**Ecosystem**

In this project, you’ll use the commands you just learned to redirect files in Ecosystem, a natural history museum exhibit.

If you get stuck during this project or would like to see an experienced developer work through it, click “**Get Help**“ to see a **project walkthrough video**.

**Tasks**

**0/15Complete**

Mark the tasks as complete by checking them off

**1.**

List all contents, including hidden files and directories, in long format, ordered by the date and time they were last modified.

Hint

ls -alt

**2.**

Use cat to view the contents of **rocks.txt**.

Hint

cat rocks.txt

**3.**

Redirect the standard output of **rocks.txt** to **mosses.txt** and use cat to view the contents of **mosses.txt**.

Hint

cat rocks.txt > mosses.txt

cat mosses.txt

**4.**

Redirect **plants.txt** as standard input to the wordcount command. Use the -l option on the wordcount command.

Hint

wc -l < plants.txt

**5.**

Append the standard output of **streams.txt** to **plants.txt**. Then use cat to view the contents of **plants.txt**.

Hint

cat streams.txt >> plants.txt

cat plants.txt

**6.**

Append the standard output of **plants.txt** to **trees.txt**. Then use cat to view the contents of **trees.txt**.

Hint

cat plants.txt >> trees.txt

cat trees.txt

**7.**

In one command, pipe the ls -l command to the head command. Then redirect the standard output of the head command to **list1.txt**.

Once you complete the above step, use cat to view the contents of **list1.txt**.

Hint

ls -l | head > list1.txt

cat list1.txt

**8.**

In one command, pipe the standard output of the ls -la command to the head command, then append the standard output to \*\* list1.txt\*\*, then pipe the standard output to the wc command.

Once you complete the above step, use cat to view the contents of **list1.txt**.

Hint

ls -la | head >> list1.txt | wc

cat list1.txt

**9.**

Sort the contents of **mammals.txt** in alphabetical order.

Hint

sort mammals.txt

**10.**

Use the uniq command to filter out duplicate, adjacent lines in **mammals.txt**

Hint

uniq mammals.txt

**11.**

In a single command, use the sort command to filter out duplicate, adjacent lines in **flowers.txt**, pipe it to the uniq command, and redirect the standard output of the uniq command to **uniq-flowers.txt**.

Once you complete the above command, use cat to view contents of **uniq-flowers.txt**

Hint

sort flowers.txt | uniq > uniq-flowers.txt

cat uniq-flowers.txt

**12.**

Use the grep command to search uppercase instances of the string ‘Mushroom’ in **fungi.txt**.

Hint

grep Mushroom fungi.txt

**13.**

Use the grep command to search uppercase or lower instances of the string ‘Mushroom’ or ‘mushroom’ in **fungi.txt**.

Hint

grep -i Mushroom fungi.txt

**14.**

Use the grep command to search for the string ‘tree’ in the **ecosystem/** directory, and output filenames with matched results. Do not output line numbers.

Hint

grep -Rl tree .

**15.**

Use the sed command to replace all instances of the word ‘Dirt’ with ‘Soils’ in **soils.txt**.

Hint

sed 's/Dirt/Soils/g' soils.txt