Salmon.Quant Documentation

Description: Perform transcript-level quantification of RNA-seq data using Salmon.
See: The Salmon User Guide for detailed usage guidelines.

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Contact: Algorithm and scientific questions: https://github.com/COMBINE-lab/salmon/issues. Module specific issues: genepattern.org/help

Summary: Quantify gene expression at transcript level using the pseudo-alignment based method "Salmon".

Source Publication: Patro R, Duggal G, Love MI, Irizarry RA, Kingsford C. Salmon provides fast and bias-aware quantification of transcript expression. Nat Methods. 2017 Apr;14(4):417-419. doi: 10.1038/nmeth.4197. Epub 2017 Mar 6. PMID: 28263959; PMCID: PMC5600148.

Basic Parameters:

Name	Description
Reads	Paired end RNA-seq reads with separate fastq.gz files for _R1 and _R2. Each pair should be named with the same sample ID and have the appropriate read suffix. Reads must be gzipped.
Transcriptome Index	The indexed transcriptome output from the Salmon.Indexer module (or comparable pipeline). File must be .tar.gz
Library Type	The relative orientation of the paired end reads. By default, salmon will attempt to autodetect the mate orientation.
Sampling	Method for assessing technical variance assessment. Necessary for downstream transcript differential expression testing with Sleuth
seqBias	Attempt to learn and correct random hexamer priming biases in the reads.
gcBias	Attempt to learn and correct GC sequence biases in the reads.
posBias	Model fragment position distribution to correct for 5' or 3' positional biases.

Advanced Parameters: See The Salmon User Guide for details on additional parameters offered in this module.

Output Files:

Name	Description
<SampleID_R1>.salmon_quant .tar.gz	Gzipped files containing each salmon quantification result named for each input R1 file.

Module Language: Shell script
Source Repository: https://github.com/genepattern/Salmon.Quant/releases/tag/v1
Docker image: combinelab/salmon:1.5.2

Version	Comment
1	Initial release.