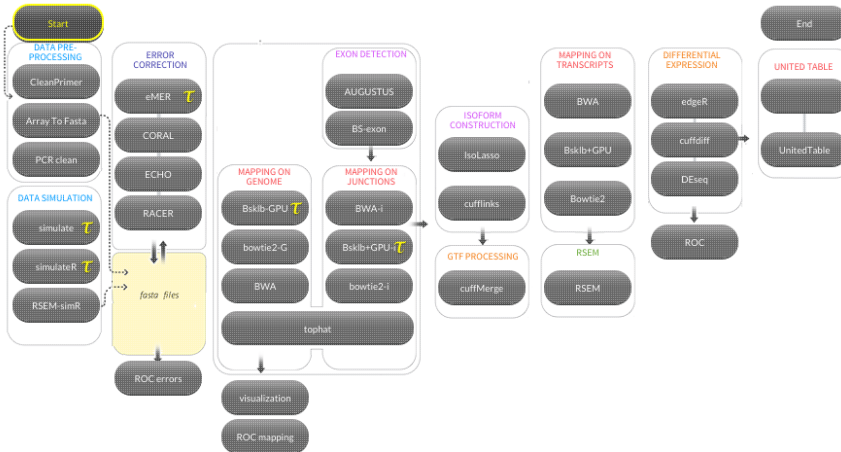


RNA-SEQ/CHIP



RNA-Seq analysis pipeline starts with a job called “Start” that compiles user selected data input options into a series of tags and generates the correct pipeline options, reducing the number of possible algorithms to the ones that can handle the input data.

Based on the highlighted buttons, now you can create your pipeline using the graphical interface. By right-clicking the selected button, you will be able to deselect it.

Some buttons will open a parameters dialog box. After selecting all the desired options, select the “end” button to give the pipeline a name, upload data and run the pipeline.

Data formats:

- fastA
- fastQ
- non-illumina (array)
- Sam/Bam
- Sra
- Gtf/Gff

[Read more...](#)