



GenEpi-BioTrain – Virtual Training 9 & 10

# Unix for beginners: Combining Files

August 21<sup>st</sup> 2024

## Additional Information



- Use the **Handout!** Everything we are presenting is already in the Handout.
- If you are a mac user and had trouble using `wget` and `readlink` yesterday, read the **macOS addendum** on EVA. Here you can find installation guides and alternative commands.

# Learning goals



Today, we will learn how to:

- Combine files
- Writing and appending to files
- Searching within files and folders
- Counting words/lines
- Redirecting output from one program to another using |
- Compressing and decompressing files
- Creating empty files



# Objectives

Specific objectives of this session:

- Redirect & Append Output to File
- Combining Files





# Objectives



Specific objectives of this session:

- **Redirect & Append Output to File**
- Combining Files

# Redirecting

command > file



Direct the output of a command to a file

ls > contentlist.txt



# Appending

command >> file



Append the output of a command to a file

`ls >> contentlist.txt`





# Objectives

Specific objectives of this session:

- Redirect & Append Output to File
- **Combining Files**



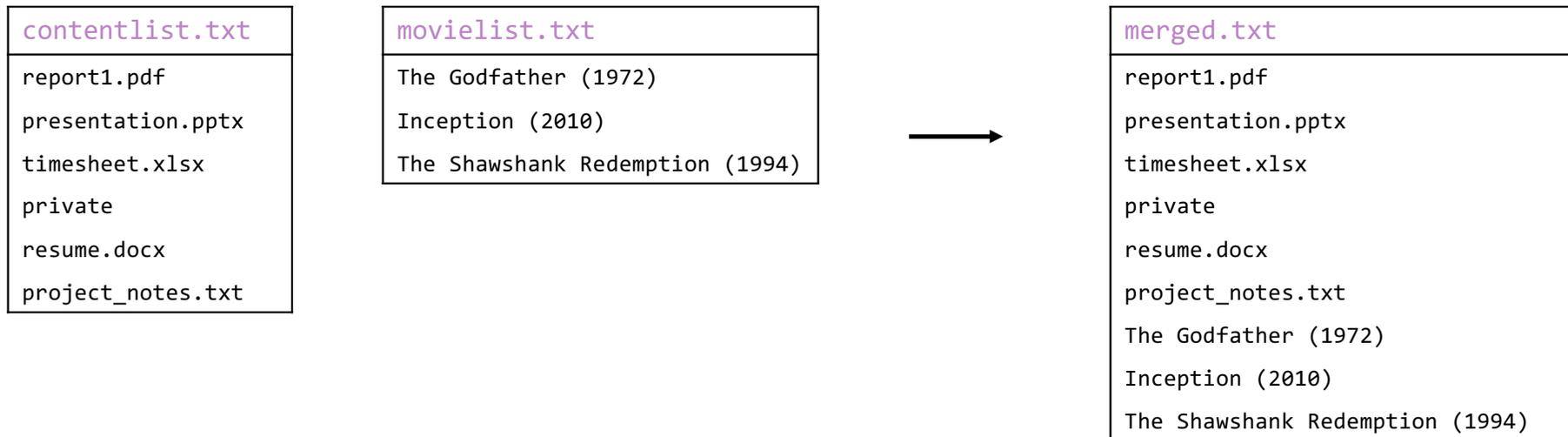
# Combining Files

```
cat file1 file2 > file3
```



concatenate multiple files into one

```
cat contentlist.txt movielist.txt > merged.txt
```



# Exploration

Exercise 1

Checkpoint: 3

Have fun! 😊



GenEpi-BioTrain – Virtual Training 9 & 10

# Unix for beginners: Searching within Files

August 21<sup>st</sup> 2024



# Objectives

Specific objectives of this session:

- `grep`: Searching within Files
- Introduction to FASTA Files



# Objectives

Specific objectives of this session:

- **grep: Searching within Files**
- Introduction to FASTA Files



# Searching

`grep [options] "pattern" file`



Searching text or files for lines that match a specified **pattern**

`grep "The" merged.txt`

merged.txt
report1.pdf
presentation.pptx
timesheet.xlsx
private
resume.docx
project_notes.txt
The Godfather (1972)
Inception (2010)
The Shawshank Redemption (1994)



The Godfather (1972)  
The Shawshank Redemption (1994)

# Searching

```
grep [options] "pattern" file
```



Searching text or files for lines that match a specified **pattern**

```
grep "the" merged.txt
```

merged.txt
report1.pdf
presentation.pptx
timesheet.xlsx
private
resume.docx
project_notes.txt
The Godfather (1972)
Inception (2010)
The Shawshank Redemption (1994)



# Searching

```
grep [options] "pattern" file
```



Searching text or files for lines that match a specified **pattern**

```
grep -i "the" merged.txt
```

merged.txt
report1.pdf
presentation.pptx
timesheet.xlsx
private
resume.docx
project_notes.txt
The Godfather (1972)
Inception (2010)
The Shawshank Redemption (1994)



The Godfather (1972)  
The Shawshank Redemption (1994)

# Searching

`grep [options] "pattern" file`



Searching text or files for lines that match a specified **pattern**

`grep -in "the" merged.txt`

<code>merged.txt</code>
report1.pdf
presentation.pptx
timesheet.xlsx
private
resume.docx
project_notes.txt
The Godfather (1972)
Inception (2010)
The Shawshank Redemption (1994)



7:The Godfather (1972)  
9:The Shawshank Redemption (1994)

# Searching

```
grep [options] "pattern" file
```



Searching text or files for lines that match a specified **pattern**

```
grep -io "the" merged.txt
```

merged.txt

```
report1.pdf  
presentation.pptx  
timesheet.xlsx  
private  
resume.docx  
project_notes.txt  
The Godfather (1972)  
Inception (2010)  
The Shawshank Redemption (1994)
```



```
The  
The
```

# Objectives

Specific objectives of this session:

- grep: Searching within Files
- **Introducing FASTA Files**



# FASTA File

A FASTA file is a text format for storing biological sequences like DNA, RNA, or proteins.

example.fasta

```
>sequence_name1 [description]
ATGCGTACGTAGCTAGCCGTAGCTAGCTAGTACG
>sequence_name2 [description]
TTGCACATAAATGTTGTCTATCTCTAATGT
```

← **Header:** Sequence name and optional description. Always starts with ">"

← **Sequence:** Nucleotide or protein sequence

# Exploration

Exercise 2

*Checkpoint: 4*

Have fun! 😊

GenEpi-BioTrain – Virtual Training 9 & 10

# Unix for beginners: Redirecting output

August 21<sup>st</sup> 2024



# Objectives

Specific objectives of this session:

- Counting
- Redirecting Output to Command



# Objectives

Specific objectives of this session:

- **Counting**
- Redirecting Output to Command

# Word count

`wc [options] [file]`



Counts the number of lines, words, and characters in a file or input

`wc contentlist.txt`

```
contentlist.txt
report1.pdf
presentation.pptx
timesheet.xlsx
private
resume.docx
project_notes.txt
The Godfather (1972)
Inception (2010)
The Shawshank Redemption (1994)
```



9

16

157

contentlist.txt

# Word count

`wc [options] [file]`



Counts the number of lines, words, and characters in a file or input

`wc contentlist.txt`

```
contentlist.txt
report1.pdf
presentation.pptx
timesheet.xlsx
private
resume.docx
project_notes.txt
The Godfather (1972)
Inception (2010)
The Shawshank Redemption (1994)
```



Lines	Words	Characters	File name
9	16	157	contentlist.txt

# Word count

`wc [options] [file]`



Counts the number of lines, words, and characters in a file or input

`wc -l contentlist.txt`

```
contentlist.txt
report1.pdf
presentation.pptx
timesheet.xlsx
private
resume.docx
project_notes.txt
The Godfather (1972)
Inception (2010)
The Shawshank Redemption (1994)
```



Lines	File name
9	contentlist.txt

# Word count

`wc [options] [file]`



Counts the number of lines, words, and characters in a file or input

`wc -c contentlist.txt`

```
contentlist.txt
report1.pdf
presentation.pptx
timesheet.xlsx
private
resume.docx
project_notes.txt
The Godfather (1972)
Inception (2010)
The Shawshank Redemption (1994)
```



Characters    File name  
157            contentlist.txt

# Objectives



Specific objectives of this session:

- Counting
- **Redirecting Output to Command**

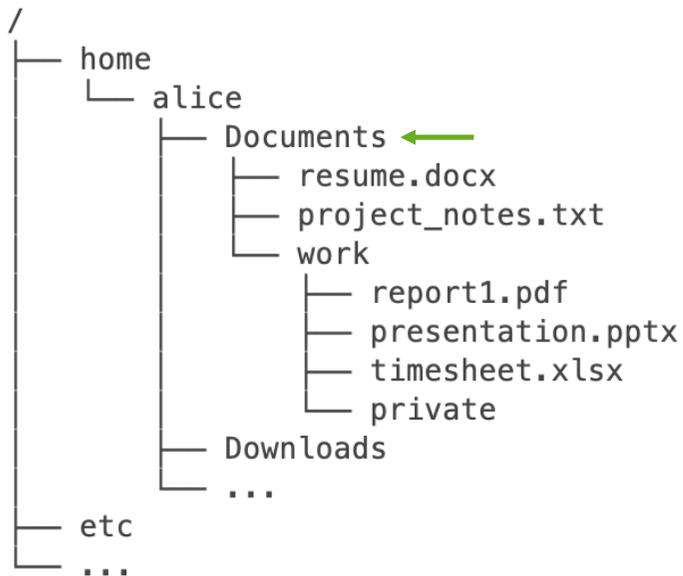
# Pipe

command | command



Takes the output of one command and use it as the input for another command

```
ls -l | grep "Apr"
```



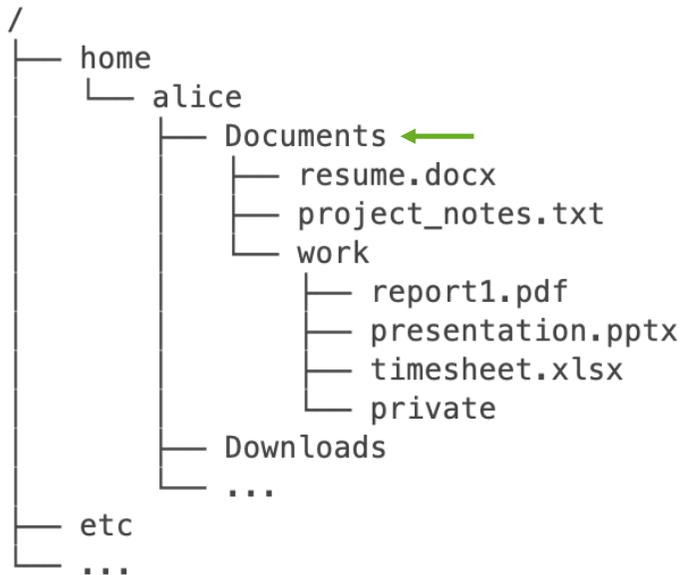
# Pipe

command | command



Takes the output of one command and use it as the input for another command

```
ls -l | grep "Apr"
```



```
-rw-r--r-- 1 alice 53579 May 13 15:22 resume.docx
-rw-r--r-- 1 alice 157017 Apr 6 07:27 project_notes.txt
drwxr-xr-x 1 alice 736 Apr 23 09:02 work
```

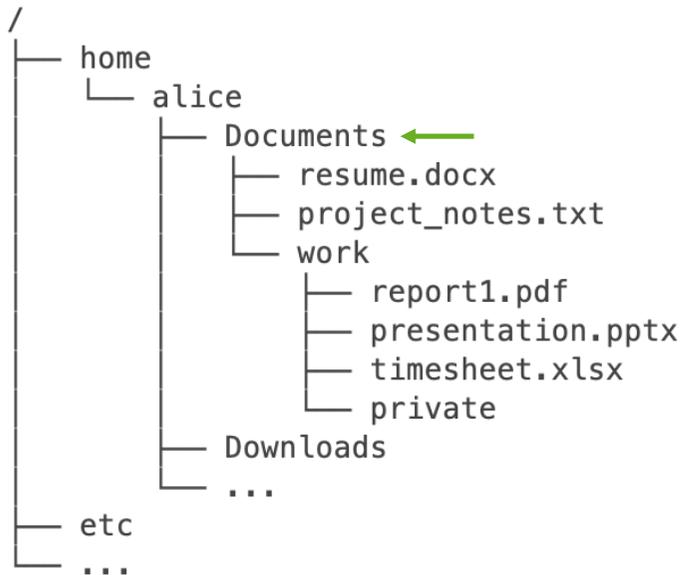
# Pipe

command | command



Takes the output of one command and use it as the input for another command

```
ls -l | grep "Apr"
```



```
-rw-r--r-- 1 alice 53579 May 13 15:22 resume.docx
-rw-r--r-- 1 alice 157017 Apr 6 07:27 project_notes.txt
drwxr-xr-x 1 alice 736 Apr 23 09:02 work
```



```
-rw-r--r-- 1 alice 157017 Apr 6 07:27 project_notes.txt
drwxr-xr-x 1 alice 736 Apr 23 09:02 work
```

# Exploration

Exercise 3

*Checkpoint: 4*

Have fun! 😊



GenEpi-BioTrain – Virtual Training 9 & 10

# Unix for beginners: Putting it all together

August 21<sup>st</sup> 2024



# Objectives

Specific objectives of this session:

- Compressing and Decompressing Files



# Compressing

`tar [options] file target`



Compress `directory` to `zip-file`

```
tar -czvf work.tar.gz ~/Documents/work/
```

Option	Description
-c	<b>C</b> reate a new archive
-x	<b>E</b> xtract files from the archive
-z	Compress the archive using <b>gzip</b>
-v	<b>V</b> erbose list the files being processed
-f	Specify the name of the archive <b>file</b>
-h	Follow symbolic links and include the actual files they point to.

# Decompressing `tar [options] file`



Decompress `zip-file`

```
tar -xzvf work.tar.gz
```

Option	Description
<code>-c</code>	<b>C</b> reate a new archive
<code>-x</code>	<b>E</b> xtract files from the archive
<code>-z</code>	Compress the archive using <b>gzip</b>
<code>-v</code>	<b>V</b> erbose list the files being processed
<code>-f</code>	Specify the name of the archive <b>file</b>
<code>-h</code>	Follow symbolic links and include the actual files they point to.

# Exploration

Exercise 4

*Checkpoint: 4*

Have fun! 😊



GenEpi-BioTrain – Virtual Training 9 & 10

# Unix for beginners: Wrapping up

August 21<sup>st</sup> 2024



# Objectives

Specific objectives of this session:

- Creating files 😊 easy – you are experts now!



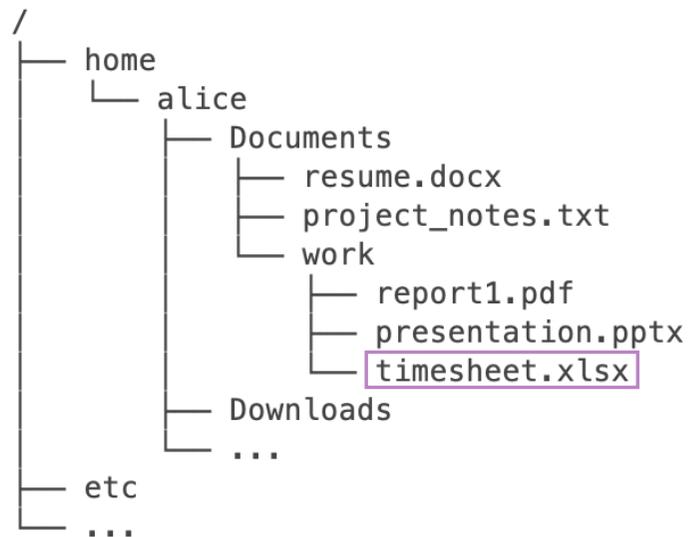
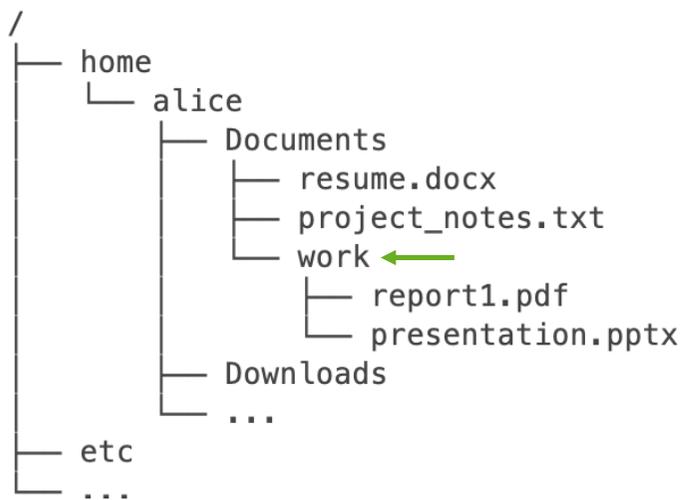
# Create File

`touch [options] file`



Create new empty file

`touch timesheet.xlsx`



# Exploration

Exercise 5

*Checkpoint: 5*

Have fun! 😊

We will meet up at 13:55

## Rounding up – Day 2



Today, we learned how to:

- Combining files
- Writing and appending to files
- Searching within files and folders
- Counting words/lines
- Redirecting output from one program to another using |
- Compressing and decompressing files
- Creating empty files

Thanks for coming  
Great job! 😊

Tomorrow we will try out the Conda ecosystem  
and how to manage different environments