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 3.13.0 of the package.

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

lens
   1    2
7122    7

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

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

So somehow 7 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
613 224 366 377  97 204 164 245 391  92 365 407 139  78 148 336 246 266 371 273
  8   9   X   Y
219 236 279  13
```

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)
>
```

Homo sapiens