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* data package to construct our object.

```
> library("annotate")

Loading required package: Biobase
Welcome to Bioconductor
         Vignettes contain introductory material.  To view,
         simply type: openVignette()
         For details on reading vignettes, see
         the openVignette help page.

> library("hu6800")
> affy <- ls(env = hu6800CHR)
> chrs <- mget(affy, env = hu6800CHR)
> lens <- sapply(chrs, length)
> table(lens)

lens
   1    2
7119   10

> chrs[lens == 2]

$D49410_at
[1] "X" "Y"

$"HG2868-HT3012_s_at"
[1] "X" "Y"

$"HG3936-HT4206_at"
[1] "X" "Y"

$J03592_at
[1] "X" "Y"

$L39064_rna1_at
[1] "X" "Y"
```

```
$M16279_at
[1] "X" "Y"

$U11090_at
[1] "X" "Y"

$U13706_at
[1] "X" "Y"

$U82668_rna1_at
[1] "X" "Y"

$X17648_at
[1] "X" "Y"
```

So somehow nine of the genes are mapped to two different chromosomes. We really should sort that out, but for now we can just put them all on the X chromosome (they are all X,Y). 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.

```
> chrs2 <- sapply(chrs, 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
678 252 417 422 108 233 181 269 445  99 589 446 150 101 170 365 281 297 430 324
  8   9   X   Y
240 254 329  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 with distance taken from the 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 <- mget(affy, env = 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)
```