

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: human
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] "human"
```

```
> dataSource(z)
```

```
[1] "hgu95av2"
```

```
> names(chromLocs(z))
```

```
[1] "1"          "10"         "10_random" "11"         "12"         "13"
[7] "14"         "15"         "16"         "17"         "17_random" "18"
[13] "19"         "1_random"   "2"          "20"         "21"         "22"
[19] "2_random"   "3"          "3_random"   "4"          "5"          "6"
[25] "6_random"   "7"          "7_random"   "8"          "8_random"   "9"
[31] "9_random"   "Un_random" "X"          "Y"          "X_random"   "15_random"
```

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

```
32991_f_at  37583_at  38355_at  31911_at  41214_at  32864_at  38182_at
-6436914 -20762489 14025441 14824111  2354783 -2300025 20654374
35885_at   31534_at  40030_at 32930_f_at 266_s_at  40097_at  31412_at
13821824   2448675   6844969 15645118 -20047720 21582794 -23063086
31412_at 34172_s_at 41138_at 36553_at 35073_at 39168_at 31415_at
23481727 1355970 2204357 -1167591 527257 -1999606 -18826051
31415_at 40435_at 938_at 34215_at 34753_at 36554_at 40342_at
19192518 -1150499 50253240 1355970 50137007 -1167591 24210865
40342_at 629_at 40436_g_at 32677_at 32677_at 1185_at 35447_s_at
25825251 50253240 -1150499 -15106321 15176762 1100815 1359802
41108_at 34477_at 34477_at 34477_at 31411_at 31411_at 31411_at
-113605 -14368927 -14418054 -14443579 23975593 25609336 -26033085
33593_at 33593_at 33593_at 35929_s_at 35929_s_at 35929_s_at 35929_s_at
-25036564 26624297 -25037125 8878028 8918640 8938985 8959253
35929_s_at 35930_at 35930_at 35930_at 35930_at 35930_at
8979583 8878028 8918640 8938985 8959253 8979583
```

```
> 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.