Project 2: Installing Bioinformatics Softwares on the terminal

N/B: You need to install and setup your conda environment with either anaconda or miniconda.

Please copy exactly what worked. Do not paraphrase. A single mismatch makes you loose your point.

1. Activate your base conda environment

```
$ wget https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86_64.sh
$ bash Miniconda3-latest-Linux-x86_64.sh
$ exec -l $SHELL
$ conda -version
$ conda activate base
```

2. Create a conda environment names funtools

```
$ conda create -n funtools
```

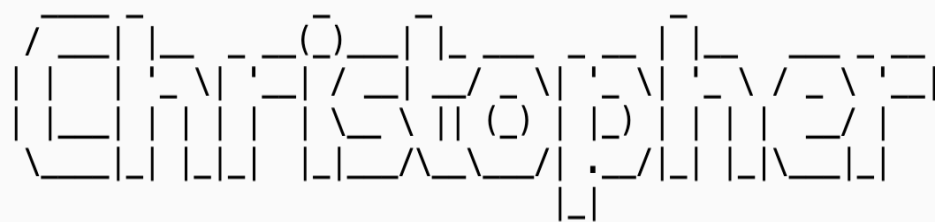3. Activate the funtools environment

```
$ conda activate funtools
```

4. Install Figlet using conda

```
$ sudo apt update
$ sudo apt install figlet
```

5. Run the following command figlet {your name}. Put a screenshot of what you see below ▱


```
(funtools) christarkaa@cloudshell:~$ figlet Christopher
  ___ _          _     _              _
 / __| |_  _ _ _(_)___| |_ ___ _ __| |_  ___ _ _
| (__| ' \| '_| (_-<|  _/ _ \ '_ \  ' \/ -_) '_|
 \___|_||_|_| |_/__/ \__\___/ .__/_||_\___|_|
                            |_|
```

6. Install bwa through the bioconda channel

```
$ conda install -c bioconda bwa
```

7. Install blast through the bioconda channel

```
$ conda install -c bioconda blast
```

8. Install samtools through the bioconda channel

```
$ conda install -c bioconda samtools
```

9. Install bedtools through the bioconda channel
```
$ conda install -c bioconda bedtools
```

10. Install spades.py through the bioconda channel

```
$ conda install -c bioconda spades
```

11. Install bcftools through the bioconda channel

```
$ conda install -c bioconda bcftools
```

12. Install fastp through the bioconda channel

```
$ conda install -c bioconda fastp
```

13. Install multiqc through the bioconda channel

```
$ conda create -n multiqc_env python=3.5
$ conda activate multiqc_env
$ conda install -c bioconda multiqc
```