Using the DNaseI hypersensitivity data from encode in R

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1 Introduction

Annotation tracks from UCSC hg18 can be used with Bioconductor to help establish genomic contexts of events or alterations. The CD4-based hypersensitivity assays are collected in the structure rawCD4 in package encoDnaseI:

```
> library(encoDnaseI)
> data(rawCD4)
> rawCD4

hg18track (storageMode: lockedEnvironment)
assayData: 382713 features, 1 samples
  element names: dataVals
protocolData: none
phenoData: none
featureData
  featureNames: 1 2 ... 382713 (382713 total)
  fvarLabels: bin chrom chromStart chromEnd
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
  pubMedIds: 16791207
Annotation:
```

At present, we can subset the data by casting a chromosome number:

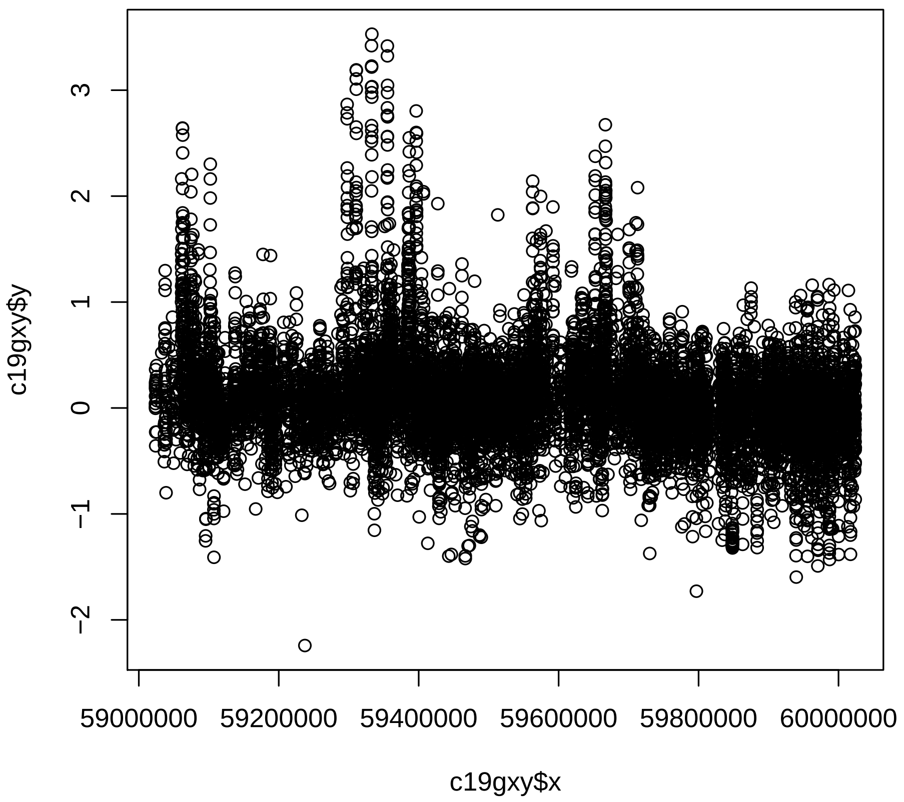
```
> c19g = rawCD4[chrnum(19)]
> c19g

hg18track (storageMode: lockedEnvironment)
assayData: 11158 features, 1 samples
  element names: dataVals
```

```
protocolData: none
phenoData: none
featureData
  featureNames: 129572 129573 ... 140729 (11158 total)
  fvarLabels: bin chrom chromStart chromEnd
  fvarMetadata: labelDescription
experimentData: use 'experimentData(object)'
  pubMedIds: 16791207
Annotation:
```

And we can get a trace of values along the chromosome:

```
> c19gxy = getTrkXY(c19g)
> plot(c19gxy)
```



2 Coupling the DnaseI series to genetics of gene expression

We would like to subset a racExSet from GGdata and look at snps that are in regions of high DNaseI sensitivity. Some infrastructure to help with this is:

```
> clipSnps = function(sms, chrn, lo, hi) {
+     allp = getSnpLocs(sms)
+     allp = allp - allp[1]
+     ok = allp >= lo & allp <= hi
+     thesm = smList(sms)[[1]]
+     rsn = colnames(thesm)
+     rid = rsn[which(ok)]
+     thesm = thesm[, rid, drop = FALSE]
+     nn = new.env()
+     tmp = list(thesm)
+     names(tmp) = as.character(chrn)
+     assign("smList", tmp, nn)
+     sms@smlEnv = nn
+     sms@activeSnpInds = which(ok)
+     sms
+ }
> rangeX = function(htrk) {
+     range(getTrkXY(htrk)$x)
+ }
```

So we get the information on expression and SNPs in chr19g and filter:

```
> library(GGtools)
> library(GGdata)
> h19 = getSS("GGdata", "19")
> rs19g = rangeX(c19g)
> library(SNPlocs.Hsapiens.dbSNP.20090506)
> c19l = getSNPlocs("chr19")
> h19locs = rbind(rsid = as.numeric(c19l[, "RefSNP_id"]), loc = as.numeric(c19l[,
+     "loc"]))
> goodlocs = which(h19locs[2, ] >= rs19g[1] & h19locs[2, ] <= rs19g[2])
> h19rsn = paste("rs", h19locs[1, goodlocs], sep = "")
> h19trim = h19[rsid(h19rsn), ]
```

A gene-specific screen can be computed as follows:

```
> oo = options()
> options(warn = 0)
> library(GGtools)
> showMethods("gwSnpTests")
```

```
Function: gwSnpTests (package GGtools)
sym="formula", sms="smlSet", cnum="cnumOrMissing", cs="missing"
sym="formula", sms="smlSet", cnum="snpdepth", cs="chunksize"
sym="formula", sms="smlSet", cnum="snpdepth", cs="missing"
```

```
> smxi1 = gwSnpTests(genesym("MXI1") ~ 1 - 1, h19trim, chrnum(19))
```

```
[1] "GI_18641367-A" "GI_18641367-I" "GI_18641369-I"
```

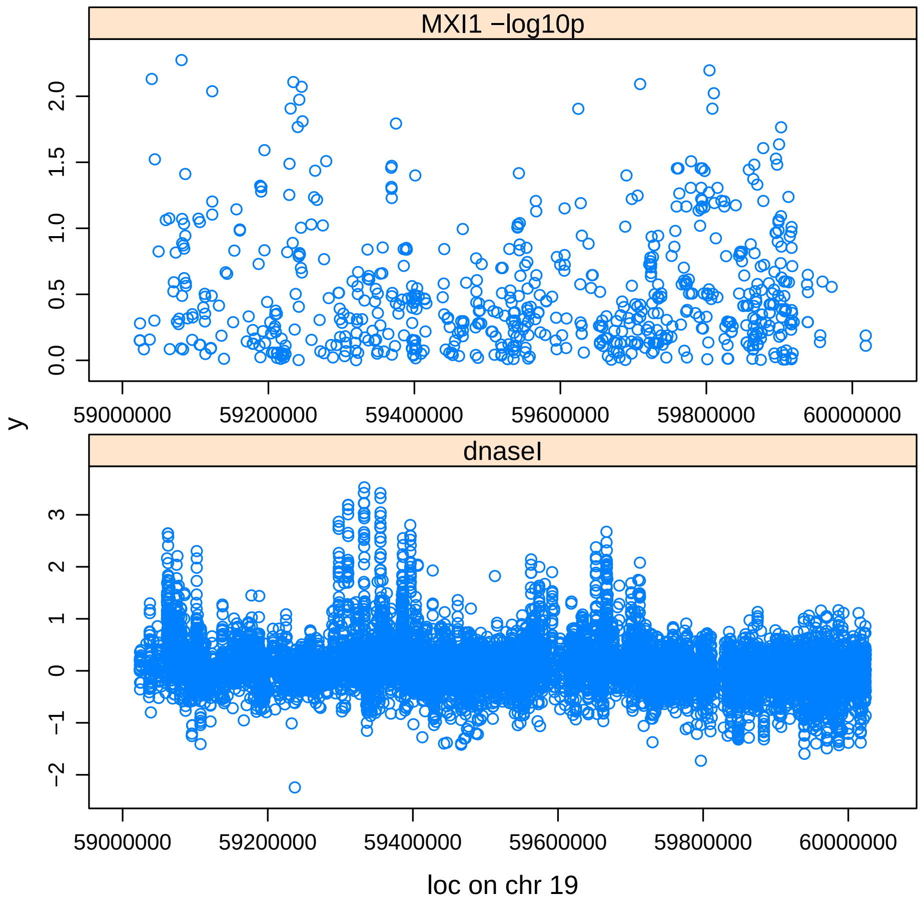
```
> smxi1
```

```
gwSnpScreenResult for gene  MXI1  [probe  GI_18641367-A ]
```

```
> options(oo)
```

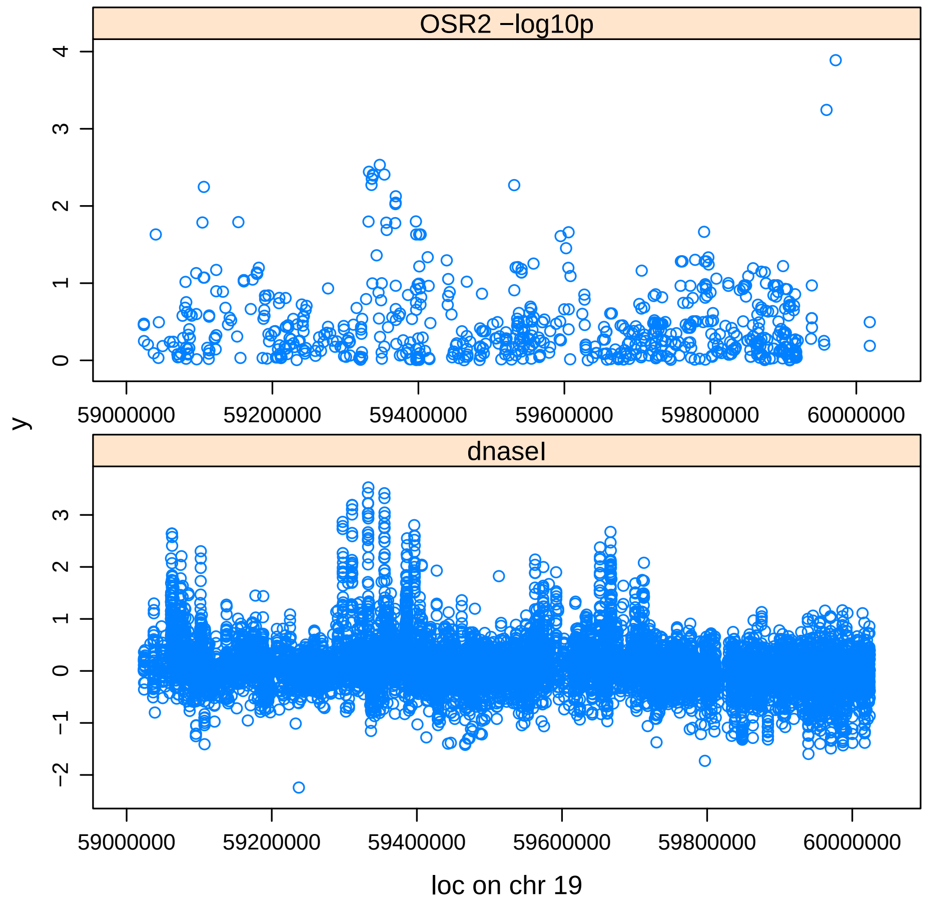
We'd like to look at the SNP screen results juxtaposed with the DnaseI results.

```
> print(juxtaPlot(c19g, smxi1, h19locs))
```



Another example:

```
> oo = options()
> options(warn = 0)
> sOSR2 = gwSnpTests(genesym("OSR2") ~ 1 - 1, h19trim, chrnum(19))
> print(juxtaPlot(c19g, sOSR2, h19locs))
> options(oo)
```



With these scores, we can find gene-snp combinations for which association is at least partly synchronized with DHS. Algorithms for systematically assessing synchronicity are in development.