Introduction to the command line with Bash: Learn useful fundamentals and make your own scripts!

interactive intro workshop

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agenda

- motivation to learn how to use command line tools
- terminal & shell
- text editor
- commandline tools
- file permissions
- transfer of files
- installing software
- customizing work environment

Motivation & Justification

- understand how the computer "thinks"
- decide the tradeoff, when do you do something manual, and when do you automate it?
- what you do in the terminal could be made into a script that can be saved for reproducibility.
- there is a plethora of open source software developed by other scientists.

show of hands ?

- Bioengineering/Biosustain/anything else?
- windows/mac/anything else
- windows users with WSL?
- who has US english or EU english keyboard layout?

How to get started with



if you are not on a linux machine



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Inside the terminal

```
bash-3.2$ bash --help
bash-3.2$ bash --version
bash-3.2$ man bash
```

command line argument:

Unless there is a particular reason, most software is designed so that -- prefixes a word and - prefixes a single character.

i.e.: ls - ltrh == ls - l - t - r - h

Inside the terminal

bash-3.2\$ which man

bash-3.2\$ man less

bash-3.2\$ less --help | less

Anatomy of a man page

NAME

The name of the command or function, followed by a one-line description of what it does.

SYNOPSIS

In the case of a command, a formal description of how to run it and what command line options it takes. For program functions, a list of the parameters the function takes and which header file contains its declaration.

DESCRIPTION

A textual description of the functioning of the command or function.

EXAMPLES

Some examples of common usage.

SEE ALSO

A list of related commands or functions.

characters, what are their names?



characters

- Backtick
- Tilde
- Double quote
- Single quote
- Slash
- Backslash
- Pipe
- Colon
- Less than

()
[]
{ }
_
*
•
,
•
>

- Exclamation ! At @ Pound/Hash # Dollar \$ Percentage % Hat/Circumflex ^
- Ampersand &
- Plus +
- Equal =

whitespace characters and line breaks

Space tab newline carriage return

lets make a folder and enter it

- pwd print working directory
- ls list files in directory
- cd change directory (you should now be in ~ your home directory mkdir bashworkshop – make a directory named bashworkshop cd bashworkshop – enter the directory (try hitting tab during typing for autocomplete)

lets say hello to the person next to us

- echo 'hej'
- name=Albert
 - echo hej \$name
 - echo "hej \$name"
 - echo 'hej \$name'
- What happens if we had used backticks?

lets make a file

- echo "hej \$name" > greeting.txt
- cat greeting.txt
- echo "hej \$name" >> greeting.txt
- What is the difference
- touch emptyfile.txt
- cat, | , > grep, sort, ...
- ls

lets make a file

- Try to redefine the \$name variable and append a new line to the greeting.txt file
 - i.e. echo "hej Jakob" >> greeting.txt

you should have different lines in the file

cat greeting.txt

cat greeting.txt | sort

cat greeting.txt | grep hej

cat greeting.txt | grep Jakob

cat greeting.txt | grep fejwlkjbfg

cat greeting.txt | grep Jakob | wc -l

lets rename the file

- mv greeting.txt greetings.txt (moving the content from one file to another)
- ls -l

what do we see in the ls –l output?

lets copy the file

• cp greetings.txt emptyfile.txt (copying the content from one file to another)

• ls -l

what exactly did we do?

• history

text editors (.txt)

- on most systems you will encounter bash as the shell, some text editors are almost always installed: nano vi
- vi can be customized. Some people prefer to install emacs or neovim
- outside the terminal you have many more choices, i.e. vscode



• if your put your text files in an office program, you risk your - will be converted to – as well as text getting Auto Capitalized etc.

lets make our first script in nano or vim

- make a file called hello.sh
- it should say hello to someone at your table when you run it.
- bash ./hello.sh
- ./hello.sh

(we need to add a line pointing to the program needed=bash) hashbang/shebang: #!/bin/bash which bash

nano – simple text editor, you can just type

hotkeys listed in bottom, ^ = Ctrl

General Terminal hotkeys:

- copy and paste in terminal is different from other programs
- Copy = Shift + Ctrl + C / Cmd + C / selecting text with cursor
- Paste = Shift + Ctrl + V / Cmd + V / middle click with cursor

What does Ctrl + C do ?????

How about Ctrl + Z ???

vim – powerful text editor

- omnipresent, it is almost always on the server you visit.
- old, origins traces back to before arrow keys
- notoriously steep learning curve

file owner and permissions

- chmod
- sudo

Downloading

- scp / sftp (command line vs interactive) i.e. filezilla
- most systems have curl or wget (download files)
- some have git (download software projects/repositories)

Software:

- mac: port / brew
- ubuntu/debian: apt / snap
- fedora: dnf / flatpak
- DTU HPC: dont install software, do `module load` instead

some websites will ask you to install software

- curl URL | bash
- Please download first to look at the code (keep the code in case you need to know what you did)
- curl –O URL
- less file
- bash file

some websites will ask you to install software

- curl | bash please be very careful if you ever have to use sudo for these types of setups
- icanhazip.com

https://major.io/p/a-new-future-for-icanhazip/

Downloading with curl or wget

• curl and wget are both useful for downloading files. will insert example download here

go to github.com/biosustain/dsp_workshop_bash copy the URL:

https://raw.githubusercontent.com/biosustain/dsp_workshop_bash/refs/heads/main/Readme.md

• curl

Downloading a repository with git

• git clone https://github.com/biosustain/dsp_workshop_bash

get / make a script

- #!/usr/bin/env bash
- #!/bin/bash
- # comment in bash
- echo 'code in bash'

Example: script.sh

```
#!/bin/bash
# Albert 2024-09-25
# Script to add sample names to the gene calls
# Loop through all .fna files in the current directory
for file in *.fna; do
    echo "Working on $file"
    # Extract filename without extension
    filename=$(basename "$file" .fna)
```

```
# Use sed to insert the filename at the start of each line beginning with '>'
    sed -i '' "s/^>/>${filename}_/" "$file"
done
```

echo "Sample name inserted into lines starting with '>' in all .fna files."

Example: script.sh

#!/bin/bash

Albert 2024-09-25

Script to add sample names to the gene calls

Loop through all .fna files in the current directory
for file in *.fna; do
 echo "Working on \$file"

```
# Extract filename without extension
filename=$(basename "$file" .fna)
```

Use sed to insert the filename at the start of each line beginning with '>'
 sed -i '' "s/^>/>\${filename}_/" "\$file"
done

echo "Sample name inserted into lines starting with '>' in all .fna files."

ssh

- get on **DTUsecure wifi** and connect to login1.hpc.dtu.dk with ssh
- try to run the command whoami in your terminal
- ssh DTUUSERNAME@ login1.hpc.dtu.dk

scp

Upload:

scp file.txt DTUUSERNAME@transfer.gbar.dtu.dk:~/
 Download:

scp DTUUSERNAME@transfer.gbar.dtu.dk:~/file.txt ~/

You can also access the directory with an sftp browser like filezilla

Takehome messages

- The best terminal is the one you already have
- There are certain unix tools you will find on almost all servers
 - bash, nano, vim, grep, sed, sort, uniq, head, tail, cat, less ...
- dont just paste/pipe things you find on the web
- use a proper text editor, not Office programs
- give your files/folders the permissions they need
- learn about git in our next workshop

Upcoming events

- November 13th 2024 Git and Github
- November 20th 2024 Data Visualization
- November 27th 2024 Nextflow

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