

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* 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"      "3_random"
[31] "5_h2_hap1" "19_random" "2_random" "8_random" "22_random"
[36] "6_random" "X_random" "1_random"

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

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