Introduction to UNIX

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22.9. 2016

Sequencing reads of 15 genomes

$\approx$ 1GB of plain text data / species

$\approx$ 640938 of pages

Why UNIX?

How to check a file??

Notepad?

not well suited for big files

Office?

Microsoft® Office™

Use at least read-only mode

Gene name errors are widespread in the scientific literature

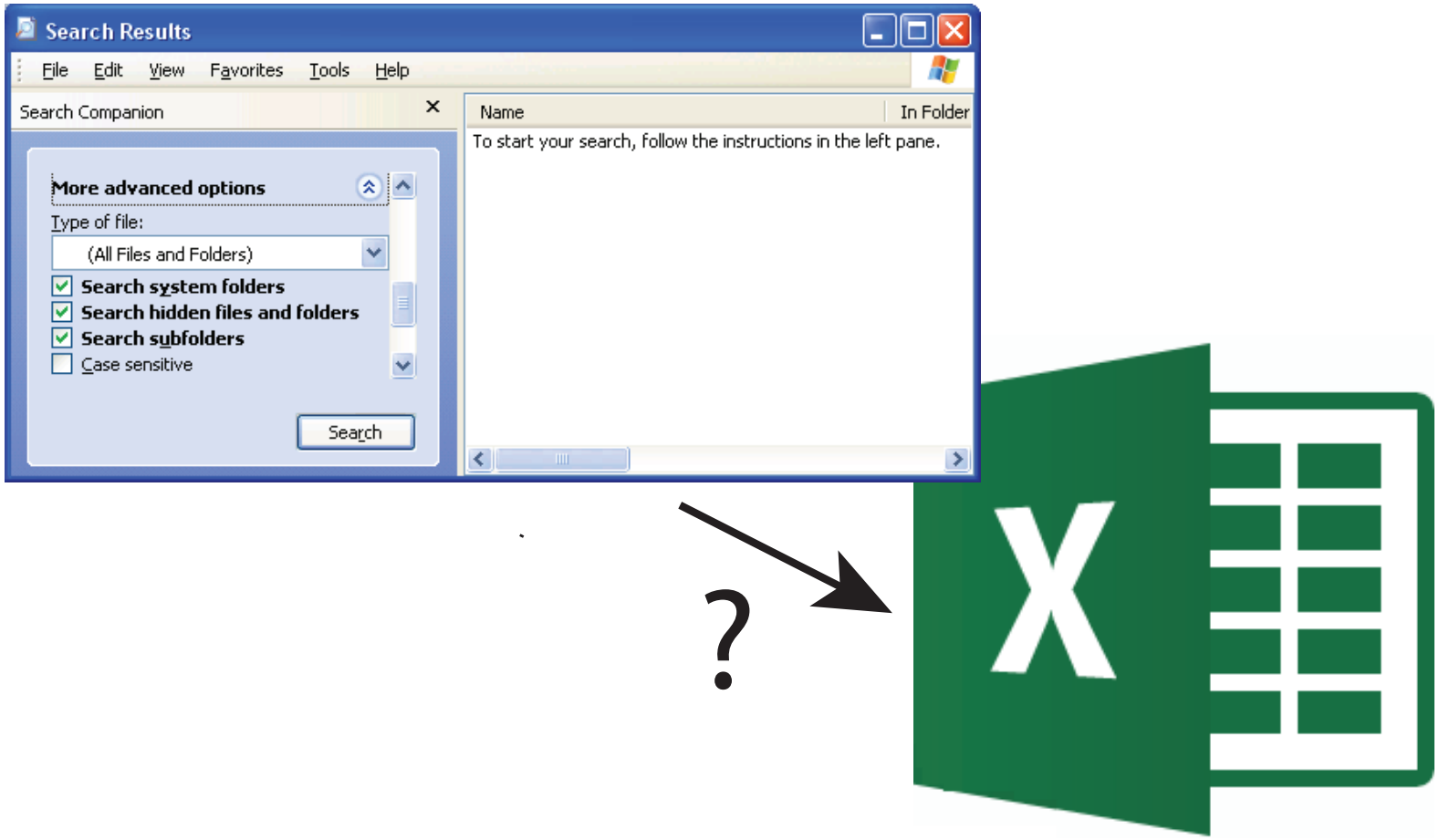
Mark Ziemann, Yotam Eren and Assam El-Osta

Genome Biology 2016 17:177 | DOI: 10.1186/s13059-016-1044-7

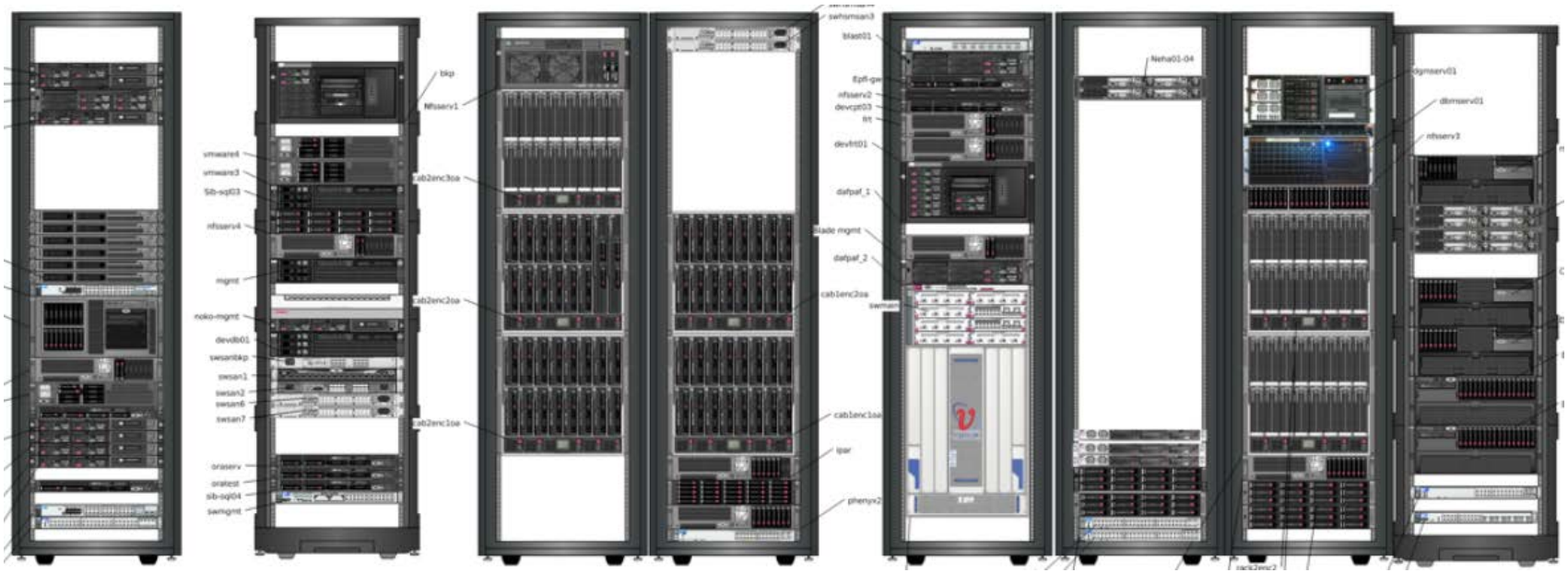
Published: 23 August 2016

Abstract

The spreadsheet software Microsoft Excel when used with default settings, is known to convert gene names to dates and floating-point numbers. A programmatic scan of leading genomics journals reveals that approximately one-fifth of papers with supplementary Excel gene lists contain erroneous gene name conversions.

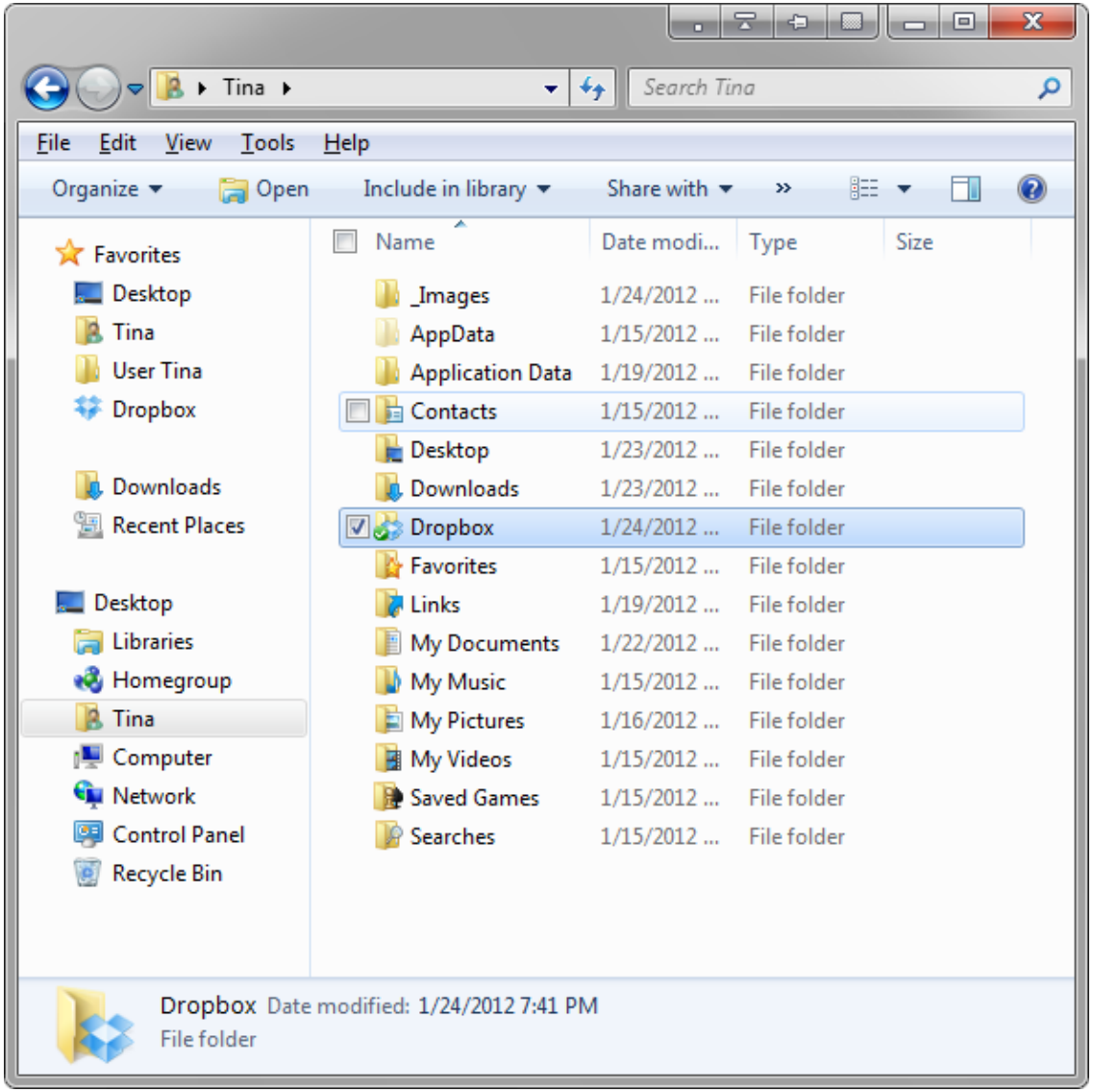

Search Results
File
Edit
View
Favorites
Tools
Help
Search Companion
More advanced options
Type of file:
(All Files and Folders)
Search system folders
Search hidden files and folders
Search subfolders
Case sensitive
Search
Name
In Folder
To start your search, follow the instructions in the left pane.
?
X

Cluster computing

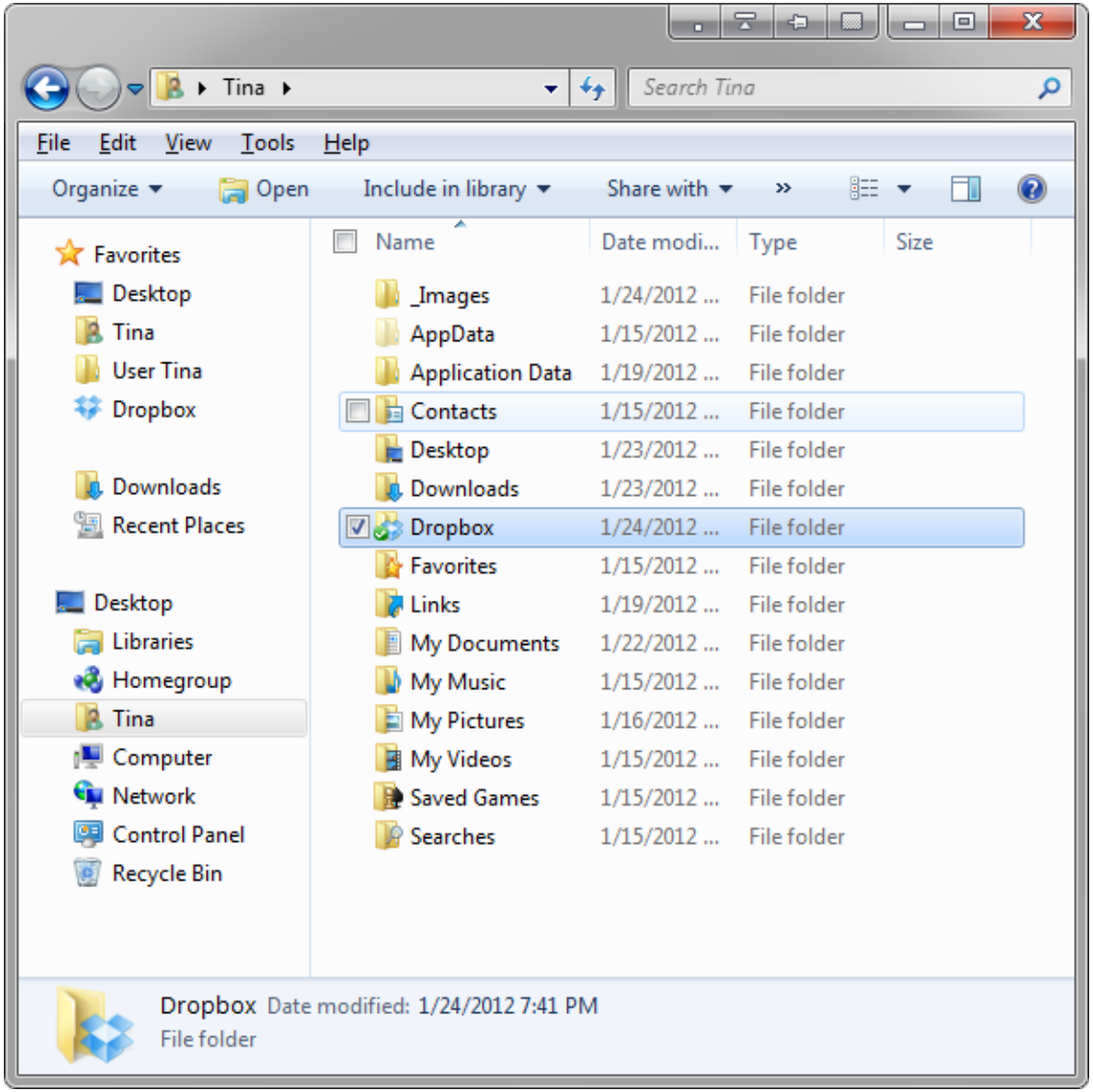


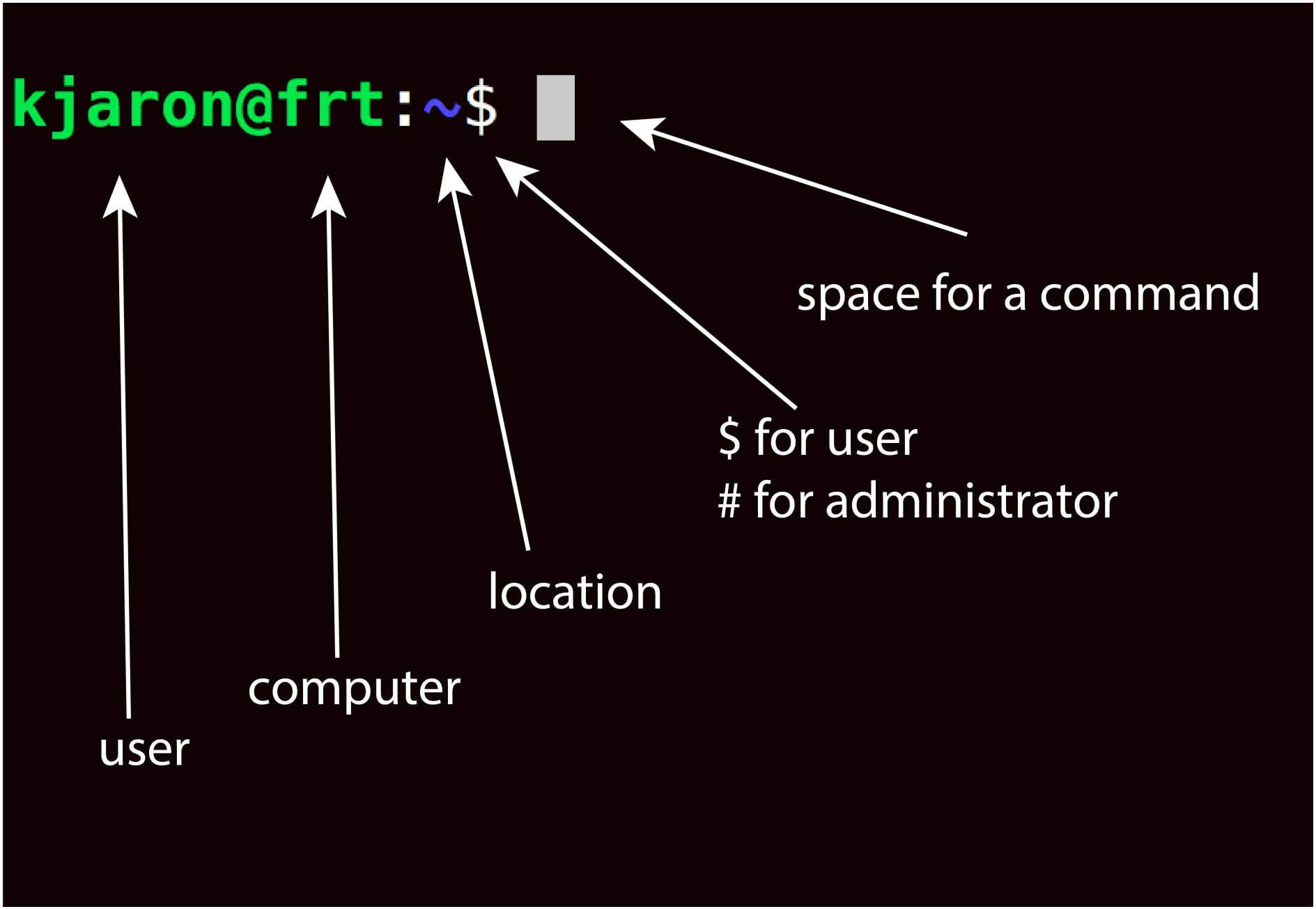
How can UNIX help us?

Command line ≈ explorer + toolbox of commands

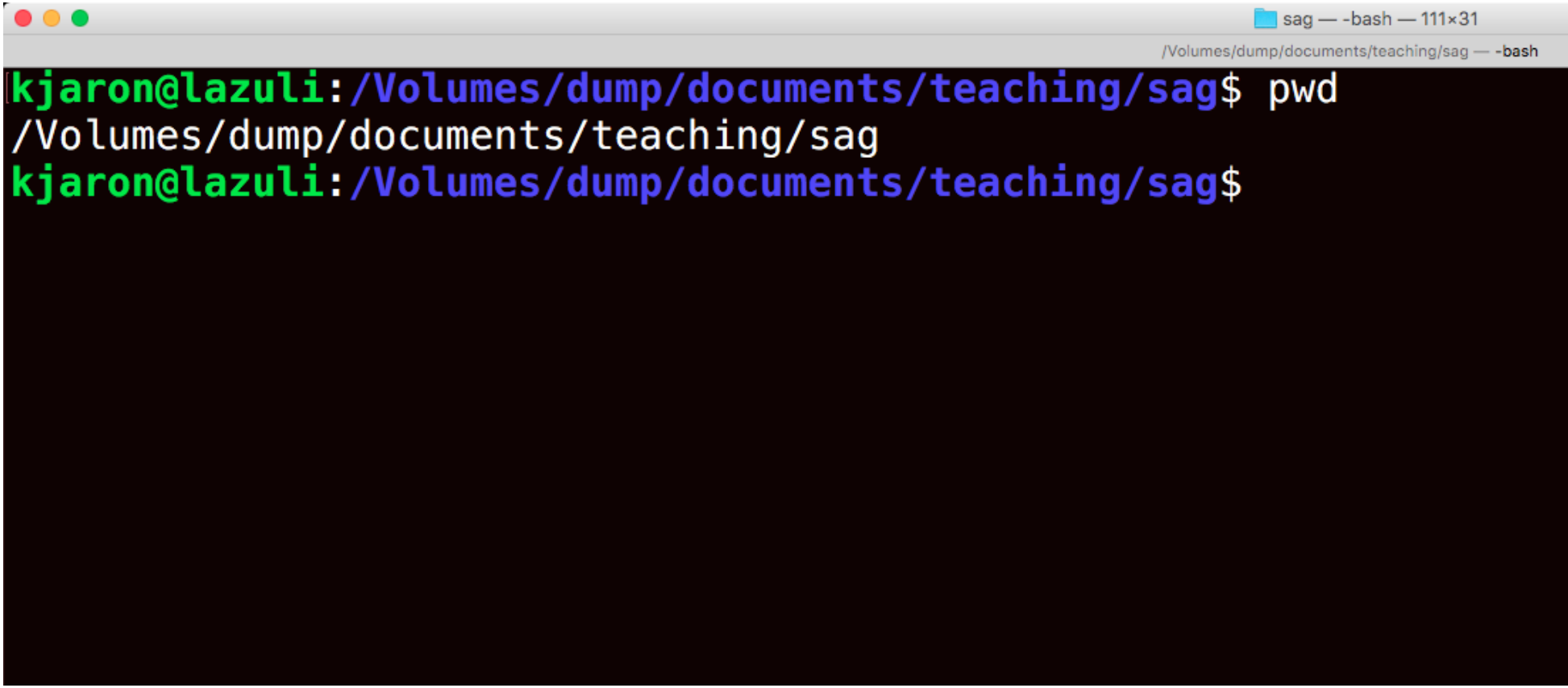


bash ≈ explorer




kjaron@frt:~$
space for a command
$ for user
# for administrator
location
computer
user

bash ≈ explorer (where am I?)



bash ≈ explorer (browse directories)

2016_spring — -bash — 111×31

/Volumes/dump/documents/teaching/sag/2016_spring — -bash

```
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$ ls
2015_autumn 2016_autumn 2016_spring
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$ cd 2016_spring/
kjaron@lazuli:/Volumes/dump/documents/teaching/sag/2016_spring$ ls
EX1                                                 Topics_Students_Assistants_SAGEII.xls
EX2                                                 fq.gz.length_extr.py
EX4                                                 kallisto
EX5                                                 qc
EvaluationMSc-MLS_Spring2016_Seq-GenomeII.pdf       rl.csv
GenDB_Pseudomonas_protegens_S5.gbk                  sag.Rproj
IGV                                                 seq.fq
LSA_PWy5G7RSaOgJ_L7_R1_002.fastq.gz                 student_reports
Pseud_protegens_S5_final.fasta                      workig_documents
Sequence-a-genome
kjaron@lazuli:/Volumes/dump/documents/teaching/sag/2016_spring$
```

bash ≈ explorer (copy and move files)

```
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$ ls
2015_autumn 2016_autumn 2016_spring
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$ cd 2016_spring/
kjaron@lazuli:/Volumes/dump/documents/teaching/sag/2016_spring$ ls
EX1                                          Topics_Students_Assistants_SAGEII.xlsx
EX2                                          fq.gz.length_extr.py
EX4                                          kallisto
EX5                                          qc
EvaluationMSc-MLS_Spring2016_Seq-GenomeII.pdf rl.csv
GenDB_Pseudomonas_protegens_S5.gbk           sag.Rproj
IGV                                          seq.fq
LSA_PWy5G7RSaOgJ_L7_R1_002.fastq.gz          student_reports
Pseud_protegens_S5_final.fasta               workig_documents
Sequence-a-genome
kjaron@lazuli:/Volumes/dump/documents/teaching/sag/2016_spring$ cp Topics_Students_Assistants_SAGEII.xlsx ..
kjaron@lazuli:/Volumes/dump/documents/teaching/sag/2016_spring$ cd ..
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$ ls
2015_autumn                              2016_spring
2016_autumn                              Topics_Students_Assistants_SAGEII.xlsx
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$ mv Topics_Students_Assistants_SAGEII.xlsx  2016_autumn/
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$
```

```
### relative paths
.      # this directory
..     # parent directory
~      # my home directory
### absolute path
/      # root directory
```

bash ≈ explorer (remove files)

```
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$ ls
2015_autumn 2016_autumn 2016_spring
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$ cd 2016_spring/
kjaron@lazuli:/Volumes/dump/documents/teaching/sag/2016_spring$ ls
EX1                                          Topics_Students_Assistants_SAGEII.xlsx
EX2                                          fq.gz.length_extr.py
EX4                                          kallisto
EX5                                          qc
EvaluationMSc-MLS_Spring2016_Seq-GenomeII.pdf rl.csv
GenDB_Pseudomonas_protegens_S5.gbk           sag.Rproj
IGV                                          seq.fq
LSA_PWy5G7RSaOgJ_L7_R1_002.fastq.gz          student_reports
Pseud_protegens_S5_final.fasta               workig_documents
Sequence-a-genome
kjaron@lazuli:/Volumes/dump/documents/teaching/sag/2016_spring$ cp Topics_Students_Assistants_SAGEII.xlsx ..
kjaron@lazuli:/Volumes/dump/documents/teaching/sag/2016_spring$ cd ..
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$ ls
2015_autumn                          2016_spring
2016_autumn                          Topics_Students_Assistants_SAGEII.xlsx
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$ mv Topics_Students_Assistants_SAGEII.xlsx  2016_autumn/
kjaron@lazuli:/Volumes/dump/documents/teaching/sag$ cd 2016_autumn/
kjaron@lazuli:/Volumes/dump/documents/teaching/sag/2016_autumn$ rm Topics_Students_Assistants_SAGEII.xlsx
kjaron@lazuli:/Volumes/dump/documents/teaching/sag/2016_autumn$ ls
1_unix_local.Rmd       1_unix_local.pdf       3_qc_and_trimming.Rmd  unix_presentation.Rmd
1_unix_local.html      2_unix_cluster.Rmd     3_qc_presentation.Rmd  unix_presentation.html
kjaron@lazuli:/Volumes/dump/documents/teaching/sag/2016_autumn$
```

```
command -<parameters> <arguments>
```

Examples:

```
ls -lah  #list long, all, human readable
ls -la ..  #list in parent directory
cp -r <what_dir> <were> # recursive
rm -rf <what dir>       # -||- , force
# careful with this one...
```

Special characters `*, ?, []`

```
$cd /
$echo b
b

$echo b*
bin boot

$echo b\*
b*

$echo B*
B*
```

OK, try it!

```
# Auto Completion by <tab>
cd /<tab><tab>   # lists all in root
cd ~/k<tab><tab> # lists all in home
```

MyUnil → Sequence a Genome II → 1_unix_local.pdf

```
# Auto Completion by <tab>
cd /<tab><tab>   # lists all in root
cd ~/k<tab><tab> # lists all in home
# Command history
<arrow_up>       # last excuted command
<Ctrl+R>         # full-text search
```

What about that toolbox?

How to check a file??

Notepad?

not well suited for big files

Office?

Microsoft® Office™

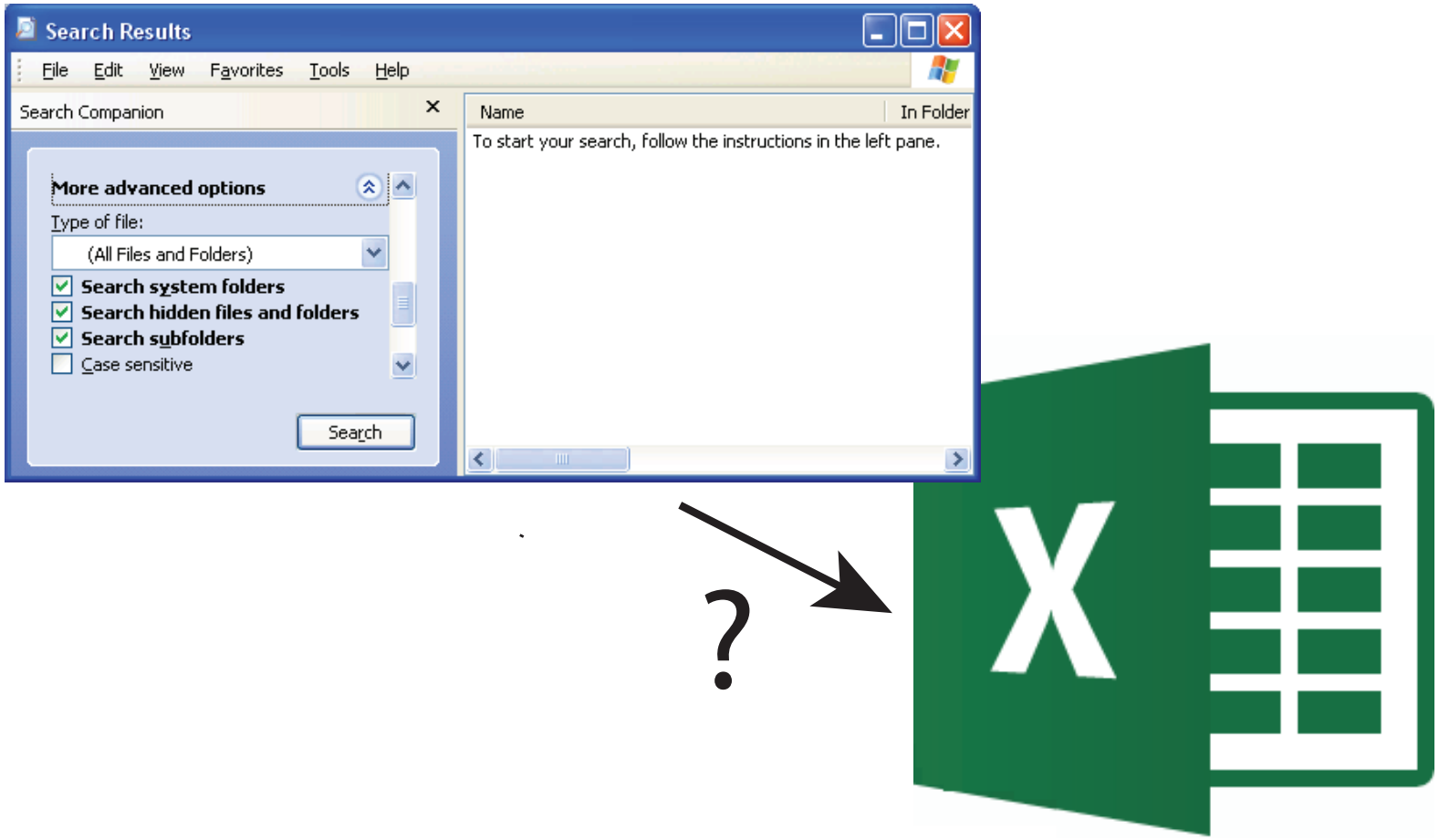
Use at least read-only mode

Look at a plain-text file

```
command <text_file>

head
tail
cat    # catenate
less   # > more; text reader

wc     # word count
tr     # transform
grep   # global regular expression print
```

IO streams - a way how to build pipes!

```
command <text_file>
            == cat <text_file> | command
echo
tail / head
cat    # catenate
less   # > more

wc     # word count
tr     # transform
grep   # global regular expression print
```


Search Results
File
Edit
View
Favorites
Tools
Help
Search Companion
More advanced options
Type of file:
(All Files and Folders)
Search system folders
Search hidden files and folders
Search subfolders
Case sensitive
Search
Name
In Folder
To start your search, follow the instructions in the left pane.
?
X

IO streams!

```
ls | wc -w
```

Streams in the service of genomics!

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

input file

```
grep -v ">" seq.fasta | \
  tr -d '\n' | wc -l
```

```
>seq1
CGATCGTCGTAGCTACGAT
>seq2
ACCGATCAAACCGTCGTAA
```

grep -v ">"

```
grep -v ">" seq.fasta | \
  tr -d "\n" | wc -l
```

```
CGATCGTCGTAGCTACGAT
ACCGATCAAACCGTCGTAA
```

tr -d "\n"

```
grep -v ">" seq.fasta | \
  tr -d "\n" | wc -l
```

CGATCGTCGTAGCTACGATACCGATCAAACCGTCGTAA

wc -l

```
grep -v ">" seq.fasta | \
  tr -d "\n" | wc -l
```

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Stream redirection overview

```
grep ">" seq.fasta          # print
grep ">" seq.fasta | wc     # pipe
grep ">" seq.fasta > file   # write
grep ">" seq.fasta >> file # append
```

Your turn

```
command <text_file>

echo
tail / head
cat    # catenate
less   # text reader

wc     # word count
tr     # transform
grep   # global regular expression print
```