



HAL
open science

sRNA-pipe A Nextflow-based pipeline for small RNA analysis

Matthias Zytnicki, Hoang-Giang Pham

► **To cite this version:**

Matthias Zytnicki, Hoang-Giang Pham. sRNA-pipe A Nextflow-based pipeline for small RNA analysis. JOBIM, Jun 2023, multi-site, France. Actes de JOBIM 2023. hal-04199064

HAL Id: hal-04199064

<https://hal.inrae.fr/hal-04199064>

Submitted on 7 Sep 2023

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution 4.0 International License

sRNA-pipe

A Nextflow-based pipeline for small RNA analysis

Matthias ZYTNICKI¹ and Hoang-Giang PHAM¹

¹Applied Mathematics and Computer Science Unit of Toulouse (MIAT)-INRAE, 24 chemin de Borde Rouge, 31320, Toulouse, France

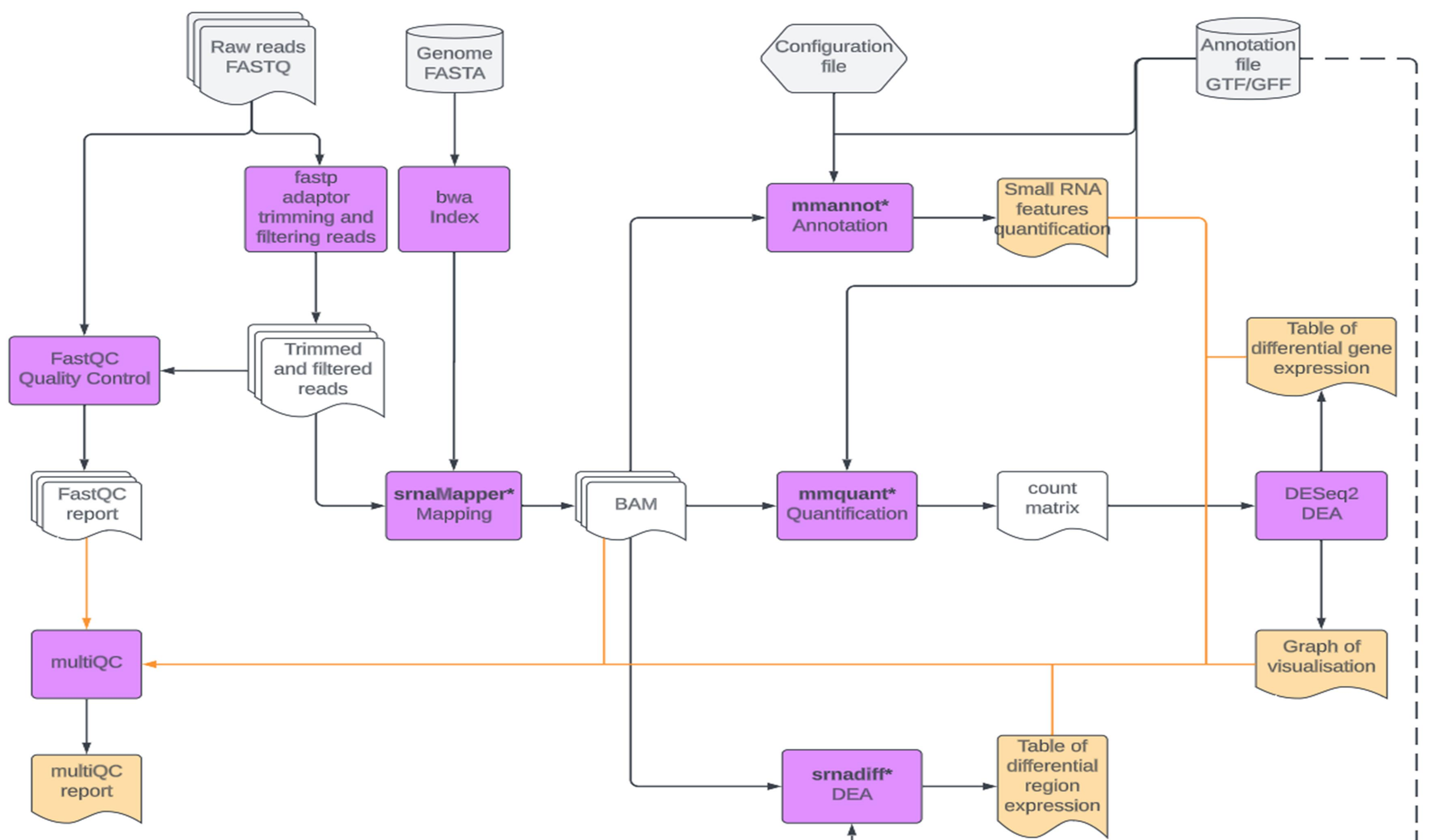
Motivation

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>