



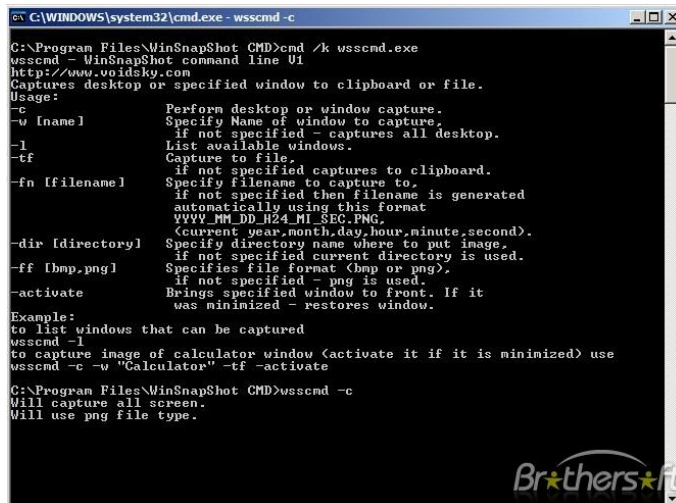
01. The shell

Erik Dassi & Davide Bressan

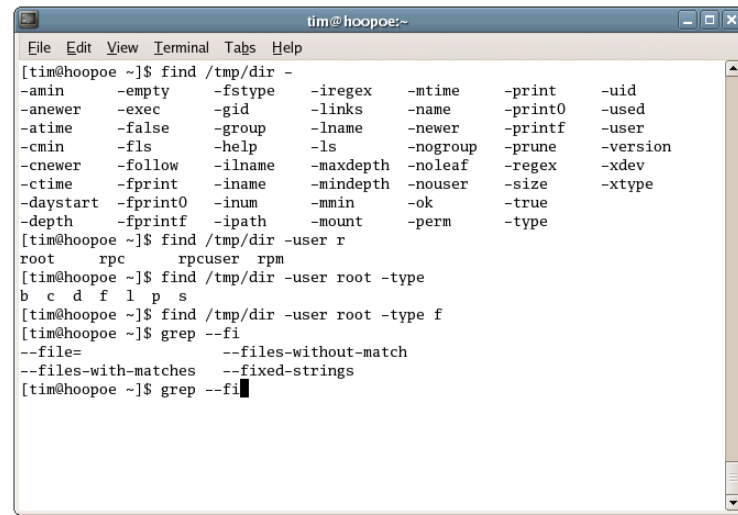
Genomics Technologies Lab

The Shell

- A command-line interpreter, the historical user interface to computer systems, also called *terminal*
- Allows to perform actions by inserting text commands
- Many types available in Linux (sh, Bash, csh, etc)



```
C:\WINDOWS\system32\cmd.exe - wsscmd -c
C:\Program Files\WinSnapShot CMD>cmd /k wsscmd.exe
wsscmd - WinSnapShot command line UI
http://www.voidsky.com
Captures desktop or specified window to clipboard or file.
Usage:
-c          Perform desktop or window capture.
-w [name]   Specify Name of window to capture,
             if not specified - captures all desktop.
-l          List available windows.
-tf         Capture to file,
             if not specified captures to clipboard.
-fn [filename] Specify filename to capture to,
             if not specified then filename is generated
             automatically using this format
             YYYY_MM_DD_H24_M1_SEC.PNG.
-dir [directory] Specify directory name where to put image,
             if not specified current directory is used.
-ff [tmp.png] Specifies file format (bmp or png),
             if not specified - png is used.
-activate   Brings specified window to front. If it
             was minimized - restores window.
Example:
to list windows that can be captured
wsscmd -l
to capture image of calculator window (activate it if it is minimized) use
wsscmd -c -w "Calculator" -tf -activate
C:\Program Files\WinSnapShot CMD>wsscmd -c
Will capture all screen.
Will use png file type.
```



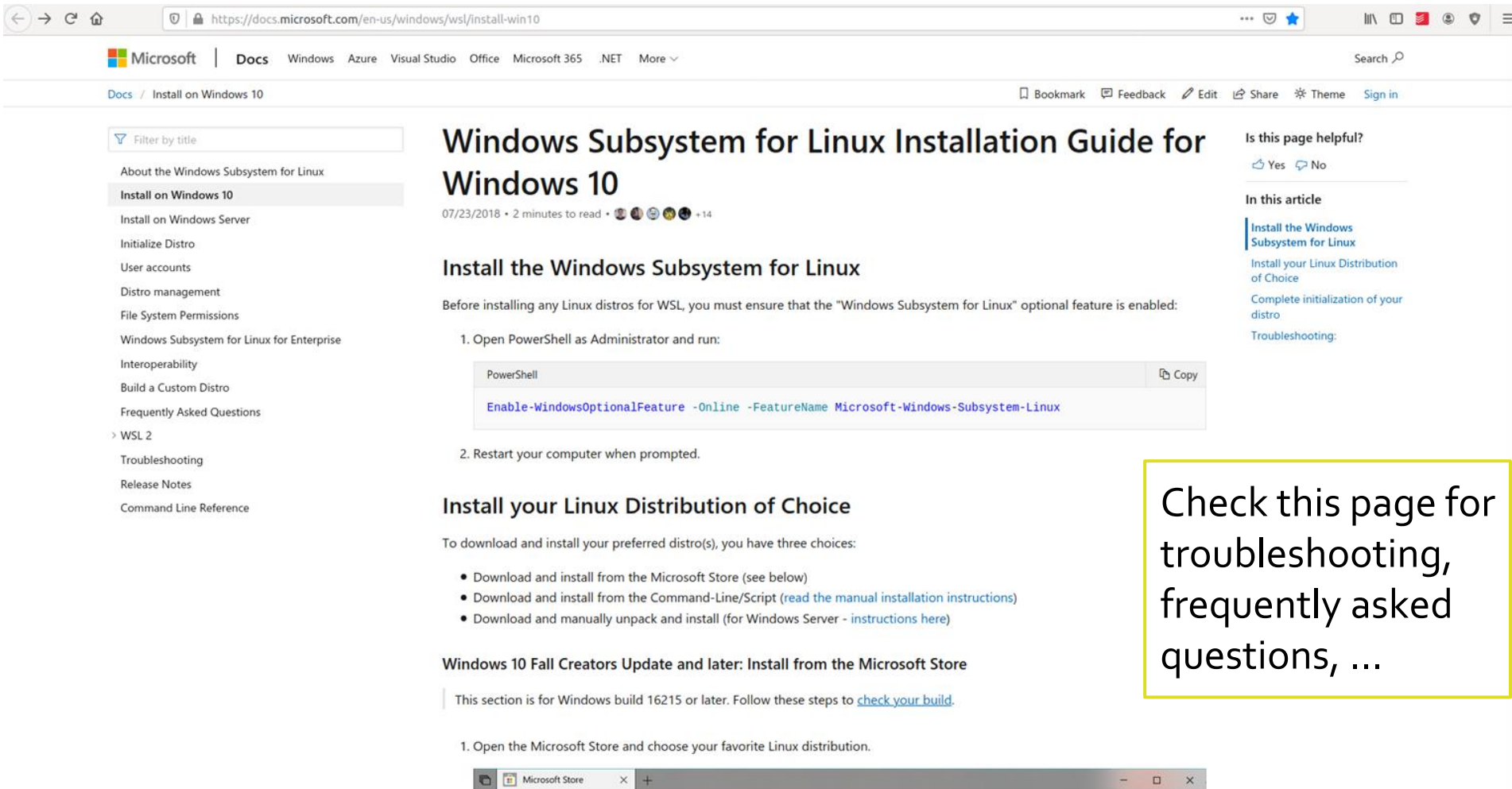
```
tim@hoopoe:~$ find /tmp/dir -
-amin      -empty      -fstype     -iregex     -mtime     -print      -uid
-anewer     -exec         -gid        -links      -name       -print0     -used
-atime      -false        -group      -lname      -newer      -printf     -user
-cmin       -fls          -help       -ls         -nogroup    -prune      -version
-cnewer     -follow       -ilname     -maxdepth   -noleaf     -regex      -xdev
-ctime      -fprint       -iname      -mindepth   -nouser     -size       -xtype
-daystart   -fprint0      -inum       -mmin       -ok         -true
-depth      -fprintf      -ipath      -mount      -perm       -type
[tim@hoopoe ~]$ find /tmp/dir -user r
root      rpc      rpcuser  rpm
[tim@hoopoe ~]$ find /tmp/dir -user root -type
b  c  d  f  l  p  s
[tim@hoopoe ~]$ find /tmp/dir -user root -type f
[tim@hoopoe ~]$ grep --fi
--file=                --files-without-match
--files-with-matches    --fixed-strings
[tim@hoopoe ~]$ grep --fi
```

What can I do with a shell ?

- List directories and files
 - Move, rename, delete and view files
 - Launch any kind of software, even the ones having a graphical interface
 - View various information on the status of your system
 - Perform complex text manipulations (with the help of some specific software)
 - ... almost anything that might come to your mind (*no coffee*, though....)
- > Run a set of commands as a script: a *pipeline* <

Install WSL for Windows

<https://docs.microsoft.com/en-us/windows/wsl/install-win10>



The screenshot shows the Microsoft Docs website for the "Windows Subsystem for Linux Installation Guide for Windows 10". The page is titled "Windows Subsystem for Linux Installation Guide for Windows 10" and is dated 07/23/2018. It includes a sidebar with navigation links such as "About the Windows Subsystem for Linux", "Install on Windows 10", "Install on Windows Server", "Initialize Distro", "User accounts", "Distro management", "File System Permissions", "Windows Subsystem for Linux for Enterprise", "Interoperability", "Build a Custom Distro", "Frequently Asked Questions", "WSL 2", "Troubleshooting", "Release Notes", and "Command Line Reference". The main content area is titled "Install the Windows Subsystem for Linux" and includes a section "Before installing any Linux distros for WSL, you must ensure that the 'Windows Subsystem for Linux' optional feature is enabled:". It lists two steps: 1. Open PowerShell as Administrator and run: `Enable-WindowsOptionalFeature -Online -FeatureName Microsoft-Windows-Subsystem-Linux` and 2. Restart your computer when prompted. Below this, it says "Install your Linux Distribution of Choice" and provides three options: Download and install from the Microsoft Store (see below), Download and install from the Command-Line/Script (read the manual installation instructions), and Download and manually unpack and install (for Windows Server - instructions here). The page also mentions "Windows 10 Fall Creators Update and later: Install from the Microsoft Store" and provides a link to "check your build". At the bottom, it says "1. Open the Microsoft Store and choose your favorite Linux distribution." and shows a small image of the Microsoft Store app icon.

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- Interoperability
- Build a Custom Distro
- Frequently Asked Questions
- WSL 2
- Troubleshooting
- Release Notes
- Command Line Reference

Windows Subsystem for Linux Installation Guide for Windows 10

07/23/2018 • 2 minutes to read • 14

Install the Windows Subsystem for Linux

Before installing any Linux distros for WSL, you must ensure that the "Windows Subsystem for Linux" optional feature is enabled:

1. Open PowerShell as Administrator and run:

```
PowerShell
```

```
Enable-WindowsOptionalFeature -Online -FeatureName Microsoft-Windows-Subsystem-Linux
```

Copy

2. Restart your computer when prompted.

Install your Linux Distribution of Choice

To download and install your preferred distro(s), you have three choices:

- Download and install from the Microsoft Store (see below)
- Download and install from the Command-Line/Script ([read the manual installation instructions](#))
- Download and manually unpack and install (for Windows Server - [instructions here](#))

Windows 10 Fall Creators Update and later: Install from the Microsoft Store

This section is for Windows build 16215 or later. Follow these steps to [check your build](#).

1. Open the Microsoft Store and choose your favorite Linux distribution.

Microsoft Store

Check this page for
troubleshooting,
frequently asked
questions, ...

Install WSL for Windows

Filter by title

WSL Documentation

- > Overview
- > Quickstart
 - Install WSL & update to WSL 2
 - Install on Windows Server
 - Create a user account & password
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- > How-to
 - Frequently Asked Questions
 - WSL 2 FAQ
 - Troubleshooting
- > Release Notes



The following links will open the Microsoft store page for each distribution:



- [Ubuntu 16.04 LTS](#)
- [Ubuntu 18.04 LTS](#)
- [Ubuntu 20.04 LTS](#)
- [openSUSE Leap 15.1](#)
- [SUSE Linux Enterprise Server 12 SP5](#)
- [SUSE Linux Enterprise Server 15 SP1](#)
- [Kali Linux](#)
- [Debian GNU/Linux](#)
- [Fedora Remix for WSL](#)

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👍 Yes 👎 No

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[Simplified Installation for Windows Insiders](#)

[Manual Installation Steps](#)

[Step 1 - Enable the Windows Subsystem for Linux](#)

[Step 2 - Check requirements for running WSL 2](#)

[Step 3 - Enable Virtual Machine feature](#)

[Step 4 - Download the Linux kernel update package](#)

[Step 5 - Set WSL 2 as your default version](#)


[Step 6 - Install your Linux distribution of choice](#)

[Install Windows Terminal \(optional\)](#)

[Set your distribution version to WSL 1 or WSL 2](#)

[Troubleshooting installation](#)

Install WSL for Windows

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Ubuntu 20.04 LTS

Canonical Group Limited • [Strumenti di sviluppo](#) > [Utilità](#)

Ubuntu 20.04 LTS on Windows allows you to use Ubuntu Terminal and run Ubuntu command line utilities including bash, ssh, git, apt and many more.

[Altro](#)



PEGI 3

Gratis

Ottieni

 [Vedi i requisiti di sistema.](#)

[Informazioni generali](#)

[Requisiti di sistema](#)

[Correlati](#)

Install WSL for Windows



Prodotto installato.

Avvia

...



Ubuntu 20.04 LTS

Canonical Group Limited • Strumenti di sviluppo > Utilità

Condividi

Ubuntu 20.04 LTS on Windows allows you to use Ubuntu Terminal and run Ubuntu command line utilities including bash, ssh, git, apt and many more.

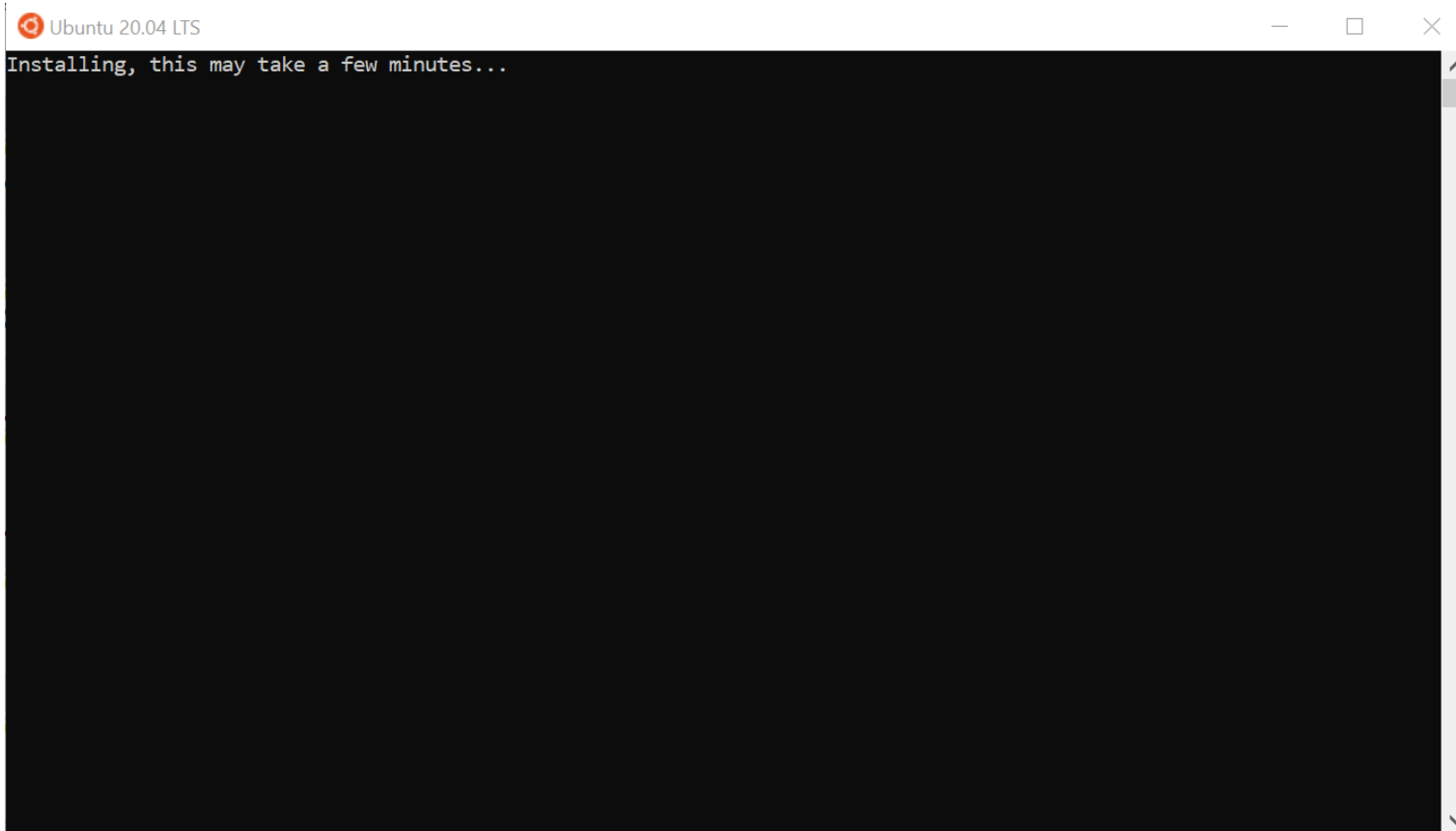
Altro



PEGI 3

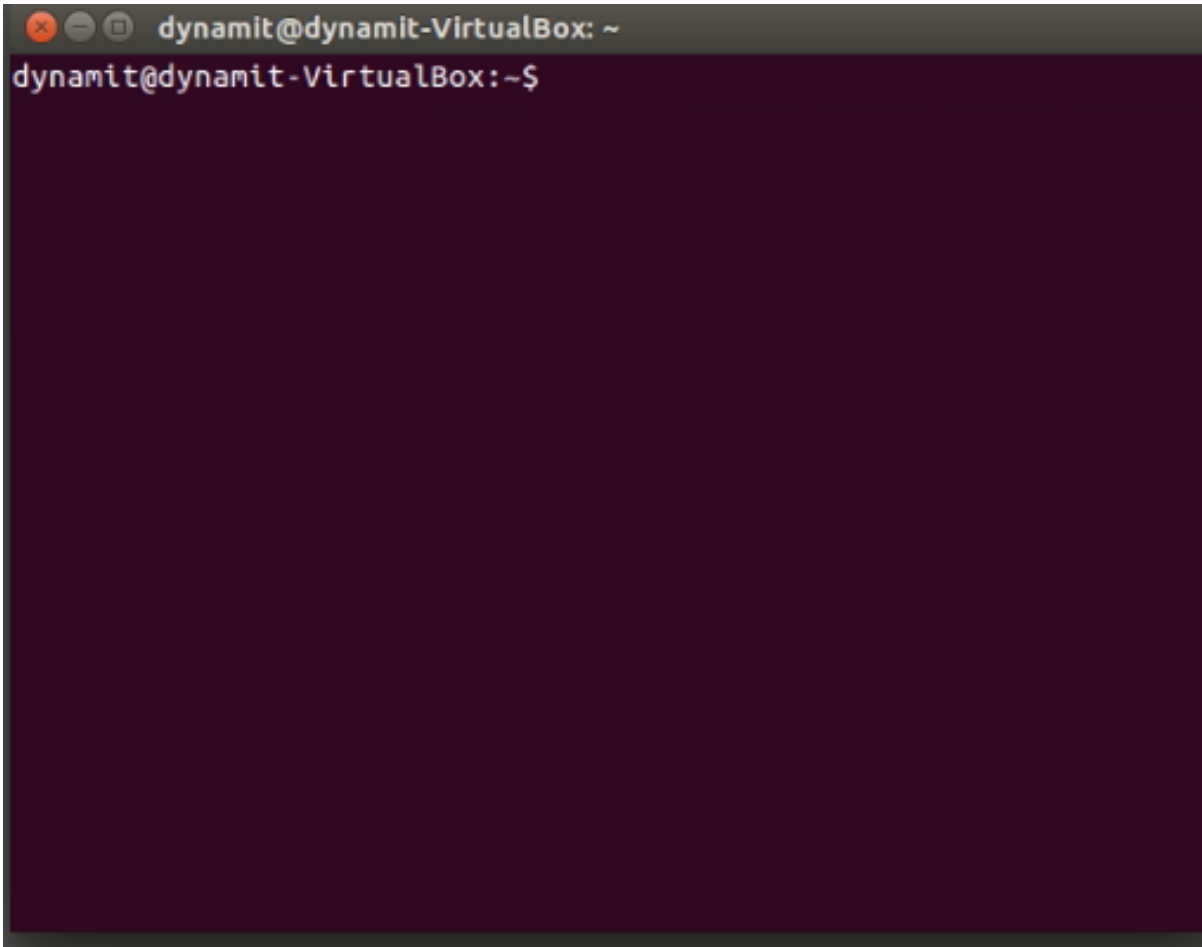
Elenco preferenze

Install WSL for Windows



Choose a username and password

Linux



```
dynamit@dynamit-VirtualBox: ~  
dynamit@dynamit-VirtualBox:~$
```

Code conventions

- Text in red surrounded by < and > signs, e.g.:

echo <text>

- Means that you have to substitute that with your text/command/folder name, e.g:

echo «Genomics Technologies '23-'24»

Hello, World!

- Print something to the shell with the command:

echo <text>

echo Hello World

- Print current time and date

echo \$(date)

- Print some text to a file (do it!)

echo <the text you want> > output.txt

Windows WSL: similar to ? C:\Users\<user>\AppData\Local\Packages\CanonicalGroupLimite.Ubuntu20.04
onWindow_79rhkp1fndgsc\LocalState\rootfs\home\<user>\output.txt

macOS: /Users/<user>/output.txt

Linux: /home/<user>/output.txt

Let's have a look around

- Check the current location:

pwd

print name of current/working directory

- List directories and files in the current location:

ls

lists everything that is in current directory

ls -lh

lists files details and human-readable sizes

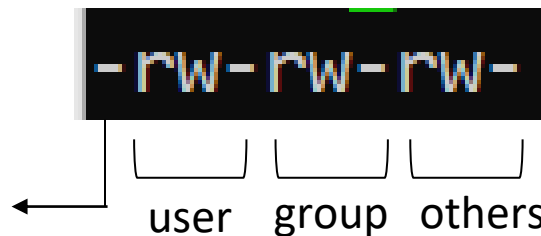
ls -lh *.txt

list only files with txt extension

File permissions:

- = file

d = directory



r = read

w = write

x = execute

- = no permission

Let's have a look around

- Move to another directory:

cd <DirectoryName>

move to that directory

cd ..

move up one level

cd

move to the home directory

- Create a new directory:

mkdir <DirectoryName>

create directory

mkdir mywork

create that directory in home directory

mkdir mywork/GTExercises

create that directory in Desktop

Moving stuff around

- Copy a file to another folder:

cp <source file> <destination file>

cp output.txt mywork/ GTExercises /output2.txt

copy to our directory in Desktop

- Move a file to another folder:

mv <source file> <destination file>

mv output.txt mywork/GTExercises/output.txt

moves the file to our directory

mv mywork/GTExercises/output.txt .

moves back the file

mv output.txt output3.txt

renames the file

Help!

- Display the user manual of the command:

man <command>

man less

- Display a usage message:

command --help

less --help

head --help

tail --help

Viewing stuff

- Display a file contents (one screen at a time):

less <filename>

less output3.txt

man less > less.txt

less less.txt

- Display the beginning or the end of a file:

head <filename> **tail** <filename>

head less.txt

head -n 200 less.txt

tail -n 200 less.txt

Pipes

- Pipes allow to forward the output of a command to the input of the next one, thus creating a chain or pipe
- A pipe is created by «|», multiple pipes can be chained in the same command
- Allow to spare commands and be more efficient
- Basic examples:

man less | head

Try more!

- Download the **mygenelist.txt** file from moodle
- Copy the file in the mywork/GTExercises directory
- Move to that directory
cd mywork/GTExercises

Sorting, counting

sort mygenelist.txt

sort lines of text files

wc mygenelist.txt

print number of lines, words and character for each file

wc -l mygenelist.txt

wc -w mygenelist.txt

wc -c mygenelist.txt

uniq mygenelist.txt

report or omit repeated lines

Cat, cut & paste

cat mygenelist.txt

create, view and concatenate files and print output

cat output2.txt mygenelist.txt

cut

print selected parts of lines

cut -f 1 mygenelist.txt

print column 1 of mygenelist.txt

paste output2.txt mygenelist.txt

merge lines of files

Text manipulation tools

- **grep** is a command looking for lines matching a pattern in a file

i.e. All lines containing «*motorcycle*»

i.e. All lines **not** containing «*wasp*»

- can use simple patterns (i.e. a word) but also regular expressions (i.e. all words beginning with *co* and ending with *er* - computer, controller, etc.)
- A basic example:

```
man more > more_manual.txt
```

```
grep less more_manual.txt
```

Grep examples

- Select non-matching lines:

```
grep -v less_more_manual.txt
```

- Reading patterns from a file:

```
grep -f patterns.txt more_manual.txt
```

Grep examples / 2

- Counting lines corresponding to matches:

```
grep -c less more_manual.txt
```

- Ignoring case (**C** = **c**, while normally **C** <> **c**):

```
grep LiNe more_manual.txt
```

```
grep -i LiNe more_manual.txt
```

- Matching whole words only:

```
grep in more_manual.txt
```

```
grep -w in more_manual.txt
```

Grep exercise

- Search in the **awk** program manual for lines including the program name «*AWK*» and also the word «*language*»
- Save the matching lines to a file
- Count the number of matching lines
- Try to use pipes!

A solution

- Pipe-extreme solution:

man awk | **grep** AWK | **grep** language > exercise.txt

man awk | **grep** AWK | **grep -c** language

A solution

- Pipe-extreme solution:

```
man awk | grep AWK | grep language > output.txt
```

```
man awk | grep AWK | grep -c language
```

- Simpler solutions not using pipes can work and are ok as well, although they are less efficient:

```
man awk > awk_manual.txt
```

```
grep AWK awk_manual.txt > tmp.txt
```

```
grep -c language tmp.txt
```

```
grep language tmp.txt > exercise.txt
```

GTF file format

The GTF (General Transfer Format) / GFF (General Feature Format) is a text file format, tab-separated and consists of one line per feature, each containing 9 columns of data, plus optional track definition lines, and "empty" columns should be denoted with a '.'

1. **seqname** - name of the chromosome or scaffold; chromosome names can be given with or without the 'chr' prefix.
2. **source** - name of the program that generated this feature, or the data source (database or project name)
3. **feature** - feature type name, e.g. Gene, Variation, Similarity
4. **start** - Start position of the feature, with sequence numbering starting at 1.
5. **end** - End position of the feature, with sequence numbering starting at 1.
6. **score** - A floating point value.
7. **strand** - defined as + (forward) or - (reverse).
8. **frame** - One of '0', '1' or '2'. '0' indicates that the first base of the feature is the first base of a codon, '1' that the second base is the first base of a codon, and so on..
9. **attribute** - A semicolon-separated list of tag-value pairs, providing additional information about each feature.

GTF file example

chr1	HAVANA	gene	11869	14409	.	+	.	gene_id	"ENSG00000223972.5"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869"; transcript_id "ENSG00000223972.5"; transcript_id "ENST00000456328.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	transcript	11869	14409	.	+	+	gene_id	"ENSG00000223972.5"; transcript_id "ENST00000456328.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	exon	11869	12227	.	+	.	gene_id	"ENSG00000223972.5"; transcript_id "ENST00000456328.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	transcript	12010	13670	.	+	+	gene_id	"ENSG00000223972.5"; transcript_id "ENST00000450305.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	exon	12010	12057	.	+	.	gene_id	"ENSG00000223972.5"; transcript_id "ENST00000450305.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	exon	12179	12227	.	+	.	gene_id	"ENSG00000223972.5"; transcript_id "ENST00000450305.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	exon	12613	12721	.	+	.	gene_id	"ENSG00000223972.5"; transcript_id "ENST00000456328.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	exon	12613	12697	.	+	.	gene_id	"ENSG00000223972.5"; transcript_id "ENST00000450305.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	exon	12975	13052	.	+	.	gene_id	"ENSG00000223972.5"; transcript_id "ENST00000450305.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	exon	13221	14409	.	+	.	gene_id	"ENSG00000223972.5"; transcript_id "ENST00000456328.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	exon	13221	13374	.	+	.	gene_id	"ENSG00000223972.5"; transcript_id "ENST00000450305.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	exon	13453	13670	.	+	.	gene_id	"ENSG00000223972.5"; transcript_id "ENST00000450305.2"; gene_type "transcribed_unprocessed_pseudogene"; gene_name "DDX11L1"; level 2; hgnc_id "HGNC:11869";
chr1	HAVANA	gene	14404	29570	.	.	.	gene_id	"ENSG00000227232.5"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	transcript	14404	29570	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	exon	14404	14501	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	exon	15005	15038	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	exon	15796	15947	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	exon	16607	16765	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	exon	16858	17055	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	exon	17233	17368	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	ENSEMBL	gene	17369	17436	.	.	.	gene_id	"ENSG00000278267.1"; gene_type "miRNA"; gene_name "MIR6859-1"; level 3; hgnc_id "HGNC:50039";
chr1	ENSEMBL	transcript	17369	17436	.	.	.	gene_id	"ENSG00000278267.1"; transcript_id "ENST00000619216.1"; gene_type "miRNA"; gene_name "MIR6859-1"; transcript type "antisense_intronic";
chr1	ENSEMBL	exon	17369	17436	.	.	.	gene_id	"ENSG00000278267.1"; transcript_id "ENST00000619216.1"; gene_type "miRNA"; gene_name "MIR6859-1"; transcript type "antisense_intronic";
chr1	HAVANA	exon	17606	17742	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	exon	17915	18061	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	exon	18268	18366	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	exon	24738	24891	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	exon	29534	29570	.	.	.	gene_id	"ENSG00000227232.5"; transcript_id "ENST00000488147.1"; gene_type "unprocessed_pseudogene"; gene_name "WASH7P"; level 2; hgnc_id "HGNC:38034"; havan
chr1	HAVANA	gene	29554	31109	.	+	.	gene_id	"ENSG00000243485.5"; gene_type "lncRNA"; gene_name "MIR1302-2HG"; level 2; hgnc_id "HGNC:52482"; tag "lncRNA host"
chr1									

Let's practice!

- Download the **hs_annotation.gtf** file from moodle
- Move it to your *GTEercises* directory
- Check where you are:

pwd

- Move in your directory

cd mywork/GTEercises

Let's practice!

1. Count how many lines are present in `hs_annotation.gtf`

Let's practice!

1. Count how many lines are present in `hs_annotation.gtf`

```
wc -l hs_annotation.gtf
```

Let's practice!

1. Count how many lines are present in `hs_annotation.gtf`

`wc -l hs_annotation.gtf`

2. Count how many genes are present in `hs_annotation.gtf`

Let's practice!

1. Count how many lines are present in `hs_annotation.gtf`

```
wc -l hs_annotation.gtf
```

2. Count how many genes are present in `hs_annotation.gtf`

```
cut -f 3 hs_annotation.gtf | grep -c gene  
cut -f 3 hs_annotation.gtf | grep gene | wc -l  
grep -w gene hs_annotation.gtf | wc -l
```

Let's practice!

1. Count how many lines are present in `hs_annotation.gtf`

```
wc -l hs_annotation.gtf
```

2. Count how many genes are present in `hs_annotation.gtf`

```
cut -f 3 hs_annotation.gtf | grep -c gene  
cut -f 3 hs_annotation.gtf | grep gene | wc -l  
grep -w gene hs_annotation.gtf | wc -l
```

3. Count how many “protein_coding” genes are present in `hs_annotation.gtf`

Let's practice!

1. Count how many lines are present in `hs_annotation.gtf`

```
wc -l hs_annotation.gtf
```

2. Count how many genes are present in `hs_annotation.gtf`

```
cut -f 3 hs_annotation.gtf | grep -c gene  
cut -f 3 hs_annotation.gtf | grep gene | wc -l  
grep -w gene hs_annotation.gtf | wc -l
```

3. Count how many “protein_coding” genes are present in `hs_annotation.gtf`

```
grep -w gene hs_annotation.gtf | grep -c protein_coding  
grep -w gene hs_annotation.gtf | grep protein_coding | wc -l
```

```
grep -w gene hs_annotation.gtf > hs_annotation_genes.gtf  
grep protein_coding hs_annotation_genes.gtf | wc -l
```

Exercises

1. Count how many genes of type “lncRNA” are present in `hs_annotation.gtf`, get their gene names and sort them alphabetically
2. Count how many gene types are present in `hs_annotation.gtf`



Questions ?

The meaning of life **./** («dot-slash»)

- Builtin commands VS custom commands

less output.txt

man less

./myscript.sh

./install.sh

. -> refers to the current directory

/ -> directory path separator

- Details here: **http://www.linfo.org/dot_slash.html**

Need Power ?

- Some (*quite a lot, indeed...*) actions can not be run by the normal user
- Needs super-user (SU) status to install specific tools or to change system settings
- If you know the SU password, you can gain temporary SU privileges (*dangerous!*)
- Just type: **sudo** «*command to execute*»

