# Introduction to Transcriptomics Analysis

## Class 03 - Basic File Navigation with Linux

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# Outline of Topics

- Exercise 1: Creating and moving into directories.
- Exercise 2: Absolute vs relative paths.
- Exercise 3: Moving, renaming and copying files.
- Exercise 4: Taking a look into the files.
- Exercise 5: Organising directories

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- Exercise 1: Creating and moving into directories.

1. Print working directory with **pwd**.
2. Using **mkdir** create a directory called Linux_exercises
3. Change the working directory to Linux_exercises with **cd**
4. Create five new directories called exercise01, exercise02, exercise03, exercise04 and exercise05
5. List all the directories with **ls** and **ls -lh**. Discuss the differences.
6. Print the working directory.
7. Change the working directory to exercise01
8. Create two new directories called test01 and test02
9. Eliminate the test01 directory with **rmdir**
10. Change the working directory to home typing **cd** with no arguments.

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- Exercise 2: Absolute vs relative paths.

1. Change the working directory to Linux_exercises and then to exercise02.
2. Create two directories, sample01 and sample02.
3. Change the directory to sample02.
4. Specify the absolute and relative paths of sample01 from your current working directory.
5. Change the working directory to home.
6. Specify the absolute and relative path of sample02 from your current working directory.
7. List the items for the directory Linux_exercises and inside this one exercise02 using ls and as argument the absolute path.
8. List the items for the directory Linux_exercises and inside this one exercise01 using ls and as argument the relative path.

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- Exercise 3: Moving, renaming and copying files.

1. Change the working directory to Linux_exercises and then to exercise03.
2. Copy the directories sample01 and sample02 from the exercise02 directory using **cp**.
3. List the items from the exercise02 directory.
4. Move the directory test02 from the exercise01 directory to your current working directory using **mv**.
5. List the items from the exercise01 directory.
6. Change the name of the test02 directory to sample03 using the command **mv**.
7. List the items for the directory exercise03
8. Change your working directory to your home.
9. Create a new directory called RNASeq

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- Exercise 4: Taking a look into the files.

1. Copy the files “Araport11_GFF3_genes_transposons.201606.gff” and “Artha_TAIR10_genome.fasta” from the directory /storage/users/RNASeq2020UNIMI/00_DATA/00_reference into the RNASeq directory.
2. Change the working directory to RNASeq.
3. Print the first ten lines of the “Artha_TAIR10_genome.fasta” file using **head**.
4. Print the last twenty lines of the “Artha_TAIR10_genome.fasta” file using **tail -n 20**.
5. Open the file “Araport11_GFF3_genes_transposons.201606.gff” with **less**. Use the arrows up and down to navigate the file. Exit from the less screen pushing the “q” key.
6. Search the lines with the character “>” in the “Artha_TAIR10_genome.fasta” file using the command **grep “>”**.
7. Redirect the output of the command grep “>” on “Artha_TAIR10_genome.fasta” using the symbol “>” again (no quotes this time) into a file called “ID_list.txt”.

- Exercise 4: Taking a look into the files.

8. Check the content of the “ID_list.txt” file using less.
9. Ignore all the lines with the character “#” using **grep -v “#”** on the file “Araport11_GFF3_genes_transposons.201606.gff”. To avoid to print the whole file in your screen pipe the output of grep -v “#” Araport11_GFF3_genes_transposons.201606.gff into a **head** command using the symbol **“|”**.
10. Cut the second column in the file “Araport11_GFF3_genes_transposons.201606.gff” using the command **cut -f 2**.
11. Change the working directory to home.

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- Exercise 5: Organising directories

1. Change the working directory to RNASeq.
2. Create a directory called 00_references
3. Move the files “Araport11_GFF3_genes_transposons.201606.gff” and “Artha_TAIR10_genome.fasta” into 00_references.
4. Delete the file “ID_list.txt”.
5. Create a directory called 01_raw_reads
6. Copy all the files from the directory /storage/users/RNASeq2020UNIMI/00_DATA/01_transcriptome into the directory 01_raw_reads.
7. Use **ls -lh** to check the size that it is being use in the directory 01_raw_reads. Alternatively use **df -lh** to check the space used in the hard drive by the directory 01_raw_reads.
8. Create the directories: 02_processed_reads, 03_mapped_reads, 04_transcript_models and 05_quantification.