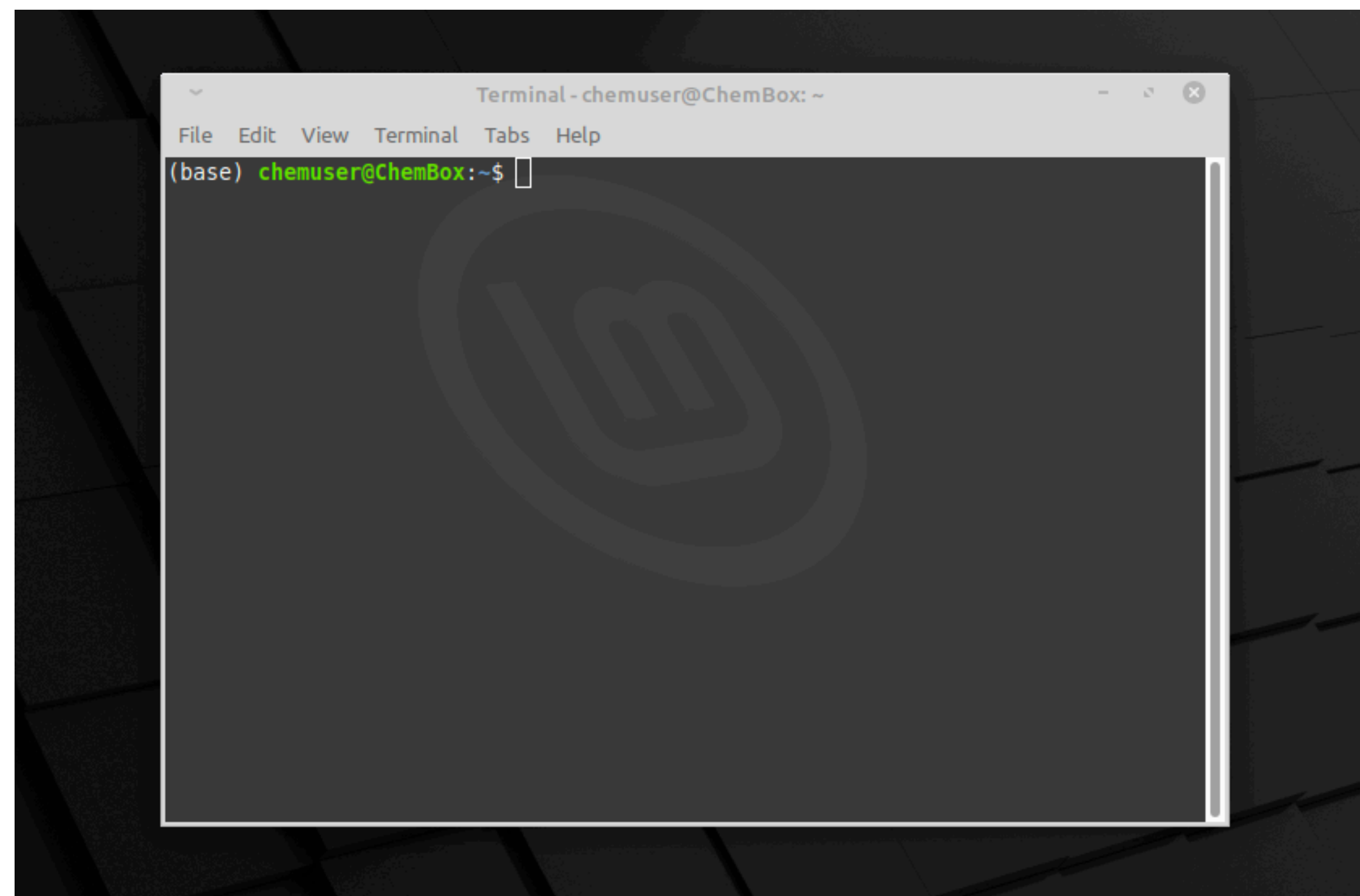
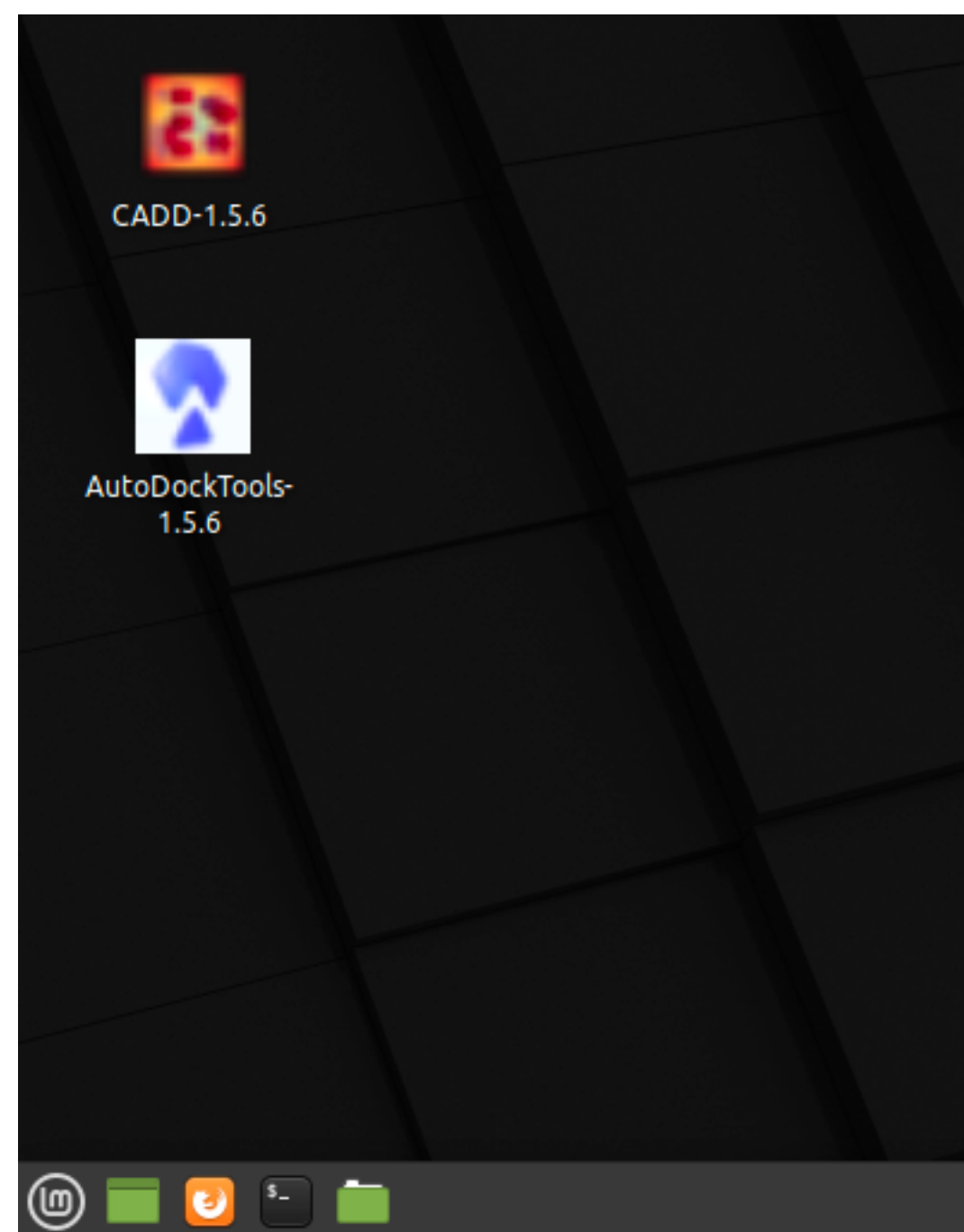


1.1.2 Tutorial: Linux terminal basics

- In this tutorial, you will learn how to navigate the Linux terminal
- The terminal is very similar to the terminal used in
 - UNIX - a predecessor
 - Mac OS X
- Useful for
 - accessing programs that run with a command line interface (CLI)
 - automation
- TODO: Create specific tasks

Starting the terminal



- In the Linux Mint VM, click on the black box in the lower left-hand corner. This opens up a terminal window.

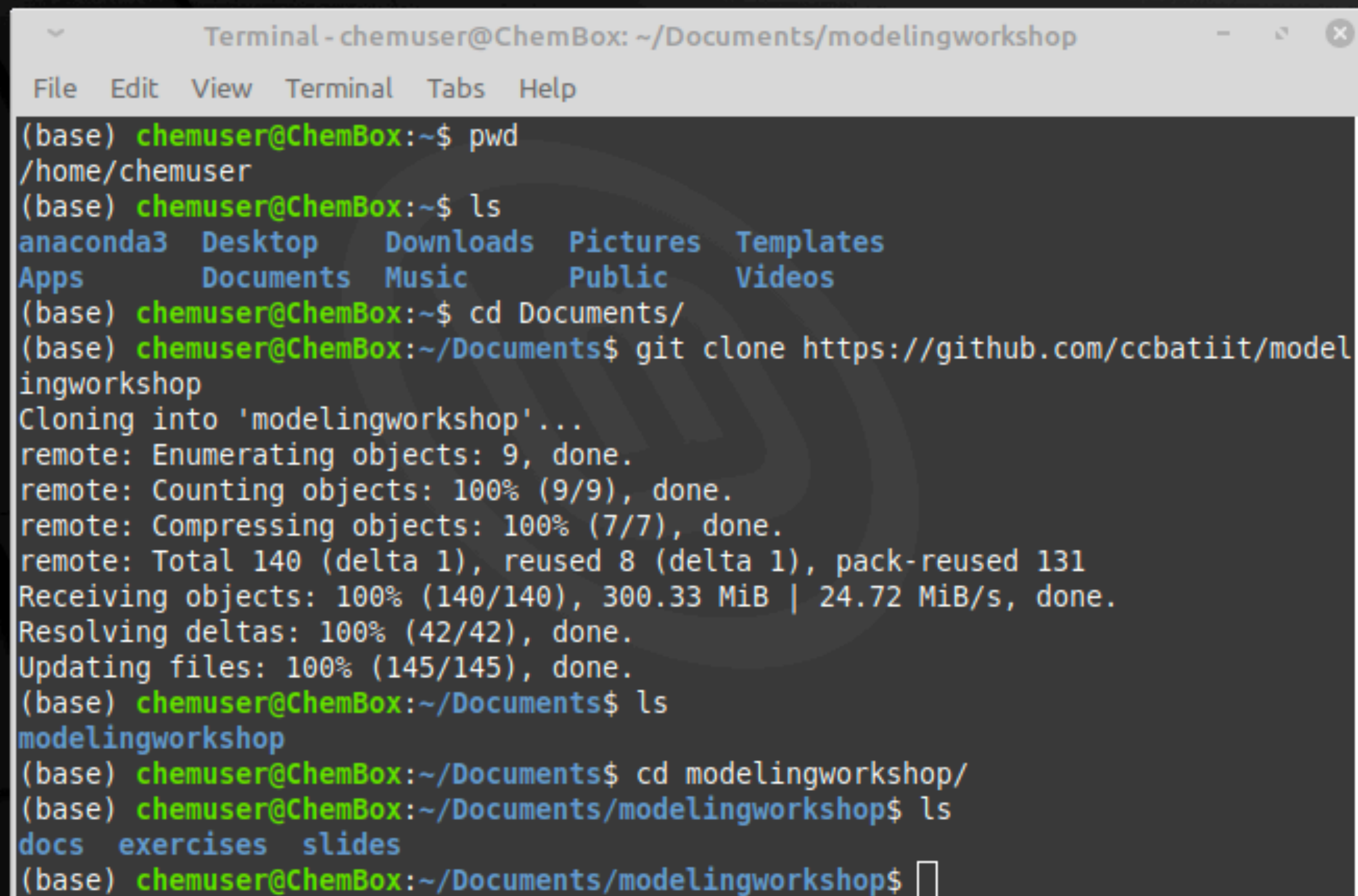
Command Line Interface (CLI)

- Computer software is usually either accessible by a
 - graphical user interface (GUI) or a
 - command line interface (CLI)
- A lot of scientific software is based on a CLI
 - it takes effort to create a GUI
 - a CLI is easier to automate
- Starting a program on the CLI looks like
 - `path_to_program/program_name required_argument1 --argument1_name argument1_value`
 - `path_to_program` can be `./` for the local directory or omitted if the program is in the `$PATH` variable
 - the number of required and optional arguments depends on the program

Basic LINUX commands

- Here are some basic commands
 - echo \$SHELL - echo reports the value of a variable. \$SHELL is the terminal interface you are using, and will affect the details of all other commands. bash is a popular shell.
 - File operations
 - ls – list files and directories
 - cp – copy files
 - rm – remove files and directories
 - mv – rename or move files and directories to another location
 - Directory management
 - pwd – describes current directory
 - cd – change directory
 - mkdir – make new directory
 - rmdir – remove directory
- Also see
 - <https://www.unixtutorial.org/basic-unix-commands>
 - An Introduction to Linux (<https://www.youtube.com/watch?v=IVquJh3DXUA>). Work with the terminal starts at 3:35

Example: Cloning the workshop files



```
Terminal - chemuser@ChemBox: ~/Documents/modelingworkshop
File Edit View Terminal Tabs Help
(base) chemuser@ChemBox:~$ pwd
/home/chemuser
(base) chemuser@ChemBox:~$ ls
anaconda3  Desktop  Downloads  Pictures  Templates
Apps       Documents Music      Public    Videos
(base) chemuser@ChemBox:~$ cd Documents/
(base) chemuser@ChemBox:~/Documents$ git clone https://github.com/ccbatiit/modelingworkshop
Cloning into 'modelingworkshop'...
remote: Enumerating objects: 9, done.
remote: Counting objects: 100% (9/9), done.
remote: Compressing objects: 100% (7/7), done.
remote: Total 140 (delta 1), reused 8 (delta 1), pack-reused 131
Receiving objects: 100% (140/140), 300.33 MiB | 24.72 MiB/s, done.
Resolving deltas: 100% (42/42), done.
Updating files: 100% (145/145), done.
(base) chemuser@ChemBox:~/Documents$ ls
modelingworkshop
(base) chemuser@ChemBox:~/Documents$ cd modelingworkshop/
(base) chemuser@ChemBox:~/Documents/modelingworkshop$ ls
docs  exercises  slides
(base) chemuser@ChemBox:~/Documents/modelingworkshop$
```