**The SRA Toolkit on the GCP (https://github.com/ncbi/sra-tools/wiki/02.-Installing-SRA-Toolkit)**

**Install sratoolkit**

wget --output-document sratoolkit.tar.gz <http://ftp-trace.ncbi.nlm.nih.gov/sra/sdk/current/sratoolkit.current-ubuntu64.tar.gz>

tar -vxzf sratoolkit.tar.gz

export PATH=$PATH:$PWD/sratoolkit.2.11.0-ubuntu64/bin

vi .bashrc //Add the command above to .bashrc

mkdir data process

vdb-config -i //Configure sratoolkit

// Download SRA data: <https://www.ncbi.nlm.nih.gov/sra/docs/sradownload/>

// https://www.ncbi.nlm.nih.gov/sra/docs/SRA-Google-Cloud/

prefetch SRR873430

Download data

// 1. RNS-seq

// Download SRA in SRA format from <https://www.ncbi.nlm.nih.gov/bioproject/206422>

prefetch SRR873430 //NOT USED <https://trace.ncbi.nlm.nih.gov/Traces/sra/?run=SRR873430>

// Download fastq from <https://trace.ddbj.nig.ac.jp/DRASearch/study?acc=SRP023539>

fastq-dump SRR873427

fastq-dump SRR873836

fastq-dump SRR873428

fastq-dump SRR873430

// Download the simulation data

wget https://bioinfo.uth.edu/VirusFinder/simulation-data.tgz?csrt=11929234083444165632

// 2. Targeted sequencing

Download 3rd party tools

// Download samtools from http://www.htslib.org/download/

wget <https://github.com/samtools/samtools/releases/download/1.13/samtools-1.13.tar.bz2>

tar xvjf samtools-1.13.tar.bz2

export PATH=$PATH:$PWD/bin/samtools-1.13 // Added to .bashrc