

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"         "1_random"   "2"
[16] "20"         "21"         "22"         "2_random"   "3"
[21] "3_random"   "4"          "4_random"   "5"          "6"
[26] "6_hla_hap1" "7"         "8"          "9"          "X"
[31] "Y"          "7_random"   "19_random"  "6_random"   "8_random"
[36] "22_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 -6777320   -19540650 13251290  20117360 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  -18318992 18685459  -23613633 25318188 1499187
40436_g_at 36553_at 31412_at   31412_at  32677_at  32677_at   41138_at
-1548871   -1565963 -22556027 22974668  -14535783 14606228 2602588
40435_at   36554_at 35073_at   31411_at  31411_at  34753_at 35447_s_at
-1548871   -1565963  555078    23468534  25102275 57552149 1758174
33665_s_at 34172_s_at 33593_at   33593_at  33593_at  41108_at  34477_at
-1355172   1754312  -24529503 26106388  -24530066 -161425  -13798393
34477_at   34477_at 35930_at   35930_at  35930_at  35930_at 35929_s_at
-13847520  -13873045 9958849    9259045   9897924   9279390 9958849
35929_s_at 35929_s_at 35929_s_at 31601_s_at 31601_s_at 31601_s_at 31601_s_at
9259045    9897924   9279390   22011373  22034914  -22364349 22011382
31601_s_at
22034923

> 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.