BINF2111 - Introduction to Bioinformatics Computing UNIX 101 - enter the coding zone



Lecture 5 - Tuesday Sep 5th, 2023

RAW Lab

Learning Objectives

- Review bonus
- Comments about data and formats

- Sort/uniq/cut commands
- PATHS
- Quiz 5

- Delete all the empty lines in the empty lines file with

- Delete all the 'all white space' with grep

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- → grep: grep -v -e '^\$' file

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- → awk: awk '!/^\$/' file
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- → grep: grep -v -e '^\$' file
- → awk: awk '!/^\$/' file
- Delete all the 'all white space' with grep
- → grep: grep -v -e '^[[:space:]]*\$' file

- Delete all the empty lines in the empty lines file with
- → grep: grep -v -e '^\$' file or egrep -v '^\$' file
- → awk: awk '!/^\$/' file
- Delete all the 'all white space' with grep
- → grep: grep -v -e '^[[:space:]]*\$' file
- → awk: awk 'NF > 0' file
- → sed '/^[[:space:]]*\$/d'

Also, in python (think Pandas)

Any one try in Python Pandas.

Bonus 4 – Python Pandas

- First use sed to convert from tsv (tab delim) to csv (column delim)

import pandas as pd

```
df = pd.read_csv('data.csv')
new_df = df.dropna() or df.dropna(inplace = True)
print(new_df.to_string()) or print(df.to_string())
```

Expression 1

^[A-Z]

Expression 2

[A-Z]\$

A regular expression would do what to this file?

head file.txt line 1 bat cat RAT line 2 RAT cat bat line 3 rat cat bat A) expression 1 acts on line 1, expression 2 acts on line 3.

B) expression 1 acts on line 2, expression 2 acts on line 1.

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head file.txt
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Expression 1

^[A-Z]

Expression 2

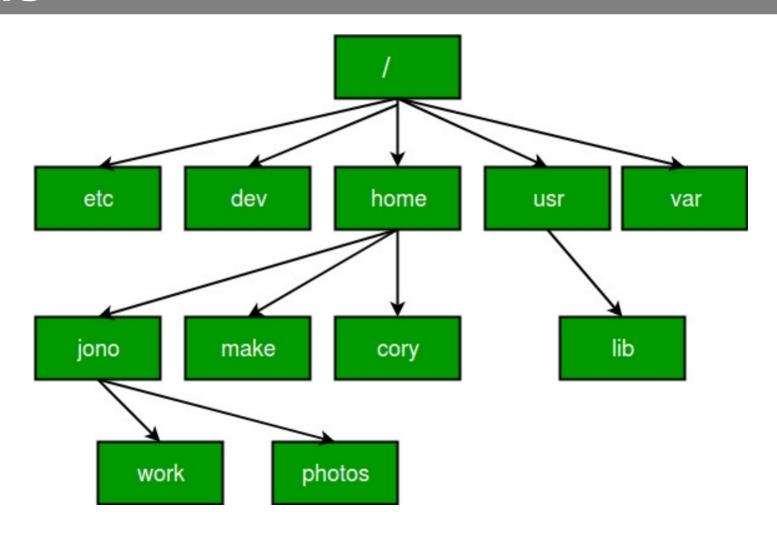
[A-Z]\$

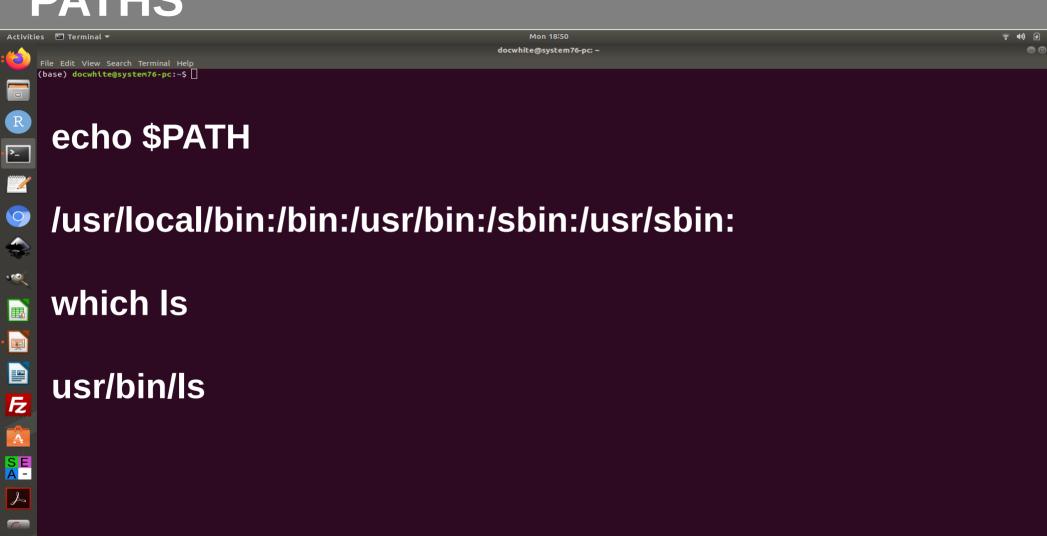
A regular expression would do what to this file?

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line 1 bat cat RAT
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A) expression 1 acts on line 1, expression 2 acts on line 3.

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echo \$PATH

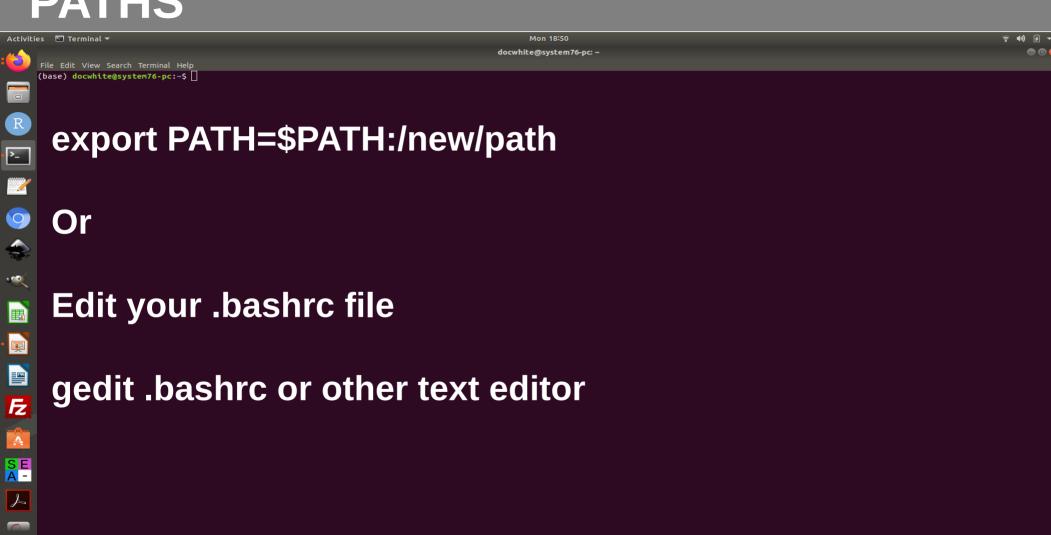
Finds which directories your shell is set to check for executable files.

This output is a list of directories where executable files are stored.

This allows you to check which programs are executable from anywhere in the shell terminal. It allows for custom directory to be executed anywhere

If your installing programs this is very helpful to know.

As some have to be in your path in order to run



General comments - data

UNDERSTAND YOUR DATA

- Expectations Format, Types, Domains, Uniqueness, etc.
- Assumptions Does it make sense to use data from X in a new context Y? Restrictions Licenses, Embargos, etc.

STANDARDIZE YOUR DATA

- Values ID mapping, Unit conversion, Adding/Removing Prefixes/Suffixes, etc.
- Columns Adding, Removing, Rearranging, Merging, Splitting, etc.
- Rows Filtering data (duplicates, missing data, not relevant to task, etc)

RECORD YOUR ANALYSIS PROCESS

- Your computer is a lab Keep a lab notebook!
- Use Version Control like GitHub or BitBucket.

General comments - data formats

Column-oriented data

- Spreadsheets, CSV, Tabular, delimited
- Fixed position
- One line per record, fixed set of fields (columns)

Key-Value data

- Multiple lines per record
- Variable number of fields/values

Hierarchical data (XML, JSON, Ontologies, etc)

- Nested usually requires a more complex parser
- Usually follow a well-defined schema.

Web-based API resources

- Issue specific commands to get different types of data
- **Infinite proprietary formats**
- Usually harder to parse but generally act like other types

General comments: Column-Oriented

Easy to browselexplore

- MOST files are this type

Best for databases

- between fields
- 1 line = 1 record
- Each record has fixed set of fields

- Delimiters are tabs or commas

Complex code not needed:

- Excel can handle small datasets
- (<1 million rows)UNIX can handle the rest

CSV

david, abdul, xi, bill mary, david, bill, abdul

wang,abdul,xi,david

TSV

David abdul xi Mary david bill bill

abdul

Wang abdul xi david

General comments - XML formats

Machine-readable

- Many tools and libraries available to parse it

Can represent complex structures

- multiple values
- nested structures

Not trivial for non-coders

```
<?xml version="1.0"?>
<!DOCTYPE Entrezgene-Set PUBLIC "-//NLM//DTD NCBI-Entrezgene, 21st Ja
<Entrezgene-Set>
<Entrezgene>
  <Entrezgene track-info>
    <Gene-track>
      <Gene-track geneid>4336</Gene-track geneid>
      <Gene-track status value="live">0</Gene-track status>
      <Gene-track_create-date>
        <Date>
          <Date std>
            <Date-std>
              <Date-std_year>1998</Date-std_year>
              <Date-std_month>8</Date-std_month>
              <Date-std day>27</Date-std day>
            </Date-std>
          </Date std>
        </Date>
      </Gene-track_create-date>
      <Gene-track_update-date>
        <Date>
          <Date std>
            <Date-std>
              <Date-std_year>2016</Date-std_year>
              <Date-std_month>12</Date-std_month>
              <Date-std_day>6</Date-std_day>
            </Date-std>
          </Date std>
        </Date>
      </Gene-track update-date>
    </Gene-track>
  </Entrezgene track-info>
  <Entrezgene_type value="protein-coding">6</Entrezgene_type>
  <Entrezgene source>
    <BioSource>
      <BioSource_genome value="genomic">1</BioSource_genome>
      <BioSource origin value="natural">1</BioSource origin>
      <BioSource org>
        <0rg-ref>
          <Org-ref taxname>Homo sapiens/Org-ref taxname>
          <Org-ref_common>human</Org-ref_common>
          <0rg-ref db>
            <Dbtag>
              <Dbtag_db>taxon</Dbtag_db>
              <Dbtag tag>
                <Object-id>
                  <Object-id_id>9606</Object-id_id>
                </Object-id>
              </Dbtag tag>
            </Dbtag>
          </0rg-ref db>
          <0rq-ref syn>
            <Org-ref_syn_E>humans</Org-ref_syn_E>
            <Org-ref_syn_E>man</Org-ref_syn_E>
          </0rq-ref_syn>
          <Org-ref_orgname>
            <OrgName>
              <OrgName_name>
```

General comments: Key-value formats

Easy to read

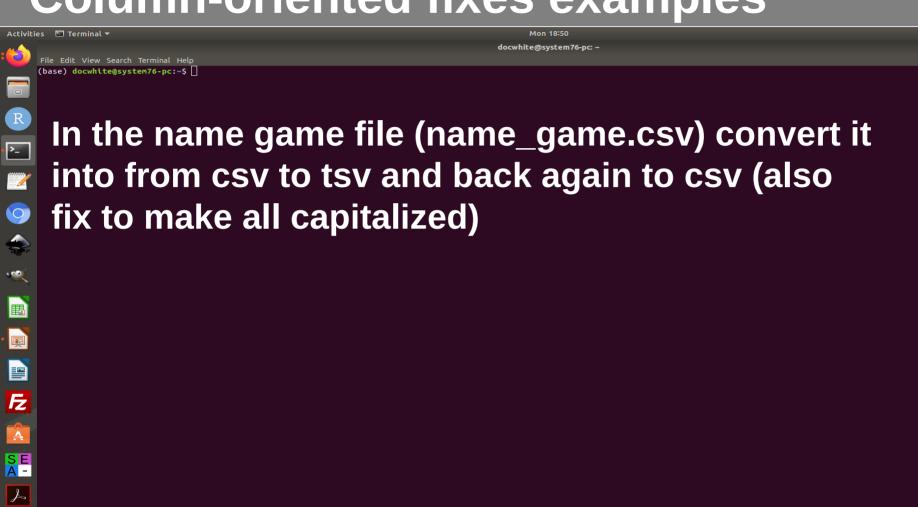
Straightforward to parse

- Delimiter for each Record
- One key-value pair per line
- Supports multiple values

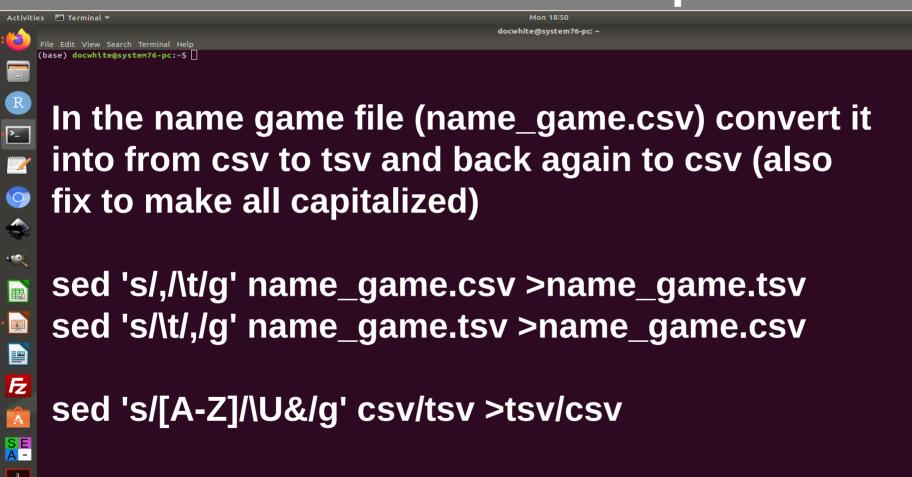
Novice coders can handle it!

```
remark: cvs version: use data-version
ontology: go
[Term]
id: GO:0000001
name: mitochondrion inheritance
namespace: biological process
def: "The distribution of mitochondria, including the mitocho
PMID:10873824. PMID:113897641
exact synonym: "mitochondrial inheritance" []
is a: GO:0048308 ! organelle inheritance
is a: GO:0048311 ! mitochondrion distribution
id: GO:0000002
name: mitochondrial genome maintenance
namespace: biological process
def: "The maintenance of the structure and integrity of the m
is a: GO:0007005 ! mitochondrion organization
[Term]
id: GO:0000003
name: reproduction
namespace: biological process
alt id: GO:0019952
alt id: GO:0050876
def: "The production of new individuals that contain some por
subset: goslim chembl
subset: goslim generic
subset: goslim pir
subset: goslim plant
subset: gosubset prok
exact synonym: "reproductive physiological process" []
xref analog: Wikipedia: Reproduction
is a: GO:0008150 ! biological process
[Term]
id: GO:0000005
name: obsolete ribosomal chaperone activity
namespace: molecular function
def: "OBSOLETE. Assists in the correct assembly of ribosomes
PMID:121509131
comment: This term was made obsolete because it refers to a c
exact synonym: "ribosomal chaperone activity" []
is obsolete: true
consider: GO:0042254
consider: GO:0044183
consider: GO:0051082
```

Column-oriented fixes examples



Column-oriented fixes examples



cut – syntax anatomy UNIX's scissors

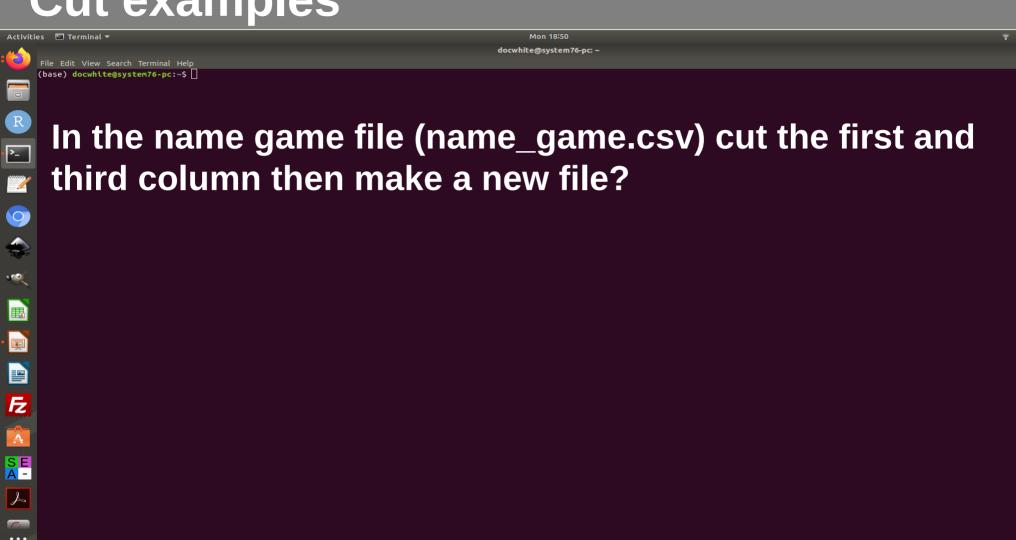
cut [options] file.txt

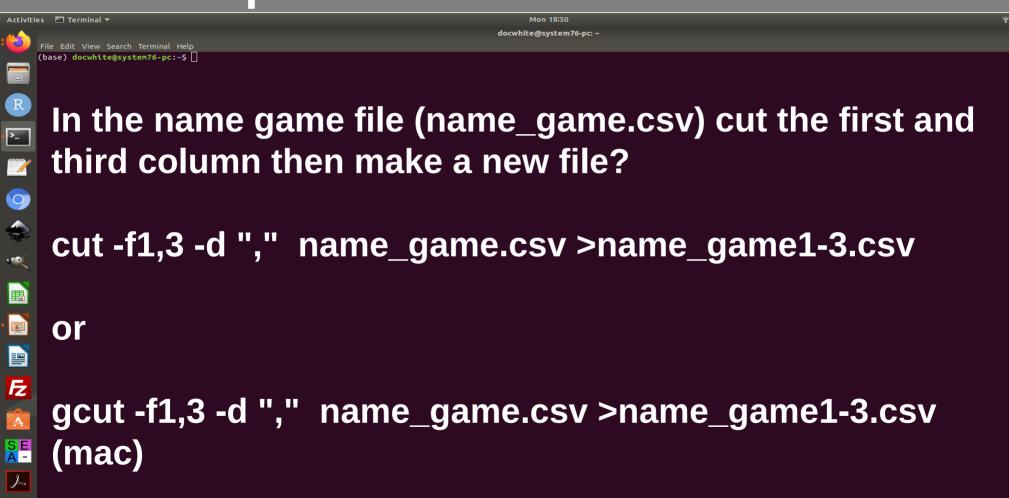
- -d (--delimiter) "," set field delimiter (default tab)
- -f (--fields=LIST) Select by specifying a field
 - -f 2 select a field to cut (left is 1)
 - -f 2-8,12 select multiple fields to cut
- -b (--bytes=LIST) Select by specifying a byte
- -c (--characters=LIST) Select by specifying a character
- --complement Complement the selection.
- -s (--only-delimited) suppress non-matches

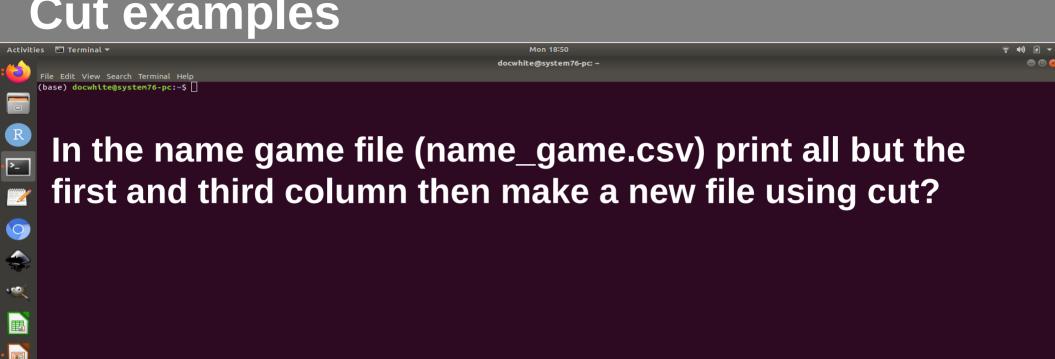
cut – syntax anatomy UNIX's scissors

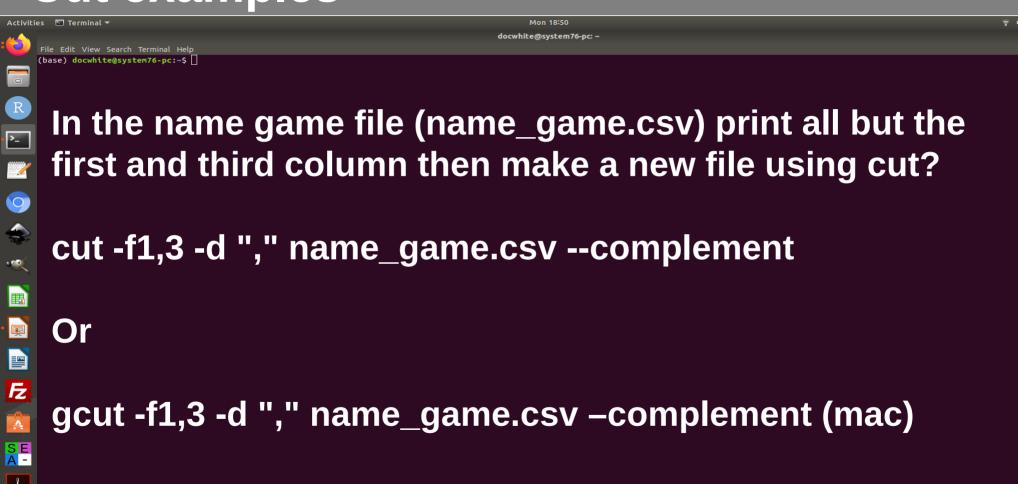
gcut [options] file.txt

Install coreutils brew install coreutils









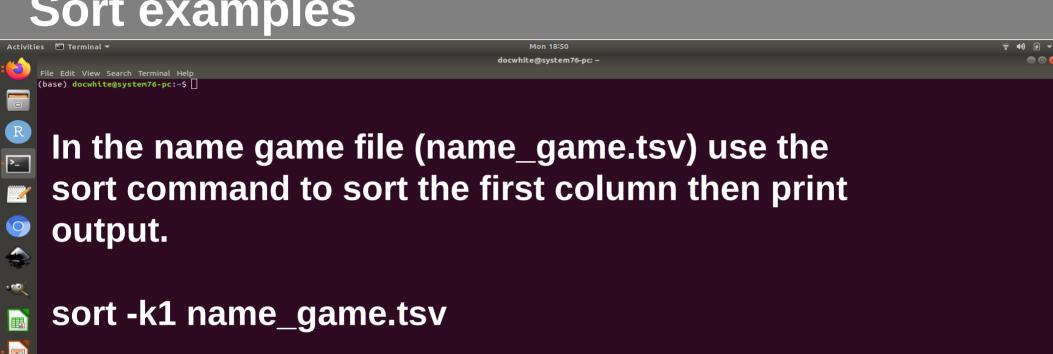
sort – syntax anatomy of sort

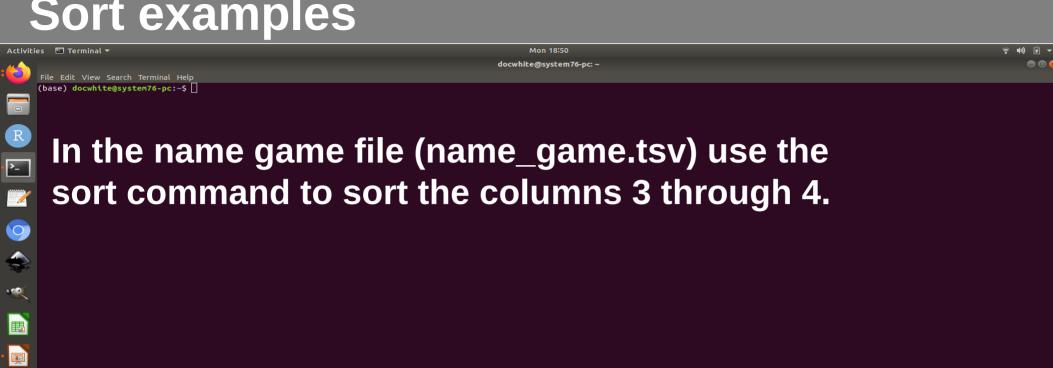
sort [options] file.txt

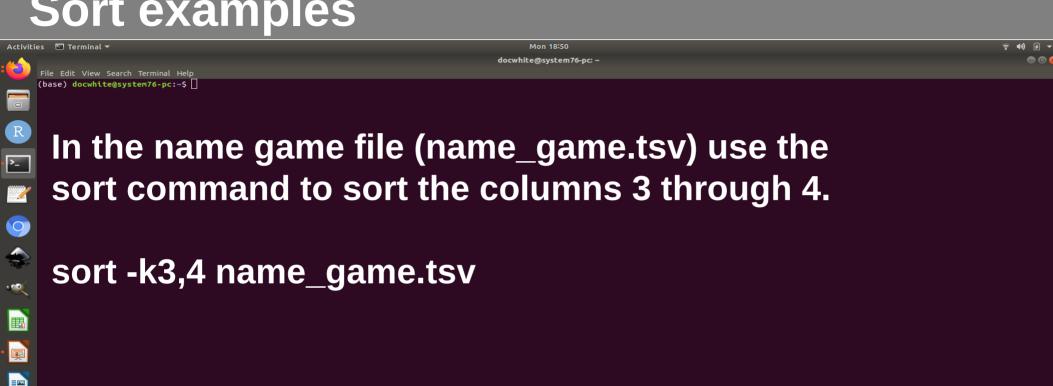
- -t "t" set the delimiter when using -k default is non-blank to blank transition
- -k 3 sort column #3 (left is 1)
- -k 2,3 sort multiple columns
- -n sort numerically
- -r reverse sort order
- -u drop duplicates from the result
- -b, --ignore-leading-blanks, ignore leading blanks
- -d, --dictionary-order consider only blanks and alphanumeric characters
- -f, --ignore-case fold lower case to upper case characters
- No options: sort alphabetically from leftmost character.

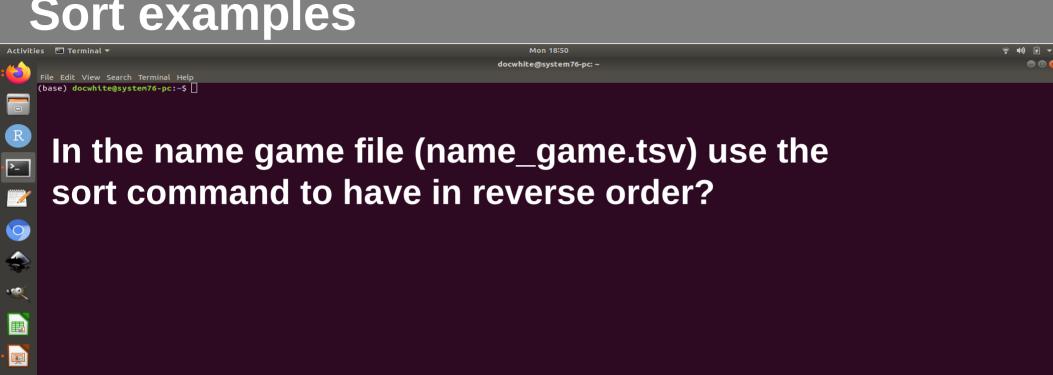


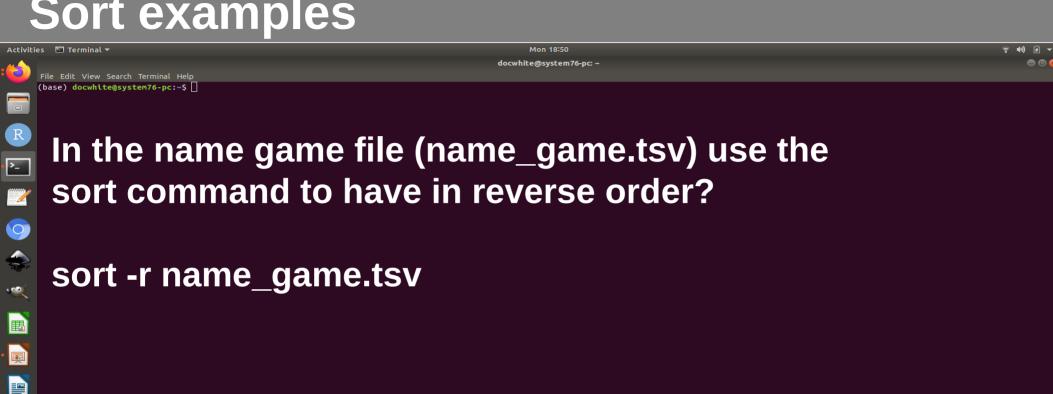
As tab (t) is default

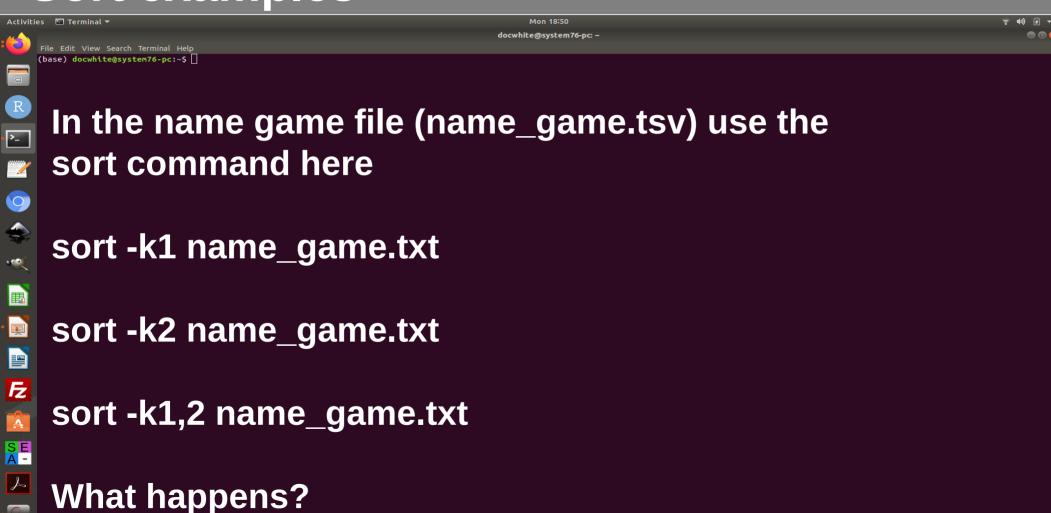








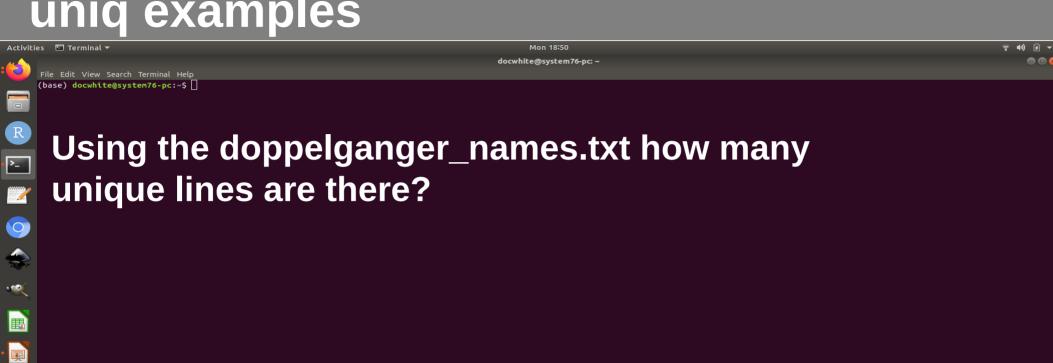


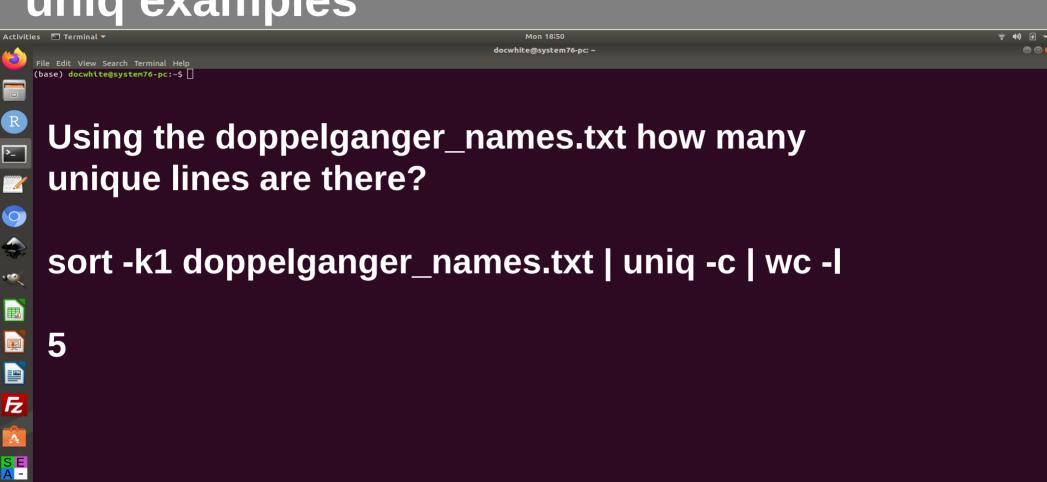


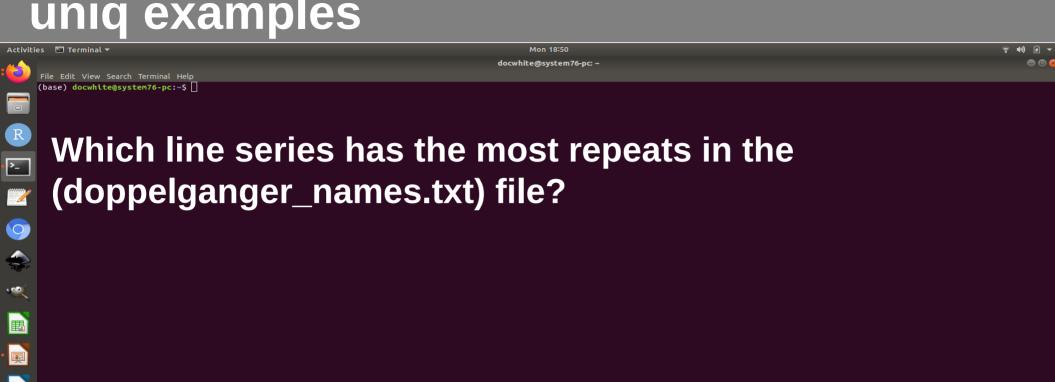
uniq – syntax anatomy of uniq

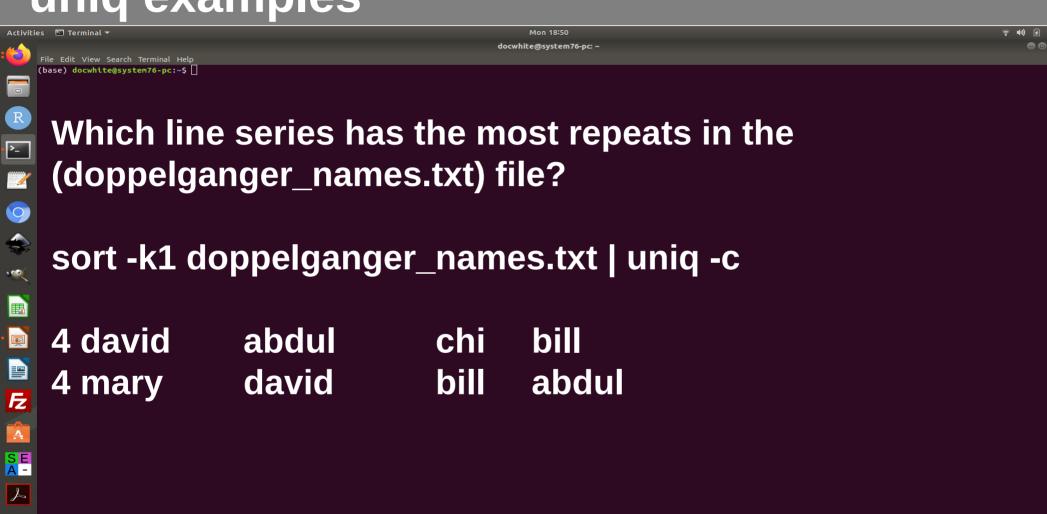
uniq [options] file.txt

- Only works on sorted files and adjacent lines!
- -c count lines for each unique value
- -d only report duplicated lines
- -u only report non-duplicated lines
- No options: drop all duplicated lines (keeps 1 copy)

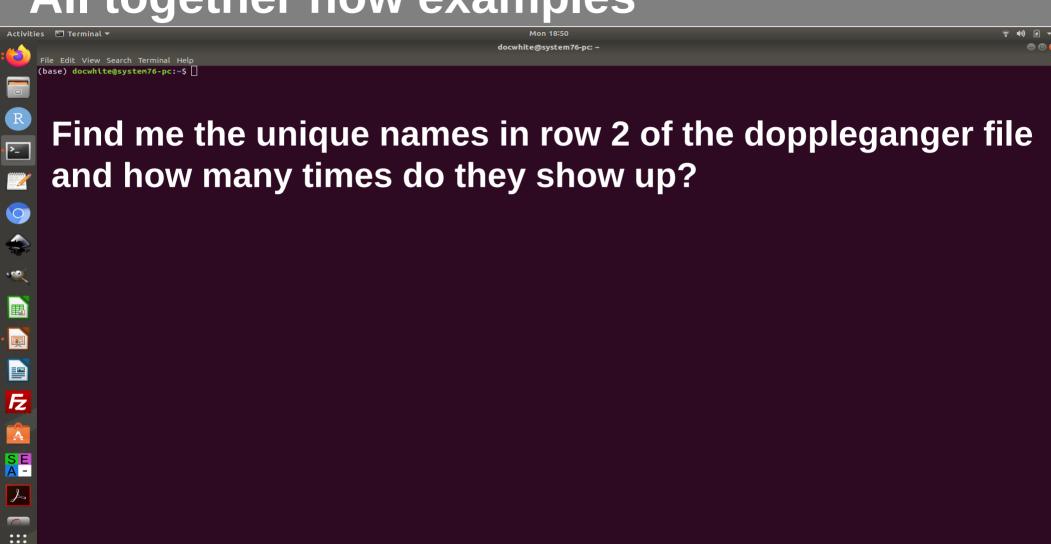




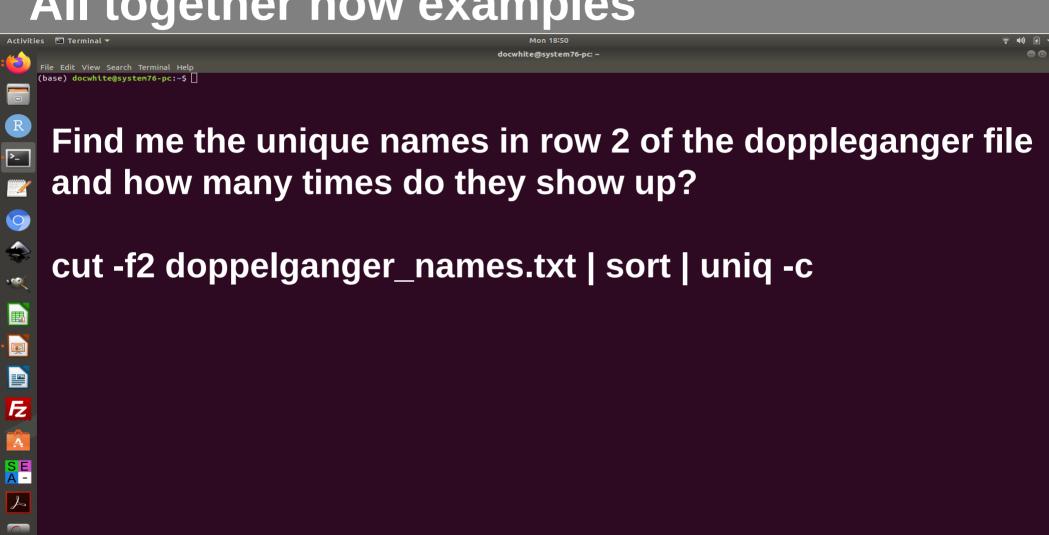




All together now examples



All together now examples



- Convert name game file (name_game.csv) to tsv with:

 \rightarrow tr

→ awk

- On canvas now