

# High-Throughput Transcriptome Analysis for Investigating Host-Pathogen Interactions

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jove.com/video/62324

## Materials

Name	Company	Catalog Number	Comments
CEMiTool	Computational Systems Biology Laboratory	1.12.2	Discovery and the analysis of co-expression gene modules in a fully automatic manner, while providing a user-friendly HTML report with high-quality graphs.
EdgeR	Bioconductor (Maintainer: Yunshun Chen [yuchen at wehi.edu.au])	3.30.3	Differential expression analysis of RNA-seq expression profiles with biological replication
EnhancedVolcano	Bioconductor (Maintainer: Kevin Blighe [kevin at clinicalbioinformatics.co.uk])	1.6.0	Publication-ready volcano plots with enhanced colouring and labeling
FastQC	Babraham Bioinformatics	0.11.9	Aims to provide a simple way to do some quality control checks on raw sequence data coming from high throughput sequencing
FeatureCounts	Bioinformatics Division, The Walter and Eliza Hall Institute of Medical Research	2.0.0	Assign mapped sequencing reads to specified genomic features
MDP	Computational Systems Biology Laboratory	1.8.0	Molecular Degree of Perturbation calculates scores for transcriptome data samples based on their perturbation from controls
R	R Core Group	4.0.3	Programming language and free software environment for statistical computing and graphics
STAR	Bioinformatics Division, The Walter and Eliza Hall Institute of Medical Research	2.7.6a	Aligner designed to specifically address many of the challenges of RNA-seq data mapping using a strategy to account for spliced alignments
Bowtie2	Johns Hopkins University	2.4.2	Ultrafast and memory-efficient tool for aligning sequencing reads to long reference sequences

Trimmomatic	THE USADEL LAB	0.39	Trimming adapter sequence tasks for Illumina paired-end and single-ended data
Get Docker	Docker	20.10.2	Create a bioinformatic environment reproducible and predictable ( <a href="https://docs.docker.com/get-docker/">https://docs.docker.com/get-docker/</a> )
WSL2-Kernel	Windows	NA	<a href="https://docs.microsoft.com/en-us/windows/wsl/wsl2-kernel">https://docs.microsoft.com/en-us/windows/wsl/wsl2-kernel</a>
Get Docker Linux	Docker	NA	<a href="https://docs.docker.com/engine/install/ubuntu/">https://docs.docker.com/engine/install/ubuntu/</a>
Docker Linux Repository	Docker	NA	<a href="https://docs.docker.com/engine/install/ubuntu/#install-using-the-repository">https://docs.docker.com/engine/install/ubuntu/#install-using-the-repository</a>
MDP Website	Computational Systems Biology Laboratory	NA	<a href="https://mdp.sysbio.tools">https://mdp.sysbio.tools</a>
Enrichr Website	MaayanLab	NA	<a href="https://maayanlab.cloud/Enrichr/">https://maayanlab.cloud/Enrichr/</a>
webCEMiTool	Computational Systems Biology Laboratory	NA	<a href="https://cemitool.sysbio.tools/">https://cemitool.sysbio.tools/</a>
gProfiler	Bioinformatics, Algorithmics and Data Mining Group	NA	<a href="https://biit.cs.ut.ee/gprofiler/gost">https://biit.cs.ut.ee/gprofiler/gost</a>
goseq	Bioconductor (Maintainer: Matthew Young [my4 at sanger.ac.uk])	NA	<a href="http://bioconductor.org/packages/release/bioc/html/goseq.html">http://bioconductor.org/packages/release/bioc/html/goseq.html</a>
SRA NCBI study	NCBI	NA	<a href="https://www.ncbi.nlm.nih.gov/bioproject/PRJNA507472/">https://www.ncbi.nlm.nih.gov/bioproject/PRJNA507472/</a>