CLIMB-TRE

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None

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1. CLIMB-TRE

1.1 Introduction

The CLIMB Trusted Research Environment (CLIMB-TRE) project provides tools with which users can upload metagenomics data, with metadata, and analyse them on CLIMB.

This site documents how to use the CLIMB-TRE tools and is distinct from more general documentation on using CLIMB. Read further for general information on how to upload or analyse data.

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1.2.2 Project Specifications

Common Structure
Learn more about required files, naming conventions and processing requirements common to all projects.

Project List

Project	Description	Uploader Specification	Analysis Specification	Template CSV
mSCAPE	Metagenomics Surveillance Collaboration and Analysis Programme	Uploader Specification	Analysis Specification	mscape-template.csv
PATH-SAFE	Pathogen Surveillance in Agriculture, Food and Environment	Uploader Specification	Analysis Specification	pathsafe-template.csv
synthSCAPE	Synthetic dataset for mSCAPE	Uploader Specification	Analysis Specification	synthscape-template.csv
openMGS	Open Meta-Genomic Surveillance	Uploader Specification	Analysis Specification	openmgs-template.csv

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2. Getting Started

2.1 Uploading data

2.1.1 Overview

Data in CLIMB-TRE is managed through a database called Onyx. To upload data into Onyx, you must deposit the appropriate files (including the metadata) into the relevant S3 bucket on CLIMB. We recommend doing this using the AWS or `s3cmd` command-line tools. For general information about how to upload data to CLIMB, see the CLIMB docs on setting up `s3cmd` locally and running `s3cmd` locally or on Bryn. You may also wish to review the overall CLIMB storage documentation.

Each CLIMB-TRE project requires data (e.g. FASTQ sequencing reads) and metadata (e.g. a CSV file). These must match the relevant specification ("spec") and be uploaded to the appropriate S3 bucket. Doing so will trigger the ingest process. Data that doesn't meet the spec will not be ingested.

Lines starting with `$` indicate commands to be entered at a terminal. The `$` represents the prompt, which might be different on your system.

2.1.2 Preparing example FASTQ files

As an example, let's imagine we want to upload the two example files in Conor Meehan's Pathogen genomics course as part of the mSCAPE project. The two files are from Hikichi et al. (2019), `DRR187559_1.fastqsanger.bz2` and `DRR187559_2.fastqsanger.bz2`, available in this Zenodo archive. You can download the files either by clicking on them in the Zenodo interface or with the common command line tools `wget`:

```
$ wget https://zenodo.org/record/4534098/files/DRR187559_1.fastqsanger.bz2
$ wget https://zenodo.org/record/4534098/files/DRR187559_2.fastqsanger.bz2
```

or `curl`:

```
$ curl -L https://zenodo.org/record/4534098/files/DRR187559_1.fastqsanger.bz2 -O
$ curl -L https://zenodo.org/record/4534098/files/DRR187559_2.fastqsanger.bz2 -O
```

These two files are bzip2 files, not gzip, which is what we need. We can convert them by piping the output from `bzcat` (which decompresses the files) to `gzip -c` (which compresses the stream and writes it to `STDOUT`) and then to new files:

```
$ bzcat DRR187559_1.fastqsanger.bz2 | gzip -c > DRR187559_1.fastq.gz
$ bzcat DRR187559_2.fastqsanger.bz2 | gzip -c > DRR187559_2.fastq.gz
```

The mSCAPE specification says that our files must have names like `mscape.[run_index].[run_id].[extension]`, where the extension is `1.fastq.gz` or `2.fastq.gz`. The `run_index` and `run_id` can in principle contain any alphanumeric characters, underscores (`_`) or hyphens ('-'), so you can rename the FASTQ files to whatever meets those requirements. At the command line, this means moving the files with something like:

```
$ mv DRR187559_1.fastq.gz mscape.test-run-index-01.test-run-id-01.1.fastq.gz
$ mv DRR187559_2.fastq.gz mscape.test-run-index-01.test-run-id-01.2.fastq.gz
```

2.1.3 Creating a metadata CSV file

Data uploads require that the FASTQ files are accompanied by a CSV file with the metadata (e.g. when the sample was taken, what type of sample it is). This CSV file must have two rows:

1. the headers, as in the project metadata specification; and
2. the actual metadata.

It's filename must match the FASTQ files but with the extension `csv` instead of `1.fastq.gz` or `2.fastq.gz` (or `fastq.gz` if your data is single ended).

For the sake of our test and getting to know the system, you should try to create such a file by hand by referring to the relevant metadata spec. The columns are documented in alphabetical order but can be given in any order. The optional columns can be omitted entirely.

Note that the `run_index` and `run_id` must *exactly* match the values implied by the FASTQ filenames. E.g., in my example above

- the `run_index` is `test-run-index-01` and
- the `run_id` is `test-run-id-01`.

The first few columns of your metadata CSV file might look like

```
run_index,run_id,biosample_id,sample_source,sample_type,...
test-run-index-01,test-run-id-01,test-sample-01,nose_and_throat,swab,...
```

with no extra spaces separating the fields.

2.1.4 Uploading files to S3 buckets

You're now ready to upload your data to one of the buckets, which we'll do using the `s3cmd` tool. There's more information about using `s3cmd` with Bryn in the CLIMB-BIG-DATA documentation on storage.

You can download `s3cmd` from the `s3cmd` download pages or install it using `pip` (perhaps in a virtual or Conda environment) with

```
$ python3 -m pip install s3cmd
```

To set `s3cmd` up to communicate with the buckets, you'll need your API keys from Bryn. You can find them by logging in to Bryn, selecting the S3 Buckets tab on the left and click the Show API Keys button that appears below the list of buckets.

You can then set up `s3cmd` with

```
$ s3cmd --configure
```

When asked for the following, you should give these answers:

- Access Key: value of `AWS_ACCESS_KEY_ID` displayed on Bryn.
- Secret Key: value of `AWS_SECRET_ACCESS_KEY` displayed on Bryn.
- Default Region [US]: leave blank.
- S3 Endpoint: `s3.climb.ac.uk`
- DNS-style bucket+hostname:port template for accessing a bucket: `%(bucket)s.s3.climb.ac.uk`

You now should be ready to upload the data. But where? The names of the S3 buckets for each project are given in the metadata specs but are usually of the form

```
[project]-[sequencing_org]-[platform]-[test_flag]
```

We'll use `mscape-public-illumina-test`, so the command to "put" the three files in the bucket would be

```
$ s3cmd put mscape.test-run-index-01.test-run-id-01.csv mscape.test-run-index-01.test-run-id-01.1.fastq.gz mscape.test-run-index-01.test-run-id-01.2.fastq.gz
s3://mscape-public-illumina-test
```

You should then see the progress of your upload (the files might be split into parts), after which you're back at the terminal.

Now what?

2.1.5 Finding the result of your upload

You won't get any feedback from `s3cmd` about the progress of your data into Onyx. When the data is received in the bucket, it announces the files to whoever is listening, which includes a program called Roz. It then starts to check the data: Are all the files present? Are they named correctly? Is the metadata well-formed? If so, the data is copied into internal project buckets and a record is added to the database, Onyx.

At this point, you can interact with your data through Onyx, which is described in the page on analysing data in Onyx.

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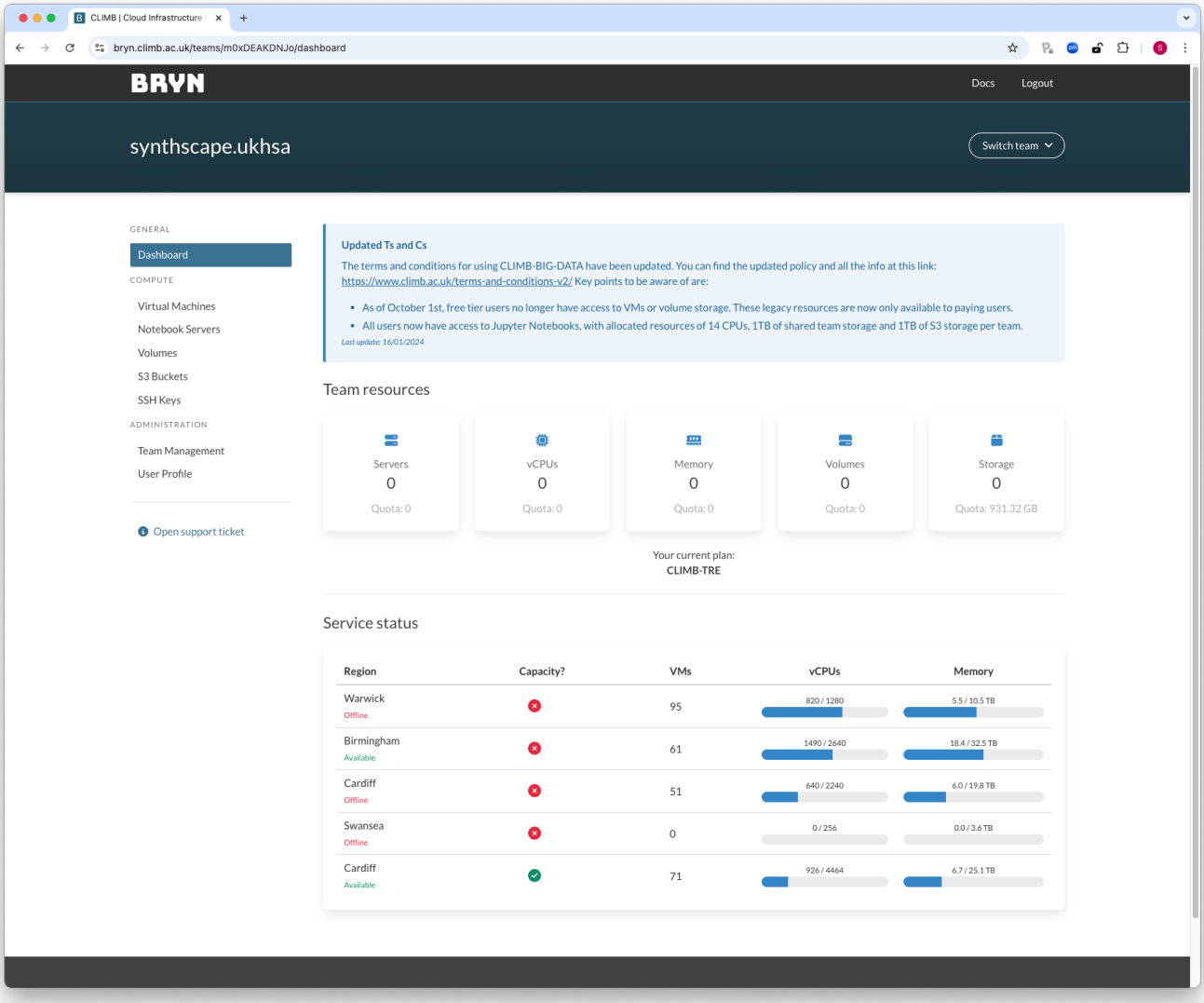
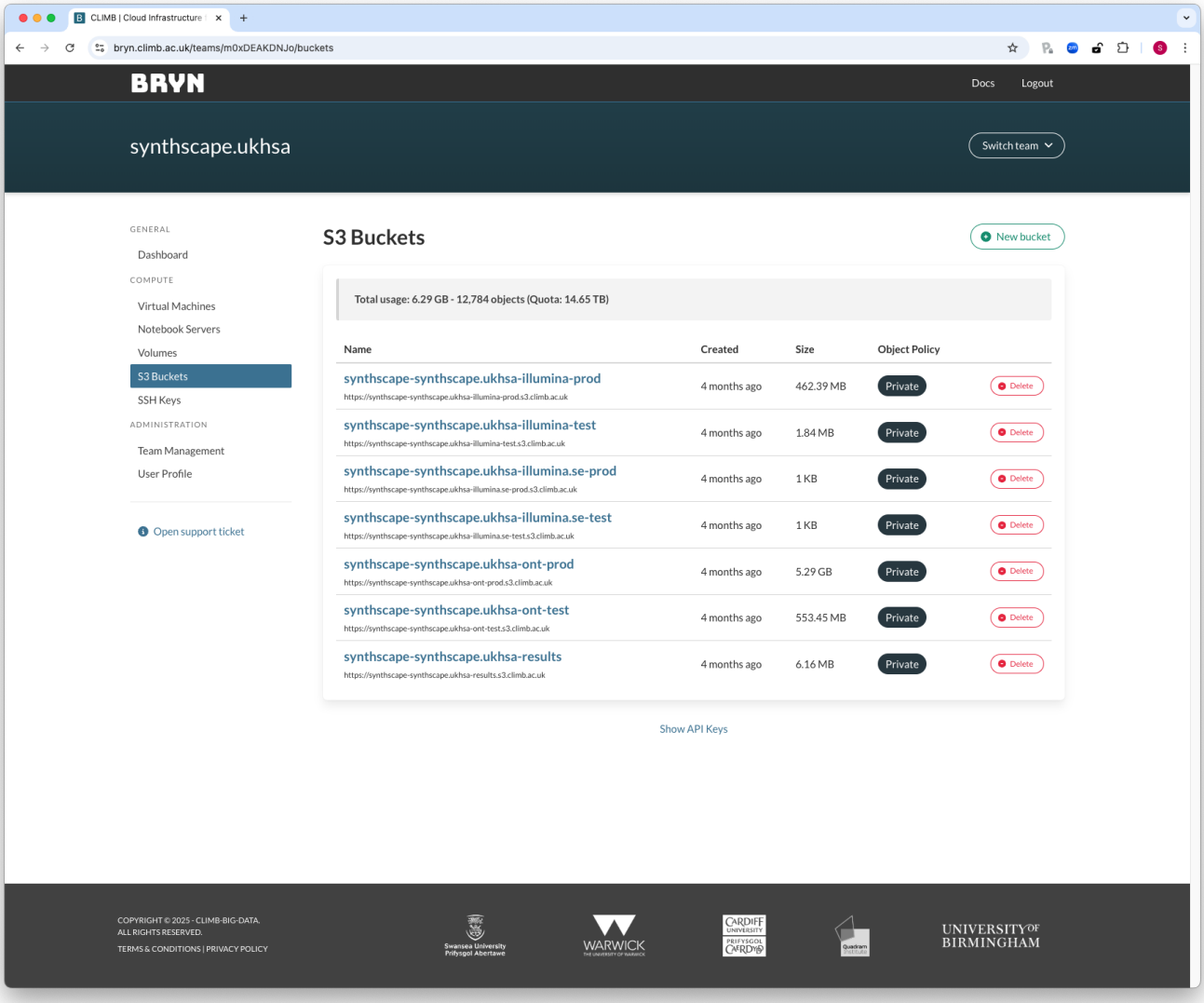
2.2 Checking Results After Submitting Data

2.2.1 Bryn GUI

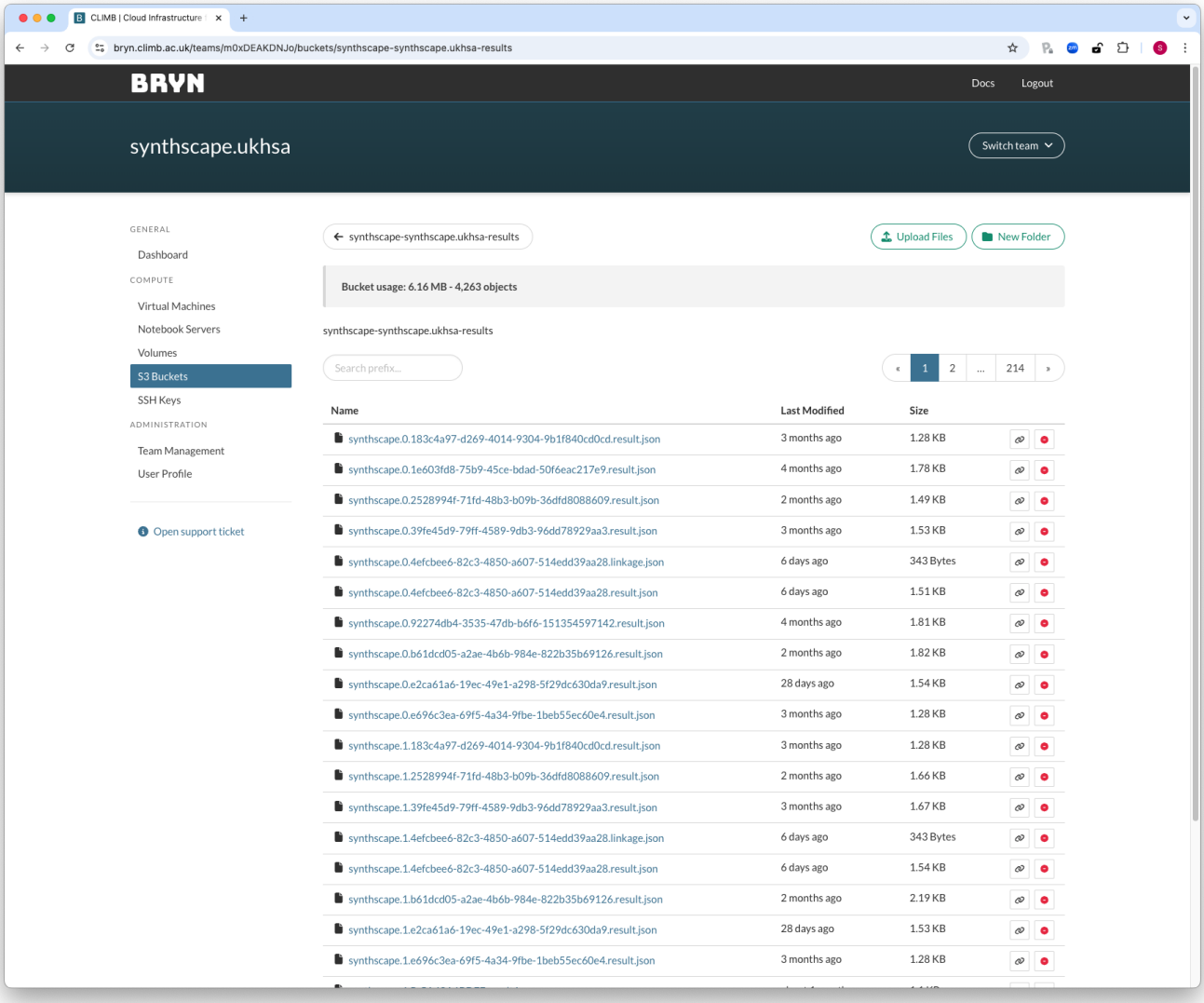
The Bryn GUI is the simplest way to check on the status of submitted data for most users. To do so, simply log in to Bryn.



Once there navigate to the "S3 Buckets" menu on the left which should look like this:



Then select the results bucket by clicking on it, the name of the results bucket will differ based on the CLIMB-TRE project and which site you belong to but the layout will be: `{project}-{bryn tenant name}-results`. Once you click on the bucket you should see a page like this:

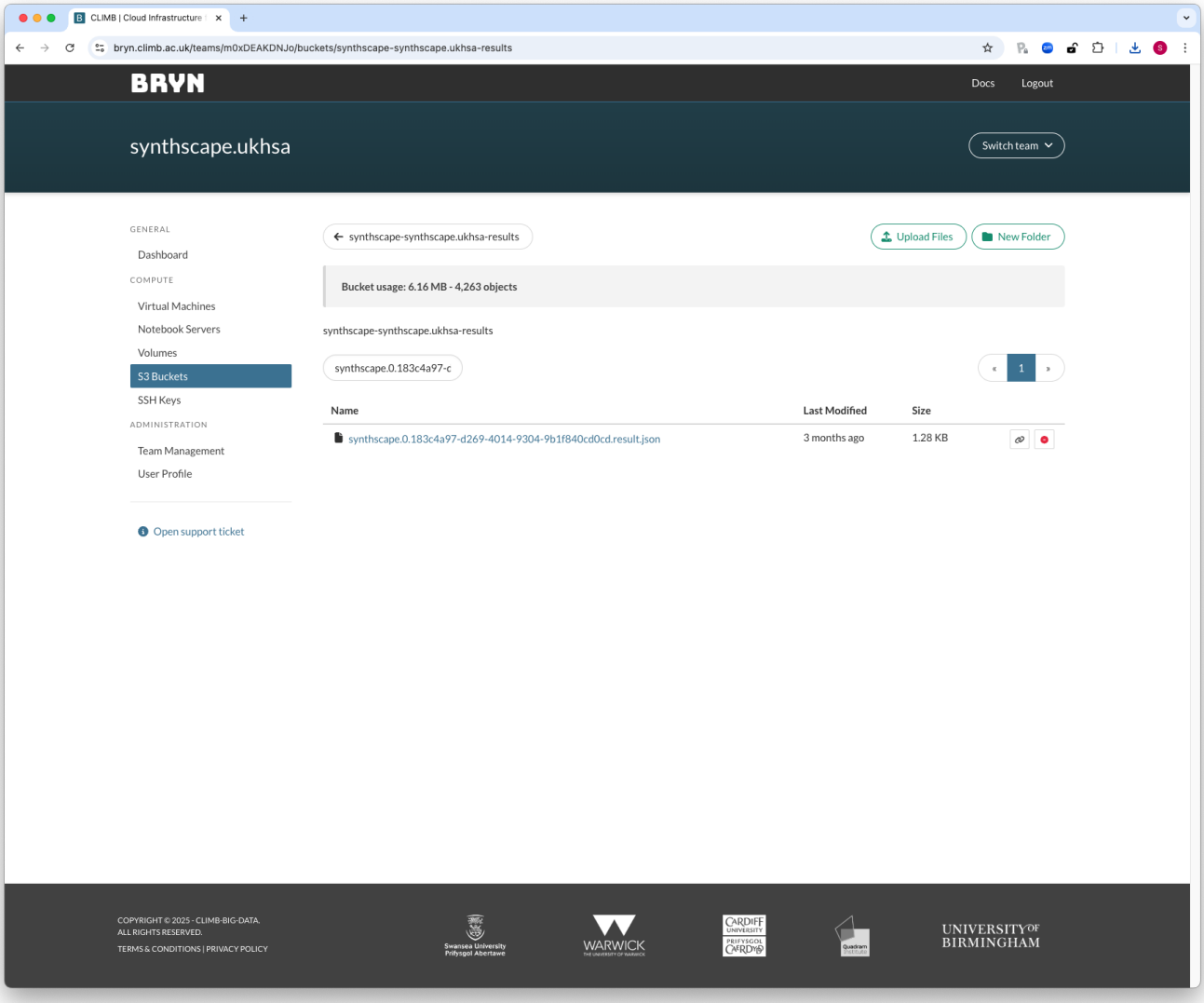


There will be up to two types of file present in this S3 bucket; result JSON files and linkage JSON files.

- Result JSON files are named with the following pattern: `{project}.{run_index}.{run_id}.result.json` and contain all the relevant information about your sample including errors during the ingest process, issues with the metadata CSV, etc.
- Linkage JSON files are named with the following pattern: `{project}.{run_index}.{run_id}.linkage.json`, these are only generated once when the ingest for that run_index and run_id has been successful and the artifact has been ingested into the dataset. It contains data which can be used to link the submitted file names with the anonymised identifiers in the main dataset, you are responsible for maintaining this linkage information and have the ability to delete it from your results bucket, if you do and lose linkage **we WILL NOT be able to establish linkage for you**.

To find the result for a specific artifact you can search, the search function requires a full match from the start of the file name, e.g. for a file named `synthscape.1.some_run_id.result.json`

- `1.some_run_id` **will not** match the file
- `synthscape.1.some_run_id` **will** match the file



Once you have found the result / linkage file you are interested in you can download it by clicking on it, be aware, these files contain private identifiers and should be treated as sensitive, we take no responsibility if you do not follow data security procedures for your trust / organisation.

A result JSON will look similar to this:


```
{
  "uuid": "f84ae65d-ec57-443a-946f-6af34bace889",
  "site": "synthscape",
  "raw_site": "synthscape.ukhsa",
  "uploaders": [
    "bryn-synthscape-ukhsa"
  ],
  "match_timestamp": 1.7286538918609505e+18,
  "artifact": "synthscape|0|183c4a97-d269-4014-9304-9b1f840cd0cd",
  "run_index": "0",
  "run_id": "183c4a97-d269-4014-9304-9b1f840cd0cd",
  "project": "synthscape",
  "platform": "ont",
  "files": {
    ".csv": {
      "uri": "s3://synthscape-synthscape.ukhsa-ont-prod/synthscape.0.183c4a97-d269-4014-9304-9b1f840cd0cd.csv",
      "etag": "0b17ccec938f4876029972c4d37dba72",
      "key": "synthscape.0.183c4a97-d269-4014-9304-9b1f840cd0cd.csv",
      "submitter": "bryn-synthscape-ukhsa",
      "parsed_fname": {
        "project": "synthscape",
        "run_index": "0",
        "run_id": "183c4a97-d269-4014-9304-9b1f840cd0cd",
        "ftype": "csv"
      }
    },
```

```
    ".fastq.gz": {
      "uri": "s3://synthscape-synthscape.ukhsa-ont-prod/synthscape.0.183c4a97-d269-4014-9304-9b1f840cd0cd.fastq.gz",
      "etag": "62adfae7ac5dcbcc3a770133e2bcf7e5",
      "key": "synthscape.0.183c4a97-d269-4014-9304-9b1f840cd0cd.fastq.gz",
      "submitter": "bryn-synthscape-ukhsa",
      "parsed_fname": {
        "project": "synthscape",
        "run_index": "0",
        "run_id": "183c4a97-d269-4014-9304-9b1f840cd0cd",
        "ftype": "fastq",
        "gzip": "gz"
      }
    }
  },
  "test_flag": false,
  "validate": false,
  "onyx_test_create_errors": {
    "source_climb_id": [
      "This CLIMB ID does not exist in mSCAPE."
    ]
  }
}
```


If the submission was successful there will be no `onyx_test_create_errors` or `ingest_errors` fields present and the `created` / `published` fields will both be "true".

Any metadata issues will be defined in the `onyx_test_create_errors` field separated by the field to which the issue applies, we hope that the errors should be fairly readable and self explanatory but if not the please contact the CLIMB-TRE team for assistance.

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2025-01-15

2.3 Analysing data

2.3.1 Overview

Once data and metadata have been ingested into the Onyx database, you can query it using the Onyx client, which provides a command line interface (CLI) and Python API. This short example demonstrates a few principal functions. More are described in the `onyx-client` documentation.

This guide also assumes that you're using a Notebook Server on CLIMB, so that once installed, the Onyx client will automatically be configured.

2.3.2 Onyx client basics

First, let's install the Onyx client, which is available through the conda-forge package `climb-onyx-client` and can thus be installed with `conda`. As advised in the CLIMB docs on installing software, you should install the client in a new Conda environment. I'll name my environment `onyx` and install `climb-onyx-client`, as well as `ipykernel` (so that the client is available in my Jupyter Notebooks).

```
jovyan:~$ conda create -n onyx ipykernel climb-onyx-client
```

Let's activate this environment.

```
jovyan:~$ conda activate onyx
```

On Bryn's Notebook Servers, the client will automatically be configured. Try running the command-line client with

```
(onyx) jovyan:~$ onyx
```

This should show you some options and commands that are available. Have a look at your own profile with

```
(onyx) jovyan:~$ onyx profile
```

and which projects you have access to with

```
(onyx) jovyan:~$ onyx projects
```

You should see `mscape` listed.

2.3.3 Querying data

As an example task, we'll see if we can find any sequencing data performed for ZymoBIOMICS sources. These are designed with a particular specification of DNA from eight bacteria and two yeasts. We can use these to see if our protocol correctly recovers the DNA fractions. I.e. if our protocol is biased.

From the command line, the main route to querying Onyx is via the `filter` command. On its own, this queries the database with *no* filters. The command

```
(onyx) jovyan:~$ onyx filter mscape
```

will produce tens of thousands of lines of JSON, so let's not do that just yet. To first see which fields are available in the database, we can use

```
(onyx) jovyan:~$ onyx fields mscape
...
├──────────────────────────────┼──────────┼──────────────┼──────────────────────────────────────────────────────────────────────────────┼──────────────────────────────────────────────────────────┤
│ extraction_enrichment_protocol │ optional │ text         │ Details of nucleic acid extraction and optional enrichment steps.            │
├──────────────────────────────┼──────────┼──────────────┼──────────────────────────────────────────────────────────────────────────────┼──────────────────────────────────────────────────────────┤
...
```

Let's search the database for entries with `zymo` (case-insensitive) in this field.

```
(onyx) jovyan:~$ onyx filter mscape --field extraction_enrichment_protocol.icontains=zymo
...
```

That should return JSON data for a few entries. You may wish to format the data as CSV or TSV with `--format csv` or `--format tsv`, respectively.

2.3.4 Inspecting some pipeline output on the command line

When data is ingested into Onyx, a taxonomic classification is automatically run. The last part of the JSON data is usually some of this, in JSON format. The complete reports can be found in the S3 buckets given in the `'taxon_report'` field. You can find this in the output you've already produced or modify the `filter` command to only request them using the `--include` flag. e.g.

```
(onyx) jovyan:~$ onyx filter mscape --field extraction_enrichment_protocol.icontains=zymo --include=taxon_reports
[
    {
        "taxon_reports": "s3://mscape-published-taxon-reports/C-FDE50853AD/"
    },
    {
        "taxon_reports": "s3://mscape-published-taxon-reports/C-04F4495068/"
    }
]
```

Multiple fields can be requested with the `--include` flag e.g.

```
(onyx) jovyan:~$ onyx filter mscape --field extraction_enrichment_protocol.icontains=zymo --include climb_id,taxon_reports
[
    {
        "climb_id": "C-FDE50853AD",
        "taxon_reports": "s3://mscape-published-taxon-reports/C-FDE50853AD/"
    },
    {
        "climb_id": "C-04F4495068",
        "taxon_reports": "s3://mscape-published-taxon-reports/C-04F4495068/"
    }
]
```

You can conversely exclude individual fields using the `--exclude` flag in the same way.

Either way, you now have the location of the taxonomy reports. Let's have a look with `s3cmd`.

```
(onyx) jovyan:~$ s3cmd ls s3://mscape-published-taxon-reports/C-FDE50853AD/
2023-11-10 12:56   146K  s3://mscape-published-taxon-reports/C-FDE50853AD/PlusPF.kraken.json
2023-11-10 12:56     2G  s3://mscape-published-taxon-reports/C-FDE50853AD/PlusPF.kraken_assignments.tsv
2023-11-10 12:56   193K  s3://mscape-published-taxon-reports/C-FDE50853AD/PlusPF.kraken_report.txt
```

The plain text report is what we're after, so let's download that with `s3cmd`:

```
(onyx) jovyan:~$ s3cmd get s3://mscape-published-taxon-reports/C-FDE50853AD/PlusPF.kraken_report.txt
download: 's3://mscape-published-taxon-reports/C-FDE50853AD/PlusPF.kraken_report.txt' -> './PlusPF.kraken_report.txt'  [1 of 1]
 197750 of 197750   100% in    0s     3.79 MB/s  done
```

If you've never seen one of these reports before, it's worth having a quick look with a tool like `less` or by opening it using the JupyterLab file browser. For reference, it's worth showing the header

```
(onyx) jovyan:~$ head -n 1 PlusPF.kraken_report.txt
% of Seqs       Clades  Taxonomies      Rank    Taxonomy ID     Scientific Name
```

The Zymo sample is prepared with 12% *Bacillus subtilis*. Let's see how much was actually reported in the results:

```
(onyx) jovyan:~$ grep "Bacillus subtilis" PlusPF.kraken_report.txt
 20.30  435278  1452    G1      653685                  Bacillus subtilis group
  0.12  2624    1952    S       1423                      Bacillus subtilis
  0.03  565     242     S1      135461                      Bacillus subtilis subsp. subtilis
  0.01  108     108     S2      1404258                       Bacillus subtilis subsp. subtilis str. OH 131.1
  ...
```

Looks like 20.3%, though classified under *Bacillus subtilis* "subgroup", rather than *Bacillus subtilis*, which reportedly only comprises 0.12% of the sample. Most of that 20.3% is under *Bacillus spizizenii*.

An important detail here is that the fraction reported in this output is not calculated in the same way as what's used in the reference values (12% for bacteria; 2% for yeasts). Let's make a fairer comparison using the JSON taxonomic data.

2.3.5 Working with database output in Python

To fairly compare the taxonomic data with the reference values in the Zymo community, we need to know the proportions of gDNA, so we need to compute the number of base pairs that were assigned to each taxon. Let's make this comparison in Python using the Onyx client's Python API.

Let's first run the same query for the Zymo data. We'll follow the examples in the Onyx documentation and run the query in a context manager.

```
import os
from onyx import OnyxConfig, OnyxEnv, OnyxClient

config = OnyxConfig(
    domain=os.environ[OnyxEnv.DOMAIN],
    token=os.environ[OnyxEnv.TOKEN],
)

with OnyxClient(config) as client:
    records = list(client.filter(
        "mscape",
        fields={
            "extraction_enrichment_protocol__icontains": "zymo",
        },
    ))
```

We've wrapped the `filter` call in a `list` because otherwise we get a generator.

If you want to inspect the data, it's a bit easier to read if formatted with indentation, which can be done using the standard `json.dumps` function:

```
import json
print(json.dumps(records[0], indent=2))  # show first record
```

In each record, the `'taxa_files'` key gives us a list of dictionaries that each has a number of reads and a mean length, the product of which is the total number of base pairs that were read for that taxon. A simple first step is to convert the taxonomic data (for the first record) into a Pandas DataFrame with

```
import pandas as pd

df = pd.DataFrame(records[0]['taxa_files'])
```

We also need to drop a few lower-level taxa that are already accounted for in higher ones. e.g. the reads for *Bacillus spizizenii TU-B-10* are among the reads counted for *Bacillus spizizenii*. A quick way of doing this is by selecting the rows that have only two words in their names.

```
df = df.loc[df['human_readable'].apply(lambda name: len(name.split()) == 2)]
```

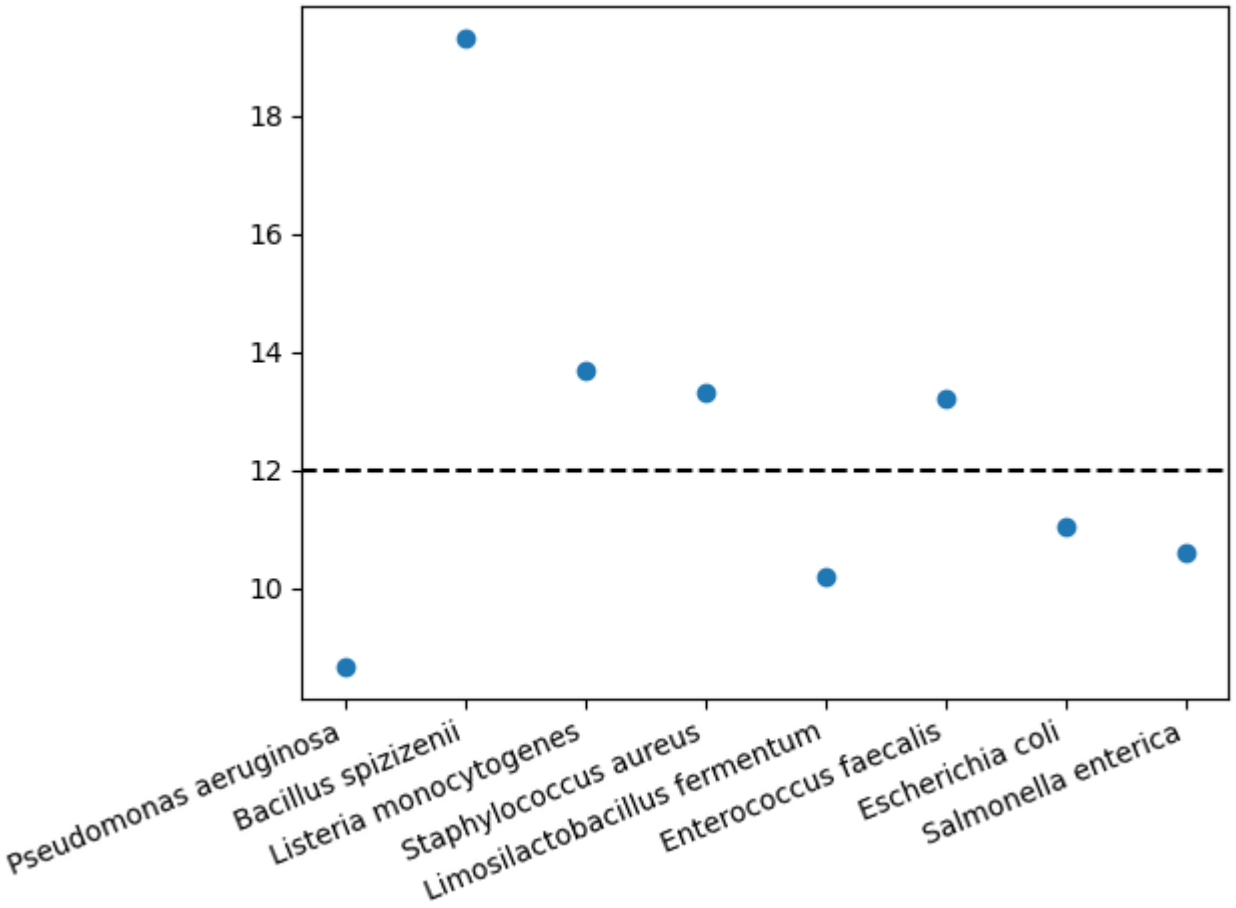
Now, let's add columns for the total number of base pairs associated with each taxon and what proportion that is of the total.

```
df['gDNA'] = df['n_reads']*df['mean_len']
df['proportion'] = df['gDNA']/df['gDNA'].sum()
```

Finally, let's make a rough plot with a black dashed line at 12%.

```
import matplotlib.pyplot as plt

plt.plot(df['human_readable'], df['proportion']*100, 'o')
plt.axhline(12, c='k', ls='--');
plt.xticks(rotation=22.5, ha='right');
```



There are some clear discrepancies—*Pseudomonas aeruginosa* is underreported and *Bacillus spizizenii* is overreported—but this matches results by e.g. Nicholls et al. (2019).

This short example is intended as a basic demonstration of what's possible in CLIMB-TRE. We're always interested to hear more examples of research questions that CLIMB-TRE can answer, so let us know if you have an example that could be included as a guide for others.

2024-03-04

2023-11-01

2.4 Analysis examples for mSCAPE

2.4.1 Retrieve all samples that contain a particular taxa e.g. `pseudomonas`

This can be done through the CLI:

```
$ onyx filter mscape --field taxa_files.human_readable.icontains=pseudomonas --format csv
```

Or through the Python API:

```
import os
from onyx import OnyxConfig, OnyxClient, OnyxEnv, OnyxField

config = OnyxConfig(
    domain=os.environ[OnyxEnv.DOMAIN],
    token=os.environ[OnyxEnv.TOKEN],
)

with OnyxClient(config) as client:
    # Filter for read sets containing "pseudomonas"
    for metadata in client.query(
        "mscape",
        query=OnyxField(taxa_files__human_readable__icontains="pseudomonas"),
    ):
        # Do analysis here
        print("CLIMB ID:", metadata["climb_id"])
        print("Published date:", metadata["published_date"])

        # The query command by default does not return taxonomic information
        # To get this, we have to call the `get` method and retrieve the samples individually
        full_metadata = client.get("mscape", metadata["climb_id"])

        # Now we can inspect the taxonomic information for the readset
        print(
            "Number of binned reads:", len(full_metadata["taxa_files"])
        )  # etc. Do more analysis
        print("Pseudomonas taxa:")
        for taxa in full_metadata["taxa_files"]:
            if "pseudomonas" in taxa["human_readable"].lower():
                print("-", taxa["human_readable"])
```

Example output for this python script:

```
CLIMB ID: C-FE89BACF2D
Published date: 2024-02-28
Number of binned reads: 3
Pseudomonas taxa:
- Pseudomonas aeruginosa
- Pseudomonas aeruginosa PA7
CLIMB ID: C-470A57DCD0
Published date: 2024-02-28
Number of binned reads: 8
Pseudomonas taxa:
- Pseudomonas aeruginosa
- Pseudomonas aeruginosa PA7
CLIMB ID: C-FB67513BE0
Published date: 2024-02-28
Number of binned reads: 4
Pseudomonas taxa:
- Pseudomonas aeruginosa
CLIMB ID: C-E49EED98E4
Published date: 2024-02-28
Number of binned reads: 3
Pseudomonas taxa:
- Pseudomonas aeruginosa
- Pseudomonas aeruginosa PA7
...
```

2.4.2 Get a CSV distribution of all binned taxa present in the dataset

Through the CLI:

```
$ onyx filter mscape --summarise taxa_files.taxon_id,taxa_files.human_readable --format csv
```

Or through the Python API:

```
import os
from onyx import OnyxConfig, OnyxClient, OnyxEnv, OnyxField
```

```
config = OnyxConfig(
    domain=os.environ[OnyxEnv.DOMAIN],
    token=os.environ[OnyxEnv.TOKEN],
)

with OnyxClient(config) as client:
    for summary_data in client.query(
        "mscape",
        summarise=["taxa_files__taxon_id", "taxa_files__human_readable"],
    ):
        # Do analysis here
        print("Taxon ID:", summary_data["taxa_files__taxon_id"])
        print("Taxon name:", summary_data["taxa_files__human_readable"])
        print("Number of readsets present:", summary_data["count"])
```

Example output for this python script:

```
Taxon ID: 1304
Taxon name: Streptococcus salivarius
Number of readsets present: 22
Taxon ID: 1305
Taxon name: Streptococcus sanguinis
Number of readsets present: 9
Taxon ID: 1313
Taxon name: Streptococcus pneumoniae
Number of readsets present: 26
Taxon ID: 1318
Taxon name: Streptococcus parasanguinis
Number of readsets present: 42
Taxon ID: 1328
Taxon name: Streptococcus anginosus
Number of readsets present: 4
...
```

2024-03-06

2024-03-06

3. Project Specifications

3.1 Project specification structure

3.1.1 Overview

All projects on CLIMB-TRE are specified in the same way.

3.1.2 Files to be provided

These are the files that must be uploaded (usually some sequencing reads and a metadata file). Submissions without the correct number of files provided will be considered incomplete and will not be processed.

3.1.3 File naming convention

This is the convention to which the provided file names must adhere.

Each of the files to be provided will use the same basename followed by specified extensions (e.g. for data versus metadata). The basename for each file is usually several fields separated by a fixed number of stops/periods (`.`).

The set of valid characters is usually limited to letters, numbers, hyphens (`-`) and underscores (`_`) but this will be specified. Filenames containing forbidden characters or extensions will not be processed.

3.1.4 File processing requirements

FASTQ

- Must be gzipped.
- Must adhere to the FASTQ format.

CSV

- Must be a plain text file with comma-delimited data.
- Must contain two rows: the first will contain the column names and the second will contain the data.
- Must have column names that match the specification exactly.
- Must not have missing data for required fields.
- Must not have invalid data (e.g. `"N/A"`) to circumvent missing data checks.
- Must not contain metadata that contradicts the file name.
- Must use the latest version of the metadata specification.

3.1.5 Metadata specification

The metadata for each project is specified in tables detailing required fields (which must not be empty) and optional fields (which can be left empty).

3.1.6 Project upload buckets

Files should be uploaded to S3 buckets hosted at the `s3.climb.ac.uk` endpoint.

The bucket names are a combination of:

- Project (e.g. `mscape`).
- Site code (e.g. `bham`).
- Platform (e.g. `illumina`).
- A flag that indicates a test (`test`) or production (`prod`) submission.

All files must be placed in the root directory of the submission buckets. Any S3 URI containing a directory will be ignored.

2024-03-12

2023-11-01

3.2 mSCAPE

3.2.1 mSCAPE Uploader Specification

Files to be provided

For *paired-end Illumina* (`illumina`) sequencing data, suppliers must provide:

- A FASTQ 1 file containing the forward sequencing reads.
- A FASTQ 2 file containing the reverse sequencing reads.
- A CSV file containing the metadata associated with sequencing the sample.

For *single-end Illumina* (`illumina.se`) sequencing data, suppliers must provide:

- A FASTQ file containing the sequencing reads.
- A CSV file containing the metadata associated with sequencing the sample.

For *ONT* (`ont`) sequencing data, suppliers must provide:

- A FASTQ file containing the sequencing reads.
- A CSV file containing the metadata associated with sequencing the sample.

Sequencing data must be dehumanised prior to submission. The ingest pipeline will reject sequencing data where the number of assigned human reads exceeds the human read rejection threshold.

File naming convention

The base filenames should be of the form

```
mscape.[run_index].[run_id].[extension]
```

where:

- `[run_index]` is an identifier that is unique within a sequencing run, e.g. a sequencing barcode identifier, or a 96-well plate co-ordinate.
- `[run_id]` is the name of the sequencing run as given by the supplier's sequencing instrument (not an internal identifier assigned by the supplier).
- `[extension]` is the file extension indicating the file type.

File name extensions

For *paired-end Illumina* sequencing data, the extensions (`[extension]`) should be:

- `1.fastq.gz` for the forward FASTQ file.
- `2.fastq.gz` for the reverse FASTQ file.
- `csv` for the CSV metadata file.

For *single-end Illumina* sequencing data, the extensions (`[extension]`) should be:

- `fastq.gz` for the forward FASTQ file.
- `csv` for the CSV metadata file.

For *ONT* sequencing data, the extensions (`[extension]`) should be:

- `fastq.gz` for the forward FASTQ file.
- `csv` for the CSV metadata file.

Platforms

- For *paired-end Illumina* sequencing data, the (`[platform]`) should be `illumina`.
- For *single-end Illumina* sequencing data, the (`[platform]`) should be `illumina.se`.
- For *ONT* sequencing data, the (`[platform]`) should be `ont`.

Valid characters

The `[run_index]`, `[run_id]` and `[extension]` must contain only:

- Letters (`A-Z`, `a-z`).
- Numbers (`0-9`).
- Hyphens (`-`).
- Underscores (`_`).

Buckets

Bucket names follow the general convention:

```
mscape-[sequencing_org]-[platform]-[test_flag]
```

If you upload your data to an incorrect bucket, it will not be processed or in the worst case may be processed incorrectly, **it is your responsibility to ensure that your data is uploaded correctly!**

Metadata specification

CSV TEMPLATE

A CSV template for uploaders can be downloaded here: mscape-template.csv

REQUIRED FIELDS

Field	Data type	Description	Restrictions
`biosample_id`	`text`	The sequencing provider's identifier for a sample.	• Max length: `50`
`run_index`	`text`	The sequencing provider's identifier for the position of a sample on a run.	• Max length: `50`
`run_id`	`text`	Unique identifier assigned to the run by the sequencing instrument.	• Max length: `100`
`input_type`	`choice`	The type of input sequenced.	• Choices: `community_standard`, `negative_control`, `positive_control`, `specimen`, `validation_material`
`sample_source`	`choice`	The source from which the sample was collected.	• Choices: `blood`, `environment`, `faecal`, `lower_respiratory`, `nose_and_throat`, `other`, `plasma`, `pleural_fluid`, `stool`, `tissue`, `upper_respiratory`, `urine`
`sample_type`	`choice`	The type of sampling method used.	• Choices: `aspirate`, `bal`, `biopsy`, `other`, `sputum`, `swab`
`spike_in`	`choice`	The type of spike-in used in the run.	• Choices: `ERCC-RNA_4456740`, `bacillus_ms2phage`, `ms2-phage`, `none`, `phix`, `tobacco_mosaic_virus`, `zymo_D6320`, `zymo_D6321`

At least one of the following fields are required:

Field	Data type	Description	Restrictions
`collection_date`	`date`	The date the sample was collected.	• Input formats: `YYYY-MM`, `YYYY-MM-DD` • Output format: `YYYY-MM-DD`
`received_date`	`date`	The date the sample was received by the sequencing centre (if collection_date unavailable).	• Input formats: `YYYY-MM`, `YYYY-MM-DD` • Output format: `YYYY-MM-DD`

OPTIONAL FIELDS

Field	Data type	Description	Restrictions
`biosample_source_id`	`text`	Unique identifier for an individual to permit multiple samples from the same individual to be linked.	• Max length: `50`
`specimen_type_details`	`choice`	Named control or standard for specimens.	• Required when `input_type` is: `specimen` • Choices: `asymptomatic`, `respiratory_infection`
`control_type_details`	`choice`	Named control or standard for positive and negative controls.	• Required when `input_type` is: `positive_control` • Required when `input_type` is: `negative_control` • Choices: `NIBSC_11/242`, `NIBSC_20/170`, `bacillus_ms2phage`, `resp_matrix_mc110`, `water_extraction_control`, `zepto_rp2.1`, `zymo-mc_D6300`
`is_approximate_date`	`bool`	The date is approximate e.g. the sample is from a public repository and it is unclear whether the date corresponds to collection or publishing.	• Default: `False`
`batch_id`	`text`	Used to identify samples prepared in the same laboratory batch (e.g. extraction, library and/or sequencing).	• Max length: `100`
`study_id`	`text`	Used to identify study or if NHS residual sample.	• Max length: `100`
`study_centre_id`	`text`	Used to identify sequencing centre.	• Max length: `100`
`sequence_purpose`	`choice`	Used to differentiate between clinical or research studies.	• Choices: `clinical`, `research`
`governance_status`	`choice`	Did the patient consent to their sample being used for research purposes or not.	• Default: `no_consent_for_research` • Choices: `consented_for_research`, `no_consent_for_research`, `open`
`iso_country`	`choice`	Country that the sample was collected in, using ISO-3166-1 alpha-2 codes (https://en.wikipedia.org/wiki/ISO_3166-1_alpha-2), unless within United Kingdom. If so, use ISO-3166-2:GB (https://	• Choices: `AD`, `AE`, `AF`, `AG`, `AI`, `AL`, `AM`, `AO`, `AQ`, `AR`, `AS`, `AT`, `AU`, `AW`, `AX`, `AZ`, `BA`, `BB`, `BD`, `BE`, ...

Field	Data type	Description	Restrictions
		en.wikipedia.org/wiki/ISO_3166-2:GB).	
`iso_region`	`choice`	Region that the sample was collected in, using the second level subdivision codes of ISO-3166-2:GB (https://www.iso.org/obp/ui/#iso:code:3166:GB).	• Requires: `iso_country` • Choices: `GB-ABC`, `GB-ABD`, `GB-ABE`, `GB-AGB`, `GB-AGY`, `GB-AND`, `GB-ANN`, `GB-ANS`, `GB-BAS`, `GB-BBD`, `GB-BCP`, `GB-BDF`, `GB-BDG`, `GB-BEN`, `GB-BEX`, `GB-BFS`, `GB-BGE`, `GB-BGW`, `GB-BIR`, `GB-BKM`, ...
`extraction_enrichment_protocol`	`text`	Details of nucleic acid extraction and optional enrichment steps.	
`library_protocol`	`text`	Details of sequencing library construction.	
`sequencing_protocol`	`text`	Details of sequencing.	
`protocol_arm`	`choice`	Used to indicate arm for protocols which have separate arms for bacterial and viral nucleic acids.	• Choices: `bacterial`, `viral`
`bioinformatics_protocol`	`text`	Detail of initial bioinformatics protocol, for example versions of basecalling software and models used, any read quality filtering/trimming employed.	
`dehumanisation_protocol`	`text`	Details of bioinformatics method used for human read removal.	
`is_public_dataset`	`bool`	The sample is from a public dataset. Please only set this after it has been made public.	• Default: `False`
`public_database_name`	`choice`	The public repository where the data is.	• Choices: `ENA`, `SRA`
`public_database_accession`	`text`	The accession for the data in the public database.	

2025-09-25

2023-11-01

3.2.2 mSCAPE Analysis Specification

ANALYSIS FIELDS

Field	Data type	Description	Res
`published_date`	`date`	The date the object was published in Onyx.	• Ou `iso`
`site`	`choice`	The site or sequencing centre providing the data.	• Ch `gosl` `pub` `uhs` `ukhs`
`climb_id`	`text`	Unique identifier for a project record in Onyx.	
`biosample_id`	`text`	The sequencing provider's identifier for a sample.	
`biosample_source_id`	`text`	Unique identifier for an individual to permit multiple samples from the same individual to be linked.	
`run_id`	`text`	Unique identifier assigned to the run by the sequencing instrument.	
`platform`	`choice`	The platform used to sequence the data.	• Ch `illu`
`input_type`	`choice`	The type of input sequenced.	• Ch `comm` `nega` `posi` `spec` `vali`
`specimen_type_details`	`choice`	Named control or standard for specimens.	• Ch `resp`
`control_type_details`	`choice`	Named control or standard for positive and negative controls.	• Ch `NIBS` `baci` `resp` `wate` `zept` `mc_l`
`sample_source`	`choice`	The source from which the sample was collected.	• Ch `envi` `lowe` `nose` `plas` `stoo` `uppe`
`sample_type`	`choice`	The type of sampling method used.	• Ch `bal` `sput`
`spike_in`	`choice`	The type of spike-in used in the run.	• Ch `RNA_` `baci` `phag` `toba` `zymo`

Field	Data type	Description	Res
spike_in_result	choice	Result assigned by scylla for the provided spike-in.	• Cl par
collection_date	date	The date the sample was collected.	• Ou YYY
received_date	date	The date the sample was received by the sequencing centre (if collection_date unavailable).	• Ou YYY
is_approximate_date	bool	The date is approximate e.g. the sample is from a public repository and it is unclear whether the date corresponds to collection or publishing.	
batch_id	text	Used to identify samples prepared in the same laboratory batch (e.g. extraction, library and/or sequencing).	
study_id	text	Used to identify study or if NHS residual sample.	
study_centre_id	text	Used to identify sequencing centre.	
sequence_purpose	choice	Used to differentiate between clinical or research studies.	• Cl res
governance_status	choice	Did the patient consent to their sample being used for research purposes or not.	• Cl con no_ ope
iso_country	choice	Country that the sample was collected in, using ISO-3166-1 alpha-2 codes (https://en.wikipedia.org/wiki/ISO_3166-1_alpha-2), unless within United Kingdom. If so, use ISO-3166-2:GB (https://en.wikipedia.org/wiki/ISO_3166-2:GB).	• Cl AG , AR , AZ ,
iso_region	choice	Region that the sample was collected in, using the second level subdivision codes of ISO-3166-2:GB (https://www.iso.org/obp/ui/#iso:code:3166:GB).	• Cl ABD GB-A GB-A GB-B GB-B GB-B GB-B
extraction_enrichment_protocol	text	Details of nucleic acid extraction and optional enrichment steps.	
library_protocol	text	Details of sequencing library construction.	
sequencing_protocol	text	Details of sequencing.	
protocol_arm	choice	Used to indicate arm for protocols which have separate arms for bacterial and viral nucleic acids.	• Cl vir
bioinformatics_protocol	text	Detail of initial bioinformatics protocol, for example versions of basecalling software and models used, any read quality filtering/trimming employed.	

Field	Data type	Description	Res
dehumanisation_protocol	text	Details of bioinformatics method used for human read removal.	
is_public_dataset	bool	The sample is from a public dataset. Please only set this after it has been made public.	
public_database_name	choice	The public repository where the data is.	• Cl
public_database_accession	text	The accession for the data in the public database.	
ingest_report	text	HTML report summarising the read profile and taxa identified.	
taxon_reports	text	Folder of all classification output files.	
human_filtered_reads_1	text	Compressed FASTQ of input reads that have been filtered for human reads.	
human_filtered_reads_2	text	Compressed FASTQ of input reads that have been filtered for human reads.	
unclassified_reads_1	text	Compressed FASTQ of input reads which could not be classified.	
unclassified_reads_2	text	Compressed FASTQ of input reads which could not be classified.	
viral_reads_1	text	Compressed FASTQ of input reads which were classified as viral.	
viral_reads_2	text	Compressed FASTQ of input reads which were classified as viral.	
viral_and_unclassified_reads_1	text	Compressed FASTQ of input reads which were classified as viral or were unclassified.	
viral_and_unclassified_reads_2	text	Compressed FASTQ of input reads which were classified as viral or were unclassified.	
total_bases	integer	Total number of bases in the input FASTQ file(s), before any filtering.	
classifier	choice	The classifier used.	• Cl
classifier_version	text	Version of the classifier used.	
classifier_db	choice	Database used for read classification.	• Cl
classifier_db_date	date	Date classifier database was produced.	• Ou YYY
ncbi_taxonomy_date	date	Date that the NCBI taxonomy dump was produced.	• Ou YYY
scylla_version	text	Version of the scylla pipeline used.	
chimera_bam	text	BAM file of the human filtered read fraction aligned to the zeus database.	
is_chimera_published	bool	Whether chimera has been run on this record or not.	
alignment_db_version	text	Version of the Zeus database used.	

Field	Data type	Description	Res
`sylph_db_version`	`text`	Sylph database version utilised to produce Sylph classifications.	
`taxa_files`	`relation`	Table of all species level taxa extracted.	
`taxa_files.taxon_id`	`integer`	The NCBI taxonomy id associated with the taxa.	
`taxa_files.human_readable`	`text`	A human readable name for the taxa.	
`taxa_files.n_reads`	`integer`	The number of reads extracted for the taxa.	
`taxa_files.total_bases`	`integer`	Total number of bases extracted for the taxa.	
`taxa_files.avg_quality`	`decimal`	The mean quality of reads extracted for the taxa.	
`taxa_files.mean_len`	`decimal`	The mean length of reads extracted for the taxa.	
`taxa_files.rank`	`choice`	The rank of the taxa.	• Cl `K`,
`taxa_files.fastq_1`	`text`	Compressed FASTQ of extracted reads for the taxa.	
`taxa_files.fastq_2`	`text`	Compressed FASTQ of extracted reads for the taxa.	
`classifier_calls`	`relation`	Table summarising the NCBI taxonomy ids, counts and ranks of all taxa found by the classifier.	
`classifier_calls.taxon_id`	`integer`	The NCBI taxonomy id associated with the taxa.	
`classifier_calls.human_readable`	`text`	A human readable name for the taxa.	
`classifier_calls.percentage`	`decimal`	The percentage of the (dehumanised) sample that the taxa represents.	
`classifier_calls.count_descendants`	`integer`	The number of reads mapping to this taxa and all descendant taxa.	
`classifier_calls.count_direct`	`integer`	The number of reads mapping directly to the taxa.	
`classifier_calls.rank`	`choice`	The rank of the taxa.	• Cl `K`,
`classifier_calls.raw_rank`	`text`	The rank of the taxa including an intermediate grading.	
`classifier_calls.is_spike_in`	`bool`	The taxa is a spike-in.	
`spike_in_info`	`relation`	Table containing taxonomic results found for the provided spike-in.	
`spike_in_info.taxon_id`	`integer`	The NCBI taxonomy id associated with the taxa.	
`spike_in_info.human_readable`	`text`	A human readable name for the taxa.	
`spike_in_info.reference_header`	`text`	Reference header for the individual sequence within the provided spike-in.	
`spike_in_info.mapped_count`	`integer`	Number of reads which aligned to a reference sequence for the provided spike-in.	

Field	Data type	Description	Res
`alignment_results`	`relation`	Table containing alignment results.	
`alignment_results.taxon_id`	`integer`	The NCBI taxonomy id associated with the taxa.	
`alignment_results.human_readable`	`text`	Human readable scientific name for the taxa.	
`alignment_results.unique_accession`	`text`	Unique reference identifier in the alignment database (everything prior to the first whitespace in the FASTA header).	
`alignment_results.accession_description`	`text`	The comment for the reference sequence within the alignment database.	
`alignment_results.sequence_length`	`integer`	Length of the reference sequence in the alignment database.	
`alignment_results.evenness_value`	`integer`	A percentage indicating how evenly read depths are distributed throughout the reference, with 0 being completely uneven, and 100 being perfectly even. Taken from https://academic.oup.com/nar/article/38/10/e116/2902812, under the “Calculation of evenness score” section, and calculated here: https://github.com/CLIMB-TRE/chimera/blob/dca3cacb949dabc902d0a12e5d11d36c6ac555fd/bin/generate_alignment_report.py#L102.	
`alignment_results.mean_depth`	`integer`	Mean of all depth values across the alignment reference.	
`alignment_results.coverage_1x`	`integer`	Percentage of the reference sequence covered with a depth of at least 1x.	
`alignment_results.coverage_10x`	`integer`	Percentage of the reference covered with a depth of at least 10x.	
`alignment_results.mapped_reads`	`integer`	Total number of reads mapped to the alignment reference.	
`alignment_results.uniquely_mapped_reads`	`integer`	Total number of reads which uniquely map to a reference and position within that reference (MAPQ >= 60).	
`alignment_results.mapped_bases`	`integer`	Approximation for the total number of bases mapped to the alignment reference, calculated from the length of the reference sequence multiplied by the mean depth of alignments to that reference.	
`alignment_results.mean_read_identity`	`decimal`	Mean of read identities across all alignments. Can be considered an approximation for identity of the source genome with the reference sequence. Calculated for each read here: https://github.com/CLIMB-TRE/chimera/blob/dca3cacb949dabc902d0a12e5d11d36c6ac555fd/bin/generate_alignment_report.py#L58	
`alignment_results.read_duplication_rate`	`decimal`	What proportion of the reads start and end in the same alignment reference position as at least one other read within the alignment. Calculated here: https://github.com/CLIMB-TRE/chimera/blob/	

Field	Data type	Description	Res
		dca3cacb949dabc902d0a12e5d11d36c6ac555fd/bin/generate_alignment_report.py#L76-L83	
alignment_results.forward_proportion	decimal	Proportion of reads which aligned to the forward strand. Between 0 and 1, with 0 indicating all reads aligned to the reverse strand, 1 the opposite. True hits should be close to 0.5 for this value for any reasonable mean depth.	
alignment_results.mean_alignment_length	decimal	Mean length of all alignments to the reference - different to mean read length aligned to the reference, since it only considers the aligned section of the reads.	
sylph_results	relation	Table containing sylph results.	
sylph_results.taxon_id	integer	The NCBI taxonomy id associated with the taxa.	
sylph_results.human_readable	text	Human readable scientific name for the taxa.	
sylph_results.gtdb_taxon_string	text	Description of the taxonomic placement of the source contig within the Sylph database using GTDBs taxon string format.	
sylph_results.gtdb_assembly_id	text	Assembly ID (often genbank accession) for the contig within the sylph database, taken from GTDB.	
sylph_results.gtdb_contig_header	text	From the origin FASTA record header as it appears in GTDB. Identical to 'Contig_name' field in sylph profile output.	
sylph_results.taxonomic_abundance	decimal	Normalized taxonomic abundance as a percentage. Identical to 'Taxonomic_abundance' in sylph profile output.	
sylph_results.sequence_abundance	decimal	Normalized sequence abundance as a percentage. Identical to 'Sequence_abundance' in sylph profile output.	
sylph_results.adjusted_ani	decimal	If coverage adjustment is possible (cov is < 3x cov): returns coverage-adjusted ANI (Average Nucleotide Identity). If coverage is too low/high: returns naive_ani. Identical to 'Adjusted_ANI' in sylph profile output.	
sylph_results.ani_confidence_interval	text	[5%,95%] confidence intervals. If coverage adjustment is possible: float-float e.g. 98.52-99.55. If coverage is too low/high: NA-NA is given. Identical to 'ANI_5-95_percentile' field in sylph profile output.	
sylph_results.effective_coverage	decimal	Estimated 'λeff' value, true value is not calculated, this is estimated based on kmers. More information is available in the sylph paper: https://www.nature.com/articles/s41587-024-02412-y. If coverage adjustment is possible, lambda estimate is given. Identical to 'Eff_cov' field in sylph profile output.	
sylph_results.effective_coverage_confidence_interval	text		

Field	Data type	Description	Res
		[5%, 95%] confidence intervals for lambda. Same format rules as 'ani_confidence_interval'. Identical to 'Lambda_5-95_percentile' field in sylph profile output.	
`sylph_results.median_kmer_cov`	`integer`	Median k-mer multiplicity for k-mers with >= 1 multiplicity. Identical to 'Median_cov' field in sylph profile output.	
`sylph_results.mean_kmer_cov`	`decimal`	Mean k-mer multiplicity for k-mers with >= 1 multiplicity. Identical to 'Mean_cov_geq1' field in sylph profile output.	
`sylph_results.containment_index`	`text`	int/int showing the containment index (number of k-mers found in sample divided by total k-mers), e.g. 959/1053. Identical to 'Containment_ind' field in sylph profile output.	
`sylph_results.naive_ani`	`decimal`	Containment ANI without coverage adjustment. Identical to 'Naive_ANI' field in sylph profile output.	
`sylph_results.kmers_reassigned`	`integer`	The number of k-mers reassigned away from the genome. Identical to 'Kmers_reassigned' field in sylph profile output.	

2024-03-13

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3.2.3 mSCAPE Changelog

All notable changes to CLIMB-TRE mSCAPE APIs, data or interchange formats that have impact to users or other pipelines should be documented in this file. Changes described here may only be a subset of all changes to a project as this log concerns itself only with changes that impact how data is provided or consumed by users or other pipelines.

The following DIPI projects are routinely using this changelog:

- `Scylla` -- ingest analysis pipeline
- `Roz` -- ingest management
- `Onyx` -- metadata database
- `Onyx-client` -- API for interacting with metadata database

The format is based on Keep a Changelog.

Issues can be reported to the mSCAPE DIPI group.

2025-09-15

ONYX

Added

- Added `ucl` (University College London) `site` option.
- Added `ukhsamanc` (UKHSA Manchester Lab) `site` option.
- Added `ukhsabris` (UKHSA Bristol Lab) `site` option.

2025-08-13

ONYX

Added

- Added `control_type_details` choice `bacillus_ms2phage`, constrained by an `input_type` of `positive_control`.
- Added optional choice field `protocol_arm`, with choices `bacterial` and `viral`.

SCYLLA

Release 2.1.0

Changed

- Large speedup of all read extract scripts
- Per read quality scores are now based on mean rather than median

2025-08-05

SCYLLA

Release 2.0.3

Changed

- Resolve missing total_length.json when no taxa files output

2025-08-05

ONYX

Added

- Added `spike_in` option `bacillus_ms2phage`.

SCYLLA

Release 2.0.2

Added

- Added `spike_in` option `bacillus_ms2phage`.

Changed

- Changed reference to --local flag in README/tests for local running to -profile local (can be combined with docker using -profile local,docker)

2025-07-02

ONYX

Added

- Added `total_bases` field, for recording the number of bases in the input FASTQ file(s), before any filtering.
- Added `taxa_files.total_bases` field, for recording the number of bases extracted for a taxa (assignable for each taxa within the `taxa_files` of a record).

SCYLLA

Release 2.0.1

Changed

- Change the exitcode for script which checks paired fastq files so that the pipeline doesn't fail loudly with mismatched headers

2025-05-08

SCYLLA

Released version 2.0.0. Given the number of changes, they are grouped by category rather than Added/Changed etc.

HCID changes

- Add `min_coverage` parameter to HCID JSON
- Update references in HCID JSON and reference file
- Update thresholds for HCID detection
- Drop requirement for classified reads at taxon/parent level for HCID to be detected (mapping sufficient)
- Output reads corresponding to HCIDs which have flagged a warning (NEW OUTPUT in `qc/<taxid>.reads.fq`)
- Output read stats for HCID reads to the warning JSON (`mapped_mean_quality` and `mapped_mean_length`)
- Add coverage information for HCID found showing how many bases have coverage at each level - in HCID JSON

Extract taxa changes

- Reworked code to interact with kraken reports and assignment files during extract steps. Found a bug where some of the counts in the summary had previously been double counted (where both a S and S1 or S2 level taxa were extracted)
- Extract reads at different levels for different domains as specified by config (`F` for Viruses, `G` for everything else)
- Only extract reads at the specific level, not sublevels (e.g. S not S1 or S2)
- Add `total_len` calculated both for input and extracted output files in the summary JSON (NEW OUTPUT `qc/total_length.json`)

- Make extraction percentages domain-specific (e.g. 1% of bacterial reads rather than 1% of classified reads) to fix zepto example
- To extract a taxon, needs to pass count threshold OR the percentage threshold (previously both) and increase the count threshold for bacteria to 500

Workflow changes

- Add workflow to reclassify the viral+unclassified fraction with a second database
- In the process, the parameters associated with kraken databases have been restructured. Replace `--k2_host` with `--kraken_database.default.host`, `--k2_port` with `--kraken_database.default.port`, `--database` with `--kraken_database.default.path` and `database_set` is now `kraken_database.default.name`. This allows a second dictionary of kraken parameters for `kraken_database.virus` to be defined if/when necessary.
- Add code to merge kraken assignment files, giving preference to second assignment file
- Add code to update kraken report, giving list of changes made to assignments
- Add a QC script to check the input file where a single fastq file is provided, so that it can warn if there are duplicate headers. This was seen in some example data and would cause big problems for the viral reclassification step when run, as read names need to be unique. If it finds duplicate/unexpectedly interleaved files, tries to correct them but then exists. The user can try rerunning with the fixed files. I considered silently handling but this approach seemed dangerous.
- Add messaging if paired reads provided and `--paired` not.
- Add a workflow to run modules (use `--module <name>`) and remove workflow definitions from within these modules
- Add a warning for incorrect Phred parsing as this is thought to be a resolved issue

Nextflow changes

- set `docker.userEmulation = true`

Other changes

- Add to README more helpful
- Review all local test commands and make sure they run as expected.

2025-03-31

ONYX

Added

- Added `nuth` (Newcastle upon Tyne Hospitals NHS Foundation Trust) as an option in the mSCAPE `site` field.

2025-03-06

ALL

- Start of changelog

2025-09-22

2025-03-06

3.3 PATH-SAFE

3.3.1 PATH-SAFE Uploader Specification

Files to be provided

- A FASTQ 1 file containing the forward sequencing reads.
- A FASTQ 2 file containing the reverse sequencing reads.
- A CSV file containing the metadata associated with sequencing the sample.

File naming convention

The base filenames should be of the form

```
pathsafe.[run_index].[run_id].[extension]
```

where:

- `[run_index]` is an identifier that is unique within a sequencing run, e.g. a sequencing barcode identifier, or a 96-well plate co-ordinate.
- `[run_id]` is the name of the sequencing run as given by the supplier's sequencing instrument (not an internal identifier assigned by the supplier).
- `[extension]` is the file extension indicating the file type.

File name extensions

The extensions (`[extension]`) should be:

- `1.fastq.gz` for the forward FASTQ file.
- `2.fastq.gz` for the reverse FASTQ file.
- `csv` for the CSV metadata file.

Valid characters

The `[run_index]`, `[run_id]` and `[extension]` must contain only:

- Letters (`A-Z`, `a-z`).
- Numbers (`0-9`).
- Hyphens (`-`).
- Underscores (`_`).

Metadata specification

CSV TEMPLATE

A CSV template for uploaders can be downloaded here: pathsafe-template.csv

REQUIRED FIELDS

Field	Data type	Description	Restrictions
`biosample_id`	`text`	The sequencing providers identifier for a sample.	• Max length: `50`
`run_index`	`text`	The sequencing provider's identifier for the position of a sample on a run.	• Max length: `50`
`run_id`	`text`	The unique identifier assigned to the run by the sequencing instrument.	• Max length: `100`
`submitted_species`	`choice`	The NCBI taxonomy id provided for the sample.	• Choices: `1639`, `28901`, `562`
`year`	`integer`	Year of sample collected if available or year of sample receipt otherwise.	• Min value: `2000`
`data_steward`	`choice`	Laboratory, organisation or agency that hold the data for the sample.	• Choices: `APHA`, `FSA`, `FSS`, `OTHER`, `PHS`, `PHW`, `SEPA`, `SSSCDRL`, `UKHSA`
`source_type`	`choice`	Source of the sample.	• Choices: `animal`, `animal_associated_environment`, `environment`, `food`, `food_associated_environment`, `human`, `human_associated_environment`, `missing`, `not_applicable`, `not_collected`, `not_provided`, `other`, `other_environment`, `restricted_access`
`country`	`choice`	The country that the sample was collected in, using ISO-3166-1 alpha-2 codes (https://en.wikipedia.org/wiki/List_of_ISO_3166_country_codes), unless within United Kingdom. If so, use ISO-3166-2:GB (https://en.wikipedia.org/wiki/ISO_3166-2:GB).	• Choices: `GB`, `GB-ENG`, `GB-NIR`, `GB-SCT`, `GB-WLS`
`sample_purpose`	`choice`	The purpose of the sample collection.	• Choices: `active_surveillance`, `not_applicable`, `not_collected`, `not_provided`, `other`, `outbreak_initiated_surveillance`, `outbreak_investigation`, `population_based_surveillance`, `research`, `restricted_access`, `routine_diagnostics`, `routine_surveillance`

OPTIONAL FIELDS

Field	Data type	Description	Restrictions
`biosample_source_id`	`text`	Unique identifier for an individual to permit multiple samples from the same individual to be linked.	• Max length: `50`
`sample_accession`	`text`	Sample accession number if sequence is publically available in SRA.	
`enterobase_barcode`	`text`	Sample barcode if sequence is publically available in EnteroBase.	
`collection_date`	`date`	Date of sample collection.	• Input formats: `YYYY-MM` • Output format: `YYYY-MM`
`receipt_date`	`date`	Date of receipt of the sample.	• Input formats: `YYYY-MM` • Output format: `YYYY-MM`
`month`	`integer`	Month of sample collected if available or month of receipt otherwise.	• Min value: `1` • Max value: `12`
`sequence_org`	`choice`	Laboratory, organisation or agency the sample has been sequenced by.	• Choices: `APHA`, `FSA`, `FSS`, `OTHER`, `PHS`, `PHW`, `SEPA`, `SSSCDRL`, `UKHSA`
`sequence_org_other`	`text`	Additional laboratory, organisation or agency the sample has been sequenced by.	• Requires: `sequence_org` • Required when `sequence_org` is: `OTHER`
`data_steward_other`	`text`	Additional laboratory, organisation or agency that hold the data for the sample.	• Requires: `data_steward` • Required when `data_steward` is: `OTHER`
`county`	`choice`	County that the sample was collected in, using the second level subdivision codes of ISO-3166-2:GB (https://www.iso.org/obp/ui/#iso:code:3166:GB).	• Requires: `country` • Choices: `GB-ABC`, `GB-ABD`, `GB-ABE`, `GB-AGB`, `GB-AGY`, `GB-AND`, `GB-ANN`, `GB-ANS`, `GB-BAS`, `GB-BBD`, `GB-BCP`, `GB-BDF`, `GB-BDG`, `GB-BEN`, `GB-BEX`, `GB-BFS`, `GB-BGE`, `GB-BGW`, `GB-BIR`, `GB-BKM`, ...
`sample_purpose_other`	`text`	Additional purpose of the sample collection.	• Requires: `sample_purpose` • Required when `sample_purpose` is: `other`
`sequencing_kit`	`text`	The sequencing kit used.	
`library_kit`	`text`	The library kit used to prep the sample.	
`is_multiplexed`	`bool`	Whether the sample was multiplexed.	
`type_of_sample`	`choice`	Type of sample used to produce the sequence.	• Default: `genomic` • Choices: `genomic`

2025-09-08

2023-11-01

3.3.2 PATH-SAFE Analysis Specification

ANALYSIS FIELDS

Field	Data type	Description	Restrictions
`published_date`	`date`	The date the object was published in Onyx.	• Output format: `iso-8601`
`site`	`choice`	Laboratory, organisation or agency the sample has been submitted by.	• Choices: `APHA`, `CGPS`, `FSA`, `FSS`, `PHS`, `SSSCDRL`, `UKHSA`
`climb_id`	`text`	Unique identifier for a project record in Onyx.	
`biosample_id`	`text`	The sequencing providers identifier for a sample.	
`biosample_source_id`	`text`	Unique identifier for an individual to permit multiple samples from the same individual to be linked.	
`run_id`	`text`	The unique identifier assigned to the run by the sequencing instrument.	
`platform`	`choice`	The platform used to sequence the data.	• Choices: `illumina`
`submitted_species`	`choice`	The NCBI taxonomy id provided for the sample.	• Choices: `1639`, `28901`, `562`
`sample_accession`	`text`	Sample accession number if sequence is publically available in SRA.	
`enterobase_barcode`	`text`	Sample barcode if sequence is publically available in EnteroBase.	
`collection_date`	`date`	Date of sample collection.	• Output format: `YYYY-MM`
`receipt_date`	`date`	Date of receipt of the sample.	• Output format: `YYYY-MM`
`month`	`integer`	Month of sample collected if available or month of receipt otherwise.	
`year`	`integer`	Year of sample collected if available or year of sample receipt otherwise.	
`sequence_org`	`choice`	Laboratory, organisation or agency the sample has been sequenced by.	• Choices: `APHA`, `FSA`, `FSS`, `OTHER`, `PHS`, `PHW`, `SEPA`, `SSSCDRL`, `UKHSA`
`sequence_org_other`	`text`	Additional laboratory, organisation or agency the sample has been sequenced by.	
`data_steward`	`choice`	Laboratory, organisation or agency that hold the data for the sample.	• Choices: `APHA`, `FSA`, `FSS`, `OTHER`, `PHS`, `PHW`, `SEPA`, `SSSCDRL`, `UKHSA`
`data_steward_other`	`text`	Additional laboratory, organisation or agency that hold the data for the sample.	

Field	Data type	Description	Restrictions
`source_type`	`choice`	Source of the sample.	• Choices: `animal`, `animal_associated_environment`, `environment`, `food`, `food_associated_environment`, `human`, `human_associated_environment`, `missing`, `not_applicable`, `not_collected`, `not_provided`, `other`, `other_environment`, `restricted_access`
`country`	`choice`	The country that the sample was collected in, using ISO-3166-1 alpha-2 codes (https://en.wikipedia.org/wiki/List_of_ISO_3166_country_codes), unless within United Kingdom. If so, use ISO-3166-2:GB (https://en.wikipedia.org/wiki/ISO_3166-2:GB).	• Choices: `GB`, `GB-ENG`, `GB-NIR`, `GB-SCT`, `GB-WLS`
`county`	`choice`	County that the sample was collected in, using the second level subdivision codes of ISO-3166-2:GB (https://www.iso.org/obp/ui/#iso:code:3166:GB).	• Choices: `GB-ABC`, `GB-ABD`, `GB-ABE`, `GB-AGB`, `GB-AGY`, `GB-AND`, `GB-ANN`, `GB-ANS`, `GB-BAS`, `GB-BBD`, `GB-BCP`, `GB-BDF`, `GB-BDG`, `GB-BEN`, `GB-BEX`, `GB-BFS`, `GB-BGE`, `GB-BGW`, `GB-BIR`, `GB-BKM`, ...
`sample_purpose`	`choice`	The purpose of the sample collection.	• Choices: `active_surveillance`, `not_applicable`, `not_collected`, `not_provided`, `other`, `outbreak_initiated_surveillance`, `outbreak_investigation`, `population_based_surveillance`, `research`, `restricted_access`, `routine_diagnostics`, `routine_surveillance`
`sample_purpose_other`	`text`	Additional purpose of the sample collection.	
`sequencing_kit`	`text`	The sequencing kit used.	
`library_kit`	`text`	The library kit used to prep the sample.	
`is_multiplexed`	`bool`	Whether the sample was multiplexed.	
`type_of_sample`	`choice`	Type of sample used to produce the sequence.	• Choices: `genomic`
`assembly`	`text`	Assembly FASTA file.	
`pathogenwatch_uuid`	`text`	UUID from Pathogenwatch.	

2024-03-14

2024-03-14

3.4 synthSCAPE

3.4.1 synthSCAPE Uploader Specification

Files to be provided

For *paired-end Illumina* sequencing data, suppliers must provide:

- A FASTQ 1 file containing the forward sequencing reads.
- A FASTQ 2 file containing the reverse sequencing reads.
- A CSV file containing the metadata associated with sequencing the sample.

For *single-end Illumina* sequencing data, suppliers must provide:

- A FASTQ file containing the sequencing reads.
- A CSV file containing the metadata associated with sequencing the sample.

For *ONT* sequencing data, suppliers must provide:

- A FASTQ file containing the sequencing reads.
- A CSV file containing the metadata associated with sequencing the sample.

Sequencing data must be dehumanised prior to submission. The ingest pipeline will reject sequencing data where the number of assigned human reads exceeds the human read rejection threshold.

File naming convention

The base filenames should be of the form

```
synthscape.[run_index].[run_id].[extension]
```

where:

- `[run_index]` is an identifier that is unique within a sequencing run, e.g. a sequencing barcode identifier, or a 96-well plate co-ordinate.
- `[run_id]` is the name of the sequencing run as given by the supplier's sequencing instrument (not an internal identifier assigned by the supplier).
- `[extension]` is the file extension indicating the file type.

File name extensions

For *paired-end Illumina* sequencing data, the extensions (`[extension]`) should be:

- `1.fastq.gz` for the forward FASTQ file.
- `2.fastq.gz` for the reverse FASTQ file.
- `csv` for the CSV metadata file.

For *single-end Illumina* sequencing data, the extensions (`[extension]`) should be:

- `fastq.gz` for the forward FASTQ file.
- `csv` for the CSV metadata file.

For *ONT* sequencing data, the extensions (`[extension]`) should be:

- `fastq.gz` for the forward FASTQ file.
- `csv` for the CSV metadata file.

Valid characters

The `[run_index]`, `[run_id]` and `[extension]` must contain only:

- Letters (`A-Z`, `a-z`).
- Numbers (`0-9`).
- Hyphens (`-`).
- Underscores (`_`).

Buckets

Bucket names follow the general convention:

```
synthscape-[sequencing_org]-[platform]-[test_flag]
```

Metadata specification

CSV TEMPLATE

A CSV template for uploaders can be downloaded here: synthscape-template.csv

REQUIRED FIELDS

Field	Data type	Description	Restrictions
`biosample_id`	`text`	The sequencing provider's identifier for a sample.	• Max length: `50`
`run_index`	`text`	The sequencing provider's identifier for the position of a sample on a run.	• Max length: `50`
`run_id`	`text`	Unique identifier assigned to the run by the sequencing instrument.	• Max length: `100`
`input_type`	`choice`	The type of input sequenced.	• Choices: `community_standard`, `negative_control`, `positive_control`, `specimen`, `validation_material`
`sample_source`	`choice`	The source from which the sample was collected.	• Choices: `blood`, `environment`, `faecal`, `lower_respiratory`, `nose_and_throat`, `other`, `plasma`, `pleural_fluid`, `stool`, `tissue`, `upper_respiratory`, `urine`
`sample_type`	`choice`	The type of sampling method used.	• Choices: `aspirate`, `bal`, `biopsy`, `other`, `sputum`, `swab`
`spike_in`	`choice`	The type of spike-in used in the run.	• Choices: `ERCC-RNA_4456740`, `bacillus_ms2phage`, `ms2-phage`, `none`, `phix`, `tobacco_mosaic_virus`, `zymo_D6320`, `zymo_D6321`

At least one of the following fields are required:

Field	Data type	Description	Restrictions
`collection_date`	`date`	The date the sample was collected.	• Input formats: `YYYY-MM`, `YYYY-MM-DD` • Output format: `YYYY-MM-DD`
`received_date`	`date`	The date the sample was received by the sequencing centre (if collection_date unavailable).	• Input formats: `YYYY-MM`, `YYYY-MM-DD` • Output format: `YYYY-MM-DD`

OPTIONAL FIELDS

Field	Data type	Description	Restrictions
`biosample_source_id`	`text`	Unique identifier for an individual to permit multiple samples from the same individual to be linked.	• Max length: `50`
`specimen_type_details`	`choice`	Named control or standard for specimens.	• Required when `input_type` is: `specimen` • Choices: `asymptomatic`, `respiratory_infection`
`control_type_details`	`choice`	Named control or standard for positive and negative controls.	• Required when `input_type` is: `positive_control` • Required when `input_type` is: `negative_control` • Choices: `NIBSC_11/242`, `NIBSC_20/170`, `bacillus_ms2phage`, `resp_matrix_mc110`, `water_extraction_control`, `zepto_rp2.1`, `zymo-mc_D6300`
`is_approximate_date`	`bool`	The date is approximate e.g. the sample is from a public repository and it is unclear whether the date corresponds to collection or publishing.	• Default: `False`
`batch_id`	`text`	Used to identify samples prepared in the same laboratory batch (e.g. extraction, library and/or sequencing).	• Max length: `100`
`study_id`	`text`	Used to identify study or if NHS residual sample.	• Max length: `100`
`study_centre_id`	`text`	Used to identify sequencing centre.	• Max length: `100`
`sequence_purpose`	`choice`	Used to differentiate between clinical or research studies.	• Choices: `clinical`, `research`
`governance_status`	`choice`	Did the patient consent to their sample being used for research purposes or not.	• Default: `no_consent_for_research` • Choices: `consented_for_research`, `no_consent_for_research`, `open`
`iso_country`	`choice`	Country that the sample was collected in, using ISO-3166-1 alpha-2 codes (https://en.wikipedia.org/wiki/ISO_3166-1_alpha-2), unless within United Kingdom. If so, use ISO-3166-2:GB (https://	• Choices: `AD`, `AE`, `AF`, `AG`, `AI`, `AL`, `AM`, `AO`, `AQ`, `AR`, `AS`, `AT`, `AU`, `AW`, `AX`, `AZ`, `BA`, `BB`, `BD`, `BE`, ...

Field	Data type	Description	Restrictions
		en.wikipedia.org/wiki/ISO_3166-2:GB).	
`iso_region`	`choice`	Region that the sample was collected in, using the second level subdivision codes of ISO-3166-2:GB (https://www.iso.org/obp/ui/#iso:code:3166:GB).	• Requires: `iso_country` • Choices: `GB-ABC`, `GB-ABD`, `GB-ABE`, `GB-AGB`, `GB-AGY`, `GB-AND`, `GB-ANN`, `GB-ANS`, `GB-BAS`, `GB-BBD`, `GB-BCP`, `GB-BDF`, `GB-BDG`, `GB-BEN`, `GB-BEX`, `GB-BFS`, `GB-BGE`, `GB-BGW`, `GB-BIR`, `GB-BKM`, ...
`extraction_enrichment_protocol`	`text`	Details of nucleic acid extraction and optional enrichment steps.	
`library_protocol`	`text`	Details of sequencing library construction.	
`sequencing_protocol`	`text`	Details of sequencing.	
`protocol_arm`	`choice`	Used to indicate arm for protocols which have separate arms for bacterial and viral nucleic acids.	• Choices: `bacterial`, `viral`
`bioinformatics_protocol`	`text`	Detail of initial bioinformatics protocol, for example versions of basecalling software and models used, any read quality filtering/trimming employed.	
`dehumanisation_protocol`	`text`	Details of bioinformatics method used for human read removal.	
`is_public_dataset`	`bool`	The sample is from a public dataset. Please only set this after it has been made public.	• Default: `False`
`public_database_name`	`choice`	The public repository where the data is.	• Choices: `ENA`, `SRA`
`public_database_accession`	`text`	The accession for the data in the public database.	
`source_climb_id`	`text`	CLIMB ID of the record used as a base dataset.	• Max length: `12`
`spiked_ids`	`array`	JSON list of taxon ids included in the spike-in.	• Default: `[]` • Array type: `integer`
`applications`	`array`	JSON list of applications.	• Default: `[]` • Array type: `text`
`methods`	`structure`	JSON dictionary containing methods.	• Default: `{}`

2025-09-08

2024-09-16

3.4.2 synthSCAPE Analysis Specification

ANALYSIS FIELDS

Field	Data type	Description	Res
published_date	date	The date the object was published in Onyx.	• Ou iso
site	choice	The site or sequencing centre providing the data.	• Ch syn
climb_id	text	Unique identifier for a project record in Onyx.	
biosample_id	text	The sequencing provider's identifier for a sample.	
biosample_source_id	text	Unique identifier for an individual to permit multiple samples from the same individual to be linked.	
run_id	text	Unique identifier assigned to the run by the sequencing instrument.	
platform	choice	The platform used to sequence the data.	• Ch ill
input_type	choice	The type of input sequenced.	• Ch com nega posi spe val
specimen_type_details	choice	Named control or standard for specimens.	• Ch resp
control_type_details	choice	Named control or standard for positive and negative controls.	• Ch NIBS baci resp wate zept mc_
sample_source	choice	The source from which the sample was collected.	• Ch envi lowe nose plas stoc uppe
sample_type	choice	The type of sampling method used.	• Ch bal spu
spike_in	choice	The type of spike-in used in the run.	• Ch RNA_ baci phag toba zymo
spike_in_result	choice	Result assigned by scylla for the provided spike-in.	• Ch part
collection_date	date	The date the sample was collected.	

Field	Data type	Description	Res
			• Ou YYY
received_date	date	The date the sample was received by the sequencing centre (if collection_date unavailable).	• Ou YYY
is_approximate_date	bool	The date is approximate e.g. the sample is from a public repository and it is unclear whether the date corresponds to collection or publishing.	
batch_id	text	Used to identify samples prepared in the same laboratory batch (e.g. extraction, library and/or sequencing).	
study_id	text	Used to identify study or if NHS residual sample.	
study_centre_id	text	Used to identify sequencing centre.	
sequence_purpose	choice	Used to differentiate between clinical or research studies.	• Ch rese
governance_status	choice	Did the patient consent to their sample being used for research purposes or not.	• Ch cons no_ open
iso_country	choice	Country that the sample was collected in, using ISO-3166-1 alpha-2 codes (https://en.wikipedia.org/wiki/ISO_3166-1_alpha-2), unless within United Kingdom. If so, use ISO-3166-2:GB (https://en.wikipedia.org/wiki/ISO_3166-2:GB).	• Ch AG , AR , AZ ,
iso_region	choice	Region that the sample was collected in, using the second level subdivision codes of ISO-3166-2:GB (https://www.iso.org/obp/ui/#iso:code:3166:GB).	• Ch ABD GB-A GB-A GB-B GB-B GB-B GB-B
extraction_enrichment_protocol	text	Details of nucleic acid extraction and optional enrichment steps.	
library_protocol	text	Details of sequencing library construction.	
sequencing_protocol	text	Details of sequencing.	
protocol_arm	choice	Used to indicate arm for protocols which have separate arms for bacterial and viral nucleic acids.	• Ch vira
bioinformatics_protocol	text	Detail of initial bioinformatics protocol, for example versions of basecalling software and models used, any read quality filtering/trimming employed.	
dehumanisation_protocol	text	Details of bioinformatics method used for human read removal.	

Field	Data type	Description	Res
`is_public_dataset`	`bool`	The sample is from a public dataset. Please only set this after it has been made public.	
`public_database_name`	`choice`	The public repository where the data is.	• Cl
`public_database_accession`	`text`	The accession for the data in the public database.	
`ingest_report`	`text`	HTML report summarising the read profile and taxa identified.	
`taxon_reports`	`text`	Folder of all classification output files.	
`human_filtered_reads_1`	`text`	Compressed FASTQ of input reads that have been filtered for human reads.	
`human_filtered_reads_2`	`text`	Compressed FASTQ of input reads that have been filtered for human reads.	
`unclassified_reads_1`	`text`	Compressed FASTQ of input reads which could not be classified.	
`unclassified_reads_2`	`text`	Compressed FASTQ of input reads which could not be classified.	
`viral_reads_1`	`text`	Compressed FASTQ of input reads which were classified as viral.	
`viral_reads_2`	`text`	Compressed FASTQ of input reads which were classified as viral.	
`viral_and_unclassified_reads_1`	`text`	Compressed FASTQ of input reads which were classified as viral or were unclassified.	
`viral_and_unclassified_reads_2`	`text`	Compressed FASTQ of input reads which were classified as viral or were unclassified.	
`total_bases`	`integer`	Total number of bases in the input FASTQ file(s), before any filtering.	
`classifier`	`choice`	The classifier used.	• Cl
`classifier_version`	`text`	Version of the classifier used.	
`classifier_db`	`choice`	Database used for read classification.	• Cl
`classifier_db_date`	`date`	Date classifier database was produced.	• Ou `YYY`
`ncbi_taxonomy_date`	`date`	Date that the NCBI taxonomy dump was produced.	• Ou `YYY`
`scylla_version`	`text`	Version of the scylla pipeline used.	
`chimera_bam`	`text`	BAM file of the human filtered read fraction aligned to the zeus database.	
`is_chimera_published`	`bool`	Whether chimera has been run on this record or not.	
`alignment_db_version`	`text`	Version of the Zeus database used.	
`sylph_db_version`	`text`	Sylph database version utilised to produce Sylph classifications.	

Field	Data type	Description	Res
source_climb_id	text	CLIMB ID of the record used as a base dataset.	
spiked_ids	array	JSON list of taxon ids included in the spike-in.	• Ar
applications	array	JSON list of applications.	• Ar
methods	structure	JSON dictionary containing methods.	
taxa_files	relation	Table of all species level taxa extracted.	
taxa_files.taxon_id	integer	The NCBI taxonomy id associated with the taxa.	
taxa_files.human_readable	text	A human readable name for the taxa.	
taxa_files.n_reads	integer	The number of reads extracted for the taxa.	
taxa_files.total_bases	integer	Total number of bases extracted for the taxa.	
taxa_files.avg_quality	decimal	The mean quality of reads extracted for the taxa.	
taxa_files.mean_len	decimal	The mean length of reads extracted for the taxa.	
taxa_files.rank	choice	The rank of the taxa.	• Cl K,
taxa_files.fastq_1	text	Compressed FASTQ of extracted reads for the taxa.	
taxa_files.fastq_2	text	Compressed FASTQ of extracted reads for the taxa.	
classifier_calls	relation	Table summarising the NCBI taxonomy ids, counts and ranks of all taxa found by the classifier.	
classifier_calls.taxon_id	integer	The NCBI taxonomy id associated with the taxa.	
classifier_calls.human_readable	text	A human readable name for the taxa.	
classifier_calls.percentage	decimal	The percentage of the (dehumanised) sample that the taxa represents.	
classifier_calls.count_descendants	integer	The number of reads mapping to this taxa and all descendant taxa.	
classifier_calls.count_direct	integer	The number of reads mapping directly to the taxa.	
classifier_calls.rank	choice	The rank of the taxa.	• Cl K,
classifier_calls.raw_rank	text	The rank of the taxa including an intermediate grading.	
classifier_calls.is_spike_in	bool	The taxa is a spike-in.	
spike_in_info	relation	Table containing taxonomic results found for the provided spike-in.	
spike_in_info.taxon_id	integer	The NCBI taxonomy id associated with the taxa.	
spike_in_info.human_readable	text	A human readable name for the taxa.	
spike_in_info.reference_header	text	Reference header for the individual sequence within the provided spike-in.	

Field	Data type	Description	Res
`spike_in_info.mapped_count`	`integer`	Number of reads which aligned to a reference sequence for the provided spike-in.	
`alignment_results`	`relation`	Table containing alignment results.	
`alignment_results.taxon_id`	`integer`	The NCBI taxonomy id associated with the taxa.	
`alignment_results.human_readable`	`text`	Human readable scientific name for the taxa.	
`alignment_results.unique_accession`	`text`	Unique reference identifier in the alignment database (everything prior to the first whitespace in the FASTA header).	
`alignment_results.accession_description`	`text`	The comment for the reference sequence within the alignment database.	
`alignment_results.sequence_length`	`integer`	Length of the reference sequence in the alignment database.	
`alignment_results.evenness_value`	`integer`	A percentage indicating how evenly read depths are distributed throughout the reference, with 0 being completely uneven, and 100 being perfectly even. Taken from https://academic.oup.com/nar/article/38/10/e116/2902812, under the “Calculation of evenness score” section, and calculated here: https://github.com/CLIMB-TRE/chimera/blob/dca3cacb949dabc902d0a12e5d11d36c6ac555fd/bin/generate_alignment_report.py#L102.	
`alignment_results.mean_depth`	`integer`	Mean of all depth values across the alignment reference.	
`alignment_results.coverage_1x`	`integer`	Percentage of the reference sequence covered with a depth of at least 1x.	
`alignment_results.coverage_10x`	`integer`	Percentage of the reference covered with a depth of at least 10x.	
`alignment_results.mapped_reads`	`integer`	Total number of reads mapped to the alignment reference.	
`alignment_results.uniquely_mapped_reads`	`integer`	Total number of reads which uniquely map to a reference and position within that reference (MAPQ >= 60).	
`alignment_results.mapped_bases`	`integer`	Approximation for the total number of bases mapped to the alignment reference, calculated from the length of the reference sequence multiplied by the mean depth of alignments to that reference.	
`alignment_results.mean_read_identity`	`decimal`	Mean of read identities across all alignments. Can be considered an approximation for identity of the source genome with the reference sequence. Calculated for each read here: https://github.com/CLIMB-TRE/chimera/blob/dca3cacb949dabc902d0a12e5d11d36c6ac555fd/bin/generate_alignment_report.py#L58	
`alignment_results.read_duplication_rate`	`decimal`	What proportion of the reads start and end in the same alignment reference position as at	

Field	Data type	Description	Res
		least one other read within the alignment. Calculated here: https://github.com/CLIMB-TRE/chimera/blob/dca3cacb949dabc902d0a12e5d11d36c6ac555fd/bin/generate_alignment_report.py#L76-L83	
`alignment_results.forward_proportion`	`decimal`	Proportion of reads which aligned to the forward strand. Between 0 and 1, with 0 indicating all reads aligned to the reverse strand, 1 the opposite. True hits should be close to 0.5 for this value for any reasonable mean depth.	
`alignment_results.mean_alignment_length`	`decimal`	Mean length of all alignments to the reference - different to mean read length aligned to the reference, since it only considers the aligned section of the reads.	
`sylph_results`	`relation`	Table containing sylph results.	
`sylph_results.taxon_id`	`integer`	The NCBI taxonomy id associated with the taxa.	
`sylph_results.human_readable`	`text`	Human readable scientific name for the taxa.	
`sylph_results.gtdb_taxon_string`	`text`	Description of the taxonomic placement of the source contig within the Sylph database using GTDBs taxon string format.	
`sylph_results.gtdb_assembly_id`	`text`	Assembly ID (often genbank accession) for the contig within the sylph database, taken from GTDB.	
`sylph_results.gtdb_contig_header`	`text`	From the origin FASTA record header as it appears in GTDB. Identical to 'Contig_name' field in sylph profile output.	
`sylph_results.taxonomic_abundance`	`decimal`	Normalized taxonomic abundance as a percentage. Identical to 'Taxonomic_abundance' in sylph profile output.	
`sylph_results.sequence_abundance`	`decimal`	Normalized sequence abundance as a percentage. Identical to 'Sequence_abundance' in sylph profile output.	
`sylph_results.adjusted_ani`	`decimal`	If coverage adjustment is possible (cov is < 3x cov): returns coverage-adjusted ANI (Average Nucleotide Identity). If coverage is too low/high: returns naive_ani. Identical to 'Adjusted_ANI' in sylph profile output.	
`sylph_results.ani_confidence_interval`	`text`	[5%,95%] confidence intervals. If coverage adjustment is possible: float-float e.g. 98.52-99.55. If coverage is too low/high: NA-NA is given. Identical to 'ANI_5-95_percentile' field in sylph profile output.	
`sylph_results.effective_coverage`	`decimal`	Estimated 'λeff' value, true value is not calculated, this is estimated based on kmers. More information is available in the sylph paper: https://www.nature.com/articles/s41587-024-02412-y. If coverage adjustment is	

Field	Data type	Description	Res
		possible, lambda estimate is given. Identical to 'Eff_cov' field in sylph profile output.	
`sylph_results.effective_coverage_confidence_interval`	`text`	[5%, 95%] confidence intervals for lambda. Same format rules as 'ani_confidence_interval'. Identical to 'Lambda_5-95_percentile' field in sylph profile output.	
`sylph_results.median_kmer_cov`	`integer`	Median k-mer multiplicity for k-mers with >= 1 multiplicity. Identical to 'Median_cov' field in sylph profile output.	
`sylph_results.mean_kmer_cov`	`decimal`	Mean k-mer multiplicity for k-mers with >= 1 multiplicity. Identical to 'Mean_cov_geq1' field in sylph profile output.	
`sylph_results.containment_index`	`text`	int/int showing the containment index (number of k-mers found in sample divided by total k-mers), e.g. 959/1053. Identical to 'Containment_ind' field in sylph profile output.	
`sylph_results.naive_ani`	`decimal`	Containment ANI without coverage adjustment. Identical to 'Naive_ANI' field in sylph profile output.	
`sylph_results.kmers_reassigned`	`integer`	The number of k-mers reassigned away from the genome. Identical to 'Kmers_reassigned' field in sylph profile output.	

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3.5 openMGS

3.5.1 openMGS Uploader Specification

Files to be provided

For *paired-end Illumina* sequencing data, suppliers must provide:

- A FASTQ 1 file containing the forward sequencing reads.
- A FASTQ 2 file containing the reverse sequencing reads.
- A CSV file containing the metadata associated with sequencing the sample.

For *single-end Illumina* sequencing data, suppliers must provide:

- A FASTQ file containing the sequencing reads.
- A CSV file containing the metadata associated with sequencing the sample.

For *ONT* sequencing data, suppliers must provide:

- A FASTQ file containing the sequencing reads.
- A CSV file containing the metadata associated with sequencing the sample.

Sequencing data must be dehumanised prior to submission. The ingest pipeline will reject sequencing data where the number of assigned human reads exceeds the human read rejection threshold.

File naming convention

The base filenames should be of the form

```
openmgs.[run_index].[run_id].[extension]
```

where:

- `[run_index]` is an identifier that is unique within a sequencing run, e.g. a sequencing barcode identifier, or a 96-well plate co-ordinate.
- `[run_id]` is the name of the sequencing run as given by the supplier's sequencing instrument (not an internal identifier assigned by the supplier).
- `[extension]` is the file extension indicating the file type.

File name extensions

For *paired-end Illumina* sequencing data, the extensions (`[extension]`) should be:

- `1.fastq.gz` for the forward FASTQ file.
- `2.fastq.gz` for the reverse FASTQ file.
- `csv` for the CSV metadata file.

For *single-end Illumina* sequencing data, the extensions (`[extension]`) should be:

- `fastq.gz` for the forward FASTQ file.
- `csv` for the CSV metadata file.

For *ONT* sequencing data, the extensions (`[extension]`) should be:

- `fastq.gz` for the forward FASTQ file.
- `csv` for the CSV metadata file.

Valid characters

The `[run_index]`, `[run_id]` and `[extension]` must contain only:

- Letters (`A-Z`, `a-z`).
- Numbers (`0-9`).
- Hyphens (`-`).
- Underscores (`_`).

Buckets

Bucket names follow the general convention:

```
openmgs-[sequencing_org]-[platform]-[test_flag]
```

Metadata specification

CSV TEMPLATE

A CSV template for uploaders can be downloaded here: openmgs-template.csv

REQUIRED FIELDS

Field	Data type	Description	Restrictions
`biosample_id`	`text`	The sequencing provider's identifier for a sample.	• Max length: `50`
`run_index`	`text`	The sequencing provider's identifier for the position of a sample on a run.	• Max length: `50`
`run_id`	`text`	Unique identifier assigned to the run by the sequencing instrument.	• Max length: `100`
`input_type`	`choice`	The type of input sequenced.	• Choices: `community_standard`, `negative_control`, `positive_control`, `specimen`, `validation_material`
`sample_source`	`choice`	The source from which the sample was collected.	• Choices: `blood`, `environment`, `faecal`, `lower_respiratory`, `nose_and_throat`, `other`, `plasma`, `pleural_fluid`, `stool`, `tissue`, `upper_respiratory`, `urine`
`sample_type`	`choice`	The type of sampling method used.	• Choices: `aspirate`, `bal`, `biopsy`, `other`, `sputum`, `swab`
`spike_in`	`choice`	The type of spike-in used in the run.	• Choices: `ERCC-RNA_4456740`, `bacillus_ms2phage`, `ms2-phage`, `none`, `phix`, `tobacco_mosaic_virus`, `zymo_D6320`, `zymo_D6321`

At least one of the following fields are required:

Field	Data type	Description	Restrictions
`collection_date`	`date`	The date the sample was collected.	• Input formats: `YYYY-MM`, `YYYY-MM-DD` • Output format: `YYYY-MM-DD`
`received_date`	`date`	The date the sample was received by the sequencing centre (if collection_date unavailable).	• Input formats: `YYYY-MM`, `YYYY-MM-DD` • Output format: `YYYY-MM-DD`

OPTIONAL FIELDS

Field	Data type	Description	Restrictions
`biosample_source_id`	`text`	Unique identifier for an individual to permit multiple samples from the same individual to be linked.	• Max length: `50`
`specimen_type_details`	`choice`	Named control or standard for specimens.	• Required when `input_type` is: `specimen` • Choices: `asymptomatic`, `gastrointestinal_infection`, `respiratory_infection`
`control_type_details`	`choice`	Named control or standard for positive and negative controls.	• Required when `input_type` is: `positive_control` • Required when `input_type` is: `negative_control` • Choices: `NIBSC_11/242`, `NIBSC_20/170`, `bacillus_ms2phage`, `resp_matrix_mc110`, `water_extraction_control`, `zepto_rp2.1`, `zymo-mc_D6300`
`is_approximate_date`	`bool`	The date is approximate e.g. the sample is from a public repository and it is unclear whether the date corresponds to collection or publishing.	• Default: `False`
`batch_id`	`text`	Used to identify samples prepared in the same laboratory batch (e.g. extraction, library and/or sequencing).	• Max length: `100`
`study_id`	`text`	Used to identify study or if NHS residual sample.	• Max length: `100`
`study_centre_id`	`text`	Used to identify sequencing centre.	• Max length: `100`
`sequence_purpose`	`choice`	Used to differentiate between clinical or research studies.	• Choices: `clinical`, `research`
`governance_status`	`choice`	Did the patient consent to their sample being used for research purposes or not.	• Default: `no_consent_for_research` • Choices: `consented_for_research`, `no_consent_for_research`, `open`
`iso_country`	`choice`	Country that the sample was collected in, using ISO-3166-1 alpha-2 codes (https://en.wikipedia.org/wiki/ISO_3166-1_alpha-2), unless within United Kingdom. If so, use ISO-3166-2:GB (https://	• Choices: `AD`, `AE`, `AF`, `AG`, `AI`, `AL`, `AM`, `AO`, `AQ`, `AR`, `AS`, `AT`, `AU`, `AW`, `AX`, `AZ`, `BA`, `BB`, `BD`, `BE`, ...

Field	Data type	Description	Restrictions
		en.wikipedia.org/wiki/ISO_3166-2:GB).	
`iso_region`	`choice`	Region that the sample was collected in, using the second level subdivision codes of ISO-3166-2:GB (https://www.iso.org/obp/ui/#iso:code:3166:GB).	• Requires: `iso_country` • Choices: `GB-ABC`, `GB-ABD`, `GB-ABE`, `GB-AGB`, `GB-AGY`, `GB-AND`, `GB-ANN`, `GB-ANS`, `GB-BAS`, `GB-BBD`, `GB-BCP`, `GB-BDF`, `GB-BDG`, `GB-BEN`, `GB-BEX`, `GB-BFS`, `GB-BGE`, `GB-BGW`, `GB-BIR`, `GB-BKM`, ...
`extraction_enrichment_protocol`	`text`	Details of nucleic acid extraction and optional enrichment steps.	
`library_protocol`	`text`	Details of sequencing library construction.	
`sequencing_protocol`	`text`	Details of sequencing.	
`protocol_arm`	`choice`	Used to indicate arm for protocols which have separate arms for bacterial and viral nucleic acids.	• Choices: `bacterial`, `viral`
`bioinformatics_protocol`	`text`	Detail of initial bioinformatics protocol, for example versions of basecalling software and models used, any read quality filtering/trimming employed.	
`dehumanisation_protocol`	`text`	Details of bioinformatics method used for human read removal.	
`is_public_dataset`	`bool`	The sample is from a public dataset. Please only set this after it has been made public.	• Default: `False`
`public_database_name`	`choice`	The public repository where the data is.	• Choices: `ENA`, `SRA`
`public_database_accession`	`text`	The accession for the data in the public database.	

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3.5.2 openMGS Analysis Specification

ANALYSIS FIELDS

Field	Data type	Description	Res
published_date	date	The date the object was published in Onyx.	• Ou
site	choice	The site or sequencing centre providing the data.	• Ch
climb_id	text	Unique identifier for a project record in Onyx.	
biosample_id	text	The sequencing provider's identifier for a sample.	
biosample_source_id	text	Unique identifier for an individual to permit multiple samples from the same individual to be linked.	
run_id	text	Unique identifier assigned to the run by the sequencing instrument.	
platform	choice	The platform used to sequence the data.	• Ch illu
input_type	choice	The type of input sequenced.	• Ch comm nega posi spec vali
specimen_type_details	choice	Named control or standard for specimens.	• Ch gast resp
control_type_details	choice	Named control or standard for positive and negative controls.	• Ch NIBS baci resp wate zept
sample_source	choice	The source from which the sample was collected.	• Ch envi lowe nose plas stoo uppe
sample_type	choice	The type of sampling method used.	• Ch biop swab
spike_in	choice	The type of spike-in used in the run.	• Ch ERCC baci phag toba zymo
spike_in_result	choice	Result assigned by scylla for the provided spike-in.	• Ch pass
collection_date	date	The date the sample was collected.	• Ou DD

Field	Data type	Description	Res
`received_date`	`date`	The date the sample was received by the sequencing centre (if collection_date unavailable).	• Ou `DD`
`is_approximate_date`	`bool`	The date is approximate e.g. the sample is from a public repository and it is unclear whether the date corresponds to collection or publishing.	
`batch_id`	`text`	Used to identify samples prepared in the same laboratory batch (e.g. extraction, library and/or sequencing).	
`study_id`	`text`	Used to identify study or if NHS residual sample.	
`study_centre_id`	`text`	Used to identify sequencing centre.	
`sequence_purpose`	`choice`	Used to differentiate between clinical or research studies.	• Ch `rese`
`governance_status`	`choice`	Did the patient consent to their sample being used for research purposes or not.	• Ch `cons` `no_` `oper`
`iso_country`	`choice`	Country that the sample was collected in, using ISO-3166-1 alpha-2 codes (https://en.wikipedia.org/wiki/ISO_3166-1_alpha-2), unless within United Kingdom. If so, use ISO-3166-2:GB (https://en.wikipedia.org/wiki/ISO_3166-2:GB).	• Ch `AI` , `AS` , `BA` ,
`iso_region`	`choice`	Region that the sample was collected in, using the second level subdivision codes of ISO-3166-2:GB (https://www.iso.org/obp/ui/#iso:code:3166:GB).	• Ch `GB-A` `GB-A` `GB-E` `GB-E` `GB-E` `GB-E`
`extraction_enrichment_protocol`	`text`	Details of nucleic acid extraction and optional enrichment steps.	
`library_protocol`	`text`	Details of sequencing library construction.	
`sequencing_protocol`	`text`	Details of sequencing.	
`protocol_arm`	`choice`	Used to indicate arm for protocols which have separate arms for bacterial and viral nucleic acids.	• Ch `vira`
`bioinformatics_protocol`	`text`	Detail of initial bioinformatics protocol, for example versions of basecalling software and models used, any read quality filtering/trimming employed.	
`dehumanisation_protocol`	`text`	Details of bioinformatics method used for human read removal.	
`is_public_dataset`	`bool`	The sample is from a public dataset. Please only set this after it has been made public.	

Field	Data type	Description	Res
public_database_name	choice	The public repository where the data is.	• Cl
public_database_accession	text	The accession for the data in the public database.	
ingest_report	text	HTML report summarising the read profile and taxa identified.	
taxon_reports	text	Folder of all classification output files.	
human_filtered_reads_1	text	Compressed FASTQ of input reads that have been filtered for human reads.	
human_filtered_reads_2	text	Compressed FASTQ of input reads that have been filtered for human reads.	
unclassified_reads_1	text	Compressed FASTQ of input reads which could not be classified.	
unclassified_reads_2	text	Compressed FASTQ of input reads which could not be classified.	
viral_reads_1	text	Compressed FASTQ of input reads which were classified as viral.	
viral_reads_2	text	Compressed FASTQ of input reads which were classified as viral.	
viral_and_unclassified_reads_1	text	Compressed FASTQ of input reads which were classified as viral or were unclassified.	
viral_and_unclassified_reads_2	text	Compressed FASTQ of input reads which were classified as viral or were unclassified.	
total_bases	integer	Total number of bases in the input FASTQ file(s), before any filtering.	
classifier	choice	The classifier used.	• Cl
classifier_version	text	Version of the classifier used.	
classifier_db	choice	Database used for read classification.	• Cl
classifier_db_date	date	Date classifier database was produced.	• Ou DD
ncbi_taxonomy_date	date	Date that the NCBI taxonomy dump was produced.	• Ou DD
scylla_version	text	Version of the scylla pipeline used.	
chimera_bam	text	BAM file of the human filtered read fraction aligned to the zeus database.	
is_chimera_published	bool	Whether chimera has been run on this record or not.	
alignment_db_version	text	Version of the Zeus database used.	
sylph_db_version	text	Sylph database version utilised to produce Sylph classifications.	
taxa_files	relation	Table of all species level taxa extracted.	
taxa_files.taxon_id	integer	The NCBI taxonomy id associated with the taxa.	

Field	Data type	Description	Res
taxa_files.human_readable	text	A human readable name for the taxa.	
taxa_files.n_reads	integer	The number of reads extracted for the taxa.	
taxa_files.total_bases	integer	Total number of bases extracted for the taxa.	
taxa_files.avg_quality	decimal	The mean quality of reads extracted for the taxa.	
taxa_files.mean_len	decimal	The mean length of reads extracted for the taxa.	
taxa_files.rank	choice	The rank of the taxa.	• Cl 0,
taxa_files.fastq_1	text	Compressed FASTQ of extracted reads for the taxa.	
taxa_files.fastq_2	text	Compressed FASTQ of extracted reads for the taxa.	
classifier_calls	relation	Table summarising the NCBI taxonomy ids, counts and ranks of all taxa found by the classifier.	
classifier_calls.taxon_id	integer	The NCBI taxonomy id associated with the taxa.	
classifier_calls.human_readable	text	A human readable name for the taxa.	
classifier_calls.percentage	decimal	The percentage of the (dehumanised) sample that the taxa represents.	
classifier_calls.count_descendants	integer	The number of reads mapping to this taxa and all descendant taxa.	
classifier_calls.count_direct	integer	The number of reads mapping directly to the taxa.	
classifier_calls.rank	choice	The rank of the taxa.	• Cl 0,
classifier_calls.raw_rank	text	The rank of the taxa including an intermediate grading.	
classifier_calls.is_spike_in	bool	The taxa is a spike-in.	
spike_in_info	relation	Table containing taxonomic results found for the provided spike-in.	
spike_in_info.taxon_id	integer	The NCBI taxonomy id associated with the taxa.	
spike_in_info.human_readable	text	A human readable name for the taxa.	
spike_in_info.reference_header	text	Reference header for the individual sequence within the provided spike-in.	
spike_in_info.mapped_count	integer	Number of reads which aligned to a reference sequence for the provided spike-in.	
alignment_results	relation	Table containing alignment results.	
alignment_results.taxon_id	integer	The NCBI taxonomy id associated with the taxa.	
alignment_results.human_readable	text	Human readable scientific name for the taxa.	
alignment_results.unique_accession	text		

Field	Data type	Description	Res
		Unique reference identifier in the alignment database (everything prior to the first whitespace in the FASTA header).	
`alignment_results.accession_description`	`text`	The comment for the reference sequence within the alignment database.	
`alignment_results.sequence_length`	`integer`	Length of the reference sequence in the alignment database.	
`alignment_results.evenness_value`	`integer`	A percentage indicating how evenly read depths are distributed throughout the reference, with 0 being completely uneven, and 100 being perfectly even. Taken from https://academic.oup.com/nar/article/38/10/e116/2902812, under the “Calculation of evenness score” section, and calculated here: https://github.com/CLIMB-TRE/chimera/blob/dca3cacb949dabc902d0a12e5d11d36c6ac555fd/bin/generate_alignment_report.py#L102.	
`alignment_results.mean_depth`	`integer`	Mean of all depth values across the alignment reference.	
`alignment_results.coverage_1x`	`integer`	Percentage of the reference sequence covered with a depth of at least 1x.	
`alignment_results.coverage_10x`	`integer`	Percentage of the reference covered with a depth of at least 10x.	
`alignment_results.mapped_reads`	`integer`	Total number of reads mapped to the alignment reference.	
`alignment_results.uniquely_mapped_reads`	`integer`	Total number of reads which uniquely map to a reference and position within that reference (MAPQ >= 60).	
`alignment_results.mapped_bases`	`integer`	Approximation for the total number of bases mapped to the alignment reference, calculated from the length of the reference sequence multiplied by the mean depth of alignments to that reference.	
`alignment_results.mean_read_identity`	`decimal`	Mean of read identities across all alignments. Can be considered an approximation for identity of the source genome with the reference sequence. Calculated for each read here: https://github.com/CLIMB-TRE/chimera/blob/dca3cacb949dabc902d0a12e5d11d36c6ac555fd/bin/generate_alignment_report.py#L58	
`alignment_results.read_duplication_rate`	`decimal`	What proportion of the reads start and end in the same alignment reference position as at least one other read within the alignment. Calculated here: https://github.com/CLIMB-TRE/chimera/blob/dca3cacb949dabc902d0a12e5d11d36c6ac555fd/bin/generate_alignment_report.py#L76-L83	
`alignment_results.forward_proportion`	`decimal`	Proportion of reads which aligned to the forward strand. Between 0 and 1, with 0 indicating all reads aligned to the reverse	

Field	Data type	Description	Res
		strand, 1 the opposite. True hits should be close to 0.5 for this value for any reasonable mean depth.	
alignment_results.mean_alignment_length	decimal	Mean length of all alignments to the reference - different to mean read length aligned to the reference, since it only considers the aligned section of the reads.	
sylph_results	relation	Table containing sylph results.	
sylph_results.taxon_id	integer	The NCBI taxonomy id associated with the taxa.	
sylph_results.human_readable	text	Human readable scientific name for the taxa.	
sylph_results.gtdb_taxon_string	text	Description of the taxonomic placement of the source contig within the Sylph database using GTDBs taxon string format.	
sylph_results.gtdb_assembly_id	text	Assembly ID (often genbank accession) for the contig within the sylph database, taken from GTDB.	
sylph_results.gtdb_contig_header	text	From the origin FASTA record header as it appears in GTDB. Identical to 'Contig_name' field in sylph profile output.	
sylph_results.taxonomic_abundance	decimal	Normalized taxonomic abundance as a percentage. Identical to 'Taxonomic_abundance' in sylph profile output.	
sylph_results.sequence_abundance	decimal	Normalized sequence abundance as a percentage. Identical to 'Sequence_abundance' in sylph profile output.	
sylph_results.adjusted_ani	decimal	If coverage adjustment is possible (cov is < 3x cov): returns coverage-adjusted ANI (Average Nucleotide Identity). If coverage is too low/high: returns naive_ani. Identical to 'Adjusted_ANI' in sylph profile output.	
sylph_results.ani_confidence_interval	text	[5%,95%] confidence intervals. If coverage adjustment is possible: float-float e.g. 98.52-99.55. If coverage is too low/high: NA-NA is given. Identical to 'ANI_5-95_percentile' field in sylph profile output.	
sylph_results.effective_coverage	decimal	Estimated 'λeff' value, true value is not calculated, this is estimated based on kmers. More information is available in the sylph paper: https://www.nature.com/articles/s41587-024-02412-y. If coverage adjustment is possible, lambda estimate is given. Identical to 'Eff_cov' field in sylph profile output.	
sylph_results.effective_coverage_confidence_interval	text	[5%, 95%] confidence intervals for lambda. Same format rules as 'ani_confidence_interval'. Identical to 'Lambda_5-95_percentile' field in sylph profile output.	
sylph_results.median_kmer_cov	integer		

Field	Data type	Description	Res
		Median k-mer multiplicity for k-mers with >= 1 multiplicity. Identical to 'Median_cov' field in sylph profile output.	
`sylph_results.mean_kmer_cov`	`decimal`	Mean k-mer multiplicity for k-mers with >= 1 multiplicity. Identical to 'Mean_cov_geq1' field in sylph profile output.	
`sylph_results.containment_index`	`text`	int/int showing the containment index (number of k-mers found in sample divided by total k-mers), e.g. 959/1053. Identical to 'Containment_ind' field in sylph profile output.	
`sylph_results.naive_ani`	`decimal`	Containment ANI without coverage adjustment. Identical to 'Naive_ANI' field in sylph profile output.	
`sylph_results.kmers_reassigned`	`integer`	The number of k-mers reassigned away from the genome. Identical to 'Kmers_reassigned' field in sylph profile output.	

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