

# 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.db` 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: 93
Chromosomes of this organism and their lengths in base pairs:
  1 : 249250621
  2 : 243199373
  3 : 198022430
  4 : 191154276
```

5 : 180915260  
6 : 171115067  
7 : 159138663  
X : 155270560  
8 : 146364022  
9 : 141213431  
10 : 135534747  
11 : 135006516  
12 : 133851895  
13 : 115169878  
14 : 107349540  
15 : 102531392  
16 : 90354753  
17 : 81195210  
18 : 78077248  
20 : 63025520  
Y : 59373566  
19 : 59128983  
22 : 51304566  
21 : 48129895  
6\_ssto\_hap7 : 4928567  
6\_mcf\_hap5 : 4833398  
6\_cox\_hap2 : 4795371  
6\_mann\_hap4 : 4683263  
6\_apd\_hap1 : 4622290  
6\_qbl\_hap6 : 4611984  
6\_dbb\_hap3 : 4610396  
17\_ctg5\_hap1 : 1680828  
4\_ctg9\_hap1 : 590426  
1\_g1000192\_random : 547496  
Un\_g1000225 : 211173  
4\_g1000194\_random : 191469  
4\_g1000193\_random : 189789  
9\_g1000200\_random : 187035  
Un\_g1000222 : 186861  
Un\_g1000212 : 186858  
7\_g1000195\_random : 182896  
Un\_g1000223 : 180455  
Un\_g1000224 : 179693  
Un\_g1000219 : 179198  
17\_g1000205\_random : 174588  
Un\_g1000215 : 172545  
Un\_g1000216 : 172294  
Un\_g1000217 : 172149  
9\_g1000199\_random : 169874  
Un\_g1000211 : 166566

```
Un_g1000213 : 164239
Un_g1000220 : 161802
Un_g1000218 : 161147
19_g1000209_random : 159169
Un_g1000221 : 155397
Un_g1000214 : 137718
Un_g1000228 : 129120
Un_g1000227 : 128374
1_g1000191_random : 106433
19_g1000208_random : 92689
9_g1000198_random : 90085
17_g1000204_random : 81310
Un_g1000233 : 45941
Un_g1000237 : 45867
Un_g1000230 : 43691
Un_g1000242 : 43523
Un_g1000243 : 43341
Un_g1000241 : 42152
Un_g1000236 : 41934
Un_g1000240 : 41933
17_g1000206_random : 41001
Un_g1000232 : 40652
Un_g1000234 : 40531
11_g1000202_random : 40103
Un_g1000238 : 39939
Un_g1000244 : 39929
Un_g1000248 : 39786
8_g1000196_random : 38914
Un_g1000249 : 38502
Un_g1000246 : 38154
17_g1000203_random : 37498
8_g1000197_random : 37175
Un_g1000245 : 36651
Un_g1000247 : 36422
9_g1000201_random : 36148
Un_g1000235 : 34474
Un_g1000239 : 33824
21_g1000210_random : 27682
Un_g1000231 : 27386
Un_g1000229 : 19913
M : 16571
Un_g1000226 : 15008
18_g1000207_random : 4262
```

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"
> ## The chromLocs list is extremely large. Let's only
> ## look at one of the elements.
> names(chromLocs(z))

 [1] "1"           "10"          "11"
 [4] "12"          "13"          "14"
 [7] "15"          "16"          "17"
[10] "18"          "19"          "2"
[13] "20"          "21"          "22"
[16] "3"           "4"           "5"
[19] "6"           "7"           "8"
[22] "9"           "X"           "Y"
[25] "17_ctg5_hap1" "6_cox_hap2" "6_ssto_hap7"
[28] "6_mcf_hap5"   "4_ctg9_hap1" "1_g1000191_random"
[31] "19_g1000209_random" "6_qbl_hap6" "6_dbb_hap3"
[34] "Un_g1000223" "6_apd_hap1" "6_mann_hap4"
```

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

31911_at 32864_at 32991_f_at 35885_at 36321_at 37583_at 40030_at
15815446 -2654895 -6733958 14813159 14774297 -21867300 7142012
40097_at 41214_at 1185_at 31534_at 31534_at 34753_at 38182_at
22737596 2709622 1405508 2803517 2803111 59213948 21729243
38182_at 40435_at 40436_g_at 41108_at 41138_at 938_at 31411_at
21729243 -1455044 -1455044 -171416 2559227 59330251 26764150
31411_at 31411_at 34477_at 34477_at 34477_at 38355_at 38355_at
-27177049 25130409 -15434913 -15409388 -15360258 15016018 15016696
38355_at 266_s_at 266_s_at 266_s_at 266_s_at 34172_s_at 34172_s_at
15017615 -21152525 -21152525 -21152525 -21152525 1660485 1660485
34215_at 34215_at 35073_at 35073_at 36553_at 36553_at 36554_at
1660485 1660485 535078 535078 -1472031 -1472031 -1472031
36554_at 39168_at 39168_at 32930_f_at 32930_f_at 32930_f_at 32930_f_at
-1472031 -2354454 -2354454 16634487 16636453 16635625 16733900
32930_f_at 33665_s_at 33665_s_at 33665_s_at 35447_s_at 35447_s_at 35447_s_at
16635384 1337692 1351570 1337692 1683940 1664347 1684025
```

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

```
[1] "X"
```

```
> chromInfo(z)
```

	1	2	3	4
	249250621	243199373	198022430	191154276
	5	6	7	X
	180915260	171115067	159138663	155270560
	8	9	10	11
	146364022	141213431	135534747	135006516
	12	13	14	15
	133851895	115169878	107349540	102531392
	16	17	18	20
	90354753	81195210	78077248	63025520
	Y	19	22	21
	59373566	59128983	51304566	48129895
	6_ssto_hap7	6_mcf_hap5	6_cox_hap2	6_mann_hap4
	4928567	4833398	4795371	4683263
	6_apd_hap1	6_qbl_hap6	6_dbb_hap3	17_ctg5_hap1
	4622290	4611984	4610396	1680828
	4_ctg9_hap1	1_g1000192_random	Un_g1000225	4_g1000194_random
	590426	547496	211173	191469
	4_g1000193_random	9_g1000200_random	Un_g1000222	Un_g1000212
	189789	187035	186861	186858
	7_g1000195_random	Un_g1000223	Un_g1000224	Un_g1000219
	182896	180455	179693	179198

17_gl000205_random	Un_gl000215	Un_gl000216	Un_gl000217
174588	172545	172294	172149
9_gl000199_random	Un_gl000211	Un_gl000213	Un_gl000220
169874	166566	164239	161802
Un_gl000218	19_gl000209_random	Un_gl000221	Un_gl000214
161147	159169	155397	137718
Un_gl000228	Un_gl000227	1_gl000191_random	19_gl000208_random
129120	128374	106433	92689
9_gl000198_random	17_gl000204_random	Un_gl000233	Un_gl000237
90085	81310	45941	45867
Un_gl000230	Un_gl000242	Un_gl000243	Un_gl000241
43691	43523	43341	42152
Un_gl000236	Un_gl000240	17_gl000206_random	Un_gl000232
41934	41933	41001	40652
Un_gl000234	11_gl000202_random	Un_gl000238	Un_gl000244
40531	40103	39939	39929
Un_gl000248	8_gl000196_random	Un_gl000249	Un_gl000246
39786	38914	38502	38154
17_gl000203_random	8_gl000197_random	Un_gl000245	Un_gl000247
37498	37175	36651	36422
9_gl000201_random	Un_gl000235	Un_gl000239	21_gl000210_random
36148	34474	33824	27682
Un_gl000231	Un_gl000229	M	Un_gl000226
27386	19913	16571	15008
18_gl000207_random			
4262			

```
> 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] 93
```

### 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.