

A new approach to SNP location metadata

VJ Carey

April 14, 2011

1 Introduction

Versions of GGtools prior to 2.3.x have a complicated approach to SNP location metadata, involving a specially constructed SQLite database. In versions of GGBase up to 3.11, some SNP location metadata support was provided. In GGBase 3.11 and beyond, users are responsible for managing their own location metadata for SNPs and genes. This can be accomplished using the `SNPlocs.Hsapiens.*` package and other annotation resources. The GGtools `cisProxScores` function shows some of the possibilities.

This vignette is retained as legacy for those who may want to retrieve earlier versions of R/Bioconductor to employ formerly supported facilities.

One class and two methods are supported.

```
> getClass("snpLocs")
> data(hsSnpLocs)
> hsSnpLocs
```

The chromosome-specific locations are generated reasonably efficiently:

```
> snpLocs.Hs(chrnum(20), rsid("rs6060535"))
```

2 Construction of serialized reference container

First, unify the name and location information from the `SNPlocs` package.

```
> humanSNPlocs = list()
> library(SNPlocs.Hsapiens.dbSNP.20071016)
> if (file.exists("humanSNPlocs.rda")) load("humanSNPlocs.rda") else {
+   for (i in c(as.character(1:22), "X", "Y")) {
+     curc = getSNPlocs(paste("chr", i, sep = ""))
+     rsid.int = as.integer(curc[, 1])
+     loc.int = as.integer(curc[, 3])
+   }
```

```
+      humanSNPlocs[[i]] = rbind(rsid = rsid.int, loc = loc.int)
+    }
+ }
```

Now get offsets for computing the chromosome-wide location values.

```
> require(org.Hs.eg.db)
> chrl = org.Hs.egCHRLENGTHS
> offs = c(0, cumsum(as.double(chrl[1:22])))
```

Now we create the environment-based container instance:

```
> el = new.env()
> getv = function(x) installed.packages()[x, "Version"]
> for (i in names(humanSNPlocs)) assign(i, humanSNPlocs[[i]], el)
> hsSnpLocs = new("snpLocs", locEnv = el, offsets = offs, organism = "Hs",
+   versions = c(org.Hs.eg.db = getv("org.Hs.eg.db"), SNPlocs.Hsapiens.dbSNP.200710
```

This object will be saved in GGBase.