

### Using data files with Python programs

In practical sessions and programming assignments, you will sometimes work with data files we provide. These might be reference genomes in FASTA format (e.g. `lambda_virus.fa`), sequencing reads in FASTQ format (e.g. `SRR835775_1.first1000.fastq`), or Python modules (e.g. `kmer_index.py`). To use a file with your Python code, you have to (a) download the file to the same computer as your Python program; use a web browser or a command-line tool like `wget` or `curl` to download it, then (b) put the file in the same directory with your Python program. Then you can open it from your Python program using the Python `open` function.

If you use Jupyter, another way to do this (which we use in the practical sessions) is with a command that starts with `!wget`. This is a shell command. But if you are using `try.jupyter.org` note that the `!wget` command will not work ("unable to resolve host address"). In this case, we recommend you either (a) use `www.wakari.io` instead, or (b) use the "upload" button in the `try.jupyter.org` interface to upload the file to the server, then skip the command that begins with `!wget`.

Best,

Ben