GHRU Bioinformatics Training Curriculum

This document contains a list of the current training streams

Training Stream	Tutorial Name and Link	Command Line	Web-based	Accompanying video	Status
Unix fundamentals	Bite-size Unix: Tmux unix session multiplexer	✔		✔	Complete
	Bite-size Unix: Navigating the file system	✔			Complete
	Bite-size Unix: File and Folder manipulation in UNIX	✔			Complete
	Bite-size Unix: redirects and pipes	✔			Complete
	Bite-size Unix: Version control	✔			Complete
	Bite-size Unix: Troubleshooting Nextflow	✔			Complete
	Bite-size Unix: Using the Vi editor	✔			Complete
	Bite-size Unix: UNIX miscellaneous tips	✔			Draft
Assembly	Genome Assembly Overview		✔		Complete
	Genome Assembly Tutorial: Command Line (CLI)	✔		✔	Complete
	Genome Assembly Tutorial: Batch Processing	✔			Complete
Antimicrobial Resistance Prediction	AMR prediction by submitting data to Pathogenwatch	✔	✔		Complete
Mapping and Phylogeny	Reference-based SNP phylogeny	✔			Draft
Server Setup	Installing Nextflow and Docker on Ubuntu 18.04	✔			Draft

Unix Fundamentals

1. **Tmux unix session multiplexer**

    Learning objectives. By completing this tutorial you will be able to
    a. Describe how to use Tmux to create long running persistent sessions on a unix machine
    b. Apply this knowledge to using Tmux to run unix scripts and software

2. B**ite-size Unix: Navigating the file system**

    Learning objectives. By viewing and applying this document you will be able to
    a. Describe the UNIX file system and how it is possible to view files and navigate the directories
    b. Show someone how to type commands and move around the file system and view directory contents

3. **Bite-size Unix: File and Folder manipulation in UNIX**

    Learning objectives. By viewing and applying this document you will be able to
    a. Demonstrate how to move, copy and delete files in UNIX
    b. Manipulate the permissions of files and directories

4. **Bite-size Unix: redirects and pipes**

    Learning objectives. By viewing and applying this document you will be able to
    a. Describe the what the redirect and pipe symbols are in UNIX
    b. Demonstrate ways of using these to write out files and join UNIX commands together

5. **Bite-size Unix: Version control**

    Learning objectives. By viewing and applying this document you will be able to
    a. Define version control and its purposes
    b. Produce a clone of a remote git repository e.g on github or gitlab and checkout specific tags

6. **Bite-size Unix: Troubleshooting Nextflow**

    Learning objectives. By viewing and applying this document you will be able to
    a. summarise how Nextflow is configured and explain how to debug a workflow task that has failed

7. **Bite-size Unix: Using the Vi editor**

    Learning objectives. By viewing and applying this document you will be able to
    a. Explain when and how you would use the Vi command line text editor
    b. Demonstrate how to use the editor to open manipulate and save text documents

8. **Bite-size Unix: UNIX miscellaneous tips**

    Learning objectives. By viewing and applying this document you will be able to learn methods for efficient use of the command line such as passwordless login, quick command retrieval and aliases

Assembly

1. **Genome Assembly Overview**

    Learning objectives: Learn how to
    a. Be able to explain the principles of *de novo* assembly
    b. Login to a Galaxy server.
    c. Upload data to a Galaxy server from a file on your local computer
    d. Access and run the software tools applying them to data you have uploaded
    e. Assemble a genome from a pair of fastq files

2. **Genome Assembly Tutorial: Command Line (CLI)**

    Learning objectives: Learn how to
    a. Set up a virtual machine
    b. Connect to a Linux server using ssh via the PuTTY program
    c. Transfer files to a Linux server using the WinSCP program
    d. Run commands on a Linux server
    e. Perform a genome assembly on the command line

3. **Genome Assembly Tutorial: Batch Processing**
   Learning objectives. In this tutorial you will learn
   a. What a workflow manager is and why they are used
   b. How Nextflow works as a workflow manager
   c. How to run Nextflow to assemble multiple samples

Antimicrobial Resistance Prediction

1. **AMR prediction by submitting data to Pathogenwatch**
   Learning objectives: In this tutorial you will learn
   a. How to format a CSV file for submission to Pathogenwatch
   b. How to upload assemblies and metadata to Pathogenwatch
   c. The basics of using Pathogenwatch
   d. How to assemble a collection of genomes, predict AMR using the abricate software from Torsten Seemann, and compare it to the analysis in Pathogenwatch.

Mapping and Phylogeny

1. **Reference-based SNP phylogeny**
   Learning Objectives. In this tutorial you will learn how to
   a. List the two main pathways for processing short read data
   b. Describe how to select a reference sequence for reference-based mapping
   c. Describe the critical steps taken when creating a phylogeny based on comparison of reads to a reference sequence
   d. Apply this knowledge to
      i. running the command line tools for processing a single sample
      ii. running Nextflow to process a batch of samples and produce a maximum-likelihood tree

Server Setup

1. **Installing Nextflow and Docker on Ubuntu 18.04**
   Learning Objectives. In this tutorial you will learn how to
   a. Add a user and give them sudo privileges
   b. Install Nextflow
   c. Install Docker

Version Control Table

Title	GHRU bioinformatics training curriculum			
Description	A document describing the current modules available in the GHRU bioinformatics training curriculum			
Created By	Anthony Underwood			
Date Created	28th January 2019			
Maintained By	Anthony Underwood			
Version Number	**Modified By**	**Modifications Made**	**Date Modified**	**Status**
1.0	Anthony Underwood	First version	28th January 2019	First Live Version
1.1	Anthony Underwood	Added lots of bite-size exercises	25th March 2019	Updated training
1.2	Anthony Underwood	Add additional mapping training	21st November 2019	Updated training