How to Assemble a chromLocation Object

In order to use the various *geneplotter* functions you will need to assemble an object of class `chromLocation`. This is relatively straightforward if you have access to a Bioconductor data package. In this example we will consider using the *hu6800.db* data package to construct our object. This vignette was built with version 2.2.0 of the package.

```
> library("annotate")
> library("hu6800.db")
> lens <- unlist(eapply(hu6800CHR, length))
> table(lens)

lens
   1    2
7118   11

> wh2 = mget(names(lens)[lens == 2], env = hu6800CHR)
> wh2[1]

$D49410_at
[1] "X" "Y"
```

So somehow 11 of the genes are mapped to two different chromosomes. Based on OMIM the these genes are localized to the so called *pseudoautosomal region* where the X and Y cromosomes are similar and there is actual recombination going on between them. So, we will take the expedient measure of assigning each of them to just one chromosome.

```
> chrs2 <- unlist(eapply(hu6800CHR, function(x) x[1]))
> chrs2 <- factor(chrs2)
> length(chrs2)

[1] 7129

> table(unlist(chrs2))

  1  10  11  12  13  14  15  16  17  18  19   2  20  21  22   3   4   5   6   7
674 253 417 430 110 241 182 270 445  98 427 443 149 100 171 367 280 295 432 319
  8   9   X   Y
234 252 328  16
```

Now we are ready to obtain the chromosome location data and orientation. The chromosome location data tells us the (approximate) location of the gene on the chromosome. The positions for both the sense and antisense strand are number of base pairs measured from the p (5' end of the sense strand) to q (3' end of the sense strand) arms. Chromosomes are double stranded and the gene is encoded on only one of those two strands. The strands are labeled plus and minus (sense and antisense). We use both the location and the orientation when making plots.

```
> strand <- as.list(hu6800CHRLOC)
> splits <- split(strand, chrs2)
> length(splits)

[1] 24

> names(splits)

 [1] "1"  "10" "11" "12" "13" "14" "15" "16" "17" "18" "19" "2"  "20" "21" "22"
[16] "3"  "4"  "5"  "6"  "7"  "8"  "9"  "X"  "Y"
```

Now we have processed the data and are ready to construct a new `chromLocation` object.

```
> newChrClass <- buildChromLocation("hu6800")
```

And finally we can test it by calling `cPlot`.

```
> library(geneplotter)
> cPlot(newChrClass)
```