

# 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"  "5_h2_hap1"
[31] "6_qbl_hap2" "6_random"  "3_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
36321_at 37583_at 38182_at 40097_at 41214_at 1185_at 31534_at
13283691 -20326690 20217829 21146998 2769622 1415508 2863111
31534_at 34753_at 35447_s_at 36553_at 36554_at 38355_at 38355_at
2863517 57623340 1674347 -1482031 -1482031 13525412 13526092
39168_at 40030_at 40030_at 40435_at 40436_g_at 41108_at 41138_at
-2414454 7202012 7202013 -1465044 -1465044 -161425 2619227
629_at 938_at 31411_at 31411_at 31411_at 34477_at 34477_at
57739639 57739639 -25586437 23539797 25173538 -13944307 -13918782
34477_at 34172_s_at 34172_s_at 34215_at 34215_at 35073_at 35073_at
-13869656 1670485 1670485 1670485 1670485 505078 505078
33665_s_at 33665_s_at 33665_s_at
1347692 1347692 1361570
```

```
> 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.