

# Using UNIX on the commandline



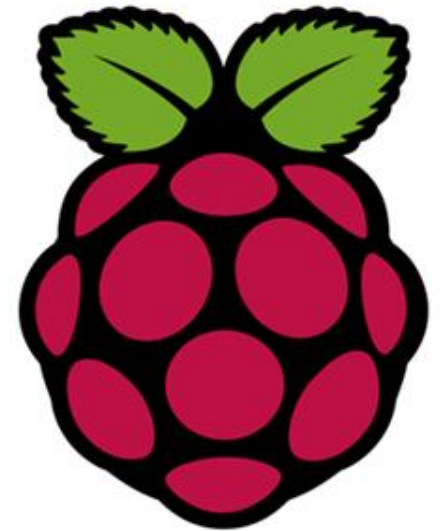
UNIX

Command line

Exercises



ORACLE®



CentOS

Gentoo: [https://de.wikipedia.org/wiki/Gentoo\\_Linux#/media/Datei:Gentoo\\_Linux\\_logo\\_matte.svg](https://de.wikipedia.org/wiki/Gentoo_Linux#/media/Datei:Gentoo_Linux_logo_matte.svg); 13.08.19

ORACLE: [https://upload.wikimedia.org/wikipedia/commons/thumb/5/50/Oracle\\_logo.svg/1920px-Oracle\\_logo.svg.png](https://upload.wikimedia.org/wikipedia/commons/thumb/5/50/Oracle_logo.svg/1920px-Oracle_logo.svg.png); 13.08.19

openSuse: <https://gitorious.org/opensuse/art/source/ecbe9f96fa4c6d2e5d1ac18a403587f925c136a5:00assets/logo/official-logo-color.svg>; 13.08.19

CentOS: <https://de.wikipedia.org/wiki/CentOS#/media/Datei:CentOS-Logo.svg>; 13.08.19

Rasbian: [https://de.wikipedia.org/wiki/Raspberry\\_Pi#/media/Datei:Raspberry\\_Pi\\_Logo.svg](https://de.wikipedia.org/wiki/Raspberry_Pi#/media/Datei:Raspberry_Pi_Logo.svg); 13.08.19



# Unix



# Windows

C:



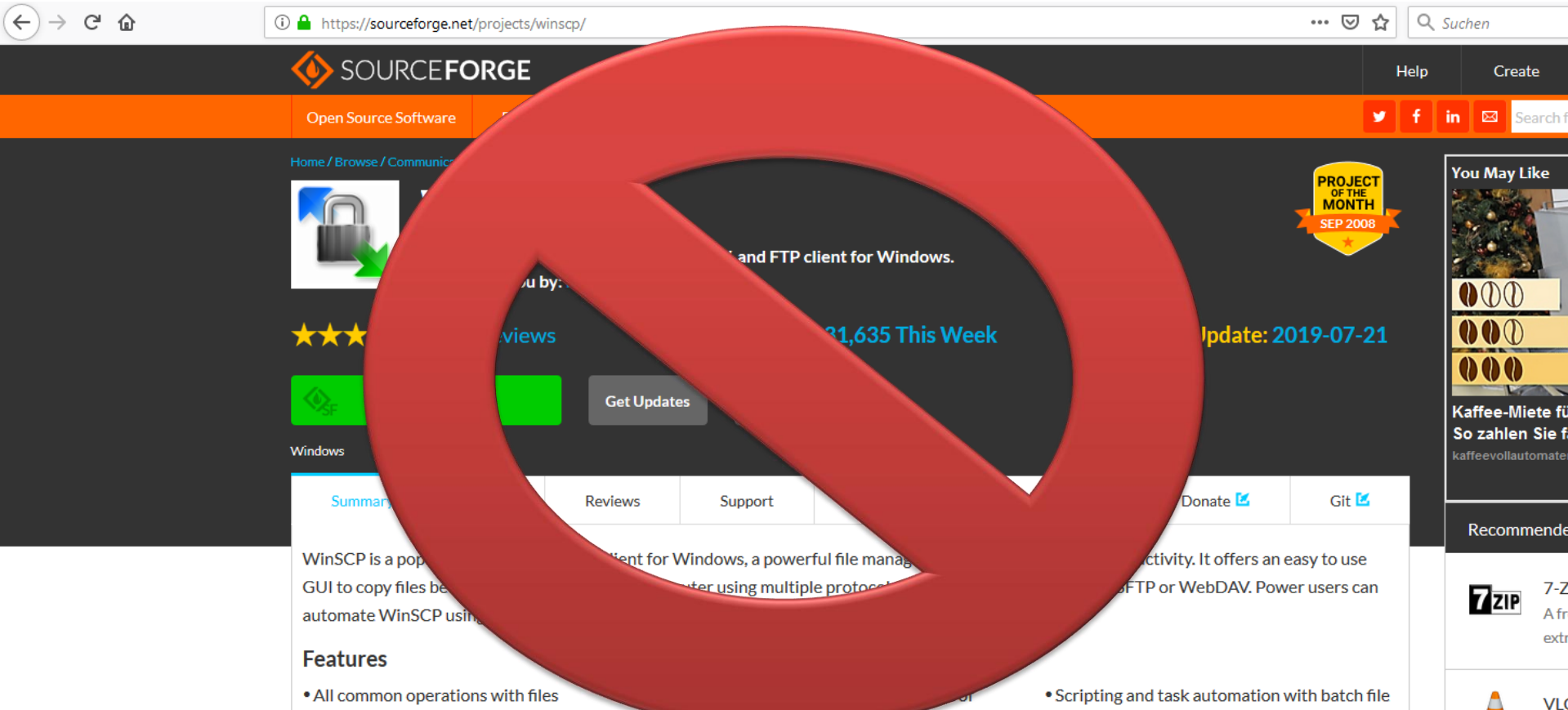
D:



E:



# Software: Packages



The image shows a screenshot of the SourceForge website for the WinSCP project. The browser address bar displays the URL <https://sourceforge.net/projects/winscp/>. The SourceForge logo is visible at the top left. The page content includes a navigation bar with 'Open Source Software', a search bar, and social media icons. A large red prohibition sign (a circle with a diagonal slash) is overlaid on the central part of the page, obscuring the main project details. Visible text includes 'WinSCP is a popular FTP client for Windows, a powerful file manager...', '31,635 This Week', and 'Update: 2019-07-21'. A 'Project of the Month' badge for 'SEP 2008' is also present. The 'Features' section lists 'All common operations with files' and 'Scripting and task automation with batch file'.

# Users, groups and the boss....



root

- can do ANYTHING

users

- constrained
- organized in groups
- substitute user do

sudo rm importantFile



By Frits Ahlefeldt

Respect

Think

Mind



Command line

**NanoPipe** New Request

Previous Request

ID ?

---

**New Request**

Target ? Upload File

Target File ?

Query File ?

Minimum Sequence Length ? 100

Email ?

Title ?

---

**Last Parameters**

Substitution Matrix	Load	Init	A	C	G	T
Use Matrix or Match Score / Mismatch Cost			5	-3	-2	-14
			-7	6	-6	-9
			-4	-6	6	-14
			-14	-9	-8	5

Gap Existence Cost (-a) ? 10

Gap Extension Cost (-b) ? 4

Insertion Existence Cost (-A) ? 17

Insertion Extension Cost (-B) ? 3

Score Matrix applies to Forward Strand (-S) ? 1

Initial Matches Position (-k) ?

Maximum Score Drop (-x) ?

Run | View Human Test Case | View Plasmodium Test Case | Set Default Parameters | Reset

```

my $s_counter = 0;
my $align_start = 0;
my $align_end = 0;
my $chr = undef;
my $cwd = ${$_[0]};
my %hash = ();
my $prevM = "";

#Search for SNP positions in maf file
open(DATA, "<.", $cwd."/calc.lastalign.maf") or die "Couldn't open maf file, $!";
while(<DATA>) {

    # Skip comments
    if($_ !~m"^#") {

        # Choose lines starting with s...
        if($_ =~m"^s\s"){
            if ($s_counter== 0) {
                # Split by any number of white spaces
                my @line_data = split ' ', $_;
                my $align_len = length $line_data[-1];
                $chr = $line_data[1];
                $chr =~ s/^chr//;
                $align_start = $line_data[2];
                $align_end = $align_len + $align_start -1;
            }
            $s_counter += 1;
        }
        elsif($_ =~m"^p\s"){
            if ($s_counter == 2){
                $s_counter = 0;
                # Split by any number of white spaces
                my @quality_data = split ' ', $_;
                my $quality = $quality_data[-1];
                if (exists ($hash{$chr})) {
                    if (exists ($hash{$chr}{$align_start})) {
                        push(@{$hash{$chr}{$align_start}}, [$align_end, $quality]);
                    }
                    else {
                        $hash{$chr}{$align_start} = [[ $align_end, $quality]];
                    }
                }
            }
        }
    }
}

```

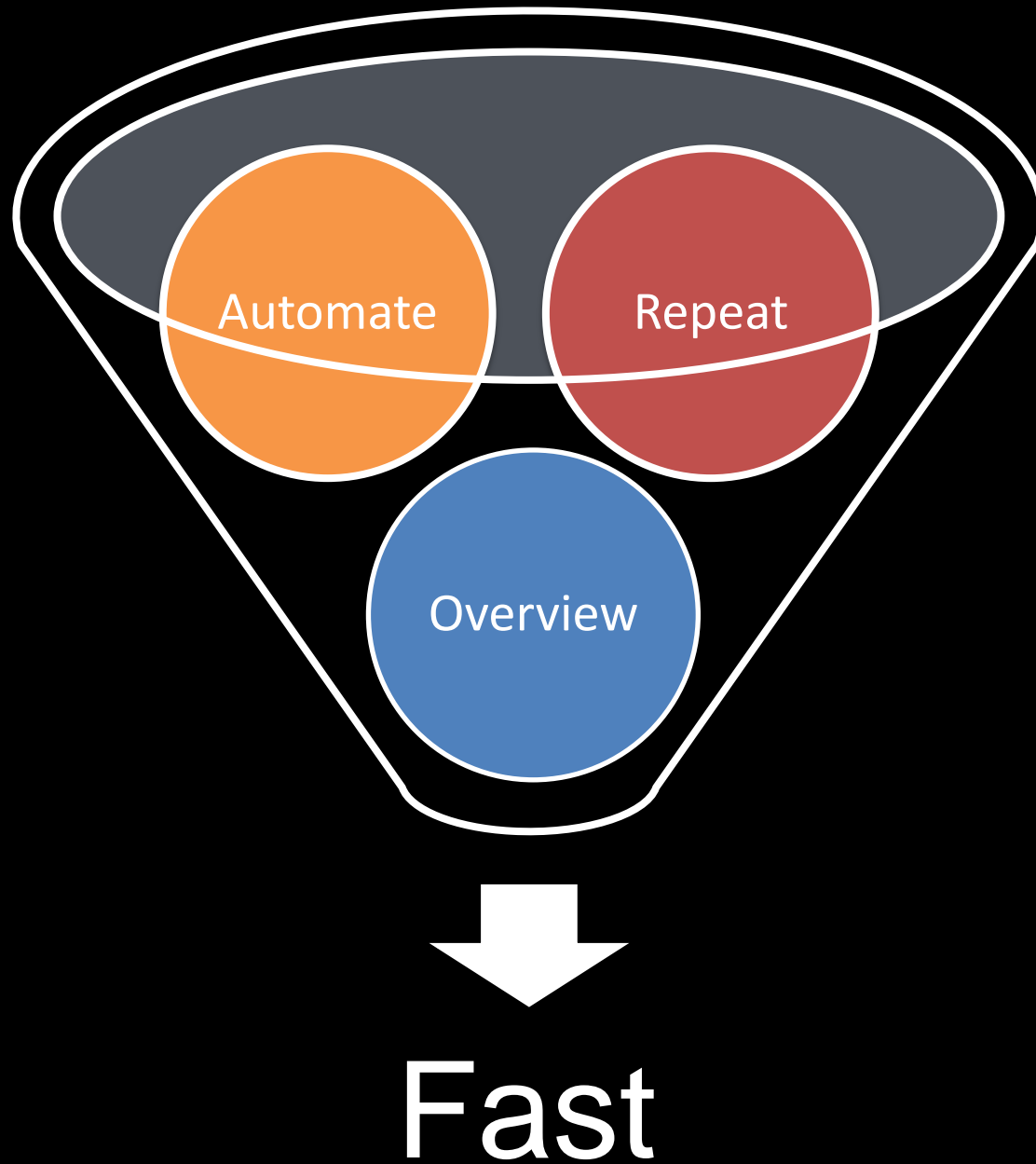
Terminal

File Edit View Search Terminal Help

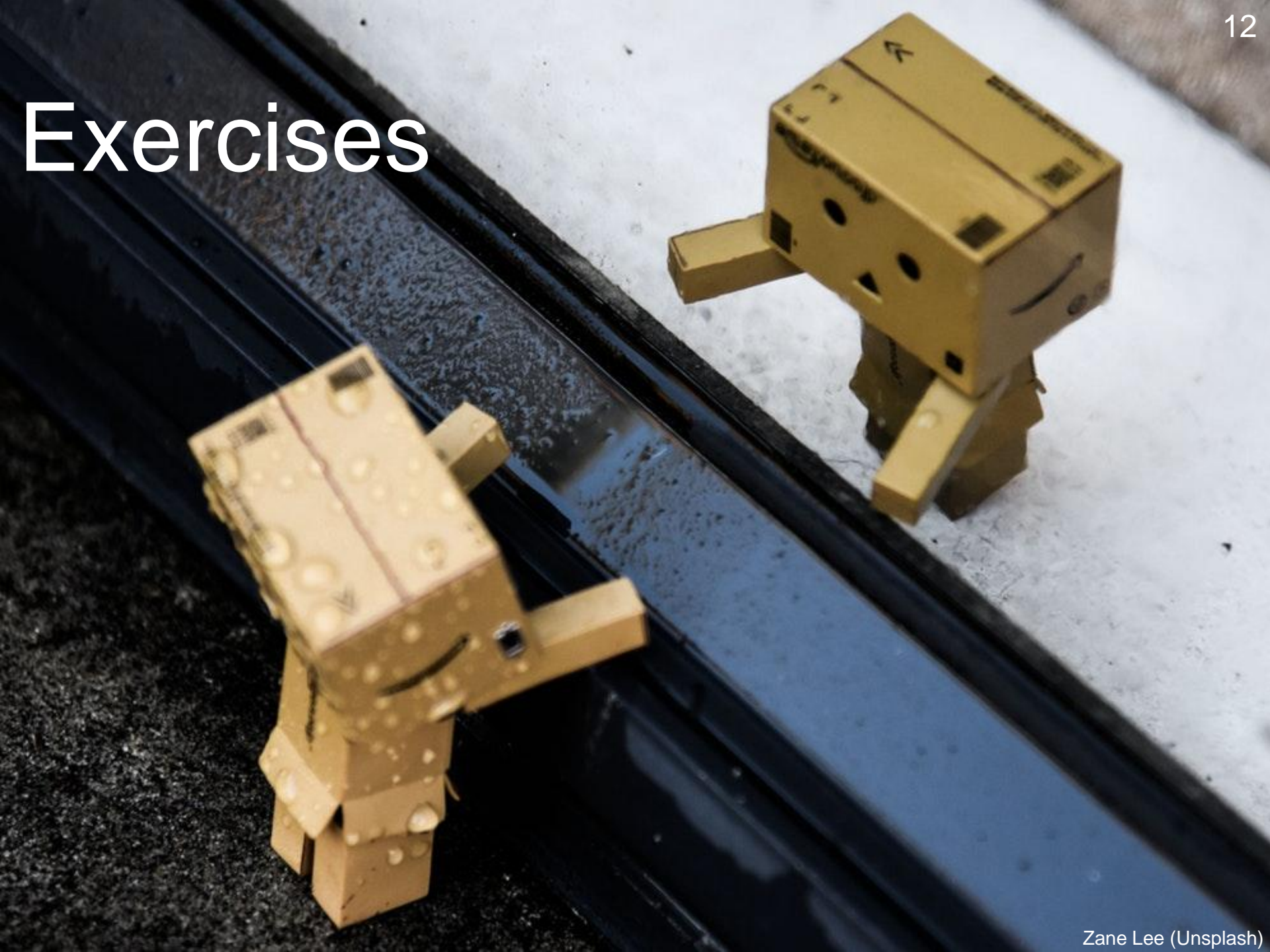
```

felixm@adminx-OptiPlex-5050:~$ nanopipe_calc.pl -q input.query -t input.target

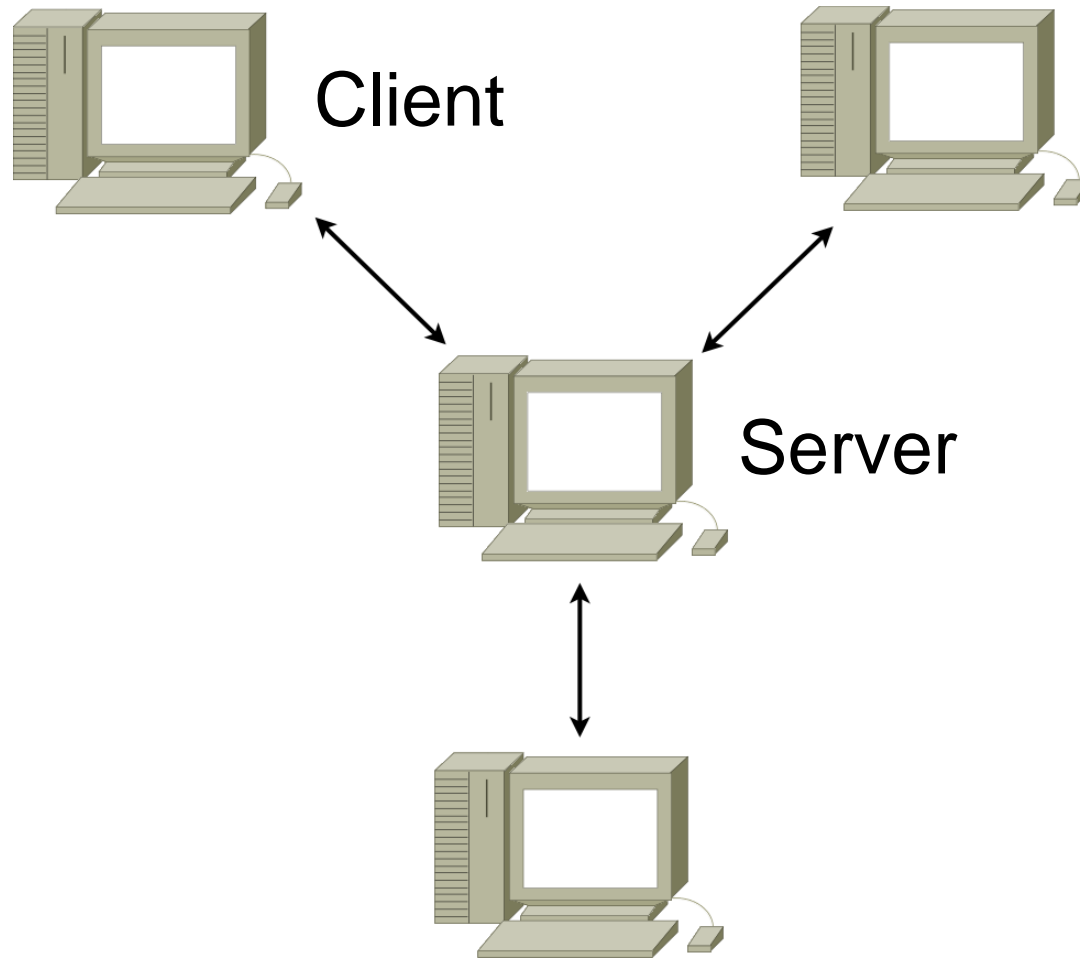
```



# Exercises



# What is a server?




# Windows

- Check bit version of Windows
  - Search for “system” using the search tool
  - Check the entry for system type

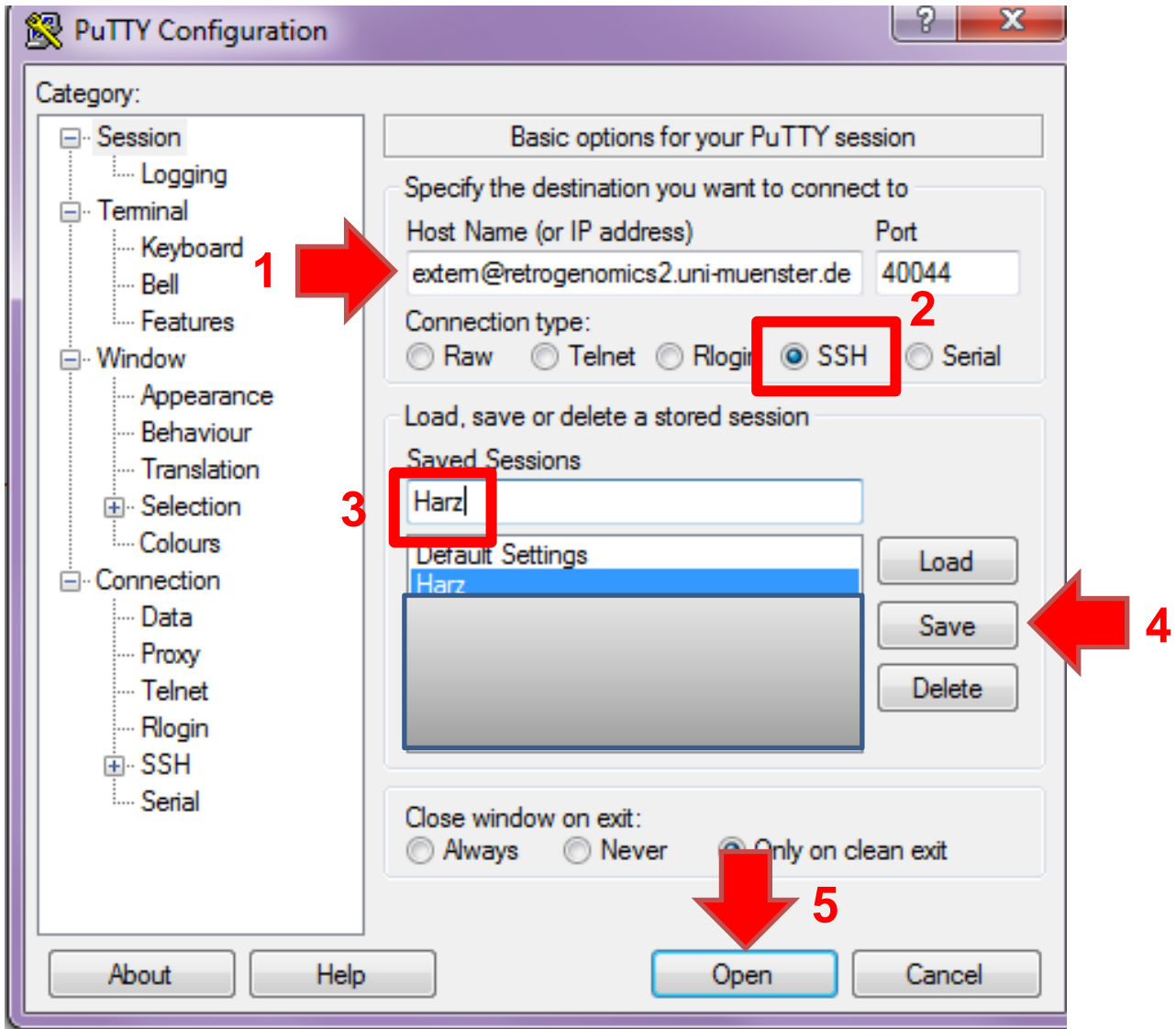
## System

---

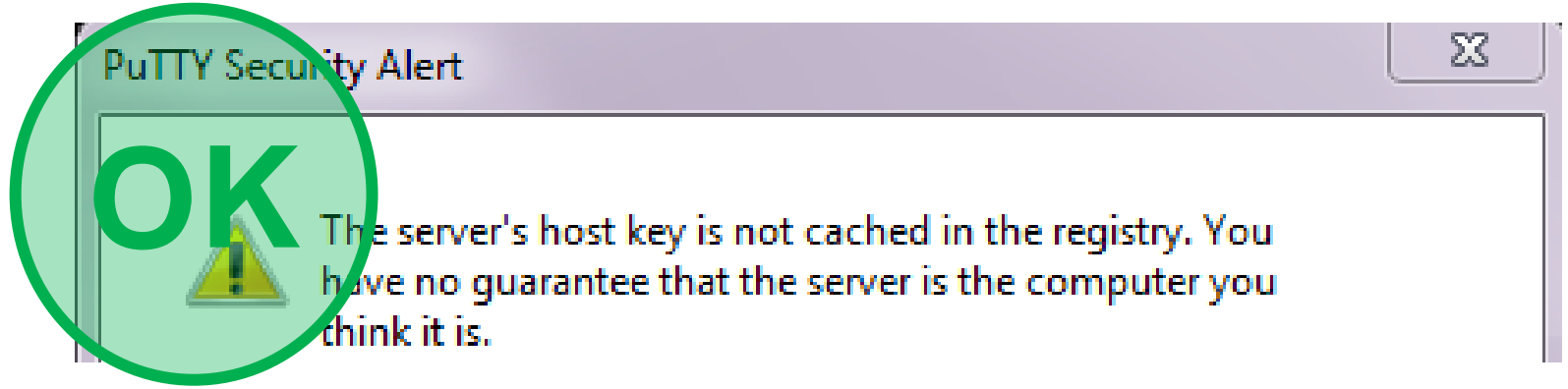
Klassifikation:	 5,9 Windows-Leistungsindex
Prozessor:	Intel(R) Core(TM) i5-3320M CPU @ 2.60GHz 2.60 GHz
Installierter Arbeitsspeicher (RAM):	8,00 GB (7,58 GB verwendbar)
Systemtyp:	64 Bit-Betriebssystem
Stift- und Fingereingabe:	Für diesen Bildschirm ist keine Stift- oder Fingereingabe verfügbar.

# Windows

- Download and install PuTTY:
  - **32-bit:**  
<https://the.earth.li/~sgtatham/putty/latest/w32/putty-0.72-installer.msi>
  - **64-bit (usually OK):**  
<https://the.earth.li/~sgtatham/putty/latest/w64/putty-64bit-0.72-installer.msi>







# UNIX/Mac

```
ssh -p 40044 extern@retrogenomics2.uni-muenster.de
```





# Home folder



list all items

ls

ls -l

put empty file

touch calender.txt

view one item

less calender.txt

print working directory

pwd

↓↑ browse history

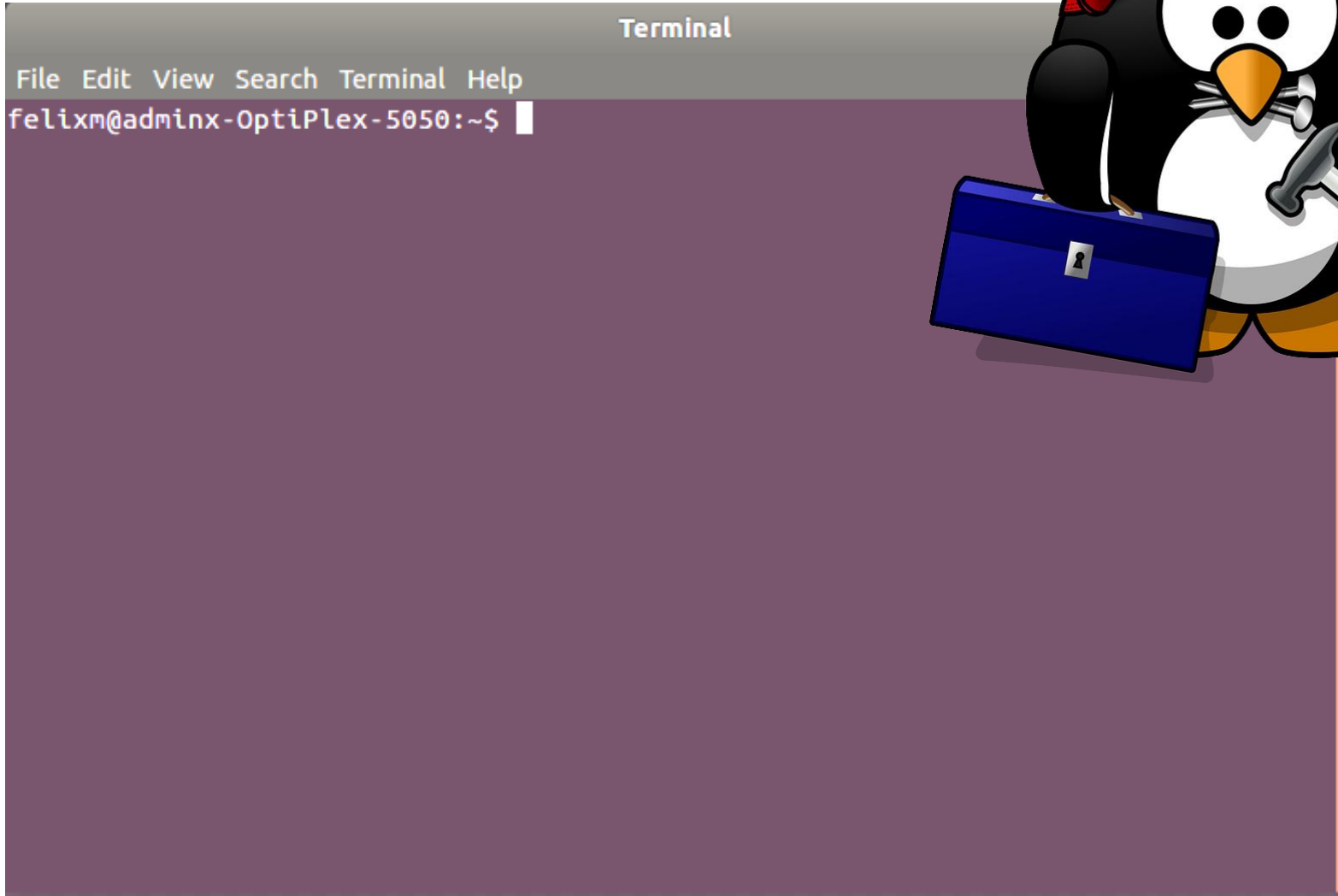
↔ auto complete

ls ≠ LS ≠ Ls

man [command] for help

top / htop: processes

ctrl + c abort



Absolute path

/building/top/hallway/1stLeft

**Boss**



../../../../top/hallway/1stLeft



**You**



/building/18th/hallway/home



Relative path





# change directory

**cd** /building/top/hallway/1stLeft

**cd** ../../../../topFloor/hallway/1stLeft

# change directory

cd /building/18th/hallway/home

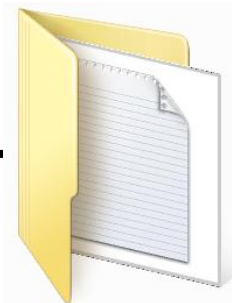
cd ../../../18th/hallway/home

cd -

cd



Documents



Harz



Map.txt

You are in the “Documents” folder.  
How do you enter the “Harz” folder?

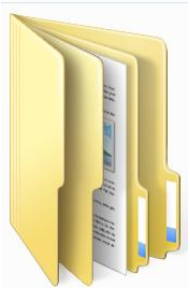
**A:** pwd

**B:** cd ..

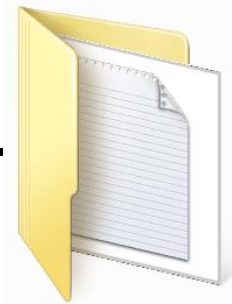
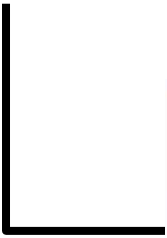
**C:** cd Harz



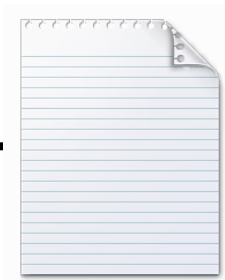
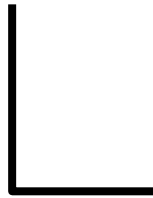
**D:** less Harz



Documents



Harz



Map.txt

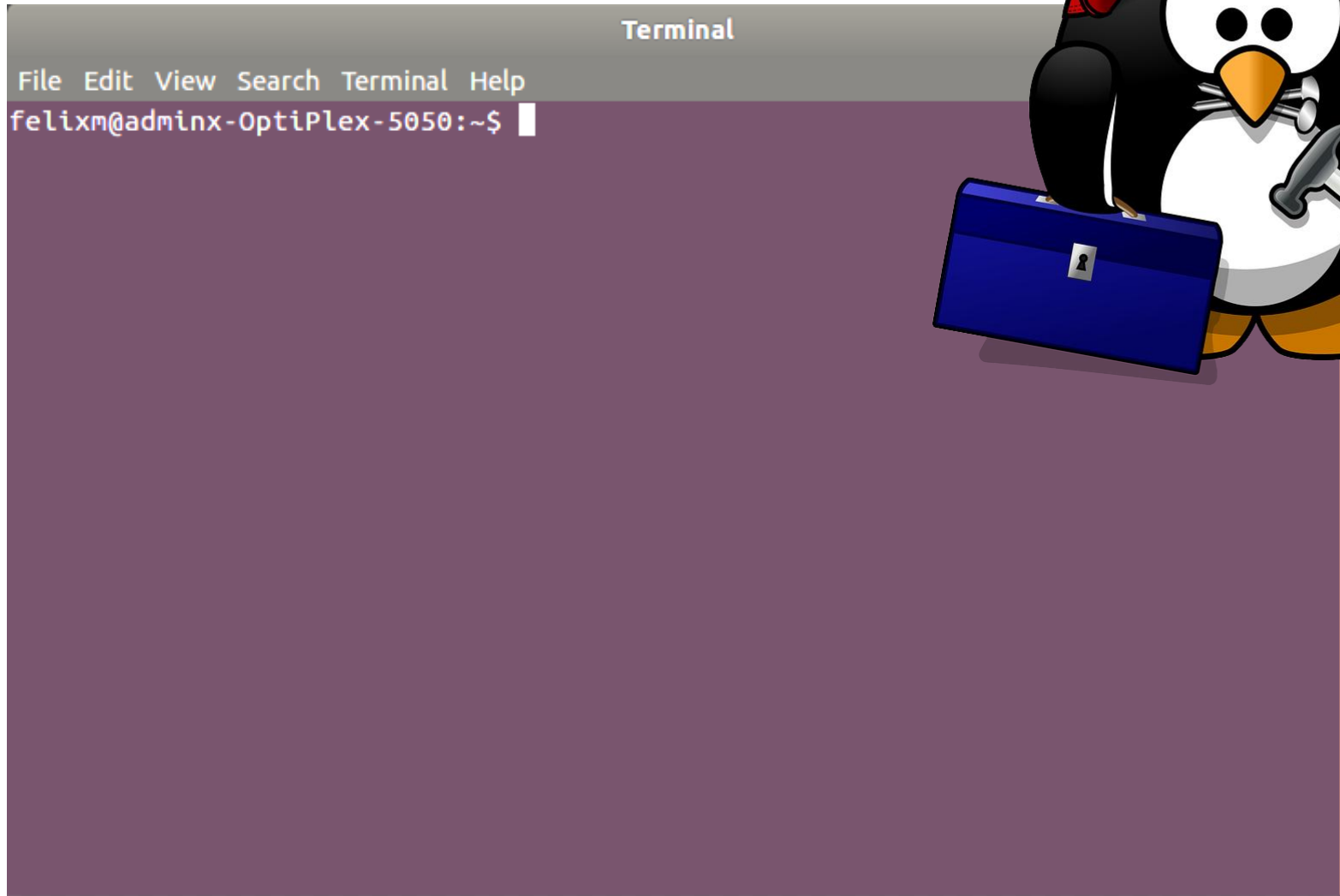
You are in the “Harz” folder.

How do you view the “Map.txt” file?

**A:**    less Map.txt    ✓

**B:**    cd Map.txt

**C:**    pwd





**m****o****v****e** contents of document place/name

**m****v** report ../Coworker/

**m****v** report FelixReport

**m****v** FelixReport ../Coworker/

**c****o****p****y** contents of document

**c****p** report ../Coworker/

**c****p** report ../Coworker/FelixReport

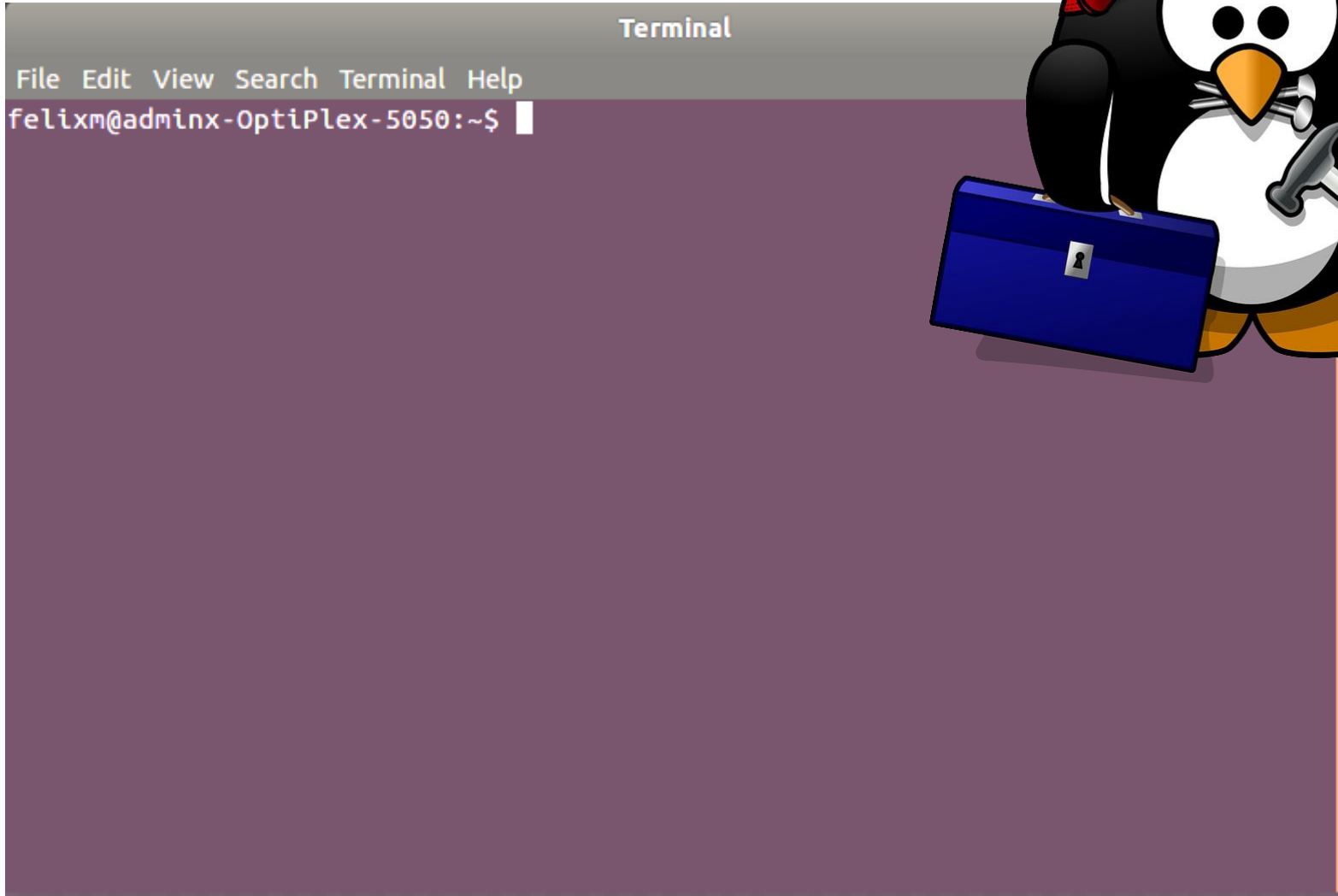


put into archive (compress):  
**zip** letter.zip report document

extract from archive (decompress):  
**unzip** letter.zip

**remove** files  
**rm** coverLetter\_2



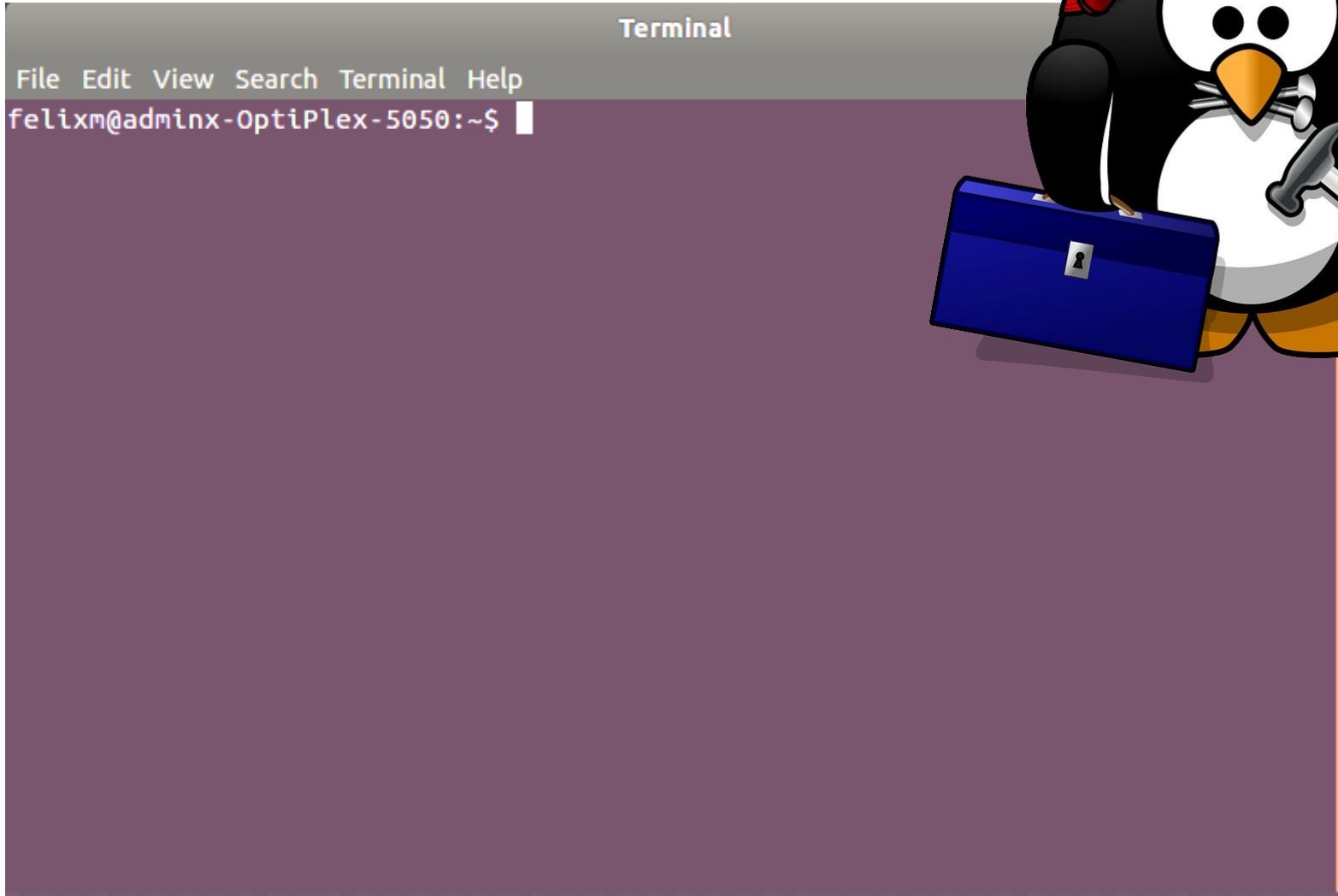




make directory  
mkdir ../NEWoffice

remove directory -r  
rm -r ../officePensioner







sort (file) contents

sort messy.txt

check for differences of files

diff final.txt final\_final.txt

global search for a regular expression and print out matched lines

grep "Secret" superSecret.txt

grep -E "^>" seq.fasta



# From screen to file



## Save

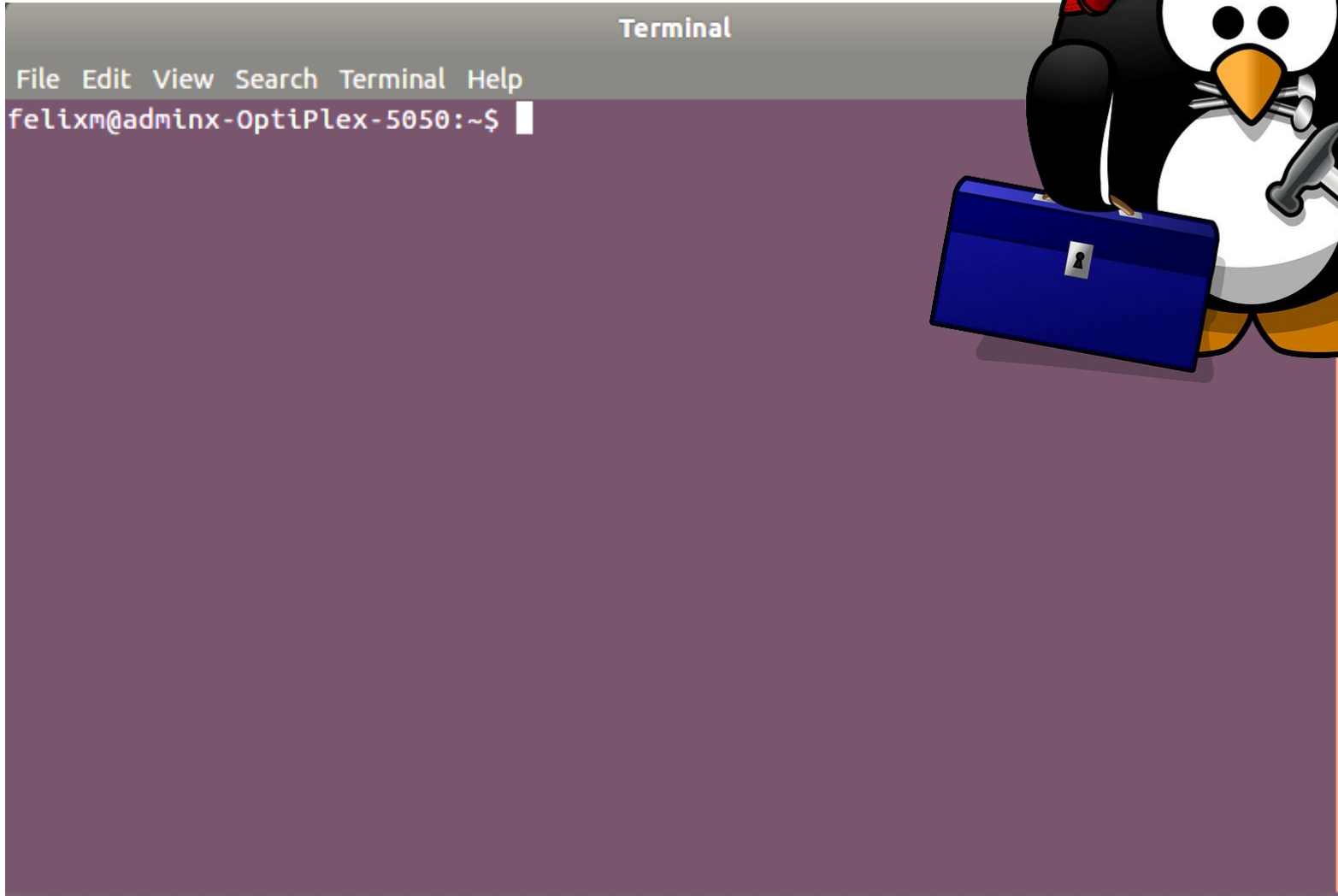
output: `./script.py > results.txt`

errors: `./script.py 2> errors.txt`

both: `./script.py > out.txt 2>&1`

## Append

`./followUp.py >> results.txt`



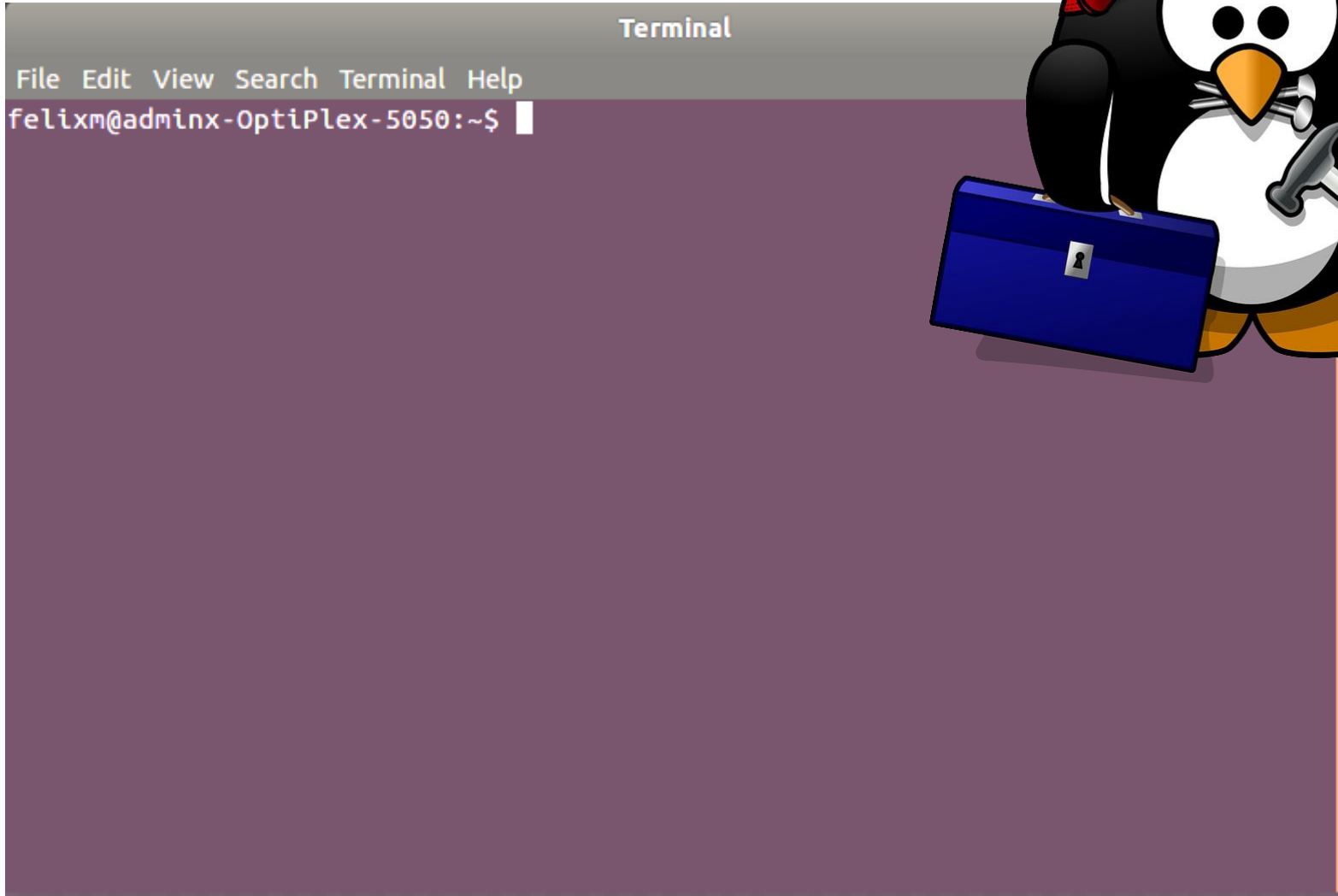


|: (anonymous) pipe

E.g.:

- 1) list all files in seq
- 2) consider only fasta files
- 3) sort by file size

```
ls -l seq/ | grep ".fasta" | sort -k5,5nr
```





E.g.:



[ryanstutorials.net  
/linuxtutorial  
/navigation.php](http://ryanstutorials.net/linuxtutorial/navigation.php)



[computerhope.com  
/unix.htm](http://computerhope.com/unix.htm)

THANK YOU!