

# BIOL 354W - Research Methods in Advance Microbiology

Version 10

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## Abstract

This protocol series will guide students through the experience of analyzing metagenomic data.

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## Protocol

Introduction to BIOL 354W, sequencing data and bioinformatics

### Step 1.

[BIOL 354W Jan 16th](#)

[BIOL 354W Jan 18th](#)

Command line tutorial

### Step 2.

In order to do bioinformatics, we first need to become comfortable using the computational language and basic skills that will allow you to analyze data.

Open this link in Chrome

 LINK:

[http://rik.smith-unna.com/command\\_line\\_bootcamp/](http://rik.smith-unna.com/command_line_bootcamp/)

 NOTES

**Marcia Smith** 29 Jan 2018

change to:

In order to do bioinformatics, we first need to become comfortable using the computational language and basic skills that will allow you to analyze data.

DNA quality assessment and assurance

### Step 3.

The first step in analyzing the sequencing data set is to assess the quality of the sequence, and then to edit the dataset in order to retain only the highest quality sequences for the following analysis.

To this end we will use: FastQC - A high throughput sequence QC analysis tool

Familiarize yourself with the software by looking at their [web page](#) - check out the video tutorial!

#### cmd COMMAND

```
scp -r username@bio-server-2.willamette.edu:/home/username/folder_with_fastqc_file ~/Desktop/
```

Now that the software has run and you have folders and files with data, you should look at the data to assess the quality and make a decision about the quality control step that we will work on next. For this you can unzip your folder where there will be detail information about the results, as well as a summary of the run. You can also download the .html file to look at the graphic representation of the run, the same format you experienced on the FastQC web and tutorial

#### 📌 NOTES

**Rosa Leon** 14 Jan 2018

You can perform the FastQC file on .fastq files and also in .fastq.gz files or compressed files

**Rosa Leon** 30 Jan 2018

This step must be done from a Terminal window that is looking at your own computer and not connected to the server

**Marcia Smith** 29 Jan 2018

Change to:

The first step in analyzing the sequencing data set is to assess the quality of the sequence, and then to edit the dataset in order to retain only the highest quality sequences for the following analysis.

### Assuring DNA sequencing quality using Trimmomatic

#### Step 4.

Trimmomatic: A flexible read trimming tool for Illumina NGS data ([Website](#))

#### Description

Trimmomatic performs a variety of useful trimming tasks for Illumina paired-end and single ended

data. The selection of trimming steps and their associated parameters are supplied on the command line.

The current trimming steps are:

- ILLUMINACLIP: Cut adapter and other illumina-specific sequences from the read.
- SLIDINGWINDOW: Perform a sliding window trimming, cutting once the average quality within the window falls below a threshold.
- LEADING: Cut bases off the start of a read, if below a threshold quality
- TRAILING: Cut bases off the end of a read, if below a threshold quality
- CROP: Cut the read to a specified length
- HEADCROP: Cut the specified number of bases from the start of the read
- MINLEN: Drop the read if it is below a specified length
- TOPHRED33: Convert quality scores to Phred-33
- TOPHRED64: Convert quality scores to Phred-64

#### cmd **COMMAND**

```
java -jar /opt/BioInfo_tools/Trimmomatic-0.36/trimmomatic-0.36.jar PE -threads 5 -
phred33 input_forward.fq.gz input_reverse.fq.gz output_forward_paired.fq.gz output_forward_
unpaired.fq.gz output_reverse_paired.fq.gz output_reverse_unpaired.fq.gz ILLUMINACLIP:/opt/
BioInfo_tools/Trimmomatic-0.36/adapters/TruSeq3-
PE.fa:2:30:10 LEADING:15 TRAILING:15 SLIDINGWINDOW:4:15 MINLEN:36
input_forward.fq.gz = " the exact name of your forward or R1 sequence file" input_reverse.fq.gz =
" the exact name of your forward or R2 sequence file" output_forward_paired.fq.gz = write in what
you would like the output to be called Eg. 3A_trimmed_R1_paired.fastq.gz"
output_forward_unpaired.fq.gz = write in what you would like the output to be called Eg.
3A_trimmed_R1_unpaired.fastq.gz" output_reverse_paired.fq.gz = write in what you would like the
output to be called Eg. 3A_trimmed_R2_paired.fastq.gz" output_reverse_unpaired.fq.gz = write in
what you would like the output to be called Eg. 3A_trimmed_R2_unpaired.fastq.gz" Try to run this
command as it is with quality of Q15 (SLIDINGWINDOW:4:15) as currently stated in the command
and then with Q30 (SLIDINGWINDOW:4:30). Record the number % of out put sequences per each.
```

### Metagenomic assembly

#### Step 5.

To assemble our metagenomes we will try two different assemblies and compare them. We will try IDBA\_UD and Megahit assemblies. These are going to be one of the most time intensive processes that we will do in the class.

Megahit github - <https://github.com/voutcn/megahit/>

Megahit article - <https://academic.oup.com/bioinformatics/article/31/10/1674/177884>

IDBA\_UD - <https://github.com/loneknightpy/idba>

IDBA\_UD article - <https://academic.oup.com/bioinformatics/article/28/11/1420/266973>

cmd **COMMAND**

```
/opt/BioInfo_tools/idba/bin/idba_ud -r merged_reads.fa -o output_dir --num_threads 5
```

Once the read files are converted into fasta and in consecutive order then the assembly can be run  
merged\_reads.fa = your new generated merged fasta sequences files exactly as you called them  
output\_dir = a folder to store the assembly output, you choose the folder name

## Assessing the quality of the assemblies

### Step 6.

We can investigate assembly statistics to compare which assembly is best between the two assemblies utilized. For this we can use a software called Quast.

Metrics based only on contigs:

- Number of large contigs (i.e., longer than 500 bp) and total length of them.
- Length of the largest contig.
- N50 (length of a contig, such that all the contigs of at least the same length together cover at least 50% of the assembly).
- Number of predicted genes, discovered either by GeneMark.hmm (for prokaryotes), GeneMark-ES or GlimmerHMM (for eukaryotes), or MetaGeneMark (for metagenomes).

cmd **COMMAND**

```
/opt/BioInfo_tools/quast/metaquast.py contig.fa --gene-finding -t 5
```

QUAST evaluates genome assemblies by computing various metrics.

## Binning assembled metagenomes with MaxBin

### Step 7.

MaxBin is a software for binning assembled metagenomic sequences based on an Expectation-Maximization algorithm.

Users provide the assembled metagenomic sequences and the reads coverage information or sequencing reads. MaxBin will report genome-related statistics, including estimated completeness, GC content and genome size in the binning summary page.

MaxBin article - <https://academic.oup.com/bioinformatics/article/32/4/605/1744462>

cmd **COMMAND**

```
perl /opt/BioInfo_tools/MaxBin-2.2.4/run_MaxBin.pl -contig "assembled_contigs.fa" -reads "interleaved reads fasta" -out "out directory" -thread 5
```

MaxBin requires the assembled contains file and also the file that contains the sequence reads  
assembled\_contigs.fa = your contigs file (remember to add the full path if you are in a different directory)  
concatenated reads fasta = the path to your reads, these reads most all be in one file

and concatenate ( or paired R1 followed by R2 reads). This you can get from your IDBA fq2fa run out directory = a directory that you create to save your bins

### Assessing the quality of your bins via CheckM

#### Step 8.

Checkm article - <http://genome.cshlp.org/content/25/7/1043>

Also check out the website for information on CheckM - [CheckM website](#)

Before running CheckM the software pplacer must be included in the PATH by adding

`export PATH="/opt/anaconda3/bin:$PATH"` to the `.bashrc` file in your home directory under the

`# User specific aliases and functions` section.

cmd **COMMAND**

```
/usr/bin/checkm lineage_wf -x fasta ./bins_folder ./checkm_out_folder -t 5
```

CheckM will assess the quality of each of your bins. All bins must be in the same directory/folder.

All bins must have a `.fasta` ending `bins_folder` = the path to the folder where your bins are located

### Use VizBin to further curate your bins

#### Step 9.

VizBin is a Java software that calculates kmer composition and creates a pictographical output that shows the similarity between contigs related to how close they are positioned to each other. We will use VizBin to help us de-contaminate our bins

VizBin will generate a visualization window. Each point represents a genomic fragment (by default of length  $\geq 1,000$ nt). VizBin is designed with the user in mind. All that is needed is a fasta file containing the sequences of interest. A step-by-step guide on using VizBin - including a description of loading the data, selecting points, and exporting the sequences represented by the selected points - is provided on the tutorial page of [VizBin's github wiki](#)

In order to run VizBin with your data you must download your bins fasta files onto your desktop.

To download go to the [VizBin page](#)

### Perform taxonomic identification using Phylosift

#### Step 10.

Phylosift software searches for single copy marker genes and finds their taxonomic classification

Before running this command take a moment to learn about the software at the [Phylosift webpage](#)

cmd **COMMAND**

```
/opt/BioInfo_tools/PhyloSift/phylosift all contigs.fasta -threads 5
```

Prokka - software for annotations

### Step 11.

Learn about how to set up a prokka run and what the outputs are by looking at the git hub [prokka webpage](#)

cmd **COMMAND**

```
/opt/BioInfo_tools/prokka-1.11/bin/prokka contigs.fasta
```

We will annotated our curated bins using PROKKA