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

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: