

Bash Task 1

1. Explore your file system!
2. Whats in your home folder?
3. How many users are there on your system?
4. Try an absolute path to get to home!

Bash Task 2

1. Create a new folder at home
2. Create an empty file in it
3. List the file
4. Rename the file
5. Move the file one level up
6. Remove the file. Test if it's really gone.
7. Remove the folder. Test if it's really gone.
8. Go to root
9. Try to create a directory in root

Bash Task 3

1. Create a directory called python_course.
2. Move the course files from your Downloads folder to the course folder
3. Unpack them with 'tar xzvf [files]'
4. What files are in there?

Bash Task 4

1. How big are your course files?
2. And how long?
3. Create a new file
4. How big and long is it?

Bash Task 5

1. Open a new file in nano
2. Write something into it
3. Save it as test1.txt
4. Do it again for a 2nd file called test2.txt
5. Cat both into a new file called test3.txt
6. Open it with less
7. Remove all 3 files in a single command (use a wildcard!).

Bash Task 6

In the following tasks we will try to analyse the file 'pristionchus_mutations.txt' in your course files. It's a list of mutations and their effects in several *Pristionchus* strains (surprise!).

Each line corresponds to one mutation. The columns stand for:

Strain-Chromosome-Contig-Position-ReferenceBase-MutatedBase-CodingState-Effect-Homologs

1. Understand the contents
2. Try head and tail
3. Create a new file containing only the Contig information.

Bash Task 7

1. Are there SNPs in an 'unc'-gene?
2. How many SNPs does the file contain in total?
3. How many SNPs are in exons?
4. How many SNPs are in exons on Contig0?

Bash Task 8

1. How many "C" are mutated?
2. How many mutations from "A" to "G"?
3. How many in MA_46?
4. Which strain has the most SNPs?

Bash Task 9

Listing 1 shows a Python script.

Listing 1: Sample Python Script With Highlighting

```
def run_and_print_dict():

    result_dict = {}

    5     for chrom in chroms:
        chrom_dict = {}

        for focal in crosses:
            focal_dict = {}

    10         for partner in crosses:
            zt_cmd = "~/software/zt_mantel_test/zt -s zt_input_%s_%s.txt zt_input_%s_%s.txt

            results = commands.getoutput(zt_cmd)
            rows = results.split("\n")
            15         for row in rows:
                if "p =" in row:
                    p = row.split()[2]
                elif "r =" in row:
                    20                     r = row.split()[2]
                focal_dict[partner] = {"p":float(p), "r":float(r)}

            chrom_dict[focal] = focal_dict

    25     result_dict[chrom] = chrom_dict

    print result_dict
    return result_dict
```

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Bash Task 10

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Example Figure

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