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sRNA-pipe

A Nextflow-based pipeline for small RNA analysis

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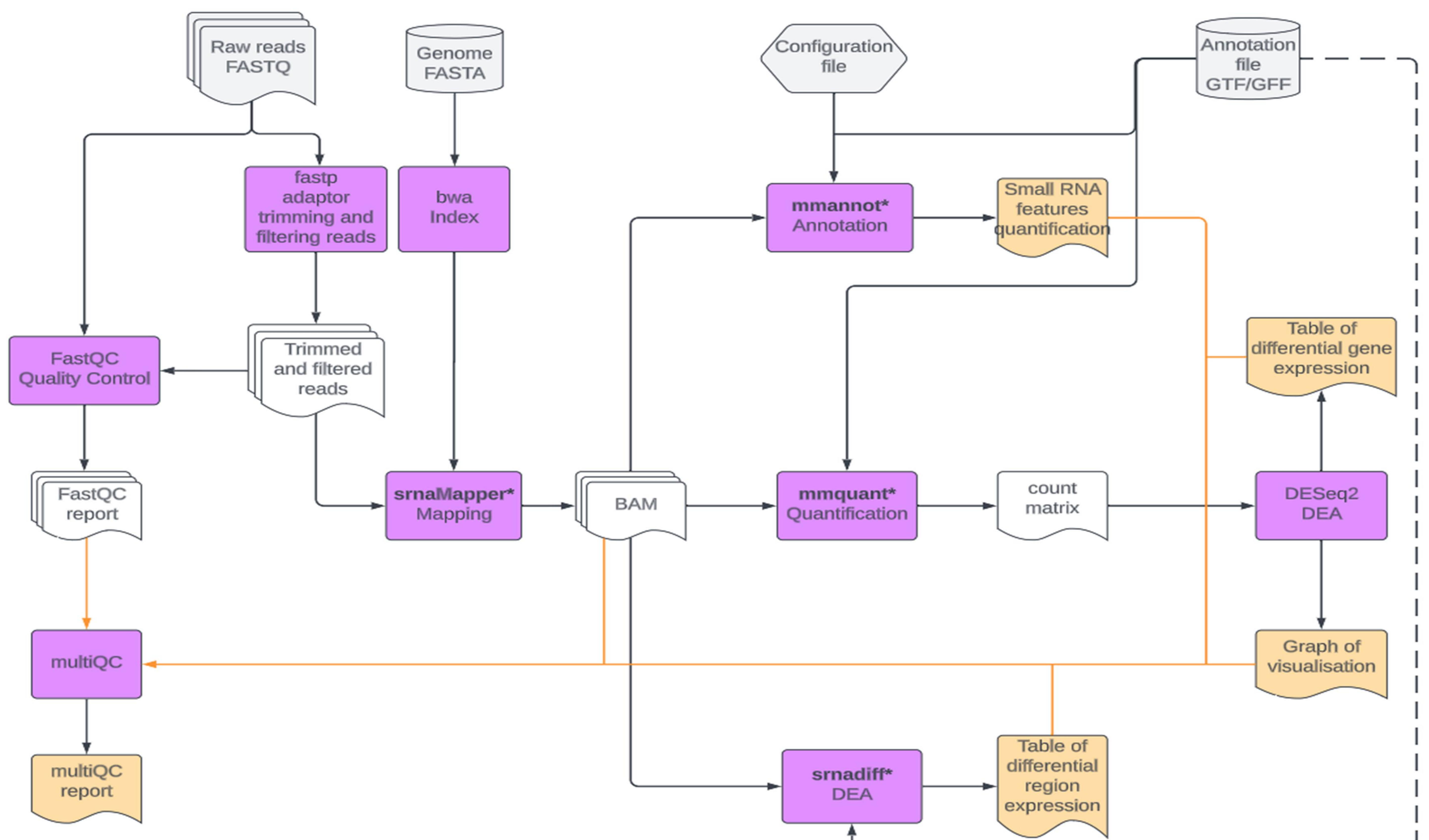
Motivation

Small RNA (sRNA) are RNA molecules shorter than 200 nucleotides, including miRNA, siRNA, piRNA, and others, which play important roles in gene regulation, cell development, and antiviral defense. Sequencing these small RNA is a state-of-the-art technique for studying their characteristics and functions. However, bioinformatic analysis of small RNA faces challenges. Due to their short length, similarity, and repetitive nature, small RNA reads often result in multi-mapping, introducing biases in mapping, annotation and quantification step. Additionally, except for miRNA, other types of small RNA are less studied, making it difficult to determine their differential gene expression.

Overview

Here, we introduce sRNA-pipe, a Nextflow pipeline developed following nf-core guidelines. This pipeline is designed to annotate various features of small RNA and perform differential analysis using tools specifically developed for small RNA analysis.

Workflow



Perspectives

- Finish the pipeline
- Benchmark on other FAIR databases
- Contribute to nf-core
- <https://github.com/phamhoanggiang262/srna-pipe>