

ProkGenomics

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Chapter 1

START HERE

I know command-line and SSH

I don't know where to start

Chapter 2

Introduction

This nextflow pipeline allows you to run several programs using a one-line command. It wraps programs to assemble, annotate, taxonomically identify, genotypic characterize and perform simple comparative genomics on prokaryotic sequencing data. This pipeline is self-contained and is NOT meant to be run in modules (not independent parts of it). This with the intention of simplifying the user interaction and the user knowledge about the bioinformatics behind this processes. However, making yourself familiar with the programs behind the scenes helps you to make informed decisions. Please go to resources to read more about what each program is doing.

2.1 Overview of the pipeline

- **Assembly, Annotation and Classification**
 - Quality control of reads (short, long, or both)
 - Cleaning reads
 - De-novo Assembly (short, long or hybrid)
 - Quality Control of the assembly and detection of contamination
 - Identification of the species in the sample
 - Identification of plasmids, phages and prophages
 - Genes Annotation
- **Comparative genomics (when genome reference provided)**
 - Coverage of reference genome
 - Identification of core genome
 - Identification of Single Nucleotide Variants (SNV)
 - Identification of rearrangements and larger deletions
- **Characterization of genes of interest (when genes sequences provided)**
 - Alignments to genes of interest
 - Summary table to identify presence, absence and truncated genes

- Generation peptides sequences from the denovo assembly

Chapter 3

Getting Started

3.1 Make sure you have Nextflow running

Before you get started with the pipeline, make sure you have installed nextflow.

If you are using a **cluster** there are high chances that nextflow is a module already installed. Please call the module. Type the following command and use **tab** after the word **nextflow** to see if you have different versions available. Ideally use the 21.10.6 version (which this pipeline has been successfully tested).

```
# if you are in a cluster
module add nextflow
```

If you can have conda installed in your system (either in your **computer** or your **server**), you could create a conda environment and install nextflow following the next commands

```
# if you can create conda env, this could work for a cluster, server or your own computer.
conda create -n nextflow
conda activate nextflow
conda install -c bioconda nextflow=21.10.6
```

Use `conda activate nextflow` every time you want to use nextflow

Alternatively, you could install nextflow using the nextflow installation instructions

3.2 Download the nextflow pipeline

Run the following command

```
# when private
```

```
git clone git@github.com:Grinter-Lab/ProkGenomics.git
```

```
# when public
```

```
git clone https://github.com/Grinter-Lab/ProkGenomics.git
```

If you have issues consulte the troubleshoot section for help

A successful download of the repository should look like this:

```
Cloning into 'ProkGenomics'...
remote: Enumerating objects: 3, done.
remote: Counting objects: 100% (3/3), done.
remote: Compressing objects: 100% (2/2), done.
remote: Total 3 (delta 0), reused 0 (delta 0), pack-reused 0
Receiving objects: 100% (3/3), done.
```

To be able to run the program from any location without using the complete path, run the following commands

```
# move to the program folder
cd ProkGenomics/
```

```
# print your working directory
pwd
```

```
# This will print your location something like: /path/to/dir/program/
```

```
# export the path of the folder into your PATH
export PATH="$PATH:/path/to/dir/program/"
```

3.3 Set up your working directory

Create a working directory for your project

```
mkdir Project1
cd Project1
```

Create a folder for your raw data

```
mkdir rawdata
cd rawdata
```

3.4 How to transfer raw data to cluster/server

Open a tab in your terminal from your local computer

```
# from tab in your local computer
# scp <location in the server, notice structue as serve:path> <location in your computer>
# notice that the wild card allows you to move all files ending in fq.gz. if your files
```

3.4. *HOW TO TRANSFER RAW DATA TO CLUSTER/SERVER* 11

```
scp *fq.gz <username>@<cluster_name>:/srv/home/username/folder/
```


Chapter 4

Run Pipeline

Remember to put the program in your `$PATH` if you haven't done it. This step has to be done every time you start a new terminal session. If you want to make this change permanent you could modify your bash profile (don't play around with it if you don't feel confident about it)

If you added the program to your `$PATH` successfully you should be able to run

```
#remember to activate the conda env if you are using one
conda activate nextflow
```

```
#run the pipeline
ProkGenomics
```

If it starts correctly, you will see something like

```
N E X T F L O W ~ version 21.10.6
Launching `main.nf` [focused_noether] - revision: eb930f0e69
```

If you don't see a version of that go to troubleshoot to look for possible solutions

4.1 Simple run

```
#remember to activate the conda env if you are using one, and if you haven't activated it yet
conda activate nextflow
```

```
#run the pipeline
ProkGenomics --sample_name '1-77321' -profile singularity
```

Parameters you can use:

Command	Description
<code>--sample_path ./rawdata/</code>	The default path for the reads is the folder rawdata in the working directory (please follow the instructions for setting up the working folder). if you have your reads somewhere else you should set this parameter to that path.
<code>--sample_name 1-77321</code>	The sample name is the prefix of your samples files. it doesn't have a default because I don't know your sample names. Please don't use sample names with spaces in them. Best approach is to use the name of the file as it comes from the sequencing facility
<code>--assembly_type short</code>	This parameter can be short long or hybrid. The default is 'short'. if you have short reads you don't have to specify this parameter. If you pick the argument long or hybrid the longreads parameter should be specify. For hybrid make sure to give a path for short and long reads.
<code>--longreads ./rawdata/longreads/ --threads 16</code>	Path to the long reads. Number of threats to use. More threats faster your processing. Make sure you know what is available for you.
<code>--outdir 1-77321</code>	The results will be in a folder in the working directory with the same sample name and _results ex. 1-77321_results.
<code>--reference reference/ReferenceGenome.fasta</code>	If you have a reference genome put the path here. This will activate all the comparative genomics steps. This file can be formatted as fasta or genbank. If you provide a genbank file your Single Nucleotide Variant file will be annotated (tell you what gene has the mutations).
<code>--adapter_file TruSeq3-PE.fa</code>	To trim your short reads you need to specify what adaptors where used when sequencing. Arguments are TruSeq2-SE.fa, TruSeq2-PE.fa, TruSeq3-PE.fa. The default is TruSeq3-PE.fa.
<code>--genes_interest GenesBD/*fasta</code>	Path to a folder that contains all genes of interest. The correct formatting is a gene per file in fasta format.

Command	Description
<code>--assembly genome_assembly.fasta</code>	If you already have an assembly you can set this parameter and the pipeline will skip all the steps of assembly

Chapter 5

Understand Outputs

This pipeline produce a folder per program run and several main outputs. The main results are described in the final report named `<sample_name>_ProkGenomics_report.html` (click hyperlink to see)

5.1 Additional outputs description

Folder structure

```
sample_name_results
  fastqc
    sample_prefix_1_fastqc.html
    sample_prefix_1_fastqc.zip
    sample_prefix_2_fastqc.html
    sample_prefix_2_fastqc.zip
    sample_prefix.R1.trim_fastqc.html
    sample_prefix.R1.trim_fastqc.zip
    sample_prefix.R1.unpaired.trim_fastqc.html
    sample_prefix.R1.unpaired.trim_fastqc.zip
    sample_prefix.R2.trim_fastqc.html
    sample_prefix.R2.trim_fastqc.zip
    sample_prefix.R2.unpaired.trim_fastqc.html
    sample_prefix.R2.unpaired.trim_fastqc.zip
    software_details.txt
  trimmomatic
    sample_prefix.R1.trim.fastq
    sample_prefix.R1.unpaired.trim.fastq
    sample_prefix.R2.trim.fastq
    sample_prefix.R2.unpaired.trim.fastq
    software_details.txt
```

```

unicyclcr
  sample_prefix
    001_spades_graph_k027.gfa
    001_spades_graph_k053.gfa
    001_spades_graph_k071.gfa
    001_spades_graph_k087.gfa
    001_spades_graph_k099.gfa
    001_spades_graph_k111.gfa
    001_spades_graph_k119.gfa
    001_spades_graph_k127.gfa
    002_depth_filter.gfa
    003_overlaps_removed.gfa
    004_bridges_applied.gfa
    005_final_clean.gfa
    assembly.fasta <<<<< Complete de novo assembly
    assembly.gfa
    unicyclcr.log
  software_details.txt
checkm
  sample_prefix.tsv <<<<< QC de novo assembly
  software_details.txt
checkv
  sample_prefix
    complete_genomes.tsv
    completeness.tsv
    contamination.tsv
    proviruses.fna
    quality_summary.tsv <<<<< Phages or Provirus detected
    viruses.fna
  software_details.txt
prokka
  sample_prefix_annotation_output
    sample_prefix.err
    sample_prefix.faa
    sample_prefix.ffn
    sample_prefix.fna
    sample_prefix.fsa
    sample_prefix.gbk <<<<< Gene Annotation
    sample_prefix.gff <<<<< Gene Annotation
    sample_prefix.log
    sample_prefix.sqn
    sample_prefix.tbl
    sample_prefix.tsv
    sample_prefix.txt
  software_details.txt
pharokka

```

```
sample_prefix_annotation_output
  sample_prefix.err
  sample_prefix.faa
  sample_prefix.ffn
  sample_prefix.fna
  sample_prefix.fsa
  sample_prefix.gbk
  sample_prefix.gff <<<< Phages or Provirus annotation
  sample_prefix.log
  sample_prefix.sqn
  sample_prefix.tbl
  sample_prefix.tsv
  sample_prefix.txt
software_details.txt
```


Chapter 6

Write Methods

Workflow of pipeline

Chapter 7

Troubleshooting

7.1 git@github.com: Permission denied

You may see this error:

```
Cloning into 'ProkGenomics'...
git@github.com: Permission denied (publickey).
fatal: Could not read from remote repository.
```

Please make sure you have the correct access rights
and the repository exists.

Note that this is a private repository, you may required to log in using your github details. Github now requires for you to setup a token key to access private repositories, please follow the github instructions to set up one

Chapter 8

Resources

<https://www.bioinformatics.babraham.ac.uk/projects/fastqc/>

<http://www.usadellab.org/cms/?page=trimmomatic>

<https://github.com/rrwick/Unicycler>

<https://singularity-tutorial.github.io/01-installation/>

Other programs

<https://bactopia.github.io/v3.0.0/>

<https://proksee.ca/>

<https://genome.usegalaxy.org.au/>

Chapter 9

Command Line Intro

If you are completely new to working with command line the following short introduction should be useful to get you started. Please read carefully this section, it will help you to understand instructions in later sections.

9.1 General syntax and conventions:

- Code or command are instructions directly given to the computer through a console or terminal window. Code or command lines in this tutorial are written with **this style** or

in this boxes

- If a string is written between `< >` it means that you have to type what that means in your case. For example: Login as: `<your_username>` this means you have to type your user name in that space without the `< >`

For example, the following instructions should look like:

```
cp <file_name> <file_destination>
```

My file name is `myfile.txt` and my file destination is `newfolder`

```
cp myfile.txt newfolder
```

- When asterisk `*` is used it means all of that kind. For example: `ls *.fasta` will print a list of all files that have the extension `.fasta`
- Every line starting with `#` is a comment. These lines are not interpreted by your computer, there are there only to give you additional information.

9.1.1 Programs:

Command lines for executing programs usually look like:

```
program --input <inputfile>
```

where

program is the program in question

--input is the option or parameter

inputfile is the argument

- Options/parameters for a program are denoted by a dash and a letter as: **-f** or a double dash and a string as: **--file**. If an option is not required but optional is often explained using **[]**, for example: **[-t 8]**
- Arguments are the input to the options/parameters. For example **-f myfile.txt**. **-f** is the option to input your file and **myfile.txt** is the argument for that option, the name of your file. The arguments are often explained using **< >**. When several arguments are possible for an option pipes are used to show the different possibilities, for example **[-f sam|bam]**. This means the option **-f** allows **sam** or **bam** formats

9.2 Basic commands:

When you enter your terminal your prompt consists of: **HOST_NAME:MACHINE CURRENT_DIRECTORY \$** everything after **\$** is your command line. You can use the following basic commands to access information or perform tasks in your computer.

- **change directory**

```
cd <name of directory you want to change to>
```

cd or cd ~ move you to your home directory

- **print working directory**

```
pwd
```

- **list your files**

```
ls
```

- **make dir*ectory**

```
mkdir <new folder name>
```

- **copy** (needs file to be copied and destination).

```
cp <path of file to be copy> <destination path>
```

9.3 Files system

- Please note that directories are structured in a hierarchical system. You have to know where you are standing to ask the computer to move to the correct

folder.

Example of folder structure:

```
      | subfolder_1
      |
main_folder
      |
      | subfolder_2
      |
      |subfolder_2.1 (YOU ARE HERE)
```

#where am I?

pwd

#shows this path: /main_folder/subfolder_2/subfolder_2.1

I want to go to the folder containing this folder

cd ..

moves to /main_folder/subfolder_2/

I want to go to the folder containing this folder and change to a folder that is there

cd ../subfolder_1

#moves to subfolder_1

Chapter 10

Connect to the cluster

10.0.1 Macs

If you are working on Mac you can directly open the terminal from applications or click the Launchpad icon in the Dock, type **Terminal** in the search field, then click Terminal. You will see a version of this:

type the following command

```
ssh <username>@<cluster_name>
```

where <username> is your authcate and the <cluster_name> is the cluster you are connecting to. Click enter, you will be asked for a password. Enter your password and click enter. Note you will not see the characters as they are typed. You are now in your home directory on the cluster.

10.0.2 Windows

If you are on a windows-based PC, you will need to download PuTTY.

In the hostname (or IP address) box, enter the hostname that you were provided, ie. <username>@<cluster_name>, where <username> where <username> is your authcate and the <cluster_name> is the cluster you are connecting to. Ensure the connection type is SSH. Click open. You will be prompted to enter your username (authcate) and password in the terminal window. Enter your credentials and click enter. Note you will not see the characters as they are typed. You are now in your home directory on the cluster.

Now you are ready to go Let's get started