

dsQTL: exploring DNA-variants associated with DNaseI hypersensitivity

VJ Carey

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1 Introduction

Degner et al. (2012) publish information on associations between DNA variants (SNP, SNV, and indels) and DNaseI hypersensitivity measures acquired via DNase-Seq.

This package includes information from the Chicago group on normalized DNase-seq data for chromosomes 2 and 17, and genotype data from chromosome 2 only.

2 The basic data structure

```
> library(dsQTL)
> data(DSQ_17)
> exptData(DSQ_17)
```

```
List of length 2
names(2): MIAME annotation
```

```
> exptData(DSQ_17)[[1]]
```

Experiment data

Experimenter name: Degner JF

Laboratory: Department of Human Genetics, University of Chicago, Chicago, Illinois 60

Contact information:

Title: DNaseI sensitivity QTLs are a major determinant of human expression variation.

URL:

PMIDs: 22307276

Abstract: A 252 word abstract is available. Use 'abstract' method.

We use summarized experiment structure for the assay data, but the imputed genotype data are kept separate, in the package, in the inst/parts folder.

The data structure on chr2, which will be used to reproduce some findings, is more mature

```
> data(DSQ_2)
> names(assays(DSQ_2))
```

```
[1] "normDHS"
```

```
> assays(DSQ_2)[[1]][1:5,1:5]
```

| | NA18486 | NA18498 | NA18499 | NA18501 | NA18502 |
|------------|------------|-------------|------------|------------|------------|
| dhs_2_1202 | -0.2684343 | -0.78076674 | -0.4840237 | 2.3894003 | -1.0813642 |
| dhs_2_1602 | -1.4445813 | 0.92170439 | 0.5812017 | 0.8627376 | 0.5186581 |
| dhs_2_2002 | 0.7624075 | -0.12340745 | -1.1821308 | 1.4253179 | 0.3125592 |
| dhs_2_7502 | 0.1242963 | 0.60788505 | 0.6754706 | -0.0452303 | 0.4876332 |
| dhs_2_8802 | -0.9554503 | -0.06016578 | -0.1990696 | 1.9383937 | -1.3758668 |

```
> rowData(DSQ_2)
```

GRanges object with 96024 ranges and 0 metadata columns:

| | seqnames | ranges | strand |
|-----------------|----------|------------------------|--------|
| | <Rle> | <IRanges> | <Rle> |
| dhs_2_1202 | chr2 | [1202, 1301] | * |
| dhs_2_1602 | chr2 | [1602, 1701] | * |
| dhs_2_2002 | chr2 | [2002, 2101] | * |
| dhs_2_7502 | chr2 | [7502, 7601] | * |
| dhs_2_8802 | chr2 | [8802, 8901] | * |
| ... | ... | ... | ... |
| dhs_2_242698102 | chr2 | [242698102, 242698201] | * |
| dhs_2_242711702 | chr2 | [242711702, 242711801] | * |
| dhs_2_242737502 | chr2 | [242737502, 242737601] | * |
| dhs_2_242737902 | chr2 | [242737902, 242738001] | * |
| dhs_2_242739902 | chr2 | [242739902, 242740001] | * |

```
-----
```

```
seqinfo: 1 sequence from an unspecified genome; no seqlengths
```

To implement the GGBase protocol for on-the-fly generation of smlSet instances from getSS queries, we have an ExpressionSet instance with specific names.

```
> data(eset, package="dsQTL")
> ex
```

```

ExpressionSet (storageMode: lockedEnvironment)
assayData: 96024 features, 70 samples
  element names: exprs
protocolData: none
phenoData
  sampleNames: NA18486 NA18498 ... NA19257 (70 total)
  varLabels: naid one ... isFounder (9 total)
  varMetadata: labelDescription
featureData: none
experimentData: use 'experimentData(object)'
Annotation:

```

The genotype data supplied by Degner et al are imputed to 1000 genomes haplotypes, and are reals in [0,2]. For simplicity the current image of the data uses the rounding of the fractional genotypes x with $\text{round}(x,0)$.

The feature data refer to the retained 100bp segments that were summarized for DNaseI hypersensitivity and found to lie in the uppermost 5% of the distribution.

```

> library(Biobase)
> fData(ex)[1:5,,drop=FALSE]

```

data frame with 0 columns and 5 rows

We can get the integrated container as

```

> library(GGBase)
> ds2 = getSS("dsQTL", "roundGT_2")

```

the name indicates that we simply rounded the imputed fractional genotypes to nearest integer.

A very restricted search is:

```

> # need to get rid of SNPlocs package getSNPlocs
> getSNPlocs = dsQTL::getSNPlocs # force
> library(GGtools)
> #library(parallel)
> #options(mc.cores=12)
> n1 = best.cis.eQTLs(smpack="dsQTL", radius=2000, geneannopk="dsQTL",
+   snpannopk="dsQTL", chrnames="2", smchrpref="roundGT_",
+   smFilter = function(x) GTFfilter(x, lower=0.05)[23810:23830,],
+   # geneApply=mclapply)
+   geneApply=lapply)

```

```

get data...build map...run smFilter...filter probes in map...tests...filter...done.
get data...build map...run smFilter...filter probes in map...tests...filter...done.
get data...build map...run smFilter...filter probes in map...tests...filter...done.

```

```
> n1
```

GGtools mcwBestCis instance. The call was:

```
best.cis.eQTLs(smpack = "dsQTL", radius = 2000, chrnames = "2",
  smchrpref = "roundGT_", geneApply = lapply, geneannopk = "dsQTL",
  snpannopk = "dsQTL", smFilter = function(x) GTFfilter(x,
  lower = 0.05)[23810:23830, ])
```

Best loci for 21 probes are recorded.

There were 102 gene:snp tests.

Top 4 probe:SNP combinations:

GRanges object with 4 ranges and 6 metadata columns:

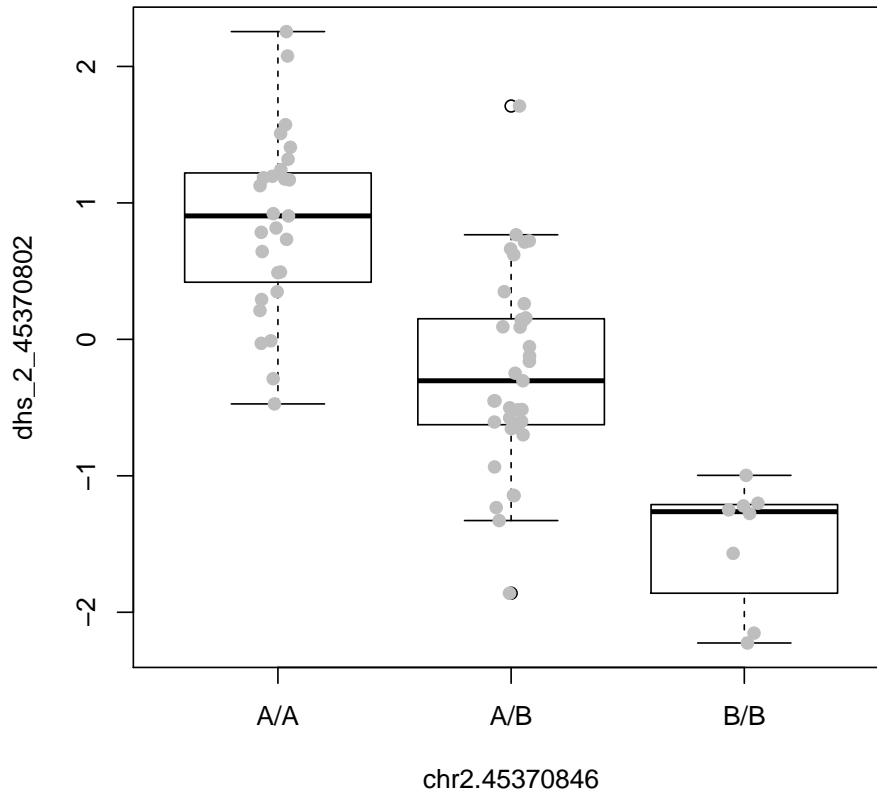
| | seqnames | ranges | strand | score | snpid |
|----------------|-----------|----------------------|-----------|-----------|---------------|
| | <Rle> | <IRanges> | <Rle> | <numeric> | <character> |
| dhs_2_45370802 | 2 | [45368802, 45372901] | * | 38.64 | chr2.45370846 |
| dhs_2_45370702 | 2 | [45368702, 45372801] | * | 29.11 | chr2.45370846 |
| dhs_2_45369802 | 2 | [45367802, 45371901] | * | 19.14 | chr2.45370846 |
| dhs_2_45304402 | 2 | [45302402, 45306501] | * | 6.82 | chr2.45302815 |
| | snploc | radiusUsed | nsnp | fdr | |
| | <integer> | <numeric> | <integer> | <numeric> | |
| dhs_2_45370802 | 45370846 | 2000 | 2 | 0 | |
| dhs_2_45370702 | 45370846 | 2000 | 2 | 0 | |
| dhs_2_45369802 | 45370846 | 2000 | 3 | 0 | |
| dhs_2_45304402 | 45302815 | 2000 | 5 | 0 | |

seqinfo: 1 sequence from an unspecified genome; no seqlengths

====

use chromsUsed(), fullreport(), etc. for additional information.

```
> plot_EvG(probeId("dhs_2_45370802"), rsid("chr2.45370846"), getSS("dsQTL", "roundGT_
+ wrapperEndo=function(x){annotation(x)="dsQTL"; x}))
```



3 Provenance

3.1 Normed DNaseI hypersensitivity scores

The dsQTL package data structures `DSQ_2` and `DSQ_17` are generated from GEO GSE31388, from which a collection of 70 compressed BED format files were acquired Aug 9 2011. These are imported using the `rtracklayer` package to obtain location and score information for all the recorded DNaseI hypersensitivity assay results. For example, after import for NA19257, we have

```
Browse[1]> x
[1] "NA19257"
Browse[1]> tmp
RangedData with 1465907 rows and 3 value columns across 22 spaces
      space          ranges |      name      score  strand
  <factor>    <IRanges> | <character> <numeric> <factor>
```

| | | | | | | |
|---------|-------|----------------------|-----|-----|-------------|-----|
| 1 | chr1 | [402, 501] | | NOT | -0.67088720 | + |
| 2 | chr1 | [502, 601] | | NOT | -1.69969288 | + |
| 3 | chr1 | [602, 701] | | NOT | 0.13520754 | + |
| ... | ... | ... | ... | ... | ... | ... |
| 1465905 | chr22 | [49571602, 49571701] | | NOT | 0.62742318 | + |
| 1465906 | chr22 | [49575102, 49575201] | | NOT | -0.09417379 | + |
| 1465907 | chr22 | [49581602, 49581701] | | NOT | -0.29496269 | + |

The scores for locations on chromosome 2 were collected using

```

> proc1 = function(x) {
+   library(rtracklayer)
+   tmp = import(paste(x, ".qnorm.bed.gz", sep=""))
+   stt = split(tmp, space(tmp))
+   obn = paste(x, "_dsq_chr2", sep="")
+   assign(obn, stt[["chr2"]])
+   save(list=obn, file=paste(obn, ".rda", sep=""))
+   NULL
+ }

```

The regions and scores reported are described in the GEO metadata as

We also provide BED file format data for each individual for the top 5% of the genome in terms of total sensitivity. This data was mapped to hg18 using a custom read-mapping algorithm which we describe in detail in the associated publication. Measures of DNase sensitivity were quantile normalized within each individual to a standard normal distribution. Each individual was corrected for GC bias and the top 4 principle (sic) components were removed from the data (See manuscript).

Score data were structured as a matrix with columns corresponding to Yoruba HapMap subject, and rows corresponding to reported hypersensitivity regions.

The `SummarizedExperiment` container is used to unite range and score data in the assays component, and allied metadata are available in `exptData` and `colData` components.

3.2 Genotype data

Textual representation of the allelic doses is provided at http://eqtl.uchicago.edu/dsQTL_data/GENOTYPES/. As of Oct 2012, these were rounded to allele counts to allow use of `snpMatrix` representation for chromosome 2 genotypes; propagation of dosage fractions will be undertaken in late 2012.

4 Session information

```
> sessionInfo()
```

```
R version 3.1.1 Patched (2014-09-25 r66681)
```

```
Platform: x86_64-unknown-linux-gnu (64-bit)
```

```
locale:
```

```
[1] LC_CTYPE=en_US.UTF-8      LC_NUMERIC=C
[3] LC_TIME=en_US.UTF-8      LC_COLLATE=C
[5] LC_MONETARY=en_US.UTF-8  LC_MESSAGES=en_US.UTF-8
[7] LC_PAPER=en_US.UTF-8     LC_NAME=C
[9] LC_ADDRESS=C             LC_TELEPHONE=C
[11] LC_MEASUREMENT=en_US.UTF-8 LC_IDENTIFICATION=C
```

```
attached base packages:
```

```
[1] splines  stats4  parallel  stats      graphics  grDevices  utils
[8] datasets  methods  base
```

```
other attached packages:
```

```
[1] GGtools_5.2.0      data.table_1.9.4    dsQTL_0.3.1
[4] GGBase_3.28.0      snpStats_1.16.0     Matrix_1.1-4
[7] survival_2.37-7    Biobase_2.26.0      GenomicRanges_1.18.1
[10] GenomeInfoDb_1.2.0 IRanges_2.0.0       S4Vectors_0.4.0
[13] BiocGenerics_0.12.0
```

```
loaded via a namespace (and not attached):
```

```
[1] AnnotationDbi_1.28.0  BBmisc_1.7          BSgenome_1.34.0
[4] BatchJobs_1.4         BiocParallel_1.0.0  Biostrings_2.34.0
[7] DBI_0.3.1             Formula_1.1-2       GenomicAlignments_1.2.0
[10] GenomicFeatures_1.18.0 Gviz_1.10.0         Hmisc_3.14-5
[13] KernSmooth_2.23-13   MASS_7.3-35         R.methodsS3_1.6.1
[16] RColorBrewer_1.0-5    RCurl_1.95-4.3      ROCR_1.0-5
[19] RSQLite_0.11.4       Rcpp_0.11.3         Rsamtools_1.18.0
[22] VariantAnnotation_1.12.0 XML_3.98-1.1        XVector_0.6.0
[25] acepack_1.3-3.3      annotate_1.44.0      base64enc_0.1-2
[28] biglm_0.9-1          biomaRt_2.22.0      biovizBase_1.14.0
[31] bit_1.1-12           bitops_1.0-6        brew_1.0-6
[34] caTools_1.17.1       checkmate_1.4        chron_2.3-45
[37] cluster_1.15.3       codetools_0.2-9     colorspace_1.2-4
[40] dichromat_2.0-0      digest_0.6.4        fail_1.2
[43] ff_2.2-13           foreach_1.4.2       foreign_0.8-61
[46] gdata_2.13.3         genefilter_1.48.1   ggplot2_1.0.0
```

| | | | |
|------|--------------------|---------------------|--------------------|
| [49] | gplots_2.14.2 | grid_3.1.1 | gtable_0.1.2 |
| [52] | gtools_3.4.1 | hexbin_1.27.0 | iterators_1.0.7 |
| [55] | lattice_0.20-29 | latticeExtra_0.6-26 | matrixStats_0.10.3 |
| [58] | munsell_0.4.2 | nnet_7.3-8 | plyr_1.8.1 |
| [61] | proto_0.3-10 | reshape2_1.4 | rpart_4.1-8 |
| [64] | rtracklayer_1.26.1 | scales_0.2.4 | sendmailR_1.2-1 |
| [67] | stringr_0.6.2 | tools_3.1.1 | xtable_1.7-4 |
| [70] | zlibbioc_1.12.0 | | |