**BIOCOMPUTING TASK**

Submit the command you used for achieving the following tasks

Command lines/fragments are written in console font and underline.

Acknowledgment: The Babraham Institute, UK.

1. Use the figlet command to draw a graphical representation of your **name**.



1. ~~xcowsay is a stupid program for making a cow talk. Tell the cow to say your name~~
   1. ~~Specify -t 0 for xcowsay. What does it mean?~~
2. In your home directory, create a folder called compare.
   1. Download this file [5MB] into your the compare directory: <https://www.bioinformatics.babraham.ac.uk/training/Introduction%20to%20Unix/unix_intro_data.tar.gz>
   2. Unzip using gunzip command
   3. Then, untar the *.tar* file with tar command
   4. Get into seqmonk\_genomes/Saccharomyces cerevisiae/EF4 and identify the rRNAs present in Mito.dat.
   5. Using cp copy Mito.dat into the compare directory.
   6. Use nano to effect the following edits:
      1. Change Mito to Mitochondrion in the ID and AC header lines
      2. Save the file and exit nano
      3. Rename the file from Mito.dat to Mitochondrion.txt
3. In task 3, in your compare directory, cd into FastQ\_Data directory.
   1. Calculate the total number of lines in lane8\_DD\_P4\_TTAGGC\_L008\_R1.fastq.gz
   2. Print the total number of lines in all fastq.gz files and save it as a new file.
4. Use conda to install the following packages on your cloud server:
   1. Seqtk
   2. Samtools
   3. fastp

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**Your codes goes here**

$ figlet Luisa

$ mkdir compare

$cd compare

$ wget <https://www.bioinformatics.babraham.ac.uk/training/Introduction%20to%20Unix/unix_intro_data.tar.gz>

$ gunzip unix\_intro\_data.tar.gz

$ tar -xvf unix\_intro\_data.tar

$ cd seqmonk\_genomes

$ cd 'Saccharomyces cerevisiae'

$ cd EF4

$ cp Mito.dat /home/luisacriollo17/compare

$ nano Mito.dat

$ mv Mito.dat /home/luisacriollo17/compare/Mitochondrion.txt

$ cd ~

$ cd compare

$ cd FastQ\_Data

$ wc -l lane8\_DD\_P4\_TTAGGC\_L008\_R1.fastq.gz

$ wc -l \*

$ wc -l \* > linesnumber.fastq.gz

$ wget https://repo.anaconda.com/miniconda/Miniconda3-latest-Linux-x86\_64.sh

$ bash Miniconda3-latest-Linux-x86\_64.sh

$ conda install -c bioconda seqtk

$ conda install -c bioconda samtools

$ conda install -c bioconda fastp