

# HowTo: Build and use chromosomal information

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## 1 Overview

The `annotate` package provides a class that can be used to model chromosomal information about a species, using one of the metadata packages provided by Bioconductor. This class contains information about the organism and its chromosomes and provides a standardized interface to the information in the metadata packages for other software to quickly extract necessary chromosomal information. An example of using `chromLocation` objects in other software can be found with the `alongChrom` function of the `geneplotter` package in Bioconductor.

## 2 The `chromLocation` class

The `chromLocation` class is used to provide a structure for chromosomal data of a particular organism. In this section, we will discuss the various slots of the class and the methods for interacting with them. Before this though, we will create an object of class `chromLocation` for demonstration purposes later. The helper function `buildChromLocation` is used, and it takes as an argument the name of a Bioconductor metadata package, which is itself used to extract the data. For this vignette, we will be using the `hgu95av2.db` package.

```
> library("annotate")
> z <- buildChromLocation("hgu95av2")
> z
```

Instance of a `chromLocation` class with the following fields:

```
Organism: Homo sapiens
Data source: hgu95av2
Number of chromosomes for this organism: 25
Chromosomes of this organism and their lengths in base pairs:
 1 : 247249719
10 : 135374737
11 : 134452384
12 : 132349534
```

13 : 114142980  
14 : 106368585  
15 : 100338915  
16 : 88827254  
17 : 78774742  
18 : 76117153  
19 : 63811651  
2 : 242951149  
20 : 62435964  
21 : 46944323  
22 : 49691432  
3 : 199501827  
4 : 191273063  
5 : 180857866  
6 : 170899992  
7 : 158821424  
8 : 146274826  
9 : 140273252  
M : 16571  
X : 154913754  
Y : 57772954

Once we have an object of the *chromLocation* class, we can now access its various slots to get the information contained within it. There are six slots in this class:

**organism:** This lists the organism that this object is describing.  
**dataSource:** Where this data was acquired from.  
**chromLocs:** A list with an element for every unique chromosome name, where each element contains a named vector where the names are probe IDs and the values describe the location of that probe on the chromosome. Negative values indicate that the location is on the antisense strand.  
**probesToChrom:** A hash table which will translate a probe ID to the chromosome it belongs to.  
**chromInfo:** A numerical vector representing each chromosome, where the names are the names of the chromosomes and the values are the lengths of those chromosomes.  
**geneSymbols:** An environment that maps a probe ID to the appropriate gene symbol.

There is a basic 'get' type method for each of these slots, all with the same name as the respective slot. In the following example, we will demonstrate these basic methods. For the `probesToChrom` and `geneSymbols` methods, the return value is an environment which maps a probe ID to other values, we will be using the probe ID '32972\_at', which was selected at random for these examples. We

are showing only part of the `chromLocs` method's output as it is quite long in its entirety.

```

> organism(z)

[1] "Homo sapiens"

> dataSource(z)

[1] "hgu95av2"

> names(chromLocs(z))

 [1] "1"           "10"          "11"          "12"          "13"
 [6] "14"          "15"          "16"          "16_random"  "17"
[11] "17_random"  "18"          "19"          "2"           "20"
[16] "21"          "22"          "3"           "4"           "4_random"
[21] "5"           "6"           "6_cox_hap1" "7"           "8"
[26] "9"           "X"           "Y"           "2_random"   "3_random"
[31] "5_h2_hap1" "6_qbl_hap2" "6_random"   "22_h2_hap1" "8_random"
[36] "19_random"  "22_random"  "1_random"

> chromLocs(z)[["Y"]]

 266_s_at  31911_at  32864_at 32930_f_at 32991_f_at  35885_at 35929_s_at
-19611913 14324840 -2714895 15145847 -6793958 13322553 9914563
 35930_at  36321_at  37583_at 38182_at  40030_at  40097_at  40342_at
 9914563 13283691 -20326688 20217829 7202013 21146998 -23684889
 41214_at  1185_at  31412_at 31412_at  31413_at  31413_at  31414_at
 2769622 1415508 -22627290 23045931 -10200764 6318471 -6334284
 31414_at  31415_at  31415_at 31534_at  31534_at  32677_at  32677_at
10183894 -18390253 18756722 2863111 2863517 -14607045 14677491
 34753_at 35447_s_at 36553_at 36554_at  38355_at  38355_at  39168_at
57623340 1674347 -1482031 -1482031 13525412 13526092 -2414454
 40435_at 40436_g_at 41108_at 41138_at 629_at 31411_at 31411_at
-1465044 -1465044 -161425 2619227 57739639 -25586437 23539797
 31411_at 31601_s_at 31601_s_at 31601_s_at 32428_at 32428_at 32428_at
25173538 -22435610 22082645 22106186 -22459152 -22435610 22082651
 34477_at 34477_at 34477_at 33593_at 33593_at 33593_at 33593_at
-13944307 -13918782 -13869656 -24601327 -24600763 26177651 26177651
33665_s_at 33665_s_at 34172_s_at 34172_s_at 34215_at 34215_at 35073_at
 1347700 1361570 1670485 1670485 1670485 1670485 505078
 35073_at
 505078

> get("32972_at", probesToChrom(z))

[1] "X"

```

```

> chromInfo(z)

      1      10      11      12      13      14      15      16
247249719 135374737 134452384 132349534 114142980 106368585 100338915 88827254
      17      18      19      2      20      21      22      3
78774742 76117153 63811651 242951149 62435964 46944323 49691432 199501827
      4      5      6      7      8      9      M      X
191273063 180857866 170899992 158821424 146274826 140273252 16571 154913754
      Y
57772954

> get("32972_at", geneSymbols(z))

[1] "NOX1"

```

Another method which can be used to access information about the particular *chromLocation* object is the `nChrom` method, which will list how many chromosomes this organism has:

```

> nChrom(z)

[1] 25

```

### 3 Summary

The *chromLocation* class has a simple design, but can be powerful if one wants to store the chromosomal data contained in a Bioconductor package into a single object. These objects can be created once and then passed around to multiple functions, which can cut down on computation time to access the desired information from the package. These objects allow access to basic but also important information, and provide a standard interface for writers of other software to access this information.