



RNA-Seq Pipeline Overview

Analysis for Walker lab

- **Prepared for:**
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 - **Process Executed on :** Feb-29-2024
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Data Access

- **Dropbox Folder:** /staging/01.RawData
- **Dropbox URL:** Error: Command 'rclone --config="rclone.conf" link remote:"/staging/01.RawData"' returned non-zero exit status 1.

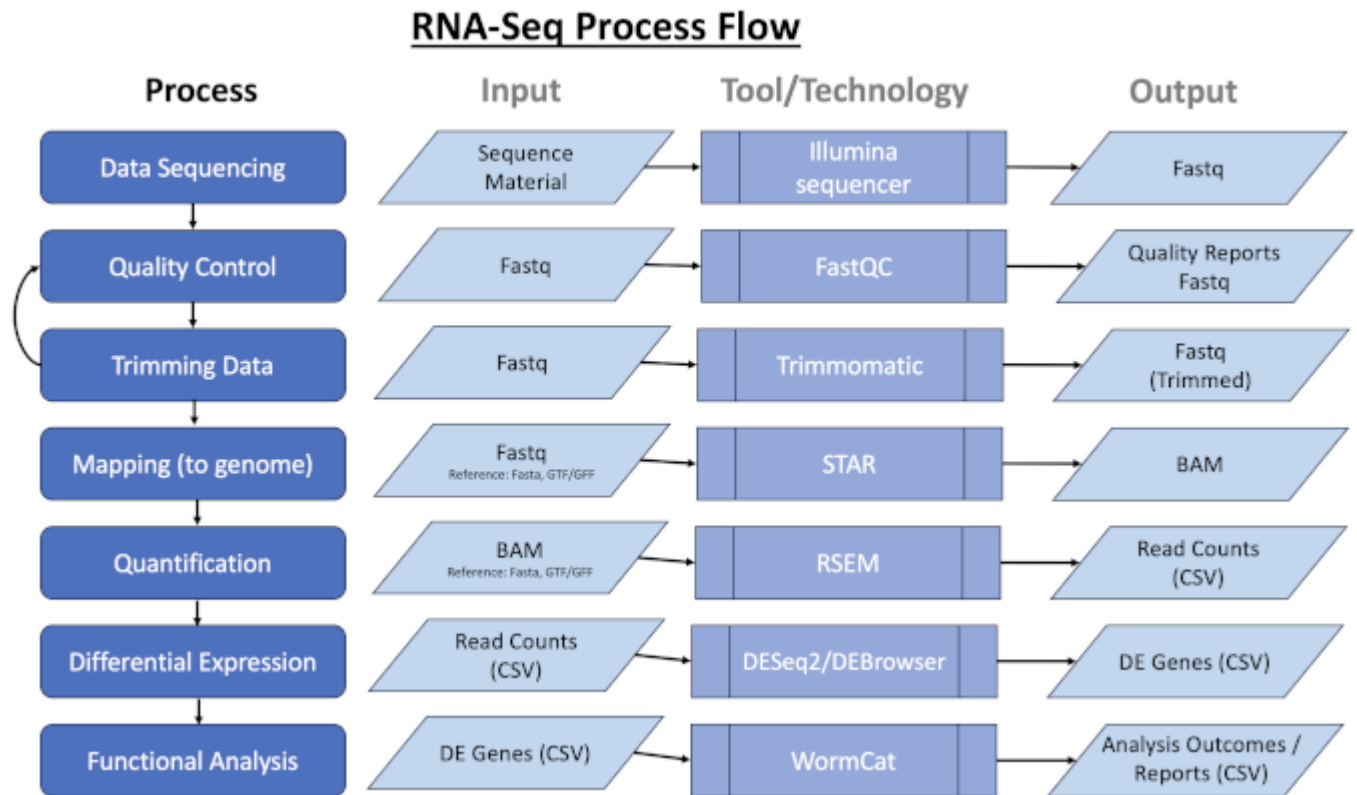
FASTQ files

Gene Index files

Gene Index based on Wormbase Version: *WS289*



RNA Seq Process



Pipeline Outputs

- MD5 Checksum Report
- FAST QC Report
- Multi QC Report
- Isoform Quantification
- Gene Quantification
- DESeq2 Gene Normalizations (Up, Down, All Expressed) & Visualizations
- WormCat Annotations and Visualizations of gene set enrichment data

Source Code

The provided tagged repository is available to create reproducible outputs from the RNA-Seq Pipeline.

Config https://github.com/DanH-UMassMed/Walker_Lab

Pipeline <https://github.com/DanH-UMassMed/RNA-Seq-Nextflow> -r v1.0.*