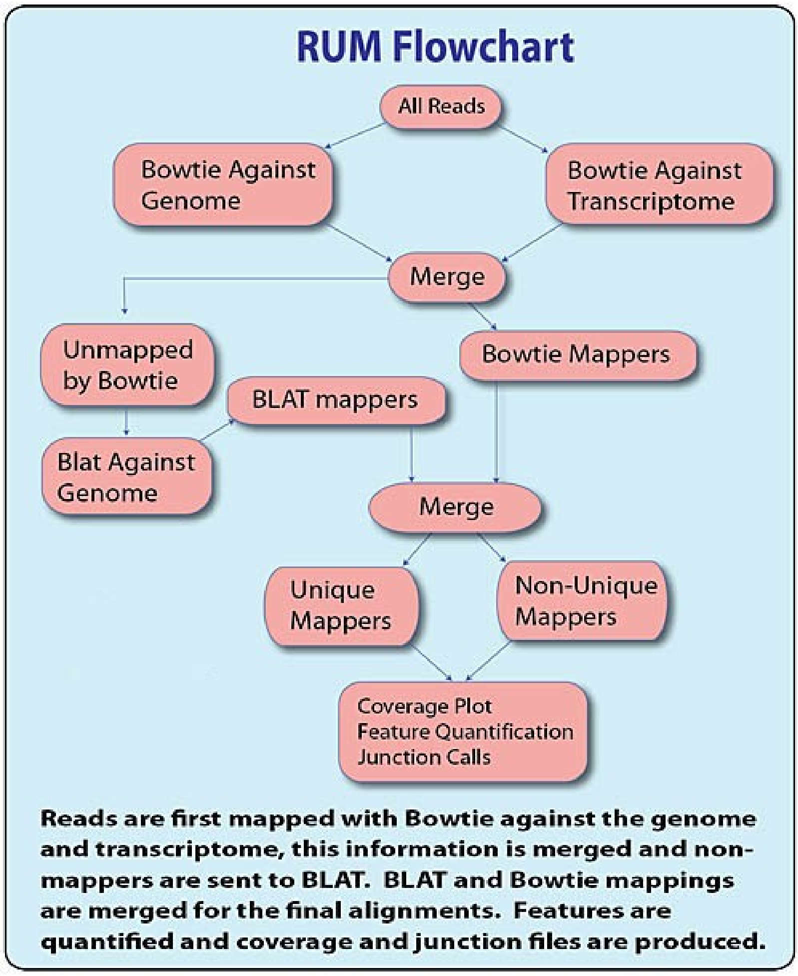
RUM (RNA-seq Unified Mapper), is RNA-Seq alignment pipeline developed at 2011. It is freely available for academic uses.



Reads are first mapped with Bowtie against the genome and transcriptome, this information is merged and non-mappers are sent to BLAT. BLAT and Bowtie mappings are merged for the final alignments. Features are quantified and coverage and junction files are produced.

To start a job, we need to type rum_runner, give it an action telling it what to do.
Actions:
rum_runner align: run the RUM pipeline
rum_runner clean: delete intermediate files
rum_runner kill: stop running and remove all output files
rum_runner stop: stop a running job
rum_runner resume: resume a stopped job
rum_runner status: check the status of a running job
rum_runner version: print out the version of RUM
rum_runner help: provide help information.

Required options for rum_runner align:
--index-dir, or -i: index directory
--name: job_name
--output or -o: output directory
--chunks: number of chunks you want to
forward_reads [reverse_reads]
options (more details about options can be found under rum_runner help align)

Required options for rum_runner help:
action name

Required options for Rum_runner other actions:
-o

Reference:

1. Comparative analysis of RNA-Seq alignment algorithms and the RNA-Seq unified mapper (RUM). Bioinformatics. 2011 Sep 15;27(18):2518-28.
2. RUM user guide. http://www.cbil.upenn.edu/RUM/userguide.php