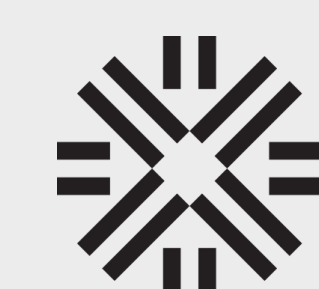


Introducing



Université de Rennes

phaseimpute

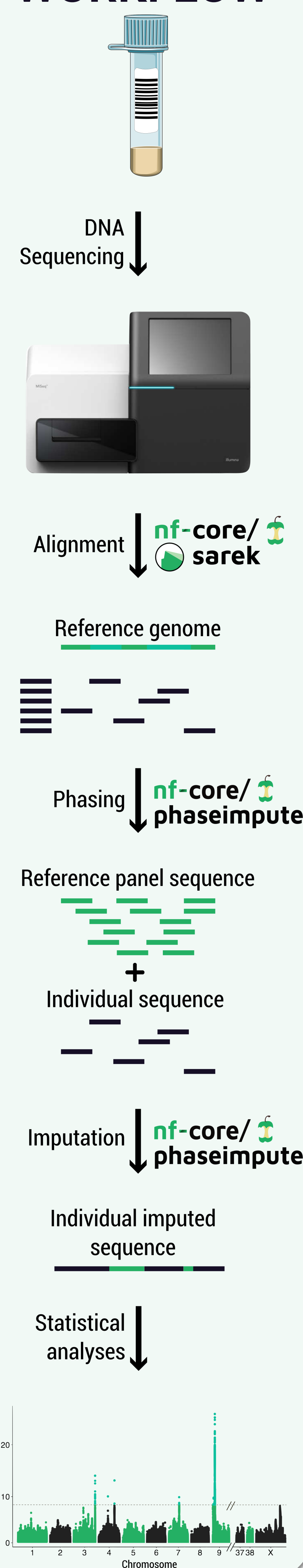
from idea to release

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² ZS Discovery, Buenos Aires, Argentina ³ Nextflow Ambassador Program

WORKFLOW

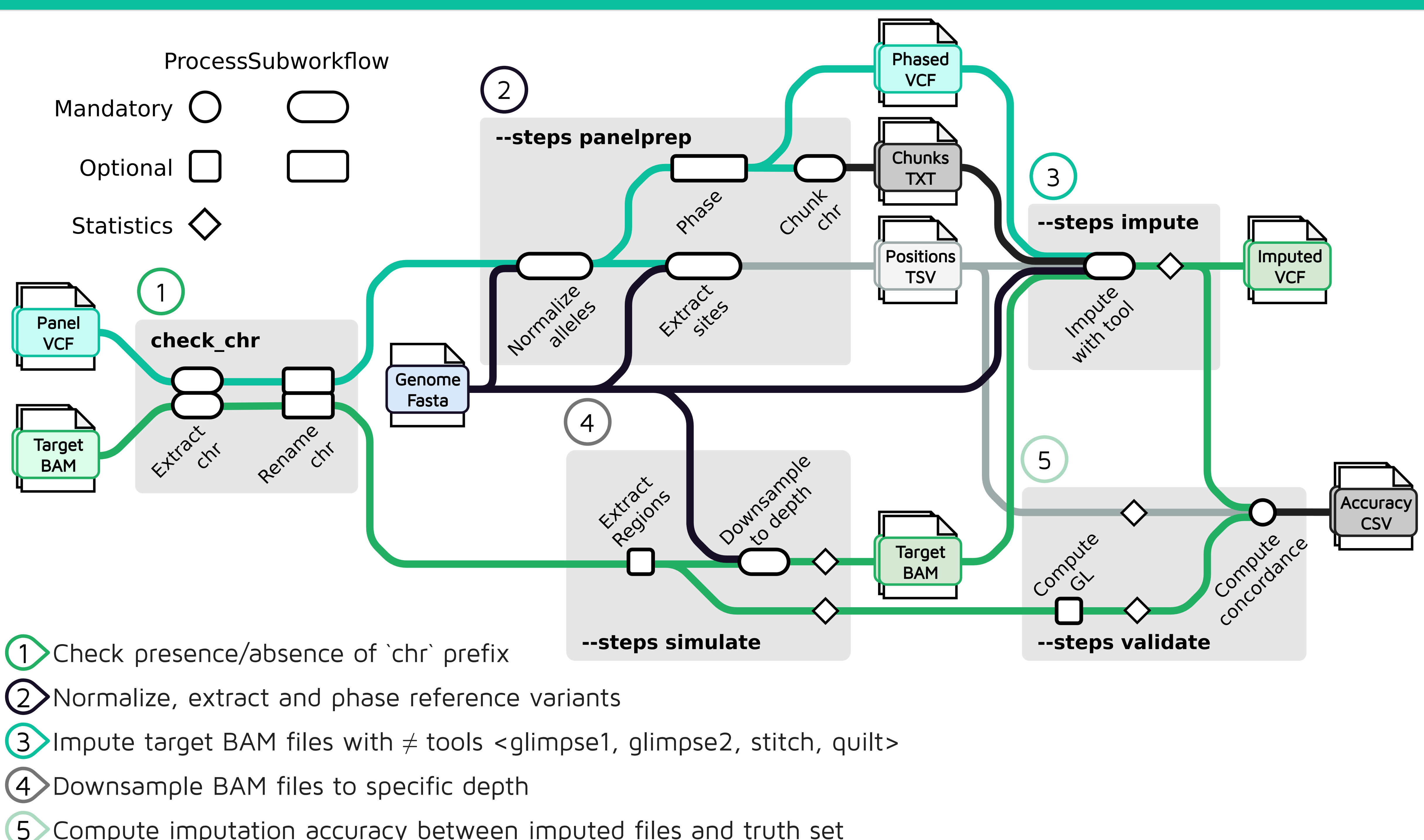


INTRODUCTION

Genome imputation is a statistical technique that enhances the resolution of genotyping SNP arrays and low-pass sequencing (<1x) by filling missing data with information from high resolution whole genome reference haplotype panels. While existing pipelines primarily focus on the imputation step and on the human species, crucial steps such as panel preparation, phasing, and imputation assessment are often overlooked.

To address this gap, we introduce **nf-core/phaseimpute**, a comprehensive pipeline to perform **panel preparation**, **genomic data simulation**, **imputation**, and **tool assessment**.

NF-CORE/PHASEIMPUTE DESIGN



DEVELOPMENT

- Back and forth with **nf-core/modules** repository
- nf-tests** for every module, function and subworkflow
- CI/CD with GitHub actions for **different use cases**
- Mega-tests** with Seqera Platform/AWS
- New imputation modules in **multiQC**

FUTURE PERSPECTIVES

- Handling of **SNP arrays data**
- Allow **batch** imputation
- Imputation of **chrX**
- Add **new imputation tools**
- Costs and environmental impacts with **nf-CO2footprint**

JOIN THE DISCUSSION !



ACKNOWLEDGMENTS

- nf-core community
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