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

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Abstract

The broadening utilisation 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 and extended pipeline for the analysis of ancient genomic data. This Nextflow pipeline aims to address three main themes: accessibility and adaptability to different computing configurations, reproducibility to ensure robust analytical standards in the field, and updating the 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 used 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 [5,6,7,8], bacteria [9,10,11], viruses [12,13], plants [14,15], palaeofaeces [16,17], dental calculus [18,19], sediments [20,21], medical slides [22], parchment [23], and most recently, ancient 'chewing gum' [24,25]. Improvement in laboratory protocols to increase yields of otherwise trace amounts of DNA has at the same time led to studies that can total hundreds of ancient individuals [26,27], spanning single [28] to thousands of organisms [18]. These differences of disciplines have led to a heterogeneous landscape in terms of the types of analyses undertaken, and their computational resource requirements [29,30]. 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 [31] DNA molecules fragment over time, resulting in ultra-short molecules [32]. These sequences have low nucleotide complexity making it difficult to identify with precision which part of the genome a read (sequenced DNA molecule) is derived from. 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 misincorporation of bases during library construction [33]. On top of this, taphonomic processes such as heat, moisture, and microbial- and burial-environment processes lead to varying rates of degradation [34,35]. The original DNA content of a sample is therefore increasingly lost over time and supplanted by younger 'environmental' DNA. Later handling by archaeologists, museum curators, and other researchers 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 [36]), they also pose specific challenges such as unspecific DNA alignment and/or low coverage and miscoding lesions that can result in low-confidence genotyping. These factors often lead to prohibitive sequencing costs when retrieving enough data for modern NGS data pipelines (such as more than 1 billion reads for a 1X depth coverage *Yersinia pestis* genome [37]), and thus require aDNA-tailored methods and techniques to overcome these challenges.

Two previously published and commonly used pipelines in the field are PALEOMIX [38] and EAGER [39]. 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 the bwa aln algorithm for ultra-short molecules [40] and mapDamage [41] for evaluation of aDNA characteristics). 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 [18,19] has become particularly common in palaeo- and archaeogenetics, given its role in revealing widespread infectious disease and possible epidemics that had previously been undetected in the archaeological record [12,13,37,42]. 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 as well as limiting the full range of possibilities from their data. Given that material from samples is limited, there are both ethical as well as economical interests to maximise analytical yield [43].

To address these shortcomings, we have completely re-implemented the latest version of the EAGER pipeline in Nextflow [44] (a domain-specific-language or 'DSL', specifically designed for the construction of omics analysis pipelines), introduced new features, and more flexible pipeline configuration. In addition, the newly named pipeline - nf-core/eager - has been developed in the context of the nf-core community framework [45], which enforces strict guidelines for best-practises in software development.

Results and Discussion

Scalability, Portability, and Efficiency

The re-implementation 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, as well as local workstations. This portability allows users to run nf-core/eager regardless of the type of computing infrastructure or cluster size (if applicable), with minimal effort or configuration. This facilitates 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 [46], Docker [47] and Singularity [48]. These are isolated sandboxes that include all software (with exact versions) required by the pipeline, in a form that is installable and runnable by users regardless of the set up of their local software environment. Another major change with nf-core/eager is that the graphical-user-interface (GUI) set up of an 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 a window system), 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, a GUI-based pipeline set up is now offered via the nf-core website (https://nf-co.re/launch), which provides a commmon GUI format across multiple pipelines as well as additional robusticity checks of input parameters for those less familiar with CLIs. Typically the output of the launch functionality is a JSON file that can be used with nf-core launch command as a single parameter (as with EAGER v1), however upcoming integration with tower.nf [49] will allow direct submission of pipelines without any command line usage.

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 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, which 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 can also reduce 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 [50]), and will be updated in each new release as new studies are published.

Finally, nf-core/eager provides improved efficiency over the original EAGER pipeline by replacing the sample-by-sample sequential processing with Nextflow's asynchronous job parallelisation, whereby multiple pipeline steps and samples are run in parallel (in addition to natively parallelised pipeline steps). This is similar to the approach taken by paleomix, however nf-core/eager expands this by utilising Nextflow's ability to customise resource settings the parameters for every job in the pipeline; reducing unnecessary resource allocation that can occur with unfamiliar users to each step of an NGS data processing pipeline. This is particularly pertinent given the increasing use of centralised HPCs or cloud computing that often use per-hour cost calculations.

Updated Workflow

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

1. Pre-processing
   - Sequencing quality control: FastQC [51]
   - Sequencing artefact clean-up (merging, adapter clipping): AdapterRemoval2 [52]
   - Pre-processing statistics generation
2. Mapping and post-processing
   - Alignment against reference genome: BWA [40,53], CircularMapper [39], Bowtie2 [55]
   - Mapping quality filtering: SAMtools [56]
   - PCR duplicate removal: DeDup [39], Picard MarkDuplicates [57]
   - Mapping statistics generation: PreSeq [58], Qualimap2 [59]
3. aDNA Evaluation and Modification
   - Damage profiling: DamageProfiler [60]
   - aDNA reads selection: PMDtools [61]
   - Damage removal: Bamutils[62]
4. Genotyping and Consensus Sequence Generation: GATK [57], ANGSD [63] VCF2Genome [39]

In nf-core/eager, all tools originally used in EAGER have been updated to their latest versions, as available on Bioconda [64] and Conda-forge [65] to ensure widespread accessibility and stability of utilised tools. The MapDamage2 (for damage profile generation) [36] and Schmutzi (for mitochondrial contamination estimation) [66] 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. As an alternative, estimation of human *nuclear* contamination estimation is now offered through ANGSD [63]. Support for the Bowtie2 aligner [55] has been updated to have default settings optimised for aDNA [67].

New tools to the basic workflow include fastp [68] 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 [69]). For genotyping, we have now included FreeBayes [70] as an alternative

to the human-focused GATK tools, and have also added pileupCaller [71] for generation of genotyping formats commonly utilised in ancient human population analysis. 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.
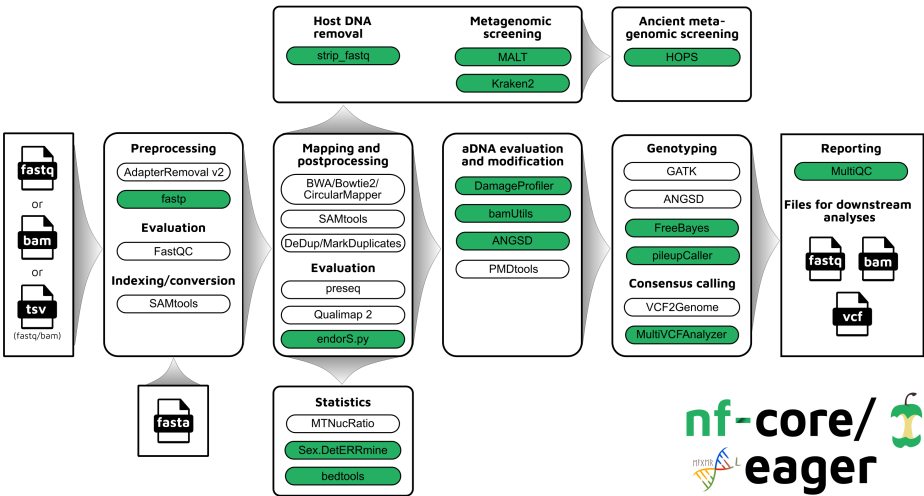

Figure 1: Simplified schematic of the nf-core/eager workflow pipeline. Green filled bubbles indicate new functionality added over the original EAGER pipeline.

We have further extended the functionality of the pipeline by adding ancient metagenomic analysis, to identify the wider taxonomic content of a sample. We have added the possibility to screen all off-target reads (not mapped to the reference genome) with two metagenomic profilers: MALT [72,73] and Kraken2 [74]. Characterisation of properties of authentic aDNA from MALT alignments is carried out with the HOPS pipeline [75]. Ancient metagenomic studies sometimes include comparative samples from living individuals [76]. To support open data, whilst respecting personal data privacy, nf-core/eager includes a 'strip_fastq' script which creates raw FASTQ files, but with all reads successfully mapped to the reference genome removed. This allows safe upload of sequencing data to public repositories after removal of identifiable (human) data.

Table 1: Comparison of usage and pipeline functionality of common ancient DNA processing pipelines. Tick represents full functionality, tilde represents partial functionality cross represents not implemented. .

Functionality	EAGER	paleomix	nf-core/eager
Command line set up	✗	✓	✓
GUI set up	✓	✗	✓
Reproducible software environments offered	✓	✗	✓
HPC scheduler integration	✗	✗	✓
Cloud computing integration	✗	✗	✓
Per-process resource optimisation	✗	~	✓
Pipeline-step parallelisation	✗	✓	✓
Sequencing lane merging	✓	✓	✓
Sequencing quality control	✓	✗	✓
Sequencing artefact removal	✗	✗	✓
Adapter clipping/read merging	✓	✓	✓

Functionality	EAGER	paleomix	nf-core/eager
Post-processing sequencing QC	✗	✗	✓
Reference mapping	✓	✓	✓
Reference mapping statistics	✓	✓	✓
Multi-reference mapping	✗	✓	✗
Mapped reads filtering	✓	✓	✓
Off-target read treatment	✓	✗	✓
Off-target metagenomic profiling	✗	✗	✓
Off-target metagenomic authentication	✗	✗	✓
Library complexity estimation	✓	✗	✓
Duplicate removal	✓	✗	✓
BAM merging	✗	✓	✓
Damage read filtering	✓	✗	✓
Contamination estimation (Human)	✓	✗	✓
Biological sex determination (Human)	✗	✗	✓
Genome coverage estimation	✓	✓	✓
Damage calculation	✓	✓	✓
Damage rescaling	✗	✓	~
SNP Calling/Genotyping	✓	~	✓
Consensus sequence generation	✓	~	✓
Regions of interest statistics	~	✓	✓

Additional functionality tailored for ancient bacterial genomics includes integration of a SNP alignment generation tool, MultiVCFAnalyzer [9], which allows assessment of cross-mapping levels from different related taxa to a reference genome - a common challenge in ancient bacterial genome reconstruction [35]. 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 [77], which can be used in cases such as for determining functional differences between ancient bacterial strains (as in [42]). 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 [78]. 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, and/or merge data from multiple sequencing runs per library. 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. This is facilitated by the optional use as input of 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 [79] report. This tool aggregates the log files of every supported tool into a single interactive report, and assists users in making a fuller assessment of their sequencing and analysis runs. We have strived to ensure that there is a corresponding MultiQC module for every tool used by nf-core/eager where possible, to enable comprehensive evaluation of all stages of the pipeline.

An overview of the entire pipeline is shown in Fig. 1, and a tabular comparison of functionality between EAGER, paleomix and nf-core/eager in 1.

To demonstrate the simultaneous genomic analysis of human DNA and metagenomic screening for putative pathogen, and improved results reporting, we re-analysed data from Barquera et al. [80], who performed a multi-discipline study of three 16th century individuals excavated from a mass burial site in Mexico City. The authors reported genetic results showing sufficient on-target human DNA (>1%) with typical aDNA damage (>20% C to T reference mismatches in the first base of the 5' ends of reads) for downstream population-genetic analysis, Y-chromosome coverage indicative that the three individuals were genetically Male, and one individual (Lab ID: SJN003) contained DNA suggesting a possible infection by *Treponema pallidum*, a species with a variety of strains that can cause diseases such as syphilis, bejel and yaws, and a second individual (Lab ID: SJN001) with the presence of Hepatitis B virus. Both results were confirmed via in-solution enrichment approaches.

We were able to successfully replicate the human and pathogen screening results in a single run of nf-core/eager. Mapping to the human reference genome (hs37d5) with BWA aln and binning of off-target reads with MALT to the NCBI Nucleotide database (2017-10-26) yielded the same results of all individuals having a biological sex of Male as well as the same frequency of C -> T miscoding lesions and short fragment lengths (characteristic of aDNA). Metagenomic hits to both pathogens from the same individuals that yielded complete genomes in the original publication were also detected. Both results and other processing statistics were identified via a single interactive MultiQC report, excerpts of which can be seen in Figure 2. The full interactive report can be seen in the supplementary information.
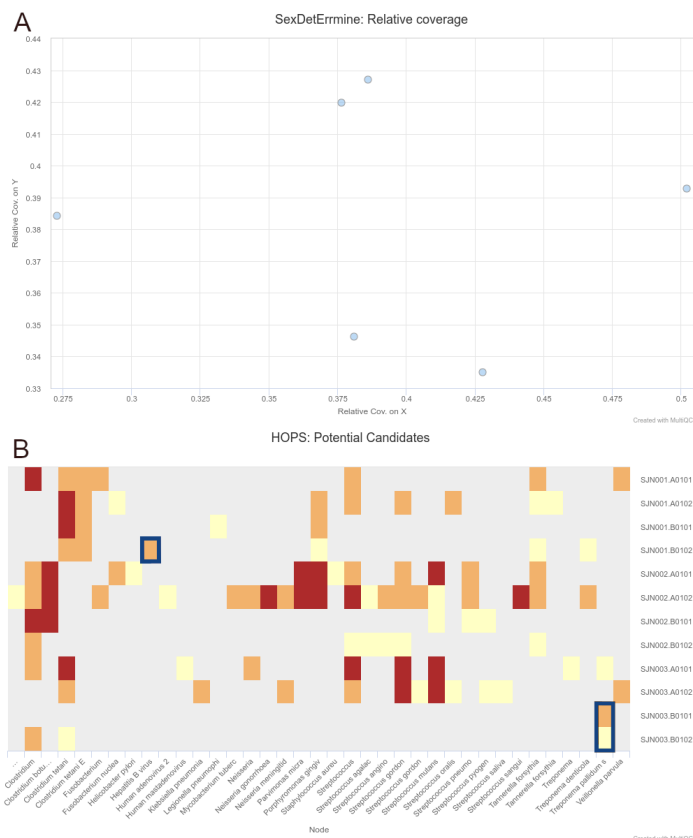
Figure 2: Sections of MultiQC report (v1.10dev) from the outcome of simultaneous human DNA and microbial pathogen screening with nf-core/eager, including **A** Sex.DetERRmine output from Male biological sex assignment with coverages on X and Y being half of that of autosomes, and **B** HOPS output with detection on of both *Treponema pallidum* and Hepatitis B virus reads. Other taxa in HOPS output represent typical oral commensal microbiota found in teeth. MultiQC v1.10 will be included in a point release of nf-core/eager, once released by the developer, but in the meantime can be manually run to get the same results as v1.9 but with the integrate HOPS heatmap. Data was shotgun data from Barquera et al. 2020 [80], and replicated results here were originally verified in the publication via enrichment methods. The full interactive reports for both MultiQC 1.9 and 1.10 can be seen in the supplementary information.

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 [81] that also gives guidance on how to interpret each section of the report - specifically in the context of NGS and aDNA. This includes best practices or expected output schematic images, which are published under CC-BY licenses to allow for use in other training material (an example can be seen in Fig. 3). We hope this open-access resource will make the study of aDNA more accessible to researchers new to the field, by providing practical guidelines on how to evaluate characteristics and effects of aDNA on downstream analyses.
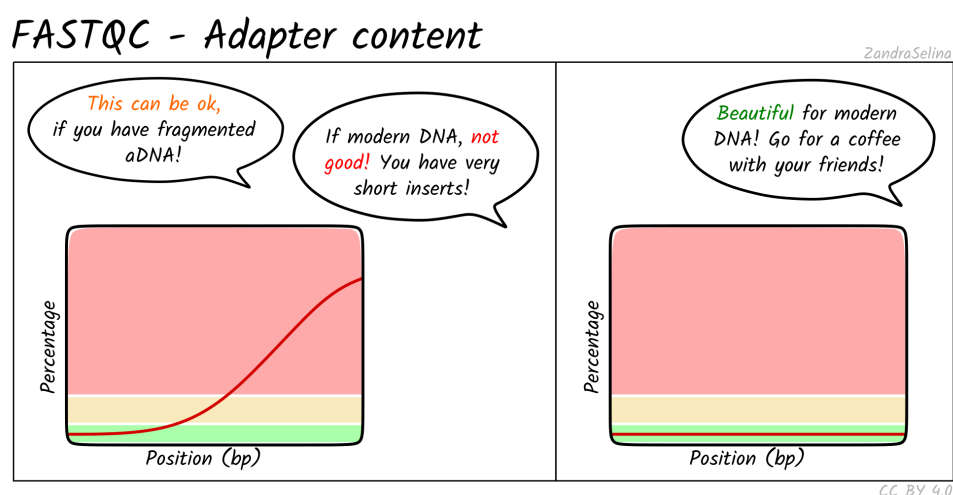
Figure 3: Example schematic images of pipeline output documentation that can assist new users in the interpretation to next-generation-sequencing aDNA processing.

The development of nf-core/eager in Nextflow and the nf-core initiative will also improve open-source development, while ensuring the high quality of 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.

Comparisons with other pipelines

We compared pipeline run-times of the three pipelines to show that the new implementation of nf-core/eager is equivalent or more efficient than EAGER or paleomix. While similar pipelines designed

for aDNA have also been released, such as ATLAS [82] or HOPS [75], these generally have been designed with specific contexts in mind (e.g. human population genetics or pathogen screening) and do not include many of the preprocessing steps required for analysing NGS data.

We ran each pipeline on a subset of Viking-age cod (*Gadus morhua*) genomic data from [4]. This data was originally run using paleomix, and was re-run here as described but with paleomix (v1.2.14), with settings for the other two pipelines as close as possible to the original paper (EAGER with v1.92.33, and nf-core/EAGER with v2.2.0dev, commit 830c22d448441e5e19508c198f530a7656c9f25d). Benchmarking environment and exact pipeline run settings can be seen in Methods and Supplementary methods. Two samples from three Illumina paired-end sequencing runs were analysed, with adapter clipping and merging (AdapterRemoval), mapping (bwa aln), duplicate removal (markduplicates) and damage profiling (paleomix: mapDamage2, EAGER and nf-core/EAGER: DamageProfiler) steps performed. We ran the commands for each tool sequentially, but repeated these batch of commands 10 times - to account for variability in the cloud service's IO connection. Run times were measured using the GNU time tool (v1.7).

Table 2: Comparison of run times in minutes between three ancient DNA pipelines. paleomix and nf-core/eager has additional runs with 'optimised' parameters with fairer computational resources matching modern multi-threading strategies for comparison. Values represent mean and standard deviation of run times in minutes .

Pipeline	Version	Environment	real	sys	user
nf-core-eager (optimised)	2.2.0dev	singularity	105.6 ± 4.6	13.6 ± 0.7	1593 ± 79.7
paleomix (optimised)	1.2.14	conda	130.6 ± 8.7	12 ± 0.7	1820.2 ± 36.9
nf-core-eager	2.2.0dev	singularity	209.2 ± 4.4	11 ± 0.9	1407.7 ± 30.2
EAGER	1.92.37	singularity	224.2 ± 4.9	22.9 ± 0.3	1736.3 ± 70.2
paleomix	1.2.14	conda	314.6 ± 2.9	10.7 ± 1	1506.7 ± 14

A summary of runtimes of the benchmarking tests can be seen in Table 2. nf-core/eager showed lowest runtimes across all three time metrics (Real: real time, System: cumulative CPU system-task times, User: cumulative CPU time of all tasks) when running on default parameters. This highlights the improved efficiency of nf-core/eager's asynchronous processing system and per-process resource customisation (here represented by nf-core/eager defaults designed for typical HPC set ups).

As a more realistic demonstration of modern computing multi-threading set ups, thread, we also re-ran paleomix with the flag –max-bwa-threads set to 4 (listed in Table 2 as 'optimised'), which is equivalent to a single bwa process of nf-core/eager. This resulted in a much faster run-time than that of default nf-core/eager, due to the approach of paleomix of mapping each lane of a library separately, whereas nf-core/eager will map all lanes of a single library merged together. Therefore, given that each library was split across three lanes, increasing the threads of bwa to 4 resulted in 12 per library, whereas nf-core/eager only gave 4 for a single bwa process of one library. While the paleomix approach is valid, we opted to retain the per-library mapping as it is often the longest running step of NGS genome-mapping pipelines, and it prevents flooding of HPC scheduling systems with many long-running jobs. Secondly, if users regularly use multi-lane data, due nf-core/eager's fine-granularity control, they can simply modify nf-core/eager's bwa process resources via config files to account for this. When we optimised parameters were used for bwa multi-threading and multiple lanes to the same number of bwa threads as the optimised paleomix run, nf-core/eager still displayed shorter runtimes. All metrics including mapped reads, percentage on-target, mean depth coverage and mean read lengths across all pipelines were extremely similar across all pipelines and replicates (see methods 3).

Conclusion

nf-core/eager is an efficient, portable, and accessible pipeline for processing ancient 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 to 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 remaining 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 [83].

Running

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

```
nextflow run nf-core/eager -r 2.2.0 -profile test,docker
```

This will download test data automatically, run the pipeline locally with all software tools containerised in a Docker image and store the output of that run in the a './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)
- 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 using different flags at the request of the user, to allow high customisation to each user's 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 2.2.0 \
-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

In additional to private locally defined profiles, we utilise a central configuration repository to enable users from various institutions to use pipelines on their particular infrastructure more easily [84]. 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 customise 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 2.2.0 -profile shh_cdag,test
```

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, the pipeline can be supplied with a tab 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 adapter removal 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 to genotyping, as shown in Figure 4.

Figure 4: 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, because 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 utilise projects such as Nextflow Tower [49] to monitor their analysis pipeline during runtime.

Output

The pipeline produces a multitude of output files in various file formats, with a more detailed listing available in the user documentation. These include metrics, statistical analysis data, and standardised 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 be emailed to users automatically, when starting the pipeline with a dedicated option (--email you@yourdomain.org).

Benchmarking

Dual Screening of Human and Microbial Pathogen DNA

Full step-by-step instructions on the set up of the demonstration (including input TSV file) can be seen in the supplementary information. To demonstrate the efficiency and conciseness of nf-core/eager pipeline in it's dual role for both human and microbial screening of ancient material, we replicated the results of Barquera et al. [80] using using v2.2.0dev (commit: e7471a78a3; Nextflow version: 20.04.1).

The following command was used to run the pipeline on the in-house servers at the Max Planck Institute for the Science of Human History, including a 2 TB memory node for running MALT against the NCBI Nt database, and therefore the centralised custom profile for this cluster was used.

```
nextflow run nf-core/eager -r dev \
-profile microbiome_screening,sdag,shh \
-with-tower \
--input 'barquera2020_pathogenscreening.tsv' \
--fasta 'ftp://ftp-
        trace.ncbi.nih.gov/1000genomes/ftp/technical/reference/phase2_referenc
        \

--bwaalnn 0.01 \
--bwaalnl 32 \
--run_bam_filtering \
--bam_discard_unmapped \
--bam_unmapped_type fastq \
--dedupper markduplicates \
--run_mtnucratio \
--run_nuclear_contamination \
--run_sexdeterrmine \
--sexdeterrmine_bedfile 'https://github.com/nf-core/test-
        datasets/raw/eager/reference/Human/1240K.pos.list_hs37d5.0based.bed.gz
        \

--run_metagenomic_screening \
--metagenomic_tool malt \
--run_maltextract \
--percent_identity 90 \
--malt_top_percent 1 \
--malt_min_support_mode 'reads' \
--metagenomic_min_support_reads 1 \
--malt_max_queries 100 \
--malt_memory_mode load \
--maltextract_taxon_list
        'https://raw.githubusercontent.com/rhuebler/HOPS/external/Resources/de
        \

--maltextract_filter def_anc \
--maltextract_toppercent 0.01 \
--maltextract_destackingoff \
--maltextract_downsamplingoff \
--maltextract_duplicateremovaloff \
--maltextract_matches \
--maltextract_megansummary \
--maltextract_percentidentity 90.0 \
--maltextract_topalignment \
--database 'malt/databases/indexed/index040/full-nt_2017-10/' \
--maltextract_ncbifiles 'resources/'
```

To include the HOPS results from metagenomic screening in the report, we re-ran MultiQC with the upcoming version v1.10 (to be integrated into nf-core/eager on the former's release). We then installed the development version of MultiQC (commit: 7584e64) as described in the MultiQC documentation [85], and ran the following command in the results directory of the nf-core/eager run, using the same configuration file.

```
multiqc . -c multiqc_config.yaml -n multiqc1_10.html -o multiqc1_10
```

Both reports can be seen in the supplementary information.

Pipeline Comparison

Full step-by-step instructions on the set up of the benchmarking, including versions can be seen in the supplementary information. EAGER (v1.92.37) and nf-core/eager (v2.2.0dev, commit: 830c22d; Nextflow v20.04.1) used the provided pre-built singularity containers for software environments, whereas for used paleomix (v1.2.14) we generated a custom conda environment (see supplementary information for the `environmental.yaml` file). Run time comparisons were performed on a 32 CPU (AMD Opteron 23xx) and 256 GB memory Red Hat QEMU Virtual Machine running the Ubuntu 18.04 operating system (Kernel 4.15.0-112). Resource parameters of each tool were only modified to specify the maximum available on the server and otherwise left as default.

The following commands were used for each pipeline, with the commands run 10 times each after cleaning up reference and results directories using a for loop. Run time was measured using GNU Time.

```
## EAGER - description of XML files can be seen in supplementary information
singularity exec \
-B ~/benchmarks/output/EAGER:/data ~/.singularity/cache/EAGER-cache/EAGER-
        GUI_latest.sif \
eagercli \
/data


## paleomix - description of input YAML files can be seen in supplementary
## information
paleomix bam_pipeline run
        ~/benchmarks/output/paleomix/makefile_paleomix.yaml


## paleomix optimised - description of input YAML files can be seen in
## supplementary information
paleomix bam_pipeline \
run ~/benchmarks/output/paleomix_optimised/makefile_paleomix.yaml \
--bwa-max-threads 4


## nf-core/eager - description of resources configuration file (-c) can be
        seen
## in supplementary information
nextflow run nf-core/eager -r dev \
--input ~/benchmarks/output/nfcore-eager-optimised/nfcore-eager_tsv.tsv \
-c ~/.nextflow/pub_eager_vikingfish.conf \
-profile pub_eager_vikingfish_optimised,pub_eager_vikingfish,singularity \
--fasta ~/benchmarks/reference/GCF_902167405.1_gadMor3.0_genomic.fasta \
--outdir ~/benchmarks/output/nfcore-eager-optimised/results/ \
-w ~/benchmarks/output/nfcore-eager-optimised/work/ \
--skip_fastqc \
--skip_preseq \
--run_bam_filtering \
--bam_mapping_quality_threshold 25 \
--bam_discard_unmapped \
--bam_unmapped_type 'discard' \
--dedupper 'markduplicates'


##nf-core/eager optimised - description of resources profile(s) with
        optimised
## bwa threads setting can be seen in supplementary information
nextflow run nf-core/eager -r dev \
--input ~/benchmarks/output/nfcore-eager-optimised/nfcore-eager_tsv.tsv \
-c ~/.nextflow/pub_eager_vikingfish.conf \
-profile pub_eager_vikingfish_optimised,pub_eager_vikingfish,singularity \
--fasta ~/benchmarks/reference/GCF_902167405.1_gadMor3.0_genomic.fasta \
--outdir ~/benchmarks/output/nfcore-eager-optimised/results/ \
-w ~/benchmarks/output/nfcore-eager-optimised/work/ \
```

```
--skip_fastqc \
--skip_preseq \
--run_bam_filtering \
--bam_mapping_quality_threshold 25 \
--bam_discard_unmapped \
--bam_unmapped_type 'discard' \
--dedupper 'markduplicates'
```

Mapping results across all pipelines showed very similar values, with low variation across replicates as can be seen in [3].

Table 3: Comparison of results values of key NGS data processing and mapping steps. All values represent mean and standard deviation across 10 replicates of each pipeline. 'qf' stands for mapping-quality filtered reads .

sample_name	category	eager	nf-core-eager	paleomix
COD076	processed_reads	71388991 ± 0	71388991 ± 0	72100142 ± 0
COD092	processed_reads	69615709 ± 0	69615709 ± 0	70249181 ± 0
COD076	mapped_qf_reads	16786467.7 ± 106.5	16786491.1 ± 89.9	16686607.2 ± 91.3
COD092	mapped_qf_reads	16283216.3 ± 71.3	16283194.7 ± 37.4	16207986.2 ± 44.4
COD076	ontarget_qf	23.5 ± 0	23.5 ± 0	23.1 ± 0
COD092	ontarget_qf	23.4 ± 0	23.4 ± 0	23.1 ± 0
COD076	dedupped_mapped_reads	12107264.4 ± 87.8	12107293.7 ± 69.7	12193415.8 ± 86.7
COD092	dedupped_mapped_reads	13669323.7 ± 87.6	13669328 ± 32.4	13795703.3 ± 47.9
COD076	mean_depth_coverage	0.9 ± 0	0.9 ± 0	0.9 ± 0
COD092	mean_depth_coverage	1 ± 0	1 ± 0	1 ± 0
COD076	mean_read_length	49.4 ± 0	49.4 ± 0	49.4 ± 0
COD092	mean_read_length	48.8 ± 0	48.8 ± 0	48.7 ± 0

Data and software availability

All pipeline 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 is the current 'dev' branch of the GitHub repository (2.2.0dev), and on publication will be released as v2.2.0. Demonstration data for dual ancient human and pathogen screening from [80] is publicly available on the European Nucleotide Archive (ENA) under project accession PRJEB37490. The human reference genome (hs37d5) and screening database (Nucleotide or 'nt', October 2017) was downloaded from National Center for Biotechnology Information FTP server. Ancient Cod genomic data from [4] used for benchmarking is publicly available on the ENA under project accession PRJEB20524. The *Gadus morhua* reference genome NCBI accession ID is: GCF_902167405.1.

This paper was collaboratively written with Manubot [86], and supplementary information such as demonstration and benchmarking environments descriptions and walk-throughs can be seen on Github at https://github.com/apeltzer/eager2-paper/ und the `supplement/` directory.

Competing Interests

No competing interests are declared.

Acknowledgements

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