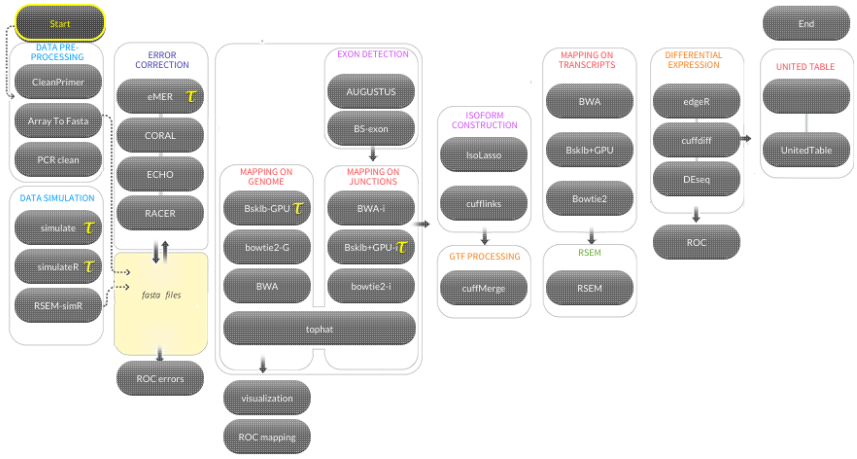
RNA-SEQ/CHIP



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.

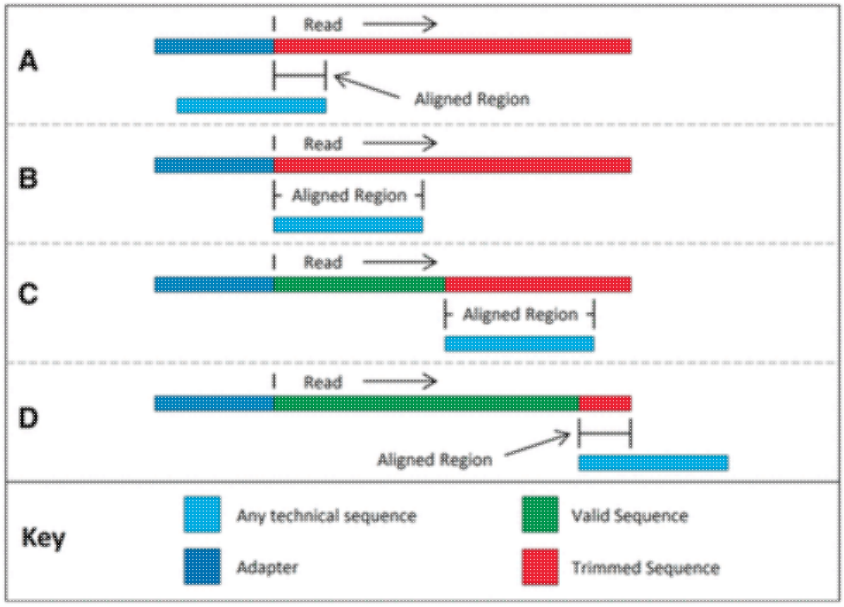
Based on the highlighted buttons, now you can create your pipeline using the graphical interface. By right-clicking the selected button, you will be able to deselect it.

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

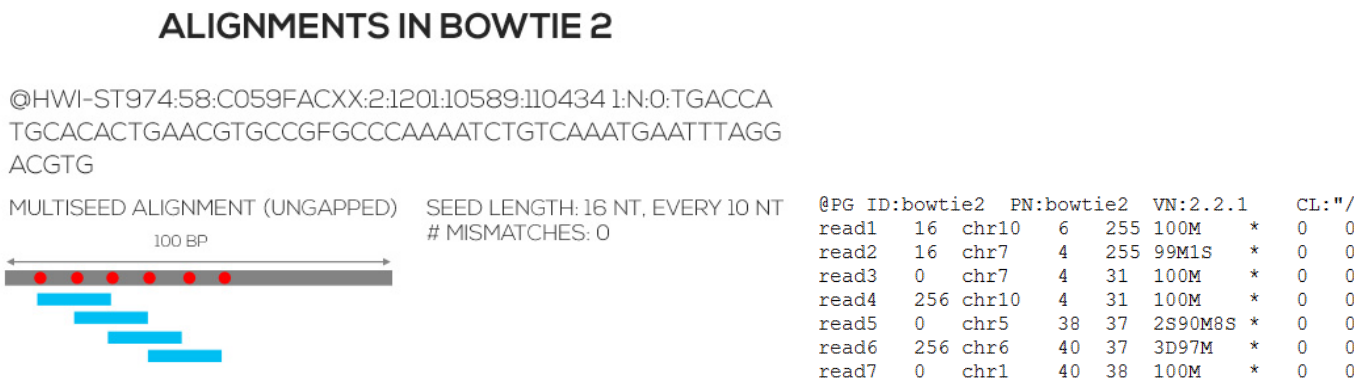
Read more...



Trimmomatic algorithm cleans raw sequencing reads from technical adapters. The Trimmomatic pre-processing step is usually performed to ensure better quality of alignment of reads on the reference genome.

For more info please see:

Bolger AM, Lohse M, Usadel B. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics*. 2014;30(15):2114-2120. doi:10.1093/bioinformatics/btu170.

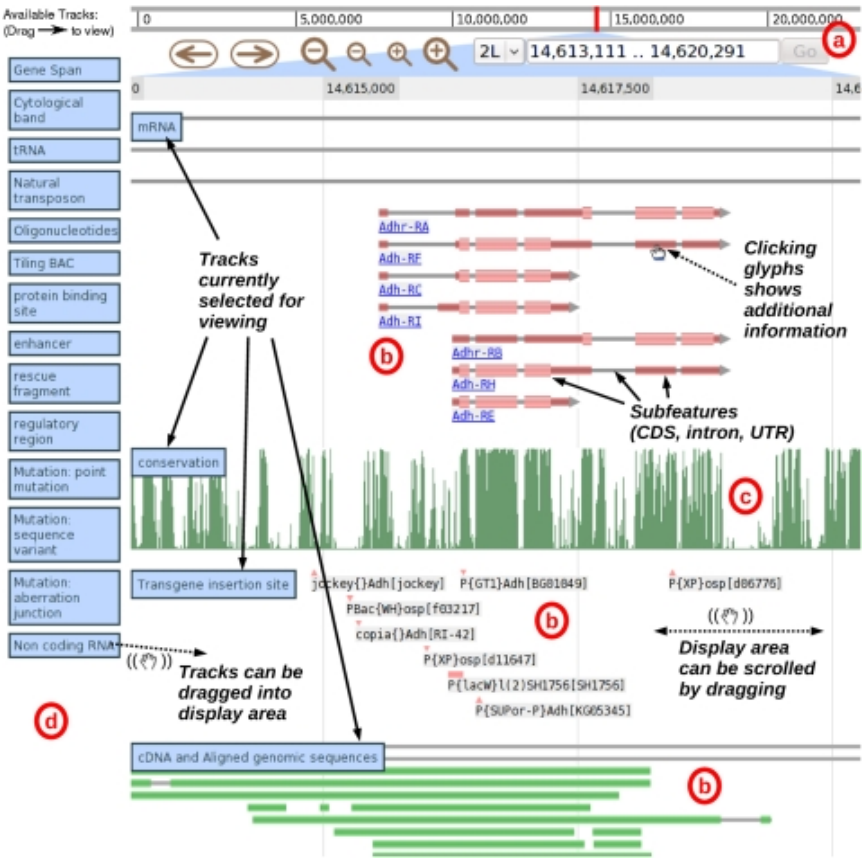


Bowtie2 is a fast alignment algorithm based on the FM-index approach on seeds substrings to align them to the genome.

For more info please see:

Langmead B, Salzberg SL. Fast gapped-read alignment with Bowtie 2. Nat Methods. 2012;9(4):357-359. doi:10.1038/nmeth.1923.

This job takes reads in fq, fa files, aligns these onto the reference genome and gives mapping result in SAM format. Each row of the SAM file contains input read name, reference read name, position on the reference read and number of mapped/skipped/inserted/deleted positions



As seen in the image above, users can view genome annotations against a reference “ruler,” with an overhead bar giving a visual indication of chromosome position. The user can navigate by dragging the display left or right or by clicking on navigation buttons; analogous buttons allow the display to be zoomed in or out. Alternatively, users can navigate directly to a region (or feature) of interest by typing the region coordinates (or feature name) into a search box. Additional annotation tracks can be added to the current display by dragging them from a reservoir bar on the left of the screen, and can be removed by dragging them back off the main display. Tracks can, similarly, be reordered by dragging. All track manipulation, as with navigation, is live and requires no page reloads

References:
https://genomebiology.biomedcentral.com/articles/10.1186/s13059-016-0924-1

After assigning a name/identifier to the pipeline, please press “*RUN PIPELINE*” button to start computations.