



## Salmon.Quant Documentation

**Description:** Perform transcript-level quantification of RNA-seq data using Salmon (v1.5.2).

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](http://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. Single-end reads are also supported (must not have the _R1 or _R2 suffix). Reads must be gzipped. Warning: Reads for the same sample must not be split across multiple fastq files.
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.

# GenePattern

**Module Language:** Shell script

**Source Repository:** <https://github.com/genepattern/Salmon.Quant/tree/v0.6>

**Docker image:** [genepattern/salmon-quant:beta](#)

Version	Comment
0.6	Initial beta release.