



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:1.4.0

GenePattern

| Version | Comment |
|---------|------------------|
| 1 | Initial release. |