
Snakemake RNA-seq pipeline

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This is the main documentation of the Snakemake RNA-seq pipeline. This pipeline takes single or paired-end mostly Illumina mRNA-seq reads and generates: 1. A quality report (multiQC format), 2. A mapping summary, 3. The gene *raw* read counts, 4. The gene *scaled* read counts

The gene raw counts can be directly used for differential gene expression with *DESeq2* <<https://www.bioconductor.org/packages/devel/bioc/vignettes/DESeq2/inst/doc/DESeq2.html>>.

A dedicated tutorial, available here <<https://scienceparkstudygroup.github.io/rna-seq-lesson/06-differential-analysis/index.html>> can be followed to perform this analysis.

1.1 Installation

To install the pipeline

1.2 Contact

Question? please contact xx

1.3 Crunchomics

Usage on crunchomics

1.4 Contact

Question? please contact xx

1.5 License

The MIT license

1.6 Contact

Question? please contact xx

INDICES AND TABLES

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