

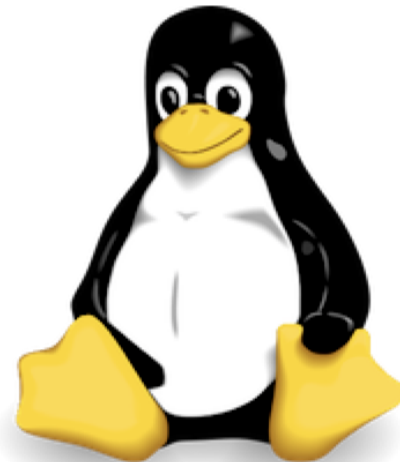
# TRANSCRIPTOMICS

## Introduction to Unix

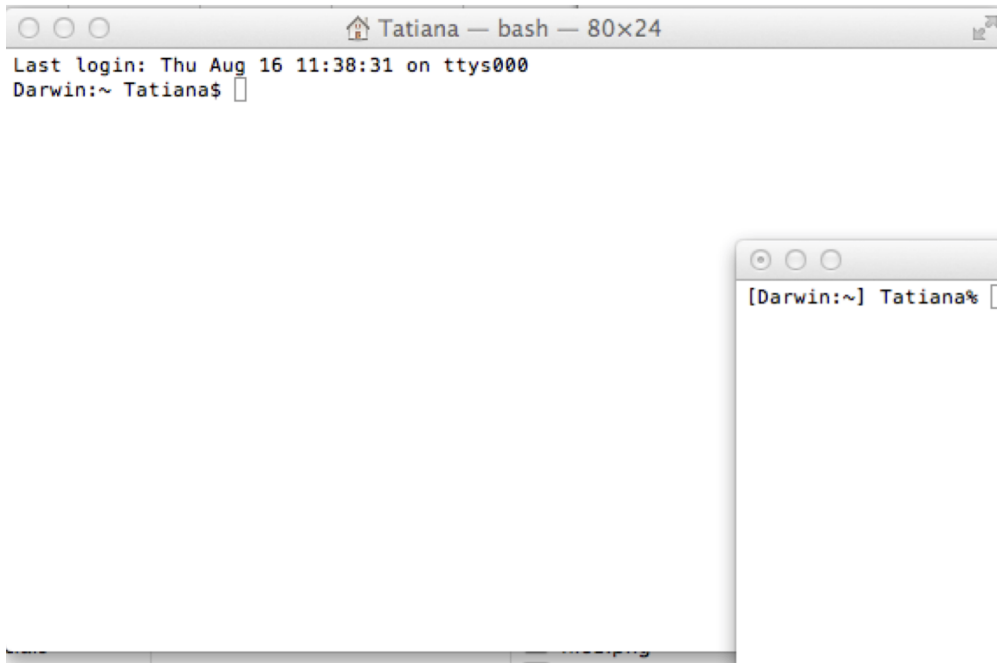
Day 01

<https://ttdorres.github.io/transcriptomics/>

# OPERATING SYSTEM



# OPERATING SYSTEM: UNIX SHELL



```
○ ○ ○ Tatiana — bash — 80x24
Last login: Thu Aug 16 11:38:31 on ttys000
Darwin:~ Tatiana$
```




```
○ ○ ○ Tatiana — csh — 80x24
[Darwin:~] Tatiana%
```

# UNIX

## Common Commands

### 1. `ls` Command (list): listing files and directories

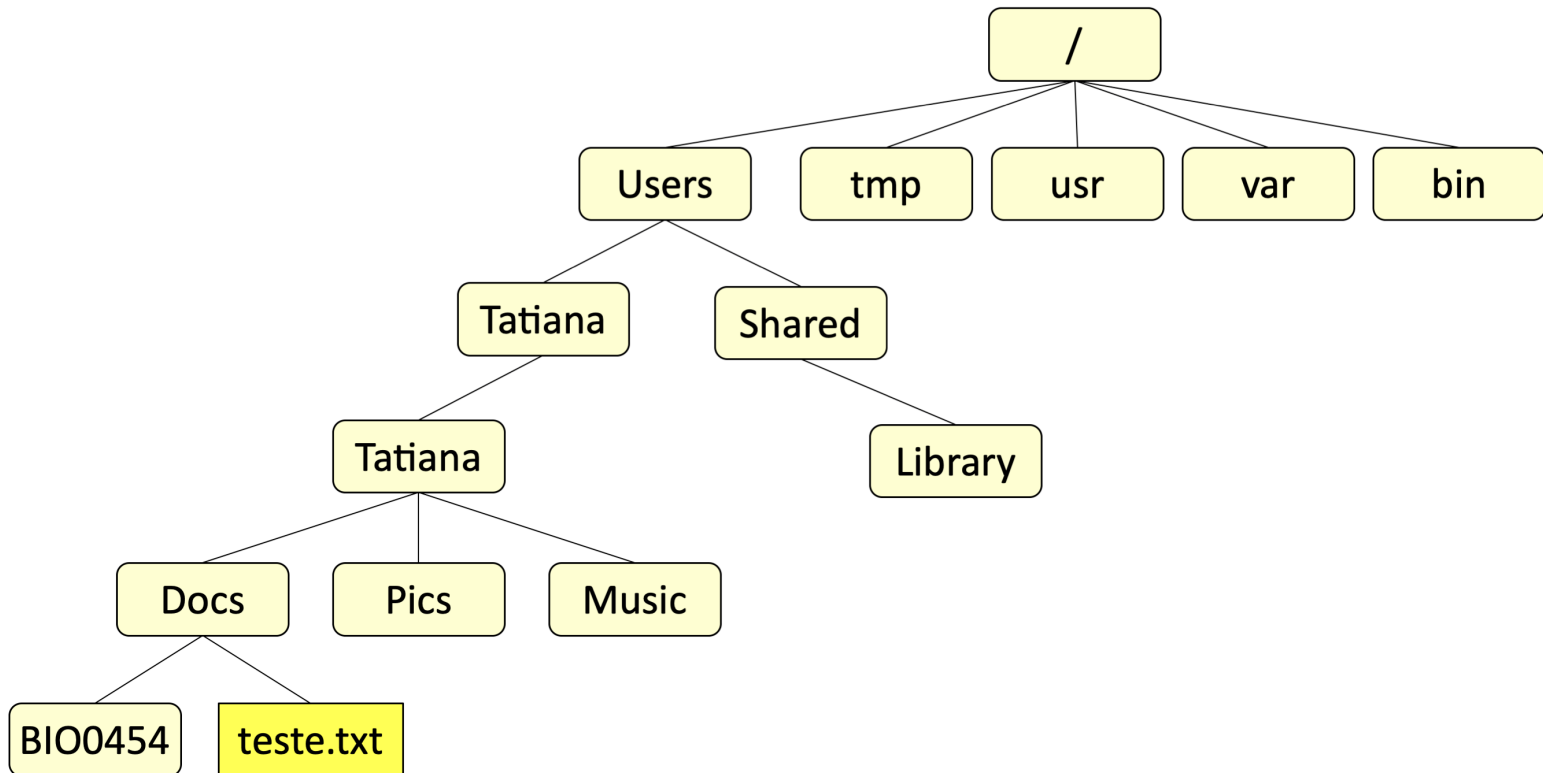
```
ls  
ls -a  
ls -l  
ls -la
```

 *man* (manual)

# UNIX

## Common Commands

### 2. Navigating directories



# UNIX

## Common Commands

### 2. Navigating directories

#### a. Check the current directory

#### b. Go to the root

#### c. Return to the home directory

# UNIX

## Common Commands

### 2. Navigating directories

a. Check the current directory: `pwd` (print working directory)

```
pwd
```

b. Go to the root

c. Return to the home directory

# UNIX

## Common Commands

### 2. Navigating directories

a. Check the current directory: `pwd` (print working directory)

```
pwd
```

b. Go to the root: `cd` (change directory)

```
cd /
```

c. Return to the home directory



# UNIX

## Common Commands

### 2. Navigating directories

a. Check the current directory: `pwd` (print working directory)

```
pwd
```

b. Go to the root: `cd` (change directory)

```
cd /
```

c. Return to the home directory: `cd`

```
cd ~
```

# UNIX

## Common Commands

### PREPARATION

On the course website, download the following files into the "home" folder:

- Fasta file: dmel-gene-r5.45.fasta
- Fasta file: metagenomics\_coral.fasta
- Fastq file: chom.txt
- File: confidential.tar.gz

<https://tttorres.github.io/transcriptomics/>

# UNIX

## Common Commands

### 3. Creating and modifying files and directories

- `mkdir` (make directory)
- `cp` (copy)
- `mv` (move)
- `rm` (remove; BE VERY CAREFUL!!!)

# UNIX

## Common Commands

### 3. Creating and modifying files and directories

a. Create the folder `myseq` in home ( `mkdir` )

b. Move the file `dme1-gene-r5.45.fasta` to `myseq` ( `mv` )

c. Go to the folder `myseq` ( `cd` )

# UNIX

## Common Commands

### 3. Creating and modifying files and directories

a. Create the folder `myseq` in home ( `mkdir` )

```
mkdir myseq
```

b. Move the file `dme1-gene-r5.45.fasta` to `myseq` ( `mv` )

c. Go to the folder `myseq` ( `cd` )

# UNIX

## Common Commands

### 3. Creating and modifying files and directories

a. Create the folder `myseq` in home ( `mkdir` )

```
mkdir myseq
```

b. Move the file `dme1-gene-r5.45.fasta` to `myseq` ( `mv` )

```
mv /mnt/c/Users/Aluno/dme1-gene-r5.45.fasta ~/myseq/
```

c. Go to the folder `myseq` ( `cd` )

# UNIX

## Common Commands

### 3. Creating and modifying files and directories

a. Create the folder `myseq` in home ( `mkdir` )

```
mkdir myseq
```

b. Move the file `dme1-gene-r5.45.fasta` to `myseq` ( `mv` )

```
mv /mnt/c/Users/Aluno/dme1-gene-r5.45.fasta ~/myseq/
```

c. Go to the folder `myseq` ( `cd` )

```
cd ~/myseq/
```

# UNIX

## Common Commands

### 3. Creating and modifying files and directories

d. Copy the file with a new name: `novo.fasta`

e. Delete the file `novo.fasta`



# UNIX

## Common Commands

### 3. Creating and modifying files and directories

d. Copy the file with a new name: `novo.fasta`

```
cp dmel-gene-r5.45.fasta novo.fasta
```

e. Delete the file `novo.fasta`

# UNIX

## Common Commands

### 3. Creating and modifying files and directories

d. Copy the file with a new name: `novo.fasta`

```
cp dmel-gene-r5.45.fasta novo.fasta
```

e. Delete the file `novo.fasta`

```
rm novo.fasta
```

# UNIX

## Common Commands

### 3. Creating and modifying files and directories

d. Move `metagenomics_coral.fasta` to `introprog` ( `mv` )

e. Move the file `chom.txt` to `introprog` ( `mv` )

f. Move the file `confidencial.tar.gz` to `introprog` ( `mv` )

# UNIX

## Common Commands

### 3. Creating and modifying files and directories

d. Move `metagenomics_coral.fasta` to `introprog` ( `mv` )

```
mv /mnt/c/Users/Aluno/meta_coral.fasta ~/introprog/
```

e. Move the file `chom.txt` to `introprog` ( `mv` )

```
mv /mnt/c/Users/Aluno/chom.txt ~/introprog/
```

f. Move the file `confidencial.tar.gz` to `introprog` ( `mv` )

```
mv /mnt/c/Users/Aluno/confidencial.tar.gz ~/introprog/
```

# UNIX

## Common Commands

### 4. Viewing files (and information)

- `head`
- `tail`
- `wc` (word count)
- `grep` (globally search a regular expression and print)

# UNIX

## Common Commands

### 4. Viewing files (and information)

**head**

head -number of lines input

```
head -10 metagenomics_coral.fasta
```

# UNIX

## Common Commands

### 4. Viewing files (and information)

**tail**

tail -number of lines input

```
tail -10 metagenomics_coral.fasta
```

# UNIX

## Common Commands

### 4. Viewing files (and information)

```
md5 / md5sum
```

```
md5 input
```

```
md5 metagenomics_coral.fasta
```



# UNIX

## Common Commands

### 4. Viewing files (and information)

`wc` #lines, words, and bytes

`wc` input

```
wc metagenomics_coral.fasta
```

# UNIX

## Common Commands

### 4. Viewing files (and information)

#### a. View the first lines of a file

#### b. View the first 20 lines of a file

#### c. View the last lines of a file

# UNIX

## Common Commands

### 4. Viewing files (and information)

#### a. View the first lines of a file

```
head dmel-gene-r5.45.fasta
```

#### b. View the first 20 lines of a file

#### c. View the last lines of a file

# UNIX

## Common Commands

### 4. Viewing files (and information)

#### a. View the first lines of a file

```
head dmel-gene-r5.45.fasta
```

#### b. View the first 20 lines of a file

```
head -20 dmel-gene-r5.45.fasta
```

#### c. View the last lines of a file

# UNIX

## Common Commands

### 4. Viewing files (and information)

#### a. View the first lines of a file

```
head dmel-gene-r5.45.fasta
```

#### b. View the first 20 lines of a file

```
head -20 dmel-gene-r5.45.fasta
```

#### c. View the last lines of a file

```
tail dmel-gene-r5.45.fasta
```

# UNIX

## Common Commands

### 4. Viewing files (and information)

**grep** #pattern search

(globally search a regular expression and print)

```
grep ">" metagenomics_coral.fasta
```

# UNIX

## Common Commands

### 4. Viewing files (and information)

**grep** #pattern search

```
grep "A" metagenomics_coral.fasta
```

# UNIX

## Common Commands

### 4. Viewing files (and information)

**grep** #pattern search

```
grep "^A" metagenomics_coral.fasta
```



# UNIX

## Common Commands

### 4. Viewing files (and information)

**grep** #pattern search

```
grep -c "^A" metagenomics_coral.fasta
```

# UNIX

## Common Commands

### 4. Viewing files (and information)

**grep** #pattern search

```
grep -n "^A" metagenomics_coral.fasta
```

# UNIX

## Common Commands

### GREP: applications

a. Count the number of sequences in a file

b. Number of sequences with the barcode "ACACGACGACT"

c. Number of sequences with the barcode "ACACGTAGTAT"

# UNIX

## Common Commands

### GREP: applications

a. Count the number of sequences in a file

```
grep -c ">" ~/introprog/metagenomics_coral.fasta
```

b. Number of sequences with the barcode "ACACGACGACT"

c. Number of sequences with the barcode "ACACGTAGTAT"

# UNIX

## Common Commands

### GREP: applications

#### a. Count the number of sequences in the file

```
grep -c ">" ~/introprog/metagenomics_coral.fasta
```

#### b. Number of sequences with the barcode "ACACGACGACT"

```
grep -c "^ACACGACGACT" ~/introprog/metagenomics_coral.fasta
```

#### c. Number of sequences with the barcode "ACACGTAGTAT"

# UNIX

## Common Commands

### GREP: applications

#### a. Count the number of sequences in the file

```
grep -c ">" ~/introprog/metagenomics_coral.fasta
```

#### b. Number of sequences with the barcode "ACACGACGACT"

```
grep -c "^ACACGACGACT" ~/introprog/metagenomics_coral.fasta
```

#### c. Number of sequences with the barcode "ACACGTAGTAT"

```
grep -c "^ACACGTAGTAT" ~/introprog/metagenomics_coral.fasta
```

# UNIX

## Common Commands

### 5. Redirecting output (and information)

- `>`
- `>>`

```
grep "^>" input >output
```

```
grep "^>" metagenomics_coral.fasta >tmp.fasta
```

# UNIX

## Common Commands

### 5. Redirecting output (and information)

- `>`
- `>>`

```
grep "^>" input >output
```

```
grep "^A" metagenomics_coral.fasta >tmp.fasta
```



# UNIX

## Most Used Commands

### 5. Redirecting Output (and Information)

- `>`
- `>>`

```
grep "^>" input >output
```

```
grep "^>" metagenomics_coral.fasta >>tmp.fasta
```

# UNIX

## Most Used Commands

### 6. File Editing

- `tr` (transliterate)

#### a. Convert uppercase to lowercase

```
tr [A-Z] [a-z] <metagenomics_coral.fasta >tmp.fasta
```

#### b. Generate the complement of the sequence

# UNIX

## Most Used Commands

### 6. File Editing

- `tr` (transliterate)

#### a. Convert uppercase to lowercase

```
tr [A-Z] [a-z] <metagenomics_coral.fasta >tmp.fasta
```

#### b. Generate the complement of the sequence

```
tr [ACGT] [tgca] <metagenomics_coral.fasta >tmp.fasta
```

# UNIX

## Most Used Commands

### 6. File Editing

- `sed` (stream **e**ditor)

1<sup>st</sup> application:

`sed s/old_text/new_text/ <input >output`

```
sed s/length/comprimento/ <meta_coral.fasta >tmp.fasta
```

# UNIX

## Most Used Commands

### 6. File Editing

- `sed` (stream **e**ditor)

**1<sup>st</sup> application:**

`sed s/old_text/new_text/ <input >output`

```
sed s/old_text/new_text/ <input >output
```

FLAGS: "N" replaces up to the N-th occurrence

"g" replaces all occurrences

# UNIX

## Most Used Commands

### 6. File Editing

- `sed` (stream **e**ditor)

**2<sup>nd</sup> application:**

`sed y/characters/characters/ <input >output`

```
sed y/ACGT/tgca/ <metagenomics_coral.fasta >tmp.fasta
```

# UNIX

## Most Used Commands

### 6. File Editing

- `sed` (stream **e**ditor)

3<sup>rd</sup> application:

`sed G <input >output`

```
sed G <metagenomics_coral.fasta >tmp.fasta
```

# UNIX

## Most Used Commands

### 6. File Editing

- `sed` (stream **e**ditor)

4<sup>th</sup> application:

`sed = <input >output`

```
sed = <metagenomics_coral.fasta >tmp.fasta
```



# UNIX

## Most Used Commands

### 6. File Editing

- `sed` (stream **e**ditor)

5<sup>th</sup> application:

`sed /pattern/d <input >output`

```
sed /length/d <metagenomics_coral.fasta >tmp.fasta
```

# UNIX

## Most Used Commands

### 7. Pipelines

- `|` (the output of one command is used as input by another)

command1 parameters | command2 parameters

```
echo 5+6 | bc
```

```
grep ">" metagenomics_coral.fasta | wc -l
```

```
tr [ACGT] [tgca] <metagenomics_coral.fasta | sed  
s/\>/\>COMP\_/_/ >tmp.fasta
```

# UNIX

## Most Used Commands

### 8. Permissions

```
tar -xvzf confidential.tar.gz
```

```
head confidential.txt
```

# UNIX

## Most Used Commands

### 8. Permissions

```
Darwin:Student Tatiana$ ls -la
total 5088
drwxr-xr-x   5 Tatiana  staff   170 Aug 22 14:02 .
drwxr-xr-x  49 Tatiana  staff  1666 Aug 22 14:02 ..
-rw-r--r--   3 Tatiana  staff 2593130 Aug 20 20:20 meta_coral.fasta
-----   1 Tatiana  staff    8 Aug 22 11:38 test1.doc
-rw-r--r--@  1 Tatiana  staff   152 Aug 22 12:18 test1.tar.gz
```

# UNIX

## Most Used Commands

### 8. Permissions

```
Darwin:Aluno Tatiana$ ls -la
total 5088
drwxr-xr-x   5 Tatiana  staff    170 22 Ago 14:02 .
drwxr-xr-x  49 Tatiana  staff   1666 22 Ago 14:02 ..
-rw-r--r--   3 Tatiana  staff  2593130 20 Ago 20:20 meta_coral.fasta
-----    1 Tatiana  staff     8 22 Ago 11:38 prova1.doc
-rw-r--r--@  1 Tatiana  staff   152 22 Ago 12:18 prova1.tar.gz
```

# UNIX

## Most Used Commands

### 8. Permissions

```
Darwin:Aluno Tatiana$ ls -la
total 5088
drwxr-xr-x  5 Tatiana  staff   170 22 Ago 14:02 .
drwxr-xr-x 49 Tatiana  staff  1666 22 Ago 14:02 ..
-rw-r--r--  3 Tatiana  staff 2593130 20 Ago 20:20 meta_coral.fasta
-----  1 Tatiana  staff    8 22 Ago 11:38 prova1.doc
-rw-r--r--@ 1 Tatiana  staff  152 22 Ago 12:18 prova1.tar.gz
```

# UNIX

## Most Used Commands

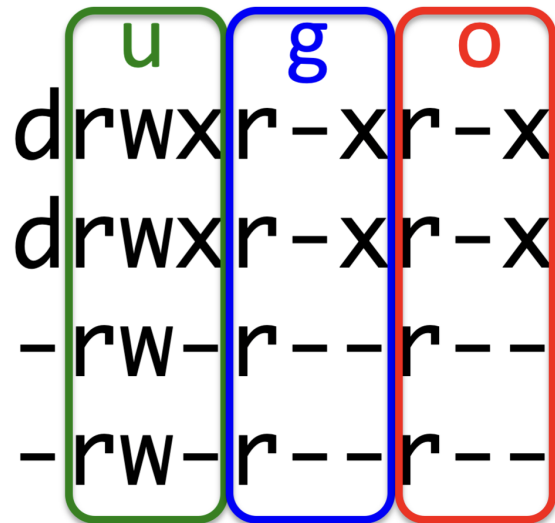
### 8. Permissions

```
drwxr-xr-x
drwxr-xr-x
-rw-r--r--
-----
-rw-r--r--
```

# UNIX

## Most Used Commands

### 8. Permissions



The diagram illustrates the structure of UNIX permissions. It consists of four rows of text: 'drwxr-xr-x', 'drwxr-xr-x', '-rw-r--r--', and '-rw-r--r--'. Above these rows are three vertical colored boxes: a green box on the left containing the letter 'u', a blue box in the middle containing the letter 'g', and a red box on the right containing the letter 'o'. The green box encloses the first character of each row ('d', 'd', '-', '-'). The blue box encloses the next three characters of each row ('r', 'w', 'x', 'r', 'w', 'x', 'r', 'w', 'x', 'r'). The red box encloses the final three characters of each row ('r', 'x', 'r', 'x', 'r', 'x', 'r', 'x', 'r', 'x').

u	g	o
d	rwxr	-xr-x
d	rwxr	-xr-x
-	rw-r	--r--
-	rw-r	--r--

read, write, execute



# UNIX

## Most Used Commands

### 8. Changing Permissions

- `chmod` (**change mode**)

FIRST FORM (symbolic):

Operator	Action
+	Add permission
-	Remove permission
=	Set permission

# UNIX

## Most Used Commands

### 8. Changing Permissions

- chmod (**change mode**)

FIRST FORM (symbolic):

```
ls -l confidential.txt
```

# UNIX

## Most Used Commands

### 8. Changing Permissions

- chmod (**change mode**)

FIRST FORM (symbolic):

```
ls -l confidential.txt
----- 1 Tatiana  staff  8 Aug 22  2012 confidential
```

# UNIX

## Most Used Commands

### 8. Changing Permissions

- chmod (**change mode**)

FIRST FORM (symbolic):

```
ls -l confidential.txt
----- 1 Tatiana  staff  8 Aug 22  2012 confidential
chmod o+wr confidential.txt
```

# UNIX

## Most Used Commands

### 8. Changing Permissions

- chmod (**change mode**)

FIRST FORM (symbolic):

```
ls -l confidential.txt
----- 1 Tatiana  staff  8 Aug 22  2012 confidential
chmod o+wr confidential.txt
ls -l confidential.txt
```

# UNIX

## Most Used Commands

### 8. Changing Permissions

- chmod (**change mode**)

FIRST FORM (symbolic):

```
ls -l confidential.txt
----- 1 Tatiana  staff  8 Aug 22  2012 confidential
chmod o+wr confidential.txt
ls -l confidential.txt
-----rw- 1 Tatiana  staff  8 Aug 22  2012 confidential
```

# UNIX

## Most Used Commands

### 8. Changing Permissions

- chmod (**change mode**)

FIRST FORM (symbolic):

```
chmod u+x confidential.txt  
ls -l confidential.txt
```

# UNIX

## Most Used Commands

### 8. Changing Permissions

- chmod (**change mode**)

FIRST FORM (symbolic):

```
chmod u+x confidential.txt
ls -l confidential.txt
---x---rw-  1 Tatiana  staff   8 Aug 22  2012 confidential
```



# UNIX

## Most Used Commands

### 8. Changing Permissions

- chmod (**change mode**)

FIRST FORM (symbolic):

```
chmod g=rx confidential.txt  
ls -l confidential.txt
```

# UNIX

## Most Used Commands

### 8. Changing Permissions

- chmod (**change mode**)

FIRST FORM (symbolic):

```
chmod g=rx confidential.txt
ls -l confidential.txt
---xr-xrw-  1 Tatiana  staff   8 Aug 22  2012 confidential
```

# UNIX

## Most Used Commands

### 8. Permissions

“-rw-r--r--” é equivalente a “644”

$r = 4, w = 2, x = 1$

	user	group	other
	rw-	r--	r--
read	4	4	4
write	2	0	0
execute	0	0	0
<hr/>			
soma	6	4	4

# UNIX

## Most Used Commands

### 8. Changing Permissions

- `chmod` (**change mode**)

SECOND FORM:

```
chmod 666 confidential.doc  
ls -l confidential.doc
```

# UNIX

## Most Used Commands

### 8. Changing Permissions

- chmod (change mode)

SECOND FORM:

```
chmod 666 confidential.doc
ls -l confidential.doc
-rw-rw-rw-@ 1 Tatiana  staff  8 Aug 22  2012 confidential
```

# UNIX

## Most Used Commands

### 8. Changing Permissions

- chmod (change mode)

SECOND FORM:

```
chmod 000 confidential.doc
ls -l confidential.doc
----- 1 Tatiana  staff  8 Aug 22  2012 confidential
```

# UNIX

## Most Used Commands

### 9. Superuser Privileges

- sudo (super user do)

sudo command

```
sudo head confidential.doc  
Password:
```