

# **Fundamentals of computational biology**

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2022-04-11

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# Preface

Here we present a course centered book of the Fundamentals of Computational Biology. We will cover several topics, from using the unix tools, the importance of package manager systems (such as homebrew and conda), sequencing technologies, sequence alignments, molecular phylogenetics, genome assembly and annotation, and variant calling analysis.

# 1 Introduction

This is a book created from markdown and executable code.

See Knuth (1984) for additional discussion of literate programming.

## 2 Welcome to the command line

In this chapter we will explore the fundamentals of the command line. That is the concepts of Unix based systems the command line (CLI) and how we can use it to access information programmatically.

## **3 Introduction to sequence analysis**

## 4 Summary

## 5 Challenges demos

### 5.1 Genome searching

In this chapter we will use several tools to download a genome from the command line. We will identify some features

#### Downloading a genome

```
ncbi-genome-download
```

#### Downloading from NCBI

The first step in this journey is to download a bunch of sequences programatically. To do so, we will use the program [ncbi-genome-download](#).

You could inspect all the options it provides, now we will set our command as the following:

```
ngd --genera "Bacillus subtilis"\  
-s refseq\  
-l complete\  
-o Data\  
--flat-output\  
--format features\  
-n bacteria\  
| head -n 10
```

Considering the following 193 assemblies for download:

GCF_000772125.1	Bacillus subtilis	ATCC 13952
GCF_000772165.1	Bacillus subtilis	ATCC 19217
GCF_000772205.1	Bacillus subtilis	Bs-916
GCF_000782835.1	Bacillus subtilis	SG6
GCF_000789295.1	Bacillus subtilis	PS832



```
GCF_000952895.1 Bacillus subtilis BS34A
GCF_000953615.1 Bacillus subtilis BS49
GCF_001015095.1 Bacillus subtilis UD1022
GCF_001037985.1 Bacillus subtilis TO-A JPC
```

## Listing files

```
ls Data | head -n 10
```

## Decompressing using gzip

```
gzip -d *
```

...

## Some files in our data dir

```
ls Data | head
```

## Importing the files into R

```
library(tidyverse)
library(fs)

all_features <- dir_ls("Data/") %>%
  map_df(read_tsv)

all_features %>%
  head()
```

...

```
library(tidyverse)
```

```
-- Attaching packages ----- tidyverse 1.3.1 --
```

```
v ggplot2 3.3.5      v purrr 0.3.4
v tibble 3.1.6       v dplyr 1.0.8
v tidyr 1.2.0        v stringr 1.4.0
v readr 2.1.2        v forcats 0.5.1
```

```
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()     masks stats::lag()
```

```
library(fs)

all_features <- dir_ls("Data/") %>%
  map_df(read_tsv)

all_features %>%
  head()
```

```
# A tibble: 0 x 0
```

## Data processing

```
all_features_grouped <- all_features %>%
  rename(feature = `# feature`) %>%
  select(assembly, feature) %>%
  group_by(assembly, feature) %>% operations
  count() %>%
  pivot_wider(names_from = feature, values_from = n) %>%
  arrange(desc(CDS))

all_features_grouped %>%
  head()
```

create a new dataset that will group by features per accession get read of the weird name of the column Select these two columns Group by these two columns to perform count the numbers of rows based on the applied group generate a wide dataset sending row names as columns Arrange descending by the number of CDSs

## References

Knuth, Donald E. 1984. “Literate Programming.” *Comput. J.* 27 (2): 97–111. <https://doi.org/10.1093/comjnl/27.2.97>.