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

Authors

- **James A. Fellows Yates**
  [0000-0001-5585-6277](#) · [jfy133](#) · [jafellowsyates](#)
  Microbiome Sciences Group, Department of Archaeogenetics, Max-Planck-Institute for the Science of Human History, Jena, Germany · Funded by Max Planck Society

- **Thiseas C. Lamnidis**
  [0000-0003-4485-8570](#) · [TCLamnidis](#) · [TCLamnidis](#)
  Population Genetics Group, Department of Archaeogenetics, Max-Planck-Institute for the Science of Human History, Jena, Germany · Funded by Max Planck Society

- **Maxime Borry**
  [0000-0001-9140-7559](#) · [maxibor](#) · [notmaxib](#)
  Microbiome Sciences Group, Department of Archaeogenetics, Max-Planck-Institute for the Science of Human History, Jena, Germany · Funded by Max Planck Society

- **Aida Andrades Valtueña**
  [0000-0002-1737-2228](#) · [aidaanva](#) · [aidaanva](#)
  Computational Pathogenomics Group, Department of Archaeogenetics, Max-Planck-Institute for the Science of Human History, Jena, Germany · Funded by Max Planck Society

- **Zandra Fagernäs**
  [0000-0003-2667-3556](#) · [ZandraFagernas](#) · [ZandraSelina](#)
  Microbiome Sciences Group, Department of Archaeogenetics, Max-Planck-Institute for the Science of Human History, Jena, Germany · Funded by Max Planck Society

- **Stephen Clayton**
  [0000-0001-5223-9695](#) · [sc13-bioinf](#)
  Department of Archaeogenetics, Max-Planck-Institute for the Science of Human History, Jena, Germany · Funded by Max Planck Society

- **Maxime U. Garcia**
  [0000-0003-2827-9261](#) · [MaxUlysse](#) · [gau](#)
  Department of Oncology-Pathology, Karolinska Institutet, Stockholm, Sweden · Funded by Barncancerfonden

- **Judith Neukamm**
  [0000-0001-8141-566X](#) · [JudithNeukamm](#) · [JudithNeukamm](#)
  Palaeogenetics Group, Institute of Evolutionary Medicine, University of Zurich, Zürich, Switzerland

- **Alexander Peltzer**
  [0000-0002-6503-2180](#) · [apeltzer](#) · [alex_peltzer](#)
  Quantitative Biology Center (QBiC), Eberhard-Karls-Universität, Tübingen, Germany

Abstract

The broadening utilization of ancient DNA (aDNA) to address archaeological, 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 genomic data. nf-core/eager builds on existing ideas and concepts introduced in the original EAGER pipeline, and improves various aspects of the analysis procedure by building on computational frameworks such as Nextflow and nf-core. The pipeline aims to address three main points: accessibility and adaptability to different research groups and their computing configurations, reproducibility to ensure robust analytical standards in the field, and updating the EAGER pipeline to the latest routine ancient genomic practises. This new version of EAGER has been developed within the nf-core initiative, to ensure high quality software development and maintenance support; contributing to a long-term lifecycle for the pipeline. nf-core/eager will assist in ensuring that ancient DNA sequencing data can be utilised by a diverse range of research groups and fields.

Introduction

Ancient DNA (aDNA) has become a widely accepted source of biological data, helping to provide new perspective for a range of fields including archaeology, ecology, cultural heritage, and palaeontology. The utilisation of next-generation-sequencing has allowed the recovery of aDNA from a wide variety of sources, including but not limited to, the skeletal remains of animals [1,2,3,4], modern and archaic humans [5,6,7], bacteria [8,9,10], viruses [11,12], plants [13,14], coprolites [15,16], dental calculus [17,18], sediments [19,20], medical slides [21], parchment [22], and most recently ancient 'chewing gum' [23,24]. Improvement in laboratory protocols to increase yields of otherwise trace amount of DNA has at the same time led to studies that can total hundreds of ancient individuals [25,26], spanning single [27] to thousands of organisms [17]. These differences of disciplines have led to a heterogeneous landscape in terms of types of analyses and require different types of computing resources for each lab [28,29]. Taking into consideration the unequal distribution of resources (and infrastructure such as internet connection), streamlined and efficient pipelines can help increase accessibility to high-quality analyses

The degraded nature of aDNA poses an extra layer of complexity to standard modern genomic analysis. Through a variety of processes [30], DNA molecules will fragment overtime resulting in ultra-short molecules [31]). These sequences have low nucleotide complexity making it difficult to identify with precision which part of the genome a read is derived from. Furthermore, when fragmentation is not a 'clean break' this can lead to uneven ends with single-stranded 'overhangs' at end of molecules, which are susceptible to chemical processes such as deamination that lead to mis-incorporation of bases during library construction [32]. On top of this, taphonomic processes such as heat, moisture, and microbial and burial environment processes lead to varying rates of degradation [33,34], where the original DNA content of a sample is lost and supplanted by modern environmental DNA. Later handling by archaeologists, museum curators, and scientists can also contribute 'modern' contamination. While these characteristics can help provide evidence towards the 'authenticity' of true aDNA sequences (e.g. aDNA C>T 'damage' profiles [35]), they also pose specific challenges such as unspecific DNA alignment and/or low coverage and miscoding lesions resulting in low-confidence genotyping. These factors often lead to prohibitive sequencing costs to retrieve enough data for modern NGS data pipelines (e.g. > 1 billion reads for a 1X depth coverage *Yersinia pestis* genome [36]), and thus require aDNA tailored methods and techniques to overcome these challenges.

Two previously published and commonly used pipelines in the field are PALEOMIX [37] and EAGER [38]. These two pipelines take a similar approach to link together standard tools used for Illumina NGS data processing (sequencing quality control, sequencing adapter removal/and or paired-end read

merging, mapping of reads to a reference genome, genotyping, etc.), but with a specific focus on tools that are designed for or well-suited for aDNA (such as bwa aln that works well on ultra-short molecules [39] and mapDamage [40] for aDNA characteristics evaluation). Yet, neither of these pipelines have had major updates to bring them in-line with current routine aDNA analyses. Metagenomic screening of off-target genomic reads for pathogens or microbiomes [17,18] has become particularly common, given its role in revealing widespread infectious disease and possible epidemics that had previously been undetected in the archaeological record [11,12,36,41]. Without easy access to the latest field-established analytical routines, aDNA studies risk being published without the necessary quality control checks that ensure aDNA authenticity and without yielding the full range of possibilities from their data.

To address these shortcomings, we have completely re-implemented the latest version of the EAGER pipeline in Nextflow [42] (a domain-specific-language (DSL), specifically designed for the construction of omics analysis pipelines), introduced new features, and more flexible pipeline configurations. In addition, the newly named pipeline - nf-core/eager - has been developed in the context of the nf-core community framework [43], which enforces strict guidelines for best-practises in software development.

Results and Discussion

Scalability, Portability, and Efficiency

The reimplementation of EAGER into Nextflow offers a range of benefits over the original custom pipeline framework.

Firstly, the new framework provides immediate integration of nf-core/eager into various job schedulers in POSIX High-Performance-Cluster (HPC) environments, cloud computing resources, and as well as local workstations. This portability allows both small and big labs to run nf-core/eager regardless of the type of computer or cluster size, with minimal effort or configuration, facilitating reproducibility and therefore maintenance of standards within the field. This is further assisted by the in-built compatibility with software environments and containers such as Conda [44], Docker[45] and Singularity [46]. These are single packages that include all the software (with exact versions) required by the pipeline, in a form that is installable and runnable regardless of the setup of their local software environment. Another major change with nf-core/eager is that the graphical-user-interface (GUI) set up of an nf-core/eager run is now replaced with a command-line-interface (CLI) as the primary user interaction mode. This is more compatible and portable with most HPCs (that may not offer display of program windows), and is in line with the vast majority of bioinformatic tools. We therefore believe this will not be a hindrance to new researchers from outside computational biology. However there are plans from Nextflow (with tower.nf [47]) and within the nf-core community to provide multiple alternatives in the near future including a CLI wizard and a web-based input GUI.

Secondly, reproducibility is made easier through the use of 'profiles' that can define configuration parameters. These profiles can be managed at different hierarchical levels. HPC-level profiles can specify parameters for the computing environment (job schedulers, cache locations for containers, maximum memory and CPU resources etc.), which can be centrally managed to ensure all users of a group use the same settings. Pipeline-level profiles, specifying default parameters for nf-core/eager itself, allow fast access to routine pipeline-run parameters via a single flag in the nf-core/eager run command, without having to configure each new run from scratch.

Compared to the original EAGER that utilised per-FASTQ XML files with hardcoded filepaths for a specific user's server, nf-core/eager allows researchers to publish the specific profile used in their runs alongside their publications, to ensure other groups can generate the same results. Usage of profiles

also reduces mistakes caused by insufficient 'prose' based reporting of program settings that can be regularly found in the literature. The default nf-core/eager profile uses parameters evaluated in different aDNA specific contexts (e.g. in [48]), and will be updated in each new release as new studies are published.

nf-core/eager provides improved efficiency over the original EAGER pipeline by replacing the sample-by-sample sequential processing with Nextflow's asynchronous parallelisation, whereby multiple pipeline steps and samples are run in parallel (in addition to single pipeline step multi-threading). This, combined with pre-defined per-process customisation of resource parameters, reduces unnecessary resource allocation that can occur with new users to each step of an NGS data processing pipeline. This is particularly pertinent given the increasing use of centralised HPCs or cloud computing, which often use per-hour cost calculations.

Updated Workflow

nf-core/eager follows a similar structural foundation to the original EAGER. Given Illumina short-read FASTQ and/or BAM files, and a reference FASTA file, this can be split into four main stages:

1. Preprocessing
   - Sequencing quality control: FastQC [49]
   - Sequencing artefact clean-up (merging, adapter clipping): AdapterRemoval2 [50]
   - Preprocessing statistics generation
2. Mapping and post- processing
   - Alignment against reference genome: BWA [39,51], CircularMapper [38]
   - Mapping quality filtering: Samtools [53]
   - PCR duplicate removal: DeDup [38], Picard MarkDuplicates [54]
   - Mapping statistics generation: PreSeq [55], Qualimap2 [56]
3. aDNA Evaluation and Modification
   - Damage profiling: DamageProfiler [57]
   - aDNA reads selection: PMDTools [58]
   - Damage removal: Bamutils[59]
   - (Human) contamination estimation: ANGSD [60]
4. Genotyping and Consensus Sequencing: GATK [54], VCF2Genome [38]

In nf-core/eager, all tools also originally used in EAGER have been updated to latest versions, as available on Bioconda [61] and Conda-forge [62] to ensure widespread accessibility and stability of utilized tools. The MapDamage2 (for damage profile generation) [35] and Schmutzi for (mitochondrial contamination estimation) [63] methods have not been carried over to nf-core/eager, the first because a more performant successor method is now available (DamageProfiler), and the latter because a stable release of the method could not be migrated to Bioconda. We anticipate that there will be an updated version of Schmutzi in the near future that will allow us to integrate the method again in nf-core/eager, once a version is released on Bioconda. Support for the Bowtie2 aligner [64] will be added in the near future, after consultation with the palaeogenetics community. New tools to the basic workflow include fastp [65] for the removal of 'poly-G' sequencing artefacts that are common in 2-colour Illumina sequencing machines (such as the increasingly popular NextSeq and NovaSeq platforms, [66]). For genotyping we have now included FreeBayes [67] as an alternative to the human-focused GATK tools. We have also maintained the possibility of using the now unsupported GATK UnifiedGenotyper, as the GATK HaplotypeCaller performs *de novo* assembly around possible variants, which may not be suitable for low-coverage aDNA data.
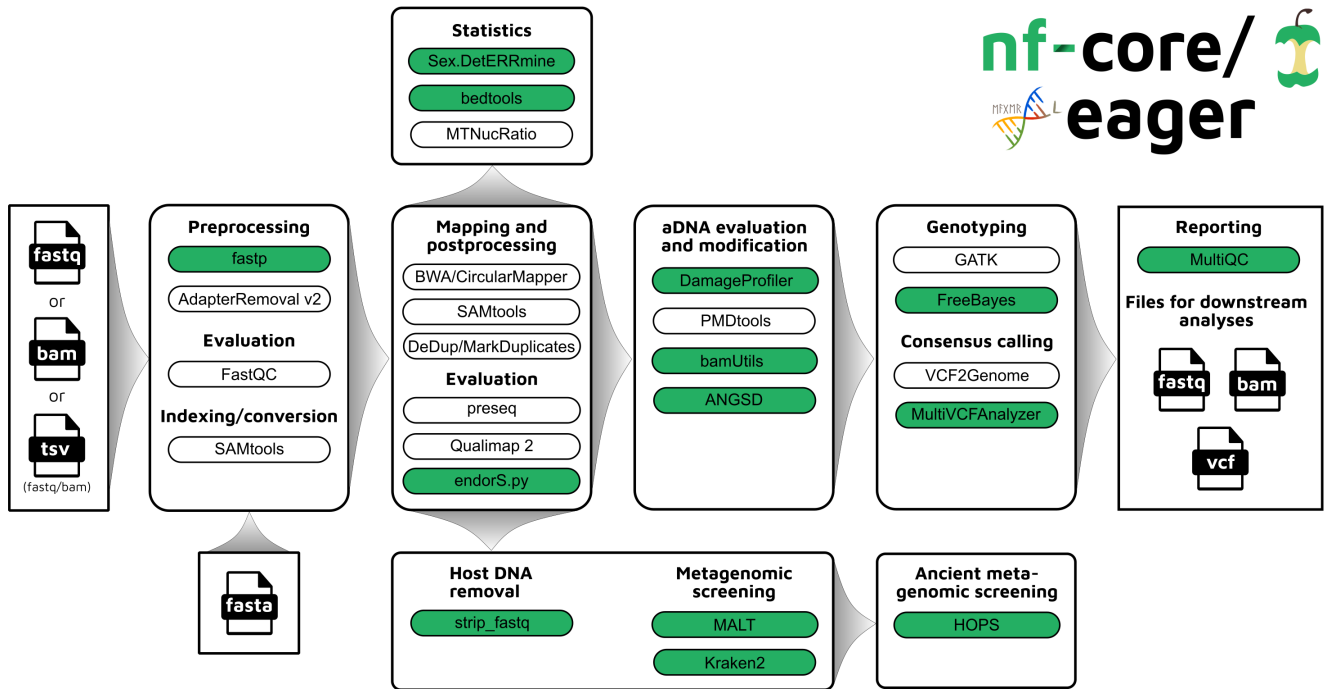
Figure 1: Simplified schematic of the nf-core/eager workflow pipeline. Green filled bubbles indicate new functionality added over the original EAGER pipeline.

We have further extended the genomic analysis functionality of the pipeline by adding ancient metagenomic analysis, to identify the wider taxonomic content of a sample. We have added the ability to screen all off-target reads (not mapped to the reference genome) with two metagenomic profilers: MALT [68,69] and Kraken2 [70]. Characterisation of properties of authentic aDNA from MALT alignments is carried out with the HOPS pipeline [71]. Ancient metagenomic studies sometimes may include comparative samples from living individuals [72]. To support open data, whilst respecting data privacy, nf-core/eager includes a 'strip_fastq' script which creates raw FASTQ files, but with reference-genome mapped reads removed. This allows safe upload of sequencing data to public repositories with identifiable human data removed.

Additional functionality tailored for ancient bacterial genomics includes integration of a SNP alignment generation tool, MultiVCFAnalyzer [8], which allows assessment of cross-mapping levels from different related taxa to a reference genome - a common challenge in ancient bacterial genome reconstruction [34]. The output SNP alignment FASTA file can then be used for downstream analyses such as phylogenetic tree construction. Simple coverage statistics of particular annotations (e.g. genes) of an input reference is offered by bedtools [73], which can be used, for example, for determining functional differences between ancient bacterial strains (as in [41]). When using a human reference genome, nf-core/eager can now also can give estimates of the biological sex of a given individual with Sex.DetERRmine [74]. A dedicated 'endogenous DNA' calculator (endorS.py) is also included to provide a percentage estimate of the sequenced reads matching the reference from the total number of reads sequenced per library.

Given the large amount of sequencing often required to yield sufficient genome coverage from aDNA data, palaeogeneticists tend to use multiple (differently treated) libraries or sequencing runs. The original EAGER pipeline could only run single libraries at a time, and in these contexts required significant manual user input in merging different FASTQ or BAM files. A major upgrade in nf-core/eager is that the new pipeline supports automated processing of complex sequencing strategies for many samples. As an alternative to direct paths to FASTQ or BAM files, the pipeline can also accepts a simple table in TSV format which includes file paths and additional metadata such as sample name, library name, sequencing lane, colour chemistry, and UDG treatment. This allows simultaneous

processing and appropriate merging of heterogeneous data from multiple sequencing runs and/or library types.

The original EAGER pipeline required users to look through many independent output directories and files to make full assessment of their sequencing data. This has now been replaced with a much more extensive MultiQC [75] report. This tool aggregates the log files of every supported tool into a single interactive report, and assists users in making fuller assessment of their sequencing and analysis runs. Most tools within nf-core/eager have a corresponding MultiQC module to enable comprehensive evaluation of all stages of the pipeline.

An overview of the entire pipeline is shown in Figure 1.

Accessibility

Alongside the interactive MultiQC report, we have written extensive documentation on all parts of running and interpreting the output of the pipeline. Given that a large fraction of aDNA researchers come from fields outside computational biology, and thus may have limited computational training, we have written documentation that also gives guidance on how to interpret each section of the report, specifically in the context of NGS and aDNA. This includes schematic images of best practices or expected output that are published under CC-BY licenses to allow for use in other training material (example in 2). We hope this open-access resource will make the study of aDNA more accessible to researchers new to the field, by providing practical guidelines how to evaluate characteristics and effects of aDNA on downstream analyses.
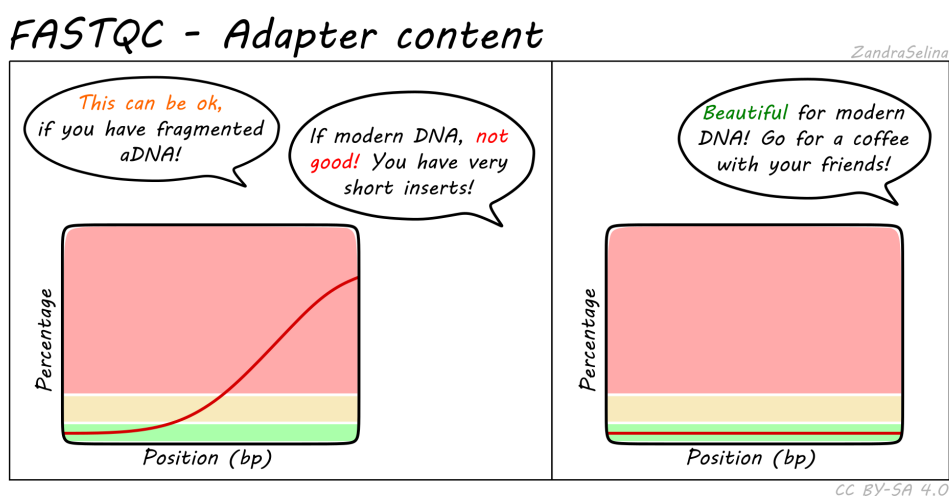
Figure 2: Example of output interpretation documentation schematic images that can assist new users in the interpretation to next-generation-sequencing aDNA processing.

The development of nf-core/eager in Nextflow and the nf-core initiative will also improve open-source community contributions to the pipeline. While Nextflow is written primarily in Groovy, the Nextflow DSL simplifies a number of concepts to an intermediate level that bioinformaticians without Java/Groovy experience can easily access (regardless of own programming language experience). Furthermore, Nextflow places ubiquitous and more widely known command-line interfaces, such as bash, in a prominent position within the code, rather than custom java code and classes. We hope this will motivate further bug fixes and feature contributions from the community, to keep the pipeline state-of-the-art and ensure a longer life-cycle. This will also be supported by the active and welcoming nf-core community who provide general guidance and advice on developing Nextflow and nf-core pipelines.

Conclusion

nf-core/eager is an efficient, portable, and accessible pipeline for processing aDNA genomic data. This re-implementation of EAGER into Nextflow and nf-core will improve reproducibility and inclusion of rapidly increasing aDNA datasets, for both large and small laboratories. Extensive documentation also enables newcomers to the field get a practical understanding on how to interpret aDNA in the context of NGS data processing. Ultimately, nf-core/eager provides easier access to the latest tools and routine screening analyses commonly used in the field, and sets up the pipeline for staying at the forefront of palaeogenetic analysis.

Methods

Installation

nf-core/eager requires a version of Java, Nextflow and either a functional Conda installation *or* Docker/Singularity container installation. A quick installation guide to follow to get started can be found in the *Quickstart* section of the nf-core/eager repository [76].

Running

After the installation, users can run the pipeline using standard test data by utilizing some of the `test` profiles we provide (e.g. using Docker):

```
nextflow run nf-core/eager -r 2.1.0 -profile test,docker
```

This will download test data automatically, run the pipeline locally with all software tools containerized in a Docker image and store the output of that run in the `./results` folder of your current directory.

The default pipeline settings assumes paired end FASTQ data and will run: FastQC; AdapterRemoval2 (merging and adapter clipping); post-clipping FastQC (for AdapterRemoval2 performance evaluation); bwa mapping (with the 'aln' algorithm); samtools flagstat (for mapping statistics); endorS.py (for endogenous DNA calculation); DeDup (for PCR amplicon deduplication); PreSeq (for library complexity evaluation); DamageProfiler and Qualimap2 (for genome coverage statistics) and the MultiQC pipeline run report. If no additional FASTA indices are given, these will also be generated.

The pipeline is highly configurable and most modules can be turned on and off at the request of the user using different flags to allow high customisation to each users needs. For example, to include metagenomic screening of off-target reads and sex determination based on on-target mappings of pre-clipped single-end data:

```
nextflow run nf-core/eager -r 2.1.0 -profile conda --input
        '/<path>/<to>/*/*R1*.fastq.gz' --single_end --fasta
        '/<path>/<to>/<reference>.fasta.gz' --skip_fastqc --
        skip_adapterremoval --run_bam_filtering --bam_discard_unmapped --
        bam_unmapped_type 'fastq' --run_metagenomic_screening --
        metagenomic_tool 'malt' --database '/<path>/<to>/<malt_database>' --
        run_sexdeterrmine
```

Profiles

We utilize a central configuration profile repository to enable users from various institutions to use pipelines on their particular infrastructure more easily [77]. There are multiple resources listed in this repository with information on how to add your own configuration profile with help from the nf-core community.

Users can customize this infrastructure profile by themselves, with the nf-core community, or with their local system administrator to make sure that the pipeline runs successfully, and can then rely on the Nextflow and nf-core framework to ensure compatibility upon further infrastructure changes. For example, in order to run the nf-core/eager pipeline at the Max Planck Institute for the Science of Human History (MPI-SHH) in Jena, users only have to run:

```
nextflow run nf-core/eager -r 2.1.0 -profile shh_cdag --input
         '/<path>/<to>/*/*{R1,R2}*.fastq.gz' --fasta
         '/<path>/<to>/<reference>.fasta.gz'
```

This runs the testing profile of the nf-core/eager pipeline with parameters specifically adapted to the HPC system at the MPI-SHH. In some cases, similar institutional configs for other institutions may already exist (originally utilised for different nf-core pipelines), so users need not write their own.

Inputs

The pipeline can be started using (raw) FASTQ files from sequencing or pre-mapped BAM files. Additionally, the pipeline requires a FASTA reference genome.

If BAM input is provided, an optional conversion to FASTQ is offered, otherwise BAM files processing will start from the post-mapping stage.

If users have complex set-ups, e.g. multiple sequencing lanes that require merging of files for example, the pipeline can be supplied with a tabular separated value (TSV) file to enable such complex data handling. Both FASTQs and BAMs can be provided in this set up. FASTQs with the same library name and sequencing chemistry but sequenced across multiple lanes will be concatenated after AdapterRemoval and prior mapping. Libraries with the sample name and with the same UDG treatment, will be merged after deduplication. If libraries with the sample name have different UDG treatment, these will be merged after the aDNA modification stage (i.e. BAM trimming or PMDtools, if turned on), prior genotyping, as shown in in Figure 3.
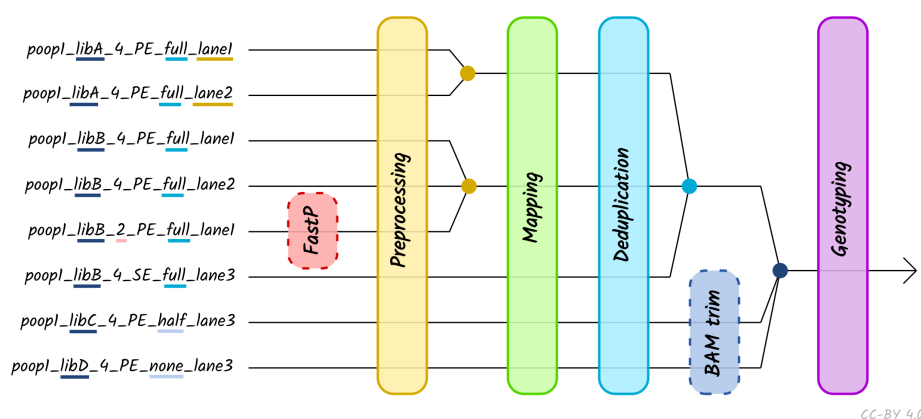
Figure 3: Schematic of different processing and merging points based on the nature of different libraries, as specified in metadata of a TSV file. Dashed boxes represent optional library-specific processes

As Nextflow will automatically download files from URLs, profiles and/or TSV files can include links to publicly available data (e.g. the ENA FTP server). This assists in reproducibility as if profiles or TSV files are uploaded with a publication, a researcher wishing to re-analyse the data in the same way can use the exact settings and merging procedures in the original publication, without having to reconstruct this from prose.

Monitoring

Users can either monitor their pipeline execution with the messages Nextflow prints to the console while running, or utilize projects such as Nextflow Tower [47] to monitor their analysis pipeline during runtime.

Output

The pipeline produces several dozen output files in various file formats, with a more detailed listing available in the user documentation. This includes metrics, statistical analysis data and standardized output files (BAM, VCF) for close inspection and further downstream analysis, as well as a MultiQC report. If an emailing daemon is set up on the server, the latter can even be emailed to users automatically, when starting the pipeline with a dedicated option (–email you@yourdomain.org).

Data and software availability

All code is available on github at https://github.com/nf-core/eager and archived with Zenodo under the DOI 10.5281/zenodo.1465061. The version of nf-core/eager that this preprint is based on the current dev branch of the GitHub repository (2.2.0dev), and on publication will be released as 2.2.0.

This paper was written with Manubot [78].

Competing Interests

No competing interests are declared.

Acknowledgements

References

1. **Complete Genomes Reveal Signatures of Demographic and Genetic Declines in the Woolly Mammoth**
   Eleftheria Palkopoulou, Swapan Mallick, Pontus Skoglund, Jacob Enk, Nadin Rohland, Heng Li, Ayça Omrak, Sergey Vartanyan, Hendrik Poinar, Anders Götherström, … Love Dalén
   Current Biology (2015-05) https://doi.org/34d
   DOI: 10.1016/j.cub.2015.04.007 · PMID: 25913407 · PMCID: PMC4439331

2. **Recalibrating Equus evolution using the genome sequence of an early Middle Pleistocene horse**
   Ludovic Orlando, Aurélien Ginolhac, Guojie Zhang, Duane Froese, Anders Albrechtsen, Mathias Stiller, Mikkel Schubert, Enrico Cappellini, Bent Petersen, Ida Moltke, … Eske Willerslev
   Nature (2013-06-26) https://doi.org/q7n
   DOI: 10.1038/nature12323 · PMID: 23803765

3. **Ancient pigs reveal a near-complete genomic turnover following their introduction to Europe**
   Laurent A. F. Frantz, James Haile, Audrey T. Lin, Amelie Scheu, Christina Geörg, Norbert Benecke, Michelle Alexander, Anna Linderholm, Victoria E. Mullin, Kevin G. Daly, … Greger Larson
   Proceedings of the National Academy of Sciences (2019-08-27) https://doi.org/gf9hnf
   DOI: 10.1073/pnas.1901169116 · PMID: 31405970 · PMCID: PMC6717267

4. **Ancient DNA reveals the Arctic origin of Viking Age cod from Haithabu, Germany**
   Bastiaan Star, Sanne Boessenkool, Agata T. Gondek, Elena A. Nikulina, Anne Karin Hufthammer, Christophe Pampoulie, Halvor Knutsen, Carl André, Heidi M. Nistelberger, Jan Dierking, … James H. Barrett
   Proceedings of the National Academy of Sciences (2017-08-22) https://doi.org/gbt8b2
   DOI: 10.1073/pnas.1710186114 · PMID: 28784790 · PMCID: PMC5576834

5. **137 ancient human genomes from across the Eurasian steppes**
   Peter de Barros Damgaard, Nina Marchi, Simon Rasmussen, Michaël Peyrot, Gabriel Renaud, Thorfinn Korneliussen, J. Víctor Moreno-Mayar, Mikkel Winther Pedersen, Amy Goldberg, Emma Usmanova, … Eske Willerslev
   Nature (2018-05-09) https://doi.org/gd8hs5
   DOI: 10.1038/s41586-018-0094-2 · PMID: 29743675

6. **A High-Coverage Genome Sequence from an Archaic Denisovan Individual**
   M. Meyer, M. Kircher, M.-T. Gansauge, H. Li, F. Racimo, S. Mallick, J. G. Schraiber, F. Jay, K. Prufer, C. de Filippo, … S. Paabo
   Science (2012-08-30) https://doi.org/q8p
   DOI: 10.1126/science.1224344 · PMID: 22936568 · PMCID: PMC3617501

7. **The genome of the offspring of a Neanderthal mother and a Denisovan father**
   Viviane Slon, Fabrizio Mafessoni, Benjamin Vernot, Cesare de Filippo, Steffi Grote, Bence Viola, Mateja Hajdinjak, Stéphane Peyrégne, Sarah Nagel, Samantha Brown, … Svante Pääbo
   Nature (2018-08-22) https://doi.org/cs64
   DOI: 10.1038/s41586-018-0455-x · PMID: 30135579 · PMCID: PMC6130845

8. **Pre-Columbian mycobacterial genomes reveal seals as a source of New World human tuberculosis**
   Kirsten I. Bos, Kelly M. Harkins, Alexander Herbig, Mireia Coscolla, Nico Weber, Iñaki Comas, Stephen A. Forrest, Josephine M. Bryant, Simon R. Harris, Verena J. Schuenemann, … Johannes Krause

Nature (2014-08-20) https://doi.org/f6nk4g
DOI: 10.1038/nature13591 · PMID: 25141181 · PMCID: PMC4550673

9. **Integrative approach using *Yersinia pestis* genomes to revisit the historical landscape of plague during the Medieval Period**
Amine Namouchi, Meriam Guellil, Oliver Kersten, Stephanie Hänsch, Claudio Ottoni, Boris V. Schmid, Elsa Pacciani, Luisa Quaglia, Marco Vermunt, Egil L. Bauer, … Barbara Bramanti
Proceedings of the National Academy of Sciences (2018-12-11) https://doi.org/ggfn3h
DOI: 10.1073/pnas.1812865115 · PMID: 30478041 · PMCID: PMC6294933

10. **Ancient genomes reveal a high diversity of Mycobacterium leprae in medieval Europe**
Verena J. Schuenemann, Charlotte Avanzi, Ben Krause-Kyora, Alexander Seitz, Alexander Herbig, Sarah Inskip, Marion Bonazzi, Ella Reiter, Christian Urban, Dorthe Dangvard Pedersen, … Johannes Krause
PLOS Pathogens (2018-05-10) https://doi.org/gdrj4v
DOI: 10.1371/journal.ppat.1006997 · PMID: 29746563 · PMCID: PMC5944922

11. **Ancient hepatitis B viruses from the Bronze Age to the Medieval period**
Barbara Mühlemann, Terry C. Jones, Peter de Barros Damgaard, Morten E. Allentoft, Irina Shevnina, Andrey Logvin, Emma Usmanova, Irina P. Panyushkina, Bazartseren Boldgiv, Tsevel Bazartseren, … Eske Willerslev
Nature (2018-05-09) https://doi.org/gddxvj
DOI: 10.1038/s41586-018-0097-z · PMID: 29743673

12. **Neolithic and medieval virus genomes reveal complex evolution of hepatitis B**
Ben Krause-Kyora, Julian Susat, Felix M Key, Denise Kühnert, Esther Bosse, Alexander Immel, Christoph Rinne, Sabin-Christin Kornell, Diego Yepes, Sören Franzenburg, … Johannes Krause
eLife (2018-05-10) https://doi.org/gdhck2
DOI: 10.7554/elife.36666 · PMID: 29745896 · PMCID: PMC6008052

13. **Ancient reveals the timing and persistence of organellar genetic bottlenecks over 3,000 years of sunflower domestication and improvement**
Nathan Wales, Melis Akman, Ray H. B. Watson, Fátima Sánchez Barreiro, Bruce D. Smith, Kristen J. Gremillion, M. Thomas P. Gilbert, Benjamin K. Blackman
Evolutionary Applications (2018-02-13) https://doi.org/gf568v
DOI: 10.1111/eva.12594 · PMID: 30622634 · PMCID: PMC6304678

14. **The origins and adaptation of European potatoes reconstructed from historical genomes**
Rafal M. Gutaker, Clemens L. Weiß, David Ellis, Noelle L. Anglin, Sandra Knapp, José Luis Fernández-Alonso, Salomé Prat, Hernán A. Burbano
Nature Ecology & Evolution (2019-06-24) https://doi.org/ggxkk8
DOI: 10.1038/s41559-019-0921-3 · PMID: 31235927

15. **The Prevotella copri Complex Comprises Four Distinct Clades Underrepresented in Westernized Populations**
Adrian Tett, Kun D. Huang, Francesco Asnicar, Hannah Fehlner-Peach, Edoardo Pasolli, Nicolai Karcher, Federica Armanini, Paolo Manghi, Kevin Bonham, Moreno Zolfo, … Nicola Segata
Cell Host & Microbe (2019-11) https://doi.org/ggc9dc
DOI: 10.1016/j.chom.2019.08.018 · PMID: 31607556 · PMCID: PMC6854460

16. **CoproID predicts the source of coprolites and paleofeces using microbiome composition and host DNA content**
Maxime Borry, Bryan Cordova, Angela Perri, Marsha Wibowo, Tanvi Prasad Honap, Jada Ko, Jie Yu,

Kate Britton, Linus Girdland-Flink, Robert C. Power, … Christina Warinner
PeerJ (2020-04-17) https://doi.org/dr8x
DOI: 10.7717/peerj.9001 · PMID: 32337106 · PMCID: PMC7169968

17. **Pathogens and host immunity in the ancient human oral cavity**
Christina Warinner, João F Matias Rodrigues, Rounak Vyas, Christian Trachsel, Natallia Shved, Jonas Grossmann, Anita Radini, Y Hancock, Raul Y Tito, Sarah Fiddyment, … Enrico Cappellini
Nature Genetics (2014-02-23) https://doi.org/r4n
DOI: 10.1038/ng.2906 · PMID: 24562188 · PMCID: PMC3969750

18. **Neanderthal behaviour, diet, and disease inferred from ancient DNA in dental calculus**
Laura S. Weyrich, Sebastian Duchene, Julien Soubrier, Luis Arriola, Bastien Llamas, James Breen, Alan G. Morris, Kurt W. Alt, David Caramelli, Veit Dresely, … Alan Cooper
Nature (2017-03-08) https://doi.org/f9szrm
DOI: 10.1038/nature21674 · PMID: 28273061

19. **Fifty thousand years of Arctic vegetation and megafaunal diet**
Eske Willerslev, John Davison, Mari Moora, Martin Zobel, Eric Coissac, Mary E. Edwards, Eline D. Lorenzen, Mette Vestergård, Galina Gussarova, James Haile, … Pierre Taberlet
Nature (2014-02-05) https://doi.org/f2zr4s
DOI: 10.1038/nature12921 · PMID: 24499916

20. **Neandertal and Denisovan DNA from Pleistocene sediments**
Viviane Slon, Charlotte Hopfe, Clemens L. Weiß, Fabrizio Mafessoni, Marco de la Rasilla, Carles Lalueza-Fox, Antonio Rosas, Marie Soressi, Monika V. Knul, Rebecca Miller, … Matthias Meyer
Science (2017-05-12) https://doi.org/b6jd
DOI: 10.1126/science.aam9695 · PMID: 28450384

21. **Plasmodium vivax Malaria Viewed through the Lens of an Eradicated European Strain**
Lucy van Dorp, Pere Gelabert, Adrien Rieux, Marc de Manuel, Toni de-Dios, Shyam Gopalakrishnan, Christian Carøe, Marcela Sandoval-Velasco, Rosa Fregel, Iñigo Olalde, … Carles Lalueza-Fox
Molecular Biology and Evolution (2020-03) https://doi.org/ggqzq2
DOI: 10.1093/molbev/msz264 · PMID: 31697387 · PMCID: PMC7038659

22. **Paging through history: parchment as a reservoir of ancient DNA for next generation sequencing**
M. D. Teasdale, N. L. van Doorn, S. Fiddyment, C. C. Webb, T. O'Connor, M. Hofreiter, M. J. Collins, D. G. Bradley
Philosophical Transactions of the Royal Society B: Biological Sciences (2015-01-19)
https://doi.org/ggqzq3
DOI: 10.1098/rstb.2013.0379 · PMID: 25487331 · PMCID: PMC4275887

23. **A 5700 year-old human genome and oral microbiome from chewed birch pitch**
Theis Z. T. Jensen, Jonas Niemann, Katrine Højholt Iversen, Anna K. Fotakis, Shyam Gopalakrishnan, Åshild J. Vågene, Mikkel Winther Pedersen, Mikkel-Holger S. Sinding, Martin R. Ellegaard, Morten E. Allentoft, … Hannes Schroeder
Nature Communications (2019-12-17) https://doi.org/ggfm6x
DOI: 10.1038/s41467-019-13549-9 · PMID: 31848342 · PMCID: PMC6917805

24. **Ancient DNA from mastics solidifies connection between material culture and genetics of mesolithic hunter–gatherers in Scandinavia**
Natalija Kashuba, Emrah Kırdök, Hege Damlien, Mikael A. Manninen, Bengt Nordqvist, Per Persson, Anders Götherström

Communications Biology (2019-05-15) https://doi.org/ggqzqz
DOI: 10.1038/s42003-019-0399-1 · PMID: 31123709 · PMCID: PMC6520363

25. **The Beaker phenomenon and the genomic transformation of northwest Europe**
Iñigo Olalde, Selina Brace, Morten E. Allentoft, Ian Armit, Kristian Kristiansen, Thomas Booth, Nadin Rohland, Swapan Mallick, Anna Szécsényi-Nagy, Alissa Mittnik, … David Reich
Nature (2018-02-21) https://doi.org/gcx74m
DOI: 10.1038/nature25738 · PMID: 29466337 · PMCID: PMC5973796

26. **The genomic history of southeastern Europe**
Iain Mathieson, Songül Alpaslan-Roodenberg, Cosimo Posth, Anna Szécsényi-Nagy, Nadin Rohland, Swapan Mallick, Iñigo Olalde, Nasreen Broomandkhoshbacht, Francesca Candilio, Olivia Cheronet, … David Reich
Nature (2018-02-21) https://doi.org/gc2n9h
DOI: 10.1038/nature25778 · PMID: 29466330 · PMCID: PMC6091220

27. **A draft genome of Yersinia pestis from victims of the Black Death**
Kirsten I. Bos, Verena J. Schuenemann, G. Brian Golding, Hernán A. Burbano, Nicholas Waglechner, Brian K. Coombes, Joseph B. McPhee, Sharon N. DeWitte, Matthias Meyer, Sarah Schmedes, … Johannes Krause
Nature (2011-10-12) https://doi.org/fk87wk
DOI: 10.1038/nature10549 · PMID: 21993626 · PMCID: PMC3690193

28. **Bioinformatics Education–Perspectives and Challenges out of Africa**
O. Tastan Bishop, E. F. Adebiyi, A. M. Alzohairy, D. Everett, K. Ghedira, A. Ghouila, J. Kumuthini, N. J. Mulder, S. Panji, H.-G. Patterton, (for the H3ABioNet Consortium, as members of The H3Africa Consortium)
Briefings in Bioinformatics (2014-07-02) https://doi.org/f67hjx
DOI: 10.1093/bib/bbu022 · PMID: 24990350 · PMCID: PMC4364068

29. **Highlights on the Application of Genomics and Bioinformatics in the Fight Against Infectious Diseases: Challenges and Opportunities in Africa**
Saikou Y. Bah, Collins Misita Morang'a, Jonas A. Kengne-Ouafo, Lucas Amenga–Etego, Gordon A. Awandare
Frontiers in Genetics (2018-11-27) https://doi.org/gfrxbz
DOI: 10.3389/fgene.2018.00575 · PMID: 30538723 · PMCID: PMC6277583

30. **Instability and decay of the primary structure of DNA**
Tomas Lindahl
Nature (1993-04) https://doi.org/d9c9vq
DOI: 10.1038/362709a0 · PMID: 8469282

31. **Nuclear DNA sequences from the Middle Pleistocene Sima de los Huesos hominins**
Matthias Meyer, Juan-Luis Arsuaga, Cesare de Filippo, Sarah Nagel, Ayinuer Aximu-Petri, Birgit Nickel, Ignacio Martínez, Ana Gracia, José María Bermúdez de Castro, Eudald Carbonell, … Svante Pääbo
Nature (2016-03-14) https://doi.org/bdcn
DOI: 10.1038/nature17405 · PMID: 26976447

32. **Patterns of damage in genomic DNA sequences from a Neandertal**
A. W. Briggs, U. Stenzel, P. L. F. Johnson, R. E. Green, J. Kelso, K. Prufer, M. Meyer, J. Krause, M. T. Ronan, M. Lachmann, S. Paabo

Proceedings of the National Academy of Sciences (2007-08-21) https://doi.org/bs4w7h
DOI: 10.1073/pnas.0704665104 · PMID: 17715061 · PMCID: PMC1976210

33. **A new model for ancient DNA decay based on paleogenomic meta-analysis**
Logan Kistler, Roselyn Ware, Oliver Smith, Matthew Collins, Robin G. Allaby
Nucleic Acids Research (2017-06-20) https://doi.org/gf58ts
DOI: 10.1093/nar/gkx361 · PMID: 28486705 · PMCID: PMC5499742

34. **A Robust Framework for Microbial Archaeology**
Christina Warinner, Alexander Herbig, Allison Mann, James A. Fellows Yates, Clemens L. Weiß,
Hernán A. Burbano, Ludovic Orlando, Johannes Krause
Annual Review of Genomics and Human Genetics (2017-08-31) https://doi.org/gf5wqv
DOI: 10.1146/annurev-genom-091416-035526 · PMID: 28460196 · PMCID: PMC5581243

35. **mapDamage2.0: fast approximate Bayesian estimates of ancient DNA damage parameters**
Hákon Jónsson, Aurélien Ginolhac, Mikkel Schubert, Philip L. F. Johnson, Ludovic Orlando
Bioinformatics (2013-07) https://doi.org/gb5g2t
DOI: 10.1093/bioinformatics/btt193 · PMID: 23613487 · PMCID: PMC3694634

36. **Early Divergent Strains of Yersinia pestis in Eurasia 5,000 Years Ago**
Simon Rasmussen, Morten Erik Allentoft, Kasper Nielsen, Ludovic Orlando, Martin Sikora, Karl-
Göran Sjögren, Anders Gorm Pedersen, Mikkel Schubert, Alex Van Dam, Christian Moliin Outzen
Kapel, … Eske Willerslev
Cell (2015-10) https://doi.org/f3mxqd
DOI: 10.1016/j.cell.2015.10.009

37. **Characterization of ancient and modern genomes by SNP detection and phylogenomic and metagenomic analysis using PALEOMIX**
Mikkel Schubert, Luca Ermini, Clio Der Sarkissian, Hákon Jónsson, Aurélien Ginolhac, Robert
Schaefer, Michael D Martin, Ruth Fernández, Martin Kircher, Molly McCue, … Ludovic Orlando
Nature Protocols (2014-04-10) https://doi.org/f5x3qm
DOI: 10.1038/nprot.2014.063 · PMID: 24722405

38. **EAGER: efficient ancient genome reconstruction**
Alexander Peltzer, Günter Jäger, Alexander Herbig, Alexander Seitz, Christian Kniep, Johannes
Krause, Kay Nieselt
Genome Biology (2016-03-31) https://doi.org/ggqzpk
DOI: 10.1186/s13059-016-0918-z · PMID: 27036623 · PMCID: PMC4815194

39. **Fast and accurate short read alignment with Burrows-Wheeler transform**
H. Li, R. Durbin
Bioinformatics (2009-05-18) https://doi.org/dqt59j
DOI: 10.1093/bioinformatics/btp324 · PMID: 19451168 · PMCID: PMC2705234

40. **mapDamage: testing for damage patterns in ancient DNA sequences**
Aurelien Ginolhac, Morten Rasmussen, M. Thomas P. Gilbert, Eske Willerslev, Ludovic Orlando
Bioinformatics (2011-08-01) https://doi.org/cn45v7
DOI: 10.1093/bioinformatics/btr347 · PMID: 21659319

41. **The Stone Age Plague and Its Persistence in Eurasia**
Aida Andrades Valtueña, Alissa Mittnik, Felix M. Key, Wolfgang Haak, Raili Allmäe, Andrej Belinskij,
Mantas Daubaras, Michal Feldman, Rimantas Jankauskas, Ivor Janković, … Johannes Krause

Current Biology (2017-12) https://doi.org/cgmv
DOI: 10.1016/j.cub.2017.10.025

42. **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 · PMID: 28398311

43. **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 · PMID: 32055031

44. **Conda — Conda documentation**https://docs.conda.io/en/latest/

45. **Empowering App Development for Developers | Docker**https://www.docker.com/

46. **Home**
Sylabs.io
https://sylabs.io/

47. **Nextflow Tower**https://tower.nf/

48. **Improving ancient DNA read mapping against modern reference genomes**
Mikkel Schubert, Aurelien Ginolhac, Stinus Lindgreen, John F Thompson, Khaled AS AL-Rasheid, Eske Willerslev, Anders Krogh, Ludovic Orlando
BMC Genomics (2012) https://doi.org/gb3ff7
DOI: 10.1186/1471-2164-13-178 · PMID: 22574660 · PMCID: PMC3468387

49. **Babraham Bioinformatics - FastQC A Quality Control tool for High Throughput Sequence Data**https://www.bioinformatics.babraham.ac.uk/projects/fastqc/

50. **AdapterRemoval v2: rapid adapter trimming, identification, and read merging**
Mikkel Schubert, Stinus Lindgreen, Ludovic Orlando
BMC Research Notes (2016-02-12) https://doi.org/gfzqhb
DOI: 10.1186/s13104-016-1900-2 · PMID: 26868221 · PMCID: PMC4751634

51. **Fast and accurate long-read alignment with Burrows–Wheeler transform**
Heng Li, Richard Durbin
Bioinformatics (2010-03-01) https://doi.org/cm27kg
DOI: 10.1093/bioinformatics/btp698 · PMID: 20080505 · PMCID: PMC2828108

52. **Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM**
Heng Li
arXiv (2013-05-28) https://arxiv.org/abs/1303.3997

53. **The Sequence Alignment/Map format and SAMtools**
H. Li, B. Handsaker, A. Wysoker, T. Fennell, J. Ruan, N. Homer, G. Marth, G. Abecasis, R. Durbin, 1000 Genome Project Data Processing Subgroup
Bioinformatics (2009-06-08) https://doi.org/ff6426
DOI: 10.1093/bioinformatics/btp352 · PMID: 19505943 · PMCID: PMC2723002

54. **The Genome Analysis Toolkit: A MapReduce framework for analyzing next-generation DNA sequencing data**
A. McKenna, M. Hanna, E. Banks, A. Sivachenko, K. Cibulskis, A. Kernytsky, K. Garimella, D. Altshuler, S. Gabriel, M. Daly, M. A. DePristo
Genome Research (2010-07-19) https://doi.org/bnzbn6
DOI: 10.1101/gr.107524.110 · PMID: 20644199 · PMCID: PMC2928508

55. **Predicting the molecular complexity of sequencing libraries**
Timothy Daley, Andrew D Smith
Nature Methods (2013-02-24) https://doi.org/gfx6f5
DOI: 10.1038/nmeth.2375 · PMID: 23435259 · PMCID: PMC3612374

56. **Qualimap 2: advanced multi-sample quality control for high-throughput sequencing data**
Konstantin Okonechnikov, Ana Conesa, Fernando García-Alcalde
Bioinformatics (2015-10-01) https://doi.org/ggxrmx
DOI: 10.1093/bioinformatics/btv566 · PMID: 26428292 · PMCID: PMC4708105

57. **Integrative-Transcriptomics/DamageProfiler: DamageProfiler v0.4.9**
Judith Neukamm, Alexander Peltzer
Zenodo (2019-11-29) https://doi.org/ggxrmz
DOI: 10.5281/zenodo.3557708

58. **Separating endogenous ancient DNA from modern day contamination in a Siberian Neandertal**
Pontus Skoglund, Bernd H. Northoff, Michael V. Shunkov, Anatoli P. Derevianko, Svante Pääbo, Johannes Krause, Mattias Jakobsson
Proceedings of the National Academy of Sciences (2014-02-11) https://doi.org/f2z5sw
DOI: 10.1073/pnas.1318934111 · PMID: 24469802 · PMCID: PMC3926038

59. **An efficient and scalable analysis framework for variant extraction and refinement from population-scale DNA sequence data**
Goo Jun, Mary Kate Wing, Gonçalo R. Abecasis, Hyun Min Kang
Genome Research (2015-06) https://doi.org/f7dz2d
DOI: 10.1101/gr.176552.114 · PMID: 25883319 · PMCID: PMC4448687

60. **ANGSD: Analysis of Next Generation Sequencing Data**
Thorfinn Sand Korneliussen, Anders Albrechtsen, Rasmus Nielsen
BMC Bioinformatics (2014-11-25) https://doi.org/gb8wpz
DOI: 10.1186/s12859-014-0356-4 · PMID: 25420514 · PMCID: PMC4248462

61. **Bioconda: sustainable and comprehensive software distribution for the life sciences**
Björn Grüning, Ryan Dale, Andreas Sjödin, Brad A. Chapman, Jillian Rowe, Christopher H. Tomkins-Tinch, Renan Valieris, Johannes Köster, The Bioconda Team
Nature Methods (2018-07-02) https://doi.org/gd2xzp
DOI: 10.1038/s41592-018-0046-7 · PMID: 29967506

62. **conda-forge | community driven packaging for conda** https://conda-forge.org/

63. **Schmutzi: estimation of contamination and endogenous mitochondrial consensus calling for ancient DNA**
Gabriel Renaud, Viviane Slon, Ana T. Duggan, Janet Kelso
Genome Biology (2015-10-12) https://doi.org/f72mvg
DOI: 10.1186/s13059-015-0776-0 · PMID: 26458810 · PMCID: PMC4601135

64. **Fast gapped-read alignment with Bowtie 2**
Ben Langmead, Steven L Salzberg
Nature Methods (2012-03-04) https://doi.org/gd2xzn
DOI: 10.1038/nmeth.1923 · PMID: 22388286 · PMCID: PMC3322381

65. **fastp: an ultra-fast all-in-one FASTQ preprocessor**
Shifu Chen, Yanqing Zhou, Yaru Chen, Jia Gu
Bioinformatics (2018-09-01) https://doi.org/gd9mrb
DOI: 10.1093/bioinformatics/bty560 · PMID: 30423086 · PMCID: PMC6129281

66. **QC Fail Sequencing » Illumina 2 colour chemistry can overcall high confidence G bases**https://sequencing.qcfail.com/articles/illumina-2-colour-chemistry-can-overcall-high-confidence-g-bases/

67. **Haplotype-based variant detection from short-read sequencing**
Erik Garrison, Gabor Marth
arXiv (2012-07-24) https://arxiv.org/abs/1207.3907

68. **MALT: Fast alignment and analysis of metagenomic DNA sequence data applied to the Tyrolean Iceman**
Alexander Herbig, Frank Maixner, Kirsten I. Bos, Albert Zink, Johannes Krause, Daniel H. Huson
bioRxiv (2016-04-27) https://doi.org/ggxkk9
DOI: 10.1101/050559

69. **Salmonella enterica genomes from victims of a major sixteenth-century epidemic in Mexico**
Åshild J. Vågene, Alexander Herbig, Michael G. Campana, Nelly M. Robles García, Christina Warinner, Susanna Sabin, Maria A. Spyrou, Aida Andrades Valtueña, Daniel Huson, Noreen Tuross, … Johannes Krause
Nature Ecology & Evolution (2018-01-15) https://doi.org/ggxkk7
DOI: 10.1038/s41559-017-0446-6 · PMID: 29335577

70. **Improved metagenomic analysis with Kraken 2**
Derrick E. Wood, Jennifer Lu, Ben Langmead
Genome Biology (2019-11-28) https://doi.org/ggfk55
DOI: 10.1186/s13059-019-1891-0 · PMID: 31779668 · PMCID: PMC6883579

71. **HOPS: automated detection and authentication of pathogen DNA in archaeological remains**
Ron Hübler, Felix M. Key, Christina Warinner, Kirsten I. Bos, Johannes Krause, Alexander Herbig
Genome Biology (2019-12-16) https://doi.org/ggxkmb
DOI: 10.1186/s13059-019-1903-0 · PMID: 31842945 · PMCID: PMC6913047

72. **Microbial differences between dental plaque and historic dental calculus are related to oral biofilm maturation stage**
Irina M. Velsko, James A. Fellows Yates, Franziska Aron, Richard W. Hagan, Laurent A. F. Frantz, Louise Loe, Juan Bautista Rodriguez Martinez, Eros Chaves, Chris Gosden, Greger Larson, Christina Warinner
Microbiome (2019-07-06) https://doi.org/ggxkmc
DOI: 10.1186/s40168-019-0717-3 · PMID: 31279340 · PMCID: PMC6612086

73. **BEDTools: a flexible suite of utilities for comparing genomic features**
Aaron R. Quinlan, Ira M. Hall
Bioinformatics (2010-03-15) https://doi.org/cmrms3
DOI: 10.1093/bioinformatics/btq033 · PMID: 20110278 · PMCID: PMC2832824

74. **Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe**
Thiseas C. Lamnidis, Kerttu Majander, Choongwon Jeong, Elina Salmela, Anna Wessman, Vyacheslav Moiseyev, Valery Khartanovich, Oleg Balanovsky, Matthias Ongyerth, Antje Weihmann, … Stephan Schiffels
Nature Communications (2018-11-27) https://doi.org/ggxkk6
DOI: 10.1038/s41467-018-07483-5 · PMID: 30479341 · PMCID: PMC6258758

75. **MultiQC: summarize analysis results for multiple tools and samples in a single report**
Philip Ewels, Måns Magnusson, Sverker Lundin, Max Käller
Bioinformatics (2016-10-01) https://doi.org/f3s996
DOI: 10.1093/bioinformatics/btw354 · PMID: 27312411 · PMCID: PMC5039924

76. **nf-core/eager**
nf-core
(2020-06-08) https://github.com/nf-core/eager

77. **nf-core/configs**
nf-core
(2020-06-05) https://github.com/nf-core/configs

78. **Open collaborative writing with Manubot**
Daniel S. Himmelstein, Vincent Rubinetti, David R. Slochower, Dongbo Hu, Venkat S. Malladi, Casey S. Greene, Anthony Gitter
PLOS Computational Biology (2019-06-24) https://doi.org/c7np
DOI: 10.1371/journal.pcbi.1007128 · PMID: 31233491 · PMCID: PMC6611653