EBERHARD KARLS UNIVERSITÄT TÜBINGEN

Quantitative Biology Center

QBiC

CRISPR gene editing analysis with nf-core/crispseq: A pipeline for targeted and screening experiments

Júlia Mir Pedrol[1*], Laurence Kuhlburger[1,2*], Marta Sanvicente García[3], Gisela Gabernet[1], Ghazaleh Tabatabai[2], Marc Güell[3], nf-core community, Sven Nahnsen[1,4]

[1]Quantitative Biology Center, Eberhard-Karls University of Tübingen, Germany.

[2]Department of Neurology & Interdisciplinary Neuro-Oncology, University Hospital Tübingen, Hertie Institute for Clinical Brain Research, Eberhard-Karls University Tübingen, Germany.

[3]Department of Medicine and Life Sciences, Universitat Pompeu Fabra, Barcelona, Spain.

[4]Biomedical Data Science, Department of Computational Science, Eberhard-Karls University of Tübingen, Germany.

*These authors contributed equally to the work.

INTRODUCTION

CRISPR-Cas9 enables precise DNA editing and can be applied to a wide range of research areas, including drug discovery, molecular biology, functional genomics, disease modeling, agriculture, and gene therapies. Its utility extends to understanding gene function, identifying therapeutic targets, and advancing precision medicine.
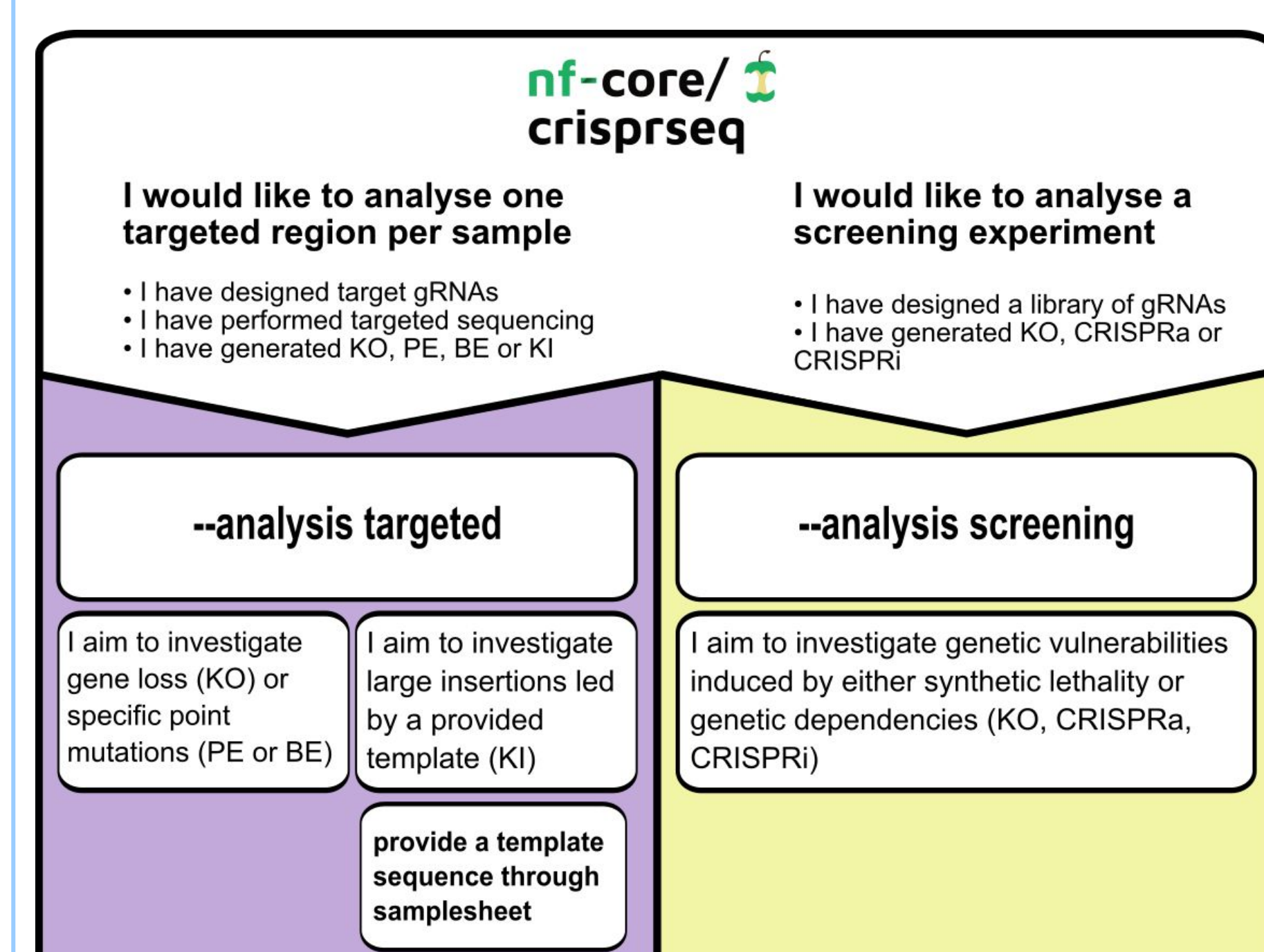
Analysing CRISPR editing results can be a daunting task, often involving the use of complex and user-unfriendly software. This complexity can challenge interpreting results, and extracting meaningful insights from the data.

nf-core/crisprseq

nf-core/crisprseq is a pipeline for the assessment of CRISPR gene editing assays. This tool facilitates the analysis of a wide range of experiments, from targeted gene edits to large-scale functional screens.

The pipeline accurately characterizes knockouts, knock-ins, base and prime editing, as well as gene modulation.
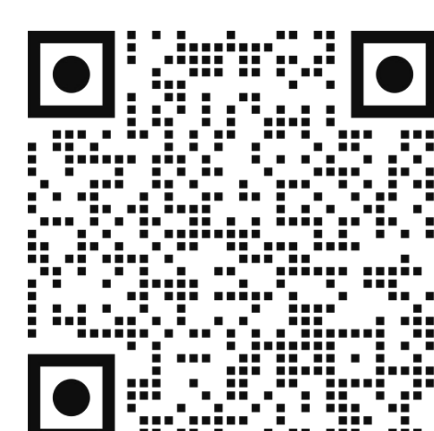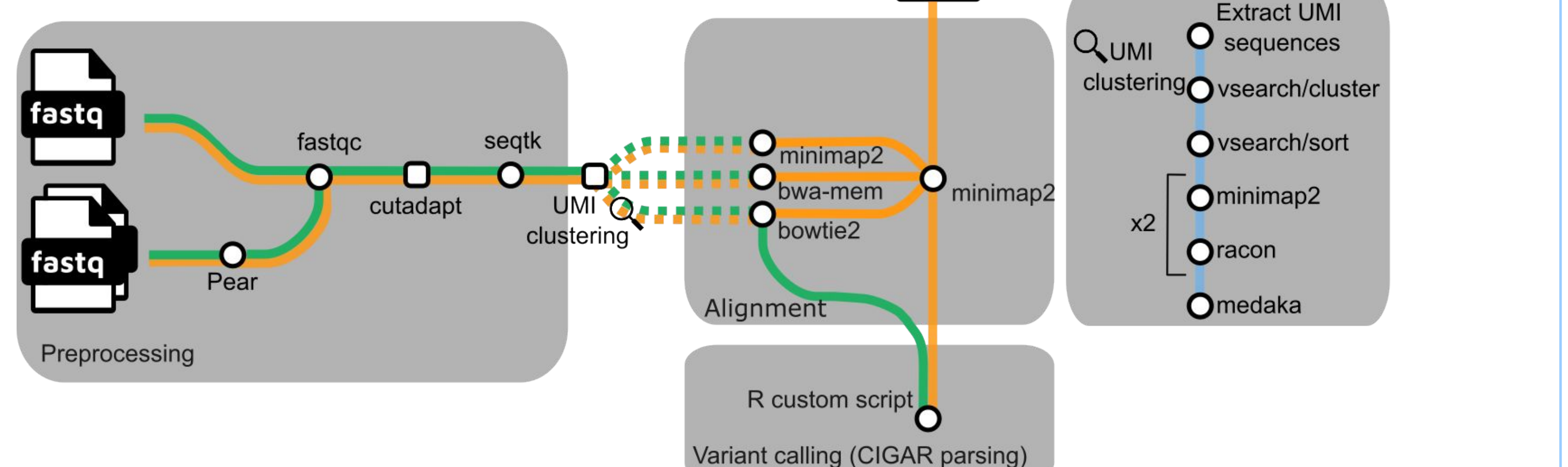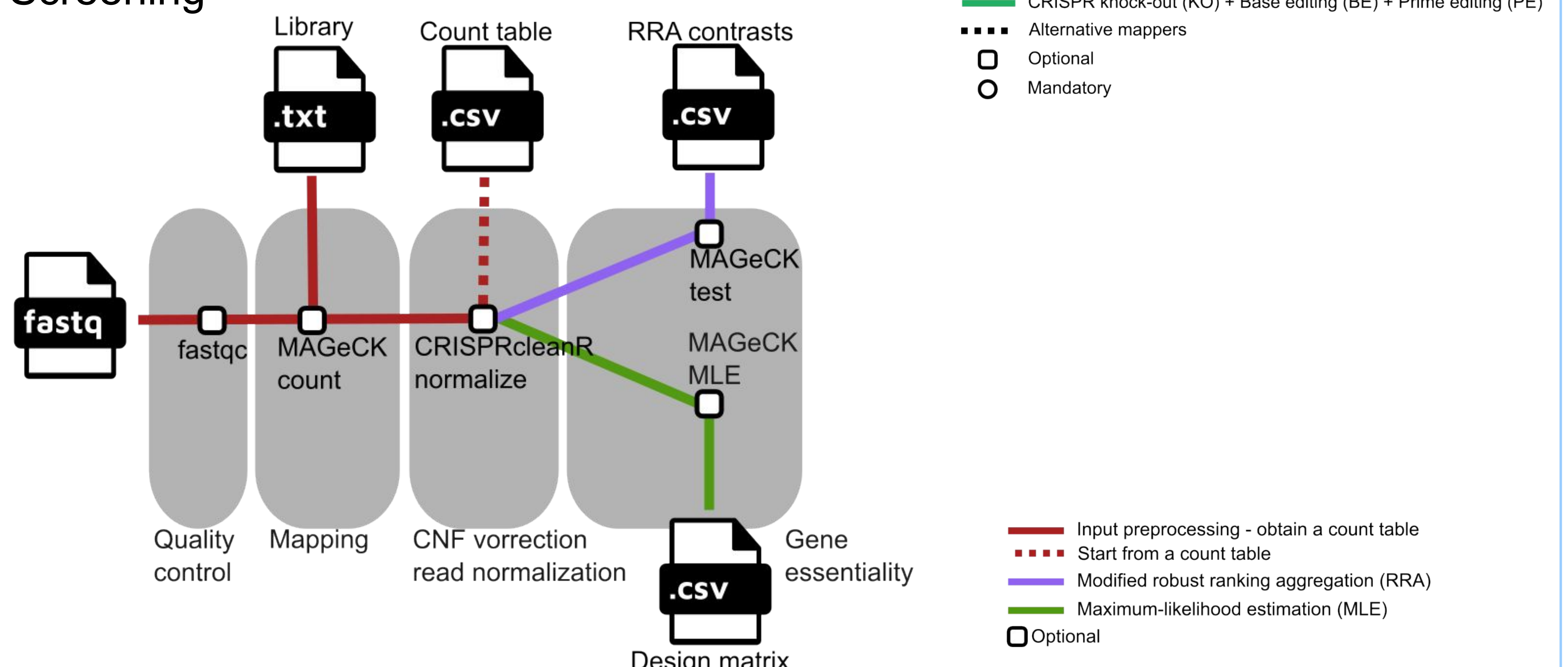
Applications

Get in touch

https://nf-co.re/crisprseq

https://github.com/nf-core/crisprseq

https://nfcore.slack.com/channels/crisprseq

Workflow