

how to make an smlSet from hapmap data

VJ Carey

October 28, 2009

1. **Raw data acquisition:** Obtain the hapmap files from the bulk data download. A typical filename is

```
genotypes_chrY_YRI_r23_nr.b36_fwd.txt.gz
```

2. use `snpMatrix read.HapMap.data` to obtain the associated `snp.matrix` and support data frame. We do this for the 24 main chromosome files. We save the `snp.matrix` for chromosome `n` to `C[nn].rda`. Be careful with the ordering of filenames – should match desired ordering of chromosomes.

3. **Create a list of `snp.matrix` of genotype data:**

```
> ofi = dir(patt = "C.*rda")
> allsm = list()
> cn = rep(NA, 24)
> for (i in 1:24) {
+   cat(i)
+   load(ofi[i])
+   fn = gsub(".rda", "", ofi[i])
+   allsm[[i]] = get(fn)[[1]]
+   cn[i] = as.character(get(fn)[[2]][1, "Chromosome"])
+   print(fn)
+   rm(fn)
+   gc()
+ }
```

Don't forget to give names 1:22, X, Y to the list elements.

4. Create an environment and assign the list created above to symbol `smList` in that environment. This environment is a valid value for the `smlEnv` slot of a `smlSet` instance.

5. The `chromInds` slot gives numerical indices indicating which chromosomes are included; see `hmceuB36.2021` in `GGtools` for an example.
6. remaining slots are as in `ExpressionSet`