Pathway/Module analysis

- Minpath: MinPath (Minimal set of Pathways) is a parsimony approach for biological pathway reconstructions using protein family predictions, achieving a more conservative, yet more faithful, estimation of the biological pathways for a query dataset. This program is configured to run on both KEGG pathways and KEGG modules.
- Pathway/Module abundance: Calculates pathway/module abundance based on functional abundances and pathway/module assignments from MinPath. Abundances are reported as the harmonic mean of functional abundances.

Pathway Descriptions

pathway_descriptions: Internal script that matches KO genes with pathway whilst displaying the total abundance in the dataset for each pathway. Pathway descriptions are also included.

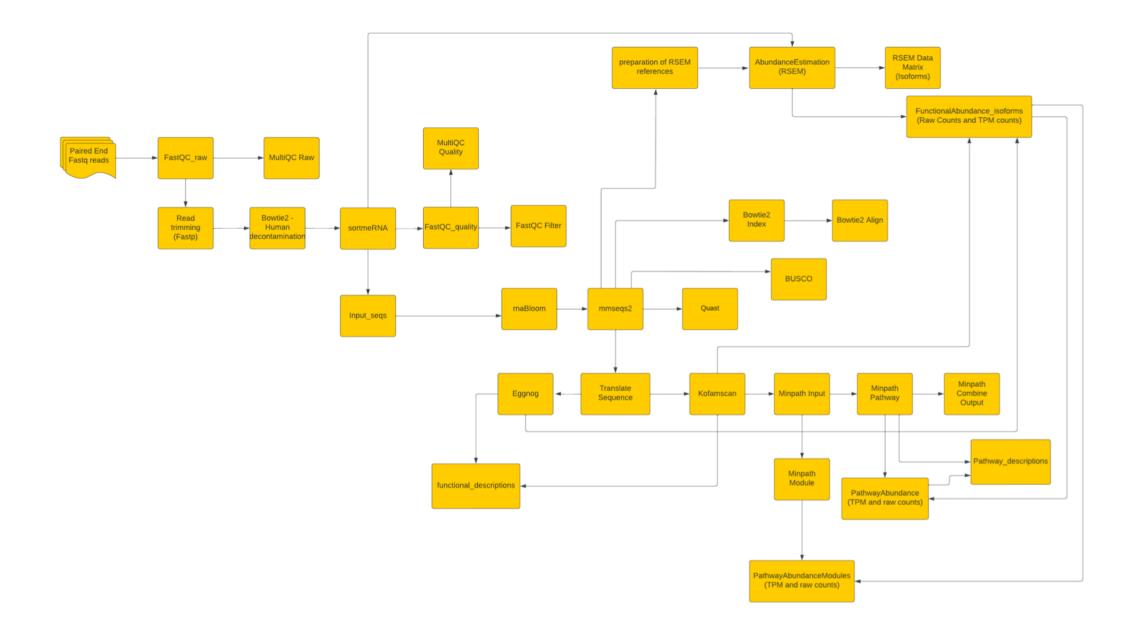


Figure 1: Overview of the Metatranscriptomics pipeline