

A new approach to SNP location metadata

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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 the current version we will use a structure derived from the SNPlocs.Hsapiens.dbSNP.* package.

One class and two methods are supported.

```
> require(GGtools)
> getClass("snpLocs")
```

```
Class "snpLocs"
```

```
Slots:
```

```
Name:      locEnv      offsets      organism      versions
Class: environment  numeric      character      character
```

```
> data(hsSnpLocs)
> hsSnpLocs
```

```
snpLocs instance, organism Hs
based on:
```

```
org.Hs.eg.db SNPlocs.Hsapiens.dbSNP.20071016
"2.2.0" "0.99.1"
```

The chromosome-specific locations are generated reasonably efficiently:

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

```
      [,1]
rsid 6060535
loc  33698936
```

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:

```
> e1 = new.env()
> getv = function(x) installed.packages()[x, "Version"]
> for (i in names(humanSNPlocs)) assign(i, humanSNPlocs[[i]], e1)
> hsSnpLocs = new("snpLocs", locEnv = e1, 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.