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NGLess is a domain-specific language for NGS (next-generation sequencing data) processing.

For questions, you can also use the nglss mailing list.

Note: If you are using NGLess for generating results in a scientific publication, please cite

For metagenomics profiling, consider using ng-meta-profile, which is a collection of predefined pipelines developed using NGLess.
NGLess is best illustrated by an example:

```python
ngless "0.11"
input = paired('ctrl1.fq', 'ctrl2.fq', singles='ctrl-singles.fq')
input = preprocess(input) using |read|:
    read = read[5:]
    read = substrim(read, min_quality=26)
    if len(read) < 31:
        discard

mapped = map(input, reference='hg19')

write(count(mapped, features=['gene']),
      ofile='gene_counts.csv',
      format=(csv))
```
CHAPTER 3

Building and installing

See the install page for more information.
Basic functionality

- preprocessing and quality control of FastQ files
- mapping to a reference genome (implemented through \texttt{bwa} by default)
- assembly of contigs
- annotation and summarization of the alignments using reference gene annotations
- much more

\texttt{Ngless} has built-in support for model organisms:
1. Homo sapiens (hg19)
2. Mus Musculus (mm10)
3. Rattus norvegicus (rn4)
4. Bos taurus (bosTau4)
5. Canis familiaris (canFam2)
6. Drosophila melanogaster (dm3)
7. Caenorhabditis elegans (ce10)
8. Saccharomyces cerevisiae (sacCer3)

and the standard library includes support for m\textsc{OTUs}, metagenomics profiling of marine samples and human gut microbiome samples. We also have standard library modules for helping users upgrading from \textsc{MOCAT} or running many samples (we have used \texttt{Ngless} on projects with >10,000 samples).

\texttt{NgLess} puts a strong emphasis on reproducibility.
ngless can be used as a traditional command line transformer utility, using the \(-e\) argument to pass an inline script on the command line.

The \(-p\) (or \(--print-last\)) argument tells ngless to output the value of the last expression to stdout.

### 5.1 Converting a SAM file to a FASTQ file

Extract file reads from a SAM (or BAM) file:

```
$ ngless -pe 'as_reads(samfile("file.sam"))' > file.fq
```

This is equivalent to the full script:

```bash
ngless "0.11" # <- version declaration, optional on the command line
samcontents = samfile("file.sam") # <- load a SAM/BAM file
reads = as_reads(samcontents) # <- just get the reads (w quality scores)
write(reads, ofname=STDOUT) # <- write them to STDOUT (default format: FASTQ)
```

This only works if the data in the samfile is single ended as we pipe out a single FQ file. Otherwise, you can always do:

```bash
ngless "0.11"
write(as_read(samfile(" file.sam")),
     ofile="output.fq")
```

which will write 3 files: output.1.fq, output.2.fq, and output.singles.fq (the first two for the paired-end reads and the last one for reads without a mate).

### 5.2 Getting aligned reads from a SAM file as FASTQ file

Building on the previous example. We can add a `select()` call to only output unmapped reads:
$ ngless -pe 'as_reads(select(samfile("file.sam"), keep_if=[(mapped)]))' > file.fq

This is equivalent to the full script:

```bash
ngless "0.11" # <- version declaration, optional on the command line
samcontents = samfile("file.sam") # <- load a SAM/BAM file
samcontents = select(samcontents, keep_if=[(mapped)]) # <- select only *mapped* reads
reads = as_reads(samcontents) # <- just get the reads (w quality scores)
write(reads, ofname=STDOUT) # <- write them to STDOUT (default format: FASTQ)
```

### 5.3 Reading from STDOUT

For a true Unix-like utility, the input should be read from standard input. This can be achieved with the special file STDIN. So the previous example now reads

```bash
$ cat file.sam | ngless -pe 'as_reads(select(samfile(STDIN), keep_if=[(mapped)]))' > _
˓→file.fq
```

Obviously, this example would more interesting if the input were to come from another programme (not just `cat`).

Full documentation

Frequently Asked Questions (FAQ)
6.1 Introduction

6.1.1 Motivation

Nearly all next generation sequence (NGS) applications rely on sequence alignment as the first analysis step. Before the alignment they require some kind of pre-processing of data, that is always dependent on the researcher interest. Our objective is to allow the creation of a pipeline of work for all the first phase of NGS analysis until the point (inclusive) of annotation. We want to do this while achieving the following goals:

- Ease the development of NGS Tools;
- Enable an easy identification of errors;
- Easily reproduce an experiment;
- Easy configuration and execution of workflows;
- Exploit available computational resources.

6.1.2 Target Users

Bioinformaticians working in a wetlab setting. Every serious biological lab in the world now needs to hire at least one. They know programming (at least basic programming), but are not method developers.
The tool can still be useful for more advanced users.

### 6.1.3 Basic Properties

- The syntax is a pythonesque syntax with Ruby-like blocks.
- The types are statically and strictly.
- Types are implicit, but limited language allows for type inference and checking.
- Quality control is implicit and mandatory (you get it for free)
- Types are domain types (biological).

### 6.2 Installation

#### 6.2.1 Bioconda (binary)

The recommended way to install NGLess is through bioconda:

```bash
conda install -c bioconda ngless
```

**Docker**

Alternatively, a docker container with NGLess is available at biocontainers:

```bash
docker run -v $PWD:/workdir -w /workdir -it quay.io/biocontainers/ngless:0.6.1--py35
ngless --version
```

Adapt the mount flags (`-v`) as needed.

#### 6.2.2 Linux (binary)

You can get a statically linked version of NGLess 0.6.1 or a nighly build of the latest development code. This should work across a wide range of Linux versions (please report any issues you encounter):

```bash
curl -O https://ngless.embl.de/releases/ngless-0.6.0-Linux64
chmod +x ngless-0.6.0-Linux64
./ngless-0.6.0-Linux64
```

This download bundles bwa, samtools and megahit (also statically linked).

If you want to try one of ngless’ builtin modules (motus, specI, ...) you can download the full nighly build zip file which includes them.

#### 6.2.3 Windows

NGLess cannot currently compile on Windows.
6.2.4 From source

Stack is the simplest way to install the necessary requirements. You should also have gcc installed (or another C-compiler).

The following sequence of commands should download and build the software:

```
git clone https://github.com/ngless-toolkit/ngless
cd ngless
make
```

The first time you run this, it will take a while as it will download all dependencies. After this ngless is ready to use!

6.2.5 With Nix

If you use nix, you can easily build and install ngless using it (these scripts also install all necessary dependencies):

```
nix-env -i -f https://github.com/luispedro/ngless-nix/archive/master.tar.gz
```

This should download the nix scripts and build ngless.

If you prefer, you can also first clone the repository:

```
git clone https://github.com/luispedro/ngless-nix
cd ngless-nix
# inspect the default.nix & ngless.nix files if you wish
nix-env -i -f .
```

6.2.6 Make targets

The following are targets in the Makefile.

- `make`: compiles NGLess and haskell dependencies
- `clean`: remove local generated files by compilation
- `check`: run tests
- `bench`: run benchmarks

6.3 NG-meta-profiler

NG-meta-profiler is a collection of predefined pipelines for processing shotgun metagenomes.

1. `human-gut.ngl` for human gut samples
2. `marine.ngl` for marine samples
3. `mouse-gut.ngl` for mouse gut samples
4. `dog-gut.ngl` for dog gut samples
5. `pig-gut.ngl` for pig gut samples

These are predefined, but users are encouraged to adapt them to their specific needs.
6.3.1 INSTALL

1. install ngless
2. install ng-meta-profiler by downloading the appropriate pipeline from github: https://github.com/ngless-toolkit/ng-meta-profiler

6.3.2 USAGE

To use the profiler, select the appropriate script (e.g., human-gut.ngl for human gut samples), put all the FastQ files from the same sample in the same directory (INPUT-DIRECTORY) with the extension .fq.gz or fastq.gz and run:

```
ngless human-gut.ngl INPUT-DIRECTORY OUTPUT-DIRECTORY
```

6.4 What’s New (History)

6.4.1 Version 1.0

User-visible improvements

- The handling of multiple annotations in count (i.e., when the user requests multiple features and/or subfeatures) has changed. The previous model caused a few issues (#63, but also mixing with collect()). Unfortunately, this means that scripts asking for the old behaviour in their version declaration are no longer supported if they use multiple features.

6.4.2 Version 0.11

Released March 15 2019 (0.11.0) and March 21 2019 (0.11.1).

Version 0.11.0 used ZStandard compression, which was not reliable (the official haskell zstd wrapper has issues). Thus, it was removed in v0.11.1. Using v0.11.0 is not recommended.

User-visible improvements

- Module samtools (version 0.1) now includes samtools_view
- Add --verbose flag to check-install mode (ngless --check-install --verbose)
- Add early checks for input files in more situations (#33)
- Support compression in collect() output (#42)
- Add smoothtrim() function

Bugfixes

- Fix bug with orf_find & prots_out argument
- Fix bug in garbage collection where intermediate files were often left on disk for far longer than necessary.
- Fix CIGAR (#92) for select() blocks
Internal improvements

- Switched to diagrams package for plotting. This should make building easier as cairo was often a complicated dependency.
- Update to LTS-13 (GHC 8.6)
- Update minimap2 version to 2.14
- Call bwa/minimap2 with interleaved fastq files. This avoids calling it twice (which would mean that the indices were read twice).
- Avoid leaving open file descriptors after FastQ encoding detection
- Tar extraction uses much less memory now (#77)

6.4.3 Version 0.10.0

Released Nov 12 2018

Bugfixes

- Fixed bug where header was printed even when STDOUT was used
- Fix to lock1’s return value when used with paths (#68 - reopen)
- Fixed bug where writing interleaved FastQ to STDOUT did not work as expected
- Fix saving fastq sets with –subsample (issue #85)
- Fix (hypothetical) case where the two mate files have different FastQ encodings

User-visible improvements

- samtools_sort() now accepts by={name} to sort by read name
- Add __extra_megahit_args to assemble() (issue #86)
- arg1 in external modules is no longer always treated as a path
- Added expand_searchdir to external modules API (issue #56)
- Support _F/_R suffixes for forward/reverse in load_mocat_sample
- Better error messages when version is mis-specified
- Support NO_COLOR standard: when NO_COLOR is present in the environment, print no colours.
- Always check output file writability (issue #91)
- paired() now accepts encoding argument (it was documented to, but mis-implemented)

Internal improvements

- NGLess now pre-emptively garbage collects files when they are no longer needed (issue #79)
6.4.4 Version 0.9.1

Released July 17th 2018

- Added NGLess preprint citation

6.4.5 Version 0.9

Released July 12th 2018

User-visible improvements

- Added allbest() method to MappedRead.
- NGLess will issue a warning before overwriting an existing file.
- Output directory contains PNG files with basic QC stats
- Added modules for gut gene catalogs of mouse, pig, and dog
- Updated the integrated gene catalog

Internal improvements

- All lock files now are continuously “touched” (i.e., their modification time is updated every 10 minutes). This makes it easier to discover stale lock files.
- The automated downloading of builtin references now uses versioned URLs, so that, in the future, we can change them without breaking backwards compatibility.

6.4.6 Version 0.8.1

Released June 5th 2018

This is a minor release and upgrading is recommended.

Bugfixes

- Fix for systems with non-working locale installations
- Much faster collect calls
- Fixed lock1 when used with full paths (see issue #68)
- Fix expansion of searchpath with external modules (see issue #56)

6.4.7 Version 0.8

Released May 6th 2018
Incompatible changes

- Added an extra field to the FastQ statistics, with the fraction of basepairs that are not ATCG. This means that uses of `qcstats` must use an up-to-date version declaration.
- In certain cases (see below), the output of `count` when using a GFF will change.

User-visible improvements

- Better handling of multiple features in a GFF. For example, using a GFF containing “gene_name=nameA,nameB” would result in:

```
nameA, nameB 1
```

Now the same results in:

```
nameA 1
nameB 1
```

This follows after [https://git.io/vpagq](https://git.io/vpagq) and the case of `Parent=AF2312,AB2812,abc-3`

- Support for `minimap2` as alternative mapper. Import the `minimap2` module and specify the `mapper` when calling `map`. For example:

```
ngless '0.8'
import "minimap2" version "1.0"
input = paired('sample.1.fq', 'sample.2.fq', singles='sample.singles.fq')
mapped = map(input, fafile='ref.fna', mapper='minimap2')
write(mapped, ofile='output.sam')
```

- Added the `<>` operator. This can be used to concatenate filepaths. `p0 <> p1` is short for `p0 + "/" + p1` (except that it avoids double forward slashes).
- Fixed a bug in `select` where in some edge cases, the sequence would be incorrectly omitted from the result. Given that this is a rare case, if a version prior to 0.8 is specified in the version header, the old behaviour is emulated.
- Added `bzip2` support to `write`.
- Added reference argument to `count`.

Bug fixes

- Fix writing multiple compressed Fastq outputs.
- Fix corner case in `select` `<Functions.html#select>`. Previously, it was possible that some sequences were wrongly removed from the output.

Internal improvements

- Faster `collect()`
- Faster FastQ processing
- Updated to `bwa 0.7.17`
- External modules now call their `init` functions with a lock
• Updated library collection to LTS-11.7

6.4.8 Version 0.7.1

Released Mar 17 2018
Improves memory usage in `count()` and the use the `when-true` flag in external modules.

6.4.9 Version 0.7

Released Mar 7 2018

New functionality in NGLess language

• Added `max_trim` argument to `filter` method of `MappedReadSet`.
• Support saving compressed SAM files
• Support for saving interleaved FastQ files
• Compute number Basepairs in FastQ stats
• Add `headers` argument to `samfile` function

Bug fixes

• Fix `count`’s mode `{intersection_strict}` to no longer behave as `{union}`
• Fix `as_reads()` for single-end reads
• Fix `select()` corner case

In addition, this release also improves both speed and memory usage.

6.4.10 Version 0.6

Released Nov 29 2017

Behavioural changes

• Changed `include_m1` default in `count()` function to `True`

New functionality in NGLess language

• Added `orf_find` function (implemented through Prodigal) for open reading frame (ORF) prediction
• Add `qcstats()` function to retrieve the computed QC stats.
• Added reference alias for a more human readable name
• Updated builtin referenced to include latest releases of assemblies
New functionality in NGLess tools

• Add --index-path functionality to define where to write indices.
• Allow citations as key in external modules (generally better citations information)
• Use multiple threads in SAM->BAM conversion
• Better error checking/script validation

Bug fixes

• Output preprocessed FQ statistics (had been erroneously removed)
• Fix --strict-threads command-line option spelling
• Version embedded megahit binary
• Fixed inconsistency between reference identifiers and underlying files

6.4.11 Version 0.5.1

Released Nov 2 2017

Fixed some build issues

6.4.12 Version 0.5

Released Nov 1 2017

First release supporting all basic functionality.

6.5 Ocean Metagenomics Functional Profiling

Note: If you are starting out with NGLess for metagenomics profiling, consider using the predefined pipeline collection, NG-meta-profiler. This tutorial is based on deconstructing a pipeline very similar to those.

In this tutorial, we will analyse a small dataset of oceanic microbial metagenomes.

Note: This tutorial uses the full Ocean Microbial Reference Gene Catalog presented in Structure and function of the global ocean microbiome Sunagawa, Coelho, Chaffron, et al., Science, 2015

This catalog contains ca. 40 million genes and requires 56GiB of RAM

1. Download the toy dataset

First download all the tutorial data:

```bash
ngless --download-demo ocean-short
```
This will download and expand the data to a directory called ocean-short.

This is a toy dataset. It is based on real data, but the samples were trimmed so that they contain only 250k paired-end reads.

The dataset is organized in classical MOCAT style. Ngless does not require this structure, but this tutorial also demonstrates how to upgrade from your existing MOCAT-based projects:

```bash
$ find
./SAMEA2621229.sampled
./SAMEA2621229.sampled/ERR594355_2.short.fq.gz
./SAMEA2621229.sampled/ERR594355_1.short.fq.gz
./SAMEA2621155.sampled
./SAMEA2621155.sampled/ERR599133_1.short.fq.gz
./SAMEA2621155.sampled/ERR599133_2.short.fq.gz
./SAMEA2621033.sampled
./SAMEA2621033.sampled/ERR594391_2.short.fq.gz
./SAMEA2621033.sampled/ERR594391_1.short.fq.gz
./tara.demo.short
./process.ngl
```

The whole script we will be using is there as well (process.ngl), so you can immediately run it with:

```bash
ngless process.ngl
```

The rest of this tutorial is an explanation of the steps in this script.

2. Preliminary imports

To run ngless, we need write a script. We start with a few imports:

```bash
ngless "0.7"
import "parallel" version "0.6"
import "mocat" version "0.0"
import "omrgc" version "0.0"
```

These will all be used in the tutorial.

3. Parallelization

We are going to process each sample separately. For this, we use the lock1 function from the parallel module (which we imported before):

```bash
samples = readlines('tara.demo.short')
sample = lock1(samples)
```

The readlines function reads a file and returns all lines. In this case, we are reading the tara.demo.short file, which contains the three samples (SAMEA2621229.sampled, SAMEA2621155.sampled, and SAMEA2621033.sampled).

lock1() is a slightly more complex function. It takes a list and locks one of the elements and returns it. It always chooses an element which has not been locked before, so you each time you run _ngless_, you will get a different sample.

4. Preprocessing

First, we load the data (the FastQ files):

```bash
input = load_mocat_sample(sample)
```

And, now, we preprocess the data:
5. Profiling using the OM-RGC

After preprocessing, we map the reads to the ocean microbial reference gene catalog:

```
input = preprocess(input, keep_singles=False) using |read|:
    read = substrim(read, min_quality=25)
    if len(read) < 45:
        discard
```

```
mapped = map(input, reference='omrgc', mode_all=True)
```

The line above is the reason we needed to import the omrgc module: it made the omrgc reference available.

```
mapped = select(mapped, keep_if={[mapped}, {unique})]
```

Now, we need to count the results. This function takes the result of the above and aggregates it different ways. In this case, we want to aggregate by KEGG KOs, and eggNOG OGs:

```
counts = count(mapped,
    features=['KEGG_ko', 'eggNOG_OG'],
    normalization={scaled})
```

7. Aggregate the results

We have done all this computation, now we need to save it somewhere. We will use the collect() function to aggregate across all the samples processed:

```
collect(counts
    current=sample,
    allneeded=samples,
    ofile='omgc.profiles.txt')
```

8. Run it!

This is our script. We save it to a file (process.ngl in this example) and run it from the command line:

```
$ ngless process.ngl
```

Note that we need a large amount (ca. 64GB) of RAM memory to be able to use the OM-RGC. You also need to run it once for each sample. However, this can be done in parallel, taking advantage of high performance computing clusters.

### 6.5.1 Full script

Here is the full script:

```
ngless "0.8"
import "parallel" version "0.0"
import "mocat" version "0.0"
import "omrgc" version "0.0"

samples = readlines('tara.demo.short')
sample = lock1(samples)
input = load_mocat_sample(sample)
```

(continues on next page)
input = preprocess(input, keep_singles=False) using |read|:
    read = substrim(read, min_quality=25)
    if len(read) < 45:
        discard

mapped = map(input, reference='omrgc', mode_all=True)
mapped = select(mapped, keep_if=\{{mapped}, {unique}\})
collect(
    count(mapped,
        features=['KEGG_ko', 'eggNOG_OG'],
        normalization={scaled}),
    current=sample,
    allneeded=samples,
    ofile='omgc.profile.txt')

6.6 Ocean Metagenomics Assembly and Gene Prediction

In this tutorial, we will analyse a small dataset of oceanic microbial metagenomes.

Note: This tutorial uses the full Ocean Microbial Reference Gene Catalog presented in Structure and function of the global ocean microbiome Sunagawa, Coelho, Chaffron, et al., Science, 2015

1. Download the toy dataset

First download all the tutorial data:

ngless --download-demo ocean-short

We are reusing the same dataset as in the Ocean profiling tutorial. It may be a good idea to read steps 1-4 of that tutorial before starting this one.

2. Preliminary imports

To run ngless, we need write a script. We start with a few imports:

ngless "0.6"

3. Preprocessing

This is as in the profiling tutorial, except that we will be working with a single sample. You could also use the parallel module to make it easier to work on all samples:

sample = 'SAMEA2621155.sampled'
input = load_mocat_sample(sample)

preprocess(input, keep_singles=False) using |read|:
    read = substrim(read, min_quality=25)
    if len(read) < 45:
        discard

4. Assembly and gene prediction

This is now very simply two calls to the function assemble and orf_find:
### 6.6.1 Full script

```python
contigs = assemble(input)
write(contigs, ofile='contigs.fna')

orfs = orf_find(contigs)
write(contigs, ofile='orfs.fna')
```

### 6.7 Human Gut Metagenomics Functional & Taxonomic Profiling

**Note:** If you are starting out with NGLess for metagenomics profiling, consider using the predefined pipeline collection, NG-meta-profiler. This tutorial is based on deconstructing a pipeline very similar to those.

In this tutorial, we will analyse a small dataset of human gut microbial metagenomes.

**Note:** This tutorial is also available as a slide presentation

1. Download the toy dataset

First download all the tutorial data:

```bash
ngless --download-demo gut-short
```

This will download and expand the data to a directory called `gut-short`.

This is a toy dataset. It is based on real data, but the samples were trimmed so that they contain only 250k paired-end reads.

The dataset is organized in classical MOCAT style. Ngless does not require this structure, but this tutorial also demonstrates how to upgrade from your existing MOCAT-based projects.

```bash
$ find ./igc.demo.short
```

(continues on next page)
The whole script we will be using is there as well (process.ngl), so you can immediately run it with:

```
ngless process.ngl
```

The rest of this tutorial is an explanation of the steps in this script.

2. Preliminary imports

To run ngless, we need write a script. We start with a few imports:

```
ngless "0.7"
import "parallel" version "0.6"
import "mocat" version "0.0"
import "motus" version "0.1"
import "igc" version "0.0"
```

These will all be used in the tutorial.

3. Parallelization

We are going to process each sample separately. For this, we use the `lock1` function from the `parallel` module (which we imported before):

```
samples = readlines('igc.demo.short')
sample = lock1(samples)
```

The `readlines` function reads a file and returns all lines. In this case, we are reading the `tara.demo.short` file, which contains the three samples (`SAMEA2621229.sampled`, `SAMEA2621155.sampled`, and `SAMEA2621033.sampled`).

`lock1()` is a slightly more complex function. It takes a list and locks one of the elements and returns it. It always chooses an element which has not been locked before, so you each time you run `ngless`, you will get a different sample.

3. Preprocessing

First, we load the data (the FastQ files):

```
input = load_mocat_sample(sample)
```

And, now, we preprocess the data:

```
input = preprocess(input, keep_singles=False) using |read|:
    read = substrim(read, min_quality=25)
```

(continues on next page)
if len(read) < 45:
    discard

4. Filter against the human genome

We want to remove reads which map to the human genome, so we first map the reads to the human genome:

```python
mapped = map(input, reference='hg19')
```

hg19 is a built-in reference and the genome will be automatically download it the first time you use it. Now, we discard the matched reads:

```python
mr = mr.filter(min_match_size=45, min_identity_pc=90, action={unmatch})
```

The `mapped` object is a set of mapped reads (i.e., the same information that is saved in a SAM/BAM file). We use the `as_reads` function to get back to reads:

```python
input = as_reads(mapped)
```

Now, we will use the `input` object which has been filtered of human reads.

5. Profiling using the IGC

**Note:** This section of the tutorial uses the Integrated Gene Catalogue and requires ca. 15GiB of RAM. Skip to step 9 if your machine does not have this much memory.

After preprocessing, we map the reads to the integrated gene catalog:

```python
mapped = map(input, reference='igc', mode_all=True)
```

The line above is the reason we needed to import the `igc` module: it made the `igc` reference available.

Now, we need to count the results. This function takes the result of the above and aggregates it different ways. In this case, we want to aggregate by KEGG KOs, and eggNOG OGs:

```python
counts = count(mapped,
               features=['KEGG_ko', 'eggNOG_OG'],
               normalization={scaled})
```

7. Aggregate the results

We have done all this computation, now we need to save it somewhere. We will use the `collect()` function to aggregate across all the samples processed:

```python
collect(counts,
        current=sample,
        allneeded=samples,
        ofile='igc.profiles.txt')
```

9. Taxonomic profiling using mOTUS

Map the samples against the `motus` reference (this reference comes with the `motus` module we imported earlier):
mapped = map(input, reference='motus', mode_all=True)

Now call the built-in `count` function to summarize your reads at gene level:

counted = count(mapped, features=['gene'], multiple={dist1})

To get the final taxonomic profile, we call the `motus` function, which takes the gene count table and performs the motus quantification. The result of this call is another table, which we can concatenate with `collect()`:

motus_table = motus(counted)
collect(motus_table,
       current=sample,
       allneeded=samples,
       ofile='motus-counts.txt')

10. Run it!

This is our script. We save it to a file (`process.ngl` in this example) and run it from the command line:

```
$ ngless process.ngl
```

*Note: You need to run this script once for each sample.* However, this can be done in parallel, taking advantage of high performance computing clusters.

### 6.7.1 Full script

Here is the full script:

```
ngless "0.7"
import "parallel" version "0.6"
import "mocat" version "0.0"
import "motus" version "0.1"
import "igc" version "0.0"
samples = readlines('igc.demo.short')
sample = lock1(samples)
input = load_mocat_sample(sample)

input = preprocess(input, keep_singles=False) using |read|:
    read = substrim(read, min_quality=25)
    if len(read) < 45:
        discard

mapped = map(input, reference='hg19')

mapped = select(mapped) using |mr|:
    mr = mr.filter(min_match_size=45, min_identity_pc=90, action={unmatch})
    if mr.flag(mapped):
        discard

input = as_reads(mapped)
```

(continues on next page)
mapped = map(input, reference='igc', mode_all=True)
counts = count(mapped,
    features=['KEGG_ko', 'eggNOG_OG'],
    normalization={scaled})
collect(counts,
    current=sample,
    allneeded=samples,
    ofile='igc.profiles.txt')
mapped = map(input, reference='motus', mode_all=True)
counted = count(mapped, features=['gene'], multiple={dist1})

motus_table = motus(counted)
collect(motus_table,
    current=sample,
    allneeded=samples,
    ofile='motus-counts.txt')

6.8 Command line options

Running `ngless --help` will show you all the command line options. Here we describe the most important ones.

Most of the command line options can be set in a configuration file, which defaults to `~/.config/ngless.conf`, but you can set this explicitly:

`--config-file ARG` Configuration files to parse

The configuration section of the manual has more information on which options can be set in the configuration file. Whenever an option is set both in the config file and on the command line, then the command line will take priority.

Note that, like configuration files, command line options **do not change the results**. Any change in the results results from changing the NGLess script. Command line options change how the results are computed, not what they should be.

6.8.1 Using multiple threads

The main option is called `--j` and sets the number of threads.

`-j,--jobs,--threads ARG` Nr of threads to use

Using `--strict-threads/--no-strict-threads` controls whether this is a strict or soft upper limit.

--strict-threads strictly respect the --threads option (by default, NGLess will, occasionally, use more threads than specified) --no-strict-threads opposite of --strict-threads

6.8.2 Paths

NGLess can generate large temporary files. By default it uses the system’s temporary directory, but it is often a good idea to set it to a path with a lot of free disk space:
6.8.3 Debugging

A few options are useful for debugging:

- `--validate-only` Only validate input, do **not** run script
- `--subsample` Subsample mode: quickly test a pipeline by discarding 99% of the input
- `--trace` Set highest verbosity mode
- `--no-trace` opposite of `--trace`
- `--keep-temporary-files` Whether to keep temporary files (default **is** delete them)
- `--no-keep-temporary-files` opposite of `--keep-temporary-files`

6.8.4 QC Reporting

- `--create-report` create the report directory --no-create-report opposite of `--create-report`
- `--html-report-directory` ARG name of output directory

6.9 Command Line Wrappers

Some of the functionality of NGLess can also be accessed using traditional command-line scripts. These are written in Python and can be installed using Python package management tools:

```bash
pip install NGLessPy
```

All of the wrappers can install NGLess if passed the `--auto-install` flag.

All of these wrappers also have Common Workflow Language so that they can be used in larger pipelines.

6.9.1 ngless-install.py

*This is only supported on Linux*

Installs NGLess either for a single user (`$HOME/.local/bin/ngless`) or globally (`/usr/local/bin`). All the other tools in this package can also install NGLess automatically.

```bash
usage: ngless-install.py [-h] [-f] [-t TARGET] [-m {user,global}] [--verbose]

optional arguments:
  -h, --help           show this help message and exit
  -f, --force          Install NGLess even if it **is** already found
  -t TARGET, --target TARGET
```

(continues on next page)
6.9.2 ngless-count.py

This is the equivalent of calling the count function from within NGLess:

```bash
usage: ngless-count.py [-h] -i INPUT -o OUTPUT [-f FEATURES]
   [-m {dist1,all1,overN,unique_only}] [--auto-install]
   [--debug]
optional arguments:
  -h, --help           show this help message and exit
  -i INPUT, --input INPUT
  -o OUTPUT, --output OUTPUT
  -f FEATURES, --features FEATURES
  -m {dist1,all1,overN,unique_only}, --multiple {dist1,all1,overN,unique_only}
  --auto-install       Install NGLess if not found in PATH
  --debug              Prints the payload before submitting to ngless
```

6.9.3 ngless-map.py

This is the equivalent of calling the map function from within NGLess.

```bash
usage: ngless-map.py [-h] -i INPUT [-i2 INPUT_REVERSE] [-s INPUT_SINGLES] -o
   OUTPUT [--auto-install] [--debug]
   (--r {sacCer3,susScr11,ce10,dm3,gg4,canFam2,rn4,bosTau4,mm10,hg19}
   \rightarrow -f FASTA)
optional arguments:
  -h, --help           show this help message and exit
  -i INPUT, --input INPUT
  -i2 INPUT_REVERSE, --input-reverse INPUT_REVERSE
  -s INPUT_SINGLES, --input-singles INPUT_SINGLES
  -o OUTPUT, --output OUTPUT
  --auto-install       Install NGLess if not found in PATH
  --debug              Prints the payload before submitting to ngless
  --r {sacCer3,susScr11,ce10,dm3,gg4,canFam2,rn4,bosTau4,mm10,hg19}, --reference
  \rightarrow {sacCer3,susScr11,ce10,dm3,gg4,canFam2,rn4,bosTau4,mm10,hg19}
  Map against a built-in reference
  -f FASTA, --fasta FASTA
  Map against a given fasta file (will be indexed if index is not available)
```
6.9.4 ngless-mapstats.py

This is the equivalent of calling the mapstats function from within NGLess. This will take a SAM/BAM file as input and produce some simple statistics.

usage: ngless-mapstats.py [-h] -i INPUT -o OUTPUT [--auto-install] [--debug]

optional arguments:
  -h, --help show this help message and exit
  -i INPUT, --input INPUT SAM/BAM/CRAM file filter
  -o OUTPUT, --output OUTPUT Output file/path for results
  --auto-install Install NGLess if not found in PATH
  --debug Prints the payload before submitting to ngless

6.9.5 ngless-select.py

This is the equivalent of calling the select function from within NGLess:

usage: ngless-select.py [-h] -i INPUT -o OUTPUT -a {keep_if,drop_if} -c {mapped,unmapped,unique} [{mapped,unmapped,unique} ...] [--auto-install] [--debug]

optional arguments:
  -h, --help show this help message and exit
  -i INPUT, --input INPUT SAM/BAM/CRAM file filter
  -o OUTPUT, --output OUTPUT Output file/path for results
  -a {keep_if,drop_if}, --action {keep_if,drop_if} Whether to keep or drop when condition are met
  -c {mapped,unmapped,unique} [{mapped,unmapped,unique} ...], --conditions {mapped, unmapped, unique} [{mapped, unmapped, unique} ...] One or more conditions to filter on
  --auto-install Install NGLess if not found in PATH
  --debug Prints the payload before submitting to ngless

6.9.6 ngless-trim.py

This is equivalent of calling the preprocess function trimming the reads (with either substrim or endstrim depending on the arguments passed. Finally, any (trimmed) reads which are not of a minimum length are discard.

usage: ngless-trim.py [-h] -i INPUT -o OUTPUT -m {substrim,endstrim} -q MIN_QUALITY [-d DISCARD] [--auto-install] [--debug]

optional arguments:
  -h, --help show this help message and exit
  -i INPUT, --input INPUT FastQ file with reads to trim
  -o OUTPUT, --output OUTPUT Output file/path for results
  -m {substrim,endstrim}, --method {substrim,endstrim} (continues on next page)
Which trimming method to use
-q MIN_QUALITY, --min-quality MIN_QUALITY
Minimum quality value
-d DISCARD, --discard DISCARD
Discard if shorter than
--auto-install Install NGLess if not found in PATH
--debug Prints the payload before submitting to ngless

6.9.7 ngless-unique.py

This is the equivalent of calling the `count` function from within NGLess:

```

optional arguments:
  -h, --help      show this help message and exit
  -i INPUT, --input INPUT
                   FastQ file to filter
  -o OUTPUT, --output OUTPUT
                   Output file/path for results
  -c MAX_COPIES, --max-copies MAX_COPIES
                   Max number of duplicate copies to keep
  --auto-install  Install NGLess if not found in PATH
  --debug         Prints the payload before submitting to ngless
```

6.10 NGLess one liners

`ngless` can be used as a traditional command line transformer utility, using the `-e` argument to pass an inline script on the command line.

The `-p` (or `--print-last`) argument tells ngless to output the value of the last expression to `stdout`.

6.10.1 Converting a SAM file to a FASTQ file

```
$ ngless -pe 'as_reads(samfile("file.sam"))' > file.fq
```

This is equivalent to the full script:

```
ngless "0.8" # <- version declaration, optional on the command line
samcontents = samfile("file.sam") # <- load a SAM/BAM file
reads = as_reads(samcontents) # <- just get the reads (w quality scores)
write(reads, ofname=STDOUT) # <- write them to STDOUT (default format: FASTQ)
```

This only works if the data in the samfile is single ended as we pipe out a single FQ file. Otherwise, you can always do:

```
ngless "0.8"
write(as_read(samfile("file.sam")),
      ofile="output.fq")
```
which will write 3 files: output.1.fq, output.2.fq, and output.singles.fq (the first two for the paired-end reads and the last one for reads without a mate).

### 6.10.2 Getting aligned reads from a SAM file as FASTQ file

Building on the previous example. We can add a `select()` call to only output unmapped reads:

```bash
$ ngless -pe 'as_reads(select(samfile("file.sam"), keep_if=[{mapped}]))' > file.fq
```

This is equivalent to the full script:

```bash
ngless "0.8" # <- version declaration, optional on the command line
samcontents = samfile("file.sam") # <- load a SAM/BAM file
samcontents = select(samcontents, keep_if=[{mapped}]) # <- select only *mapped* reads
reads = as_reads(samcontents) # <- just get the reads (w quality scores)
write(reads, ofname=STDOUT) # <- write them to STDOUT (default format: FASTQ)
```

### 6.10.3 Reading from STDIN

For a true Unix-like utility, the input should be read from standard input. This can be achieved with the special file STDIN. So the previous example now reads:

```bash
$ cat file.sam | ngless -pe 'as_reads(select(samfile(STDIN), keep_if=[{mapped}]))' > _
       → file.fq
```

Obviously, this example would more interesting if the input were to come from another programme (not just `cat`).

### 6.11 Preprocessing FastQ Data

Preprocessing FastQ files consists of quality trimming and filtering of reads as well as (possible) elimination of reads which match some reference which is not of interest.

#### 6.11.1 Quality-based filtering

Filtering reads based on quality is performed with the `preprocess` function, which takes a block of code. This block of code will be executed for each read. For example:

```bash
ngless "0.8"
input = fastq('input.fq.gz')
input = preprocess(input) using |r|:
  r = substrim(r, min_quality=20)
  if len(r) < 45:
    discard
```

If it helps you, you can think of the `preprocess` block as a `foreach` loop, with the special keyword `discard` that removes the read from the collection. Note that the name `r` is just a variable name, which you choose using the `|r|` syntax.

Within the preprocess block, you can modify the read in several ways:
• you can trim it with the indexing operator: `r[trim5:]` or `r[:trim3]`

• you can call `substrim`, `endtrim` or `smoothtrim` to trim the read based on quality scores. `substrim` finds the longest substring such that all bases are above a minimum quality (hence the name, which phonetically combines substring and trim). `endtrim` chops bases off the ends and `smoothtrim` averages quality scores using a sliding window before applying `substrim`.

• you can test for the length of the sequence (before or after trimming). For this, you use the `len` function (see example above).

• you can test for the average quality score (using the `avg_quality()` method).

You can combine these in different ways. For example, the behaviour of the `fastx quality trimmer` can be recreated as:

```python
preprocess(input) using |r|:
    r = endtrim(r, min_quality=20)
    if r.fraction_at_least(20) < 0.5:
        discard
    if len(r) < 45:
        discard
```

### Handling paired end reads

When your input is paired-end, the `preprocess` call above will handle each mate independently. Three things can happen:

1. both mates are discarded,
2. both mates are kept (i.e., not discarded),
3. one mate is kept, the other discarded.

The only question is what to do in the third case. By default, the `preprocess` call keep the mate turning the read into an unpaired read (a single), but you can change that behaviour by setting the `keep_singles` argument to `False`:

```python
preprocess(input, keep_singles=False) using |r|:
    r = substrim(r, min_quality=20)
    if len(r) < 45:
        discard
```

Now, the output will consist of only paired-end reads.

### 6.11.2 Filtering reads matching a reference

It is often also a good idea to match reads against some possible contaminant database. For example, when studying the host associated microbiome, you will often want to remove reads matching the host. It is almost always a good to at least check for human contamination (during lab handling).

For this, you map the reads against the human genome:

```python
mapped_hg19 = map(input, reference='hg19')
```

Now, `mapped_hg19` is a set of mapped reads. Mapped reads are reads, their qualities, plus additional information of how they matched. Mapped read sets are the internal `ngless` representation of SAM files.

To filter the set, we will `select`. Like `preprocess`, `select` also uses a block for the user to specify the logic:
We first set a minimum match size and identity percentage to avoid spurious hits. **We keep the reads but unmatch** them (i.e., we clear any information related to a match). Then, we discard any reads that match by checking the flag \{mapped\}.

Finally, we convert the mapped reads back to simple reads using the `as_reads` function (this discards the matching information):

```python
input = as_reads(mapped_hg19)
```

Now, `input` can be passed to the next step in the pipeline.

### 6.12 NGLess Builtin Functions

These are the built-in NGLess functions. Make sure to check the standard library as well.

#### 6.12.1 fastq

Function to load a FastQ file:

```python
in = fastq('input.fq')
```

**Argument:**

String

**Return:**

ReadSet

**Arguments by value:**

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>encoding</td>
<td>Symbol ([auto], [33], [64], [sanger], [solexa])</td>
<td>no</td>
<td>{auto}</td>
</tr>
</tbody>
</table>

Possible values for `encoding` are:

- \{sanger\} or \{33\} assumes that the file is encoded using sanger format. This is appropriate for newer Illumina outputs.
- \{solexa\} or \{64\} assumes that the file is encoded with a 64 offset. This is used for older Illumina/Solexa machines.
- \{auto\}: use auto detection. This is the default.

When loading a data set, quality control is carried out and statistics can be visualised in a graphical user interface (GUI). Statistics calculated are:
• percentage of guanine and cytosine (%GC)
• number of sequences
• minimum/maximum sequence length
• mean, median, lower quartile and upper quality quartile for each sequence position

If not specified, the encoding is guessed from the file.

Gzip and bzip2 compressed files are transparently supported (determined by file extension, .gz and .bz2 for gzip and bzip2 respectively).

### 6.12.2 paired

Function to load a paired-end sample, from two FastQ files:

```plaintext
in = paired('input.1.fq', 'input.2.fq', singles='input.3.fq')
```

`paired()` is an exceptional function which takes two unnamed arguments, specifying the two read files (first mate and second mate) and an optional `singles` file (which contains unpaired reads).

**Argument:**

String, String

**Return:**

ReadSet

**Arguments by value:**

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>encoding</td>
<td>Symbol (<code>{auto}</code>, <code>{33}</code>, <code>{64}</code>, <code>{sanger}</code>, <code>{solexa}</code>)</td>
<td>no</td>
<td><code>{auto}</code></td>
</tr>
<tr>
<td>singles</td>
<td>String</td>
<td>no</td>
<td><code>•</code></td>
</tr>
</tbody>
</table>

The `encoding` argument has the same meaning as for the `fastq()` function:

- `{sanger}` or `{33}` assumes that the file is encoded using sanger format. This is appropriate for newer Illumina outputs.
- `{solexa}` or `{64}` assumes that the file is encoded with a 64 offset. This is used for older Illumina/Solexa machines.
- `{auto}`: use auto detection. This is the default.

### 6.12.3 group

Groups a list of ReadSet objects into a single ReadSet:
rs1 = paired('data0.1.fq.gz', 'data0.2.fq.gz')
rs2 = paired('data1.1.fq.gz', 'data1.2.fq.gz')
rs = group([rs1, rs2], name='input')

**Arguments by value:**

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td>String</td>
<td>no</td>
<td></td>
</tr>
</tbody>
</table>

**Argument**

List of ReadSet

**Returns**

ReadSet

### 6.12.4 samfile

Loads a SAM file:

s = samfile('input.sam')

This function takes no keyword arguments. BAM files are also supported (determined by the filename), as are sam.gz files.

**Returns**

MappedReadSet

**Arguments by value:**

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>name</td>
<td>String</td>
<td>no</td>
<td></td>
</tr>
<tr>
<td>header</td>
<td>String</td>
<td>no</td>
<td></td>
</tr>
</tbody>
</table>

New in version 0.7: The header argument was added in version 0.7

- The name argument names the group (for count(), for example).
- The headers argument can be used if the SAM headers are kept in a separate file.
6.12.5 qcstats

New in version 0.6: This functionality was not available prior to 0.6
Returns the auto-computed statistics:

```python
write(qcstats({fastq}), ofile='fqstats.txt')
```

**Returns**
CountsTable

**Argument**

{fastq}: FastQ statistics {mapping}: Mapping statistics

6.12.6 countfile

Loads a TSV file:

```python
c = countfile('table.tsv')
```

This function takes no keyword arguments. If the filename ends with “.gz”, it is assumed to be a gzipped file.

**Returns**
CountTable

6.12.7 as_reads

Converts from a MappedReadSet to a ReadSet:

```python
reads = as_reads(samfile('input.sam'))
```

6.12.8 unique

Function that given a set of reads, returns another which only retains a set number of copies of each read (if there are any duplicates). An example:

```python
input = unique(input, max_copies=3)
```

**Argument:**

ReadSet

**Return:**

ReadSet
Arguments by value:

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>max_copies</td>
<td>Integer</td>
<td>no</td>
<td>2</td>
</tr>
</tbody>
</table>

The optional argument **max_copies** allows to define the number of tolerated copies (default: 2).

Two short reads with the same nucleotide sequence are considered copies, independently of quality and identifiers.

This function is currently limited to single-end samples.

### 6.12.9 preprocess

This function executes the given block for each read in the ReadSet. Unless the read is **discarded**, it is transferred (after transformations) to the output. For example:

```python
inputs = preprocess(inputs) using |read|:
    read = read[3:]
```

**Argument:**

ReadSet

**Return:**

ReadSet

Arguments by value:

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>keep_singles</td>
<td>bool</td>
<td>no</td>
<td>true</td>
</tr>
</tbody>
</table>

When a paired-end input is being preprocessed in single-mode (i.e., each mate is preprocessed independently, it can happen that on eof the mates is discarded, while the other is kept). The default is to collect these into the singles pile. If **keep_singles** if false, however, they are discarded.

This function also performs quality control on its output.

### 6.12.10 map

The function map, maps a ReadSet to reference. For example:

```python
mapped = map(input, reference='sacCer3')
mapped = map(input, fafile='ref.fa')
```

**Argument:**

ReadSet
Return:

MappedReadSet

Arguments by value:

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>reference</td>
<td>String</td>
<td>no</td>
<td></td>
</tr>
<tr>
<td>fafile</td>
<td>String</td>
<td>no</td>
<td></td>
</tr>
<tr>
<td>block_size_megabases</td>
<td>Integer</td>
<td>no</td>
<td></td>
</tr>
<tr>
<td>mode_all</td>
<td>Bool</td>
<td>no</td>
<td></td>
</tr>
</tbody>
</table>

The user must provide either a path to a FASTA file in the fafile argument or the name of a built-in reference using the reference argument. The fafile argument supports search path expansion.

A list of datasets provided by NGLess can be found at Available Reference Genomes.

To use any of these, pass in the name as the reference value:

```python
mapped_hg19 = map(input, reference='hg19')
```

NGLess does not ship with any of these datasets, but they are downloaded lazily: i.e., the first time you use them, NGLess will download and cache them. NGLess will also index any database used the first time it is used.

The option `block_size_megabases` turns on low memory mode (see the corresponding section in the mapping documentation).

The option `mode_all=True` can be passed to include all alignments of both single and paired-end reads in the output SAM/BAM.

### 6.12.11 mapstats

Computes some basic statistics from a set of mapped reads (number of reads, number mapped, number uniquely mapped).

**Argument**

MappedReadSet

**Return**

CountTable
6.12.12 select

select filters a MappedReadSet. For example:

\[
\text{mapped} = \text{select} \{\text{mapped}, \text{keep}_\text{if}=[\{\text{mapped}\}]\}
\]

**Argument:**

MappedReadSet

**Return:**

MappedReadSet

**Arguments by value:**

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>keep_if</td>
<td>[Symbol]</td>
<td>no</td>
<td>•</td>
</tr>
<tr>
<td>drop_if</td>
<td>[Symbol]</td>
<td>no</td>
<td>•</td>
</tr>
<tr>
<td>paired</td>
<td>Bool</td>
<td>no</td>
<td>true</td>
</tr>
</tbody>
</table>

At least one of keep_if or drop_if should be passed, but not both. They accept the following symbols:

- {mapped}: the read mapped
- {unmapped}: the read did not map
- {unique}: the read mapped to a unique location

If keep_if is used, then reads are kept if they pass all the conditions. If drop_if they are discarded if they fail to any condition.

By default, select operates on a paired-end read as a whole. If paired=False is passed, however, then link between the two mates is not considered and each read is processed independently.

6.12.13 count

Given a file with aligned sequencing reads (ReadSet), count() will produce a counts table depending on the arguments passed. For example:

\[
\text{counts} = \text{count} \{\text{mapped}, \text{min}=2, \text{mode}=\text{union}, \text{multiple}=\{\text{dist1}\}\}
\]

**Argument:**

MappedReadSet
Return:

CountTable

Arguments by value:

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default value</th>
</tr>
</thead>
<tbody>
<tr>
<td>gff_file</td>
<td>String</td>
<td>no*</td>
<td></td>
</tr>
<tr>
<td>functional_map</td>
<td>String</td>
<td>no*</td>
<td></td>
</tr>
<tr>
<td>features</td>
<td>[ String ]</td>
<td>no</td>
<td>'gene'</td>
</tr>
<tr>
<td>subfeatures</td>
<td>[ String ]</td>
<td>no</td>
<td></td>
</tr>
<tr>
<td>mode</td>
<td>Symbol</td>
<td>no</td>
<td>{union}</td>
</tr>
<tr>
<td>multiple</td>
<td>Symbol</td>
<td>no</td>
<td>{dist1}</td>
</tr>
<tr>
<td>strand</td>
<td>Bool</td>
<td>no</td>
<td>false</td>
</tr>
<tr>
<td>normalization</td>
<td>Symbol</td>
<td>no</td>
<td>{raw}</td>
</tr>
<tr>
<td>include_minus1</td>
<td>Bool</td>
<td>no</td>
<td>true</td>
</tr>
<tr>
<td>min</td>
<td>Integer</td>
<td>no</td>
<td>0</td>
</tr>
<tr>
<td>discard_zeros</td>
<td>Bool</td>
<td>no</td>
<td>false</td>
</tr>
<tr>
<td>reference</td>
<td>String</td>
<td>no</td>
<td></td>
</tr>
</tbody>
</table>

If the features to count are ["seqname"], then each read will be assigned to the name of reference it matched and only an input set of mapped reads is necessary. For other features, you will need extra information. This can be passed using the gff_file or functional_map arguments. If you had previously used a reference argument for the map() function, then you can also leave this argument empty and NGLess will use the corresponding annotation file.

The gff_file and functional_map arguments support search path expansion.

features: which features to count. If a GFF file is used, this refers to the “features” field.

subfeatures: this is useful in GFF-mode as the same feature can encode multiple attributes (or, in NGLess parlance, “subfeatures”). By default, NGLess will look for the "ID" or "gene_id" attributes.

mode indicates how to handle reads that (partially) overlap one or more features. Possible values for mode are {union},{intersection_non_empty} and {intersection_strict} (default: {union}). For every position of a mapped read, collect all features into a set. These sets of features are then handled in different modes.

• {union} the union of all the sets. A read is counted for every feature it overlaps.

• {intersection_non_empty} the intersection of all non-empty sets. A read is only counted for features it exclusively overlaps, even if partially.

• {intersection_strict} the intersection of all the sets. A read is only counted if the entire read overlaps the same feature(s).

Consider the following illustration of the effect of different mode options:

(continues on next page)
How to handle multiple mappers (inserts which have more than one “hit” in the reference) is defined by the `multiple` argument:

- `{unique_only}`: only use uniquely mapped inserts
- `{all1}`: count all hits separately. An insert mapping to 4 locations adds 1 to each location
- `{1overN}`: fractionally distribute multiple mappers. An insert mapping to 4 locations adds 0.25 to each location
- `{dist1}`: distribute multiple reads based on uniquely mapped reads. An insert mapping to 4 locations adds to these in proportion to how uniquely mapped inserts are distributed among these 4 locations.

Argument `strand` represents whether the data are from a strand-specific (default is `false`). When the data is not strand-specific, a read is always overlapping with a feature independently of whether maps to the same or the opposite strand. For strand-specific data, the read has to be mapped to the same strand as the feature.

`min` defines the minimum amount of overlaps a given feature must have, at least, to be kept (default: 0, i.e., keep all counts). If you just want to discard features that are exactly zero, you should set the `discard_zeros` argument to `True`.

`normalization` specifies if and how to normalize to take into account feature size:

- `{raw}` (default) is no normalization
- `{normed}` is the result of the `{raw}` mode divided by the size of the feature
- `{scaled}` is the result of the `{normed}` mode scaled up so that the total number of counts is identical to the `{raw}` (within rounding error)

Unmapped inserts are included in the output if `{include_minus1}` is true (default: `False`). New in version 0.6: Before version 0.6, the default was to not include the -1 fraction.

### 6.12.14 substrim

Given a read finds the longest substring, such that all bases are of at least the given quality. The name is a construction of “substring trim”. For example:

```python
read = substrim(read, min_quality=25)
```

**Argument:**

- `ShortRead`
Return:

ShortRead

Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>min_quality</td>
<td>Integer</td>
<td>yes</td>
<td></td>
</tr>
</tbody>
</table>

min_quality parameter defines the minimum quality accepted.

### 6.12.15 endtrim

Given a read, trim from both ends (5’ and 3’) all bases below a minimal quality. For example:

```python
read = endtrim(read, min_quality=25)
```

**Argument:**

ShortRead

**Return:**

ShortRead

Arguments

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>min_quality</td>
<td>Integer</td>
<td>yes</td>
<td></td>
</tr>
</tbody>
</table>

min_quality parameter defines the minimum quality value.

### 6.12.16 smoothtrim

This trims with the same algorithm as subtrim but uses a sliding window to average base qualities. For example:

```python
read = smoothtrim(read, min_quality=15, window=4)
```

Quality values of bases at the edges of each read are repeated to allow averaging with quality centered on each base. For instance a read:

<table>
<thead>
<tr>
<th>Sequence</th>
<th>A T C G</th>
<th>with a window</th>
<th>A A T C G G</th>
</tr>
</thead>
<tbody>
<tr>
<td>Quality</td>
<td>28 25 14 12</td>
<td>of size 3 becomes</td>
<td>28 28 25 14 12 12</td>
</tr>
</tbody>
</table>

and is smoothed:
at which point `substrim` is applied for trimming.

Quality scores are returned to their original value after trimming.

**Argument:**

ShortRead

**Return:**

ShortRead

**Arguments**

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>min_quality</td>
<td>Integer</td>
<td>yes</td>
<td></td>
</tr>
<tr>
<td>window</td>
<td>Integer</td>
<td>yes</td>
<td></td>
</tr>
</tbody>
</table>

`min_quality` parameter defines the minimum quality accepted for the sub-sequence. `window` parameter defines the number of bases to average over.

**6.12.17 write**

Writes an object to disk.

**ReadSet**

**Argument:**

Any

**Return:**

Void
Arguments by value:

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>ofile</td>
<td>String</td>
<td>yes</td>
<td>yes</td>
</tr>
<tr>
<td>format</td>
<td>String</td>
<td>no</td>
<td>yes</td>
</tr>
</tbody>
</table>

The argument `ofile` is where to write the content.

The output format is typically determined from the `ofile` extension, but the `format` argument overrides this. Supported formats:

- CountsTable: `{tsv}` (default) or `{csv}`: use TAB or COMMA as a delimiter
- MappedReadSet: `{sam}` (default) or `{bam}
- ReadSet: FastQ format, optionally compressed (depending on the extension).

6.12.18 print

Print function allows to print a NGLessObject to IO.

**Argument:**

NGLessObject

**Return:**

Void

Arguments by value:

none

6.12.19 readlines

Reads a text file and returns a list with all the strings in the file

**Argument**

string: the filename
Example

`readlines` is useful in combination with the `parallel` module, where you can then use the `lock1` function to process a large set of inputs:

```python
sample = lock1(readlines('samplelist.txt'))
```

6.12.20 assemble

assemble

Implementation

`assemble()` uses the MEGAHIT assembler.

Arguments

ReadSet

Returns

string : generated file

Arguments by value:

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>__extra_megahit_arg</code></td>
<td>List of str</td>
<td>no</td>
<td>[]</td>
</tr>
</tbody>
</table>

`__extra_megahit_arg` is passed directly to megahit with no checking.

6.12.21 orf_find

`orf_find` finds open reading frames (ORFs) in a sequence set:

```python
contigs = assemble(input)
orf = select(contigs, is_metagenome=True)
```

Argument:

SequenceSet

Return:

SequenceSet
Arguments by value:

<table>
<thead>
<tr>
<th>Name</th>
<th>Type</th>
<th>Required</th>
<th>Default Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>is_metagenome</td>
<td>Bool</td>
<td>yes</td>
<td></td>
</tr>
<tr>
<td>coords_out</td>
<td>FilePath</td>
<td>no</td>
<td></td>
</tr>
<tr>
<td>prots_out</td>
<td>FilePath</td>
<td>no</td>
<td></td>
</tr>
</tbody>
</table>

Implementation

NGLess uses Prodigal as the underlying gene finder.

6.13 Methods

Methods are invoked using an object-oriented syntax. For example:

```python
mapped = select(mapped) using |mr|:
    mr = mr.pe_filter()
```

They can also take arguments:

```python
mapped = select(mapped) using |mr|:
    mr = mr.filter(min_match_size=30)
```

6.13.1 Short reads

Short reads have the following methods:

- `avg_quality()`: the average quality (as a double)
- `fraction_at_least(q)`: the fraction of bases of quality greater or equal to `q`
- `n_to_zero_quality()`: transform the quality scores so that any `N` (or `n`) bases in the sequence get a quality of zero.

6.13.2 Mapped reads

Mapped reads contain several methods. *None of these methods changes its argument, they return new values.* The typical approach is to reassign the result to the same variable as before (see examples above).

- `pe_filter`: only matches where both mates match are kept.
- `flag`: Takes one of `{mapped}` or `{unmapped}` and returns true if the reads were mapped (in a paired-end setting, a read is considered mapped if at least one of the mates mapped).
- `some_match`: Takes a reference name and returns True if the read mapped to that reference name.
• **allbest**: eliminates matches that are not as good as the best. For NGLess, the number of errors (given by the **NM** field) divided by the length of the longest match is the fractional distance of a match. Thus, a match with 3 errors over 100 bp is considered better than a match with 0 errors over 90bps.

**filter**

`filter` takes a mapped read and returns a mapped read according to several criteria:

- **min_match_size**: minimum match size
- **min_identity_pc**: minimum percent identity (considered over the matching location, trimming on the left and right are excluded).
- **max_trim**: maximum number of bases trimmed off the ends. Use 0 to specify only global matches.

If more than one test is specified, then they are combined with the AND operation (i.e., all conditions have to be fulfilled for the test to be true).

The default is to discard mappings that do not pass the test, but it can be changed with the **action** argument, which must be one of {drop} (default: the read is excluded from the output), or {unmatch} (the read is changed so that it no longer reports matching).

You can pass the flag **reverse** (i.e., `reverse=True`) to reverse the sign of the test.

### 6.14 Standard library

#### 6.14.1 Parallel module

This module allows you to run several parallel computations. It provides two functions: `lock1` and `collect`.

`lock1` :: [string] -> string takes a list of strings and returns a single element. It uses the filesystem to obtain a lock file so that if multiple processes are running at once, each one will return a different element. Ngless also marks results as `finished` once you have run a script to completion.

The intended usage is that you simply run as many processes as inputs that you have and ngless will figure everything out.

For example:

```bash
ngless "0.6"
import "parallel" version "0.6"
samples = ['Sample1', 'Sample2', 'Sample3']
current = lock1(samples)
```

Now, current will be one of 'Sample1', 'Sample2', or 'Sample3'. You can use this to find your input data:

```bash
input = paired("data/" + current + ".1.fq.gz", "data/" + current + ".2.fq.gz")
```

Often, it’s a good idea to combine `lock1` with `readlines` (a function which returns the contents of all the non-empty lines in a file as a list of strings):

```bash
samples = readlines('samples.txt')
current = lock1(samples)
input = paired("data/" + current + ".1.fq.gz", "data/" + current + ".2.fq.gz")
```

You now use `input` as in any other ngless script:
mapped = map(input, reference='hg19')
write(input, ofile='outputs/'+current+ '.bam')
counts = count(mapped)
write(counts, ofile='outputs/'+current+ '.txt')

This will result in both BAM files and counts being written to the outputs/ directory. The module also adds the collect function which can paste all the counts together into a single table, for convenience:

collect(
    counts,
    current=current,
    allneeded=samples,
    ofile='outputs/counts.txt.gz')

Now, only when all the samples in the allneeded argument have been processed, does ngless collect all the results into a single table.

**Full “parallel” example**

```python
ngless "0.8"
import "parallel" version "0.6"

sample = lock1(readlines('input.txt'))
input = fastq(sample)
mapped = map(input, reference='hg19')
collect(count(mapped, features=['seqname']),
    current=sample,
    allneeded=readlines('input.txt'),
    ofile='output.tsv')
```

Now, you can run multiple ngless jobs in parallel and each will work on a different line of input.txt.

**Parallel internals**

Normally this should be invisible to you, but if you are curious or want to debug an issue, here are the gory details:

The function lock1() will create a lock file in a sub-directory of ngless-locks. This directory will be named by the hash value of the script. Thus, any change to the script will force all data to be recomputed. This can lead to over-computation but it ensures that you will always have the most up to date results (ngless’ first priority is correctness, performance is important, but not at the risk of correctness). Similarly, collect() will use hashed values which encode both the script and the position within the script (so that if you have more than one collect() call, they will not clash).

Lock files have their modification times updated once every 10 minutes while NGLess is running. This allows the programme to easily identify stale files. The software is very conservative, but any lock file with a modification time older than one hour is considered stale and removed. Note that because NGLess will write always create its outputs atomically, the worst that can happen from mis-identifying a stale lock (for example, you had a compute node which lost network connectivity, but it comes back online after an hour and resumes processing) is that extra computation is wasted, the processes will never interfere in a way that you get erroneous results.

### 6.14.2 Samtools module

This module exposes two samtools functionalities: sorting (samtools_sort) and selecting reads in regions of interest (samtools_view).
import "samtools" version "0.0"
input = samfile('input.bam')
sam_regions = samtools_view(input, bed_file="interesting_regions.bed")
write(sam_regions, ofile='interesting.sam')

```
samtools_view :: mappedreadset -> mappedreadset
returns a subset of the mapped reads that overlap with the regions specified in the BED file.
```

import "samtools" version "0.0"
to_sort = samfile('input.bam')
name_sorted = samtools_sort(to_sort, by=(name))
write(name_sorted, ofile='input.name_sorted.bam')

```
samtools_sort :: mappedreadset -> mappedreadset
returns a sorted version of the dataset.
```

Internally, both function call ngless’ version of samtools while respecting your settings for the use of threads and temporary disk space. When combined with other functionality, ngless can also often stream data into/from samtools instead of relying on intermediate files (these optimizations should not change the visible behaviour, only make the computation faster).

### 6.14.3 Mocat module

import "mocat" version "0.6"

This is a MOCAT compatibility layer to make it easier to adapt projects from MOCAT to ngless.

**Functions**

load_mocat_sample :: string -> readset
this function takes a directory name and returns a set of reads by scanning the directory for (compressed) FastQ files. This is slightly more flexible than MOCAT2 in terms of the patterns in matches. In particular, the following extensions are accepted:

- fq
- fq.gz
- fq.bz2
- fastq
- fastq.gz
- fastq.bz2

Paired-end reads are assumed to be split into two files, with matching names with .1/_2 appended. _1/_2 as is used by the European Nucleotide Archive (ENA) is also accepted.

coord_file_to_gtf :: string -> string
this function takes a MOCAT-style .coord, converts it internally to a GTF file and returns it.

Example usage:
ngless "0.6"
import "mocat" version "0.6"

sample = load_mocat_sample('Sample1')
mapped = map(sampled, fafile='data/catalog.padded.fna')
write(count(mapped, gff_file=coord_file_to_gtf('data/catalog.padded.coord')), ofile='counts.txt')

This module can be combined with the parallel module (see above) to obtain a very smooth upgrade from MOCAT to ngless.

6.15 Modules

To add a module to ngless there are two options: external or internal modules. External modules are the simplest option.

6.15.1 External modules

External modules can perform two tasks:

1. Add new references to ngless
2. Add functions to ngless

Adding references makes them available to the `map()` call using the `reference` argument and (optionally) allows for calls to `count()` without specifying any annotation file.

Like everything else in ngless, these are versioned for reproducibility so that the resulting script implicitly encodes the exact version of the databases used.

Functions in external modules map to command line calls to a script you provide.

6.15.2 How to define an external module

You can use the example module in the ngless source for inspiration. That is a complete, functional module.

A module is defined by an YaML file.

Every module has a name and a version:

```
name: 'module'
version: '0.0.0'
```

Everything else is optional.

References

References are added with a `references` section, which is a list of references. A reference contains a `fasta-file` and (optionally) a `gtf-file`. For example:

```
references:
  - name: 'ref'
```

(continues on next page)
Note that the paths are relative to the module directory. The GTF file may be gzipped.

**Initialization**

An `init` section defines an initialization command. This will be run **before** anything else in any script which imports this module. The intention is that the module can check for any dependencies and provide the user with an early error message instead of failing later after. For example:

```yaml
init:
  init_cmd: './init.sh'
  init_args:
    - "Hello"
    - "World"
```

will cause ngless to run the command `./init.sh Hello World` whenever a user imports the module.

**A note about paths:** paths you define in the module.yaml file are **relative to the Yaml file itself**. Thus you put all the necessary scripts and data in the module directory. However, the scripts are run with the current working directory of wherever the user is running the ngless protocol (so that any relative paths that the user specifies work as expected). To find your data files inside your module, ngless sets the environmental variable `NGLESS_MODULE_DIR` as the path to the module directory.

**Functions**

To add new functions, use a `functions` section, which should contain a list of functions encoded in YaML format. Each function has a few required arguments:

- `nglName` the name by which the function will be called **inside** of an ngless script.
- `arg0` the script to call for this function. Note that the user will never see this.

For example:

```yaml
functions:
  -
    nglName: "test"
    arg0: ".:/run-test.sh"
```

will enable the user to call a function `test()` which will translate into a call to the `run-test.sh` script (see the note above about paths).

You can also add arguments to your function, naturally. Remember that ngless functions can have only one unnamed argument and any number of named arguments. To specify the unnamed argument add a `arg1` section, with the key `atype` (argument type):  

```yaml
arg1:
  atype: <one of 'readset'/ 'mappedreadset'/ 'counts'/ 'str'/ 'flag'/ 'int'/ 'option'>
```

The arguments of type `readset`, `mappedreadset`, and `counts` are passed as paths to a file on disk. **Your command is assumed to not change these, but make a copy if necessary. Bad things will happen if you change the files.** You can specify more details on which kind of file you expect with the following optional arguments:
The flags can_gzip/can_bzip2 indicate whether your script can accept compressed files (default: False). can_stream indicates whether the input can be a pipe (default: False, which means that an intermediate file will always be used).

For example, if your tool wants a SAM file (and never a BAM file), you can write:

```
arg1:
  atype: mappedreadset
  filetype: sam
```

ngless will ensure that your tool does receive a SAM file (including converting BAM to SAM if necessary).

Finally, additional argument are specified by a list called additional. Entries in this list have exactly the same format as the arg1 entry, except that they have a few extra fields. The extra field name is mandatory, while everything else is optional:

```
additional:
  -
    name: <name>
    atype: <as for arg1: 'readset'/mappedreadset'/...>
    def: <default value>
    required: true/false
```

Arguments of type flag have an optional extra argument, when-true which is a list of strings which will be passed as extra arguments when the flag is true. You can also just specify a single string. If when-true is missing, ngless will pass an option of the form --name (i.e., a double-dash then the name used). For example:

```
additional:
  -
    name: verbose
    atype: flag
    def: false
    when-true: "-v"
  -
    name: complete
    atype: flag
    def: false
    when-true:
      - "--output=complete"
      - "--no-filter"
```

All other argument types are passed to your script using the syntax --name=value if they are present or if a default has been provided.

Arguments of type option map to symbols in ngless and require you to add an additional field allowed specifying the universe of allowed symbols. Ngless will check that the user specifies arguments from the allowable universe. For example:

```
additional:
  -
    atype: 'option'
    name: 'verbosity'
```
def: 'quiet'
allowed:
    - 'quiet'
    - 'normal'
    - 'loud'

If you do not have a fixed universe for your argument, then it should be a str argument.

The required flag determines whether the argument is required. Note that arguments with a default argument are automatically optional (ngless may trigger a warning if you mark an argument with a default as required).

To return a value, you must request that ngless generate a new temporary file for the script to generate output to. Therefore, you need to specify a return section, with three parameters: rtype (return type, see below), name the name of the argument to use, and extension the file extension of the output type.

```python
return:
    rtype: "counts"
    name: "ofile"
    extension: "sam"
```

rtype must be one of "void", "counts", "readset", or "mappedreadset".

If you plan to make use of search path expansion, in order for NGLess to expand the argument prior to passing it to the external module you need to set atype: "str" and expand_searchpath: true.

```python
additional:
    - atype: 'str'
      name: 'reference'
      expand_searchpath: true
```

### Citation

Finally, if you wish to, you can add one or more citations:

```python
citation: "A paper which you want to be listed when users import your module"
```

This will be printed out whenever users use your module and thus will help you get exposure.

If you have more than one citation, you can use the citations key and provide a list:

```python
citations:
    - "Paper 1"
    - "Paper 2"
```

### 6.15.3 Internal Modules

This is very advanced as it requires writing Haskell code which can then interact very deeply with the rest of ngless.

For an example, you can look at the example internal module. If you want to get started, you can ask about details on the ngless user mailing list.
6.16 NGLess Constants

In NGLess, any variable written in uppercase is a constant, i.e., can only be assigned to once. In addition, there are builtin constants defined by NGLess.

6.16.1 Built in constants

- ARGV
  This is string array which contains the arguments passed to the script

- STDIN
  Use in place of a filename to read from standard input

- STDOUT
  Use in place of a filename to write to standard output

For example:

```plaintext
ngless '0.9'

input = samfile(STDIN)
input = select(input) using |mr|:
  if mr.flag({mapped}):
    discard
write(input, ofile=STDOUT, format={bam})
```

This file reads a sam stream from stdin, filters it (using the `select` call) and writes to standard output in `bam` format.

6.17 Available Reference Genomes

NGLess provides builtin support for the most widely used model organisms (human, mouse, yeast, C. elegans, ...; see the full table below). This makes it easier to use the tool when using these organisms as some knowledge is already built in.

6.17.1 Genome references available

NGLess provides archives containing data sets of organisms. Is also provided gene annotations that provide information about protein-coding and non-coding genes, splice variants, cDNA and protein sequences, non-coding RNAs.

The following table represents organisms provided by default:
<table>
<thead>
<tr>
<th>Name</th>
<th>Description</th>
<th>Assembly</th>
<th>Ensembl</th>
</tr>
</thead>
<tbody>
<tr>
<td>bosTau4</td>
<td>bos_taurus</td>
<td>UMD3.1</td>
<td>75</td>
</tr>
<tr>
<td>ce10</td>
<td>caenorhabditis_elegans</td>
<td>WBCel235</td>
<td>75</td>
</tr>
<tr>
<td>canFam3</td>
<td>canis_familiaris</td>
<td>CanFam3.1</td>
<td>75</td>
</tr>
<tr>
<td>dm6</td>
<td>drosophila_melanogaster</td>
<td>BDGP6</td>
<td>90</td>
</tr>
<tr>
<td>dm5</td>
<td>drosophila_melanogaster</td>
<td>BDGP5</td>
<td>75</td>
</tr>
<tr>
<td>gg5</td>
<td>gallus_gallus</td>
<td>Gallus_gallus-5.0</td>
<td>90</td>
</tr>
<tr>
<td>gg4</td>
<td>gallus_gallus</td>
<td>GalGal4</td>
<td>75</td>
</tr>
<tr>
<td>hg38.p10</td>
<td>homo_sapiens</td>
<td>GRCh38.p10</td>
<td>90</td>
</tr>
<tr>
<td>hg38.p7</td>
<td>homo_sapiens</td>
<td>GRCh38.p7</td>
<td>85</td>
</tr>
<tr>
<td>hg19</td>
<td>homo_sapiens</td>
<td>GRCh37</td>
<td>75</td>
</tr>
<tr>
<td>mm10.p5</td>
<td>mus_musculus</td>
<td>GRCm38.p5</td>
<td>90</td>
</tr>
<tr>
<td>mm10.p2</td>
<td>mus_musculus</td>
<td>GRCm38.p2</td>
<td>75</td>
</tr>
<tr>
<td>rn6</td>
<td>rattus_norvegicus</td>
<td>Rnor_6.0</td>
<td>90</td>
</tr>
<tr>
<td>rn5</td>
<td>rattus_norvegicus</td>
<td>Rnor_5.0</td>
<td>75</td>
</tr>
<tr>
<td>sacCer3</td>
<td>saccharomyces_cerevisiae</td>
<td>R64-1-1</td>
<td>75</td>
</tr>
<tr>
<td>susScr11</td>
<td>sus_scrofa</td>
<td>Sscrofa11.1</td>
<td>90</td>
</tr>
</tbody>
</table>

These archives are all created using versions 75, 85 and 90 of Ensembl.

### 6.17.2 Automatic installation

The built-in datasets are downloaded the first time they are used. They are downloaded to the user home directory and stored in `home/.ngless/genomes`.

### 6.17.3 Manual installation

It is possible to install data sets locally, before running any script. They can be installed in **User** mode or in **Root** mode.

To install locally (organism bos taurus), use the following command:

```bash
$ ngless --install-reference-data bosTau4
```

If you install as a super-user, then the dataset will be available for all users:

```bash
$ sudo ngless --install-reference-data bosTau4
```

When attempting to install an organism if is returned **True** it means that the organism is already installed, and there is no reason to install again. Otherwise, a progress bar is displayed to provide information on the download.

### 6.17.4 Data Set Structure

This section provides the technical details necessary if you wish to build your own reference for others to use automatically. For most users, it will likely be easier to directly specify the references in the ngless script.

The archives provided by NGLess contain BWA index files, the genome reference file and a gene annotation file.

```
Name.tar.gz
   ├── Sequence
   │   └──
```

(continues on next page)
The basename of Description.tar.gz (Description) will have the description name of the respective organism (i.e, Mus_musculus.tar.gz).

### 6.18 Taxonomic profiling using mOTUs with ngless

You can use ngless to compute mOTU profiles. This requires the use of the (standard) motus module:

```bash
ngless "0.8"
import "motus" version "0.1"
```

This module (with the motus database) will be downloaded the first time you use it.

You can use all the ngless functionality to load and preprocess your data:

```python
input = paired('input.1.fq.gz', 'input.2.fq.gz')
files = preprocess(input, keep_singles=False) using |read|:
    read = substrim(read, min_quality=25)
    if len(read) < 45:
        discard
```

Producing the motus tables is done in three steps.

1. Map the samples against the motus reference (this reference comes with the motus module we imported earlier):

   ```python
   mapped = map(files, reference='motus', mode_all=True)
   ```

2. call the built-in count function to summarize your reads at gene level, optionally adding include_minus1=true if you want to also obtain the fraction of unknown reads (-1). This is the default behavior from version 0.6 onwards:

   ```python
   counted = count(mapped, features=\['gene\'], multiple={dist1})
   ```

3. call the motus function, which takes the gene count table and performs the motus quantification. The result of this call is another table, which can then be written out with the standard write call:

   ```python
   table = motus(counted)
   write(table, ofile='motus-counts.txt')
   ```

This function is the only special function introduced by the motus module, everything else is standard ngless.

You can see a full worked out example in the examples/motus.ngl recipe.
6.19 Configuration

Note: ngless’ results do not change because of configuration or command line options. The ngless script always has complete information on what is computed. What configuration options change are details of how the results are computed such as where to store intermediate files and how many CPU cores to use.

Ngless gets its configuration options from the following sources:

1. Defaults/auto-configuration
2. A global configuration file
3. A user configuration file (typically $HOME/.config/ngless.conf)
4. A configuration file present in the current directory'
5. A configuration file specified on the command line
6. Command line options

In case an option is specified more than once, the order above determines priority: later options take precedence.

6.19.1 Configuration file format

NGLess configuration files are text files using assignment syntax. Here is a simple example, setting the temporary directory and enabling auto-detection of the number of threads:

```
temporary-directory = "/local/ngless-temp/
jobs = "auto"
```

6.19.2 Options

jobs: number of CPUs to use. You can use the keyword auto to attempt auto-detection (see below).

strict-threads: by default, NGLess will, in certain conditions, use more CPUs than specified by the jobs argument (in bursts of activity). This happens, for example, when it calls an external short-read-mapper (such as bwa). By default, it will pass the threads argument through to bwa. However, it will still be processing bwa's output using its own threads. This will result in small bursts of activity where the CPU usage is above jobs. If you specify --strict-threads, however, then this behavior is curtailed and it will never use more threads than specified (in particular, it will call bwa using one thread fewer than specified, while restricting itself to a single thread, thus even peak usage is at most the number of specified threads).

temporary-directory: where to keep temporary files. By default, this is the system defined temporary directory (either /tmp or the value of the $TEMPDIR environment variable on Unix).

color: whether to use color output. Defaults to auto (i.e., print color if the output is a terminal), no (never use color), force (use color even if writing to a file or pipe), yes (synonym of force).

print-header: whether to print ngless banner (version info...).

user-directory: user writable directory to cache downloads (default is system dependent, on Linux, typically $HOME/.local/share/ngless/.

user-data-directory: user writable directory to cache data (default is a data directory inside the user-directory [see above]).

index-path: user writable directory to store indices and similar data.
global-data-directory: global data directory.

**Debug options**

keep-temporary-files: whether to keep temporary files after the end of the programme.
trace (only command line): print a lot of internal information.

**Auto-detection of the number of CPUs**

If the option auto is passed as the number of jobs (either on the command line or in the configuration file), ngless will inspect the environment looking for a small set of clues as to how many CPUs to use. In particular, it will make use of these variables:

- OMP_NUM_THREADS
- NSLOTS
- LSB_DJOB_NUMPROC
- SLURM_CPUS_PER_TASK

If none are found (or they do not contain a single number), an error is produced.

### 6.20 Search path expansion

**Note:** Search path expansion is a very powerful feature. It can be abused to defeat NGLess’ reproducibility mechanisms and to obscure which reference information is being used. However, if used correctly, it can greatly simplify file management and enhance reproducibility.

NGLess supports a search path system to find references. Certain functions (such as map()) support search path expansion. For example, you can write:

```python
map(input, fafile="<>/my-reference.fa")
```

Then if the search path consists of "/opt/ngless-references/", the expanded version will be "/opt/ngless-references/my-reference.fa".

#### ## Named and unnamed search paths

You can have named and unnamed paths in your search path. The rules are a bit complex (see below), but it makes sense if you see examples:

```python
map(input, fafile="<references>/my-reference.fa")
```

With the search path ["references=/opt/ngless-refs"] will result in "/opt/ngless-refs/my-reference.fa".

With the search path ["internal=/opt/ngless-internal", "references=/opt/ngless-refs"] will also result in "/opt/ngless-refs/my-reference.fa" as the internal path will not be matched.

With the search path ["internal=/opt/ngless-internal", "references=/opt/ngless-refs", "/opt/ngless-all"] now it will result in ["/opt/ngless-refs/my-reference.fa", "/opt/ngless-all/my-reference.fa"] as the unnamed path will always match. Since there is more than one result, both are checked (in order).
Using <> (as in the example above) will use only unnamed paths.

## Setting the search path

The search path can be passed on the command line:

```
ngless script.ngl --search-path "references=/opt/ngless"
```

Alternatively, you can set it on the ngless configuration file:

```
search-path = ["references=/opt/ngless"]
```

Note that the search path is a list, even if it contains a single element.

## Rules

1. If a path matches <([^>]*>), then it is path expanded.
2. The search path (which is a list of named and unnamed search paths) is filtered. A path is kept on the list if it is an unnamed path or if the name matches the requested pattern (references requests “references”; <> never matches so that only unnamed paths are kept).
3. Paths are tested in order and the first path referring to an existing file is kept.

Similarly

### 6.21 Reproducible Computation With NGLess

NGLess has several built-in features to make it easier to achieve reproducible research.

All information that is needed to run a result is contained in the NGLess script. There is no command line or configuration option which changes the results: they only change the way in which the computation was run (what information was printed on the console, where intermediate files were saved, &c).

The version annotations that NGLess requires also enhance reproducibility while allowing us to update NGLess going forward.

#### 6.21.1 Annotate results with input script

The `write()` function call supports the argument `auto_comments` which will add (as comments) meta information to the output. In particular, you can use the `{script}` auto comment to add the script to your output. For example:

```
ngless '0.8'
mapped = samfile('input.bam')

counted = count(mapped, features=['seqname'])
write(counted,
        ofile='output.txt',
        auto_comments=[{script}]) # <<< ADD SCRIPT
```

This will add the script to your output. Thus, it will be easy to see how the output was generated.

You can also use `{date}`, which will output a string with the date in which the script was run (note that the result is no longer reproducible at the Byte level as each run will contain a different date/time). Finally, the `comment` argument allows for any free text string:
Finally, you can use the magical \{hash\} auto comment:

```plaintext
write(counted,
ofile="output.txt",
comment="For my awesome Science publication",
avto_comments=\{\{script\}\, \{hash\}\})
```

This will add a hash string to the output describing the computational path to compute the result. This is smarter than a simple hash of the script as it does not consider code that is not necessary to generate the script or elements such as variable names (i.e., if you change the variable names, the hash will stay the same as it is the same computational path).

The `collect()` function also support the same arguments.

### 6.22 Frequently Asked Questions

This is a list of questions we have regularly gotten on the project. See below for questions about the ngless language.

#### 6.22.1 Why a new domain-specific language instead of a library in Python (or another existing language)?

First of all, you can actually use NGLess through Python, using NGLessPy.

However, the native mode of NGLess is using its internal DSL (domain specific language). There are several advantages to this approach:

1. Fast error checking which can speed up the development process. For example, static type checking, which is known to many programmer. In general, we do a lot of error checking before even starting interpretation. We perform syntax and error checking, but we can also check some conditions that can be tricky to express with simple types only (e.g., certain parameter combinations can be illegal). We also pre-check all the input files (so even if you only use a particular file in step 5 of your process, we check if it exists even before running steps 1 through 4). We even do some things like: if you use step 1 to compute to name of the input file that will be used in step 5, we will check it immediately after step 1. Same for output files. If you issue a `write()` call using `output/results.txt` as your output filename, we will check if a directory named output exists and is writable. We also try to be helpful in the error messages (mispelled a parameter value? Here’s an error, but also my best guess of what you meant + all legal values). I really care about error messages.

2. By controlling the environment more than would be typical with a Python library (or any other language), we can also get some reproducibility guarantees. Note too that we declare the version of every script so that we can update the interpreter in the future without silently changing the behaviour of older ones.

3. Using a domain specific language makes the resulting scripts very readable even for non-experts as there is little boilerplate.

4. Finally, we needed the result to be fast and languages such as Python often add a lot of overhead.

#### 6.22.2 Is the language extensible?

Yes.
While the basic types and syntax of the language are fixed, it is not hard to add external modules that introduce new functions. These can be described with a YAML file and can use any command line tool.

Add new model organisms can similarly be done with simple YAML file.

More advanced extensions can be done in Haskell, but this is considered a solution for advanced users.

### 6.22.3 Couldn’t you just use Docker/Bioboxes?

Short answer: Bioboxes gets us part of the way there, but not all of it; however, if we think of these technologies as complements, we might get more out of them.

Longer answer:

Several of the goals of ngless can be fulfilled with a technology such as bioboxes. Namely, we can obtain reproducibility of computation, including across platforms using bioboxes without having to bother with ngless. However, the result is less readable than an ngless script, which is another important goal of ngless. An ngless script can be easily submitted as supplemented methods to a journal publication and even be easily scrutinized by a knowledgeable reviewer in an easier way than a Docker container.

Furthermore, the fact that we work with a smaller domain than a Docker-based solution (we only care about NGS) means that we can provide the users a better experience than is possible with a generic tool. In particular, when the user makes a mistake (and all users will make mistakes), we can diagnose it faster and provide a better error message than is possible to do with Bioboxes.

### 6.22.4 What is the relationship of ngless to the Common Workflow Language?

Like for the question above, we consider ngless to be related to but not overlapping with the CWL (Common Workflow Language).

In particular, much of functionality of ngless can also be accessed in CWL workflow, using our command line wrappers all of which have CWL wrappers.

Additionally, (with some limitations), you can embedded a generic NGLess script within a larger CWL workflow by using the `--export-cwl` functionality. For example, to automatically generate a wrapper for a script called `my-script.ngl`, call:

```bash
ngless --export-cwl=wrapper.cwl my-script.ngl
```

The automatically generated `wrapper.cwl` file can now be used as a CWL tool within a larger pipeline. See more in the [CWL page](#).

### 6.22.5 How does ngless interact with job schedulers and HPC clusters?

Generally speaking, it does not. It can be used with HPC clusters, whereby you simply run a job that calls the ngless binary.

The parallel module can be used to split large jobs in many tasks, so that you can run multiple ngless instances and they collaborate. It is written such that does not depend on the HPC scheduler and can, thus, be used in any HPC system (or even, for smaller jobs, on a single machine).
6.22.6 Questions about the ngless language

6.22.7 Can I pass command line arguments to a script?

Yes, you can. Just add them as additional arguments and they will be available inside your script as ARGV.

6.22.8 What are symbols (in the ngless language)?

If you are familiar with the concept, you can think of them as enums in other languages. Whenever a symbol is used in the argument to a function, this means that that function takes only one of a small number of possible symbols for that argument. This improves error checking and readability.

6.22.9 Does the select function work on inserts (considering both mates) or per-read (treating the data as single-ended)?

By default, select considers the insert as a whole, but you can have it consider each read as single-end by using setting the paired argument to False.

6.23 NGLessPy: NGLess in Python

Note As of Oct 2017, NGLess is considered beta software (we believe it works, but there may still be a few rough edges), while NGLessPy is alpha software (very experimental).

6.23.1 Install

```
pip install NGLessPy
```

(or from source, using the standard python setup.py install)

6.23.2 Basic Tutorial

This tutorial expects a certain familiarity with general ngless concepts and functions.

We start by importing the NGLess object:

```
from ngless import NGLess
```

We now build an NGLess.NGLess object, giving it the version of ngless we wish (this is like the version declaration at the top of an NGLess file):

```
sc = NGLess.NGLess('0.8')
```

To simplify the rest of the script, we are going to use the short name e to refer to the environment of the script we are generating. The environment is what will hold the ngless variables we will use:

```
e = sc.env
```

We can import ngless modules using the import_ function (using name and version):

6.23. NGLessPy: NGLess in Python
Now, we can use all NGLess functionality. Functions get an underscore at the end, like this:

```python
e.sample = sc.load_mocat_sample_('testing')
```

`preprocess_` is special because it takes a block in ngless, which maps to it taking a function in Python. We can use decorator syntax to do it all compactly:

```python
@sc.preprocess_(e.sample, using='r')
def proc(bk):
    # bk is the block environment, where 'r' is defined
    bk.r = sc.substrim_(bk.r, min_quality=25)
```

Now, we map against `hg19` and filter it. As you can see, ngless functions are called with an extra underscore and variables are kept in the `e` object:

```python
e.mapped = sc.map_(e.sample, reference='hg19')
e.mapped = sc.select_(e.mapped, keep_if=['{mapped}'])
sc.write_(e.mapped, ofile='ofile.sam')
```

Finally, we execute the resulting script:

```python
sc.run(auto_install=True)
```

This will even install NGLess if it is not available in the PATH.

### 6.23.3 Full script

```python
from ngless import NGLess
sc = NGLess.NGLess('0.8')
e = sc.env
sc.import_('mocat', '0.0')

e.sample = sc.load_mocat_sample_('testing')
@sc.preprocess_(e.sample, using='r')
def proc(bk):
    # bk is the block environment, where 'r' is defined
    bk.r = sc.substrim_(bk.r, min_quality=25)

e.mapped = sc.map_(e.sample, reference='hg19')
e.mapped = sc.select_(e.mapped, keep_if=['{mapped}'])
sc.write_(e.mapped, ofile='ofile.sam')
sc.run(auto_install=True)
```
6.24 Common Workflow Language Integrations

6.24.1 Simple operations

Simple NGLess operations can be performed through the command line wrappers, all of which have a CWL tool description.

6.24.2 Automatic CWL export of NGLess scripts

An NGLess script that conforms to certain rules can be exported as a CWL tool using the `--export-cwl` option:

```
ngless script.ngl --export-cwl=tool.cwl
```

The rules are simple: the script must use ARGV for its inputs and outputs. For example, this is a conforming script:

```
ngless "0.8"

mapped = samfile(ARGV[1])

mapped = select(mapped, drop_if=[{mapped}])

write(mapped, ofile=ARGV[2])
```

The resulting tool will take two arguments, specifying its input and output.

6.25 Advanced options

6.25.1 Subsample mode

Subsample mode simply throws away >90% of the data. This allows you to quickly check whether your pipeline works as expected and the output files have the expected format. Subsample mode should never be used in production.

To use it, pass the option `--subsample` on the command line:

```
ngless --subsample script.ngl
```

will run script.ngl in subsample mode, which will probably run much faster than the full pipeline, allowing to quickly spot any issues with your code. A 10 hour pipeline will finish in a few minutes (sometimes in just seconds) when run in subsample mode.

Note: subsample mode is also a way to make sure that all indices exist. Any map() calls will check that the necessary indices are present: if a fafile argument is used, then the index will be built if necessary; if a reference argument is used, then the necessary datasets are downloaded if they have not previously been obtained.

Subsample mode also changes all your write() so that the output files include the subsample extension. That is, a call such as:

```
write(output, ofile='results.txt')
```

will automatically get rewritten to:
write(output, ofile='results.txt.subsample')

This ensures that you do not confuse subsampled results with the real thing.

## 6.26 NGLess Language

This document describes the NGLess language.

### 6.26.1 Tokenization

Tokenization follows the standard C-family rules. A word is anything that matches `[A-Za-z_] [A-Za-z_0-9]*`. The language is case-sensitive. All files are assumed to be in UTF-8.

Both LF and CRLF are accepted as line endings (Unix-style LF is preferred).

A semicolon (;) can be used as an alternative to a new line. Any spaces (and only space characters) following a semicolon are ignored. *This feature is intended for inline scripts at the command line (passed with the \(-e\) option), its use for scripts is heavily discouraged and may trigger an error in the future.*

Script-style (# to EOL), C-style (/\* to */\*) and C++-style (/\// to EOL) comments are all recognised. Comments are effectively removed prior to any further parsing as are empty lines.

Strings are denoted with single or double quotes and standard backslashed escapes apply (\n for newline, ...).

A symbol is denoted as a token surrounded by curly braces (e.g., `{symbol}` or `{gene}`).

Integers are specified as decimals `[0-9]+` or as hexadecimals `0x[0-9a-fA-F]+`.

### 6.26.2 Version declaration

The first line (ignoring comments and empty lines) of an NGLess file MUST be a version declaration:

```
ngless "0.9"
```

### 6.26.3 Module Import Statements

Following the version statement, optional import statements are allowed, using the syntax `import "<MODULE>" version "<VERSION>"`. For example:

```
import "batch" version "1.0"
```

This statement indicates that the `batch` module, version 1.0 should be used in this script. Module versions are independent of NGLess versions.

Only a predefined set of modules can be imported (these are shipped with NGLess). To import user-written modules, the user MUST use the `local import` statement, e.g.:

```
local import "batch" version "1.0"
```

Import statements MUST immediately follow the version declaration.
Blocks

Blocks are defined by indentation in multiples of 4 spaces. To avoid confusion, TAB characters are not allowed. Blocks are used for conditionals and `using` statements.

6.26.4 Data types

NGless supports the following basic types:

- String
- Integer
- Double
- Bool
- Symbol
- Filename
- Shortread
- Shortreadset
- Mappedread
- Mappedreadset

In addition, it supports the composite type List of X where X is a basic type. Lists are built with square brackets (e.g., [1,2,3]). All elements of a list must have the same data type.

String

A string can start with either a quote (U+0022, " ) or a single quote (U+0027, ’ ) or and end with the same character. They can contain any number of characters.

Special sequences start with \. Standard backslashed escapes can be used as LF and CR (\n and \r respectively), quotation marks (\' ) or slash (\\).

Integer

Integers are specified as decimals [0-9]+ or as hexadecimals 0x[0-9a-fA-F]+. The prefix – denotes a negative number.

Double

Doubles are specified as decimals [0-9]+ with the decimal point serving as a separator. The prefix – denotes a negative number.

Doubles and Integers are considered numeric types.

Boolean

The two boolean constants are True and False (which can also be written true or false).
Symbol

A symbol is denoted as a token surrounded by curly braces (e.g., `{symbol}` or `{drop}`). Symbols are used as function arguments to indicate that there is only a limited set of allowed values for that argument. Additionally, unlike Strings, no operations can be performed with Symbols.

6.26.5 Variables

NGless is a statically typed language and variables are typed. Types are automatically inferred from context. Assignment is performed with = operator:

```
variable = value
```

A variable that is all uppercase is a constant and can only be assigned to once.

6.26.6 Operators

Unary

The operator (-) returns the symmetric of its numeric argument.
The operator `len` returns the length of a ShortRead.
The operator `not` negates its boolean argument

6.26.7 Binary

All operators can only be applied to numeric types. Mixing integers and doubles returns a double. The following binary operators are used for arithmetic:

```
+ - < > >= <= == !=
```

The + operator can also perform concatenation of String objects.
The `<>` operator is used to concatenate two Strings while also adding a ‘/’ character between them. This is useful for concatenating file paths.

6.26.8 Indexing

Can be used to access only one element or a range of elements in a ShortRead. To access one element, is required an identifier followed by an expression between brackets. (e.g, x[10]).

To obtain a range, is required an identifier and two expressions separated by a ‘:’ and between brackets. Example:

- x[:] - from position 0 until length of variable x
- x[10:] - from position 10 until length of variable x
- x[:10] - from position 0 until 10
6.26.9 Conditionals

Conditionals work as in Python. For example:

```plaintext
if 5 > 10:
    val = 10
else:
    val = 20
```

6.26.10 Functions

Functions are called with parentheses:

```plaintext
result = f(arg, arg1=2)
```

Functions have a single positional parameter, all other must be given by name:

```plaintext
unique(reads, max_copies=2)
```

The exception is constructs which take a block: they take a single positional parameter and a block. The block is passed using the `using` keyword:

```plaintext
reads = preprocess(reads) using |read|:
    block
    ...
```

The `|read|` syntax defines an unnamed (lambda) function, which takes a variable called `read`. The function body is the following block.

There is no possibility of defining new functions within the language. Only built-in functions or those added by modules can be used.

6.26.11 Methods

Methods are called using the syntax `object . methodName ( <ARGS> )`. As with functions, one argument may be unnamed, all others must be passed by name.

6.26.12 Grammar

This is the extended Backus-Naur form grammar for the NGLess language (using the ISO 14977 conventions). Briefly, the comma (,) is used for concatenation, [x] denotes optional, and {x} denotes zero or more of x.

```plaintext
string = ? a quoted string, produced by the tokenizer ? ;
word = ? a word produced by the tokenizer ? ;
eol =
    ','
    | '\n' {'\n'}
    ;
ngless = [header], body;
```

(continues on next page)
header = {eol}, ngless_version, {eol}, {import}, {eol}
ngless_version = "ngless", string, eol;
import = ["local"], "import", string, "version", string, eol;
body = {expression, eol};
expression =
    conditional
    | "discard"
    | "continue"
    | assignment
    | innerexpression
    ;
innerexpression = left_expression, binop, innerexpression
    | left_expression
    ;
left_expression = uoperator
    | method_call
    | indexexpr
    | base_expression
    ;
base_expression = pexpression
    | funccall
    | listexpr
    | constant
    | variable
    ;
pexpression = '(', innerexpression, ')';
constant =
    "true"
    | "True"
    | "false"
    | "False"
    | double
    | integer
    | symbol
    ;
double = integer, '.', integer;
integer = digit, {digit};
digit = '0' | '1' | '2' | '3' | '4' | '5' | '6' | '7' | '8' | '9';
symbol = '{', word, '}';
indentation = ' ', {' '};
binop = '+', '|', '*', '{', '}', '!', '!', '='
      | "=" | ">" | ">=" | ">=" | ">=" | ">=" | ">="
      | "+" | "-";
uoperator =
    lenop
    | unary_minus
    ;
Mapping is one of the major functions of NGLess. Here we describe, in more detail, some of its functionality.

Mapping is implemented using bwa. As of version 0.6, NGLess uses bwa 0.7.15.

By default, bwa is called with default parameters. If the mode_all argument is set to true, then \(-a\) is passed to bwa.

### 6.27.1 Low memory mode

As databases get very large, memory requirements can grow very large. In order to make large databases accessible to users without access to large memory machines, NGLess implements a simple heuristic: it splits the input database into smaller blocks, processes each one in turn and combines the results at the end.
To enable low-memory mode, use the `block_size_megabases` in the script. Set it to a value that is less than the available memory.

A FAQ is why the memory requirements are not a configuration option and must be specified in the script. As low memory mode is heuristic, it can potentially change results. As NGLess aims to capture all parameters that can change the result inside the script, it must be specified as an argument to `map()`.

### 6.27.2 Using SOAPAligner

**Note:** Support for SOAPAligner is experimental (as of version 0.6)

You can use SOAPAligner as an alternative to bwa using the following code:

```python
import "soap" version "0.0"

input = ....

mapped = map(input, mapper="soap")
```

Note that, unlike the case for bwa, SOAPAligner is not bundled with NGLess and must be in the PATH to be used.

### 6.28 Software used by NGLess

NGLess internally uses a few other packages to implement specific functionality. As we believe in giving appropriate credit, these packages are printed in the citation list of any script that uses them.

NGLess version 0.6 uses the following software tools:

- Samtools (used for SAM/BAM handling as well as in the `samtools` module: version 1.6
- BWA (used for `map`): version 0.7.15
- Prodigal (used for `orf_find`): version 2.6.3 (with a patch to fix a bug [submitted upstream])