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Welcome page

On this website you will find a short tutorial that will provide guidance in how to use bash and the command line interface.

The first few pages will introduce you how to set up a terminal and document your code.

Afterwards, the actual tutorial will begin, in which we will assume the role of a researcher who just received amplicon sequencing data from a sequencing center and wants to start analysing this data using the command line interface. This tutorial is divided into two main parts:

1. In the first section, we will learn how to organize and how to view and exploring the data on the filesystem. We will start with some basic operations to assess with how much data we work with and extract information from our files.
2. After becoming familiar with the command line, we will learn how to analyze our data on an HPC (since often analysing large datasets on a personal computer can become quite resource intensive). We will learn how to connect to an HPC, download some software to assess the quality of our sequencing data and submit jobs to computational nodes. If you do not have access to an HPC you can follow most parts on your own computer as the dataset we provide is a small one.

For information not covered in this tutorial, check out [IBED's bioinformatics guidance page](#).