***--Prerequisite: Linux Os(ubuntu preferred) and CONDA (package and environment management system).***

***--PASTE the 3 scripts i.e analysis.sh,variantcalling.sh and viral.yml inside the "Directory” with fastq files***

***--Fastq files should be in format name\_1.fastq and name\_2.fastq for P.E forward and reverse end respectively and name.fastq for single end. “Directory” must contain either P.E reads or S.E reads not both.Make separate directory for S.E and P.E if required and paste the 3 files in both directories.***

***--Terminal will ask the user to enter “S” for Single end reads and “P” for paired end reads.***

***--Open the "directory" in terminal and type "bash analysis.sh"***

***--Terminal will ask the user to enter the location of the genome. "Enter the location as /home/USER/directoryname/genome.fa"***