

# nf-core/cutandrun - A reproducible, portable and interpretable Nextflow pipeline for analysis of CUT&RUN, CUT&TAG and TIP-Seq datasets

Dr Christopher Cheshire, Charlotte West, Tamara Hodgetts

Briscoe Lab, The Francis Crick Institute, UK

## Motivation

The exploration of transcription factors (TFs) and epigenetic modifications such as histone marks is central to unravelling the complexities of gene regulation. The development of the CUT&RUN, CUT&Tag, and TIPseq protocols represents progressive iterations on the theme of targeting DNA-bound proteins and constitute a significant improvement of data quality when compared to CHIP-Seq.

These methodologies utilize either MNase or Tn5 transposase to cut and insert DNA at targeted sites. Although each protocol has its unique strengths, the core processing steps for these methods share substantial similarities, particularly in the initial stages of data analysis. This commonality in data processing presents an opportunity for a unified bioinformatics solution. The nf-core/cutandrun pipeline is engineered to harness this common ground, providing a singular, robust pipeline capable of analysing data across all three protocols. This consolidated approach not only streamlines the analysis workflow but also fosters consistency and reproducibility in the data analysis process, thereby aiding direct comparison between the protocols.

## Overview

Here we present nf-core/cutandrun, a best-practice bioinformatic analysis workflow for sequencing data generated from the CUT&RUN, CUT&Tag and TIP-Seq protocols.

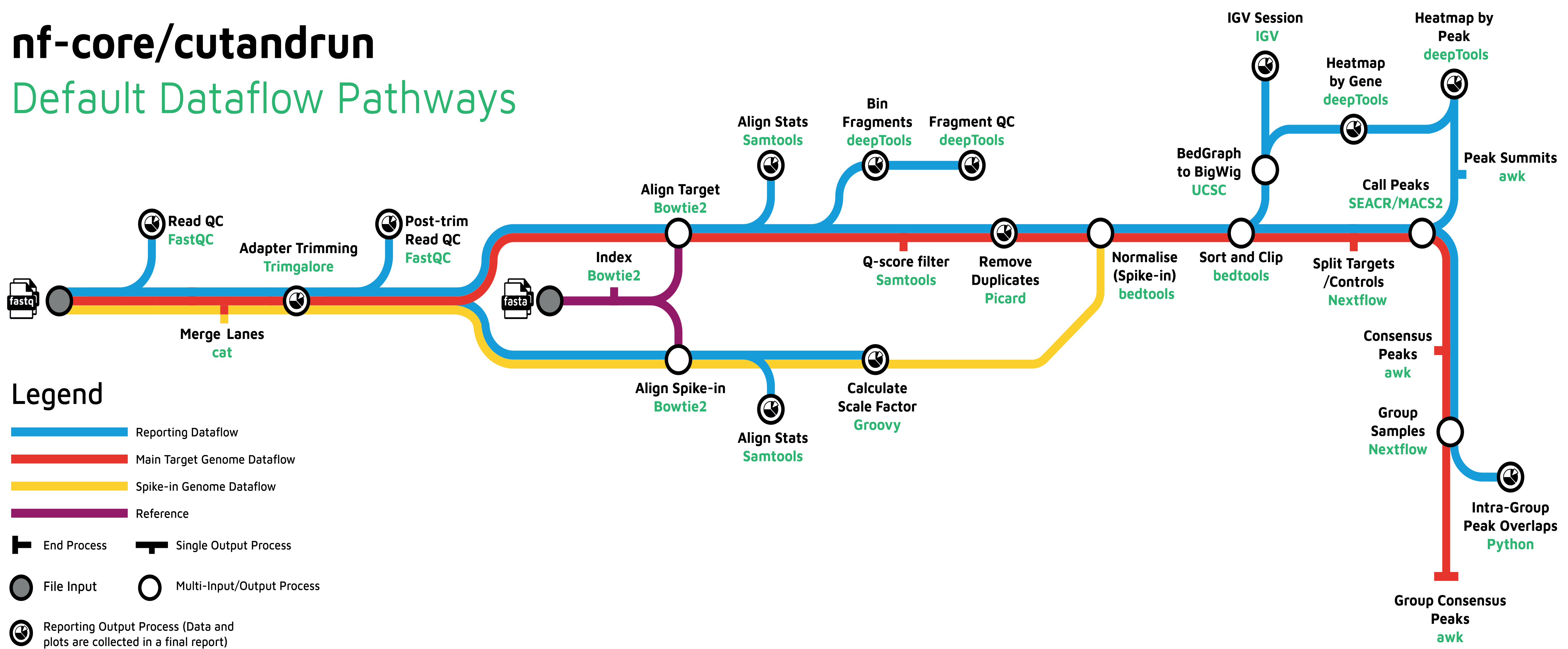
The pipeline supports a rich set of experimental design options including spike-ins, IgG controls, technical replicates and antibody groupings as well as comprehensive quality metric reporting. nf-core/cutandrun is designed to the tenets of portability, reproducibility and interpretability.

nf-core/cutandrun runs on a wide range of execution environments, operating systems and platforms. It is designed to be used with the minimum of technical knowledge, but allows users with wide range of biological expertise to obtain the results they need.

The pipeline is regularly updated using continuous integration automated deployment and is supported by over 200 tests.

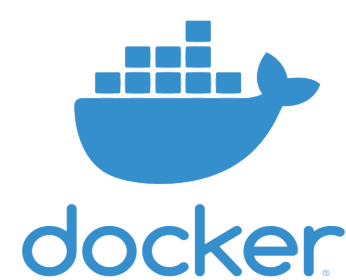
## nf-core/cutandrun

### Default Dataflow Pathways

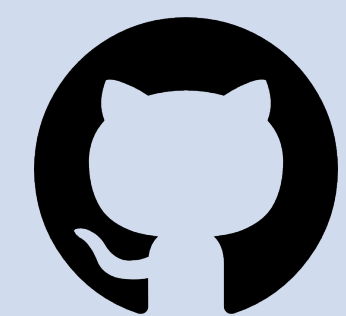


## Supports

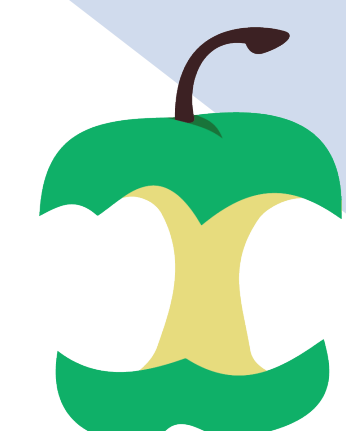
nextflow



nf-core #cutandrun



nf-core/cutandrun



nf-co.re/join

## Explore, Comment, Contribute

