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 3.2.3 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
606 219 354 372  96 203 163 236 375  91 350 400 138  85 146 329 244 262 358 266
  8   9   X   Y
217 233 275  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.

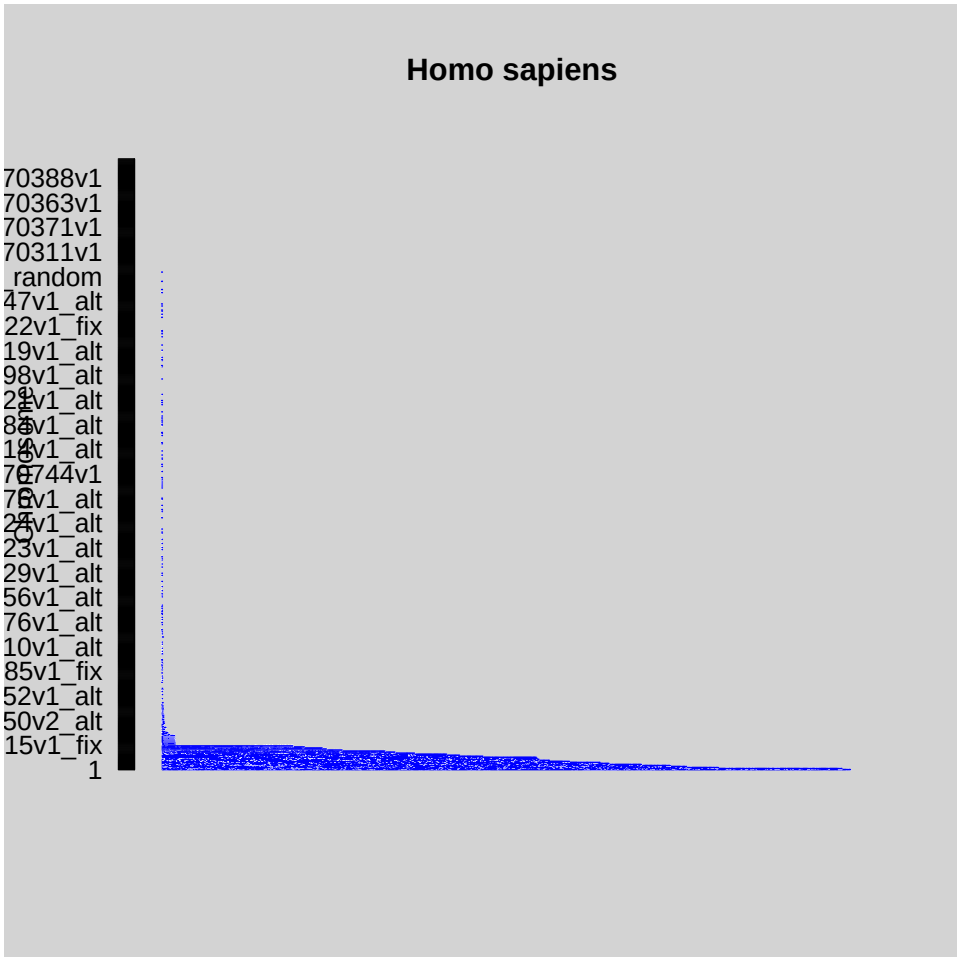
```
> strand <- as.list(hu6800CHRLOC)
> splits <- split(strand, chrs2)
> length(splits)

[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
70388v1
70363v1
70371v1
70311v1
random
47v1_alt
22v1_fix
19v1_alt
98v1_alt
21v1_alt
86v1_alt
14v1_alt
744v1
76v1_alt
24v1_alt
23v1_alt
29v1_alt
56v1_alt
76v1_alt
10v1_alt
85v1_fix
52v1_alt
50v2_alt
15v1_fix
1