

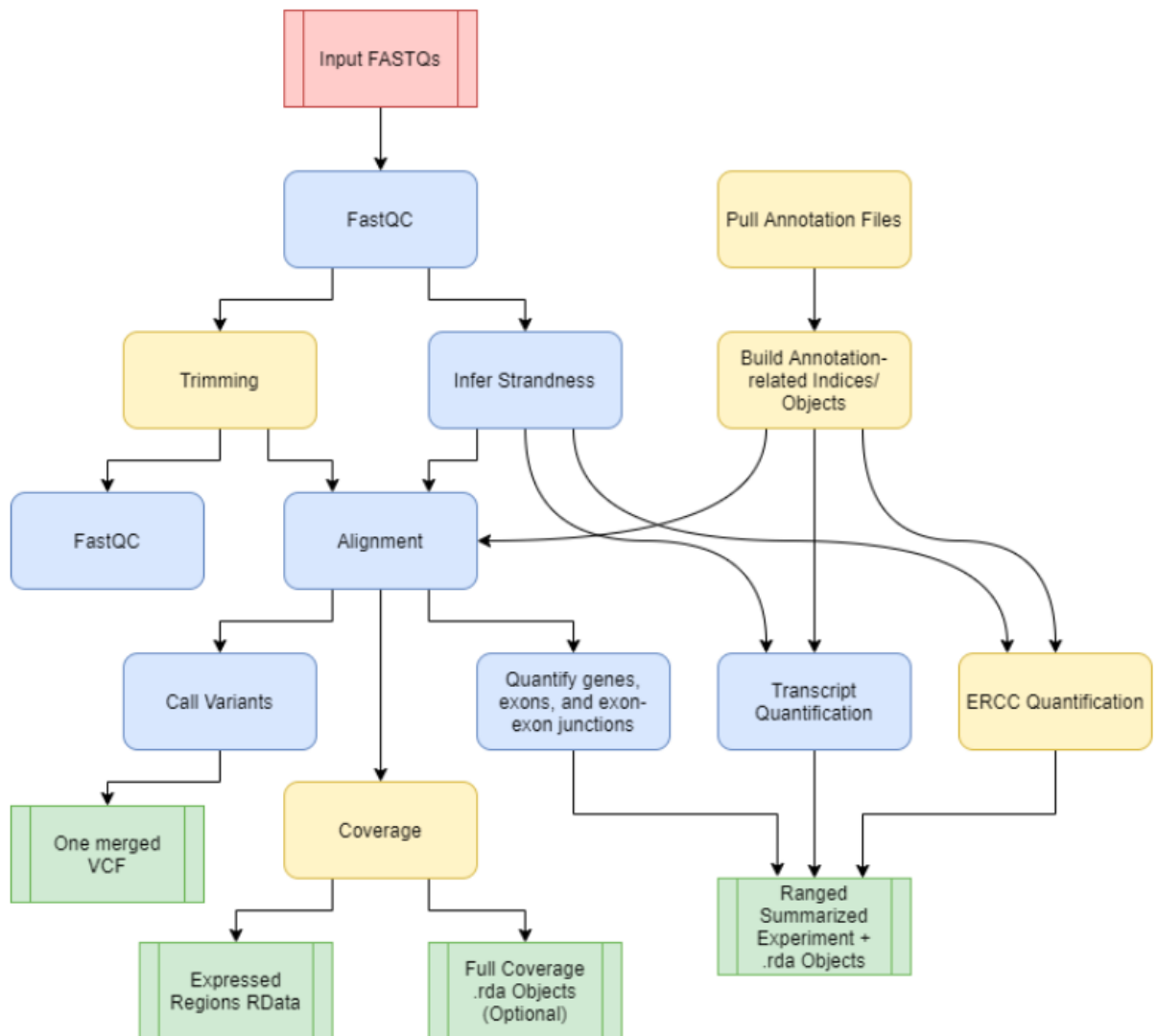


# Datos de RNA-seq a través de recount3

▼ Class	Bioinformática
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🔗 Materials	
☰ Profesor	Leonardo Collado
☑ Reviewed	<input type="checkbox"/>
▼ Type	Lecture

## Procesar datos crudos (FASTQ)

Ejemplo: <https://www.biorxiv.org/content/10.1101/2020.12.11.386789v1>



## 10 Differential expression analysis | R/Bioconductor-powered Team Data Science

To learn about differential expression analysis we used the data from the SPEAQeasy-example website we made. This involves work mostly by Nicholas J. Eagles, Joshua M. Stolz, and Louise Huuki. In particular, we followed the set of activities described in detail at [SPEAQeasy-example/bootcamp\\_intro](https://lcolladotor.github.io/bioc_team_ds/differential-expression-analysis.html).

[https://lcolladotor.github.io/bioc\\_team\\_ds/differential-expression-analysis.html](https://lcolladotor.github.io/bioc_team_ds/differential-expression-analysis.html)

## Proyectos recount

Procesa datos de RNA-seq públicos, esto ayudo a desarrollar métodos de expresión diferencial.

- Ayuda a que todos podamos analizar los datos sin importar quien tiene acceso a high performance computing (HPC) (clústers para procesar datos).
- Es como democratizar el acceso a los datos ^^

## Usando recount3

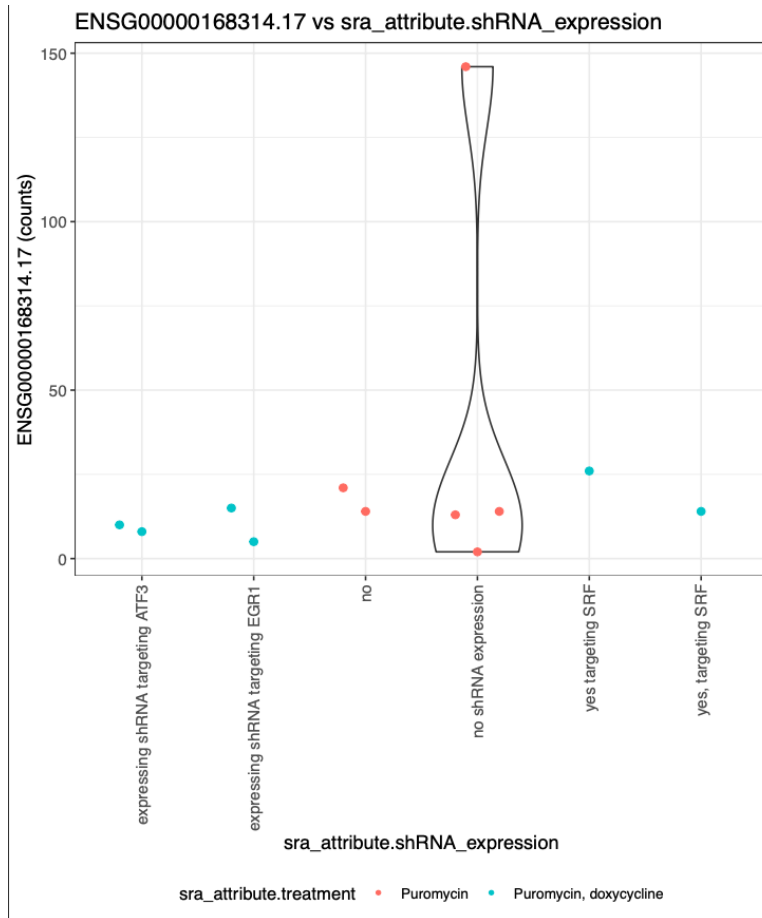
Explore and download data from the recount3 project

The recount3 package enables access to a large amount of uniformly processed RNA-seq data from human and mouse. You can download RangedSummarizedExperiment objects at <http://research.libd.org/recount3/index.html>

recount3

## Ejercicio

Replicar la imagen usando iSEE



### recount3: human and mouse public RNA-seq data

recount3 provides processed RNA-seq data for human and mouse in file formats similar to recount2 (Figure 1.1), which at its core is based on coverage bigWig files and exon-exon

<http://research.libd.org/recount3-docs/docs/index.html#study-explorer>

