

# Package ‘dsQTL’

April 14, 2020

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

**Version** 0.24.0

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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, DNaseSeqData, NCI, Project1000genomes, BiocViews

**git\_url** <https://git.bioconductor.org/packages/dsQTL>

**git\_branch** RELEASE\_3\_10

**git\_last\_commit** 471fb5b

**git\_last\_commit\_date** 2019-10-29

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

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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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