HowTo: Build and use chromosomal information

Jeff Gentry

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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"         "1_random"   "2"
[16] "20"         "21"         "22"         "22_random"  "2_random"
[21] "3"          "3_random"   "4"          "4_random"   "5"
[26] "6"          "6_hla_hap1" "7"          "8"          "9"
[31] "X"          "Y"          "19_random"  "6_random"   "8_random"
[36] "7_random"   "X_random"

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

32930_f_at   31911_at 32991_f_at   266_s_at   35885_at   38182_at   40097_at
  15074584   14253577   -6777319  -19540650   13251290   20142460   21075735
  31534_at   40030_at   41214_at   38355_at   32864_at   37583_at     629_at
   2846906    7185374    2752983   13454907   -2698256  -20255427   57668376
  39168_at   34215_at   31415_at   31415_at   40342_at   40342_at    1185_at
  -2397815    1754312  -18318990   18685459   25318188  -23613632    1499187
40436_g_at   36553_at   31412_at   31412_at   32677_at   32677_at   41138_at
  -1548871   -1565963  -22556027   22974668  -14535782   14606228    2602588
  40435_at   36554_at   35073_at   34753_at 35447_s_at 33665_s_at 34172_s_at
  -1548871   -1565963     555078   57552143    1758174   -1355172    1754312
  33593_at   33593_at   33593_at   41108_at   34477_at   34477_at   34477_at
 -24529503   26106388  -24530066    -161425  -13798393  -13847520  -13873045
  31411_at   31411_at   31411_at 31601_s_at 31601_s_at 31601_s_at 31601_s_at
  23468534   25102275  -25515176   22011373   22034914  -22364349  -22387891
31601_s_at 31601_s_at   35930_at   35930_at   35930_at   35930_at   35930_at
  22011382   22034923    9218433    9259045    9279390    9918236    9938519
  35930_at 35929_s_at 35929_s_at 35929_s_at 35929_s_at 35929_s_at 35929_s_at
   9958849    9218433    9259045    9279390    9918236    9938519    9958849

> 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.