

Linux command line and nf-core introduction

Edoardo Piombo

Let' download stuff

Windows people should do the following:

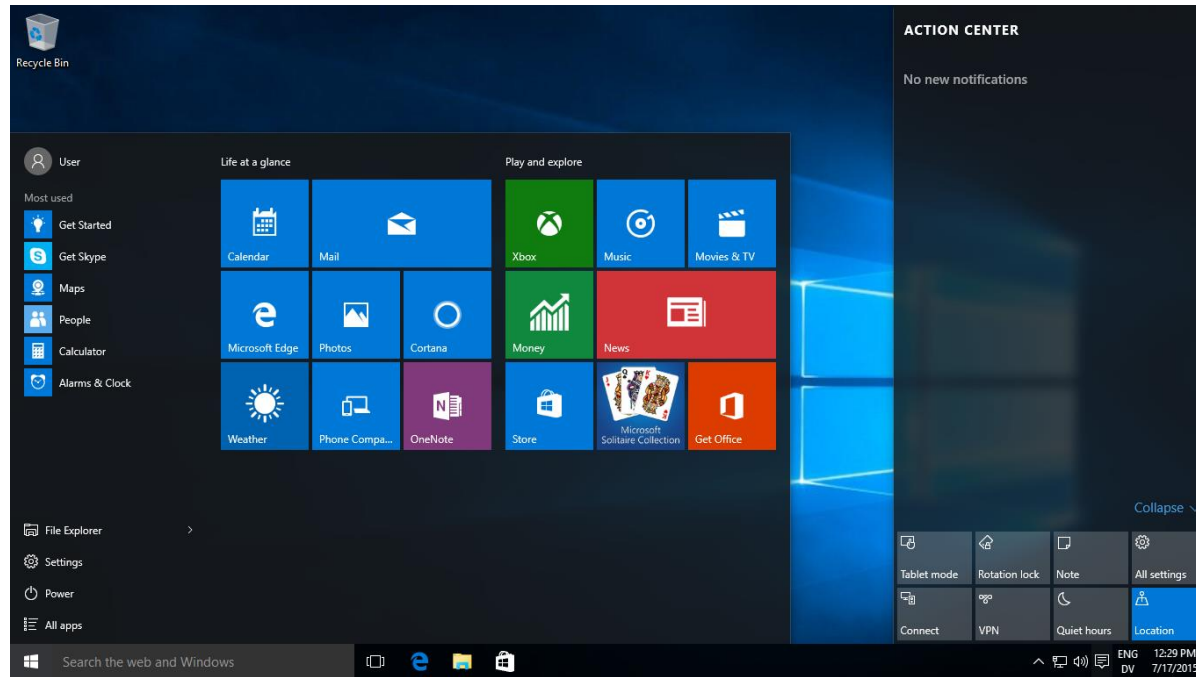
- download moba X term from here: <https://mobaxterm.mobatek.net/>
- Do “new session”
- Choose “shell”
- Choose “bash”
- Enter “open /home/mobaxterm” to open the directory in the file explorer

People using Macs or Linux just need to open a terminal:

- Mac: <https://support.apple.com/guide/terminal/open-or-quit-terminal-apd5265185d-f365-44cb-8b09-71a064a42125/mac>
- Linux: <https://ubuntu.com/tutorials/command-line-for-beginners#3-opening-a-terminal>

There are different ways of interacting with computers

Graphical user interface (GUI)

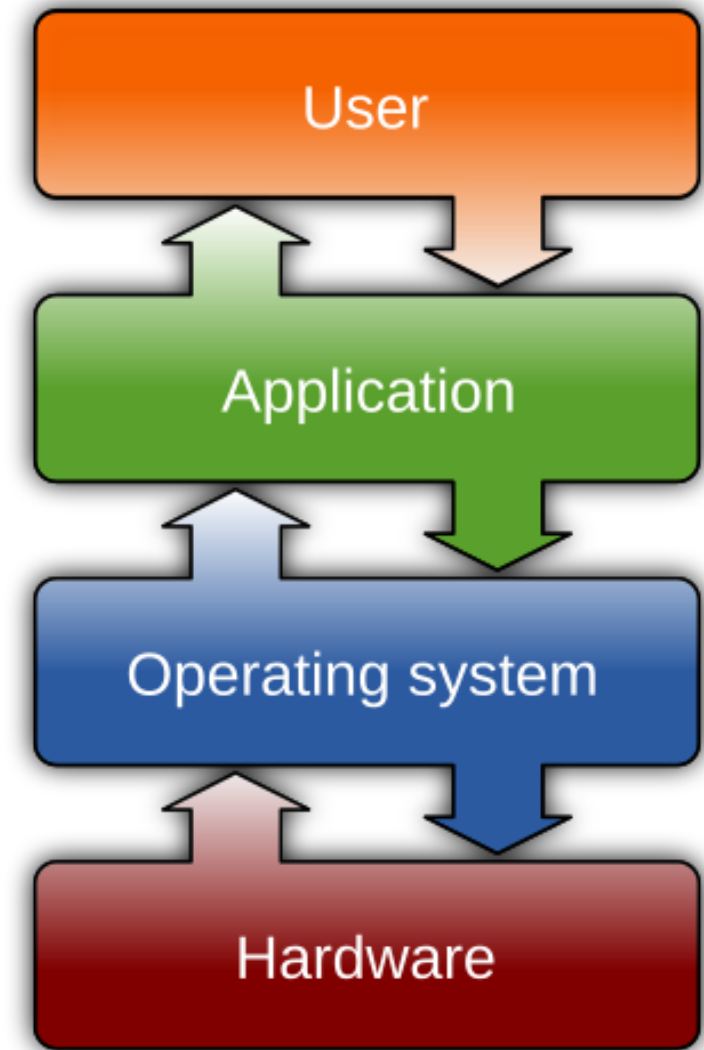


Command-line (or text) interface (CLI). Also called shell

```
javatpoint@javatpoint-Inspiron-3542: ~  
File Edit View Search Terminal Help  
javatpoint@javatpoint-Inspiron-3542:~$ date  
Wed Apr  1 19:53:16 IST 2020  
javatpoint@javatpoint-Inspiron-3542:~$ cal  
April 2020  
Su Mo Tu We Th Fr Sa  
    1  2  3  4  
  5  6  7  8  9 10 11  
12 13 14 15 16 17 18  
19 20 21 22 23 24 25  
26 27 28 29 30  
javatpoint@javatpoint-Inspiron-3542:~$ pwd  
/home/javatpoint  
javatpoint@javatpoint-Inspiron-3542:~$ ls  
Akash      display      hello.sh      newfile      Public      Templates  
Demo.txt   Documents    key@ssh       nohup.out    Python      Videos  
Demo.txt~  Downloads    key@ssh.pub   output       Python-3.8.0  
Desktop    examples.desktop Music          Pictures     snap  
javatpoint@javatpoint-Inspiron-3542:~$
```

Linux

- Operating system (OS)
- Microsoft Windows, MacOS, and **Linux**
- Linux – Versatile, open source, free,
used on supercomputers.
- The most common way to run complex bioinformatic analyses, on supercomputers or your own pc, is to use the **Bash shell.**



What we will do today

- Tutorial about the bash shell

Break

- Learning about **nf-core**
- Exercise about **nf-core**

Downloading this presentation

- Go to this link:
<https://github.com/EdoardoPiombo/nf-core-introduction>

- Click on “Presentation.pdf”
or “Presentation.pptx”

EdoardoPiombo Uploaded presentation		84b9ce6 · 27 minutes ago	🕒 9 Commits
📁 raw	Delete raw/fastq_1	31 minutes ago	
📁 solutions	Add files via upload	2 weeks ago	
📄 LICENSE	Initial commit	2 weeks ago	
📄 Presentation.pdf	Uploaded presentation	27 minutes ago	
📄 Presentation.pptx	Uploaded presentation	27 minutes ago	
📄 README.md	Update README.md	2 weeks ago	
📄 example_sample_sheet.csv	Added empty files to test pipelines	2 weeks ago	
📄 genes_coordinates.gff	Added empty files to test pipelines	2 weeks ago	
📄 genome_file.fasta	Added empty files to test pipelines	2 weeks ago	
📄 install_nextflow.sh	Create install_nextflow.sh	2 weeks ago	

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Click on “download raw file” and then open the downloaded presentation.

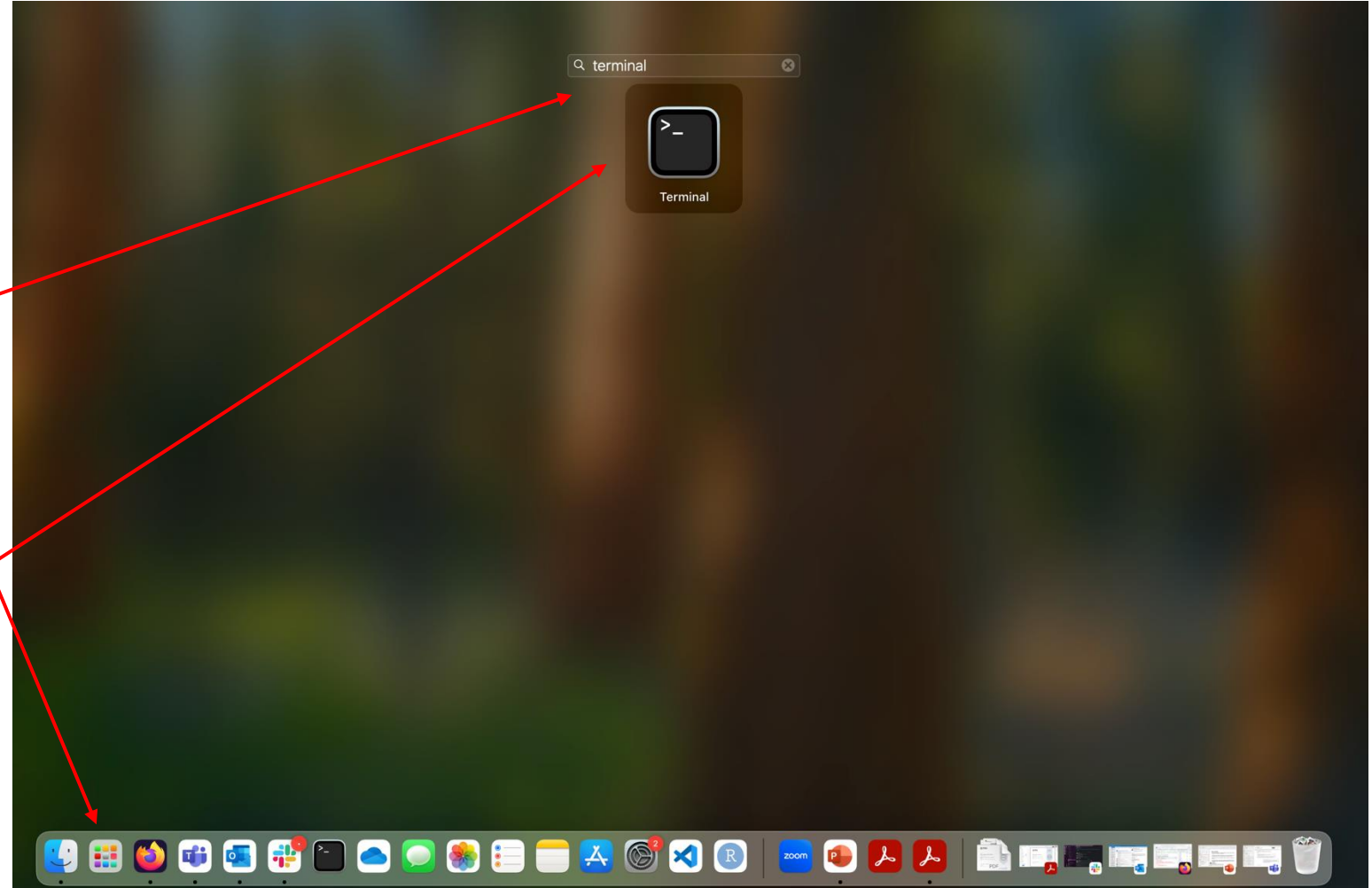


[View raw](#)

(Sorry about that, but we can't show files that are this big right now.)

Open a terminal: Mac

- Open launchpad
- Write “terminal” in the search bar.
- Click on Terminal



Open a terminal: Mac

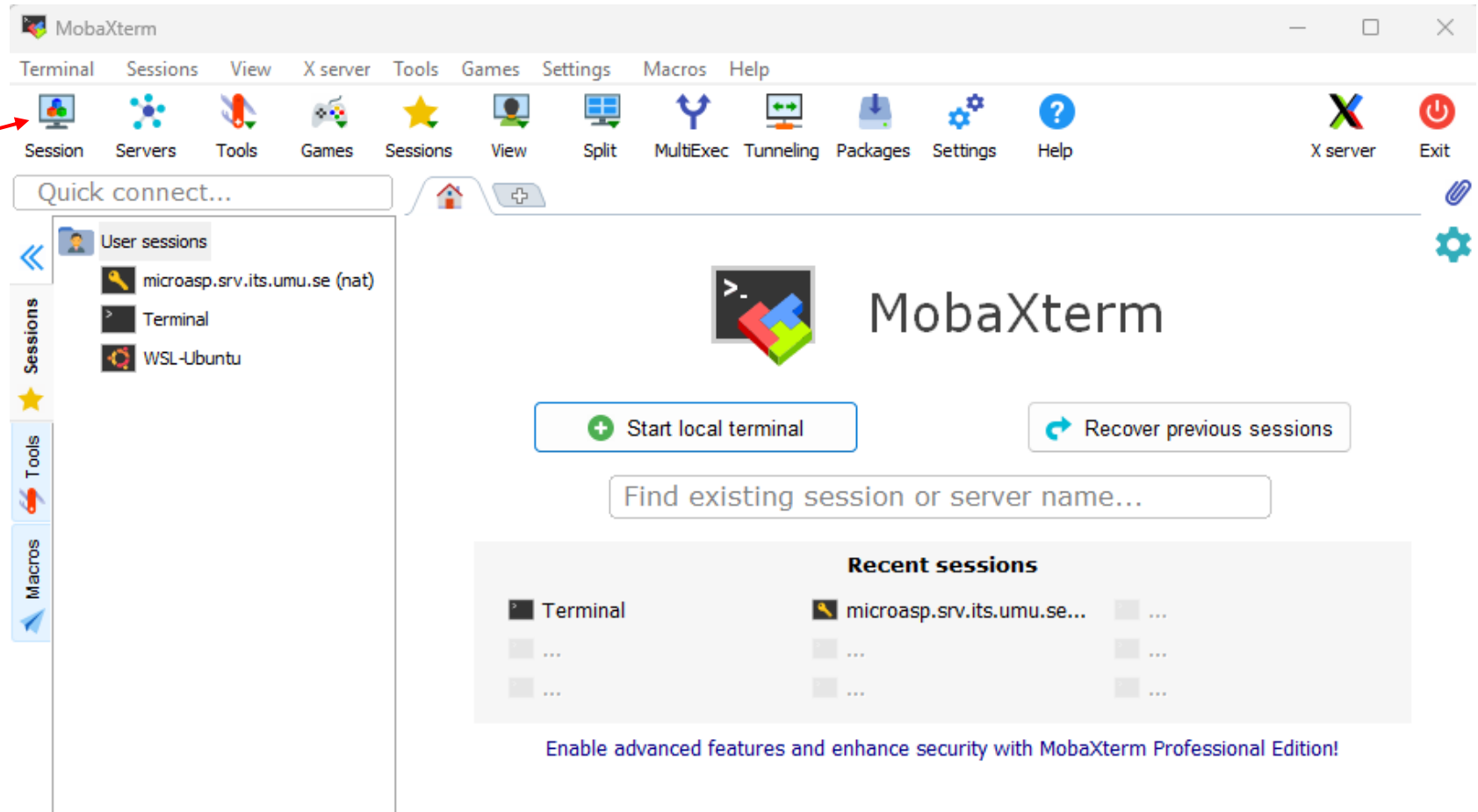
- You should see something like this

A screenshot of a macOS terminal window. The title bar at the top shows three colored window control buttons (red, yellow, green) on the left, followed by a blue folder icon and the text "edoardo — -zsh — 80x24". The main content area of the terminal displays the text "Last login: Wed May 21 08:53:53 on console" followed by the prompt "(base) edoardo@client227-209 ~ %" and a black cursor block.

```
edoardo — -zsh — 80x24
Last login: Wed May 21 08:53:53 on console
(base) edoardo@client227-209 ~ %
```

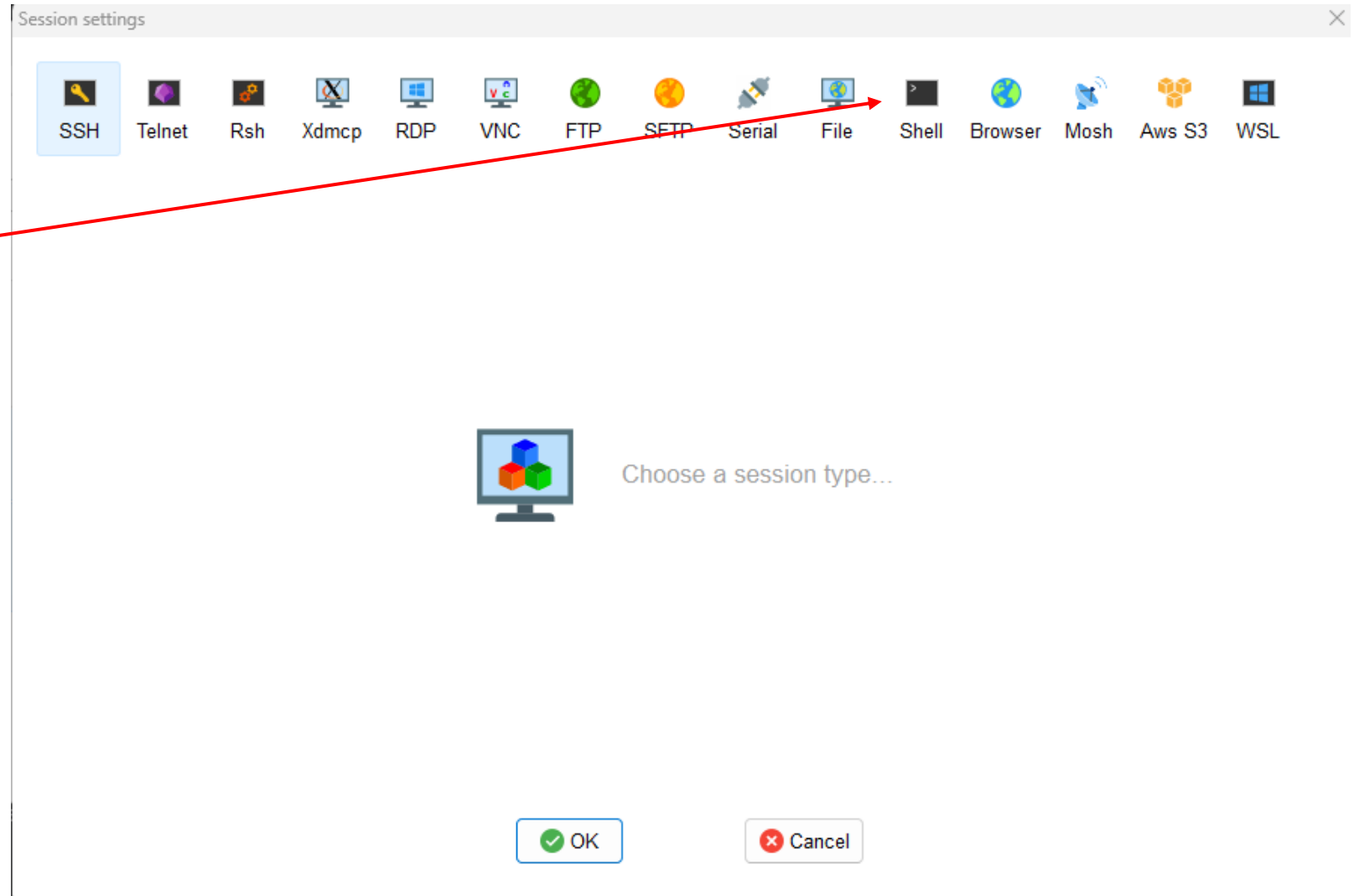
Open a terminal: Windows

- Open MobaXterm
- Start a new session



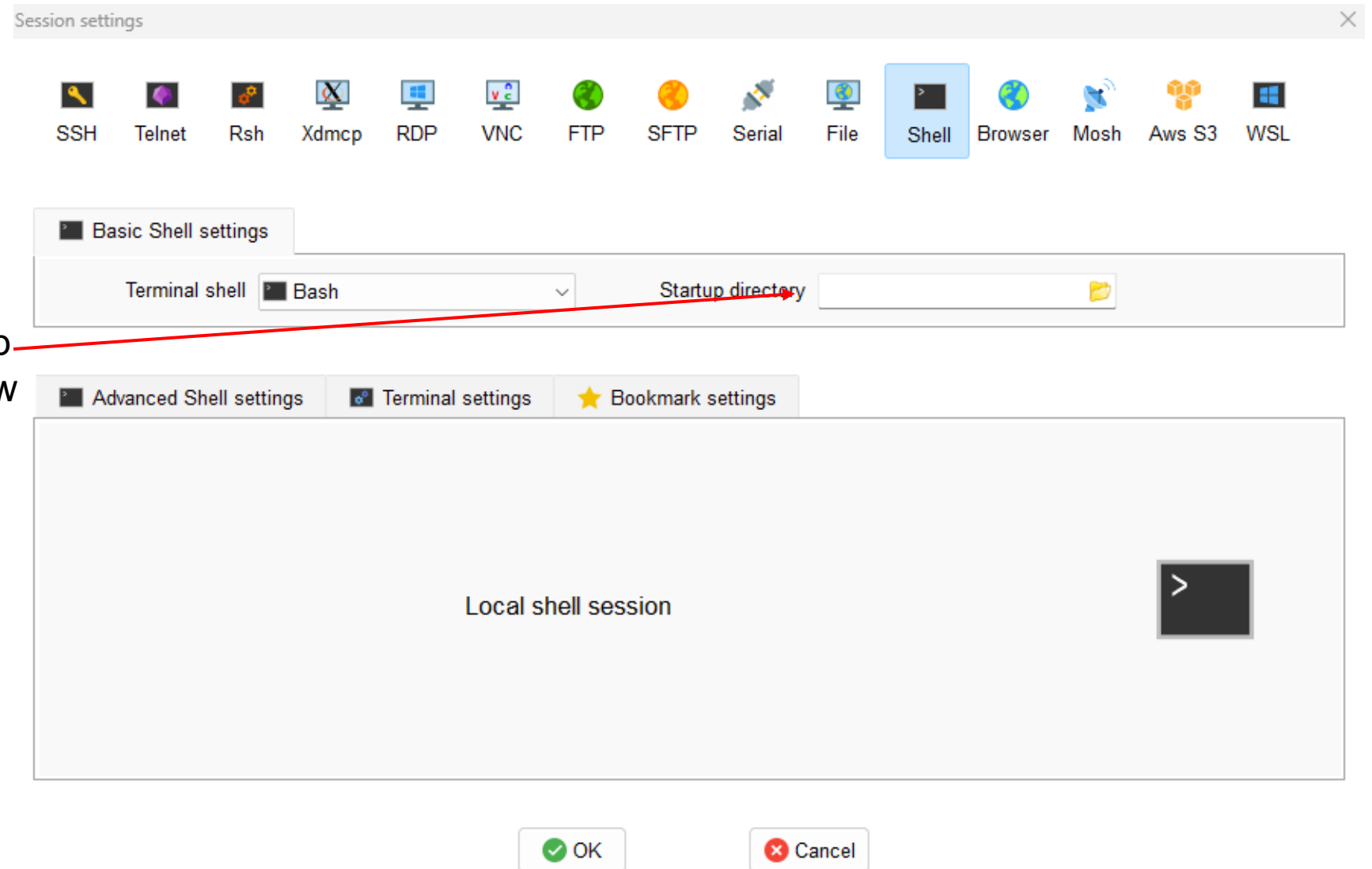
Open a terminal: Windows

- Open MobaXterm
- Start a new session
- Select “shell”



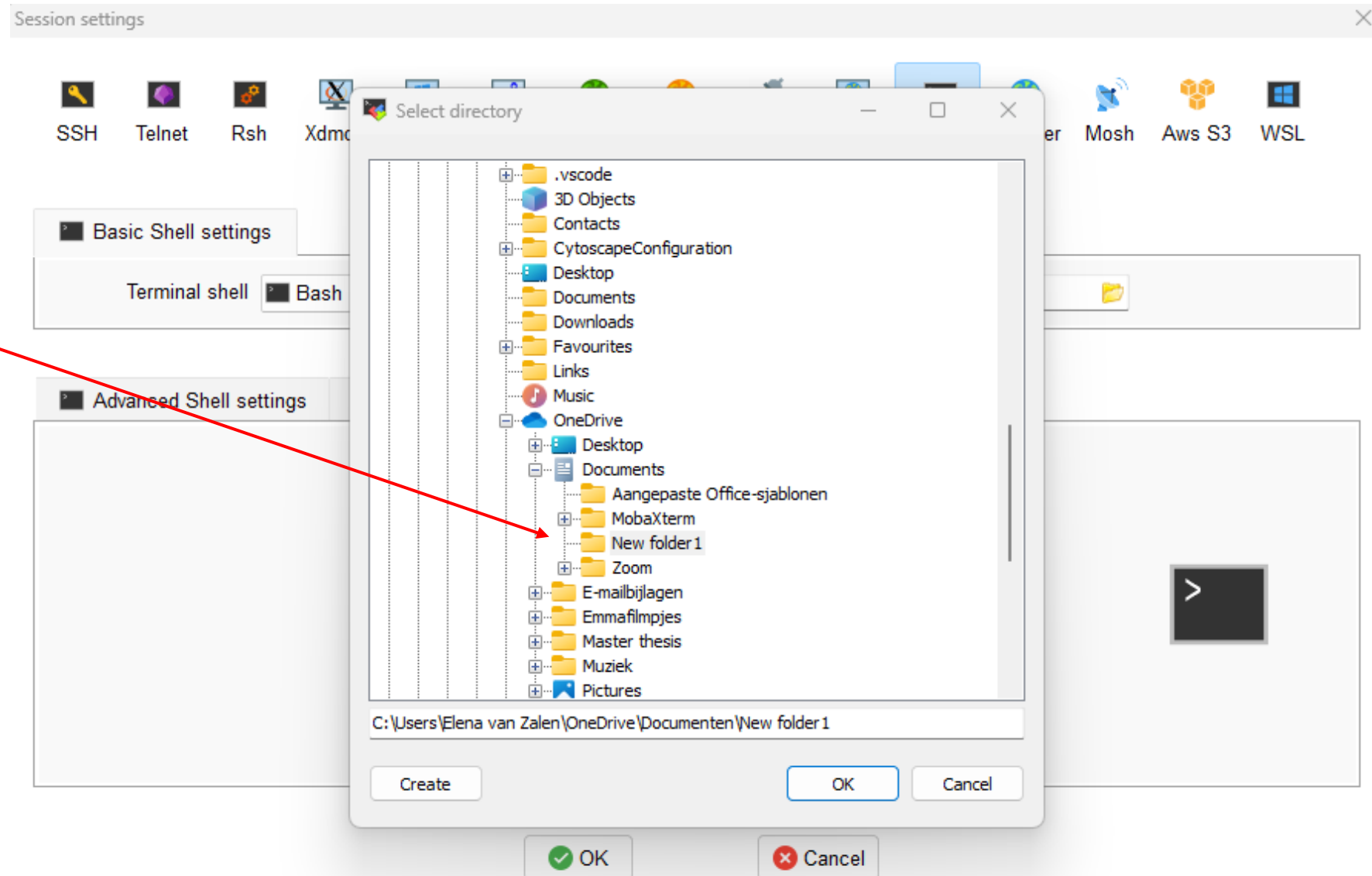
Open a terminal: Windows

- Open MobaXterm
- Start a new session
- Select “shell”
- Select an empty startup directory or make a new one



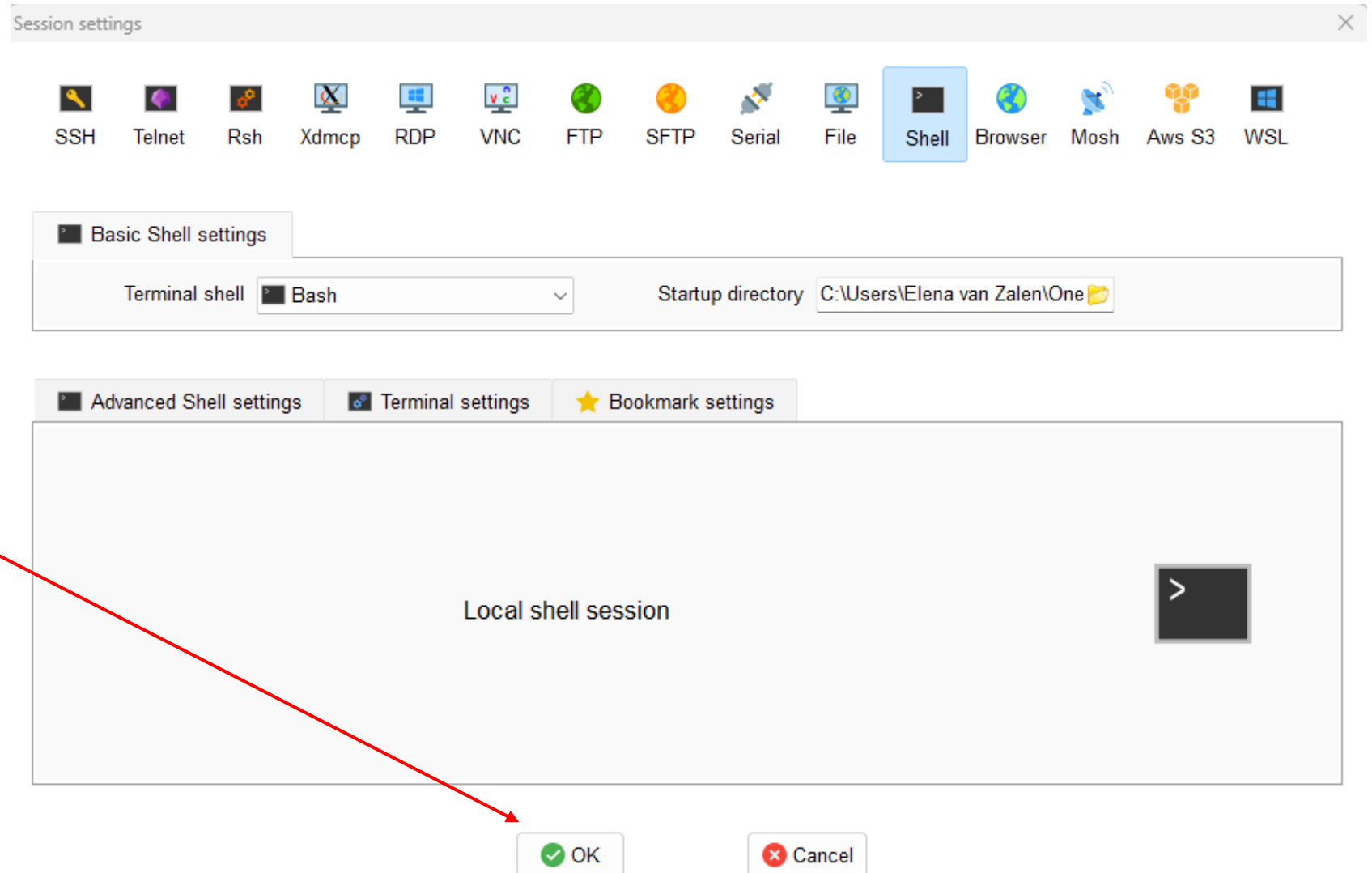
Open a terminal: Windows

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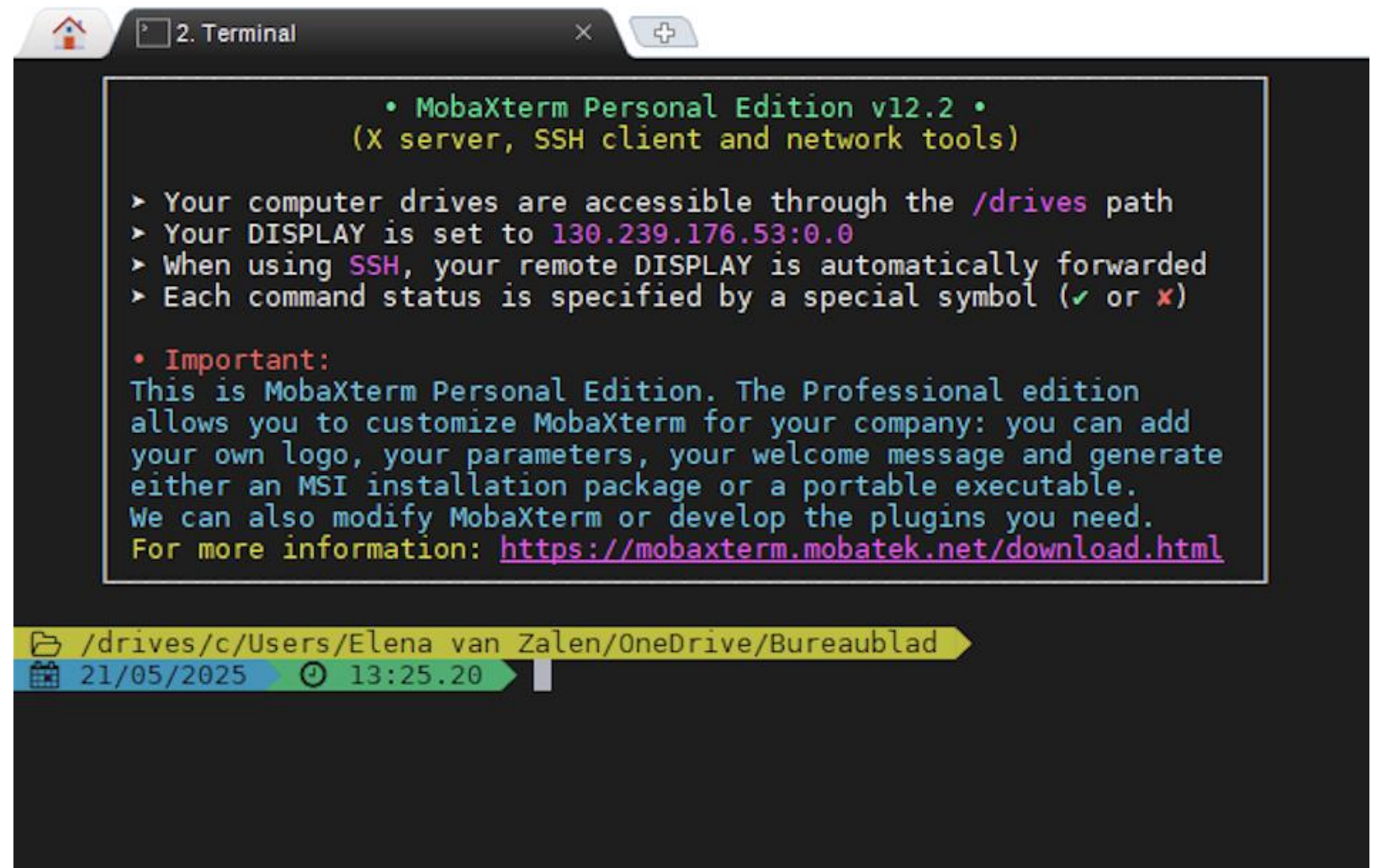
Open a terminal: Windows

- Open MobaXterm
- Start a new session
- Select “shell”
- Select an empty startup directory or make a new one
- Click “OK” to open a terminal



Open a terminal: Windows

- Open MobaXterm
- Start a new session
- Select “shell”
- Select an empty startup directory or make a new one
- Click “OK” to open a terminal
- You should see something like this



The screenshot shows a terminal window titled "2. Terminal". The window displays the MobaXterm welcome message, which includes the version number (v12.2) and a list of features. Below the welcome message, the current directory path is shown as `/drives/c/Users/Elena van Zalen/OneDrive/Bureaublad`. A red arrow points from the text "something like this" in the list to the terminal window.

```
• MobaXterm Personal Edition v12.2 •  
(X server, SSH client and network tools)  
  
➤ Your computer drives are accessible through the /drives path  
➤ Your DISPLAY is set to 130.239.176.53:0.0  
➤ When using SSH, your remote DISPLAY is automatically forwarded  
➤ Each command status is specified by a special symbol (✓ or ✗)  
  
• Important:  
This is MobaXterm Personal Edition. The Professional edition  
allows you to customize MobaXterm for your company: you can add  
your own logo, your parameters, your welcome message and generate  
either an MSI installation package or a portable executable.  
We can also modify MobaXterm or develop the plugins you need.  
For more information: https://mobaxterm.mobatek.net/download.html  
  
/drives/c/Users/Elena van Zalen/OneDrive/Bureaublad  
21/05/2025 13:25.20
```

Software carpentry tutorial

Go to this link:

<https://swcarpentry.github.io/shell-novice/index.html>

Follow the instructions, completing these two sections:

1: Introducing the Shell

2: Navigating Files and Directories

What is nf-core?

From their website: *A global community effort to collect a curated set of open-source analysis pipelines built using Nextflow.*

When starting a new project requiring bioinformatics analyses, it is not a bad idea to check the nf-core website to see if they have a pipeline prepared to run the analysis of the type of data you have:

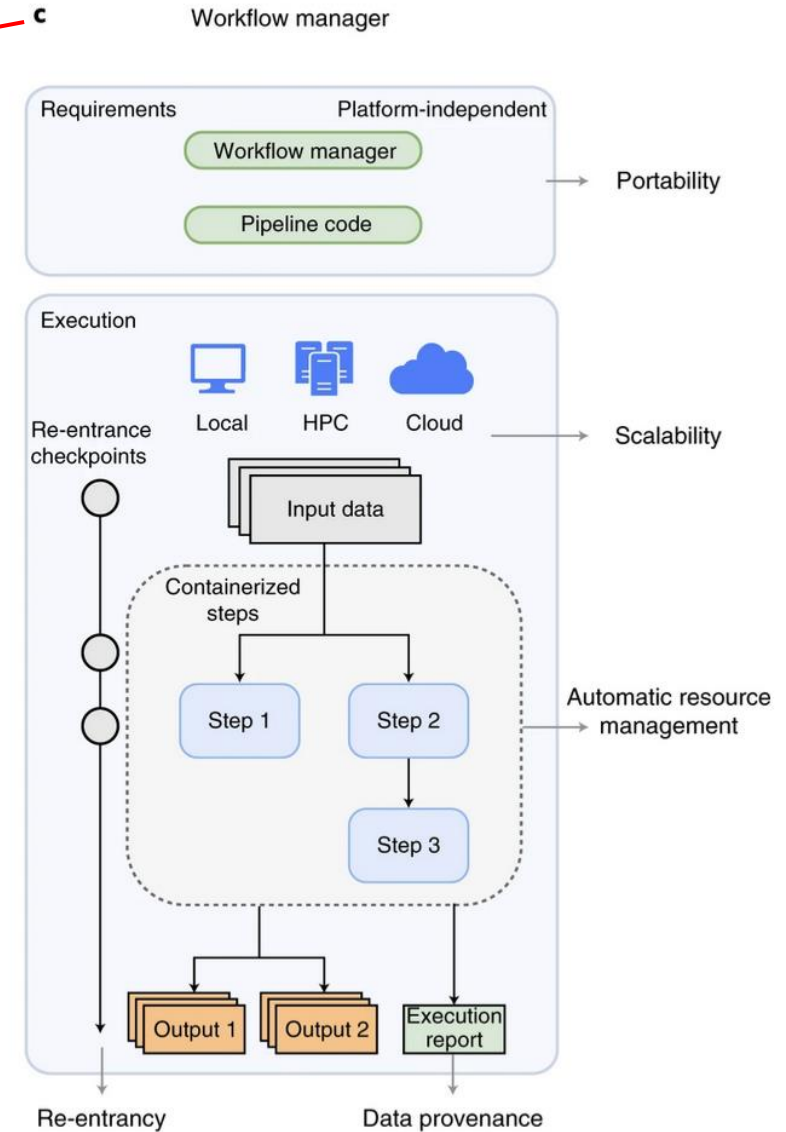
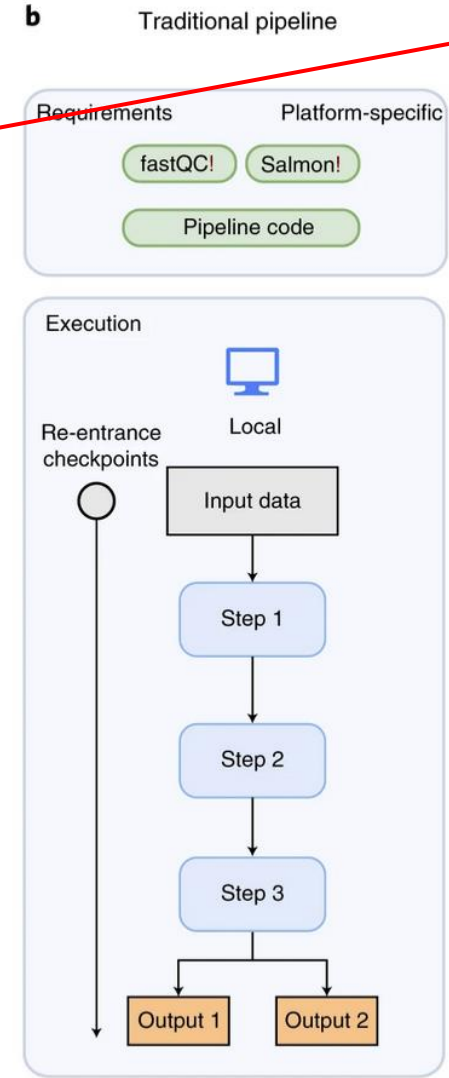
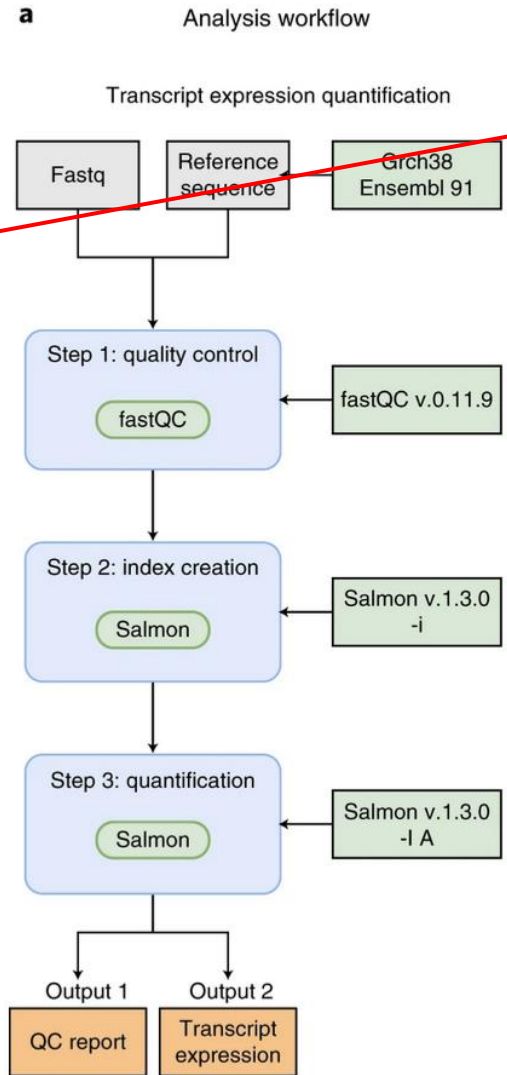
<https://nf-co.re/>

Visually:

Nextflow is the software allowing this

Nf-core is a repository of nextflow pipelines built for different bioinformatics applications

Source:
Wratten, L., Wilm, A. & Göke, J.
Reproducible, scalable, and shareable analysis pipelines with bioinformatics workflow managers. Nat Methods 18, 1161–1168 (2021)



How to edit files

- In the rest of the lesson, you will edit a variety of files. They are all txt files organized in specific ways, such as **json** files.
- To edit them, use simple text editors and not word, as word tends to add metacharacters that are not correctly interpreted by the softwares we will use.
- Good text editors to use are TextEdit (for Mac) and Notepad or WordPad (for windows).
- A more complex one to use (very good, but with many functionalities that may be confusing) is VScode (<https://code.visualstudio.com/download>), which works on every system.

Running the rnaseq pipeline

- Download my github repository by entering in your shell the following command:
`git clone https://github.com/EdoardoPiombo/nf-core-introduction.git`
- Follow the instructions in the README file to do the exercise.
- You have solutions in the “solutions” folder if you are stuck.
- When you are done, feel free to check out the other pipelines and see if there is something that could help you with your work:

<https://nf-co.re/pipelines/>