

nf-core/taxprofiler: highly parallelised and flexible pipeline for metagenomic taxonomic classification and profiling

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1 Abstract

Metagenomic classification tackles the problem of characterising the taxonomic source of all DNA sequencing reads in a sample. A common approach to address the differences and biases between the many different taxonomic classification tools is to run metagenomic data through multiple classification tools and databases. This, however, is a very time-consuming task when performed manually - particularly when combined with the appropriate preprocessing of sequencing reads before the classification.

Here we present nf-core/taxprofiler, a highly parallelised read-processing and taxo-

36 nomic classification pipeline. It is designed for the automated and simultaneous clas-
 37 sification and/or profiling of both short- and long-read metagenomic sequencing li-
 38 braries against a 11 taxonomic classifiers and profilers as well as databases within a
 39 single pipeline run. Implemented in Nextflow and as part of the nf-core initiative, the
 40 pipeline benefits from high levels of scalability and portability, accommodating from
 41 small to extremely large projects on a wide range of computing infrastructure. It has
 42 been developed following best-practise software development practises and commu-
 43 nity support to ensure longevity and adaptability of the pipeline, to help keep it up to
 44 date with the field of metagenomics.

45 2 Introduction

46 Whole-genome, metagenomic sequencing offers strong benefits to the taxonomic clas-
 47 sification of DNA samples over targeted approaches (Eloe-Fadrosh et al. 2016; Florian
 48 P. Breitwieser, Lu, and Salzberg 2019). While metabarcoding approaches targeting
 49 the 16S rRNA or other marker genes are widely used due to low cost and large, di-
 50 verse reference databases (Yilmaz et al. 2014; Lynch and Neufeld 2015), metagenomic
 51 approaches have been gaining popularity with the increasingly lower costs of, for
 52 example, shotgun sequencing. These metagenomic analyses with whole microbial
 53 genome as references have been shown to provide a similar level of taxonomic res-
 54 olution (Hillmann et al. 2018). However they also have the added benefit of having
 55 greater reusability potential of the data, such as for whole genome and/or functional
 56 classification (Sharpton 2014; Quince et al. 2017).

57 Taxonomic classifiers (sometimes referred to as taxonomic bidders) aim to identify
 58 the original ‘taxonomic source’ of a given DNA sequence (Ye et al. 2019; Meyer et al.
 59 2022; Govender and Eyre 2022). In metagenomics, this typically consists of comparing
 60 millions of DNA reads (sequenced DNA molecules) against hundreds or thousands
 61 of reference genomes either via sequence alignment or ‘k-mer matching’ (Sharpton
 62 2014; Sun et al. 2021). The reference genome with the most similar match to the
 63 read is then considered the most likely original ‘source’ organism of that sequence. In
 64 this article we will also refer to ‘taxonomic profilers’. We consider these as classifiers
 65 that also try to infer sequence abundance (i.e. re-assignment of counts to the most
 66 likely source based on the distribution of other hits) or biological relative abundance
 67 of the organism in the original sample (by coverage of expected marker genes, copy
 68 number estimations etc.), in addition to the simple read classification (Nayfach and
 69 Pollard 2016). We will use classifiers and profilers interchangeably throughout the
 70 publication.

71 Having to identify the original source of the many DNA sequences out of the many ref-
 72 erence genomes in a time and computationally efficient manner is a difficult problem.
 73 In many cases biologists are not just interested as to which organism of each DNA
 74 sequence comes from, but also in using this information to infer the original ‘cellular’
 75 (or natural) abundance of each organism of the given environment - something that
 76 is very difficult due to the biases inherent to DNA extraction and sequencing. There-
 77 fore a plethora of tools have been developed to address these challenges, all with their

own biases and specific contexts (Sczyrba et al. 2017; Meyer et al. 2022). Furthermore, each tool often produces tool-specific output formats making it difficult to efficiently cross compare results. Thus, no established ‘gold standard’ classifier tool or method currently exists.

One solution to addressing the problem of choice among the range of different tools is to run all of them in parallel, and cross compare the results. This can be useful both for benchmarking studies (e.g. Sczyrba et al. 2017; Meyer et al. 2022), but also to build consensus profiles whereby confidence of a particular taxonomic identification can be increased when it is detected by multiple tools (McIntyre et al. 2017; Ye et al. 2019).

A second challenge in taxonomic classification (and arguably a larger one) is a question of databases. As with tools, there is no one set ‘gold standard’ database. Different questions and contexts require different databases, such as when a researcher wants to search for both bacterial and viral species in samples, but as an extension of this, taxonomic classifiers often will need different settings for each database. Furthermore, as genomic sequencing becomes cheaper and more efficient, the number of publicly available reference genomes is rapidly increasing (Nasko et al. 2018). Consequently, the size of reference databases of taxonomic classifiers is also growing, often outpacing the computational capacity available to researchers. In fact, while this was one of the main motivations behind classifiers such as Kraken2 (Wood, Lu, and Langmead 2019), these algorithmic techniques are already becoming insufficient (Wright, Comeau, and Langille 2023).

Finally, with the decrease of costs, the possibility for larger and larger metagenomic sequencing datasets increases, leading to increasing sample sizes in studies. This is exemplified by the doubling of the number of metagenomes on the European Bioinformatic Institute’s MGnify database within just two years (Mitchell et al. 2019).

Altogether this highlights the need for methods to efficiently profile many samples using many tools. Manually setting up bioinformatic jobs for classification tasks for each database and settings against different tools on traditional academic computing infrastructure (e.g. high performance computing clusters or ‘HPC’ clusters) can be very tedious. Additionally, particularly for very large sample sets, there is increasing use of cloud platforms that have greater scalability than traditional HPCs. Being able to reliably and reproducibly execute taxonomic classification tasks across infrastructure with minimal intervention would therefore be a boon for the metagenomics field.

In recent years, workflow managers such as Nextflow (Di Tommaso et al. 2017) or Snakemake (Mölder et al. 2021) have become highly popular in bioinformatics. These frameworks provide for developers robust workflow execution with different HPC scheduling tools and software provisioning systems, ensuring maximum portability and efficient in different computational contexts. While a range of metagenomic pipelines already exist (a non-exhaustive list being for example, StaG-mwc by Boulund et al. 2023; MetaMeta by Piro, Matschkowski, and Renard 2017; TAMA by Sim et al. 2020; UGENE by Rose et al. 2019; and Sunbeam by Clarke et al. 2019), few

121 leverage workflow managers to make multi-step workflows easier to use in HPC or
122 cloud infrastructure. Furthermore, often these pipelines aim to carry out multiple
123 different types of metagenomic analyses (e.g. also performing functional or assembly
124 analyses, such as Morais et al. 2022; Boulund et al. 2023) of which each step has
125 fewer options of tools and may execute functionality unwanted by the end user.

126 Here we present nf-core/taxprofiler (<https://nf-co.re/taxprofiler>), a pipeline designed
127 to allow users to efficiently and simultaneously taxonomically classify or profile
128 short- and long-read sequencing data. At the time of writing it supports 11 clas-
129 sifiers and an arbitrary number of databases per classifier in a single pipeline run.
130 nf-core/taxprofiler utilises Nextflow (Di Tommaso et al. 2017) to ensure efficiency,
131 portability, and scalability, and has been developed within the nf-core initiative of
132 Nextflow pipelines (Ewels et al. 2020) to ensure high quality coding practises and
133 user accessibility. It includes detailed documentation and a graphical-user-interface
134 (GUI) execution interface in addition to a standard command-line-interface (CLI).

135 3 Description

136 nf-core/taxprofiler aims to facilitate three main steps of a typical whole-genome,
137 metagenomic sequencing analysis workflow (Chiu and Miller 2019, Figure 1). A
138 longer description of the available functionality and motivations can be seen in the
139 [Supplementary Information](#).

140 In brief, nf-core/taxprofiler can accept short- (e.g. Illumina) and/or long-read
141 (e.g. Nanopore) FASTQ or FASTA files. These are supplied to the pipeline in the
142 form of a TSV file that includes basic sample and sequencing library metadata. The
143 pipeline can then be executed either via a standard Nextflow command-line-interface
144 execution or graphical-user-interface through either the open-source and free nf-core
145 launch page (<https://nf-co.re/launch>) or the commercial (with free-tier) Nextflow
146 tower (<https://tower.nf>) solution. Examples of the command-line execution and
147 nf-core launch GUI can be seen in the [Supplementary Information](#).

148 The pipeline can perform a range of metagenomics appropriate read preprocessing
149 steps, such adapter removal, read merging, low-sequence complexity filtering, host-
150 or contamination removal, and/or per-sample run merging. All of these steps are
151 optional, and are aimed at removing possible sequencing artefacts that may result in
152 false positive taxonomic classification hits or improve classification efficiency. Most
153 of these steps also provide options of different tools to account for user preference.

154 After pre-processing, nf-core/taxprofiler can perform simultaneous profiling of pre-
155 processed reads with up to as many as 11 different taxonomic classifiers or profilers
156 (Table 1). Additionally on top of this, also simultaneously for each of the classifiers,
157 an arbitrary number of databases as supplied by the user. As of version 1.1.0, the
158 following classifiers and profilers are available: Kraken2 (Wood, Lu, and Langmead
159 2019), Bracken (Lu et al. 2017), KrakenUniq (F. P. Breitwieser, Baker, and Salzberg
160 2018), Centrifuge (Kim et al. 2016), MALT (Vågane et al. 2018), DIAMOND (Buchfink,
161 Reuter, and Drost 2021), Kaiju (Menzel, Ng, and Krogh 2016), MetaPhlAn (Blanco-

162 Míguez et al. 2023), mOTUs (Ruscheweyh et al. 2022), ganon (Piro et al. 2020), and
 163 KMCP (Shen et al. 2023). Databases are also supplied via a input TSV file, which
 164 also allows per-database custom classification parameters - meaning a given database
 165 can be supplied multiple times each with different parameters or multiple different
 166 databases per profiler. All classifiers with secondary steps to generate or convert to
 167 additional output file formats are also included.

168 Post-processing of taxonomic profiles include standardisation and aggregation of pro-
 169 files , i.e. merging of multiple profiles into a single multi-sample table for easier com-
 170 parison between profilers, with the tool TAXPASTA (Beber et al. 2023), and visualisa-
 171 tion of profiles with Krona (Ondov, Bergman, and Phillippy 2011) where supported.

172 All relevant preprocessing statistics are displayed in an interactive and dynamic Mul-
 173 tiQC report (Ewels et al. 2020).

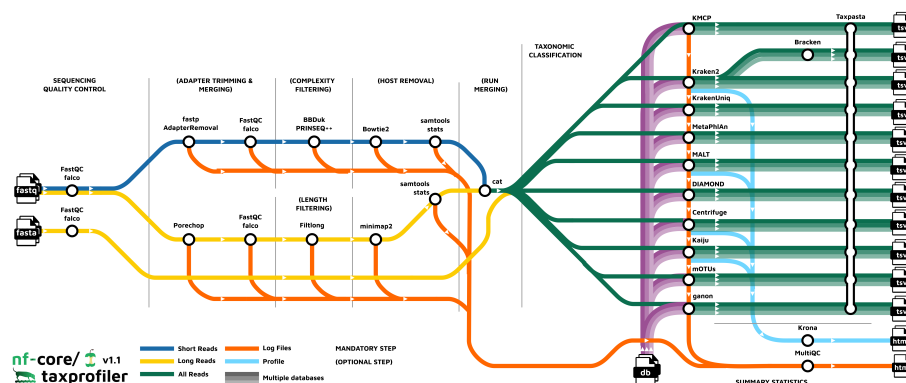


Figure 1: Visual overview of the nf-core/taxprofiler workflow. nf-core/taxprofiler can take in FASTQ (short or long reads) or FASTA files (long reads), that will optionally go through sequencing quality control (e.g. with FastQC), read preprocessing (e.g. removal of adapters), complexity filtering, host removal, and run merging before performing taxonomic classification and/or profiling with a user-selected range of tools and databases. Output from all classifiers and profilers are standardised into a common taxon table format, and when supported visualisations of the profiles are generated.

Table 1: List of nf-core/taxprofiler supported taxonomic/classifiers profilers as of version 1.1 and their approximate method and supported input database types. Primary algorithm refers to the algorithm type used for sequencing matching. Reference type refers to the typical sequence type used in database construction of the tool. Sequencing matching type refers to which ‘molecular alphabet’ is primarily used for matching between a query (read) and a reference (genome/gene).

Tool	Primary Algorithm	Reference Type	Sequence Matching Type
Kraken2	k-mer based	whole-genome	Nucleotide
Kaiju	k-mer based	whole-genome	Amino Acid
Bracken	k-mer based	whole-genome	Nucleotide
KrakenUniq	k-mer based	whole-genome	Nucleotide
ganon	k-mer based	whole-genome	Nucleotide
KMCP	k-mer based	whole-genome	Nucleotide
MALT	alignment based	whole-genome	Nucleotide/Amino Acid
DIAMOND	alignment based	whole-genome	Amino Acid
Centrifuge	alignment based	whole-genome	Nucleotide
MetaPhlAn	alignment based	marker-gene	Nucleotide
mOTUS	alignment based	marker-gene	Nucleotide

nf-core/taxprofiler comes with extensive documentation for general usage, short- and long- parameter help texts, and output file descriptions. To ensure maximum accessibility, these are available in pipeline results as markdown files (<https://github.com/nf-core/taxprofiler>), on the nf-core website (<https://nf-co.re/taxprofiler>) and for the parameter help texts on the command line via standard --help. The output documentation also aims to guide users as the most suitable files for different types of downstream analysis

4 Discussion

A range of pipelines already exists for taxonomic profiling, however, each have their own particular purpose and capabilities. We compared the functionality of nf-core/taxprofiler against four other recently published or released pipelines, selected based on their similarity of purpose to nf-core/taxprofiler. The selection criteria and a more detailed comparison between the five pipelines can be seen in the [Supplementary Information](#). Overall, while there was a general similarity across all pipelines, nf-core/taxprofiler showed the largest number of options for pipeline execution accessibility, and user choice. This is facilitated through the use of an established workflow manager (with Nextflow supporting 7 software environment/container systems), support for both CLI and GUI execution, and by the number of supported classifiers. Furthermore, it is unique in that is the only pipeline to support supplying multiple database for all of the tools in a single pipeline run.

Table 2: Comparison of functionality with four recent taxonomic pipelines with similar functionality. A more detailed textual comparison can be found in the [Supplementary Information](#). Category keys are as follows: I - Information, R - Reproducibility, A - Accessibility, P - Portability, S - Scalability, F - Functionality.

Category	Criterion	StaG-mwc	sunbeam	Unipro UGENE	tama	nf-core/taxprofiler
I	Source code URL	https://github.com/ctmrbio/stag-mwc	https://github.com/sunbeam-labs/sunbeam	https://github.com/ugeneunipro/ugene	https://github.com/kimlab/TAMA	https://github.com/nf-core/taxprofiler/
I	Evaluated version	0.7.0	4	48	githash: 3a22c8f	1.1.0
I	Last release date	2023-06-13	2023-08-08	2023-08-08	2022-03-02	2023-09-19
I	Publication year	Unpublished	2019	2019	2020	This publication
I	Publication DOI	Unpublished	10.1186/s40168-019-0658-x	10.1093/bioinformatics/bt184	10.1093/bioinformatics/bt184	This publication
R	Pipeline versioning	Yes	Yes	Yes	No	Yes
R	Software versioning	Yes	Yes	Yes	Yes	Yes
R	Nr. software environments or container engines supported	2	2	0	1	7
A	Installation documentation	Yes	Yes	Yes	Yes	Yes
A	Usage documentation	Yes	Yes	Yes	Yes	Yes
A	Output documentation	Yes	Yes	Yes	Yes	Yes
A	CLI execution interface	Yes	Yes	No	Yes	Yes
A	GUI execution interface	No	No	Yes	No	Yes

Category	Criterion	StaG-mwc	sunbeam	Unipro UGENE	tama	nf-core/taxprofiler
A/S	Integration a scheduling systems	Yes	Yes	No	No	Yes
P/A	Nr. supported operating systems	2	1	3	1	2
P	Local machine integration	Yes	Yes	Yes	Yes	Yes
P/S	HPC scheduler integration	Yes	Yes	No	No	Yes
P/S	Cloud computing integration	Unsure	Unsure	No	No	Yes
P/S	Integration with multiple scheduling systems	Partial	Partial	No	No	Yes
S	Per-process resource optimisation	Yes	Yes	Yes	No	Yes
F	Short read support	Yes	Yes	Yes	Yes	Yes
F	Long read support	No	No	Yes	No	Yes
F	Read preprocessing	Yes	Yes	Yes	Yes	Yes
F	Sequencing depth estimation	Yes	No	No	No	No
F	Complexity filtering	No	Yes	No	No	Yes
F	Host removal	Yes	Yes	Partial	No	Yes
F	Nr. supported taxonomic classifiers/profilers	7	3	3	3	11
F	Graphical run reports	Yes	No	No	No	Yes
F	Standardised profiles	No	No	No	Yes	Yes

Category	Criterion	StaG-mwc	sunbeam	Unipro UGENE	tama	nf-core/taxprofiler
F	Multiple database supported	Partial	No	No	No	Yes
F	Metagenomic assembly	No	Yes	No	No	No
F	Visualisation	No	No	No	No	Partial

Another important advantage of nf-core/taxprofiler is that it is being developed within the nf-core community (<https://nf-co.re>), that provides strong long-term support for the continued community-based development and maintenance of its pipelines. In this framework, we will continue to add additional preprocessing, metagenomic classification, and profiling tools as they become established and as requested by the metagenomics community. For example, we feel that the inclusion of steps such as sequencing saturation estimation as already being performed by a similar pipeline StaG-mwc (<https://github.com/ctmrbio/stag-mwc>) would be beneficial to the nf-core/taxprofiler workflow (possibly with dedicated tools such as Nonpareil, Rodriguez-R et al. 2018), and/or more performant complexity filtering tools such as Komplexity as offered by the sunbeam metagenomics pipeline (Clarke et al. 2019). Additional tools that could be added for short-read classification could include sourmash (Titus Brown and Irber 2016) that provides scalable sequence to sequence comparison or other marker gene reference tools such as tools such as METAXA2 (Bengtsson-Palme et al. 2015) that use shotgun sequencing reads to recover 16S sequences from metagenomic samples. Adding additional classifiers also applies to extend support to other sequencing platforms; nf-core/taxprofiler already supports Nanopore long-read data, however the use of long-read PacBio data for metagenomic data is growing in interest (Portik, Brown, and Pierce-Ward 2022). We are therefore considering adding dedicated preprocessing steps for this type of sequencing data.

A remaining major challenge for metagenomics researchers (and not supported in the same workflow by any of the compared pipelines above) is the construction of databases for each profiling tool. Given there still are no curated, high-quality ‘gold standard’ databases in metagenomics, and while nf-core/taxprofiler allows the profiling against multiple databases and settings in parallel, currently the pipeline still requires users to construct these manually and to supply to the pipeline. While we feel this is currently a reasonable investment as such databases are typically repeatedly re-used, we are exploring the possibility to add an additional complementary workflow in the pipeline to allow automated database construction of all classification tools, given a set of FASTA reference files.

Finally, once an overall taxonomic profile is generated, researchers often wish to validate hits through more sensitive and accurate methods such as with read-mapping alignment. While read alignment is supported by other pipelines such as StaG-mwc,

228 this happens in-parallel to the taxonomic profiling and requires prior expectation of
229 which reference genomes to map against. Instead, nf-core/taxprofiler could be eas-
230 ily extended to have a validation step similar to the approach of the ancient DNA
231 metagenomic pipeline aMeta (Pochon et al. 2022). Utilising Nextflow’s execution par-
232 allelism, the input sequences could be aligned back to the reference genomes of only
233 those species with hits resulting from the taxonomic classification, but with dedicated
234 accurate short- or long-read aligners. In addition to the more precise classification,
235 post-classification read-alignment could also be particularly useful for researchers in
236 palaeogenomics who wish to use tools other than KrakenUniq for initial classification
237 (as in aMeta), where alignment information can be used to authenticate ancient DNA
238 within their samples, but also in clinical metagenomics to identify potential pathogens
239 at much finer resolution (e.g. down to strain level).

240 Another motivation for developing nf-core/taxprofiler, despite the large number of ex-
241 isting metagenomics pipelines, is that by establishing a taxonomic profiling pipeline
242 within the nf-core ecosystem, it is possible to begin building both standalone but
243 also an integrated suite of powerful interconnected pipelines for the major stages
244 of metagenomic workflows. Existing microbial- and metagenomics- related pipelines
245 within the nf-core initiative include nf-core/ampliseq (Straub et al. 2020), nf-core/mag
246 (Krakau et al. 2022), and nf-core/funcscan (<https://nf-co.re/funcscan>). We expect over
247 time the ability to link inputs and outputs of each workflow to develop comprehensive
248 metagenomic analyses, while still maintaining powerful standalone pipelines, provid-
249 ing maximal user choice but with familiar interfaces.

250 5 Conclusion

251 nf-core/taxprofiler is an accessible, efficient, and scalable pipeline for metagenomic
252 taxonomic classification and profiling that can be executed on anywhere from laptops
253 to the cloud. To our knowledge, the pipeline offers the largest number of taxonomic
254 profilers across similar pipelines, providing flexibility for users not just on choice of
255 profiling tool but also with databases and database settings within a single run. With
256 the development within the open and welcoming nf-core community and with best-
257 practise development infrastructure, we look forward to further contributions and in-
258 volvement of the wider metagenomics community, and also we hope that through de-
259 tailed documentation and a range of execution options, nf-core/taxprofiler will make
260 reproducible and high-throughput metagenomics more accessible for a wide range of
261 disciplines.

262 6 Code Availability

263 nf-core/taxprofiler source code is available on GitHub at [https://github.com/nf-core/](https://github.com/nf-core/taxprofiler)
264 [taxprofiler](https://github.com/nf-core/taxprofiler), and each release is archived on Zenodo (latest version DOI: [10.5281/zen-](https://doi.org/10.5281/zenodo.7728364)
265 [odo.7728364](https://doi.org/10.5281/zenodo.7728364))

266 The version of the pipeline described in this paper is version 1.1.0 (release specific

267 Zenodo archive DOI: [10.5281/zenodo.8358147](https://doi.org/10.5281/zenodo.8358147))

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283 **9 Conflict of Interest Statement**

284 M.E.B. is a cofounder of Unseen Bio ApS, a company that offers gut microbiome pro-
285 filing to consumers, however had no role in study design, data collection and analysis,
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287 conflicts of interest to declare.

10 Supplementary Information

10.1 Implementation

10.1.1 Input and Execution

The pipeline can be executed via typical Nextflow commands (Code Block 1), or using the standard nf-core 'launch' GUI (Figure 2), making the pipeline accessible for both computationally experienced as well as less experienced researchers. In addition to the general usage and parameter documentation of the pipeline (<https://nf-co.re/taxprofiler>). The GUI offers immediate assistance and guidance to users on what each parameter does, both in short- and long-form, with long-form parameter descriptions additionally describing which tool-specific parameters are being modified for each pipeline parameter (<https://nf-co.re/launch/?pipeline=taxprofiler>). The GUI also includes controlled user input by providing strict drop-down lists and input validation prior execution of the pipeline (Figure 2) to reduce the risk of typos and other mistakes, which is in contrast to the command-line interface that only includes validation at pipeline run-time.

Listing 1 Example nf-core/taxprofiler command for running short-read quality control, removal of host DNA and executing the k-mer based Kraken2 and marker gene alignment MetaPhlAn tools.

```
$ nextflow run nf-core/taxprofiler \
  -r 1.1.0 \
  -profile singularity,<institute> \
  --input <samplesheet.csv> \
  --databases <database.csv> \
  --perform_shortread_qc \
  --shortread_qc_minlength 20 \
  --preprocessing_qc_tool falco \
  --run_host_removal --hostremoval_reference 'host_genome.fasta' \
  --run_kraken2 --kraken2_save_reads \
  --run_metaphlan \
  --run_krona \
  --run_profile_standardisation
```

An example nf-core command line execution of the pipeline can be seen in Code Block 1, where two input files are supplied: one file specifying paths of FASTQ files of metagenomic samples and necessary metadata for preprocessing (such as sample ID and sequencing platform), and the second file specifying paths to the user-defined databases with per-database classification parameters. Various parameters are available to select different preprocessing steps, and provide additional configuration such as tool selection and value options. Note that even if a user supplies a given database in the database input sheet, the corresponding profiling tool must still be activated

Preprocessing short-read QC options

Launch

--shortread_qc_minlength

15

?

Specify the minimum length of reads to be retained

Specifying a minimum read length filtering can speed up profiling by reducing the number of short unspecific reads that need to be match/aligned to the database.

Modifies tool parameter(s):

- removed from reads --length_required
- AdapterRemoval: --min length

--perform_shortread_complexityfilter

☐ True
☒ False

?

Turns on nucleotide sequence complexity filtering

--shortread_complexityfilter_tool

bdduk

[Select an option]
bdduk
prinseqplusplus
fastp

?

Specify which tool to use for complexity filtering

--shortread_complexityfilter_entropy

?

Specify the minimum sequence entropy level for complexity filtering

--shortread_complexityfilter_bdduk_windowsize

50

?

On this page

Nextflow command-line flags

> Input/output options

Preprocessing general QC options

Preprocessing short-read QC options

Preprocessing long-read QC options

Preprocessing host removal options

Preprocessing run merging options

Profiling options

Postprocessing and visualisation options

Show hidden params

Figure 2: Screenshot of the nf-core pipeline launch graphical user interface with nf-core/taxprofiler options displayed. The web browser-based interface provides guidance for how to configure each pipeline parameter by providing both short and long help descriptions to help guide users in which contexts to configure each parameter. Additional elements such as radio buttons, drop down menus, and background regular expressions check for validity of input. When pressing launch, a prepared configuration file and command is provided that can be copied and pasted by the user into the terminal

311 with the corresponding pipeline parameter (e.g. `--run_kraken2`). Per-classifier flags
312 are also available for the optional saving of additional non-profile output files. Alter-
313 natively to command line flags, parameters can be specified via pre-configured YAML
314 format files, with which (provided no hardcoded paths are included) can be re-used
315 across pipeline runs.

316 All nf-core pipelines are strictly versioned (specified with the Nextflow `-r` flag), and to
317 ensure reproducibility, each version of the pipeline has a fixed set of software used for
318 each step of the pipeline. The fixed set of software are controlled through the use of
319 the conda package manager or containers (Docker, or Apptainer - previously known
320 as Singularity, etc) from the stable Bioconda (Grüning et al. 2018) or BioContainers
321 (Veiga Leprevost et al. 2017) repositories. This, coupled with the intrinsic Nextflow
322 ability to execute on most infrastructure whether that is a local laptop (resource re-
323 quirements permitting), traditional HPC, as well across common cloud providers also
324 makes nf-core/taxprofiler a very portable pipeline that can be used in many contexts.

325 10.1.2 Preprocessing

326 Preprocessing steps in nf-core/taxprofiler are aimed at removing laboratory and se-
327 quencing artefacts that may influence taxonomic profiling, either for computing re-
328 source consumption or and/or false-positive or false-negative classification reasons.
329 First sequencing quality control with FastQC (Andrews 2010) or Falco (Sena Brandine
330 and Smith 2021) is carried out. Falco was included for reduced memory requirements,
331 in particular for long read sequencing data. Artificial library adapter sequences added
332 during sequencing reduce sequencing matching accuracy by reducing sequence speci-
333 ficity, and in some cases, may result in false-positive hits due to adapter sequence con-
334 tamination in reference genomes (Schäffer et al. 2018; F. P. Breitwieser, Baker, and
335 Salzberg 2018)¹. Additionally, paired-end merging may provide longer sequences
336 that will allow for more specific classification when paired-end alignment is not sup-
337 ported by a given classifier. For these tasks nf-core/taxprofiler can apply either fastp
338 (Chen et al. 2018) or AdapterRemoval2 (Schubert, Lindgreen, and Orlando 2016) for
339 short reads, and currently Porechop (Wick et al. 2017) for Oxford Nanopore long-read
340 data. For both short and long reads, FastQC or Falco is run again to allow assessment
341 on the performance of the adapter removal and/or pair-merging step.

342 Low complexity sequences, e.g. sequences containing long stretches of mono- or
343 di-nucleotide repeats provide little specific genetic information that contribute to
344 taxonomic identification, as they can align to many different reference genomes
345 (Schmieder and Edwards 2011; Clarke et al. 2019). Including such reads during
346 taxonomic profiling can increase run-time and memory usage for little gain, as
347 during lowest-common-ancestor (LCA) classification steps they will be assigned to

¹For an ‘infamous’ case of adapter sequences in a published eukaryotic genome, see the following blog posts

Graham Etherington: <https://web.archive.org/web/20201219022000/http://grahametherington.blogspot.com/2014/09/why-you-should-qc-your-reads-and-your.html?m=1> why-you-should-qc-your-reads-and-your.html
Sixing Huang: <https://web.archive.org/web/20220904205331/https://dgg32.medium.com/carp-in-the-soil-1168818d2191>

(Accessed 2023-08-25)

high-level taxonomic ranks (e.g. Kingdom). nf-core/taxprofiler performs removal of these reads through complexity filtering algorithms as provided by fastp, BBDuk (Bushnell 2022), or PRINSEQ++ (Cantu, Sadural, and Edwards 2019). Long read sequences often do not have such reads, as lengths are sufficient enough to capture greater sequence diversity - but it is sometimes desirable to only classify reads longer than a certain length - as these provide more precise taxonomic information (Dilthey et al. 2019; Portik, Brown, and Pierce-Ward 2022). Therefore, nf-core/taxprofiler can remove reads shorter than a user-defined length using Filtlong.

Removing host DNA is another common preprocessing step in metagenomic studies. This can help speed up run-time, particularly in microbiome studies, where detection of microbes are of interest. Furthermore, host-contamination of reference genomes in public databases is common (Longo, O'Neill, and O'Neill 2011; Kryukov and Imanishi 2016; Florian P. Breitwieser et al. 2019). Therefore, the removal of such sequences can help decrease the risk of false positive taxonomic assignment. To remove multiple hosts or other sequences, all reference genomes can be combined into a single FASTA reference file. Short read host removal can be carried out with Bowtie2 (Langmead and Salzberg 2012; Langmead et al. 2019) and minimap2 (Li 2018) for long reads, both in combination with SAMtools (Li et al. 2009; Danecek et al. 2021), where reads are aligned against the reference genome and the off-target (unaligned) reads are then converted back to FASTQ format for classification.

Finally, nf-core/taxprofiler can optionally perform 'run merging' where multiple FASTQ files from the same sample but have been sequenced over multiple lanes are concatenated together to generate one profile per sample or library. The final set of reads used for profiling can be optionally saved for downstream re-use. Throughout all steps, relevant statistics and log files are generated and used both for the final pipeline run report as well as saved into the results directory of the pipeline run for further inspection where necessary.

10.1.3 Profiling

There are many types of metagenomic profiling techniques, from profiling against whole-genome references with alignment or k-mer based approaches, to methods involving alignment to species-specific marker-gene families (Quince et al. 2017; Ye et al. 2019). nf-core/taxprofiler aims to support and include all established classification or profiling tools as requested by the community.

The choice of tools used in a pipeline run is up to the user, with a tool being executed when both the corresponding database and --run_<tool> flag is provided. Specific classification settings for each tool and database are specified in the database CSV input sheet. Some tools also have pipeline level command-line flags for controlling certain aspects of output files.

The following classifiers and profilers are supported in version 1.1.0 of nf-core/taxprofiler: Kraken2 (Wood, Lu, and Langmead 2019), Bracken (Lu et al. 2017), KrakenUniq (F. P. Breitwieser, Baker, and Salzberg 2018), Centrifuge (Kim et al. 2016), MALT (Vågene et al. 2018), DIAMOND (Buchfink, Reuter, and Drost 2021),

390 Kaiju (Menzel, Ng, and Krogh 2016), MetaPhlAn (Blanco-Míguez et al. 2023), mOTUs
391 (Ruscheweyh et al. 2022), ganon (Piro et al. 2020), KMCP (Shen et al. 2023).

392 By default, nf-core/taxprofiler produces the default per-sample taxonomic classifica-
393 tion profile output from a tool or a tool’s report generation tool. The output is nor-
394 mally in the form of counts per reference sequencing, with additional statistics about
395 the hits of a particular organism (estimated sequence abundance, taxonomic level etc.).
396 Users can also optionally request output of per-read classification output and output
397 such as classified and unclassified reads in FASTQ format, where supported.

398 The pipeline provides high efficiency, particularly during the metagenomic classifica-
399 tion stage, through the inherent parallelisation provided by Nextflow. While metage-
400 nomic classification is comparatively computationally intensive (in terms of mem-
401 ory and execution time; due to a combination of sequencing depth and number of
402 reference genomes), Nextflow automatically optimises the execution order of all the
403 steps in pipeline, maximising the number parallel running of multiple profilers and/or
404 databases at any given time point, as far as the available computational resources al-
405 low. For local machines such as laptops or desktops, Nextflow will automatically
406 detect all available computational resources, but this is customisable using Nextflow
407 configuration files. For HPC and cloud infrastructure, users typically have to define
408 the computational infrastructural environment the pipeline is being executed on (CPU
409 or memory limitations, queues, instance types, etc.). To facilitate the pipeline compu-
410 tational configuration, nf-core/taxprofiler supports use of more than 90 pre-defined
411 centralised generic and pipeline-specific institutional Nextflow configurations as pro-
412 vided by nf-core/configs (<https://nf-co.re/configs>). However, of course users are still
413 welcome to supply their own custom configuration files as with any typical Nextflow
414 run, further refining computational limitations or execution specifications.

415 **10.1.4 Post-profiling**

416 In metagenomic studies, it is common practise to compare the profiles among many
417 samples, and the results of multiple profiles are normally stored in ‘taxon tables’, i.e,
418 counts per reference taxon (rows), for each sample (columns). When available, nf-
419 core/taxprofiler supports the option to produce the ‘native’ taxon table of each classi-
420 fication tool when multiple samples are run.

421 One of the challenges that researchers face when comparing multiple taxonomic clas-
422 sifiers or profilers is the heterogenous output formats that are produced, that often
423 require custom parsing and merging scripts for each tool to standardise. To facilitate
424 more user-friendly cross-comparisons between tools, nf-core/taxprofiler utilises the
425 TAXPASTA tool (Beber et al. 2023) to generate standardised profiles and generate
426 multi-sample tables.

427 Summary statistics for the entire pipeline are visualised and displayed in a customis-
428 able MultiQC report (Ewels et al. 2020). When supported, quality control of data and
429 pipeline runs are shown for manual verification. Krona plots (Ondov, Bergman, and
430 Phillippy 2011) can also optionally be generated for supported tools to help provide
431 further visualisation of taxonomic profiles.

432 10.1.5 Output

433 To summarise, the main default output from nf-core/taxprofiler are both classifier
434 ‘native’ and standardised single- and multi-sample taxonomic profiles with counts
435 per-taxon and an interactive MultiQC run report with all run statistics, in addition to
436 the raw log files themselves where available.

437 The MultiQC run report displays statistics and summary visualisations for all steps of
438 the pipeline where possible, lists of versions for all tools of each step of the pipeline.
439 It also provides a dynamically-constructed text for the recommended ‘methods’ for
440 reporting how the pipeline was executed (including relevant citations) that users can
441 use in their own publications.

442 Optional outputs can include other types of profiles (e.g. per read classification) and
443 in other formats as produced by the tools themselves, as well as raw reads from pre-
444 processing steps and output visualisations from Krona. Nextflow resource usage and
445 trace reports are also by default produced for users to check pipeline performance.

446 10.2 Comparison with other solutions

447 nf-core/taxprofiler has been specifically developed for the analysis of whole-genome,
448 *metagenomic* sequencing data. While other types of taxonomic profiling data such
449 as 16S amplicon sequencing are well established fields with a range of popular high-
450 quality and best-practise tools pipelines (e.g. Blanco-Míguez et al. 2023; Schloss et
451 al. 2009) and databases (DeSantis et al. 2006; Yilmaz et al. 2014), ‘gold standard’
452 tools and databases for metagenomics remain much less established. Thus, the need
453 for highly-multiplexed classification is more desirable for the newer metagenomics
454 methods.

455 We searched Google Scholar for open-source pipelines published or released in the last
456 5 years (at the time of writing, since 2018) that were designed primarily for metage-
457 nomic classification screening, that supported at least 2 classifiers, had at least one
458 preprocessing step and were not specifically targeted at read classification of spe-
459 cific domains of taxa (e.g. viruses or bacteriophages only). We also included an addi-
460 tional open-source but unpublished pipeline at the recommendations of the authors
461 of the pipeline due to the functional overlap to nf-core/taxprofiler. We then evalu-
462 ated the pipelines based on their publications and documentation for typical metage-
463 nomic profiling workflow steps. We used a range of criteria related to expectations of
464 modern bioinformatic workflows that can be summarised in the following four cate-
465 gories: reproducibility, accessibility, scalability, and portability (Wratten, Wilm, and
466 Göke 2021). After searching, we selected the following pipelines for comparison with
467 nf-core/taxprofiler that matched the specific criteria described above: sunbeam (v4,
468 Clarke et al. 2019), Unipro UGENE (v48, Rose et al. 2019), TAMA (githash: 3a22c8f,
469 Sim et al. 2020), and StaG-mwc (0.7.0, Boulund et al. 2023).

470 In terms of accessibility, all pipelines have documentation describing the installation
471 steps, usage instructions, and output files. However, there are varying levels of de-
472 tail and comprehensiveness. In particular, StaG-mwc and nf-core/taxprofiler have

the most detailed descriptions of all possible output files for every supported module, whereas Unipro UGENE and sunbeam have very minimal to possibly unfinished output documentation. For execution options, most of the pipelines provide CLI execution, except for Unipro UGENE which offers only GUI-based pipeline set-up (despite a command-line execution of the GUI generated configuration). In particular, nf-core/taxprofiler is the only pipeline providing both CLI and GUI interfaces for pipeline run execution.

Criteria covering portability also overlap with accessibility, as it implies options for and ease of different users running on different types of computing infrastructure, whether that is on their own laptop, on an HPC cluster, or in the cloud. Unipro UGENE is the only pipeline that explicitly states support for execution on all three major operating systems (Linux, OSX, Windows), whereas StaG-mwc and nf-core/taxprofiler can be run on unix operating systems (albeit possibly on Windows via Windows Subsystem for Linux (WSL)), and sunbeam and TAMA are only being supported on Linux.

While all pipelines support ‘local’ machine execution (e.g. personal laptops or desktops), a large portion of academic users execute computationally intensive bioinformatic tasks on HPC clusters. In these contexts, pipeline task submissions are normally managed by job schedulers, thus integration with schedulers is an important criterion for running large multi-step and parallelised pipelines. The three pipelines leveraging workflow managers (Snakemake and Nextflow) support integration with schedulers (StaG-mwc, sunbeam, and nf-core/taxprofiler) with nf-core/taxprofiler supporting the most by far (>10 scheduling systems) as natively offered by Nextflow. This allows the greatest possible choice for users in terms of which HPC infrastructure they can execute their pipeline on. As an extension of this, only nf-core/taxprofiler has explicit support for cloud computing (e.g. AWS, GCP, or Microsoft Azure) as provided by Nextflow, again maximising user choice and portability when it comes to running the pipeline.

In terms of scalability, the aforementioned integration with schedulers and cloud computing support implicitly maximises efficiency and parallelisation of pipeline runs, providing good scalability for varying numbers of input files and steps in the pipeline. Again, the three workflow manager based pipelines provide scalability, whereas there is no mention neither Unipro UGENE nor TAMA in reference to parallel task execution. Furthermore, all pipelines except TAMA, allowed per-process customisation of computational resources, something critical for maximising efficient scalability to ensure only the necessary resources for a given step of a pipeline are requested.

In terms of reproducibility, all five pipelines are good at ensuring reproducibility in terms of pipeline and software versioning (allowing re-execution of pipeline runs using the same software), with only TAMA not having stable versioned releases. However, installing software manually across different infrastructures can result in variability in the execution of each software² (Di Tommaso et al. 2017). The current most

²As demonstrated in this blogpost from Paweł Przytuła: <https://web.archive.org/web/20230320223436/https://appsilon.com/reproducible-research-when-your-results-cant-be-reproduced/> (Accessed 2023-08-25)

popular solution to the problem of inconsistent software environments is to use container engines such as Docker or Apptainer to run container images which are isolated, deterministic computing environments which can be executed by any system providing a container runtime. Only Unipro UGENE does not document the use of a container system, with nf-core/taxprofiler offering the biggest choice for users, again, courtesy of Nextflow with 6 different engine systems at the time of writing.

Finally, we compared metagenomics related functionality between the pipelines. All pipelines support short-read FASTQ input, but only nf-core/taxprofiler explicitly reports long-read support, while the documentation in Unipro UGENE states that assembled contigs are possible input to some of the profilers. All pipelines support read preprocessing (adapter clipping, and merging). In terms of tools used for preprocessing, Trimmomatic (Bolger, Lohse, and Usadel 2014) is popular across the other pipelines but is not supported in nf-core/taxprofiler. Only sunbeam and nf-core/taxprofiler support complexity filtering to remove low sequence diversity reads. In fact within sunbeam, the authors developed their own dedicated, performant complexity filtering tool Komplexity (Clarke et al. 2019). Most pipelines support some form of host removal (only TAMA did not support this), and it is likely possible with Unipro UGENE (although not directly described). In all cases, host removal consists of mapping processed reads with an aligner and using the off-target reads for downstream profiling (as implemented in nf-core/taxprofiler), however StaG-mwc has an additional separate metagenomic host removal step with Kraken2. nf-core/taxprofiler supports by far the largest number of taxonomic classifiers and profilers at 11 as of v1.1.0 - providing the greatest choice to users - with StaG-mwc offering 7, and the remaining pipelines only 3. Only nf-core/taxprofiler and partly StaG-mwc explicitly support running each profiler with multiple databases. nf-core/taxprofiler is the only pipeline that supports running an arbitrary number of different metagenomic profiler databases each with their own settings. This makes it a useful for tool parameter comparison, testing different databases, or reducing the size of each database (e.g. per domain) to make it more flexibility for running on smaller computational infrastructure. StaG-mwc allows multiple references for their short-read alignment steps rather than the metagenomic profilers. For output, nf-core/taxprofiler, StaG-mwc, and sunbeam (via an extension) support a singular run report for summarising all preprocessing step. Only nf-core/taxprofiler and TAMA produce standardised output for all taxonomic profilers, the former with the dedicated standalone tool TAXPASTA (Beber et al. 2023). However Unipro UGENE additionally offers a ‘consensus’ profile using WEVOTE (Metwally et al. 2016).

To summarise, many of the pipelines reviewed here offer similar functionality, with particularly StaG-mwc having a strong overlap with nf-core/taxprofiler. Thus, users in most cases will be able to select the pipeline depending on which framework they feel most comfortable with. However the advantages of nf-core/taxprofiler mainly come from the offering of the greatest choice of tools, as well the particular benefits provided by Nextflow. It provides the greatest number of computational infrastructure types the pipeline can be executed on, and container systems can be used to ensure reproducibility, as well the support of the nf-core community due to the centralised pool of ‘plug-and-play’ modules to make it easier to update the pipeline over

558 time to add new tools classifiers.

559 The functionality offered by other pipelines not currently supported by nf-
560 core/taxprofiler include sequencing saturation estimation (StaG-mwc), taxonomy-
561 free composition comparison (StaG-mwc), functional profiling (StaG-mwc), *de novo*
562 assembly (sunbeam), and reference mapping (StaG-mwc, sunbeam). We do not
563 plan to support *de novo* assembly or functional profiling in nf-core/taxprofiler as
564 we feel these are already better served by other existing dedicated pipelines within
565 the nf-core ecosystem: nf-core/mag for *de novo* assembly, (Krakau et al. 2022)
566 and nf-core/funcscan for functional profiling (<https://nf-co.re/funcscan>), as well as
567 elsewhere e.g. MetaWRAP (Uritskiy, DiRuggiero, and Taylor 2018).

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