BiocGenerics (>= 0.11.3),S4Vectors (>= 0.5.10)"
.. .. .$. Imports : chr "stats4"
.. .. .$. LinkingTo : chr "S4Vectors"
.. .. .$. Suggests : chr "XVector, GenomicRanges, BSgenome.Celegans.UCSC.ce2, RUnit"
.. .. .$. License : chr "Artistic-2.0"
.. .. .$. ExtraLicenses: chr "The following files in the 'src' directory are licensed for all use by Jim Kent, in a manner compatible with the Artistic 2.0"| __truncated__
.. .. .$. Collate : chr "subsetting-internals.R Vector-class-leftovers.R Hits-class-leftovers.R List-class-leftovers.R List-comparison.R AtomicList-cl"| __truncated__
.. .. .$. Packaged : chr "2014-11-22 02:23:42 UTC; biocbuild"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-23 12:09:59 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/IRanges/M
.. .. .$. S4Vectors :List of 14
.. .. .$. Package : chr "S4Vectors"
.. .. .$. Title : chr "S4 implementation of vectors and lists"
.. .. .$. Description: chr "The S4Vectors package defines the Vector and List virtual classes and a set of generic functions that extend the semantic of"| __truncated__
.. .. .$. Version : chr "0.5.10"
.. .. .$. Author : chr "H. Pages, M. Lawrence and P. Aboyoun"
.. .. .$. Maintainer : chr "Bioconductor Package Maintainer <maintainer@bioconductor.org>"
.. .. .$. biocViews : chr "Infrastructure, DataRepresentation"
.. .. .$. Depends : chr "R (>= 3.1.0), methods, utils, stats, stats4, BiocGenerics (>=0.11.3)"
.. .. .$. Imports : chr "methods, utils, stats, stats4, BiocGenerics"
.. .. .$. Suggests : chr "IRanges, RUnit"
.. .. .$. License : chr "Artistic-2.0"
.. .. .$. Collate : chr "S4-utils.R utils.R normarg-utils.R vector-utils.R isSorted.R logical-utils.R int-utils.R str-utils.R eval-utils.R DataTable-c"| __truncated__
.. .. .$. Packaged : chr "2014-11-21 05:53:32 UTC; biocbuild"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-23 12:06:19 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/S4Vectors/M
.. .. .$. BiocGenerics :List of 14
.. .. .$. Package : chr "BiocGenerics"
.. .. .$. Title : chr "S4 generic functions for Bioconductor"
.. .. .$. Description: chr "S4 generic functions needed by many Bioconductor packages."
.. .. .$. Version : chr "0.13.2"
.. .. .$. Author : chr "The Bioconductor Dev Team"
.. .. .$. Maintainer : chr "Bioconductor Package Maintainer <maintainer@bioconductor.org>"
.. .. .$. biocViews : chr "Infrastructure"
.. .. .$. Depends : chr "methods, utils, graphics, stats, parallel"
.. .. .$. Imports : chr "methods, utils, graphics, stats, parallel"
.. .. .$. Suggests : chr "Biobase, S4Vectors, IRanges, GenomicRanges, AnnotationDbi, oligoClasses, oligo, affyPLM, flowClust, affy, RUnit, DESeq2"
.. .. .$. License : chr "Artistic-2.0"
.. .. .$. Collate : chr "S3-classes-as-S4-classes.R append.R as.data.frame.R as.list.R as.vector.R cbind.R do.call.R duplicated.R eval.R Extremes.R fu"| __truncated__

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.. .. .$. $ Packaged : chr "2014-11-18 04:14:48 UTC; biocbuild"
.. .. .$. $ Built : chr "R 3.2.0; ; 2014-11-19 00:52:20 UTC; unix"
.. .. .$. $ attr(*, "class")= chr "packageDescription"
.. .. .$. $ attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/BiocGener
.. .. .$. $ BatchJobs :List of 20
.. .. .$. $ Package : chr "BatchJobs"
.. .. .$. $ Title : chr "Batch computing with R."
.. .. .$. $ Description : chr "Provides Map, Reduce and Filter variants to generate jobs on batch
computing systems like PBS/Torque, LSF, SLURM and Sun G" | __truncated__
.. .. .$. $ Author : chr "Bernd Bischl <bernd_bischl@gmx.net>, Michel Lang <michellang@gmail.com>"
.. .. .$. $ Maintainer : chr "Bernd Bischl <bernd_bischl@gmx.net>"
.. .. .$. $ URL : chr "https://github.com/tudo-r/BatchJobs"
.. .. .$. $ BugReports : chr "https://github.com/tudo-r/BatchJobs/issues"
.. .. .$. $ MailingList : chr "batchjobs@googlegroups.com"
.. .. .$. $ License : chr "BSD_2_clause + file LICENSE"
.. .. .$. $ Depends : chr "R (>= 2.15.0), BBmisc (>= 1.8), methods"
.. .. .$. $ Imports : chr "brew, checkmate (>= 1.5), DBI, digest, fail (>= 1.2), RSQLite(>= 1.0.0),
sendmailR, stats, stringr, utils"
.. .. .$. $ Suggests : chr "MASS, testthat"
.. .. .$. $ LazyData : chr "yes"
.. .. .$. $ ByteCompile : chr "yes"
.. .. .$. $ Version : chr "1.5"
.. .. .$. $ Packaged : chr "2014-10-30 18:49:07 UTC; bischl"
.. .. .$. $ NeedsCompilation: chr "no"
.. .. .$. $ Repository : chr "CRAN"
.. .. .$. $ Date/Publication: chr "2014-10-30 20:13:25"
.. .. .$. $ Built : chr "R 3.2.0; ; 2014-11-03 09:48:06 UTC; unix"
.. .. .$. $ attr(*, "class")= chr "packageDescription"
.. .. .$. $ attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/BatchJobs/M
.. .. .$. $ BBmisc :List of 20
.. .. .$. $ Package : chr "BBmisc"
.. .. .$. $ Title : chr "Miscellaneous helper functions for B. Bischl."
.. .. .$. $ Description : chr "Miscellaneous helper functions for and from B. Bischl and some other
guys at TU Dortmund, mainly for package development."
.. .. .$. $ Authors@R : chr "c(person(\"Bernd\", \"Bischl\", email = \"bernd_bischl@gmx.net\", role
= c(\"aut\", \"cre\")), person(\"Michel\", \"Lang\" | __truncated__
.. .. .$. $ URL : chr "https://github.com/berndbischl/BBmisc"
.. .. .$. $ BugReports : chr "https://github.com/berndbischl/BBmisc/issues"
.. .. .$. $ License : chr "BSD_3_clause + file LICENSE"
.. .. .$. $ Encoding : chr "UTF-8"
.. .. .$. $ Imports : chr "stats, checkmate"
.. .. .$. $ Suggests : chr "testthat, microbenchmark"
.. .. .$. $ LazyData : chr "yes"
.. .. .$. $ ByteCompile : chr "yes"
.. .. .$. $ Version : chr "1.8"
.. .. .$. $ Packaged : chr "2014-10-30 17:28:43 UTC; bischl"
.. .. .$. $ Author : chr "Bernd Bischl [aut, cre], Michel Lang [aut], Jakob Bossek [aut], Daniel Horn
[aut], Jakob Richter [aut]"

```



```

.. .. .$ Maintainer : chr "Bernd Bischl <bernd_bischl@gmx.net>"
.. .. .$ NeedsCompilation: chr "yes"
.. .. .$ Repository : chr "CRAN"
.. .. .$ Date/Publication: chr "2014-10-30 19:34:48"
.. .. .$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-03 09:47:48 UTC; unix"
.. .. .$- attr(*, "class")= chr "packageDescription"
.. .. .$- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/BBmisc/Me
.. .. .$ BiocStyle :List of 11
.. .. .$ Package : chr "BiocStyle"
.. .. .$ Title : chr "Standard styles for vignettes and other Bioconductor documents"
.. .. .$ Description : chr "Provides standard formatting styles for Bioconductor PDF and HTML
documents. Package vignettes illustrate use and fun"|__truncated__
.. .. .$ Version : chr "1.5.3"
.. .. .$ Author : chr "Martin Morgan, Andrzej Oles, Wolfgang Huber"
.. .. .$ Maintainer : chr "Bioconductor Package Maintainer <maintainer@bioconductor.org>"
.. .. .$ Suggests : chr "knitr (>= 1.7), rmarkdown, BiocGenerics, RUnit"
.. .. .$ biocViews : chr "Software"
.. .. .$ License : chr "Artistic-2.0"
.. .. .$ VignetteBuilder: chr "knitr"
.. .. .$ Built : chr "R 3.2.0; ; 2014-11-25 15:28:08 UTC; unix"
.. .. .$- attr(*, "class")= chr "packageDescription"
.. .. .$- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/BiocStyle/M
.. .. .$ rmarkdown :List of 19
.. .. .$ Package : chr "rmarkdown"
.. .. .$ Type : chr "Package"
.. .. .$ Title : chr "Dynamic Documents for R"
.. .. .$ Version : chr "0.3.3"
.. .. .$ Date : chr "2014-09-08"
.. .. .$ Author : chr "JJ Allaire, Jonathan McPherson, Yihui Xie, Hadley Wickham, Joe Cheng,
Jeff Allen"
.. .. .$ Maintainer : chr "JJ Allaire <jj@rstudio.com>"
.. .. .$ Description : chr "Convert R Markdown documents into a variety of formats including
HTML, MS Word, PDF, and Beamer."
.. .. .$ Depends : chr "R (>= 3.0)"
.. .. .$ Imports : chr "tools, utils, knitr (>= 1.6), yaml (>= 2.1.5), htmltools (>=0.2.4), caTools"
.. .. .$ Suggests : chr "shiny (>= 0.10.1), testthat, digest"
.. .. .$ SystemRequirements: chr "pandoc (>= 1.12.3) -http://johnmacfarlane.net/pandoc"
.. .. .$ URL : chr "http://rmarkdown.rstudio.com"
.. .. .$ License : chr "GPL-3"
.. .. .$ Packaged : chr "2014-09-17 11:35:12 UTC; jjallaire"
.. .. .$ NeedsCompilation : chr "no"
.. .. .$ Repository : chr "CRAN"
.. .. .$ Date/Publication : chr "2014-09-17 18:12:29"
.. .. .$ Built : chr "R 3.2.0; ; 2014-10-14 13:44:44 UTC; unix"
.. .. .$- attr(*, "class")= chr "packageDescription"
.. .. .$- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/rmarkdown/
.. .. .$ knitr :List of 22
.. .. .$ Package : chr "knitr"

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.. .. .$. Type : chr "Package"
.. .. .$. Title : chr "A General-Purpose Package for Dynamic Report Generation in R"
.. .. .$. Version : chr "1.8"
.. .. .$. Date : chr "2014-11-11"
.. .. .$. Authors@R : chr "as.person(c( \"Adam Vogt [ctb]\", \"Alastair Andrew [ctb]\", \"Alex Zvoleff [ctb]\", \"Ashley Manton [ctb]\"|__truncated__
.. .. .$. Maintainer : chr "Yihui Xie <xie@yihui.name>"
.. .. .$. Description : chr "This package provides a general-purpose tool for dynamic report generation in R, which can be used to deal with any type o"|__truncated__
.. .. .$. Depends : chr "R (>= 2.14.1)"
.. .. .$. Imports : chr "evaluate (>= 0.5.5), digest, formatR (>= 1.0), highr (>= 0.4),markdown (>= 0.7.4), stringr (>= 0.6), tools"
.. .. .$. Suggests : chr "testit, rgl, codetools, rmarkdown, XML, RCurl"
.. .. .$. License : chr "GPL"
.. .. .$. URL : chr "http://yihui.name/knitr/"
.. .. .$. BugReports : chr "https://github.com/yihui/knitr/issues"
.. .. .$. VignetteBuilder : chr "knitr"
.. .. .$. Collate : chr "'block.R' 'cache.R' 'citation.R' 'utils.R' 'plot.R' 'defaults.R' 'concordance.R' 'engine.R' 'themes.R' 'highlight.R' 'header.'"|__truncated__
.. .. .$. Packaged : chr "2014-11-11 04:22:18 UTC; yihui"
.. .. .$. Author : chr "Adam Vogt [ctb], Alastair Andrew [ctb], Alex Zvoleff [ctb], Ashley Manton [ctb], Brian Diggs [ctb], Cassio Perei"|__truncated__
.. .. .$. NeedsCompilation: chr "no"
.. .. .$. Repository : chr "CRAN"
.. .. .$. Date/Publication: chr "2014-11-11 09:04:50"
.. .. .$. Built : chr "R 3.2.0; ; 2014-11-16 03:47:54 UTC; unix"
.. .. .- attr(*, "class")= chr "packageDescription"
.. .. .- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/knitr/Meta/p
.. .. .$. weaver :List of 13
.. .. .$. Package : chr "weaver"
.. .. .$. Title : chr "Tools and extensions for processing Sweave documents"
.. .. .$. Version : chr "1.33.0"
.. .. .$. Author : chr "Seth Falcon"
.. .. .$. Description: chr "This package provides enhancements on the Sweave() function in the base package. In particular a facility for caching code "|__truncated__
.. .. .$. Maintainer : chr "Seth Falcon <seth@userprimary.net>"
.. .. .$. License : chr "GPL-2"
.. .. .$. Depends : chr "R (>= 2.5.0), digest, tools, utils, codetools"
.. .. .$. Suggests : chr "codetools"
.. .. .$. biocViews : chr "Infrastructure"
.. .. .$. LazyLoad : chr "yes"
.. .. .$. Packaged : chr "2014-10-14 02:47:30 UTC; biocbuild"
.. .. .$. Built : chr "R 3.2.0; ; 2014-10-16 00:54:03 UTC; unix"
.. .. .- attr(*, "class")= chr "packageDescription"
.. .. .- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/weaver/Meta/p
.. .. .$. codetools :List of 14
.. .. .$. Package : chr "codetools"
.. .. .$. Version : chr "0.2-9"

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.. .. .$. Priority : chr "recommended"
.. .. .$. Author : chr "Luke Tierney <luke-tierney@uiowa.edu>"
.. .. .$. Description : chr "Code analysis tools for R"
.. .. .$. Title : chr "Code Analysis Tools for R"
.. .. .$. Depends : chr "R (>= 2.1)"
.. .. .$. Maintainer : chr "Luke Tierney <luke-tierney@uiowa.edu>"
.. .. .$. License : chr "GPL"
.. .. .$. Packaged : chr "2014-08-18 19:30:24 UTC; luke"
.. .. .$. NeedsCompilation: chr "no"
.. .. .$. Repository : chr "CRAN"
.. .. .$. Date/Publication: chr "2014-08-21 10:48:50"
.. .. .$. Built : chr "R 3.2.0; ; 2014-10-15 20:02:22 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/codetools/Meta
.. .. .$. digest :List of 15
.. .. .$. Package : chr "digest"
.. .. .$. Version : chr "0.6.4"
.. .. .$. Date : chr "$Date: 2013-12-02 21:56:30 -0600 (Mon, 02 Dec 2013) $"
.. .. .$. Author : chr "Dirk Eddelbuettel <edd@debian.org> with contributions by Antoine Lucas,
Jarek Tuszynski, Henrik Bengtsson, Simon Urbanek, "l__truncated__
.. .. .$. Maintainer : chr "Dirk Eddelbuettel <edd@debian.org>"
.. .. .$. Title : chr "Create cryptographic hash digests of R objects"
.. .. .$. Description : chr "The digest package provides a function 'digest()' for the creation of
hash digests of arbitrary R objects (using the md5, sh"l__truncated__
.. .. .$. Depends : chr "R (>= 2.4.1)"
.. .. .$. License : chr "GPL-2"
.. .. .$. URL : chr "http://dirk.eddelbuettel.com/code/digest.html"
.. .. .$. Packaged : chr "2013-12-03 04:02:00.357418 UTC; edd"
.. .. .$. NeedsCompilation: chr "yes"
.. .. .$. Repository : chr "CRAN"
.. .. .$. Date/Publication: chr "2013-12-03 07:39:12"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.3.0; 2014-08-13 10:42:11 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/digest/Meta
.. .. .$. BiocInstaller:List of 12
.. .. .$. Package : chr "BiocInstaller"
.. .. .$. Title : chr "Install/Update Bioconductor and CRAN Packages"
.. .. .$. Description: chr "Installs/updates Bioconductor and CRAN packages"
.. .. .$. Version : chr "1.17.1"
.. .. .$. Author : chr "Dan Tenenbaum and Biocore Team"
.. .. .$. Maintainer : chr "Bioconductor Package Maintainer <maintainer@bioconductor.org>"
.. .. .$. biocViews : chr "Software"
.. .. .$. Depends : chr "R (>= 3.2.0)"
.. .. .$. Suggests : chr "RUnit, BiocGenerics"
.. .. .$. License : chr "Artistic-2.0"
.. .. .$. Packaged : chr "2014-10-15 20:33:04 UTC; biocbuild"
.. .. .$. Built : chr "R 3.2.0; ; 2014-10-15 21:00:06 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"

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... ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/BiocInstall
.. ..$ loadedOnly:List of 40
.. ..$ AnnotationDbi :List of 16
.. ..$ Package : chr "AnnotationDbi"
.. ..$ Title : chr "Annotation Database Interface"
.. ..$ Description : chr "Provides user interface and database connection code for annotation
data packages using SQLite data storage."
.. ..$ Version : chr "1.29.10"
.. ..$ Author : chr "Herve Pages, Marc Carlson, Seth Falcon, Nianhua Li"
.. ..$ Maintainer : chr "Bioconductor Package Maintainer<maintainer@bioconductor.org>"
.. ..$ Depends : chr "R (>= 2.7.0), methods, utils, stats4, BiocGenerics (>=0.11.2), Biobase (>=
1.17.0), GenomeInfoDb(>= 0.99.17)"
.. ..$ Imports : chr "methods, utils, DBI, RSQLite, stats4, BiocGenerics, Biobase,S4Vectors"
.. ..$ Suggests : chr "DBI (>= 0.2-4), RSQLite (>= 0.6-4), hgu95av2.db, GO.db,org.Sc.sgd.db,
org.At.tair.db, KEGG.db, RUnit,TxDb.Hsapiens.UCSC.hg1" | __truncated__
.. ..$ Collate : chr "00RTobjs.R unlist2.R AllGenerics.R AllClasses.R FlatBimap.RSQLite.R
AnnDbObj-lowAPI.R Bimap.R GOTerms.R BimapFormatting.RBimap" | __truncated__
.. ..$ License : chr "Artistic-2.0"
.. ..$ biocViews : chr "Annotation, Microarray, Sequencing, GenomeAnnotation"
.. ..$ VignetteBuilder: chr "knitr"
.. ..$ Packaged : chr "2014-11-22 02:40:14 UTC; biocbuild"
.. ..$ Video : chr "https://www.youtube.com/watch?v=8qvGNTVz3Ik"
.. ..$ Built : chr "R 3.2.0; ; 2014-11-23 12:09:48 UTC; unix"
.. ..- attr(*, "class")= chr "packageDescription"
.. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/AnnotationI
.. ..$ base64enc :List of 15
.. ..$ Package : chr "base64enc"
.. ..$ Version : chr "0.1-2"
.. ..$ Title : chr "Tools for base64 encoding"
.. ..$ Author : chr "Simon Urbanek <Simon.Urbanek@r-project.org>"
.. ..$ Maintainer : chr "Simon Urbanek <Simon.Urbanek@r-project.org>"
.. ..$ Depends : chr "R (>= 2.9.0)"
.. ..$ Enhances : chr "png"
.. ..$ Description : chr "This package provides tools for handling base64 encoding. It is more
flexible than the orphaned base64 package."
.. ..$ License : chr "GPL-2 | GPL-3"
.. ..$ URL : chr "http://www.rforge.net/base64enc"
.. ..$ Packaged : chr "2014-06-26 14:47:44 UTC; svnuser"
.. ..$ NeedsCompilation: chr "yes"
.. ..$ Repository : chr "CRAN"
.. ..$ Date/Publication: chr "2014-06-26 17:15:25"
.. ..$ Built : chr "R 3.2.0; x86_64-apple-darwin13.3.0; 2014-08-13 10:45:21 UTC; unix"
.. ..- attr(*, "class")= chr "packageDescription"
.. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/base64enc/M
.. ..$ Biobase :List of 15
.. ..$ Package : chr "Biobase"
.. ..$ Title : chr "Biobase: Base functions for Bioconductor"
.. ..$ Version : chr "2.27.0"

```

```

.. .. ..$ Author : chr "R. Gentleman, V. Carey, M. Morgan, S. Falcon"
.. .. ..$ Description: chr "Functions that are needed by many other packages or which replace R
functions."
.. .. ..$ Suggests : chr "tools, tkWidgets, ALL, RUnit, golubEsets"
.. .. ..$ Depends : chr "R (>= 2.10), BiocGenerics (>= 0.3.2), utils"
.. .. ..$ Imports : chr "methods"
.. .. ..$ Maintainer : chr "Bioconductor Package Maintainer<maintainer@bioconductor.org>"
.. .. ..$ License : chr "Artistic-2.0"
.. .. ..$ Collate : chr "tools.R strings.R environment.R vignettes.R packages.RAllGenerics.R
VersionsClass.R VersionedClasses.Rmethods-VersionsNull."| __truncated__
.. .. ..$ LazyLoad : chr "yes"
.. .. ..$ biocViews : chr "Infrastructure"
.. .. ..$ Packaged : chr "2014-10-14 01:23:01 UTC; biocbuild"
.. .. ..$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-10-16 00:54:06 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/Biobase/M
.. .. ..$ BiocParallel :List of 18
.. .. ..$ Package : chr "BiocParallel"
.. .. ..$ Type : chr "Package"
.. .. ..$ Title : chr "Bioconductor facilities for parallel evaluation"
.. .. ..$ Version : chr "1.1.6"
.. .. ..$ Authors@R : chr "c( person(\"Bioconductor Package Maintainer\", email=\"maintainer@bioconductor.org\",
role=\"cre\"), person(\"| __truncated__
.. .. ..$ Description : chr "This package provides modified versions and novel implementation of
functions for parallel evaluation, tailored to us"| __truncated__
.. .. ..$ biocViews : chr "Infrastructure"
.. .. ..$ License : chr "GPL-2 | GPL-3"
.. .. ..$ Depends : chr "methods"
.. .. ..$ Imports : chr "parallel, foreach, tools, BatchJobs, BBmisc, BiocGenerics"
.. .. ..$ Suggests : chr "doParallel, snow, Rmpi, GenomicRanges,RNAseqData.HNRNPC.bam.chr14,
Rsamtools, GenomicAlignments,ShortRead, RUnit, BiocStyle"| __truncated__
.. .. ..$ Collate.unix : chr "AllGenerics.R BiocParallelParam-class.R ErrorHandling.Rbpbackend-
methods.R bpisup-methods.R bplapply-methods.Rbpmapply-meth"| __truncated__
.. .. ..$ Collate.windows: chr "AllGenerics.R BiocParallelParam-class.RErrorHandling.R bpbackend-
methods.R bpisup-methods.Rbplapply-methods.R bpmapply-meth"| __truncated__
.. .. ..$ VignetteBuilder: chr "knitr"
.. .. ..$ Packaged : chr "2014-11-20 04:56:05 UTC; biocbuild"
.. .. ..$ Author : chr "Bioconductor Package Maintainer [cre], Martin Morgan [aut], Michel Lang
[aut], Ryan Thompson [aut]"
.. .. ..$ Maintainer : chr "Bioconductor Package Maintainer <maintainer@bioconductor.org>"
.. .. ..$ Built : chr "R 3.2.0; ; 2014-11-23 12:05:30 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/BiocParallel
.. .. ..$ biomaRt :List of 15
.. .. ..$ Package : chr "biomaRt"
.. .. ..$ Version : chr "2.23.5"
.. .. ..$ Title : chr "Interface to BioMart databases (e.g. Ensembl, COSMIC ,Wormbaseand
Gramene)"

```

```

.. .. .$ Author : chr "Steffen Durinck <durincks@gene.com>, Wolfgang Huber"
.. .. .$ Contributors: chr "Sean Davis <sdavis2@mail.nih.gov>, Francois Pepin, VinceS. Buffalo"
.. .. .$ Maintainer : chr "Steffen Durinck <durincks@gene.com>"
.. .. .$ Depends : chr "methods"
.. .. .$ Imports : chr "utils, XML, RCurl, AnnotationDbi"
.. .. .$ Suggests : chr "annotate"
.. .. .$ biocViews : chr "Annotation"
.. .. .$ Description : chr "In recent years a wealth of biological data has become available in
public data repositories. Easy access to these valuable dat"|__truncated__
.. .. .$ License : chr "Artistic-2.0"
.. .. .$ LazyLoad : chr "yes"
.. .. .$ Packaged : chr "2014-11-22 02:27:50 UTC; biocbuild"
.. .. .$ Built : chr "R 3.2.0; ; 2014-11-23 12:10:13 UTC; unix"
.. .. .$- attr(*, "class")= chr "packageDescription"
.. .. .$- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/biomaRt/M
.. .. .$ Biostrings :List of 17
.. .. .$ Package : chr "Biostrings"
.. .. .$ Title : chr "String objects representing biological sequences, and matchingalgorithms"
.. .. .$ Description: chr "Memory efficient string containers, string matching algorithms, and
other utilities, for fast manipulation of large biolo"|__truncated__
.. .. .$ Version : chr "2.35.4"
.. .. .$ Author : chr "H. Pages, P. Aboyoun, R. Gentleman, and S. DebRoy"
.. .. .$ Maintainer : chr "H. Pages <hpages@fhcrc.org>"
.. .. .$ biocViews : chr "SequenceMatching, Genetics, Sequencing, Infrastructure,DataImport,
DataRepresentation"
.. .. .$ Depends : chr "R (>= 2.8.0), methods, BiocGenerics (>= 0.11.3), S4Vectors (>=0.2.2),
IRanges (>= 2.1.2), XVector (>= 0.7.1)"
.. .. .$ Imports : chr "graphics, methods, stats, utils, BiocGenerics, IRanges,XVector, zlibbioc"
.. .. .$ LinkingTo : chr "S4Vectors, IRanges, XVector"
.. .. .$ Enhances : chr "Rmpi"
.. .. .$ Suggests : chr "BSgenome (>= 1.13.14), BSgenome.Celegans.UCSC.ce2 (>=1.3.11),
BSgenome.Dmelanogaster.UCSC.dm3 (>= 1.3.11),BSgenome.Hsapiens"|__truncated__
.. .. .$ License : chr "Artistic-2.0"
.. .. .$ LazyLoad : chr "yes"
.. .. .$ Collate : chr "00datacache.R utils.R IUPAC_CODE_MAP.R AMINO_ACID_CODE.RGENETIC_CODE.R
XStringCodec-class.R seqtype.R XString-class.RXStrin"|__truncated__
.. .. .$ Packaged : chr "2014-11-12 02:28:16 UTC; biocbuild"
.. .. .$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-16 03:48:31 UTC; unix"
.. .. .$- attr(*, "class")= chr "packageDescription"
.. .. .$- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/Biostrings/M
.. .. .$ bit :List of 19
.. .. .$ Package : chr "bit"
.. .. .$ Type : chr "Package"
.. .. .$ Title : chr "A class for vectors of 1-bit booleans"
.. .. .$ Version : chr "1.1-12"
.. .. .$ Date : chr "2012-01-17"
.. .. .$ Author : chr "Jens Oehlschlaegel <Jens.Oehlschlaegel@truecluster.com>"
.. .. .$ Maintainer : chr "Jens Oehlschlaegel <Jens.Oehlschlaegel@truecluster.com>"

```

```

.. .. .$. Depends : chr "R (>= 2.9.2)"
.. .. .$. Description : chr "bitmapped vectors of booleans (no NAs), coercion from and to logicals,
integers and integer subscripts; fast boolean op"| __truncated__
.. .. .$. License : chr "GPL-2"
.. .. .$. LazyLoad : chr "yes"
.. .. .$. ByteCompile : chr "yes"
.. .. .$. Encoding : chr "latin1"
.. .. .$. URL : chr "http://ff.r-forge.r-project.org/"
.. .. .$. Packaged : chr "2014-04-08 21:51:43 UTC; jens"
.. .. .$. NeedsCompilation: chr "yes"
.. .. .$. Repository : chr "CRAN"
.. .. .$. Date/Publication: chr "2014-04-09 09:54:10"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.3.0; 2014-08-13 10:46:11 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/bit/Meta/pac
.. .. .$. bitops :List of 13
.. .. .$. Package : chr "bitops"
.. .. .$. Version : chr "1.0-6"
.. .. .$. Date : chr "2013-08-17"
.. .. .$. Author : chr "S original by Steve Dutky <sdutky@terpalum.umd.edu> initial R port and
extensions by Martin Maechler; revised and modi"| __truncated__
.. .. .$. Maintainer : chr "Martin Maechler <maechler@stat.math.ethz.ch>"
.. .. .$. Title : chr "Bitwise Operations"
.. .. .$. Description : chr "Functions for bitwise operations on integer vectors."
.. .. .$. License : chr "GPL (>= 2)"
.. .. .$. Packaged : chr "2013-08-17 15:58:57 UTC; maechler"
.. .. .$. NeedsCompilation: chr "yes"
.. .. .$. Repository : chr "CRAN"
.. .. .$. Date/Publication: chr "2013-08-17 21:10:34"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.3.0; 2014-08-13 10:45:57 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/bitops/Meta
.. .. .$. brew :List of 13
.. .. .$. Package : chr "brew"
.. .. .$. Type : chr "Package"
.. .. .$. Title : chr "Templating Framework for Report Generation"
.. .. .$. Version : chr "1.0-6"
.. .. .$. Date : chr "2010-09-30"
.. .. .$. Author : chr "Jeffrey Horner"
.. .. .$. Maintainer : chr "Jeffrey Horner <jeffrey.horner@gmail.com>"
.. .. .$. Description : chr "brew implements a templating framework for mixing text and R code
for report generation. brew template syntax is simil"| __truncated__
.. .. .$. License : chr "GPL-2"
.. .. .$. Packaged : chr "2011-04-13 14:36:39 UTC; hornerj"
.. .. .$. Repository : chr "CRAN"
.. .. .$. Date/Publication: chr "2011-04-13 15:16:08"
.. .. .$. Built : chr "R 3.2.0; ; 2014-08-13 10:45:25 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"

```

```

.. .. .- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/brew/Meta/
.. .. .$ BSgenome :List of 15
.. .. .$ Package : chr "BSgenome"
.. .. .$ Title : chr "Infrastructure for Biostrings-based genome data packages"
.. .. .$ Description: chr "Infrastructure shared by all the Biostrings-based genome data packages
"
.. .. .$ Version : chr "1.35.8"
.. .. .$ Author : chr "Herve Pages"
.. .. .$ Maintainer : chr "H. Pages <hpages@fhcrc.org>"
.. .. .$ biocViews : chr "Genetics, Infrastructure, DataRepresentation,SequenceMatching, Anno-
tation, SNP"
.. .. .$ Depends : chr "R (>= 2.8.0), methods, BiocGenerics (>= 0.1.2), S4Vectors (>=0.5.10),
IRanges (>= 2.1.3), GenomeInfoDb (>= 1.1.4),GenomicRa"|__truncated__
.. .. .$ Imports : chr "methods, stats, BiocGenerics, S4Vectors, IRanges, XVector,GenomeInfoDb,
GenomicRanges, Biostrings, Rsamtools, rtracklayer"
.. .. .$ Suggests : chr "BiocInstaller, BSgenome.Celegans.UCSC.ce2 (>= 1.3.11),BSgenome.Hsapiens.UCSC.hg19
(>= 1.3.11),BSgenome.Hsapiens.UCSC.hg19.m"|__truncated__
.. .. .$ License : chr "Artistic-2.0"
.. .. .$ LazyLoad : chr "yes"
.. .. .$ Collate : chr "utils.R OnDiskLongTable-class.R OnDiskNamedSequences-class.RSNPlocs-
class.R InjectSNPsHandler-class.R XtraSNPlocs-class.RBS"|__truncated__
.. .. .$ Packaged : chr "2014-11-21 02:41:48 UTC; biocbuild"
.. .. .$ Built : chr "R 3.2.0; ; 2014-11-23 12:12:06 UTC; unix"
.. .. .- attr(*, "class")= chr "packageDescription"
.. .. .- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/BSgenome/
.. .. .$ checkmate :List of 19
.. .. .$ Package : chr "checkmate"
.. .. .$ Type : chr "Package"
.. .. .$ Title : chr "Fast and versatile argument checks"
.. .. .$ Description : chr "Tests and assertions to perform frequent argument checks. A substantial
part of the package was written in C to minimize a"|__truncated__
.. .. .$ Version : chr "1.5.0"
.. .. .$ Author : chr "Michel Lang <michellang@gmail.com>, Bernd Bischl <bernd_bischl@gmx.net>"
.. .. .$ Maintainer : chr "Michel Lang <michellang@gmail.com>"
.. .. .$ URL : chr "https://github.com/mlg/checkmate"
.. .. .$ BugReports : chr "https://github.com/mlg/checkmate/issues"
.. .. .$ NeedsCompilation: chr "yes"
.. .. .$ ByteCompile : chr "yes"
.. .. .$ Encoding : chr "UTF-8"
.. .. .$ Depends : chr "R (>= 2.15.0)"
.. .. .$ Suggests : chr "testthat"
.. .. .$ License : chr "BSD_3_clause + file LICENSE"
.. .. .$ Packaged : chr "2014-10-18 20:58:35 UTC; lang"
.. .. .$ Repository : chr "CRAN"
.. .. .$ Date/Publication: chr "2014-10-19 01:41:06"
.. .. .$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-03 09:46:42 UTC; unix"
.. .. .- attr(*, "class")= chr "packageDescription"
.. .. .- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/checkmate/

```



```

.. .. .$ DBI :List of 17
.. .. .$ Package : chr "DBI"
.. .. .$ Version : chr "0.3.1"
.. .. .$ Title : chr "R Database Interface"
.. .. .$ Author : chr "R Special Interest Group on Databases (R-SIG-DB)"
.. .. .$ Maintainer : chr "Hadley Wickham <hadley@rstudio.com>"
.. .. .$ Depends : chr "R (>= 2.15.0), methods"
.. .. .$ Suggests : chr "testthat, RSQLite"
.. .. .$ Description : chr "A database interface (DBI) definition for communication between R
and relational database management systems. All cl"| __truncated__
.. .. .$ License : chr "LGPL (>= 2)"
.. .. .$ URL : chr "https://github.com/rstats-db/DBI"
.. .. .$ BugReports : chr "https://github.com/rstats-db/DBI/issues"
.. .. .$ Collate : chr "'DObject.R' 'DBConnection.R' 'DBDriver.R' 'DBResult.R' 'compliance.R'
'keywords.R' 'quote.R' 'util.R'"
.. .. .$ Packaged : chr "2014-09-23 21:42:02 UTC; hadley"
.. .. .$ NeedsCompilation: chr "no"
.. .. .$ Repository : chr "CRAN"
.. .. .$ Date/Publication: chr "2014-09-24 07:27:12"
.. .. .$ Built : chr "R 3.2.0; ; 2014-10-14 13:46:57 UTC; unix"
.. .. .$- attr(*, "class")= chr "packageDescription"
.. .. .$- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/DBI/Meta/p
.. .. .$ evaluate :List of 18
.. .. .$ Package : chr "evaluate"
.. .. .$ Type : chr "Package"
.. .. .$ Title : chr "Parsing and evaluation tools that provide more details than thedefault."
.. .. .$ Version : chr "0.5.5"
.. .. .$ Date : chr "2014-04-30"
.. .. .$ Authors@R : chr "c(person(\"Hadley\", \"Wickham\", role = \"aut\"), person(\"Yihui\",
\"Xie\", role = c(\"cre\", \"ctb\"), email = \"xie@yi\"| __truncated__
.. .. .$ Description : chr "Parsing and evaluation tools that make it easy to recreate the command
line behaviour of R."
.. .. .$ License : chr "GPL"
.. .. .$ Depends : chr "R (>= 2.14.0)"
.. .. .$ Imports : chr "stringr (>= 0.6.2)"
.. .. .$ Suggests : chr "testthat, lattice, ggplot2"
.. .. .$ Packaged : chr "2014-04-29 19:01:11 UTC; yihui"
.. .. .$ Author : chr "Hadley Wickham [aut], Yihui Xie [cre, ctb], Barret Schloerke [ctb]"
.. .. .$ Maintainer : chr "Yihui Xie <xie@yihui.name>"
.. .. .$ NeedsCompilation: chr "no"
.. .. .$ Repository : chr "CRAN"
.. .. .$ Date/Publication: chr "2014-04-29 22:08:31"
.. .. .$ Built : chr "R 3.2.0; ; 2014-08-13 14:37:13 UTC; unix"
.. .. .$- attr(*, "class")= chr "packageDescription"
.. .. .$- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/evaluate/Meta/p
.. .. .$ fail :List of 18
.. .. .$ Package : chr "fail"
.. .. .$ Type : chr "Package"

```

```

.. .. .$. Title : chr "File Abstraction Interface Layer (FAIL) mimicking a key-valuestore"
.. .. .$. Description : chr "More comfortable interface to work with a directory of R data or source
files"
.. .. .$. Version : chr "1.2"
.. .. .$. Author : chr "Michel Lang <michellang@gmail.com>"
.. .. .$. Maintainer : chr "Michel Lang <michellang@gmail.com>"
.. .. .$. URL : chr "https://github.com/mllg/fail"
.. .. .$. License : chr "BSD_3_clause + file LICENSE"
.. .. .$. Imports : chr "BBmisc"
.. .. .$. Suggests : chr "testthat"
.. .. .$. ByteCompile : chr "yes"
.. .. .$. Collate : chr "'helper.R' 'methods.R' 'zzz.R' 'cache.R' 'fail.R' 'worker.R' 'sail.R' 'back-
ends.R' 'constructor.R'"
.. .. .$. Packaged : chr "2013-09-19 11:29:30 UTC; lang"
.. .. .$. NeedsCompilation: chr "no"
.. .. .$. Repository : chr "CRAN"
.. .. .$. Date/Publication: chr "2013-09-19 14:12:29"
.. .. .$. Built : chr "R 3.2.0; ; 2014-08-13 10:47:54 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/fail/Meta/pa
.. .. .$. fastmatch :List of 12
.. .. .$. Package : chr "fastmatch"
.. .. .$. Version : chr "1.0-4"
.. .. .$. Title : chr "Fast match() function"
.. .. .$. Author : chr "Simon Urbanek <simon.urbanek@r-project.org>"
.. .. .$. Maintainer : chr "Simon Urbanek <simon.urbanek@r-project.org>"
.. .. .$. Description : chr "Package providing a fast match() replacement for cases that require
repeated look-ups. It is slightly faster than R's '|__truncated__
.. .. .$. License : chr "GPL-2"
.. .. .$. URL : chr "http://www.rforge.net/fastmatch"
.. .. .$. Packaged : chr "2012-01-21 10:09:18 UTC; svnuser"
.. .. .$. Repository : chr "CRAN"
.. .. .$. Date/Publication: chr "2012-01-21 10:22:24"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-03 19:06:30 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/fastmatch/M
.. .. .$. ff :List of 19
.. .. .$. Package : chr "ff"
.. .. .$. Version : chr "2.2-13"
.. .. .$. Date : chr "2012-03-29"
.. .. .$. Title : chr "memory-efficient storage of large data on disk and fast accessfunctions"
.. .. .$. Author : chr "Daniel Adler <dadler@uni-goettingen.de>, Christian Glaeser <chris-
tian_glaeser@gmx.de>, Oleg Nenadic <onenadi@uni-goettingen.de>"
.. .. .$. Maintainer : chr "Jens Oehlschlaegel <Jens.Oehlschlaegel@truecluster.com>"
.. .. .$. Depends : chr "R (>= 2.10.1), bit (>= 1.1-12), utils"
.. .. .$. Suggests : chr "biglm"
.. .. .$. Description : chr "The ff package provides data structures that are stored on disk but
behave (almost) as if they were in RAM by transparently '|__truncated__

```

```

.. .. .$. License : chr "GPL-2 | file LICENSE"
.. .. .$. LazyLoad : chr "yes"
.. .. .$. ByteCompile : chr "yes"
.. .. .$. Encoding : chr "latin1"
.. .. .$. URL : chr "http://ff.r-forge.r-project.org/"
.. .. .$. Packaged : chr "2014-04-07 21:16:45 UTC; root"
.. .. .$. NeedsCompilation: chr "yes"
.. .. .$. Repository : chr "CRAN"
.. .. .$. Date/Publication: chr "2014-04-09 09:54:20"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.3.0; 2014-08-13 10:47:26 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/ff/Meta/pack
.. .. .$. ffbase :List of 27
.. .. .$. Package : chr "ffbase"
.. .. .$. Maintainer : chr "Edwin de Jonge <edwindjonge@gmail.com>"
.. .. .$. License : chr "GPL-3"
.. .. .$. Title : chr "Basic statistical functions for package ff"
.. .. .$. Type : chr "Package"
.. .. .$. LazyLoad : chr "yes"
.. .. .$. Author : chr "Edwin de Jonge, Jan Wijffels, Jan van der Laan"
.. .. .$. Description : chr "Basic (statistical) functionality for package ff"
.. .. .$. Version : chr "0.11.3"
.. .. .$. URL : chr "http://github.com/edwindj/ffbase"
.. .. .$. Date : chr "2013-11-1"
.. .. .$. Depends : chr "ff (>= 2.2-11),bit,R (>= 2.12.0)"
.. .. .$. Imports : chr "fastmatch"
.. .. .$. Suggests : chr "testthat,parallel,LaF,biglm"
.. .. .$. RemoteType : chr "github"
.. .. .$. RemoteHost : chr "api.github.com"
.. .. .$. RemoteRepo : chr "ffbase"
.. .. .$. RemoteUsername: chr "edwindj"
.. .. .$. RemoteRef : chr "master"
.. .. .$. RemoteSha : chr "e55a420f1d14fa2674ebcdaae9571861737362b3"
.. .. .$. RemoteSubdir : chr "pkg"
.. .. .$. GithubRepo : chr "ffbase"
.. .. .$. GithubUsername: chr "edwindj"
.. .. .$. GithubRef : chr "master"
.. .. .$. GithubSHA1 : chr "e55a420f1d14fa2674ebcdaae9571861737362b3"
.. .. .$. GithubSubdir : chr "pkg"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-03 19:06:31 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/ffbase/Meta
.. .. .$. foreach :List of 20
.. .. .$. Package : chr "foreach"
.. .. .$. Type : chr "Package"
.. .. .$. Title : chr "Foreach looping construct for R"
.. .. .$. Version : chr "1.4.2"
.. .. .$. Author : chr "Revolution Analytics, Steve Weston"

```

```

.. .. ..$ Maintainer : chr "Revolution Analytics <packages@revolutionanalytics.com>"
.. .. ..$ Description : chr "Support for the foreach looping construct. Foreach is an idiom that
allows for iterating over elements in a collectio"| __truncated__
.. .. ..$ Depends : chr "R (>= 2.5.0)"
.. .. ..$ Imports : chr "codetools, utils, iterators"
.. .. ..$ Suggests : chr "randomForest"
.. .. ..$ Enhances : chr "compiler, doMC, RUnit, doParallel"
.. .. ..$ License : chr "Apache License (== 2.0)"
.. .. ..$ Repository : chr "CRAN"
.. .. ..$ Repository/R-Forge/Project : chr "foreach"
.. .. ..$ Repository/R-Forge/Revision : chr "25"
.. .. ..$ Repository/R-Forge/DateTimeStamp: chr "2014-04-10 18:54:16"
.. .. ..$ Date/Publication : chr "2014-04-11 07:52:42"
.. .. ..$ Packaged : chr "2014-04-10 20:16:29 UTC; rforge"
.. .. ..$ NeedsCompilation : chr "no"
.. .. ..$ Built : chr "R 3.2.0; ; 2014-08-13 10:46:17 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/foreach/Met
.. .. ..$ formatR :List of 18
.. .. ..$ Package : chr "formatR"
.. .. ..$ Type : chr "Package"
.. .. ..$ Title : chr "Format R Code Automatically"
.. .. ..$ Version : chr "1.0"
.. .. ..$ Date : chr "2014-08-25"
.. .. ..$ Author : chr "Yihui Xie"
.. .. ..$ Maintainer : chr "Yihui Xie <xie@yihui.name>"
.. .. ..$ Description : chr "This package provides a function tidy_source() to format R source
code. Spaces and indent will be added to the code automa"| __truncated__
.. .. ..$ Suggests : chr "codetools, shiny, testit, knitr"
.. .. ..$ License : chr "GPL"
.. .. ..$ URL : chr "http://yihui.name/formatR"
.. .. ..$ BugReports : chr "https://github.com/yihui/formatR/issues"
.. .. ..$ VignetteBuilder : chr "knitr"
.. .. ..$ Packaged : chr "2014-08-24 21:04:31 UTC; yihui"
.. .. ..$ NeedsCompilation: chr "no"
.. .. ..$ Repository : chr "CRAN"
.. .. ..$ Date/Publication: chr "2014-08-25 00:55:00"
.. .. ..$ Built : chr "R 3.2.0; ; 2014-10-15 20:02:23 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/formatR/Me
.. .. ..$ GenomicAlignments:List of 16
.. .. ..$ Package : chr "GenomicAlignments"
.. .. ..$ Title : chr "Representation and manipulation of short genomic alignments"
.. .. ..$ Description: chr "Provides efficient containers for storing and manipulating short genomic
alignments (typically obtained by aligning short re"| __truncated__
.. .. ..$ Version : chr "1.3.10"
.. .. ..$ Author : chr "Hervé Pagès, Valerie Obenchain, Martin Morgan"
.. .. ..$ Maintainer : chr "Bioconductor Package Maintainer <maintainer@bioconductor.org>"

```

```

.. .. .$. biocViews : chr "Genetics, Infrastructure, DataImport, Sequencing, RNASeq, SNP, Coverage, Alignment"
.. .. .$. Depends : chr "R (>= 2.10), methods, BiocGenerics (>= 0.11.3), S4Vectors (>=0.5.10), IRanges (>= 2.1.12), GenomeInfoDb (>= 1.1.20), Genomic" | __truncated__
.. .. .$. Imports : chr "methods, stats, BiocGenerics, S4Vectors, IRanges, GenomicRanges, Biostrings, Rsamtools, BiocParallel"
.. .. .$. LinkingTo : chr "S4Vectors, IRanges"
.. .. .$. Suggests : chr "ShortRead, rtracklayer, BSgenome, GenomicFeatures, RNAseqData.HNRNPC.bam.chr14, pasillaBamSubset, TxDb.Hsapiens.UCSC.hg19.kno" | __truncated__
.. .. .$. License : chr "Artistic-2.0"
.. .. .$. Collate : chr "utils.R cigar-utils.R GAlignments-class.R GAlignmentPairs-class.R GAlignmentsList-class.R GappedReads-class.R OverlapEncoding" | __truncated__
.. .. .$. Video : chr "https://www.youtube.com/watch?v=2KqBSbkfhRo ,https://www.youtube.com/watch?v=3PK_jx44QTS"
.. .. .$. Packaged : chr "2014-11-21 05:37:33 UTC; biocbuild"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-23 12:12:23 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/GenomicAI"
.. .. .$. GenomicFeatures :List of 15
.. .. .$. Package : chr "GenomicFeatures"
.. .. .$. Title : chr "Tools for making and manipulating transcript centric annotations"
.. .. .$. Version : chr "1.19.6"
.. .. .$. Author : chr "M. Carlson, H. Pages, P. Aboyoun, S. Falcon, M. Morgan, D. Sarkar, M. Lawrence"
.. .. .$. License : chr "Artistic-2.0"
.. .. .$. Description : chr "A set of tools and methods for making and manipulating transcript centric annotations. With these tools the user can" | __truncated__
.. .. .$. Maintainer : chr "Bioconductor Package Maintainer<maintainer@bioconductor.org>"
.. .. .$. Depends : chr "BiocGenerics (>= 0.1.0), S4Vectors (>= 0.1.5), IRanges (>=1.99.1), GenomeInfoDb (>= 1.1.3), GenomicRanges (>= 1.17.12), Anno" | __truncated__
.. .. .$. Imports : chr "methods, DBI (>= 0.2-5), RSQLite (>= 0.8-1), Biostrings (>=2.23.3), rtracklayer (>= 1.25.2), biomaRt (>= 2.17.1), RCurl, uti" | __truncated__
.. .. .$. Suggests : chr "org.Mm.eg.db, BSgenome, BSgenome.Hsapiens.UCSC.hg19 (>=1.3.17), BSgenome.Celegans.UCSC.ce2, BSgenome.Dmelanogaster.UCSC.dm3 " | __truncated__
.. .. .$. Collate : chr "utils.R Ensembl.utils.R findCompatibleMarts.R TxDb-class.R FeatureDb-class.R makeTxDb.R makeTxDbFromUCSC.R makeTxDbFromBiomar" | __truncated__
.. .. .$. VignetteBuilder: chr "knitr"
.. .. .$. biocViews : chr "Genetics, Infrastructure, Annotation, Sequencing, GenomeAnnotation"
.. .. .$. Packaged : chr "2014-11-04 03:50:57 UTC; biocbuild"
.. .. .$. Built : chr "R 3.2.0; ; 2014-11-04 21:46:14 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/GenomicFea"
.. .. .$. grid :List of 11
.. .. .$. Package : chr "grid"
.. .. .$. Version : chr "3.2.0"
.. .. .$. Priority : chr "base"
.. .. .$. Title : chr "The Grid Graphics Package"
.. .. .$. Author : chr "Paul Murrell <paul@stat.auckland.ac.nz>"
.. .. .$. Maintainer : chr "R Core Team <R-core@r-project.org>"

```

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.. .. ..$ Description: chr "A rewrite of the graphics layout capabilities, plus some support for
interaction"
.. .. ..$ Imports : chr "grDevices"
.. .. ..$ Suggests : chr "lattice"
.. .. ..$ License : chr "Part of R 3.2.0"
.. .. ..$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-10-14 13:30:58 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/grid/Meta/p
.. .. ..$ htmltools :List of 18
.. .. ..$ Package : chr "htmltools"
.. .. ..$ Type : chr "Package"
.. .. ..$ Title : chr "Tools for HTML"
.. .. ..$ Version : chr "0.2.6"
.. .. ..$ Date : chr "2014-07-30"
.. .. ..$ Author : chr "RStudio, Inc."
.. .. ..$ Maintainer : chr "Joe Cheng <joe@rstudio.com>"
.. .. ..$ Description : chr "Tools for HTML generation and output"
.. .. ..$ Depends : chr "R (>= 2.14.1)"
.. .. ..$ Imports : chr "utils, digest"
.. .. ..$ Suggests : chr "markdown, testthat"
.. .. ..$ Enhances : chr "knitr"
.. .. ..$ License : chr "GPL (>= 2)"
.. .. ..$ Packaged : chr "2014-09-08 16:45:00 UTC; jcheng"
.. .. ..$ NeedsCompilation: chr "no"
.. .. ..$ Repository : chr "CRAN"
.. .. ..$ Date/Publication: chr "2014-09-08 19:23:28"
.. .. ..$ Built : chr "R 3.2.0; ; 2014-10-14 13:44:43 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/htmltools/M
.. .. ..$ iterators :List of 18
.. .. ..$ Package : chr "iterators"
.. .. ..$ Type : chr "Package"
.. .. ..$ Title : chr "Iterator construct for R"
.. .. ..$ Version : chr "1.0.7"
.. .. ..$ Author : chr "Revolution Analytics"
.. .. ..$ Maintainer : chr "Revolution Analytics <packages@revolutionanalytics.com>"
.. .. ..$ Description : chr "Support for iterators, which allow a programmer to traverse through all
the elements of a vector, list, or other colle"l __truncated__
.. .. ..$ Depends : chr "R (>= 2.5.0), utils"
.. .. ..$ Suggests : chr "RUnit"
.. .. ..$ License : chr "Apache License (== 2.0)"
.. .. ..$ Repository : chr "CRAN"
.. .. ..$ Repository/R-Forge/Project : chr "foreach"
.. .. ..$ Repository/R-Forge/Revision : chr "25"
.. .. ..$ Repository/R-Forge/DateTimeStamp: chr "2014-04-10 18:54:16"
.. .. ..$ Date/Publication : chr "2014-04-11 07:52:44"
.. .. ..$ Packaged : chr "2014-04-10 20:15:28 UTC; rforge"
.. .. ..$ NeedsCompilation : chr "no"

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.. .. ..$ Built : chr "R 3.2.0; 2014-08-13 10:46:16 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/iterators/Me
.. .. ..$ lattice :List of 22
.. .. ..$ Package : chr "lattice"
.. .. ..$ Version : chr "0.20-29"
.. .. ..$ Date : chr "2014/04/01"
.. .. ..$ Priority : chr "recommended"
.. .. ..$ Title : chr "Lattice Graphics"
.. .. ..$ Author : chr "Deepayan Sarkar <deepayan.sarkar@r-project.org>"
.. .. ..$ Maintainer : chr "Deepayan Sarkar <deepayan.sarkar@r-project.org>"
.. .. ..$ Description : chr "Lattice is a powerful and elegant high-level data visualization system,
with an emphasis on multivariate data, that is su"| __truncated__
.. .. ..$ Depends : chr "R (>= 2.15.1)"
.. .. ..$ Suggests : chr "KernSmooth, MASS"
.. .. ..$ Imports : chr "grid, grDevices, graphics, stats, utils"
.. .. ..$ Enhances : chr "chron"
.. .. ..$ LazyLoad : chr "yes"
.. .. ..$ LazyData : chr "yes"
.. .. ..$ License : chr "GPL (>= 2)"
.. .. ..$ URL : chr "http://lattice.r-forge.r-project.org/"
.. .. ..$ BugReports : chr "http://r-forge.r-project.org/projects/lattice/"
.. .. ..$ Packaged : chr "2014-04-03 11:25:19 UTC; deepayan"
.. .. ..$ NeedsCompilation: chr "yes"
.. .. ..$ Repository : chr "CRAN"
.. .. ..$ Date/Publication: chr "2014-04-04 08:55:57"
.. .. ..$ Built : chr "R 3.2.0; x86_64-apple-darwin13.3.0; 2014-08-13 10:32:02 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/lattice/Meta
.. .. ..$ limma :List of 15
.. .. ..$ Package : chr "limma"
.. .. ..$ Version : chr "3.23.1"
.. .. ..$ Date : chr "2014/10/20"
.. .. ..$ Title : chr "Linear Models for Microarray Data"
.. .. ..$ Description: chr "Data analysis, linear models and differential expression for microarray
data."
.. .. ..$ Author : chr "Gordon Smyth [cre,aut], Matthew Ritchie [ctb], Jeremy Silver [ctb], James
Wettenhall [ctb], Natalie Thorne [ctb], Davis McCarth"| __truncated__
.. .. ..$ Maintainer : chr "Gordon Smyth <smyth@wehi.edu.au>"
.. .. ..$ License : chr "GPL (>=2)"
.. .. ..$ Depends : chr "R (>= 2.3.0), methods"
.. .. ..$ Suggests : chr "statmod (>= 1.2.2), splines, locfit, MASS, ellipse, affy,vsn, AnnotationDbi,
org.Hs.eg.db, GO.db, illuminaio, BiasedUrn"
.. .. ..$ LazyLoad : chr "yes"
.. .. ..$ URL : chr "http://bioinf.wehi.edu.au/limma"
.. .. ..$ biocViews : chr "ExonArray, GeneExpression, Transcription,AlternativeSplicing, Differ-
entialExpression,DifferentialSplicing, GeneSetEnrichmen"| __truncated__
.. .. ..$ Packaged : chr "2014-10-21 01:24:05 UTC; biocbuild"

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.. .. .$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-03 09:47:06 UTC; unix"
.. .. .$- attr(*, "class")= chr "packageDescription"
.. .. .$- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/limma/Meta
.. .. .$ Matrix :List of 26
.. .. .$ Package : chr "Matrix"
.. .. .$ Version : chr "1.1-4"
.. .. .$ Date : chr "2014-06-14"
.. .. .$ Priority : chr "recommended"
.. .. .$ Title : chr "Sparse and Dense Matrix Classes and Methods"
.. .. .$ Author : chr "Douglas Bates <bates@stat.wisc.edu> and Martin Maechler"
.. .. .$ Maintainer : chr "Martin Maechler <mmaechler+Matrix@gmail.com>"
.. .. .$ Contact : chr "Doug and Martin <Matrix-authors@R-project.org>"
.. .. .$ Description : chr "Classes and methods for dense and sparse matrices and operations on
them using LAPACK and SuiteSparse."
.. .. .$ Depends : chr "R (>= 2.15.2), methods"
.. .. .$ Imports : chr "graphics, grid, stats, utils, lattice"
.. .. .$ Suggests : chr "expm, MASS"
.. .. .$ Enhances : chr "MatrixModels, graph, SparseM, sfsmisc"
.. .. .$ Encoding : chr "UTF-8"
.. .. .$ LazyData : chr "no"
.. .. .$ LazyDataNote : chr "not possible, since we use data/*R *and* our classes"
.. .. .$ ByteCompile : chr "yes"
.. .. .$ BuildResaveData : chr "no"
.. .. .$ License : chr "GPL (>= 2)"
.. .. .$ LicenseNote : chr "The Matrix package includes libraries AMD, CHOLMOD,COLAMD,
CSparse and SPQR from the SuiteSparse collection of TimDavis. A"| __truncated__
.. .. .$ URL : chr "http://Matrix.R-forge.R-project.org/"
.. .. .$ Packaged : chr "2014-06-14 16:22:31 UTC; maechler"
.. .. .$ NeedsCompilation: chr "yes"
.. .. .$ Repository : chr "CRAN"
.. .. .$ Date/Publication: chr "2014-06-15 20:26:23"
.. .. .$ Built : chr "R 3.2.0; x86_64-apple-darwin13.3.0; 2014-08-13 10:32:13 UTC; unix"
.. .. .$- attr(*, "class")= chr "packageDescription"
.. .. .$- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/Matrix/Meta
.. .. .$ RCurl :List of 21
.. .. .$ Package : chr "RCurl"
.. .. .$ Version : chr "1.95-4.3"
.. .. .$ Title : chr "General network (HTTP/FTP/...) client interface for R"
.. .. .$ Author : chr "Duncan Temple Lang"
.. .. .$ SystemRequirements: chr "libcurl (version 7.14.0 or higher)http://curl.haxx.se. On Linux
systems, you will often have toexplicitly install libcurl-d"| __truncated__
.. .. .$ Maintainer : chr "Duncan Temple Lang <duncan@r-project.org>"
.. .. .$ Description : chr "The package allows one to compose general HTTP requests and pro-
vides convenient functions to fetch URIs, get & post "| __truncated__
.. .. .$ License : chr "BSD"
.. .. .$ Depends : chr "R (>= 2.7.0), methods, bitops"
.. .. .$ Imports : chr "methods"
.. .. .$ Suggests : chr "Rcompression, XML"

```



```

.. .. .$. URL : chr "http://www.omegahat.org/Rcurl"
.. .. .$. Limitations : chr "One doesn't yet have full control over the contents of aPOST form such
as specifying files, content type. Errorhandling use"| __truncated__
.. .. .$. Note : chr "This will be used generally to communicate with HTTP servers andspecifically
in the SOAP package, HTML forms and for accessin"| __truncated__
.. .. .$. Check : chr "To run R CMD check, one really needs network access. It is anHTTP client!
This can be problematic as a Web site may be down"| __truncated__
.. .. .$. Collate : chr "aClassesEnums.R bitClasses.R xbits.R base64.R binary.SClasses.S curl.S
curlAuthConstants.R curlEnums.R curlError.RcurlInfo."| __truncated__
.. .. .$. Packaged : chr "2014-07-29 09:31:41 UTC; ligges"
.. .. .$. NeedsCompilation : chr "yes"
.. .. .$. Repository : chr "CRAN"
.. .. .$. Date/Publication : chr "2014-07-29 11:53:00"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.3.0; 2014-08-13 10:47:04 UTC; unix"
.. .. .$.- attr(*, "class")= chr "packageDescription"
.. .. .$.- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/Rcurl/Meta
.. .. .$. Rsamtools :List of 18
.. .. .$. Package : chr "Rsamtools"
.. .. .$. Type : chr "Package"
.. .. .$. Title : chr "Binary alignment (BAM), FASTA, variant call (BCF), and tabixfile import"
.. .. .$. Version : chr "1.19.10"
.. .. .$. Author : chr "Martin Morgan, Herv\`e Pag\`es, Valerie Obenchain, Nathaniel Hayden"
.. .. .$. Maintainer : chr "Bioconductor Package Maintainer<maintainer@bioconductor.org>"
.. .. .$. Description: chr "This package provides an interface to the 'samtools', 'bcftools', and
'tabix' utilities (see 'LICENCE') for m"| __truncated__
.. .. .$. URL : chr "http://bioconductor.org/packages/release/bioc/html/Rsamtools.html"
.. .. .$. License : chr "Artistic-2.0 | file LICENSE"
.. .. .$. LazyLoad : chr "yes"
.. .. .$. Depends : chr "methods, S4Vectors (>= 0.5.8), IRanges (>= 1.99.17),GenomeInfoDb (>=
1.1.3), GenomicRanges (>= 1.17.19), XVector(>= 0.5.3),"| __truncated__
.. .. .$. Imports : chr "utils, BiocGenerics (>= 0.1.3), zlibbioc, bitops"
.. .. .$. Suggests : chr "GenomicAlignments, ShortRead (>= 1.19.10), GenomicFeatures,TxDb.Dmelanogaster.UCSC.dm3.
KEGG.db,TxDb.Hsapiens.UCSC."| __truncated__
.. .. .$. LinkingTo : chr "S4Vectors, IRanges, XVector, Biostrings"
.. .. .$. biocViews : chr "DataImport, Sequencing, Coverage, Alignment, QualityControl"
.. .. .$. Video : chr "https://www.youtube.com/watch?v=Rfon-DQYbWA&list=UUqaMSQd_h-
2EDGsU6WDiX0Q"
.. .. .$. Packaged : chr "2014-11-19 03:27:06 UTC; biocbuild"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-23 12:11:46 UTC; unix"
.. .. .$.- attr(*, "class")= chr "packageDescription"
.. .. .$.- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/Rsamtools/M
.. .. .$. SQLite :List of 18
.. .. .$. Package : chr "SQLite"
.. .. .$. Version : chr "1.0.0"
.. .. .$. Title : chr "SQLite Interface for R"
.. .. .$. Authors@R : chr "as.person(c( \"Hadley Wickham <hadley@rstudio.com> [aut, cre]\",
\"David A. James [aut]\", \"Seth Falcon [aut]\"))"| __truncated__
.. .. .$. Description : chr "This package embeds the SQLite database engine in R and provides an

```

```

interface compliant with the DBI package. The sou"| __truncated__
.. .. ..$ Depends : chr "R (>= 2.10.0), DBI (>= 0.3.1), methods"
.. .. ..$ Suggests : chr "testthat"
.. .. ..$ License : chr "LGPL (>= 2)"
.. .. ..$ URL : chr "https://github.com/rstats-db/RSQLite"
.. .. ..$ BugReports : chr "https://github.com/rstats-db/RSQLite/issues"
.. .. ..$ Collate : chr "'ConnectionExtensions.R' 'Connection.R' 'Driver.R' 'Connect.R' 'ConnectionRead.R'
'ConnectionTransactions.R' 'ConnectionWrite'"| __truncated__
.. .. ..$ Packaged : chr "2014-10-24 18:38:41 UTC; hadley"
.. .. ..$ Author : chr "Hadley Wickham [aut, cre], David A. James [aut], Seth Falcon [aut], SQLite
Authors [ctb] (for the included SQLite sou"| __truncated__
.. .. ..$ Maintainer : chr "Hadley Wickham <hadley@rstudio.com>"
.. .. ..$ NeedsCompilation: chr "yes"
.. .. ..$ Repository : chr "CRAN"
.. .. ..$ Date/Publication: chr "2014-10-25 01:58:48"
.. .. ..$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-03 09:47:17 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/RSQLite/M
.. .. ..$ rtracklayer :List of 16
.. .. ..$ Package : chr "rtracklayer"
.. .. ..$ Title : chr "R interface to genome browsers and their annotation tracks"
.. .. ..$ Version : chr "1.27.5"
.. .. ..$ Author : chr "Michael Lawrence, Vince Carey, Robert Gentleman"
.. .. ..$ Depends : chr "R (>= 2.10), methods, GenomicRanges (>= 1.19.3)"
.. .. ..$ Imports : chr "XML (>= 1.98-0), BiocGenerics (>= 0.11.3), S4Vectors (>=0.5.4), IRanges
(>= 2.1.6), XVector (>= 0.5.8), GenomeInfoDb(>= 1.1"| __truncated__
.. .. ..$ Suggests : chr "BSgenome (>= 1.33.4), humanStemCell, microRNA (>= 1.1.1),genefilter,
limma, org.Hs.eg.db, hgu133plus2.db,BSgenome.Hsapiens."| __truncated__
.. .. ..$ LinkingTo : chr "S4Vectors, IRanges, XVector"
.. .. ..$ Description : chr "Extensible framework for interacting with multiple genome browsers
(currently UCSC built-in) and manipulating annotatio"| __truncated__
.. .. ..$ Maintainer : chr "Michael Lawrence <michafla@gene.com>"
.. .. ..$ License : chr "Artistic-2.0"
.. .. ..$ ExtraLicenses: chr "The files in the 'src/ucsc' directory are licensed forall use by Jim
Kent, in a manner compatible with the Artistic2.0 lice"| __truncated__
.. .. ..$ Collate : chr "io.R web.R ranges.R trackDb.R browser.R ucsc.R gff.R bed.Rwig.R utils.R
bigWig.R chain.R quickload.R twobit.R fasta.Rtabix."| __truncated__
.. .. ..$ biocViews : chr "Annotation,Visualization,DataImport"
.. .. ..$ Packaged : chr "2014-11-15 02:54:37 UTC; biocbuild"
.. .. ..$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-16 03:49:19 UTC; unix"
.. .. ..- attr(*, "class")= chr "packageDescription"
.. .. ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/rtracklayer/
.. .. ..$ sendmailR :List of 16
.. .. ..$ Package : chr "sendmailR"
.. .. ..$ Version : chr "1.2-1"
.. .. ..$ Title : chr "send email using R"
.. .. ..$ Description : chr "Package contains a simple SMTP client which provides a portable
solution for sending email, including attachment, from"| __truncated__

```

```

... ..$ Authors@R : chr "c(person(\"Olaf\", \"Mersmann\", role=c(\"aut\", \"cre\"), email=\"olafm@p-
value.net\"), person(\"Quinn\", \"Weber\", \"|__truncated__
... ..$ Depends : chr "R (>= 3.0.0)"
... ..$ Imports : chr "base64enc"
... ..$ License : chr "GPL-2"
... ..$ LazyData : chr "yes"
... ..$ Packaged : chr "2014-09-21 11:16:23 UTC; olafm"
... ..$ Author : chr "Olaf Mersmann [aut, cre], Quinn Weber [ctb]"
... ..$ Maintainer : chr "Olaf Mersmann <olafm@p-value.net>"
... ..$ NeedsCompilation: chr "no"
... ..$ Repository : chr "CRAN"
... ..$ Date/Publication: chr "2014-09-21 13:32:55"
... ..$ Built : chr "R 3.2.0; ; 2014-10-14 13:47:56 UTC; unix"
... ..- attr(*, "class")= chr "packageDescription"
... ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/sendmailR/M
... ..$ snpStats :List of 16
... ..$ Package : chr "snpStats"
... ..$ Title : chr "SnpMatrix and XSnpmatrix classes and methods"
... ..$ Version : chr "1.17.0"
... ..$ Date : chr "2014-08-17"
... ..$ Author : chr "David Clayton <dc208@cam.ac.uk> "
... ..$ Description: chr "Classes and statistical methods for large SNP association studies, ex-
tending the snpMatrix package"
... ..$ Maintainer : chr "David Clayton <dc208@cam.ac.uk>"
... ..$ Depends : chr "R(>= 2.10.0), survival, Matrix, methods"
... ..$ Imports : chr "graphics, grDevices, stats, utils, BiocGenerics, zlibbioc"
... ..$ Suggests : chr "hexbin"
... ..$ License : chr "GPL-3"
... ..$ Collate : chr "ss.R contingency.table.R convert.R compare.R glm-test.Rimputation.R
indata.R long.R misc.R ld.R mvtests.R pedfile.Routdata."|__truncated__
... ..$ LazyLoad : chr "yes"
... ..$ biocViews : chr "Microarray, SNP, GeneticVariability"
... ..$ Packaged : chr "2014-10-14 01:53:09 UTC; biocbuild"
... ..$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-10-16 00:54:21 UTC; unix"
... ..- attr(*, "class")= chr "packageDescription"
... ..- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/snpStats/Me
... ..$ splines :List of 10
... ..$ Package : chr "splines"
... ..$ Version : chr "3.2.0"
... ..$ Priority : chr "base"
... ..$ Imports : chr "graphics, stats"
... ..$ Title : chr "Regression Spline Functions and Classes"
... ..$ Author : chr "Douglas M. Bates <bates@stat.wisc.edu> and William N. Venables
<Bill.Venables@csiro.au>"
... ..$ Maintainer : chr "R Core Team <R-core@r-project.org>"
... ..$ Description: chr "Regression spline functions and classes"
... ..$ License : chr "Part of R 3.2.0"
... ..$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-10-14 13:30:58 UTC; unix"

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.. .. .- attr(*, "class")= chr "packageDescription"
.. .. .- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/splines/Meta
.. .. .$ stringr :List of 15
.. .. .$ Package : chr "stringr"
.. .. .$ Maintainer : chr "Hadley Wickham <h.wickham@gmail.com>"
.. .. .$ License : chr "GPL-2"
.. .. .$ Title : chr "Make it easier to work with strings."
.. .. .$ Type : chr "Package"
.. .. .$ Author : chr "Hadley Wickham <h.wickham@gmail.com>"
.. .. .$ Description : chr "stringr is a set of simple wrappers that make R's string functions more
consistent, simpler and easier to use. It doe"| __truncated__
.. .. .$ Version : chr "0.6.2"
.. .. .$ Depends : chr "R (>= 2.14)"
.. .. .$ Suggests : chr "testthat (>= 0.3)"
.. .. .$ Collate : chr "'c.r' 'checks.r' 'count.r' 'detect.r' 'dup.r' 'extract.r' 'length.r' 'locate.r'
'match.r' 'modifiers.r' 'pad-trim.r' 'replace'| __truncated__
.. .. .$ Packaged : chr "2012-12-05 21:47:03 UTC; hadley"
.. .. .$ Repository : chr "CRAN"
.. .. .$ Date/Publication: chr "2012-12-06 08:39:59"
.. .. .$ Built : chr "R 3.2.0; ; 2014-08-13 10:45:29 UTC; unix"
.. .. .- attr(*, "class")= chr "packageDescription"
.. .. .- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/stringr/Meta
.. .. .$ survival :List of 19
.. .. .$ Title : chr "Survival Analysis"
.. .. .$ Maintainer : chr "Terry M Therneau <therneau.terry@mayo.edu>"
.. .. .$ Priority : chr "recommended"
.. .. .$ Package : chr "survival"
.. .. .$ Version : chr "2.37-7"
.. .. .$ Depends : chr "stats, utils, graphics, splines, R (>= 2.13.0)"
.. .. .$ LazyData : chr "Yes"
.. .. .$ LazyLoad : chr "Yes"
.. .. .$ ByteCompile : chr "Yes"
.. .. .$ Authors@R : chr "c(person(c(\"Terry\", \"M\"), \"Therneau\", email=\"therneau.terry@mayo.edu\",
role=c(\"aut\"| __truncated__
.. .. .$ Description : chr "survival analysis: descriptive statistics, two-sample tests, parametric
accelerated failure models, Cox model. Delayed entry"| __truncated__
.. .. .$ License : chr "LGPL (>= 2)"
.. .. .$ URL : chr "http://r-forge.r-project.org"
.. .. .$ Packaged : chr "2014-01-22 13:49:28 UTC; therneau"
.. .. .$ Author : chr "Terry M Therneau [aut, cre], Thomas Lumley [ctb, trl] (original S->R port
and maintainer until 2009)"
.. .. .$ NeedsCompilation: chr "yes"
.. .. .$ Repository : chr "CRAN"
.. .. .$ Date/Publication: chr "2014-01-22 17:48:51"
.. .. .$ Built : chr "R 3.2.0; x86_64-apple-darwin13.3.0; 2014-08-13 10:33:52 UTC; unix"
.. .. .- attr(*, "class")= chr "packageDescription"
.. .. .- attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/survival/Meta
.. .. .$ VariantAnnotation:List of 18

```

```

.. .. .$. Package : chr "VariantAnnotation"
.. .. .$. Type : chr "Package"
.. .. .$. Title : chr "Annotation of Genetic Variants"
.. .. .$. Description: chr "Annotate variants, compute amino acid coding changes, predict coding
outcomes"
.. .. .$. Version : chr "1.13.12"
.. .. .$. Authors@R : chr "c(person(\"Valerie\", \"Obenchain\", role=c(\"aut\", \"cre\"), email=\"vobencha@fhcrc.org\"),
person(\"Martin\", \"|__truncated__
.. .. .$. License : chr "Artistic-2.0"
.. .. .$. Depends : chr "R (>= 2.8.0), methods, BiocGenerics (>= 0.7.7), GenomeInfoDb(>=
1.1.3), GenomicRanges (>= 1.19.7), Rsamtools (>= 1.19.4)"
.. .. .$. Imports : chr "utils, DBI, zlibbioc, Biobase, S4Vectors (>= 0.2.3), IRanges(>= 1.99.28),
XVector (>= 0.5.6), Biostrings (>= 2.33.5), Annota"|__truncated__
.. .. .$. Suggests : chr "RUnit, BSgenome.Hsapiens.UCSC.hg19, TxDb.Hsapiens.UCSC.hg19.knownGene, SNPlocs.Hsapiens
__truncated__
.. .. .$. LinkingTo : chr "S4Vectors, IRanges, XVector, Biostrings, Rsamtools"
.. .. .$. LazyLoad : chr "yes"
.. .. .$. biocViews : chr "DataImport, Sequencing, SNP, Annotation, Genetics"
.. .. .$. Video : chr "https://www.youtube.com/watch?v=Ro0IHQ_J-I&list=UUqaMSQd_h-
2EDGsU6WDiX0Q"
.. .. .$. Packaged : chr "2014-11-20 04:00:42 UTC; biocbuild"
.. .. .$. Author : chr "Valerie Obenchain [aut, cre], Martin Morgan [aut], Michael Lawrence [aut],
Stephanie Gogarten [ctb]"
.. .. .$. Maintainer : chr "Valerie Obenchain <vobencha@fhcrc.org>"
.. .. .$. Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-23 12:12:37 UTC; unix"
.. .. .$. attr(*, "class")= chr "packageDescription"
.. .. .$. attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/VariantAnn
.. .. .$. XML :List of 19
.. .. .$. Package : chr "XML"
.. .. .$. Version : chr "3.98-1.1"
.. .. .$. Author : chr "Duncan Temple Lang (duncan@r-project.org)"
.. .. .$. Maintainer : chr "Duncan Temple Lang <duncan@r-project.org>"
.. .. .$. Title : chr "Tools for parsing and generating XML within R and S-Plus."
.. .. .$. Depends : chr "R (>= 1.2.0), methods, utils"
.. .. .$. Imports : chr "methods"
.. .. .$. Suggests : chr "bitops, RCurl"
.. .. .$. SystemRequirements: chr "libxml2 (>= 2.6.3)"
.. .. .$. Description : chr "This package provides many approaches for both reading and creating
XML (and HTML) documents (including DTDs), both lo"|__truncated__
.. .. .$. Note : chr "In version 2.4.0 of this package, a new approach to garbagecollection has been
implemented and it is experimental. You cand"|__truncated__
.. .. .$. URL : chr "http://www.omegahat.org/R/XMLSchema"
.. .. .$. License : chr "BSD"
.. .. .$. Collate : chr "AAA.R DTD.R DTDClasses.R DTDDRef.R SAXMethods.S XMLClasses.R applyDOM.R
assignChild.R catalog.R createNode.R dynSupports.Rerr"|__truncated__
.. .. .$. Packaged : chr "2013-06-20 13:45:20 UTC; ripley"
.. .. .$. NeedsCompilation : chr "yes"
.. .. .$. Repository : chr "CRAN"

```

```

.. .. .$ Date/Publication : chr "2013-06-20 15:50:33"
.. .. .$ Built : chr "R 3.2.0; x86_64-apple-darwin13.3.0; 2014-08-13 10:46:02 UTC; unix"
.. .. .$ attr(*, "class")= chr "packageDescription"
.. .. .$ attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/XML/Meta/
.. .. .$ XVector :List of 15
.. .. .$ Package : chr "XVector"
.. .. .$ Title : chr "Representation and manipulation of external sequences"
.. .. .$ Description: chr "Memory efficient S4 classes for storing sequences \"externally\" (behind
an R external pointer, or on disk)."
.. .. .$ Version : chr "0.7.2"
.. .. .$ Author : chr "H. Pages and P. Aboyoun"
.. .. .$ Maintainer : chr "H. Pages <hpages@fhcrc.org>"
.. .. .$ biocViews : chr "Infrastructure, DataRepresentation"
.. .. .$ Depends : chr "R (>= 2.8.0), methods, BiocGenerics (>= 0.11.3), S4Vectors (>=0.2.0),
IRanges (>= 2.1.2)"
.. .. .$ Imports : chr "methods, BiocGenerics, S4Vectors, IRanges"
.. .. .$ LinkingTo : chr "S4Vectors, IRanges"
.. .. .$ Suggests : chr "Biostrings, drosophila2probe, RUnit"
.. .. .$ License : chr "Artistic-2.0"
.. .. .$ Collate : chr "SharedVector-class.R SharedRaw-class.R SharedInteger-class.RSharedDouble-
class.R XVector-class.R XRaw-class.RXInteger-class"|__truncated__
.. .. .$ Packaged : chr "2014-11-06 05:08:02 UTC; biocbuild"
.. .. .$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-11-07 15:41:56 UTC; unix"
.. .. .$ attr(*, "class")= chr "packageDescription"
.. .. .$ attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/XVector/Me
.. .. .$ zlibbioc :List of 13
.. .. .$ Package : chr "zlibbioc"
.. .. .$ Type : chr "Package"
.. .. .$ Title : chr "An R packaged zlib-1.2.5"
.. .. .$ Version : chr "1.13.0"
.. .. .$ Author : chr "Martin Morgan"
.. .. .$ Maintainer : chr "Bioconductor Package Maintainer <maintainer@bioconductor.org>"
.. .. .$ Description: chr "This package uses the source code of zlib-1.2.5 to create libraries for
systems that do not have these available via other"|__truncated__
.. .. .$ URL : chr "http://bioconductor.org/packages/release/bioc/html/Zlibbioc.html"
.. .. .$ License : chr "Artistic-2.0 + file LICENSE"
.. .. .$ LazyLoad : chr "yes"
.. .. .$ biocViews : chr "Infrastructure"
.. .. .$ Packaged : chr "2014-10-14 02:39:15 UTC; biocbuild"
.. .. .$ Built : chr "R 3.2.0; x86_64-apple-darwin13.4.0; 2014-10-16 00:54:05 UTC; unix"
.. .. .$ attr(*, "class")= chr "packageDescription"
.. .. .$ attr(*, "file")= chr "/Users/stvjc/ExternalSoft/R-devel-dist/R.framework/Versions/3.2/Resources/library/zlibbioc/Me
.. .. attr(*, "class")= chr "sessionInfo"

```

Details

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

lower bound

Examples

```
data(filtFDR)
filtFDR
```

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)

```

manhWngr	<i>manhattan plot with named GRanges</i>
----------	--

Description

manhattan plot with named GRanges

Usage

```
manhWngr(store, probeid = "ENSG00000183814.10", sym = "LIN9", fdrsupp, namedGR, slstyle = "NCBI", xlab,
```

Arguments

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

Examples

```
require(geuvStore)
require(gQTLBase)
reg = partialRegistry()
store = ciseStore(reg, addProbeMap=TRUE, addRangeMap=FALSE)
data(hmm878)
data(filtFDR)
manhWngr(store, fdrsupp=filtFDR, namedGR=hmm878)
```

queryVCF	<i>obtain SnpMatrix from VCF genotypes</i>
----------	--

Description

obtain SnpMatrix from VCF genotypes

Usage

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

Arguments

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

Value

a list of length two

readout	output of readVcf
sm	output of genotypeToSnpMatrix run on the read result

Examples

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

senstab	<i>create a plottable table for eQTL sensitivity analysis visualization</i>
---------	---

Description

create a plottable table for eQTL sensitivity analysis visualization

Usage

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

Arguments

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

Details

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

Value

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

Examples

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

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

```

# and specify 15 cpu for BatchJobs in .BatchJobs.R

sens1 = makeRegistry("sens1", file.dir="sens1",
  packages=c("gQTLstats", "dplyr"),
  src.files="parms.R") # note parms.R

sens4One = function(z) {
  load("../bigStore.rda") # get a ciseStore instance
  ans = storeToFDRByProbe(bigStore, xprobs=seq(.01,.99,.01), # xprobs
    # needs to be chosen with care
  filter=function(x) x[which(x$MAF >= parms[z,1] &
    x$mindist <= parms[z,2])])
  ans = setFDRfunc(ans, span=.35) # span can be important
  list(fdrsups=ans, parms=parms[z,])
}

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

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

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

```

setFDRfunc	<i>estimate and store function relating association scores to approximate plug-in FDR</i>
------------	---

Description

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

Usage

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

Arguments

FDRsupp instance of [FDRsupp-class](#)

fudge	if FDR is zero, a log or logistic transform will fail; we add the small positive number fudge to avoid this
zthresh	for association scores greater than this value, a hard value of FDR 0 is assigned
...	arguments passed to <code>lo</code> for the smooth model relating association score to FDR at selected quantiles of the association score distribution

Value

returns an updated `FDRsupp-class` instance

Examples

```
data(filtFDR)
filtFDR2 = setFDRfunc(filtFDR)
```

storeToStats	<i>extract a vector from store results as ff (out of memory reference); support statistical reductions</i>
--------------	--

Description

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

Usage

```
storeToQuantiles(store, field,
  probs=c(seq(0,.999,.001), 1-(c(1e-4,1e-6,1e-6,1e-7))),
  ids = NULL, ..., checkField = FALSE, filter=force)
storeToHist(store,
  getter = function(x) as.numeric(S4Vectors::as.matrix(mcols(x)[,
  c("permScore_1", "permScore_2", "permScore_3")])), breaks, ids=NULL,
  filter=force)
storeToFDR(store, xprobs = c(seq(0, 0.999, 0.001), 1 - (c(1e-04,
  1e-06, 1e-06, 1e-07))), xfield = "chisq",
  getter = function(x) as.numeric(S4Vectors::as.matrix(mcols(x)[,
  c("permScore_1", "permScore_2", "permScore_3")])), nperm=3,
  filter=force)
```

Arguments

store	instance of <code>ciseStore-class</code>
field	character tag, length one, must be name of a numeric field in the result set (typically something like 'chisq' in the GRanges generated by <code>cisAssoc</code>)
xfield	as field, for FDR computation, see Details.
ids	job ids to be used; if NULL, process all jobs
breaks	boundaries of histogram bins

...	supplied to makeRegistry for a temporary registry: typically will be a vector of package names if additional packages are needed to process results
checkField	if TRUE steps will be taken to verify that the tag to which 'field' evaluates is present in result in the first job
probs	numeric vector of probabilities with values in [0,1]. See quantile.ff .
xprobs	percentiles of the empirical distribution of the association statistic at which FDR estimates are recorded.
getter	function of a single argument that extracts a numeric vector of association scores obtained under permutation
nperm	number of genome-wide permutations recorded in the store (or, in special cases, retrieved for nonstandard versions of getter
x	instance of FDRsupp
filter	function accepting and returning GRanges instance, executed when cisAssoc result is loaded to modify that result, defaults to no-op

Details

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

Value

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

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

storeToFDR and storeToFDRByProbe return an instance of FDRsupp class

Note

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

Examples

```
stopifnot(require(geuvStore))
require(BatchJobs)
require(gQTLBase)
reg = partialRegistry()
store = ciseStore(reg, addProbeMap=FALSE, addRangeMap=FALSE)
library(doParallel)
if (.Platform$OS.type == "windows") {
  registerDoSEQ()
} else registerDoParallel(cores=max(c(detectCores()-1,1)))
smchisq = storeToFF( store, "chisq", ids=store@validJobs[1:3])
smchisq
qs = storeToQuantiles( store, "chisq", ids = store@validJobs[1:5],
  probs=seq(.1,.9,.1) )
qs
```

```
hh = storeToHist( store, ids = store@validJobs[1:5], breaks=
  c(0,q5,1e9) )
hh$counts
fd = storeToFDR( store, xprobs=c(seq(.05,.95,.05),.99,.999) )
tail(getTab(fd),4)
sss = storeToFDRByProbe( store , xprobs=c(seq(.05,.95,.05),.99) )
tail(getTab(sss),4)
```

txsPlot

visualize transformed FDR against transformed association statistics

Description

visualize transformed FDR against transformed association statistics

Usage

```
txsPlot(FDRsupp)
```

Arguments

FDRsupp an instance of [FDRsupp-class](#)

Examples

```
data(filtFDR)
txsPlot(filtFDR)
```

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