

# Reproducible portable and efficient ancient genome reconstruction



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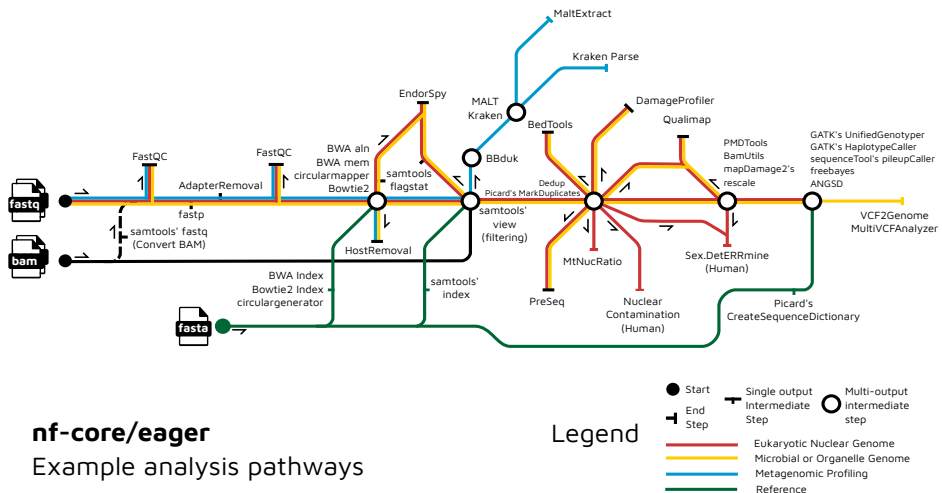
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## Motivation

- Ancient DNA is now an established data source for many fields
- Previous pipelines do not scale to today's sample-sizes
- Previous pipelines do not include now-routine palaeogenomic analyses or latest tools

## Latest tools and workflows

- For Parallel metagenomic screening of off-target reads
- Latest genotypers and consensus callers
- New statistics reporting (feature coverage, biological sex)

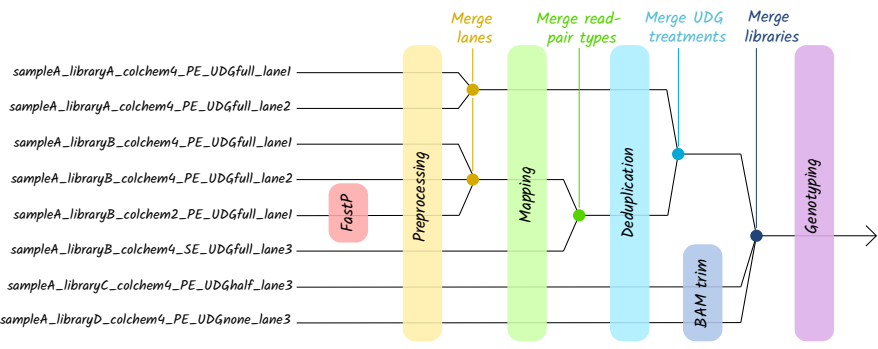


## Reproducible, portable and efficient

- Scalable: **tight integration** with HPC cluster schedulers
- Same run, any infrastructure via containers & **institutional profiles**

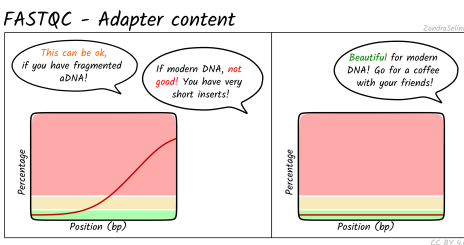
```
$ nextflow run nf-core/eager -profile singularity,mpi-shh <pipeline_parameters>
$ nextflow run nf-core/eager -profile docker,globe <pipeline_parameters>
```

Automated processing of complex sequencing strategies



## Accessibility

- Scalable and **interactive reports**
- GUI** and command-line.
- Extensive documentation (usable for teaching, CC-BY)



## Get involved!

- nf-core/eager**
- feature requests**
- bug reports**
- contribute code**

<https://nf-co.re/join>  
**nfcore - #eager**

Thurs. @ 13:00 CEST:  
**Live Demo**

Training? Contact me!  
Click:

Click on **URLs!**

## Acknowledgements

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## Publication

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