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Intro to Linux

(... and the command line interface)

Overview

- Why Linux?
- Your computing environment
- Using ThinLinc
- The command line interface (CLI/terminal/shell)
- Linux directory structure: Navigating in the File system
- Working with files
- Pipes and redirections
- Where to find help?
- SSH + FTP

Why use Linux?

- **The biggest part of the software used in the field of bioinformatics is largely written for POSIX systems (such as Linux and UNIX).**

Why use Command Line Interface (CLI)?

- **Many tools do not come with a Graphical User Interface (GUI)**
 - High effort to develop good GUIs.
 - Displaying of GUI often not possible (e.g. via SSH clients).

CentOS 8

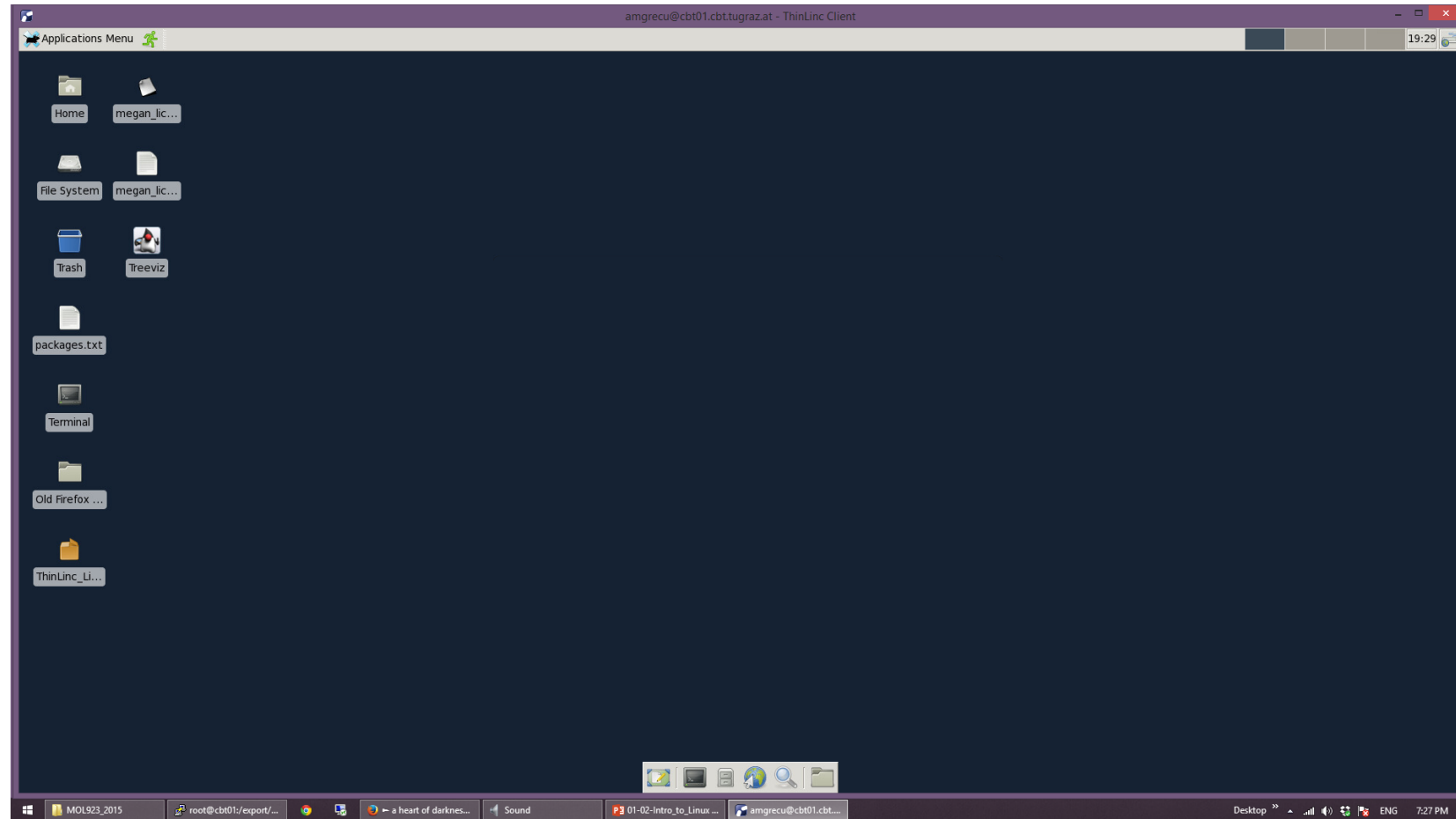
- Open Linux distribution built upon Red Hat Enterprise Linux (RHEL).
- Linux is a multi-access, multi-tasking system:
 - multiple users may be logged in and run multiple tasks on one machine at the same time, sharing resources (CPUs, memory, disk space) .
 - This is what you will be doing during the course.

Your computing environment


- In this class you will be using a **thin client**.
- A thin client refers to either a software program or to an actual computer that relies heavily on another computer to do most of its work.
- You get access to computational resources that would not be available in a “normal” computer, such as the one you use at work or at home.
- Bioinformatic Software needs only to be installed on the server
- The server we will be using is contains
 - 2 CPUs x 32 cores + hyperthreading = 128 threads
 - 2TB RAM
 - Graphic card with 24 GB
 - access to 100 TB storage

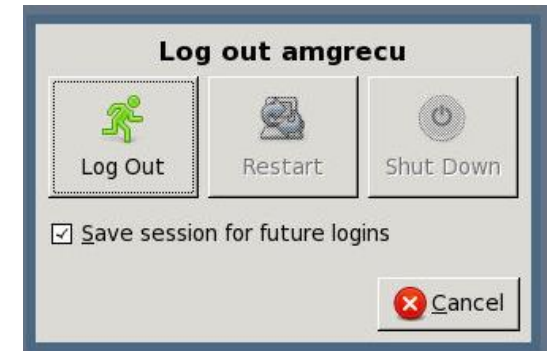


Welcome to your Linux desktop (remote desktop)



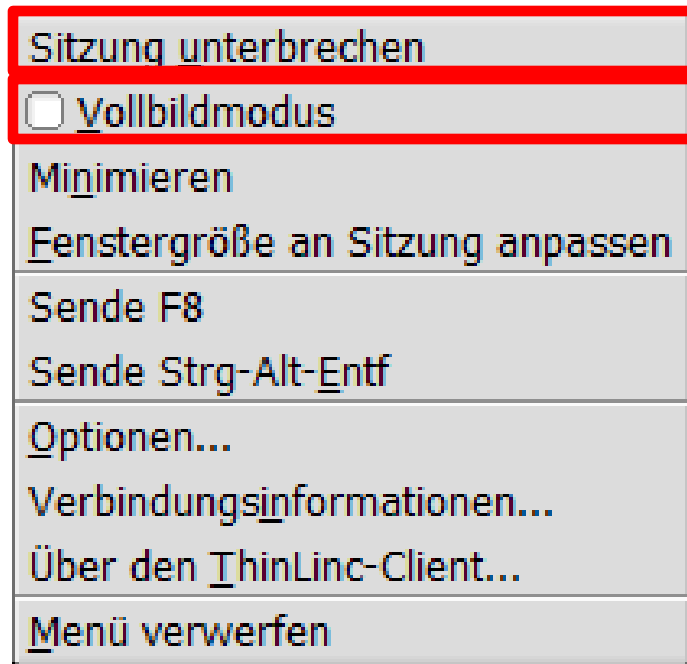
Logging out of your session

- At the end of each class please log out of your session.
- To log out simply click this icon  at the top left of your screen.
- A dialog like the one on the right will appear, make sure you have selected “Save this session for future logins” and then click the “Log Out” button.
- You will be returned to the initial desktop of the thin client.



Session control: **F8**

- Pressing F8 during your ThinLinc remote desktop session gives you access to a few more options.



- **Disconnect session:**

Preserves your session!

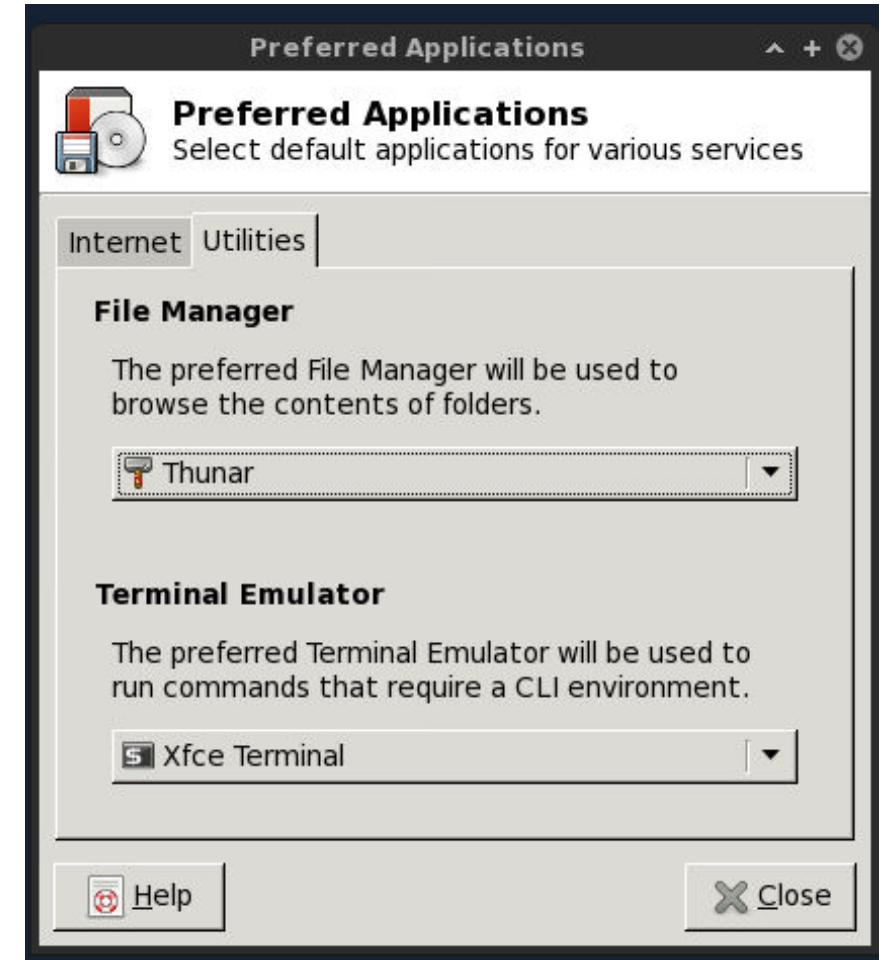
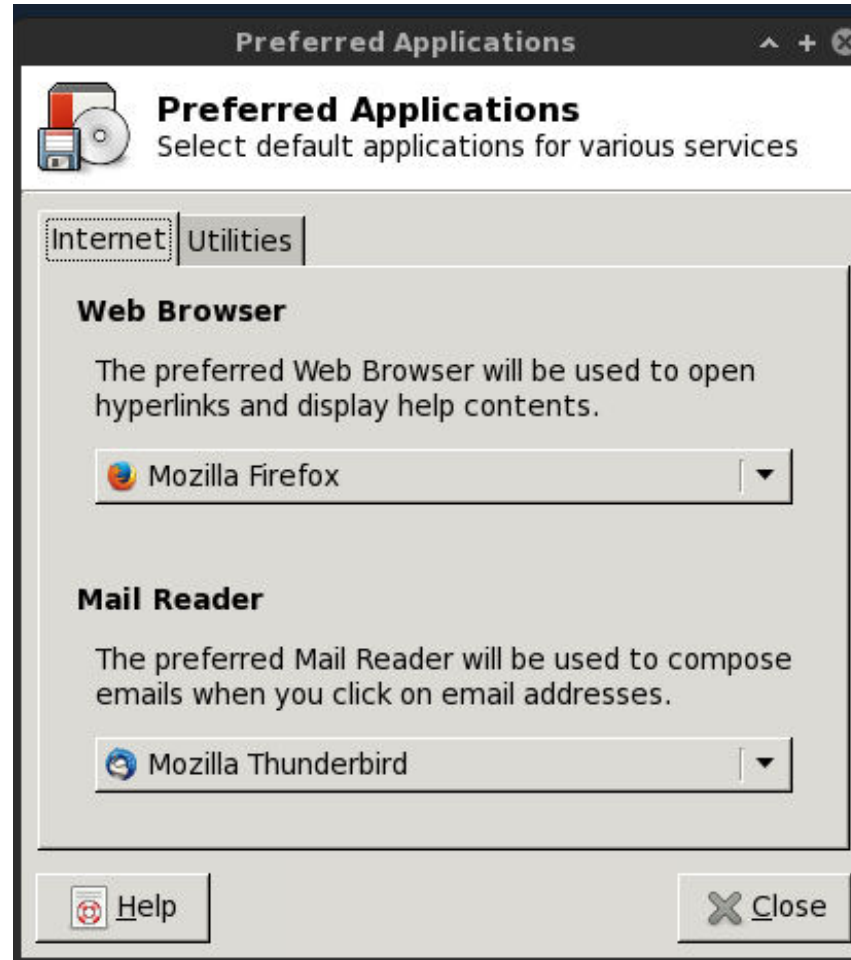
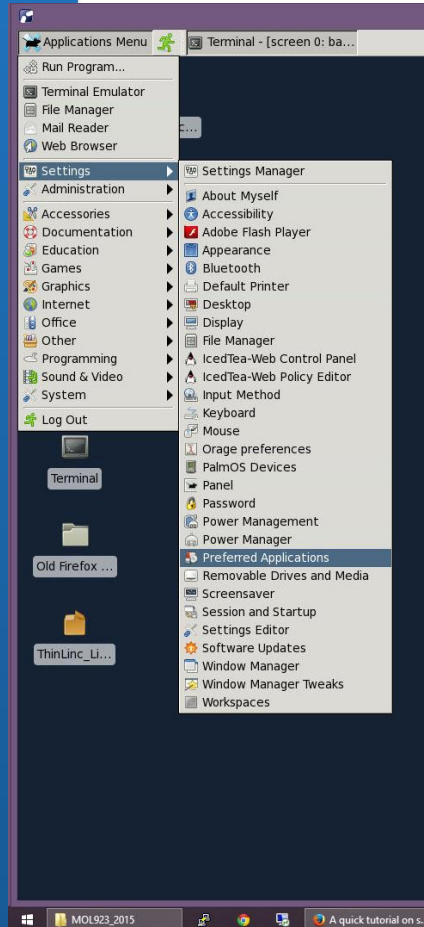
→ programs stay running

- **Full Screen mode:**

Switches on windowed mode.

→ allows you to toggle between local and remote environment.

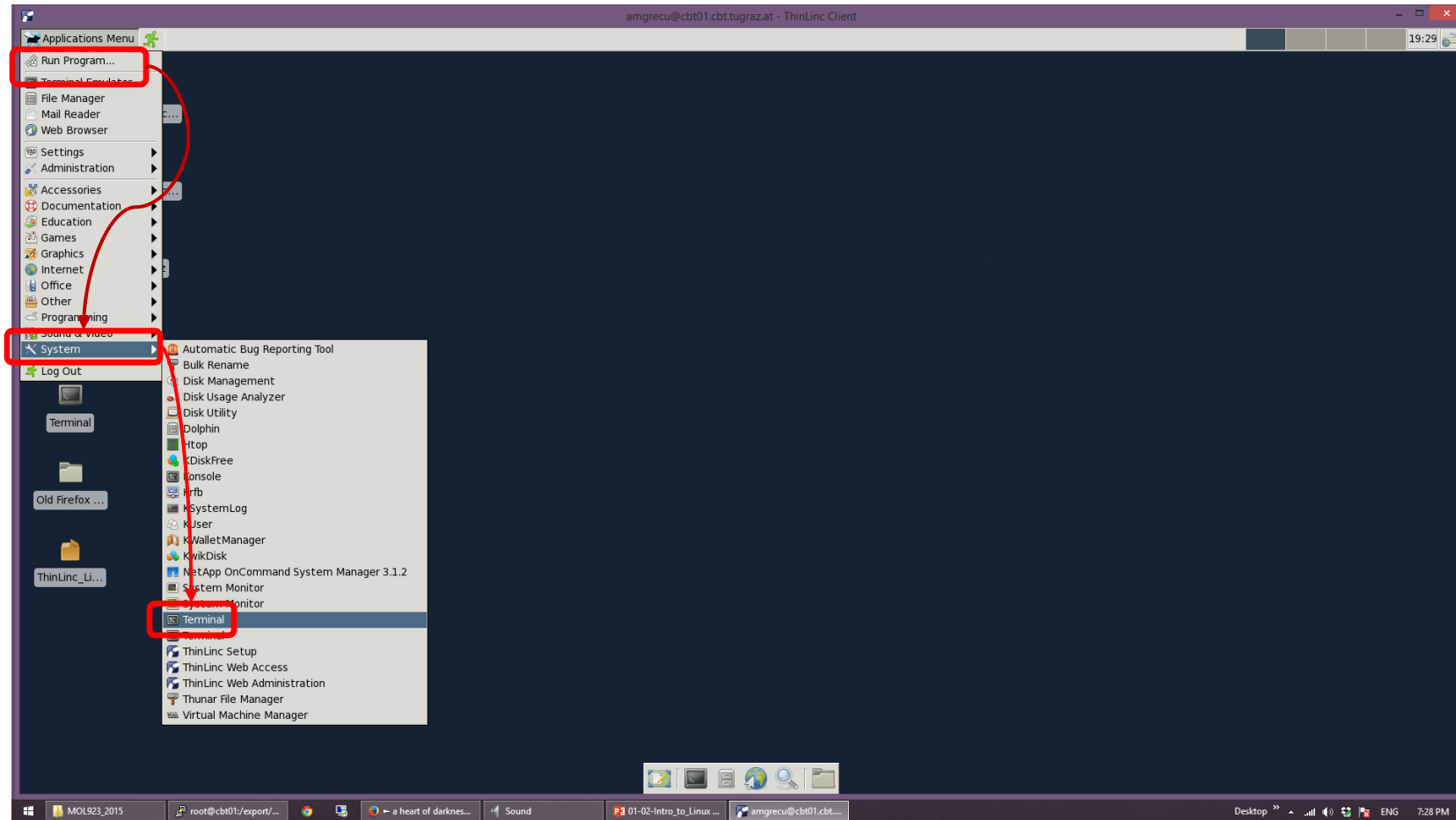
Before we begin

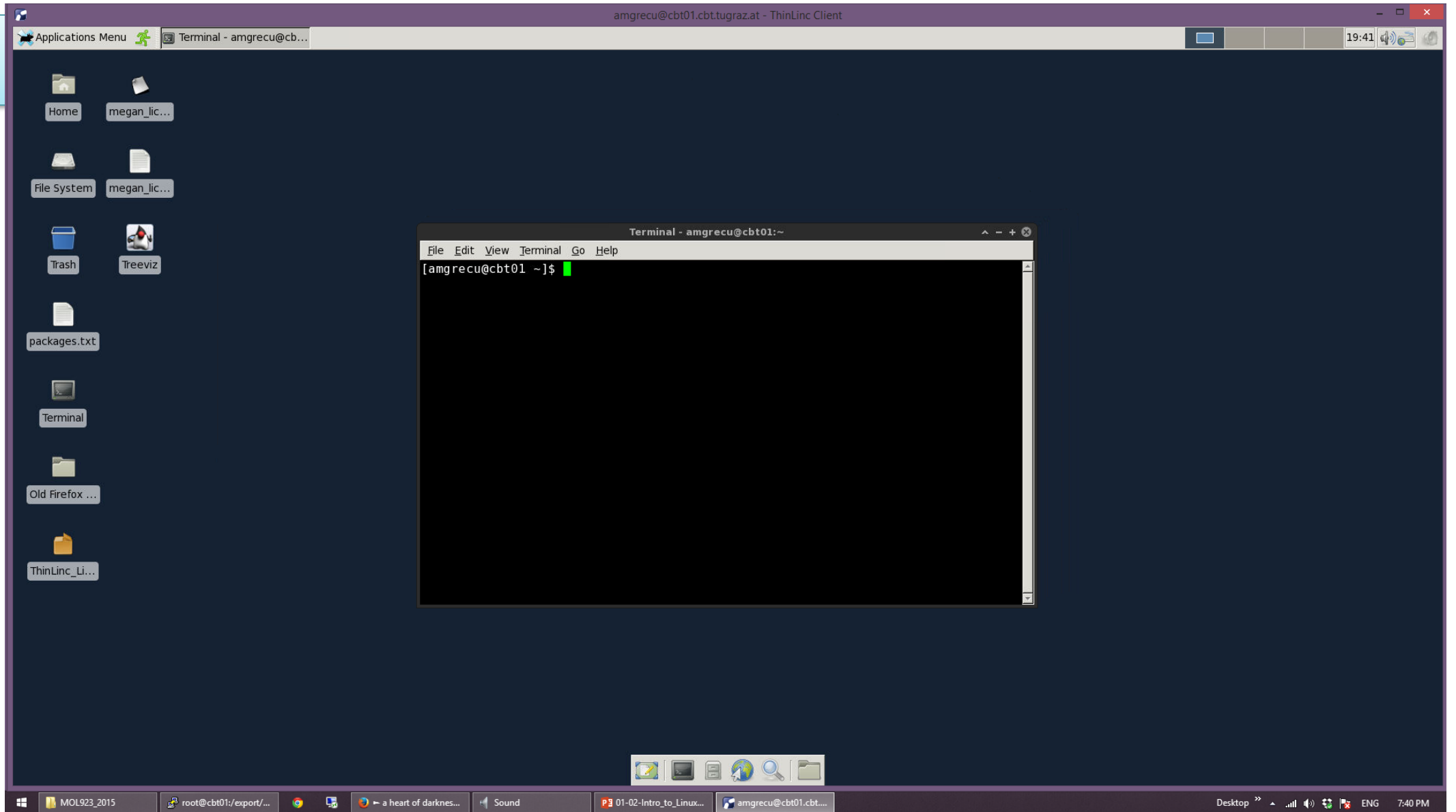


The command line interface (CLI)

- The CLI is a **text-based interface** that allows computer users to type commands that get executed by the operating system.
- You call programs, modify files and control your system just by writing a bit of text.
- We will be using the CLI to do most of the lab tasks in this class.
- There are different types of Unix **shells** or CLIs available, the one we are using is called **Bash**. Other good examples are tcsh, zsh, ksh, csh, fish...
- A command shell is characterized by the available commands.

How to open a shell window

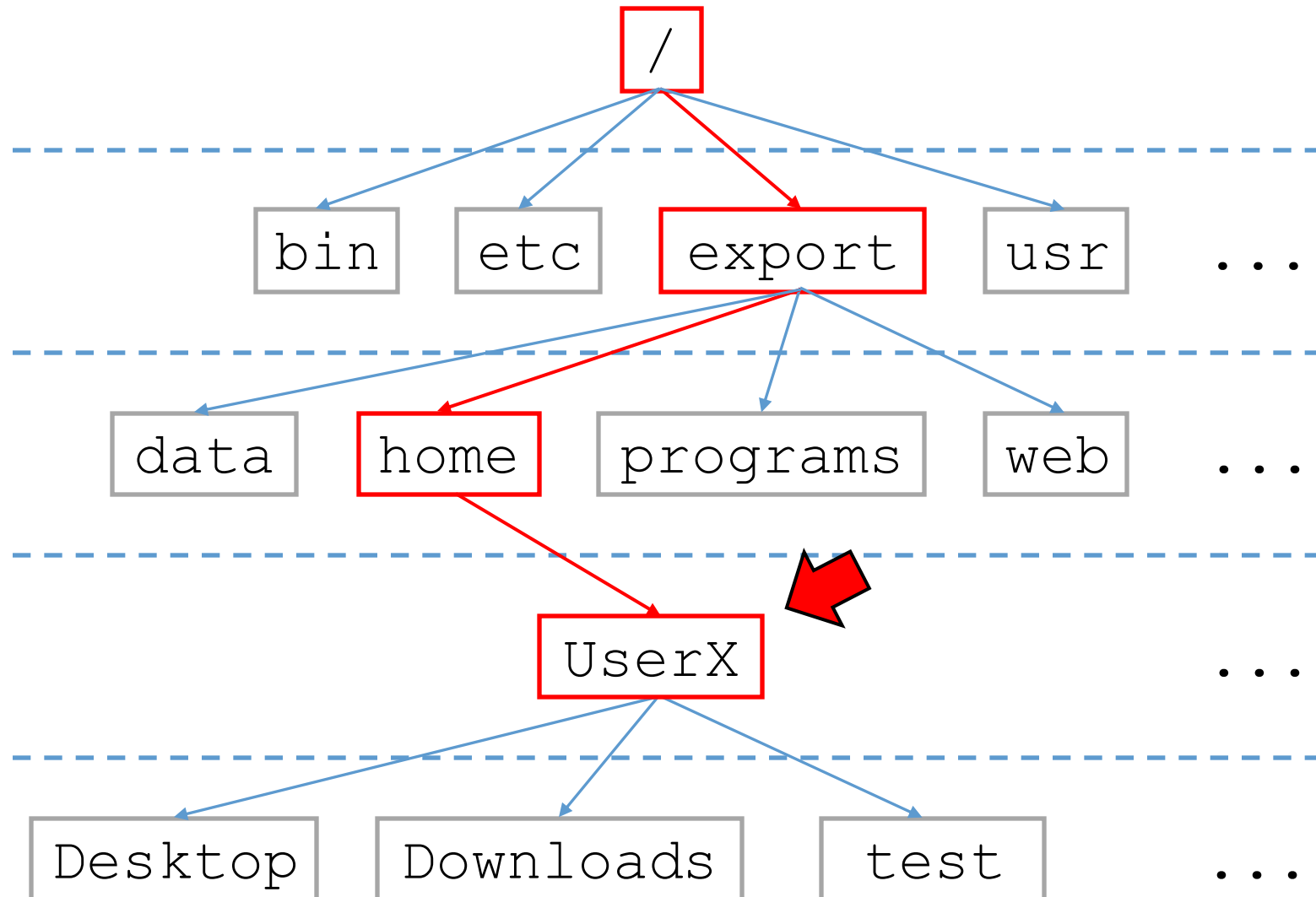




Linux directory structure

- No drive letters like **C:**
- Lowest level of the **File-Tree** is the **root** symbol **/**
- **External** storage devices are mounted to the file tree.
- For example our external storage is mounted at **/export/**
- **2 most important folders** we will be using in this course:
 - **/export/home/username** – your user **home directory**
 - similar to the Windows C:\Users\User
 - **/export/programs** – contains all the **bioinformatics software** used in the course.

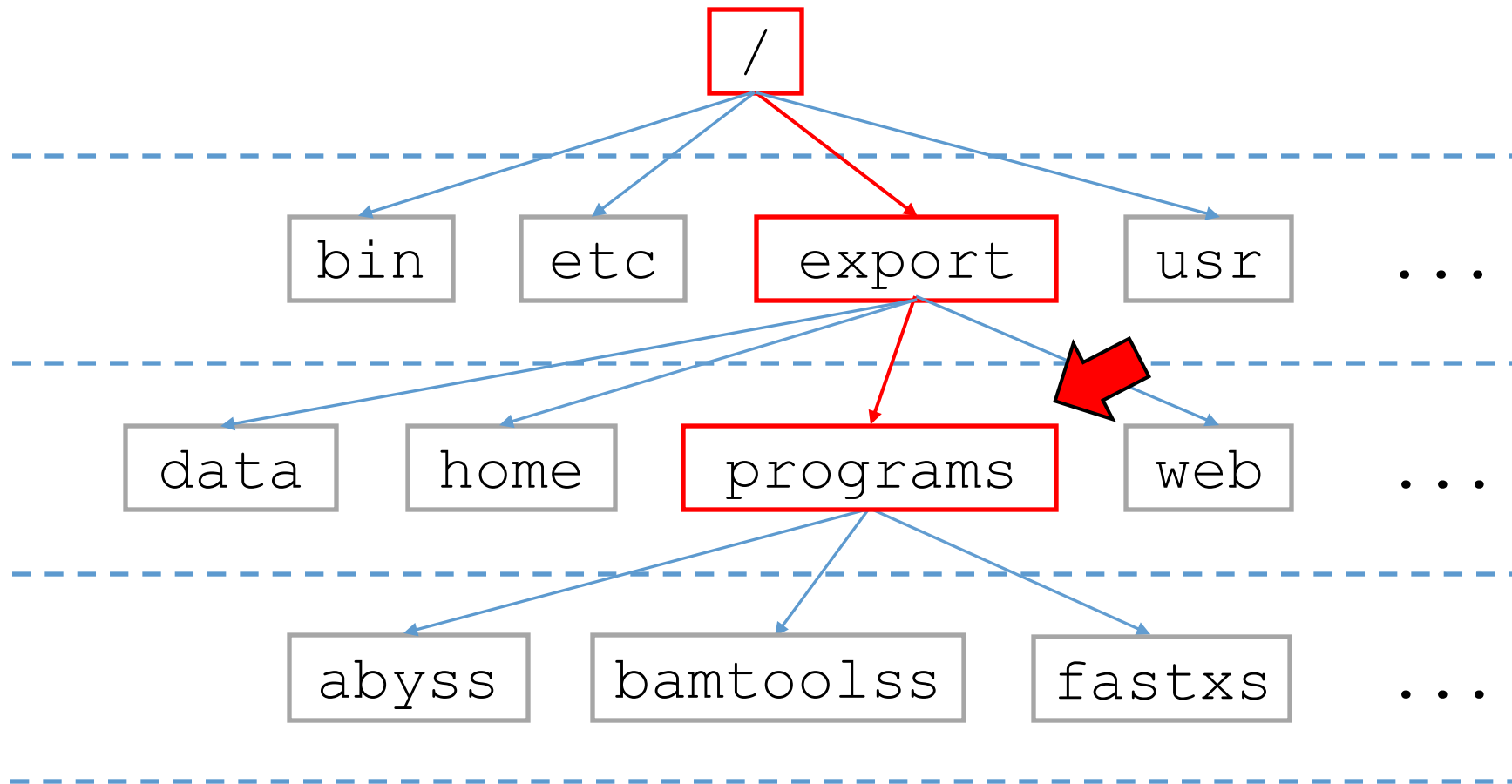
Filetree: **/export/home/UserX/**



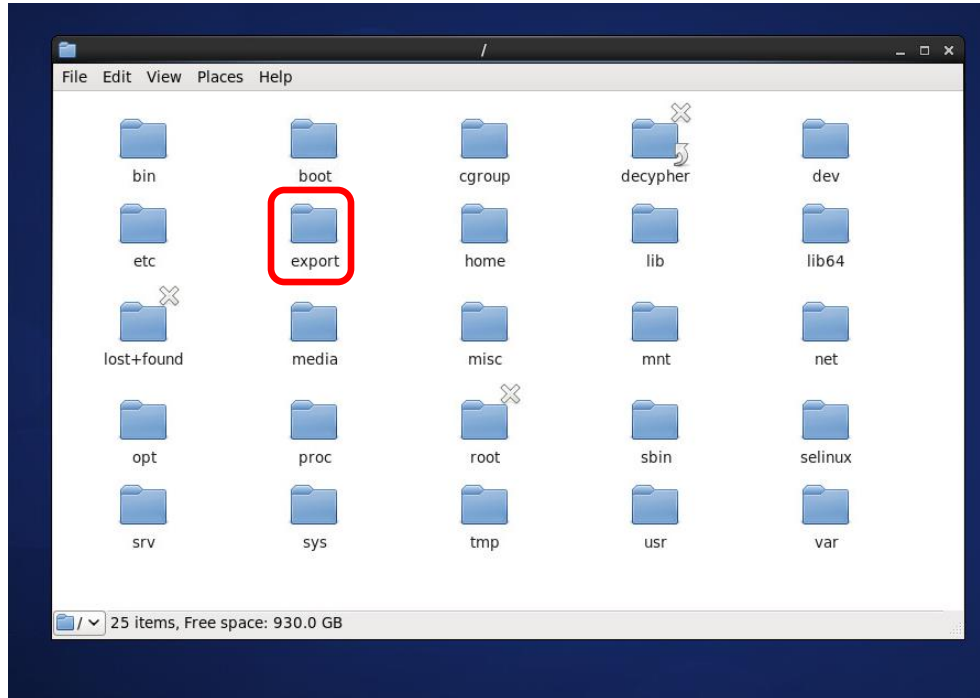
Navigating in the file system: Basic commands

- First: Open a file-browser (**Thunar**) for visual aid.
- You start at your home directory.
 - The symbol **~** references your home directory!
- **Changedirectory: **cd****
- Type: `cd /export/programs/`
- **List the content of the directory: **ls****
- Switch back to your home directory:
 - `cd ~`
 - `cd /export/home/username`

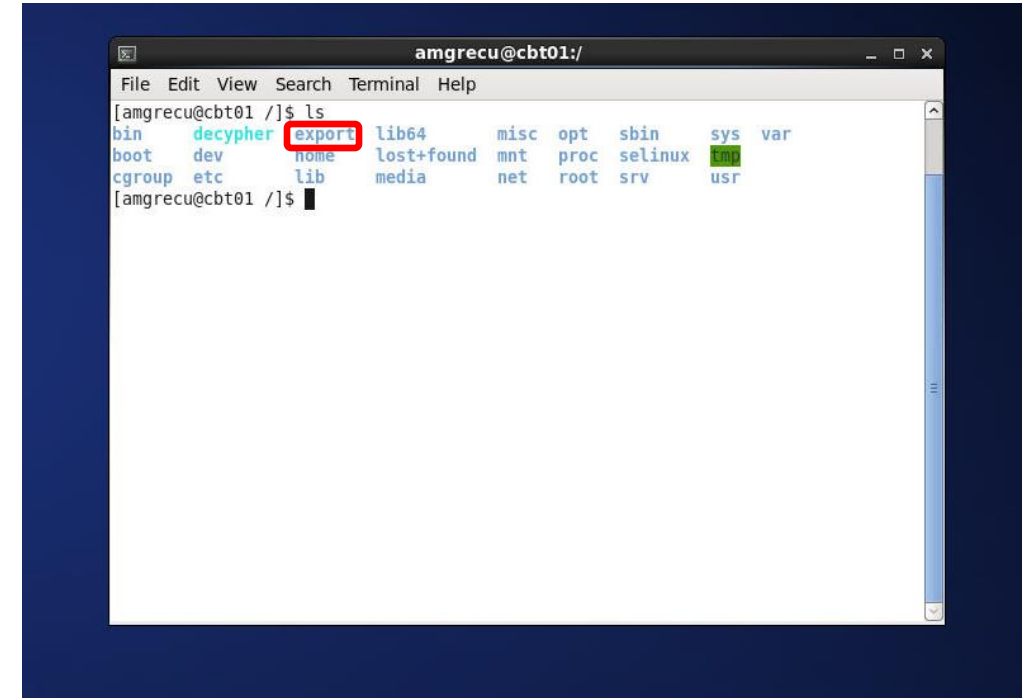
Filetree: `/export/programs/`



GUI



CLI



Linux directory structure at the root - /
Graphical User Interface (GUI) versus command line view

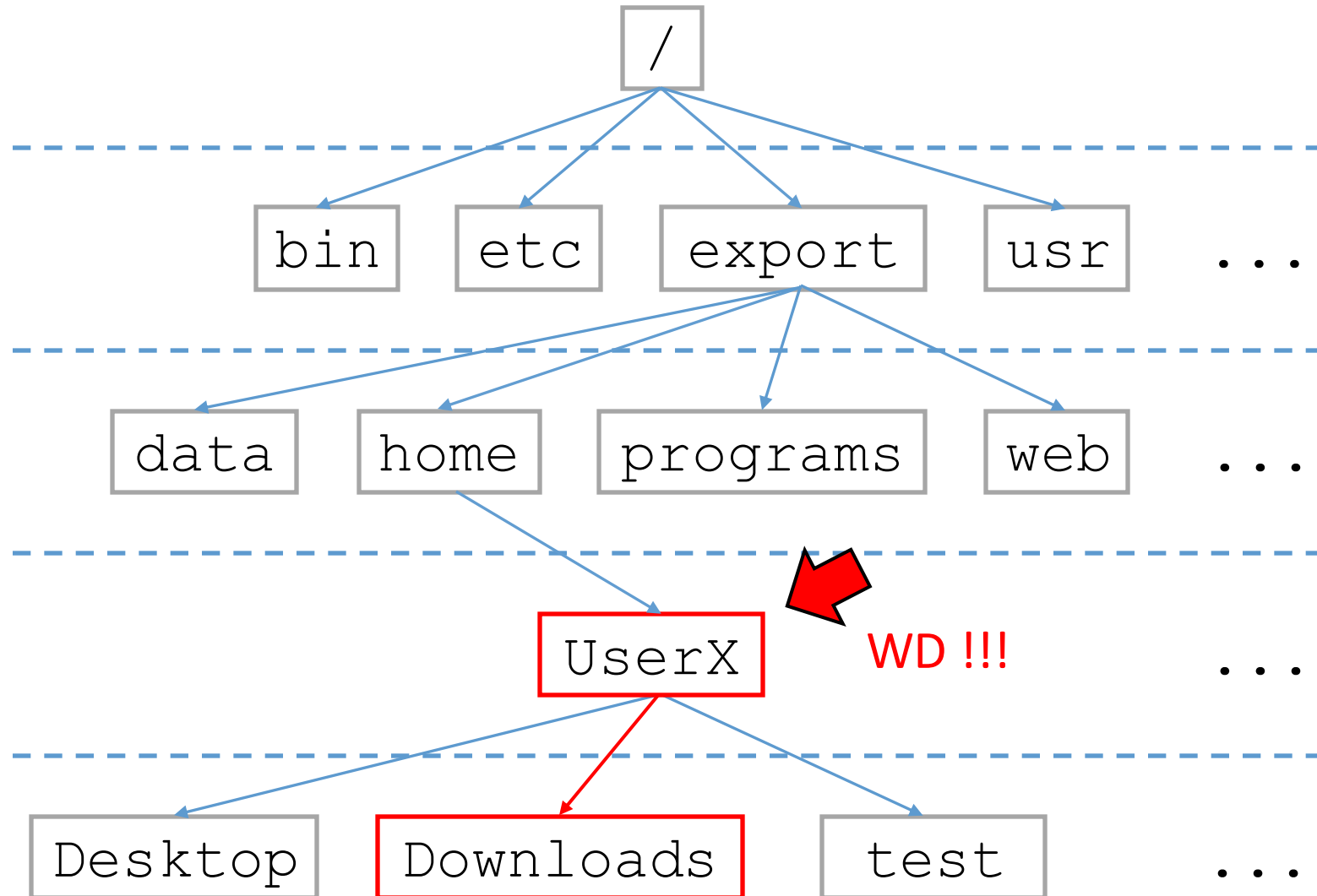
The **prompt** [testuser@cbt04 ~]\$

- [username@machine directory]\$
- Name of the user with which you are logged in.
- Name of the server on which you are.
- Name of the directory in which you currently are.
- Where is testuser?

Important: Relative and absolute paths:

- **Absolute:** `/export/programs/samtools/`
 - always begins with root
- **Relative:**
 - Relative to your current position (**working directory**)
 - Shortcuts:
 - `~` your **home** directory
 - `.` **this** directory (where you currently are)
 - `..` **parent** directory (upper directory)
- To see where you are at the moment:
 - **pwd** command: (print working directory).

WD: [UserX@cbt04 ~]\$ Downloads/



Navigating in the file system: Directories and Files: Essential commands:

- **Make** a new **dire**ctory: **mkdir**
 - Make sure you are in your home directory (**pwd!**)
 - Type: `mkdir test`
 - Type: `ls`
 - Type: `cd test/`
 - Type: `ls`
 - Type: `cd ..`
 - Type: `ls`

The manual:

- Every UNIX and Linux machine comes with built-in help for most of its commands and programs.
 - Type “**man**” followed by the command name
 - To leave:
 - q
 - For Scrolling:
 - Arrow Up or Down for one line up or down
 - Page Down or Ctrl-F for one page down
 - Page Up or Ctrl-B for one page up
 - To search
 - A slash, then your search term, then enter. e.g. /list
 - n to go to the next occurrence of the search term
- Even “man” itself has a manpage. Type `man man` into the terminal.

The manual: List

- **Type:** `man ls`
- Use `ls -alh` in the current directory.
 - **-a** `--all`
 - **-l** use a long listing format
 - **-h**, `--human-readable`: print sizes in human readable format (e.g., 1K 234M 2G)

Listing directory content

- Use `ls -alh` in the current directory.

```
amgrecu@cbt01:~  
-rw-----. 1 amgrecu ucalgary  54 Mar 31 09:13 .python_history  
-rw-r--r--. 1 root      root    599K Apr 16 13:26 root.bmp  
-rw-r--r--. 1 amgrecu root     62K Apr 16 13:25 root.png  
-rw-r--r--. 1 amgrecu ucalgary 144K Mar 10 03:53 SCDHB3.pdb  
drwx-----. 2 amgrecu ucalgary 4.0K Dec 16 07:46 .ssh  
drwxrwxrwx. 6 amgrecu ucalgary 4.0K Jan 19 13:40 .t_coffee  
drwxr-xr-x. 2 amgrecu ucalgary 4.0K Jan 26 07:14 Templates  
lrwxrwxrwx. 1 amgrecu ucalgary  43 Apr 15 12:15 thindrives -> /var/opt/thinlinc/sessions/  
amgrecu/2/drives  
drwx-----. 4 amgrecu ucalgary 4.0K Apr 16 13:19 .thumbnails  
-rw-r-----. 1 amgrecu ucalgary 91M Jan 29 10:09 tl-4.3.0-server.zip  
drwxr-xr-x. 2 amgrecu ucalgary 4.0K Jan 26 07:14 Videos  
-rw-----. 1 amgrecu ucalgary 9.4K Apr 15 12:38 .viminfo  
drwxr-xr-x. 2 amgrecu ucalgary 4.0K Apr 16 13:32 .vnc  
-rw-----. 1 amgrecu ucalgary 503 Apr 16 14:13 .Xauthority  
-rw-----. 1 amgrecu ucalgary 5.4K Feb 10 06:54 .xsession-errors  
-rw-----. 1 amgrecu ucalgary 3.4K Feb 10 02:13 .xsession-errors.old  
drwxr-xr-x. 2 amgrecu ucalgary 32K Jan 30 07:04 zalina  
drwxr-xr-x. 2 amgrecu ucalgary 12K Mar 11 09:29 zalina_new  
drwxr-xr-x. 2 amgrecu ucalgary 32K Feb  4 05:55 zalina_tcoffee  
[amgrecu@cbt01 ~]$
```

permissions

Owner user
and group

size

file last
accessed

name
blue - directory

Useful things to know

- Use **Up/Down arrow keys** – this will cycle through recently executed commands.
- Use the **TAB key** – this will often present you with a list of choices after typing a part of a command (more on this in a moment).
- **history** command: list all recently used commands

Tab Completion

- Writing every single character of a command is tedious. But your shell can help you!
- Press the Tab key while writing commands, directories or file names.
- Press once to complete until the last **unambiguous** character (you will hear a beep if there are no suggestions or you have ambiguous options).
- Press **twice** to show all completion options.



Tab Completion



- More examples:
 - bow<tab> -> bowtie and you hear a beep
 - bowtie<tab><tab> :

```
File Edit View Terminal Go Help
[amgrecu@cbt01 ~]$ bowtie
bowtie          bowtie2-build-l  bowtie2sam.pl    bowtie-build-s
bowtie2         bowtie2-build-s  bowtie-align-l   bowtie-inspect
bowtie2-align-l bowtie2-inspect  bowtie-align-s   bowtie-inspect-l
bowtie2-align-s bowtie2-inspect-l bowtie-build      bowtie-inspect-s
bowtie2-build   bowtie2-inspect-s bowtie-build-l
[amgrecu@cbt01 ~]$ bowtie
```

– bowtie2s<tab> → bowtie2sam.pl

Tab Completion

- Examples:
- Commands:
 - `cuffl<tab> -> cufflinks`
- Directories:
 - `ls /ex<tab> -> ls /export`
- Files:
 - `cp /export/data/mol923/c<tab>`
– `-> cp /export/data/mol923/completion-example.txt`



The **touch** command:

- `touch [FILENAME]`
- Update the **access and modification times** of a file.
- Creates a **new file** if the specified file does not exist.

- Enter your `test` directory.
- Type: `touch testfile`
- List the content of the directory.

The **mv** command: Move!

- `mv [target] [destination]`
- **Moves** a file to a new location.
- Also renames the file if desired.

- Create a new directory `test2`
- **Type:** `mv testfile test2/`
- Enter `test2` and list the content of the directory.
- **Type:** `mv testfile mytestfile`
- List again

The **cp** command: Copy!

- `cp [target] [destination]`
- Creates an exact **copy** of a target file.
- Type: `cp mytestfile ..`
- Switch to the parent directory and list the content.

The **rm** command: Remove!

- `rm [Filename]`
- `rm [Filename1] [Filename2] [Filename3]...`
- **Removes the respective file.... Once and for all!**
- Be especially careful with the `rm` command
- **Type:** `rm mytestfile`
- **Type:** `man rm`
- What do the switches `-r` and `-f` mean?

Removing directories

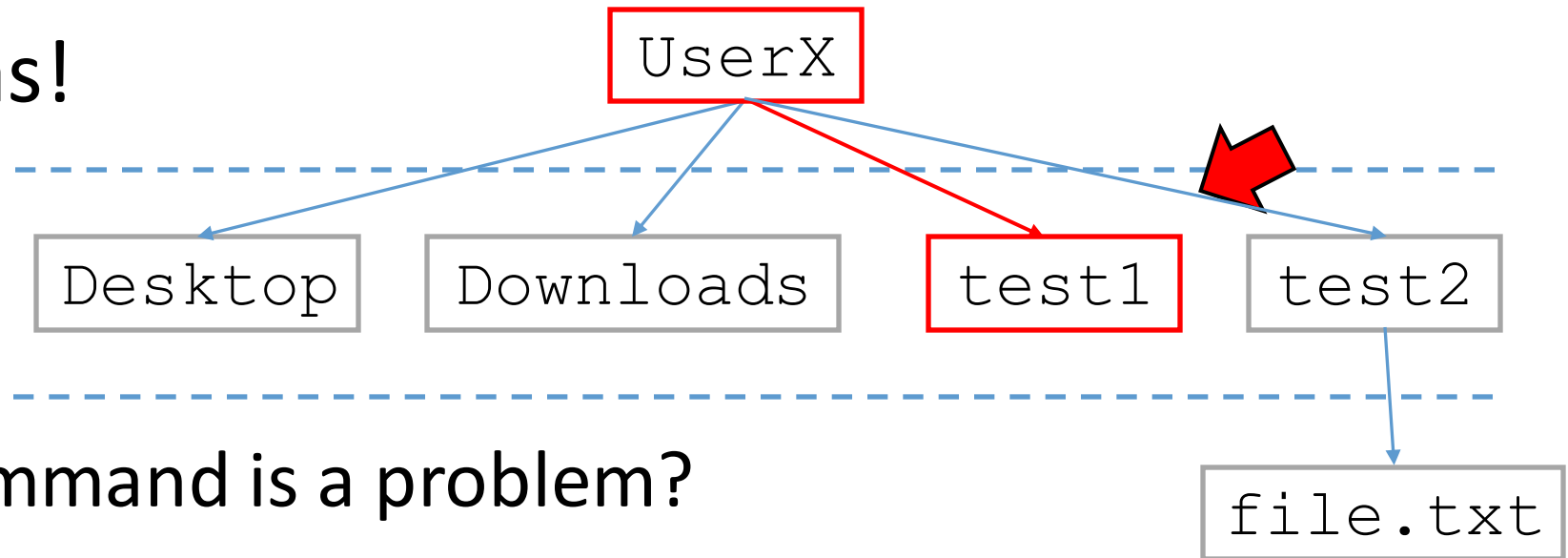
- `rmdir /export/home/klash/new_dir` - Remove directory called "new_dir" in /export/home/klash – will fail if the directory is not empty
- `rm -rf /export/home/klash/new_dir` - Remove directory called "new_dir" in /export/home/klash with all its content (i.e. all files and subdirectories will be gone)
- `rm -rf new_dir` - Remove directory called "new_dir" in current directory with all its content (i.e. all files and subdirectories will be gone)

`rm -rf` is a very dangerous command! Once you have deleted something it is GONE!

There is no "Recycle Bin"! There are no backups!

Check carefully what you are deleting!

Gotchas!



- Which command is a problem?

[UserX@cbt04 test]\$

- `rm -rf ~/test2/file.txt`
- `rm -rf ~ /test2/file.txt`
- `rm -rf / test2/file.txt`
- `rm -rf /test2/file.txt`
- `rm -rf ../test2/file.txt`
- `rm -rf ../test2/ file.txt`

Naming Files – Best Practices

- **case-sensitive** - `MyFile`, `myfile`, `myFile` are all different
- Use only **letters** (upper- and lower-case), **numbers** from 0 to 9, a dot (.), and **underscore**
- Avoid other characters! They may have special meaning in Linux (&, \$, *, ..)
- No **spaces** in filenames!

File permissions:

- The `chmod` command (**change modifier**) is used to change file permissions:
 - 4= read
 - 2= write
 - 1= execute
- Myself, Group, World
 - `chmod 700 filename`
 - 7 = read + write + execute.

Executing programs:

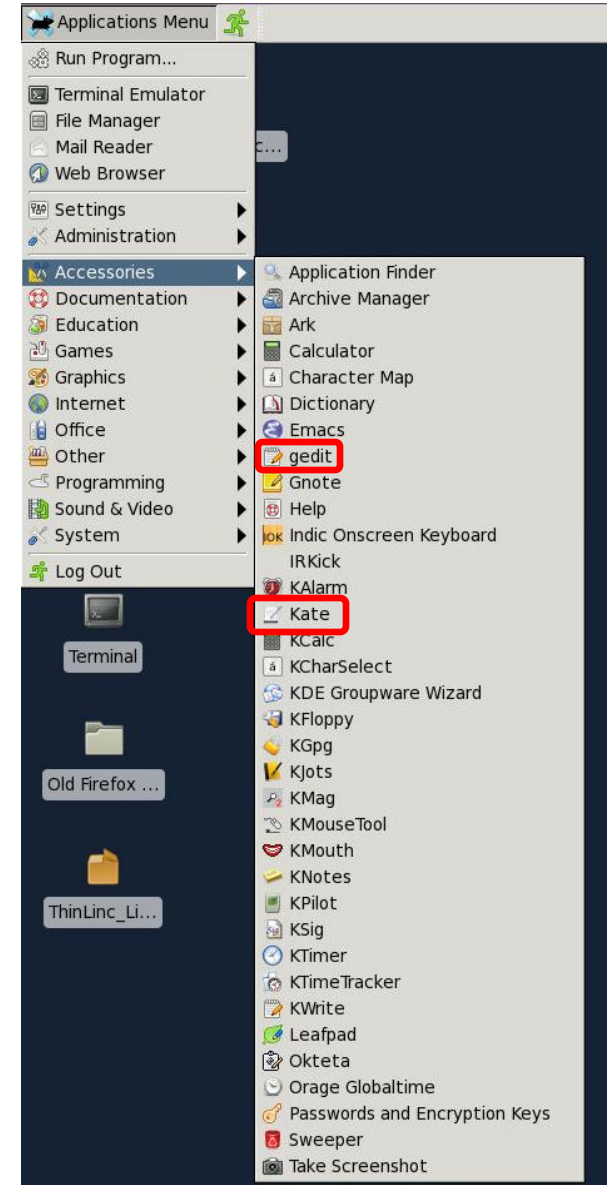
- Explicit (absolute path):
 - `/usr/local/bin/samtools`
- From working directory:
 - `cd /usr/local/bin/`
 - `./samtools`
- From **environment** (Path variable!):
 - `Samtools`
 - Has to be predefined.

Executing programs: Prompt

- When command is executed: Prompt appears in new line.
- Visible when the terminal is ready to accept commands.
- If a command takes longer:
 - Prompt will appear as soon as command is finished
 - Can abort running process with Ctrl+C [Strg+C]
- Nothing printed: Everything went well
 - Messages usually only in case of errors

Editing text files

- User-friendly options (GUI):
 gedit
 Kate
- More advanced suggestions:
 nano
- You can call them from CLI:
 nano filename
 gedit filename
 kate filename
- In the course we will generally be using gedit



Where to find help No.2?

- Not every command has a man page.
 - However most commands have built-in help output:
- ```
cp --help
blastn -help
cufflinks -h
```
- It's usually one of “-h”, “--help”, “-help” or similar
  - You can pipe the output into a pager (use q to leave; up/down arrow Ctrl-F/Ctrl-B to navigate)

```
cp --help | less
```



## Where to find help No.3?

- Also, there is plenty of help on the Internet
  - <http://www.google.com>  
Most problems can be solved by Googling. Basically, just type all related words into the search field.
  - <http://stackoverflow.com/>  
Ask specific questions here. General questions are usually already answered. You can find them through the search field, but usually they're the top hits on Google anyway.
  - <https://www.biostars.org/>  
“Stackoverflow for Biologists”
  - <http://seqanswers.com/>  
Forum about Bioinformatics tools and –omics data processing tools

## UNIX Tutorials

- <http://people.ischool.berkeley.edu/~kevin/unix-tutorial/toc.html>
- <http://www.ee.surrey.ac.uk/Teaching/Unix/unixintro.html>
- Cheat sheet, german:  
<https://github.com/linuxtage/commands-cheatsheet/raw/master/cheatsheet.pdf>
- Software Carpentry tutorial:  
<https://swcarpentry.github.io/shell-novice/>

## Getting files in and out of my home computer

- Filezilla or WinSCP
- <https://filezilla-project.org/>
- Connect to „cbt04.cbt.tugraz.at“
- Use Port **22**



Server:  Benutzername:  Passwort:  Port:   ▼

Lokal: /Users/Christoph\_Sensen\_Graz/Downloads/ ▼

- ▶ Downloads
- ▶ Dropbox
- ▶ Library
- ▶ Movies
- ▶ Music
- ▶ Pictures
- ▶ Public

| Dateiname ^             | Dateigröße | Dateityp       | Zuletzt geändert   |
|-------------------------|------------|----------------|--------------------|
| ..                      |            |                |                    |
| H6_v2.00                |            | Verzeichnis    | 28.04.2016 11:3... |
| LS100_FW_v140_Mac       |            | Verzeichnis    | 28.04.2016 19:4... |
| SAP_GUI_Java-7.30-Ma... |            | Verzeichnis    | 02.05.2016 11:0... |
| - Genomic Sequencing.a  | 50678      | Adobe PDF d... | 24.03.2016 21:1... |
| .DS_Store               | 6148       | Datei          | 02.05.2016 11:0... |
| .localized              | 0          | Datei          | 20.05.2015 17:0... |
| 119213_PDF.pdf          | 1521009    | Adobe PDF d... | 03.05.2016 16:0... |
| 119252_PDF.pdf          | 1380487    | Adobe PDF d... | 03.05.2016 16:0... |
| 119287_PDF.pdf          | 1419130    | Adobe PDF d... | 03.05.2016 16:0... |

59 Dateien und 3 Verzeichnisse. Gesamtgröße: 668975726 Bytes

| Server/Lokale Datei | Richtung | Datei auf Server | Größe | Priorität | Status |
|---------------------|----------|------------------|-------|-----------|--------|
|---------------------|----------|------------------|-------|-----------|--------|

Server: ▼

| Dateiname ^ | Dateigröße | Dateityp | Zuletzt geändert | Berechtigung | Besitz |
|-------------|------------|----------|------------------|--------------|--------|
|-------------|------------|----------|------------------|--------------|--------|

Derzeit mit keinem Server verbunden

Nicht verbunden.

**Zu übertragende Dateien** Fehlgeschlagene Übertragungen Erfolgreiche Übertragungen

## Assessment:

- Answer the following question within your report:
  - What is the difference between an absolute and a relative path? Give examples.
  - What do the following shortcuts mean?
    - ~
    - .
    - ..
  - What is the effective difference between following commands? Describe the results.
    - `[user@cbt04 ~]$ cp /export/data/mol923/Protein_example/ ./test/`
    - `[user@cbt04 ~]$ cp -r /export/data/mol923/Protein_example/ ./test/`



## Emergency Assistance

- Klaus Schliep [klaus.schliep@tugraz.at](mailto:klaus.schliep@tugraz.at)