**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, check out the **project walkthrough video** which can be found at the bottom of the page after the final step of the project.

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.

Stuck? Get a hint

**2.**

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

Stuck? Get a hint

**3.**

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

Stuck? Get a hint

**4.**

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

Stuck? Get a hint

**5.**

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

Stuck? Get a hint

**6.**

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

Stuck? Get a hint

**7.**

In one command, pipe the ls -lcommand 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**.

Stuck? Get a hint

**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 wccommand.

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

Stuck? Get a hint

**9.**

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

Stuck? Get a hint

**10.**

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

Stuck? Get a hint

**11.**

In a single command, use the sortcommand 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**

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**12.**

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

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**13.**

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

Stuck? Get a hint

**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.

Stuck? Get a hint

**15.**

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