

Seminar III: R/Bioconductor

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Note: Questions through the forum please. Those who are not from the sixth LCG
generation send us an email so we can register you on the forum.

Abstract

With the following exercises you'll practice creating some advanced plots.
You'll have to explain every plot.

1 lattice

1. Using our object `t1`, create a histogram of the BAC sizes with one panel per chromosome.
2. With the object `t2` from class, first normalize the position variable per chromosome (use `tapply` to find out the max values per chromosome). Then create density plots for your normalized position variable. Every chromosome has to have its own panel.

3. For chromosomes X and Y, and using the normalized position variable, make a densityplot grouping the information by the reference allele. For each chromosome, separate the data by the AK1.allele variable¹. Your resulting plot should have 8 panels.
4. (Optional) Check out the `latticeExtra` package and make a plot with one of its functions.

2 plotrix

1. Using the original `t2` object, plot for every chromosome the mean position with error bars. We did something very similar with `t1` on class.
2. Create a bar plot with the table information for the following data:

```
> df <- data.frame(G1 = c(25, 5, 20), G2 = c(30, 6, 22), G3 = c(40,  
+      6, 18))  
> df
```

```
   G1 G2 G3  
1 25 30 40  
2  5  6  6  
3 20 22 18
```

3. (Optional) With whichever data you want, create an interesting plot using `hierobarp`. Don't use the default examples.

¹Remember that you can use more than 1 factor