

# HowTo: Build and use chromosomal information

Jeff Gentry

April 25, 2007

## 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* 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 : 246127941
 2 : 243615958
 3 : 199344050
 4 : 191731959
```

```

5 : 181034922
6 : 170914576
7 : 158545518
8 : 146308819
9 : 136372045
10 : 135037215
11 : 134482954
12 : 132078379
13 : 113042980
14 : 105311216
15 : 100256656
16 : 90041932
17 : 81860266
18 : 76115139
19 : 63811651
20 : 63741868
21 : 46976097
22 : 49396972
X : 153692391
Y : 50286555
M : 16571

```

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" "6_qbl_hap2" "7"
[26] "8"          "9"          "X"          "Y"          "22_random"
[31] "5_h2_hap1" "8_random"   "2_random"   "3_random"   "19_random"
[36] "X_random"   "1_random"

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

32991_f_at  37583_at  38355_at  31911_at  41214_at  32864_at  38182_at
-6793959  -20326690  13526170  14324840  2769622  -2714896  20213723
35885_at   31534_at  40030_at  32930_f_at  266_s_at  40097_at  31412_at
13322553   2863545   7202013  15145847  -19611913  21146998  -22627290
31412_at  34172_s_at  41138_at  36553_at  35073_at  39168_at  31415_at
23045931   1670485   2619227  -1482031   505078   -2414454  -18390255
31415_at  40435_at  34215_at  34753_at  36554_at  40342_at  40342_at
18756722   -1465044   1670485  57623412  -1482031  -23684896  25389451
629_at  40436_g_at  32677_at  32677_at  1185_at  35447_s_at  41108_at
57739639   -1465044  -14607046  14677491  1415508   1674347   -161425
34477_at  34477_at  34477_at  31411_at  31411_at  31411_at  33593_at
-13944308  -13918783  -13869656  23539797  25173538  -25586439  -24600763
33593_at  33593_at  35929_s_at  35929_s_at  35929_s_at  35929_s_at  35930_at
26177651  -24601329   9275684   9296029   9914563   9975488   9275684
35930_at  35930_at  35930_at  33665_s_at  33665_s_at  31601_s_at  31601_s_at
9296029   9914563   9975488   1361570   1347700   22082636   22106177
31601_s_at 31601_s_at 31601_s_at 31601_s_at
-22435611  -22459154  22082645  22106186

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

[1] "X"

> chromInfo(z)
```

1	2	3	4	5	6	7	8
246127941	243615958	199344050	191731959	181034922	170914576	158545518	146308819
9	10	11	12	13	14	15	16
136372045	135037215	134482954	132078379	113042980	105311216	100256656	90041932
17	18	19	20	21	22	X	Y
81860266	76115139	63811651	63741868	46976097	49396972	153692391	50286555
M							
16571							

```
> 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.