

BIOL 354W - Research Methods in Advance Microbiology

Version 2

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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 get comfortable using the computational language and basic skills that will allow you to

Open this link in Chrome

 LINK:

http://rik.smith-unna.com/command_line_bootcamp/

DNA quality assessment and assurance

Step 3.

The first step to analyzing a sequencing dataset is to assess what is the quality of the sequence information and to edit your data set to retain only the highest quality sequences for all analysis that will follow.

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

Familiarize your self 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 decision about the quality control step that we will work on next. For this you can unzip you 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

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

Metagenomic assembly

Step 4.

To assemble our metagenomes we will try two different assemblies and compare them. First we will try IDBA_UD and Megahit assemblies.