



H3ABioNet

Pan African Bioinformatics Network for H3Africa

16SrRNA Intermediate Bioinformatics Online Course: Int_BT_2019

Introduction to the command line and R

Introduction to the command line

Practical



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16SrRNA Intermediate Bioinformatics Online Course:
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Trainer name

Intro

For this practical we are going to go through the Software Carpentry's Introduction to Unix shell.

Please ask your teaching assistant what is the appropriate why for you to get to a shell / command line. Whether it is working on your own machine, a remote server or working on a compute node by launching an interactive job.

The breakdown the specific sections can be found [here](#)

We will focus on

1. [Introducing the shell](#)
2. [Navigating files and directories](#)
3. [Working with files and directories](#)
4. [Pipes and filters](#)

You have 20 minutes to spend on each section. After that we will quickly run through the section, look at the solutions and key points and then move on to the next.

You would have received an assignment with questions for each section that needs to be filled in and returned.

Intro

First we need to setup the data you would be working with. Follow the instructions [here](#).

- `wget http://swcarpentry.github.io/shell-novice/data/data-shell.zip`
- `unzip data-shell.zip`

The `data-shell` directory contains the data that you will be working with.

Now you are setup and ready and can move onto section [1](#), then [2](#), then [3](#) and finally [4](#).

Note: In this practical we will not be doing the section Loops, Shell Scripts, Finding Things and Shell Extras. Feel free to work through those section in your own time because it contains tools and methods that will improve your command line efficiency.