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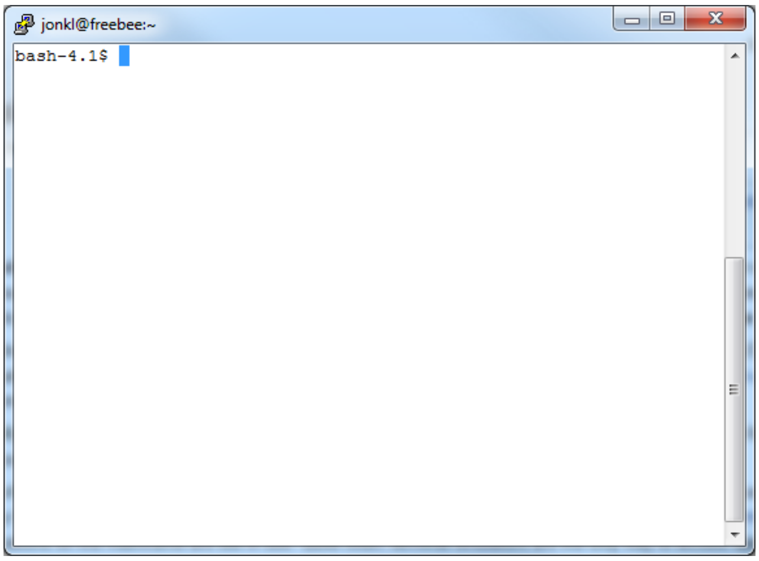
# Unix basics exercise – MBV-INFX410

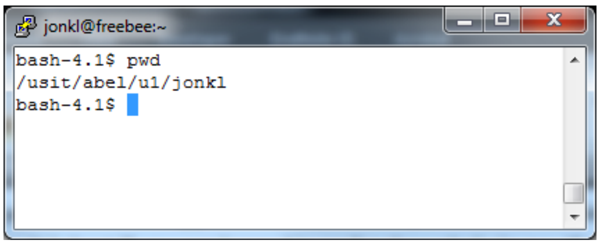
In order to start this exercise, you need to be logged in on a UNIX computer with a terminal window open on your computer. It is best if you are logged in on freebee.abel.uio.no. If you do not know how to open a terminal window, like the one below, on your desktop, please contact one of the instructors and get help.



```
bash-4.1$
```

In the terminal window you have a Unix shell open with a command-line (a shell prompt) where you can type your commands. The command-line interpreter will execute your commands. There are several alternative and widely used Unix shells, for example C shell (csh), Bourne shell (sh), tcsh (used to be default at UiO), and Bourne-again shell (bash) (now default at UiO). In this exercise we will use bash. Hopefully you already have a bash shell running. If you are uncertain, type "bash" at the command prompt and press enter. Now you have opened a bash shell inside the other shell, and you are ready to start.

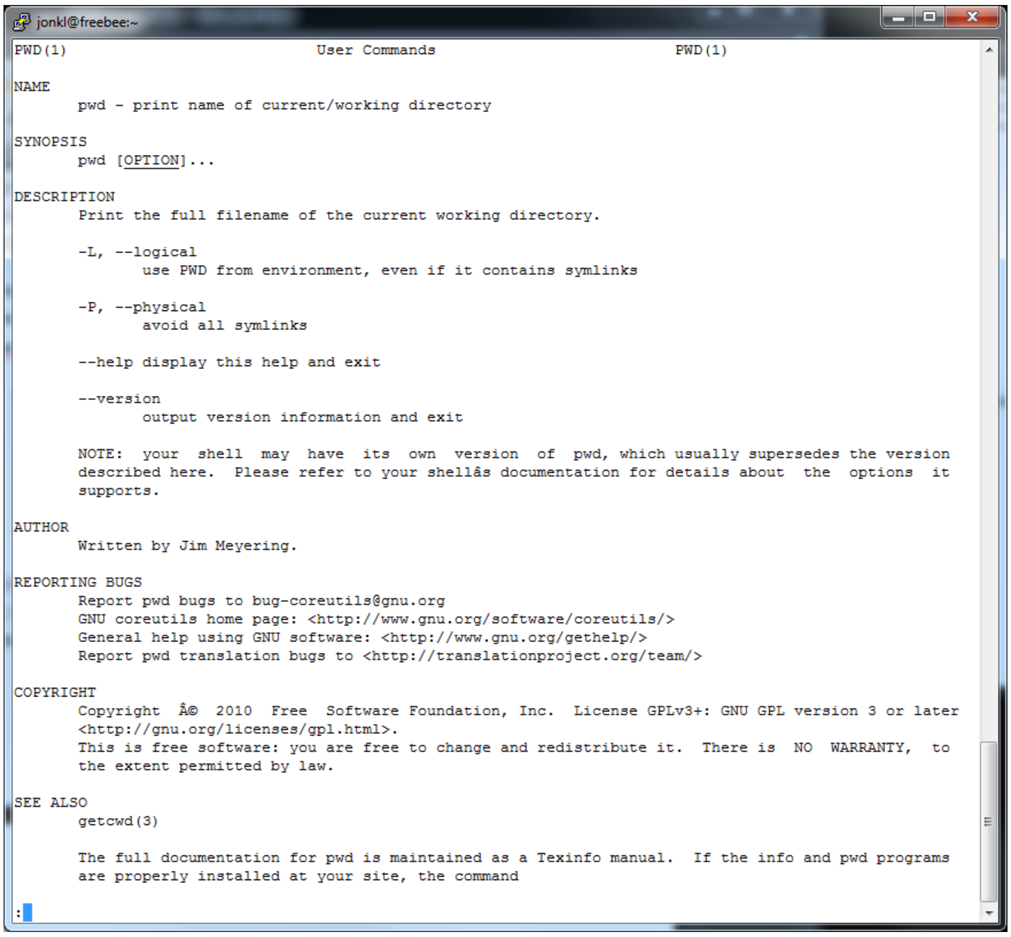
1. Your first command will be *pwd* (short for *print working directory*). It will tell you exactly where in the file system hierarchy you are, *i.e.* the full pathname of the directory you are in. Type *pwd* and press enter.



```
bash-4.1$ pwd
/usit/abel/u1/jonkl
bash-4.1$
```

The command-line interpreter have interpreted you command. It knows that *pwd* is a program and runs that program. The output from the program was sent to your screen and the interpreter is waiting for a new command. What is your "current directory"? This is "Unix-speak" for "the directory you are in right now".

2. Your second Unix command is *man*. It will show the manual pages for other Unix commands. Type *man pwd*. Then press enter. (You always press enter to make the interpreter start working on your command. Therefore we will not repeat this below!)



```
PWD(1)                           User Commands                          PWD(1)

NAME
       pwd - print name of current/working directory

SYNOPSIS
       pwd [OPTION]...

DESCRIPTION
       Print the full filename of the current working directory.

       -L, --logical
              use PWD from environment, even if it contains symlinks

       -P, --physical
              avoid all symlinks

       --help display this help and exit

       --version
              output version information and exit

       NOTE:  your  shell  may  have  its  own  version  of  pwd, which usually supersedes the version
       described here.  Please refer to your shellâs documentation for details about  the  options  it
       supports.

AUTHOR
       Written by Jim Meyering.

REPORTING BUGS
       Report pwd bugs to bug-coreutils@gnu.org
       GNU coreutils home page: <http://www.gnu.org/software/coreutils/>
       General help using GNU software: <http://www.gnu.org/gethelp/>
       Report pwd translation bugs to <http://translationproject.org/team/>

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       <http://gnu.org/licenses/gpl.html>.
       This is free software: you are free to change and redistribute it.  There is  NO  WARRANTY,  to
       the extent permitted by law.

SEE ALSO
       getcwd(3)

       The full documentation for pwd is maintained as a Texinfo manual.  If the info and pwd programs
       are properly installed at your site, the command

:
```

You get a lot of information about the *pwd* command. Press the letter "q" on your keyboard to leave the so-called man-page (the manual page for *pwd*).

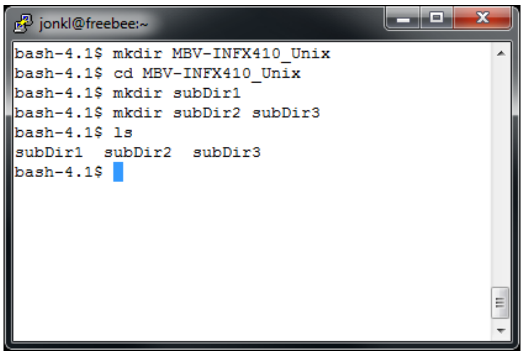
3. There is also a man-page for the command *man*. Try typing "*man man"*. You will see that while *pwd* was rather simple, *man* has many options and you can give it many different arguments. You can go up and down in the manual page by using "arrow up", "arrow down", "page up" and "page down" on your keyboard. Try this. There is a "-h" option for *man*. What will it do? Leave the man-pages (by pressing "q") and try it out by typing "*man -h"* on the command-line. What do you get?

The man-pages are very useful if you know the command you want to use, but you have forgotten some details about how to use it or what options you may use. Make sure you use the *man* command often later in this exercise!

4. Very useful and important commands are *ls* (lists all files in a directory), *cd* (change directory, go to a different directory), and *mkdir* (make directory, create a new directory)

   Write these commands (with enter after each line)

   *mkdir MBV-INFX410_Unix*
   *cd MBV-INFX410_Unix*
   *mkdir subDir1*
   *mkdir subDir2 subDir3*
   *ls*



```
bash-4.1$ mkdir MBV-INFX410_Unix
bash-4.1$ cd MBV-INFX410_Unix
bash-4.1$ mkdir subDir1
bash-4.1$ mkdir subDir2 subDir3
bash-4.1$ ls
subDir1  subDir2  subDir3
bash-4.1$
```

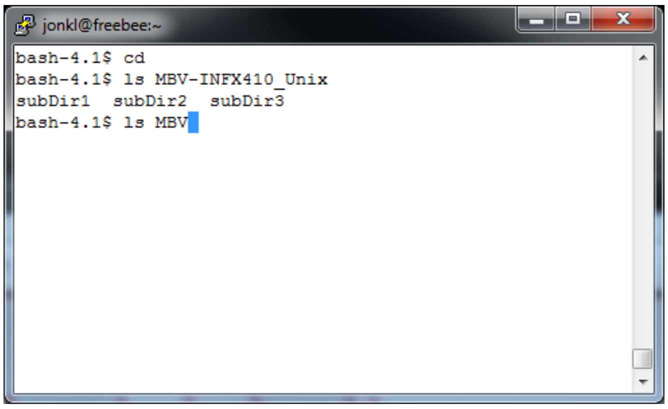
   You have made a new directory called MBV-INFX410_Unix, you went into that directory and created first 1 and then 2 new directories. Finally you listed all files in your "current directory", *i.e.* the directory you are in.

5. Here are some other commands with explanations

   *cd ..* (you will go from the directory you are in and up one level in the directory tree)
   *cd ../..* (you will go up 2 levels in the directory tree)
   *cd .* (nothing happens! You changed directory to the directory you are in)
   *cd ~/* (go to your "home directory", the directory you came to when you logged in)
   *cd* (this will do exactly the same as the previous line. If you "get lost" you can always type *cd* to go home...)
   *ls -l* (shows all files in your current directory, but with more information)
   *ls -la* (also shows "hidden files", *i.e.* files with a name that starts with a ".". These are often configuration files that you do not want to see)

   Try out these commands. Experiment with walking around in the directory tree and see what you can find out.

6. Type *cd* to get to your home directory and type *ls MBV-INFX410_Unix* to see what is in this directory. It is a lot of work, and a waste of time, to type the whole "*MBV-INFX410_Unix*". If you type *ls MBV* and press the Tab key, the shell will try to finish what you are writing. Most likely you only have one directory and "*ls MBV*" turns into "*ls MBV-INFX410_Unix*" after you have pressed Tab.



```
bash-4.1$ cd
bash-4.1$ ls MBV-INFX410_Unix
subDir1  subDir2  subDir3
bash-4.1$ ls MBV
```

Now go into the MBV-INFX410_Unix directory by using *cd*, but do not type the full directory name. Use the Tabbing-trick instead. Ok?

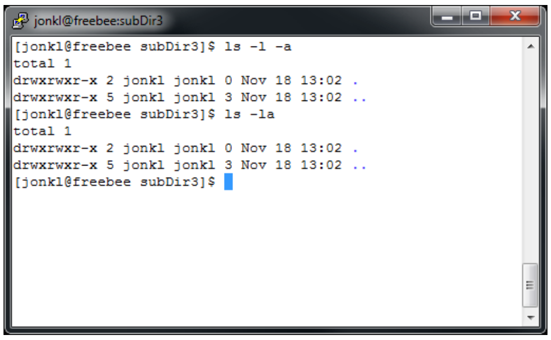
Type *cd s* and press Tab. Now there are several options, and the shell will not know if you want to go into subDir1, subDir2, or subDir3. If you press Tab twice, you get the options listed. Type *2* and enter and you are in ~/MBV-INFX410_Unix/subDir2. Type *pwd* to find out where you are in the complete directory tree. This shows you the “full path” or “absolute path”.

Make sure you use the Tab key a lot. *It will save you a lot of time and typing!*

7. Other useful things you can do are:

   Press “Ctrl” key and then (without letting go of Ctrl) “e”. This will take you to the end of the command line. Make sure you have written something after the prompt. If not, you are already at the end! This combination of keystrokes would usually be written “<ctrl>-e” or just “^e”. You can also go back and forth in the text on the command line by using the “arrow left” and “arrow right” keys. And you can delete text with the “Delete” and “Backspace” keys. Try this out!

   Other useful stuff:
   <ctrl>-a: Go to start of line, just after the prompt
   <ctrl>-k: Delete everything after the cursor
   <ctrl>-c: Kills (stops) a job that is running
   <ctrl>-z: Suspends a job that is running. A suspended job can be restarted.
8. Go into the directory ~/MBV-INFX410_Unix/subDir3 and make sure it is empty by running the command *ls -l -a*.



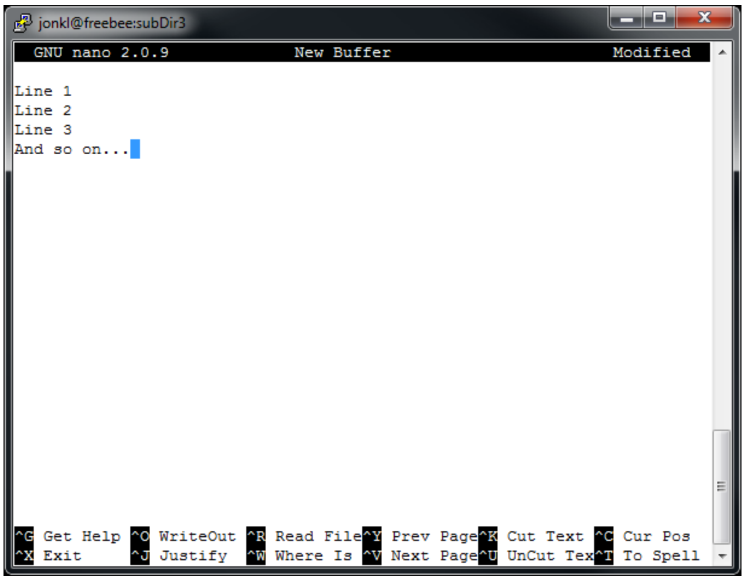
```
[jonkl@freebee subDir3]$ ls -l -a
total 1
drwxrwxr-x 2 jonkl jonkl 0 Nov 18 13:02 .
drwxrwxr-x 5 jonkl jonkl 3 Nov 18 13:02 ..
[jonkl@freebee subDir3]$ ls -la
total 1
drwxrwxr-x 2 jonkl jonkl 0 Nov 18 13:02 .
drwxrwxr-x 5 jonkl jonkl 3 Nov 18 13:02 ..
[jonkl@freebee subDir3]$
```

Above, you see that subDir3 is empty. There might appear to be two “files” there, but they are “.”, the directory you are in, and “..”, the directory above. Also note that the commands *ls -la* and *ls -l -a* will do exactly the same thing. For *ls* you can combine the arguments like this. This is not the case for all commands.

Now we want to open a text editor. Type *nano*. Inside the text editor you can type text, go up and down with the arrow keys and use delete and backspace. At the bottom of the editor, you see some keystrokes you may use to do various tasks. For example, “^x” or <ctrl>-x will exit the text editor and bring you back to the shell command line. Try this (but do not save any files yet)!

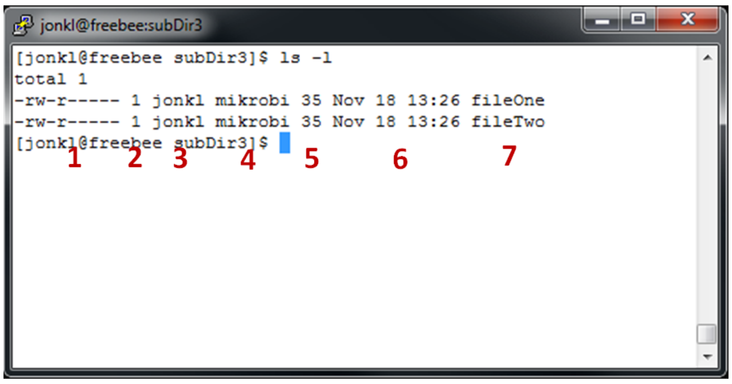
9. Nano is an extremely simple text editor. If you are more serious about using Unix you should learn something else, most likely emacs or vi. We will use nano for this exercise, but if you have a different favourite text editor, use that.

   Open nano and type in the text shown below.



```
  GNU nano 2.0.9               New Buffer                        Modified

Line 1
Line 2
Line 3
And so on...









^G Get Help ^O WriteOut ^R Read File^Y Prev Page^K Cut Text ^C Cur Pos
^X Exit     ^J Justify  ^W Where Is ^V Next Page^U UnCut Tex^T To Spell
```

Save this text as a text file by typing <ctrl>-o and calling the file “fileOne”. Save it again, but this time call it “fileTwo”. Now exit nano (<ctrl>-x). Use *ls -l* to list the files you just wrote and the information about them.



```
[jonkl@freebee subDir3]$ ls -l
total 1
-rw-r----- 1 jonkl mikrobi 35 Nov 18 13:26 fileOne
-rw-r----- 1 jonkl mikrobi 35 Nov 18 13:26 fileTwo
[jonkl@freebee subDir3]$
```

In the above window you see information about these two files in my current shell. Here is what it all means:

| **Number/position** | **Value** | **Explanation** |
|---|---|---|
| **1, 1st letter** | - | - means regular file<br>d means directory |
| **1, 2nd - 4th letter** | rw- | Access rights for the file owner (I can both read the file and modify/write to it, as well as delete it) |
| **1, 5th - 7th letter** | r-- | Access for all members of the group (here: mikrobi). The group members can open the file but not modify or delete it |
| **1, 8th - 10th letter** | --- | Access for everyone else. Users that are not members of the user group mikrobi cannot open the file (or modify it) |
| **2** | 1 | Number of hard links to the file (ignore this) |
| **3** | jonkl | User name of the file owner |
| **4** | mikrobi | Group of users that the file belongs two |
| **5** | 35 | Size of the file in bytes |
| **6** | Nov 18 13:26 | Date and time the file was last modified |
| **7** | fileOne | File name |

By modifying the accession rights you can make files and directories accessible to everyone on the computer, to only certain groups or to only yourself. The command *groups* will show which groups you are a member of. Try it! These are also useful:

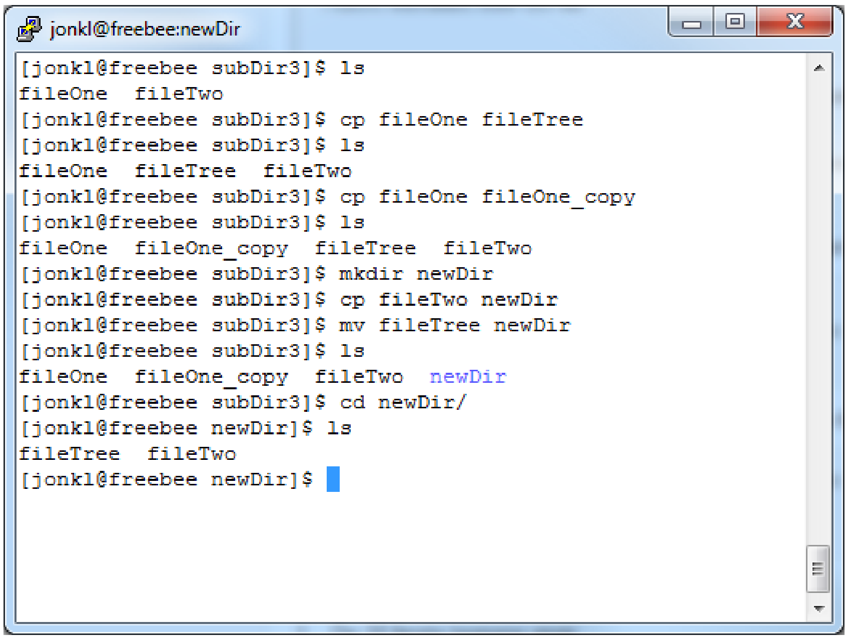
- *chmod* will modify the accessions, *i.e.* the string "-rw-r-----" to something else
- *chown* will change the owner and/or group of a file

We do not have time to try this now, but you can use the man-pages and experiment later.

Note how useful this can be! For example, if you are involved in two (top secret) projects, you can make two user groups, group1 and group2. You can then have files and directories that can be viewed (or modified) by only yourself, only members of group1, only members of group2, or all users on the computer. Maybe you will only allow group1 members to run a certain program, while only group2 members are allowed to see your holiday photos? The system is very flexible!

10. The commands *cp* (make a copy of a file), *mv* (move a file), and *rm* (remove a file) are very useful. By the way, to remove a directory use *rmdir*.

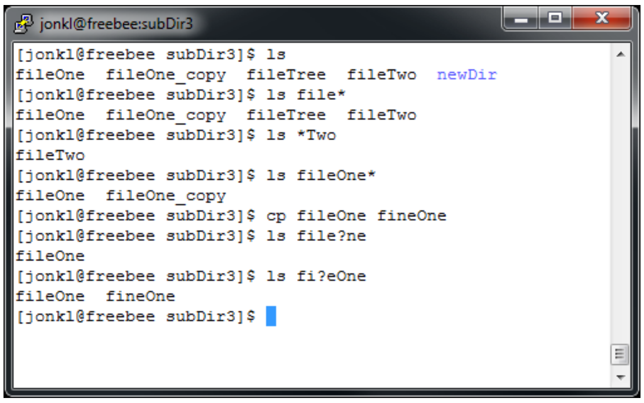
    Go to ~/MBV-INFX410_Unix/subDir3 where you still have the two files fileOne and fileTwo. Try the commands in the window below.



```
[jonkl@freebee subDir3]$ ls
fileOne  fileTwo
[jonkl@freebee subDir3]$ cp fileOne fileTree
[jonkl@freebee subDir3]$ ls
fileOne  fileTree  fileTwo
[jonkl@freebee subDir3]$ cp fileOne fileOne_copy
[jonkl@freebee subDir3]$ ls
fileOne  fileOne_copy  fileTree  fileTwo
[jonkl@freebee subDir3]$ mkdir newDir
[jonkl@freebee subDir3]$ cp fileTwo newDir
[jonkl@freebee subDir3]$ mv fileTree newDir
[jonkl@freebee subDir3]$ ls
fileOne  fileOne_copy  fileTwo  newDir
[jonkl@freebee subDir3]$ cd newDir/
[jonkl@freebee newDir]$ ls
fileTree  fileTwo
[jonkl@freebee newDir]$ 
```

    Make sure you understood what you did! Also make sure you use the Tab-key in order to avoid a lot of typing.

11. Learn to use the wildcards "*" (matches zero or more characters) and "?" (matches any single character). For examples, see the window below.



```
[jonkl@freebee subDir3]$ ls
fileOne  fileOne_copy  fileTree  fileTwo  newDir
[jonkl@freebee subDir3]$ ls file*
fileOne  fileOne_copy  fileTree  fileTwo
[jonkl@freebee subDir3]$ ls *Two
fileTwo
[jonkl@freebee subDir3]$ ls fileOne*
fileOne  fileOne_copy
[jonkl@freebee subDir3]$ cp fileOne fineOne
[jonkl@freebee subDir3]$ ls file?ne
fileOne
[jonkl@freebee subDir3]$ ls fi?eOne
fileOne  fineOne
[jonkl@freebee subDir3]$
```

12. Create some more directories, copy and move files, and finally remove some of the directories and files you created.

    Be very careful with *rm* and *rmdir*. If you remove files and directories, they are gone, and you will not get them back!
13. Copying and pasting text is of course very useful. In order to copy text from somewhere in the terminal window, click and drag to mark the text you want to copy. Then right click on the command line to paste in this text. (This might work slightly differently depending on your laptop and/or mouse. If you are stuck, ask one of the teachers)

    When you have learned to copy and paste within the terminal window you are ready to continue!
14. Open this webpage in a web browser: http://www.uniprot.org/uniprot/O15527 Click on the orange "fasta" box at the right hand side to get to the following page: http://www.uniprot.org/uniprot/O15527.fasta

    Copy the whole Fasta-sequence including the header. On a Microsoft Windows laptop you would mark the text and press <ctrl>-c. Open the nano text editor in your terminal window and paste in the text by right clicking in that window. You might have to experiment a bit, as copying and pasting will depend on computer/mouse and other settings. If you get stuck, as a teacher!

    Save the file by pressing <ctrl>-x, type "y" (yes) and type a file name (call it "O15527.fasta"). Exit nano and make sure you have created a file with the correct name.

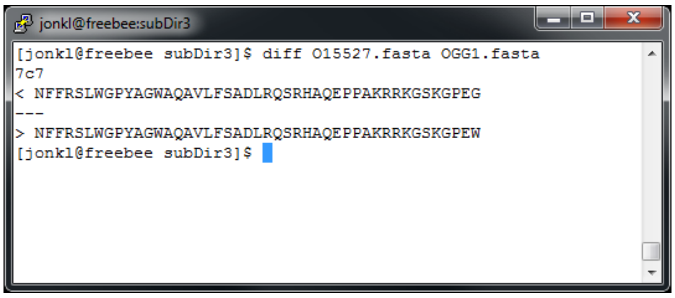
    Repeat the procedure with the text here:
    http://www.uniprot.org/uniprot/Q92736.fasta

    Save this as a file named RYR2.fasta.

15. A useful command to just list all the text in a text file is *cat*. Try *cat O15527.fasta* and *cat RYR2.fasta*. What happens?
16. Note that you, on the command line, can go back and forth in old commands by using the “arrow up” and “arrow down” keys. In this way you can access old commands and run them again. Or you can modify them and run. Try it out. This also saves a lot of typing!
17. The *cat* command will show you the whole file. If the file is long, the top will just disappear out of view at the top of the screen. A useful alternative is the *more* command. Try *more RYR2.fasta*. When you press “enter” *more* will show you one more line of text. Pressing the space bar, gives you one extra page of text. Does it work?
18. In the Unix shell we have something called “standard input” (STDIN) and “standard output” (STDOUT). Put simply, STDIN is what you type on the keyboard, while STDOUT is what is shown on the screen. This is the default. You can redirect STDIN and STDOUT. First try, as before, *cat O15527.fasta*. Then try

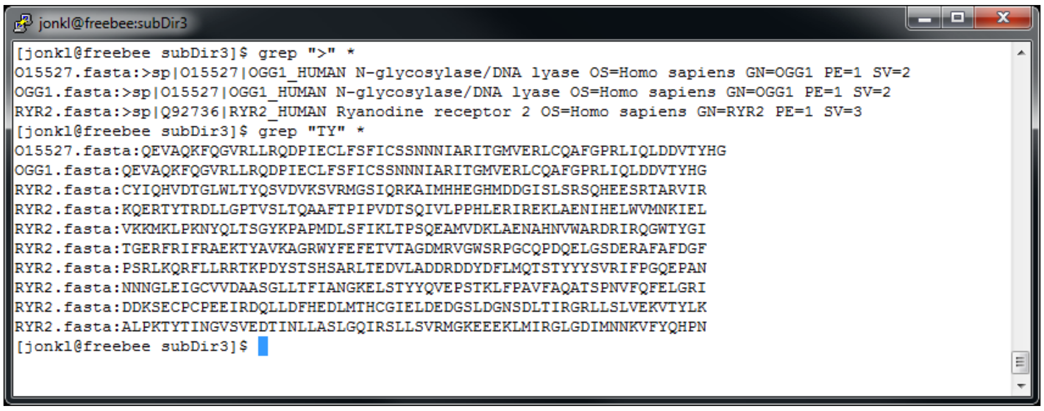
    *cat O15527.fasta > OGG1.fasta*

    Apparently nothing happens, but this is because the output wasn’t sent to the screen. Instead it was redirected into the new file OGG1.fasta. Do *cat* on that file to check. Ok?
19. Open the file OGG1.fasta in nano and change the C-terminal G (glycine) to W (tryptophan). A mutation, right! Now save the file again with the modification.
20. Another useful command is *diff*. Try *diff O15527.fasta OGG1.fasta*. What happens? Use the manual pages for *diff* if you didn’t get it or you want to know more.



```
[jonkl@freebee subDir3]$ diff O15527.fasta OGG1.fasta
7c7
< NFFRSLWGPYAGWAQAVLFSADLRQSRHAQEPPAKRRKGSKGPEG
---
> NFFRSLWGPYAGWAQAVLFSADLRQSRHAQEPPAKRRKGSKGPEW
[jonkl@freebee subDir3]$
```

21. The command *grep* will show you all the lines in one or several text files that contains a pattern, for example like this:



```
[jonkl@freebee subDir3]$ grep ">" *
O15527.fasta:>sp|O15527|OGG1_HUMAN N-glycosylase/DNA lyase OS=Homo sapiens GN=OGG1 PE=1 SV=2
OGG1.fasta:>sp|O15527|OGG1_HUMAN N-glycosylase/DNA lyase OS=Homo sapiens GN=OGG1 PE=1 SV=2
RYR2.fasta:>sp|Q92736|RYR2_HUMAN Ryanodine receptor 2 OS=Homo sapiens GN=RYR2 PE=1 SV=3
[jonkl@freebee subDir3]$ grep "TY" *
O15527.fasta:QEVAQKFQGVRLLRQDPIECLFSFICSSNNNIARITGMVERLCQAFGPRLIQLDDVTYHG
OGG1.fasta:QEVAQKFQGVRLLRQDPIECLFSFICSSNNNIARITGMVERLCQAFGPRLIQLDDVTYHG
RYR2.fasta:CYIQHVDTGLWLTYQSVDVKSVRMGSIQRKAIMHHEGHMDDGISLSRSQHEESRTARVIR
RYR2.fasta:KQERTYTRDLLGPTVSLTQAAFTPIPVDTSQIVLPPHLERIREKLAENIHELWVMNKIEL
RYR2.fasta:VKKMKLPKNYQLTSGYKPAPMDLSFIKLTPSQEAMVDKLAENAHNVWARDRIRQGWTYGI
RYR2.fasta:TGERFRIFRAEKTYAVKAGRWYFEFETVTAGDMRVGWSRPGCQPDQELGSDERAFAFDGF
RYR2.fasta:PSRLKQRFLLRRTKPDYSTSHSARLTEDVLADDRDDYDFLMQTSTYYYSVRIFPGQEPAN
RYR2.fasta:NNNGLEIGCVVDAASGLLTFIANGKELSTYYQVEPSTKLFPAVFAQATSPNVFQFELGRI
RYR2.fasta:DDKSECPCPEEIRDQLLDFHEDLMTHCGIELDEDGSLDGNSDLTIRGRLLSLVEKVTYLK
RYR2.fasta:ALPKTYTINGVSVEDTINLLASLGQIRSLLSVRMGKEEEKLMIRGLGDIMNNKVFYQHPN
[jonkl@freebee subDir3]$
```

22. We want to get access to some GenBank data from the GenBank ftp site. Google "genbank ftp site" to find where it is. Google can be useful...

    Hope you found it? It is here ftp://ftp.ncbi.nih.gov/genbank

    Open this link in your browser. You find an awful lot of files, some of them are quite big. You can find information about the data here

    ftp://ftp.ncbi.nih.gov/genbank/gbrel.txt
    ftp://ftp.ncbi.nih.gov/genbank/README.genbank

    Click on the file gbphg1.seq.gz in the GenBank ftp directory in your web browser and then save it to ~/MBV-INFX410_Unix/subDir1. This means you have to find this directory on your laptop. Hope you have mounted your UiO home area on your laptop... If you are having problems, ask one of the teachers!

    This file is in a "packed" format. It has been packed with the gzip program. To unpack, type *gunzip gbphg1.seq.gz*. Type *ls -lh* to see some information about the file. The *-h* option means that you get the file size in a more convenient format. The file is very big, 239 Mb! *This value was 204 Mb in 2012 and will change every time GenBank is updated.*

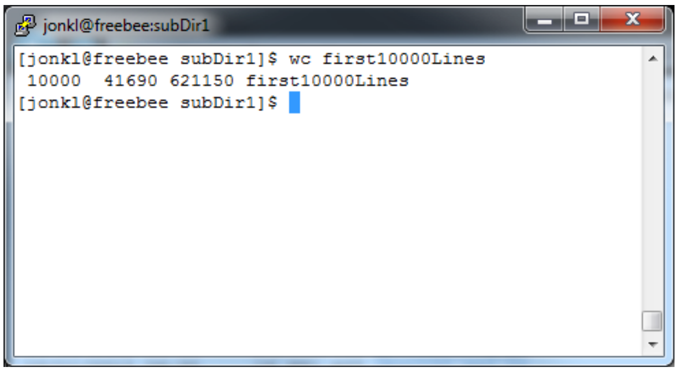
    ***PLEASE! When you have finished doing this exercise, delete this file (and other big files). We do not want to fill up your home area and the UiO computers with data that you absolutely do not need!!***

    The file contains most the phage data in GenBank. The rest is in gbphg2.seq, but we will not look into that now. Do *more gbphg1.seq* to start reading from the top. What is the accession number of the first entry? (AB000833)
23. Are there anyone called Hansen that submitted any of the data? Try *grep Hansen gbphg1.seq*.

24. The commands *head -n 20* and *tail -n 50* will print out the first 20 and the last 50 lines of a given file (but you can of course choose the number of lines you want). Try

    *head -n 200 gbphg1.seq*
    *tail -n 60 gbphg1.seq*
    *head -n 10000 gbphg1.seq > first10000Lines*

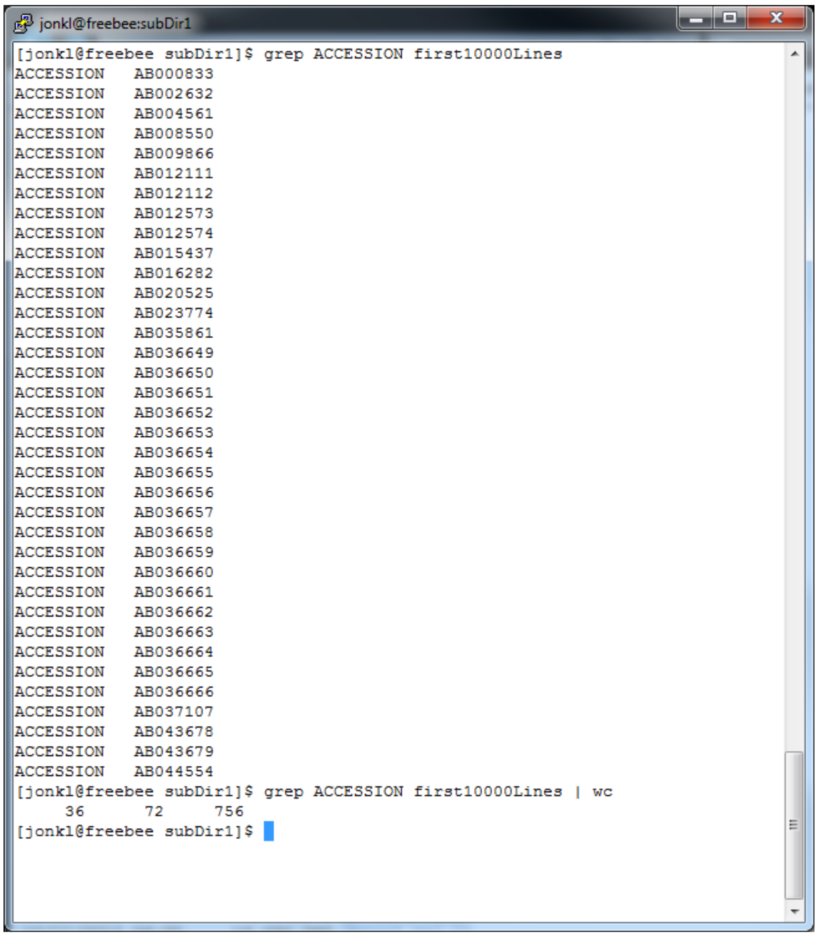
    The command *wc* counts the number of words in a file, for example *wc first10000Lines*:



```
[jonkl@freebee subDir1]$ wc first10000Lines
 10000  41690 621150 first10000Lines
[jonkl@freebee subDir1]$
```

    There are 10000 lines, 41690 words and 621150 bytes of information in the file. *Actually, it is 41687 and 621140 in November 2013, and this will most likely change when GenBank is updated next time.*

    The "|" (the "pipe") will send the STDOUT of one command into the STDIN of the next. What happens here?:



```
[jonkl@freebee subDir1]$ grep ACCESSION first10000Lines
ACCESSION   AB000833
ACCESSION   AB002632
ACCESSION   AB004561
ACCESSION   AB008550
ACCESSION   AB009866
ACCESSION   AB012111
ACCESSION   AB012112
ACCESSION   AB012573
ACCESSION   AB012574
ACCESSION   AB015437
ACCESSION   AB016282
ACCESSION   AB020525
ACCESSION   AB023774
ACCESSION   AB035861
ACCESSION   AB036649
ACCESSION   AB036650
ACCESSION   AB036651
ACCESSION   AB036652
ACCESSION   AB036653
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ACCESSION   AB036662
ACCESSION   AB036663
ACCESSION   AB036664
ACCESSION   AB036665
ACCESSION   AB036666
ACCESSION   AB037107
ACCESSION   AB043678
ACCESSION   AB043679
ACCESSION   AB044554
[jonkl@freebee subDir1]$ grep ACCESSION first10000Lines | wc
     36      72     756
[jonkl@freebee subDir1]$
```
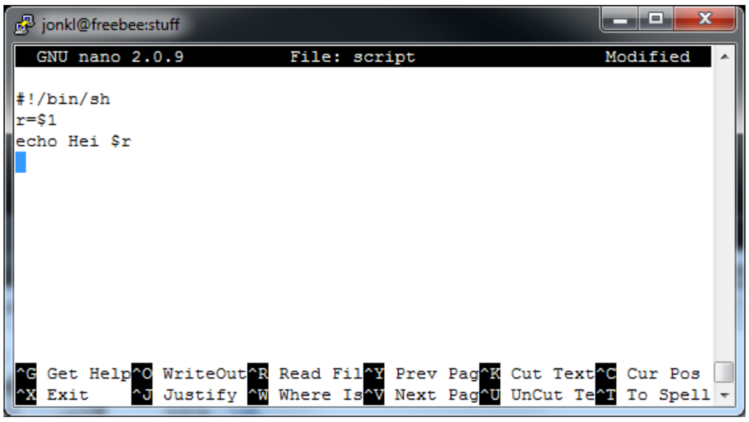

First, all the lines with "ACCESSION" is printed out. Then, instead of printing this out to the screen, the output is sent to the *wc* command. It counts 36 lines. It is 36 "ACCESSION" in the file. Easier than counting manually! How many lines have "ACCESSION" in them in gbphg1.seq?

25. Finally in this exercise we will try some very simple shell scripts. Shell scripts are small programs that are doing tasks that also could have been done step by step by a person on the command line. Go into ~/MBV-INFX410_Unix/subDir2, which should be empty (or else remove the files that are there). Copy fileOne from ../subDir3 here.
26. Open nano and type the following,



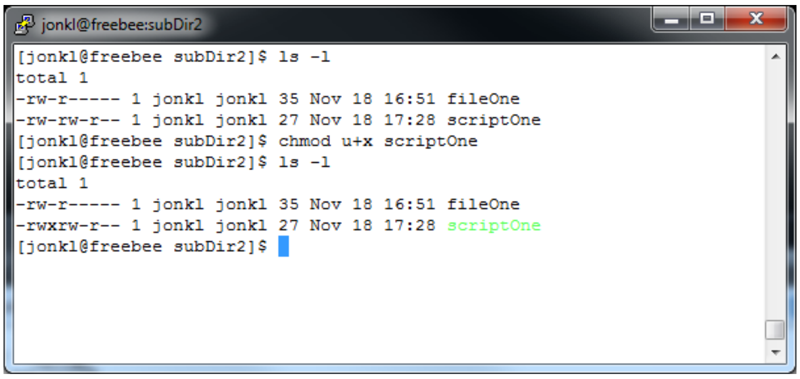
```
  GNU nano 2.0.9              File: script                        Modified

#!/bin/sh
r=$1
echo Hei $r
```

What does this mean?

| | |
|---|---|
| #!/bin/sh | The rest of this script should be interpreted by the sh shell |
| r=$1 | The variable r (that is $r) gets the contents of the first argument on the command line |
| echo Hei $r | "Hei" and then the variable content is written to STDOUT |

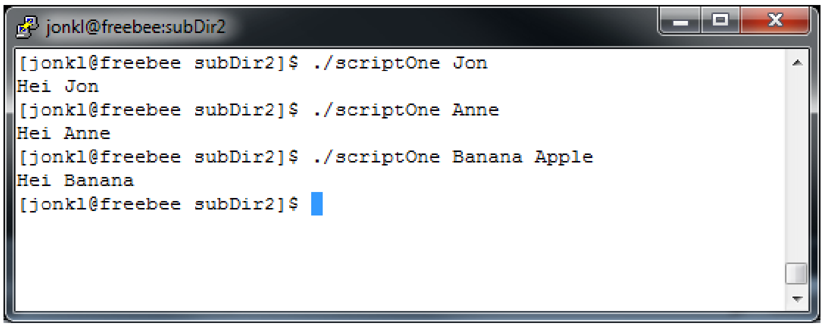
Save the script as "scriptOne". The "#!" on the first line, two first characters, is called a shebang (from "hash" and "bang", *i.e.* exclamation mark). It tells the shell that the rest of the script should be interpreted by the program /bin/sh (Bourne shell). If it had been "#!/usr/bin/python" or "#!/usr/bin/perl" that would have indicated that this instead was a python or perl script, respectively.

Most likely you have a problem, since scriptOne is not an executable program that the shell thinks it can run as a program. However, the command *chmod u+x scriptOne* will fix that:



```
[jonkl@freebee subDir2]$ ls -l
total 1
-rw-r----- 1 jonkl jonkl 35 Nov 18 16:51 fileOne
-rw-rw-r-- 1 jonkl jonkl 27 Nov 18 17:28 scriptOne
[jonkl@freebee subDir2]$ chmod u+x scriptOne
[jonkl@freebee subDir2]$ ls -l
total 1
-rw-r----- 1 jonkl jonkl 35 Nov 18 16:51 fileOne
-rwxrw-r-- 1 jonkl jonkl 27 Nov 18 17:28 scriptOne
[jonkl@freebee subDir2]$
```

The "rw-" in position 2-4 is changed to rwx, for the user (that is where the "u" comes from). The user can now, in addition to reading from and writing to the file, execute it (*i.e.* run it as a program). Now let us do that:



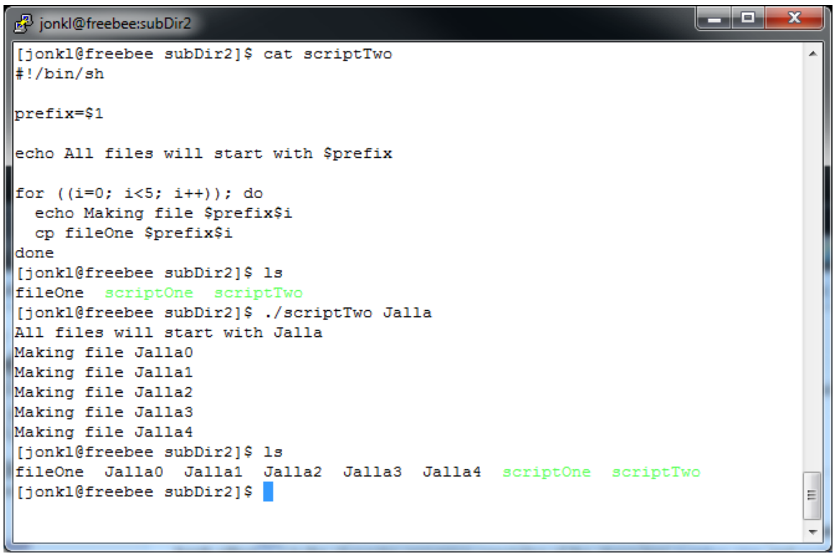
```
[jonkl@freebee subDir2]$ ./scriptOne Jon
Hei Jon
[jonkl@freebee subDir2]$ ./scriptOne Anne
Hei Anne
[jonkl@freebee subDir2]$ ./scriptOne Banana Apple
Hei Banana
[jonkl@freebee subDir2]$
```

You have to put the "./" in front of the name of your script. If you do not, (most likely) the shell will not know where to look for it. As you see, you type the name of the executable file (including the file path to it) and some words. It will repeat back to you “Hei” and the first word. Not very advanced, but you first script!

27. Now try typing in this script

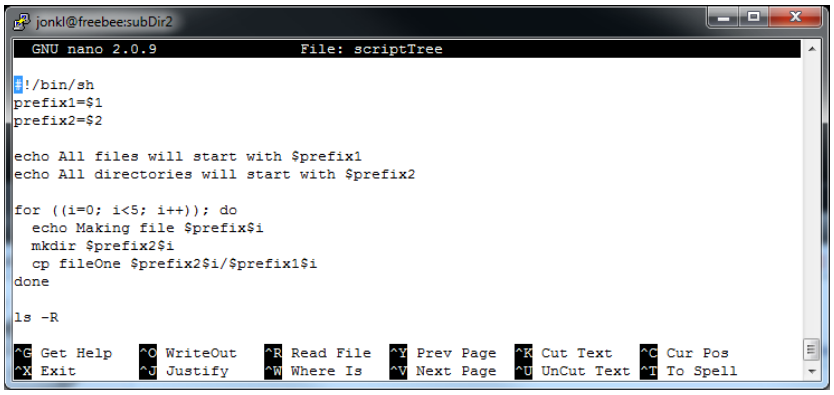
```
#!/bin/sh
prefix=$1
echo All files will start with $prefix
for ((i=0; i<5; i++)); do
   echo Making file $prefix$i
   cp fileOne $prefix$i
done
```

Save it as scriptTwo, make it executable (with *chmod*) and run it with an argument. What do you think it will do?



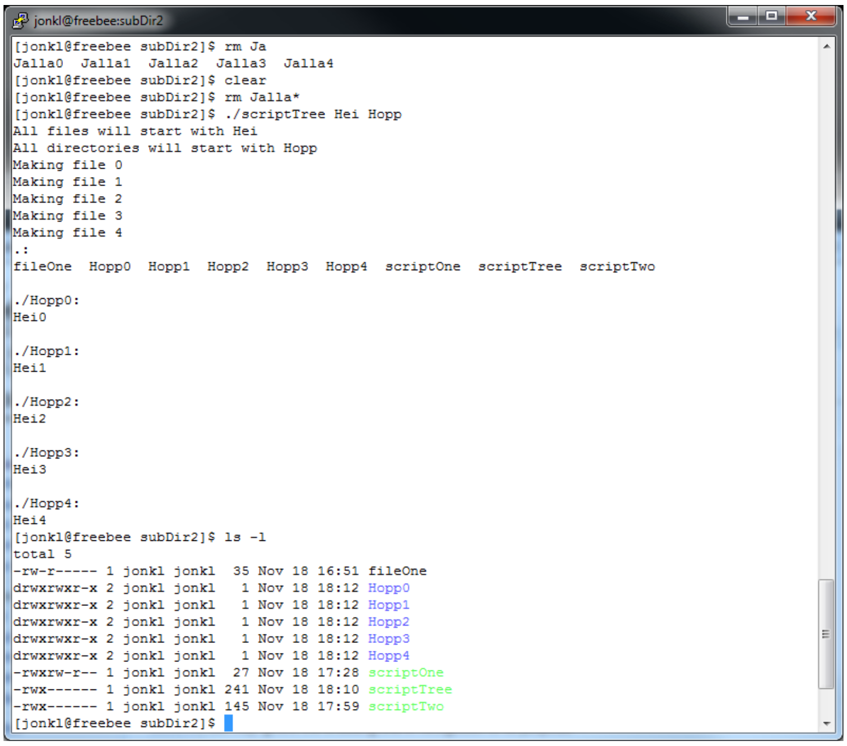
```
[jonkl@freebee subDir2]$ cat scriptTwo
#!/bin/sh

prefix=$1

echo All files will start with $prefix

for ((i=0; i<5; i++)); do
  echo Making file $prefix$i
  cp fileOne $prefix$i
done
[jonkl@freebee subDir2]$ ls
fileOne  scriptOne  scriptTwo
[jonkl@freebee subDir2]$ ./scriptTwo Jalla
All files will start with Jalla
Making file Jalla0
Making file Jalla1
Making file Jalla2
Making file Jalla3
Making file Jalla4
[jonkl@freebee subDir2]$ ls
fileOne  Jalla0  Jalla1  Jalla2  Jalla3  Jalla4  scriptOne  scriptTwo
[jonkl@freebee subDir2]$
```

The script makes 5 copies of fileOne, each called Jalla0, Jalla2 etc, or whatever prefix you entered on the command line. A final example here,



```
  GNU nano 2.0.9                    File: scriptTree

#!/bin/sh
prefix1=$1
prefix2=$2

echo All files will start with $prefix1
echo All directories will start with $prefix2

for ((i=0; i<5; i++)); do
  echo Making file $prefix$i
  mkdir $prefix2$i
  cp fileOne $prefix2$i/$prefix1$i
done

ls -R

^G Get Help  ^O WriteOut  ^R Read File  ^Y Prev Page  ^K Cut Text   ^C Cur Pos
^X Exit      ^J Justify   ^W Where Is   ^V Next Page  ^U UnCut Text ^T To Spell
```

Here it runs...



```
[jonkl@freebee subDir2]$ rm Ja
Jalla0  Jalla1  Jalla2  Jalla3  Jalla4
[jonkl@freebee subDir2]$ clear
[jonkl@freebee subDir2]$ rm Jalla*
[jonkl@freebee subDir2]$ ./scriptTree Hei Hopp
All files will start with Hei
All directories will start with Hopp
Making file 0
Making file 1
Making file 2
Making file 3
Making file 4
.:
fileOne  Hopp0  Hopp1  Hopp2  Hopp3  Hopp4  scriptOne  scriptTree  scriptTwo

./Hopp0:
Hei0

./Hopp1:
Hei1

./Hopp2:
Hei2

./Hopp3:
Hei3

./Hopp4:
Hei4
[jonkl@freebee subDir2]$ ls -l
total 5
-rw-r----- 1 jonkl jonkl  35 Nov 18 16:51 fileOne
drwxrwxr-x 2 jonkl jonkl   1 Nov 18 18:12 Hopp0
drwxrwxr-x 2 jonkl jonkl   1 Nov 18 18:12 Hopp1
drwxrwxr-x 2 jonkl jonkl   1 Nov 18 18:12 Hopp2
drwxrwxr-x 2 jonkl jonkl   1 Nov 18 18:12 Hopp3
drwxrwxr-x 2 jonkl jonkl   1 Nov 18 18:12 Hopp4
-rwxrw-r-- 1 jonkl jonkl  27 Nov 18 17:28 scriptOne
-rwx------ 1 jonkl jonkl 241 Nov 18 18:10 scriptTree
-rwx------ 1 jonkl jonkl 145 Nov 18 17:59 scriptTwo
[jonkl@freebee subDir2]$
```

What does it do?

(When I run it with the arguments Hei and Hopp, it creates directory Hopp0 with a single copy of fileOne called Hei0, Hopp1 with Hei1 and so on... Finally it does an *ls -R*) Check the man pages for *ls* to find out what *-R* is doing.

28. To exit the shell, type *exit* or press <ctrl>-d.

Get more inspiration here

- Trond Hasle Amundsens Linux/UNIX guide for UiO: http://www.uio.no/tjenester/it/maskin/linux/hjelp/tips/guide.html
- bash programming in INF3331 by Hans Petter Langtangen and co-workers: http://www.uio.no/studier/emner/matnat/ifi/INF3331/h12/bash.pdf
- EMBnet "A Quick Guide UNIX": http://www.embnet.org/sites/default/files/quickguides/guideUNIX.pdf
- Or just search the web. There is lots of useful tutorials for basic and advanced Unix and scripting

Thanks to Trond Hasle Amundsens Linux/UNIX guide and Merete Molton Worrens "Basic Unix commands" for inspiration for this exercise!