

# Seminar III: R/Bioconductor

August-December 2009

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September 17, 2009

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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

The following exercise will make sure that you can use the `GenomeGraphs` package.

## 1 GenomeGraphs

1. Download the following paper by Durinck, Bullard, Spellman and Dudoit:  
<http://www.ncbi.nlm.nih.gov/pubmed/19123956>
2. Reproduce figure 3 from the paper. Its just a matter of extracting the code from the text :)
3. Make a new plot with some re-ordering: invert the order of tracks. Meaning that you'll have conservation on top, followed by the Lee data, then David -,

David +, Nagalakshmi, + gene region, genome axis, and finally - gene region. Change the colors of all the tracks to any ones you like (without repeating them). Finally, add a text overlay with your username on the conservation track around positions 1301700 to 1301900. You might prefer to build each `gdObject` like in the class (a, b, c, ...) and then create the list when you use `gdPlot`.

4. Explain every "make..." command :)