

# Package ‘dsQTL’

April 13, 2017

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

**Version** 0.12.0

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

**Depends** R (>= 2.15.0), utils, Biobase, SummarizedExperiment, GGBase  
(>= 3.31.1)

**Suggests** GGtools, rtracklayer

**License** Artistic-2.0

**LazyLoad** yes

**biocViews** ExperimentData, Genome, SequencingData, DNASEqData, NCI,  
Project1000genomes, BiocViews

**NeedsCompilation** no

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## 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 `RangedSummarizedExperiment`.

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

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

### Author(s)

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### 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$ALT, "DNAStrngSetList")) x$ALT = DNAStrngSetList(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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