

Reproducible, portable, and efficient ancient genome reconstruction with nf-core/eager

This manuscript ([permalink](#)) was automatically generated from [apeltzer/eager2-paper@affc8b3](#) on April 5, 2020.

Authors

- **James A. Fellows Yates**

 [0000-0001-5585-6277](#) ·  [jfy133](#) ·  [jfy133](#)

Department of Archaeogenetics, Max-Planck-Institute for the Science of Human History · Funded by Grant XXXXXXXX

- **Theseas**

 [XXXX-XXXX-XXXX-XXXX](#) ·  [thi](#) ·  [placeholder](#)

Department of Something, University of Whatever · Funded by Grant XXXXXXXX

- **Maxime Borry**

 [XXXX-XXXX-XXXX-XXXX](#) ·  [placeholder](#) ·  [placeholder](#)

Department of Something, University of Whatever · Funded by Grant XXXXXXXX

- **Aida**

 [XXXX-XXXX-XXXX-XXXX](#) ·  [placeholder](#) ·  [placeholder](#)

Department of Something, University of Whatever · Funded by Grant XXXXXXXX

- **Zandra**

 [XXXX-XXXX-XXXX-XXXX](#) ·  [placeholder](#) ·  [placeholder](#)

Department of Something, University of Whatever · Funded by Grant XXXXXXXX

- **Stephen**

 [XXXX-XXXX-XXXX-XXXX](#) ·  [placeholder](#) ·  [placeholder](#)

Department of Something, University of Whatever · Funded by Grant XXXXXXXX

- **Maxime Garcia**

 [XXXX-XXXX-XXXX-XXXX](#) ·  [placeholder](#) ·  [placeholder](#)

Department of Something, University of Whatever · Funded by Grant XXXXXXXX

- **Judith**

 [XXXX-XXXX-XXXX-XXXX](#) ·  [placeholder](#) ·  [placeholder](#)

Department of Something, University of Whatever · Funded by Grant XXXXXXXX

- **Alexander Peltzer**

 [0000-0002-6503-2180](#) ·  [apeltzer](#) ·  [alex_peltzer](#)

Translational Medicine & Clinical Pharmacology, Boehringer Ingelheim Pharma GmbH & CO KG, Biberach an der Riss

Abstract

The increasing utilization of ancient DNA (aDNA) to address anthropological, palaeontological and biological questions is resulting in a rising diversity in the size of laboratories and scale of analyses being performed. In the context of this heterogeneous landscape, we present [nf-core/eager](#), an advanced and entirely redesigned pipeline for the analysis of ancient DNA molecular data. nf-core/eager builds on existing ideas and concepts introduced in the original EAGER pipeline@doi:10.1186/s13059-016-0918-z, and improves various aspects of the analysis procedure by building on computational frameworks such as Nextflow [1](#) and nf-core [2](#). The pipeline aims to address three main points: adaptability to different project sizes, reproducibility to ensure robust standards, and extensibility to ensure that new standard analyses (including metagenomic screening) are accessible to research groups of all sizes. The new version of EAGER has been developed within the nf-core initiative, to ensure high quality software development and maintenance support - which will contribute to a long-term lifecycle for the pipeline. nf-core/eager will assist in ensuring that the power of Next Generation Sequencing (NGS) ancient DNA analysis expand to many different applications in the field of ancient DNA research.

Introduction

This is a simple test with a doi citation for EAGER v1@doi:10.1186/s13059-016-0918-z.

References

1. Nextflow enables reproducible computational workflows

Paolo Di Tommaso, Maria Chatzou, Evan W Floden, Pablo Prieto Barja, Emilio Palumbo, Cedric Notredame

Nature Biotechnology (2017-04-11) <https://doi.org/gfj52z>

DOI: [10.1038/nbt.3820](https://doi.org/10.1038/nbt.3820) · PMID: [28398311](https://pubmed.ncbi.nlm.nih.gov/28398311/)

2. The nf-core framework for community-curated bioinformatics pipelines

Philip A. Ewels, Alexander Peltzer, Sven Fillinger, Harshil Patel, Johannes Alneberg, Andreas Wilm, Maxime Ulysse Garcia, Paolo Di Tommaso, Sven Nahnsen

Nature Biotechnology (2020-02-13) <https://doi.org/ggk3qh>

DOI: [10.1038/s41587-020-0439-x](https://doi.org/10.1038/s41587-020-0439-x) · PMID: [32055031](https://pubmed.ncbi.nlm.nih.gov/32055031/)