



Degree in Computer Science and Engineering | Practical Software Workshop

Practical Software Workshop (STI-S) ASSESSMENT #1: DNA

2018/19

COMMANDS IN LINUX

Goals

The goals of this assessment are:

- Learn the basic commands in Unix.
- Understand how to work with files and foulders.
- Search, sorte and edit files.

WRITTEN REPORT

In this assessment students have to deliver together the solutions of exercises 1 to 5, in a text file, and the file naLnuT.txt generated, inside a folder called G11XXEYY, where 11XX is the number of your group, and YY is the number of your partner.

It is requested to deliver in Moodle, packaged and compressed with the format: G11XXEYY.tar.gz





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Introduction

In this exercise you will use the file all.frn.tar.gz, which you must download from Moodle to your computer. This file includes DNA code files for various living beings.

Write the commands in Unix needed to perform the tasks requested in each section below.

Exercise 1

Unzip and unpack the file all.fm.tar.gz in a folder called All.

Exercise 2

Create a list sorted by size of all files (genetic codes, or DNA) ending in T.frn that belong to all subfolders of All whose name starts with L.

Here T is the number corresponding to your team (partner) in class, and L is the first letter of the name of one of the team members.

Copy the list into a file called naLnuT.

Exercise 3

Choose the longest file in the list naLnuT.

Copy the corresponding file into a subfolder called Na.

Find all occurrences of the Codom (a string of 3 characters) "ACG" in this file (the DNA). Proceed recursively for all DNAs in the Na folder.

Show on screen the number of ACG appearances.

Exercise 4

Translate the ACG, ACA, ACC and ACT codons into their associated amino acid, Thr. Also transfer the CCT, CCC, CCA and CCG codes into the amino acid Pro. That is, change the characters.

Exercise 5

Repeat the whole process in the previous exercises, but now in a single sequence of commands.