Command line

A nice introduction to using Bash can be found here.

Some other sources include Bash Scripting Tutorial and the Linux Tutorial.

Some selected examples can be found in bash.pdf.

The bash interpreter

Bash is one of the most commonly used interpreters (languages) you will find on a typical Linux system.

When writing programs in *Bash* you will be able to use all the structures and functionality you expect from any other language, e.g. *Python*.)

Bash programs are scripts that start with a special first line.

```
#!/bin/bash
echo "Hello World"
```

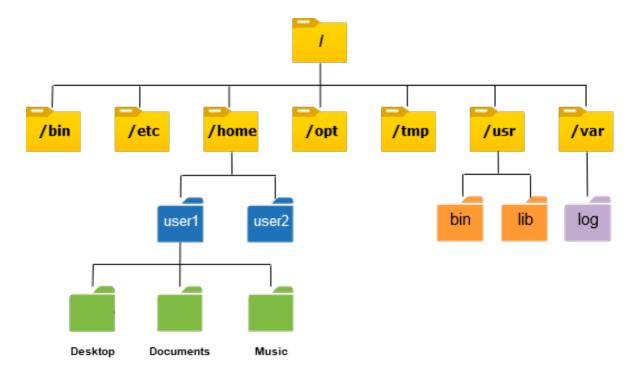
Store message into variable first.

```
#!/bin/bash
# declare STRING variable
STRING="Hello World"
#print variable on a screen
echo $STRING
```

The first line looks like it is commented out, because it starts with '#', but it is not. It instructs the command line interpreter to start the script in Bash (program /bin/bash).

1. Linux basics

Folder structure:



- files
 - Is
 - cp

cp datoteke/primer.fasta kopija.fasta

- rm
- cat, less
- gzip, zless

gzip kopija.fasta # dobimo kopija.fasta.gz
 less kopija.fasta.gz
 zless kopija.fasta.gz

awk

awk {'print \$1 " text " \$2'} datoteke/osebe.txt

folders

cd folder/path
 mkdir folder
 rmdir folder

renaming and moving files

mv from_name.txt to_name.txt

- programs
 - run a python script

2. Writing and running simple bash examples

- structure of a bash script
 - \$ chmod +x simple.sh
- variables
 - global vs. local
- arithmetics
 - compute average weight in bash datoteke/teze.txt

```
#!/bin/bash
   echo "hello world"

declare -i sum
   declare -i cn
   sum=0
while read line; do
       sum=$sum+$line
       echo $line;
       cn=$cn+1
   done < datoteke/teze.txt

echo "vsota: $sum"
   echo "n:" $cn
   echo "povprečje:" $sum/$cn
   echo "povprečje2:" $[ $sum/$cn ]
   echo "povprečje3:" $(( $sum/$cn ))</pre>
```

- arguments
 - modify script to accept any input file
- running other programs within scripts
- user input
- if else
- comparisons
 - arithmetic
 - string
- loops for iterating thru files, mostly
 - for
 - while

3. Pipelines

- Redirections of stdin, stdout, stderr to files
- Redirections with pipe
- Working on multiple files
 - Average of averages
 - Genome composition, one genome per file

Vaje

Napisi pythonov program, ki sprejme ime datotek in izracuna povprečje vrednosti.

```
average.py
#!/srv/conda/envs/notebook/bin/python
import sys
fin_name = sys.argv[1]

sum = 0
cn = 0
for line in open(fin_name):
    sum += float(line)
    cn += 1

if cn > 0:
    print(sum/cn)
```

Napisi pythonov program, ki sprejme vsebino iz stdin in izracuna povprečje vrednosti.

```
average_stdin.py
#!/srv/conda/envs/notebook/bin/python
import sys
fin = sys.stdin

sum = 0
cn = 0
for line in fin:
    sum += float(line)
    cn += 1

if cn > 0:
    print(sum/cn)
Program pričakuje novo vrednost (v novi vrstici) ali konec vnašanja (Ctrl+D).
```

napisi skripto v bash, ki pozene average.py na vsaki datoteki teze

```
pozeni_vse.sh
#!/bin/bash

for fn in datoteke/teze*.txt; do
    python average.py $fn
    # ./average.py $fn
    # cat $f | ./average.py
done
```

Napiši program, ki prebere vsako od datotek z zaporedji v datoteke/qwerty-dna/*.txt in za vsako izpiše sestavo a, t, c in g

```
prestej_dna.py
#!/srv/conda/envs/notebook/bin/python
import sys
def prestej(s):
    frek = {}
    for c in s:
        frek[c] = frek.get(c, 0) + 1
    return frek
fin_name = sys.argv[1]
print(prestej(open(fin_name).read()))
Kličemo v programu prestej_vse.sh:
#!/bin/bash
for f in datoteke/qwerty-dna.txt; do
    echo "Procesiram $f"
    ./prestej_dna.py $f
done
```

Datoteko datoteke/qwerty-dna.txt rabij na posamezne datoteke.

```
for f in `awk {'print $1'} datoteke/qwerty-dna.txt`; do
    grep "$f" datoteke/qwerty-dna.txt | awk {'print $2'} > $f.txt
done
```