Package 'dsQTL'

October 7, 2015

Title dsQTL, data excerpt from Degner et al. 2012 Nature letter

Version 0.6.0

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

Description dsQTL, excerpt from Degner et al. 2012 Nature letter on DNA variants associated with DnaseI hypersensitivity

Suggests

Depends R (>= 2.15.0), utils, GenomicRanges, Biobase, GGBase

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

License Artistic-2.0

LazyLoad yes

biocViews ExperimentData, Genome, SequencingData, DNASeqData, NCI, Project1000genomes, BiocViews

NeedsCompilation no

R topics documented:

`dsQTL-package` *dsQTL, data excerpt from Degner et al. 2012 Nature letter*

Description

dsQTL, excerpt (and complete image, added March 2013) from Degner et al. 2012 Nature letter on DNA variants associated with DnaseI hypersensitivity

Details

Package:	dsQTL
Version:	0.0.26
Suggests:	
Depends:	R (>= 2.15.0), utils, GenomicRanges, Biobase, GGBase
License:	Artistic-2.0
LazyLoad:	yes
biocViews:	genetics, HighThroughputSequencingData, ExperimentData
Packaged:	2014-02-01 17:21:58 UTC; biocbuild
Built:	R 3.1.0; ; 2014-02-13 03:35:19 UTC; unix

This package has two main components. First, a selection of genotype and DNase-seq data for illustration of dsQTL identification. Second, a complete image of the filtered DHS assay results is available in SummarizedExperiment.

The slide deck for the Feb 2012 Seattle Bioconductor workshop has illustrations.

A utility function `SE2ES` will create an ExpressionSet instance from a SummarizedExperiment as serialized here.

Author(s)

VJ Carey <stvjc@channing.harvard.edu>

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

References

PMID 22307276

Examples

```
#
# this chunk illustrates how to use a cluster to iterate cis-association
# testing, with 1000G VCF as the genotype source.  doChr sets up a
# request for chunked iteration over DHS sites in one chromosome
# upon completion a single GRanges is saved to disk
#
## Not run:
library(BatchJobs)
library(GGtools)
library(dsQTL)
data(DHStop5_hg19)

doChr = function(ctag="chr5") {
 regobn = paste0("reg", ctag)
 idtag = paste0("run", ctag)
 assign(regobn, makeRegistry( id = idtag,  seed=123, file.dir=paste0("run", ctag, "dir"),
  packages=c("Rsamtools", "VariantAnnotation", "rtracklayer",
  "GGtools", "dsQTL")))
```

```
 cfun = function(chrtag) function(inds) {
  vcfpath = function(chrn="chr9") {
      patt = "[YOUR PATH TO 1000Genomes_Phase1_v3/ALL HERE]/ALL.
      sub("
      }
  if (!exists("DHStop5_hg19")) data(DHStop5_hg19)
  c1.tf = TabixFile(vcfpath(chrtag))
  cisAssoc( DHStop5_hg19[inds,], vcf.tf=c1.tf, rhs=~1, cisradius=1000,
     stx=force, vtx=force, snfilt=function(x) gsub("chr", "", x),
     genome="hg19", assayind=1 )
  }

 inds2 = which(seqnames(DHStop5_hg19)==ctag)

 indset = as.list( GGtools:::ivector(inds2, chunkSize=100) )

 batchMap( get(regobn), cfun(ctag), indset )

 save(list=regobn, file=paste0(regobn, ".rda"))

 submitJobs( get(regobn), job.delay = function(n,i) 10 )
 waitForJobs( get(regobn) )

 fixer = function(x) { if (!is(x$ALT, "DNAStringSetList")) x$ALT = DNAStringSetList(x$ALT); x}

 fullobn = paste0("dsqfull_", ctag)

 assign(fullobn, reduceResults(get(regobn), fun=function(aggr, job, res, ...) unlist(GRangesList(c(fixer(aggr),
    fixer(res))))))

 save(list=fullobn, file=paste0(fullobn, ".rda"))

}

doChr("chr18")

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

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