

Integrate Salmon to MultiQC

CSE – 549 COMPUTATIONAL BIOLOGY

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# PURPOSE

MultiQC is a tool used for analyzing multiple sequencing samples together. The tool itself can parse through different types of outputs and generate reports. So, for example, if a folder contains output of multiple runs of Salmon, a transcript quantification and mapping tool for RNA sequences, MultiQC will be able to parse through them, read the log files, determine which tool was run on the samples, filter out features and generate a report using them. The purpose of this project is to make modules for MultiQC that are Salmon-specific.

# SCOPE

* Plot GC bias related output of Salmon to MultiQC
* Plot 5’ and 3’ biases output of Salmon to MultiQC
* Plot GC bias related output of Salmon to MultiQC
* Generate Heatmap

# APPROACH

# RESULTS