

# Wallaby Viral Assembly Pipeline

Version 0.6  
12/14/17

Copyright 2017 by Shawn Rupp  
[Shawn.M.Rupp@asu.edu](mailto:Shawn.M.Rupp@asu.edu)

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## Introduction

Wallaby is a series of scripts for automating the assembly and local alignment of viral DNA sequencing data.

### *Dependencies:*

Python3  
FastQC v0.11.3  
Trimmomatic v0.36  
ABYSS 2.0.2  
Kiwi v0.2 or above  
MySQL  
Cython  
NCBI Blast+ 2.2.31+  
usearch v10.0.240

## Installation

Note: FastQC, Trimmomatic, and SPAdes must all be downloaded in the /opt/ folder.

### *FastQC*

FastQC can be downloaded [here](#). Download the zipped file into the /opt/ directory and unzip it.

### *Trimmomatic*

Trimmomatic can be downloaded [here](#). Download the zipped file into the /opt/ directory and unzip it.

### *SPAdes*

SPAdes 3.11 can be downloaded for Linux with the following:

```
wget http://cab.spbu.ru/files/release3.11.1/SPAdes3.11.1Linux.tar.gz
tar xzf SPAdes3.11.1Linux.tar.gz
rm SPAdes3.11.1Linux/ SPAdes/
```

Make sure the directory name is changed to “SPAdes”.

### *ABYSS*

ABYSS can be downloaded [here](#). Follow their instructions to compile and install the program. Be sure to export the path to the compiled binaries.

### *Wallaby*

Download the repository:

```
git clone https://github.com/icwells/Wallaby.git
```

## Kiwi

If you wish to run BLAST or ublast, download Kiwi into the same parent directory as Wallaby (i.e. next to it) and follow the instructions in it's ReadMe.

```
git clone https://github.com/icwells/Kiwi.git
```

## Getting Started

### Manifest File

Paired-end fastq reads are given to Wallaby in a simple tab-delimited text file. The first column contains the absolute path to each read (both forward and reverse). The second column contains the batch name: all reads with the same batch name will be assembled together and the final assembly will have that batch's name. The final column is the name of each individual sample. There should be exactly two files with a given sample name: the forward reads and the reverse reads.

path/to/forward/read.fastq.gz	batch1	sample1
path/to/reverse/read.fastq.gz	batch1	sample2
path/to/forward/read.fastq.gz	batch2	sample1
path/to/reverse/read.fastq.gz	batch2	sample2

In the event that each pair of reads is to be assembled together, then the batch and sample names can be the same. The fastq files may or may not be gzipped.

### config.txt

Since Wallaby has many options, it uses a configuration file for some of the more basic options which are likely to stay the same between runs. These options include the number of threads, k (the length of k-mers for ABySS and default minimum length for Trimmomatic), trim settings for Trimmomatic (can use any valid Trimmomatic setting), the path to the database directory for running BLAST/ublast, and your MySQL username.

Any line starting with “#” will be ignored. When changing settings, be sure to leave a space between the equal sign and the setting (needless to say, don't change the setting name or the program will not recognize it).

When initially downloaded, it is named “example\_config.txt” and it must be copied or renamed to “config.txt”. This is to prevent an edited configuration file from being overwritten if “git pull” is run. It must remain in the Wallaby directory and must be named “config.txt”.

### Running Wallaby

```
python wallaby.py i path/to/manifest o path/to/output/directory
```

Wallaby will run FastQC on all input files, read the results, and call Trimmomatic on any files that failed per base sequence quality. It will also print the name of any files which may still contain adapters. These steps can be skipped with the “--noqc” flag.

Next, Wallaby will call SPAdes or ABySS and make one assembly per input batch. It will then call `filterMetagenomicSequences.py` on the contig assemblies to sort contigs by descending length and identify putative circular sequences. It will write three output files: one for all contigs, one for circular contigs, and for all contigs with a minimum length greater than 250bp. The last file will contain circular contigs in both linear and circular formats in addition to the remaining linear contigs.

Note: SPAdes may require super user privileges depending on the system you are using. If this is the case, type “sudo” before the command.

Lastly, Wallaby will perform local alignments using each of the minimum 250bp contig files against the appropriate database in the directory specified in the configuration file. The “--blast” flag will indicate that BLAST should be run; otherwise, `ublast` will be run since it is faster. A translated nucleotide search (i.e. `blastx`) will be run against the protein database. All hits with an e-value less than or equal to  $1 \times 10^{-5}$  will be subset and a nucleotide search (i.e. `blastn`) will be run against the nucleotide database. The output will then be concatenated with data from the MySQL database to provide more informative results. This step can be skipped with the “--noblast” flag and can be skipped to with the “--align” flag, allowing it to be run separately or resumed if it is interrupted.

## Scripts

### *wallaby.py*

Wraps all of the analyses programs. All functions for calling third party programs are contained in `assemblyPipeline.py`, but this script is only callable through `wallaby`.

```
python wallaby.py
  -h, --help      show this help message and exit
  -i I            Path to manifest file (formatted in three tab separated
                  columns:
                  paths to fastqs, batch name (all reads for a sample
                  set), sample
                  name (PE reads)).
  -o O            Path to output directory. All output will be written
                  here.
  --spades        Runs SPAdes in metagenomic mode(ABySS is run by
                  default).
  --noqc          Skip FastQC and Trimmomatic.
  --trim          Resumes pipeline from Trimmomatic step.
  --assemble      Resumes pipeline from ABySS/SPAdes step.
  --noblast       Ublast/Blast will not be run on sorted contigs.
  --ublast        Runs ublast on sorted contigs (blast is run by
                  default).
  --align         Resume pipeline from blast/ublast.
```

*filterMetagenomicSequences.py*

This script will order contigs by length, update headers, and identify circular sequences.

```
python filterMetagenomicSequences.py
  h, help  show this help message and exit
  i        Path to input fasta file.
```