



Laboratorio 01

Introducción a Bioconductor para análisis de secuencias

Genómica para bioinformática INB320

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¿Qué es Bioconductor?

- Proyecto abierto para análisis estadísticos en genómica
- usa R como base
- Comunidad de usuarios y desarrolladores.
Reuniones anuales, material educativo en línea, etc.

Hoy día vamos a...

Introduction to Bioconductor for Sequence Data

Bioconductor enables the analysis and comprehension of high- throughput genomic data. We have a vast number of packages that allow rigorous statistical analysis of large data while keeping technological artifacts in mind. Bioconductor helps users place their analytic results into biological context, with rich opportunities for visualization. Reproducibility is an important goal in *Bioconductor* analyses. Different types of analysis can be carried out using *Bioconductor*, for example

- Sequencing : RNASeq, ChIPSeq, variants, copy number..
- Microarrays: expression, SNP, ...
- Domain specific analysis : Flow cytometry, Proteomics ..

For these analyses, one typically imports and works with diverse sequence-related file types, including fasta, fastq, BAM, gtf, bed, and wig files, among others. *Bioconductor* packages support import, common and advanced sequence manipulation operations such as trimming, transformation, and alignment including quality assessment.

<https://www.bioconductor.org/help/workflows/sequencing/>

etapas/análisis en azul y paquetes de Bioconductor/R en rosado

