

Genome visualization using Bioconductor packages

Nociones Básicas de Bioinformática y Genómica
(*Máster en Bioinformática, Universidad de Valencia*)

David Montaner

2015-05-25

Genome browsers

- Ensembl: embedded in their web page
http://www.ensembl.org/Homo_sapiens/Location/View?r=6:133017695-133161157
- UCSC: <http://genome.ucsc.edu/cgi-bin/hgGateway>
- CIPF: GenomeMaps
<http://www.genomemaps.org/?region=6:133017695-133161157>
- Broad Institute: Integrative Genomics Viewer: runs locally.
Good for NGS data.

Many other indicated in the [Wikipedia](#) page

Genome browsers

Advantages

- Easy to use
- Databases are provided

Disadvantages

- Not fully customize
- Not all species or databases available

Bioconductor

Bioconductor is a repository of R packages aimed at the analysis of high-throughput genomic data.

Install

Open an R session as *Super User (root)* and type.

```
source("http://bioconductor.org/biocLite.R")  
biocLite()
```

See dealer's [here](#)

Packages for genome visualization

- **Gviz**: integrated visualization of known genomic information and new experimental data.
- **ggbio**: detailed views of particular genomic regions, as well as genome-wide overviews.
- **Sushi**: integrative genomic visualizations

Install Gviz

```
source("http://bioconductor.org/biocLite.R")  
biocLite("Gviz")
```