Refrence of Homework2

https://www.ncbi.nlm.nih.gov/books/NBK553888/	Single-End vs. Paired-End Sequencing in RNA-Seq
https://www.ncbi.nlm.nih.gov/books/NBK279675/	Efficiency, Depth, Coverage, Accuracy,
https://training.galaxyproject.org/training-material/topics/sequence-analysis/tutorials/quality-control/tutorial.html	Galaxy Platform in Genetics
https://www.bioinformatics.babraham.ac.uk/projects/fastqc/?ref=labworm	FastQC
https://link.springer.com/chapter/10.1007/978-3-662-48986-4_3638	Feature of 5' UTR,3UTR
https://bioinformaticsonline.com/blog/view/44713/understanding-rna-seq-normalization-methods-tpm-vs-fpkm-vs-cpm?wish=stop	FPKM,TPM,PKM
https://usegalaxy.org	Galaxy Platform in Genetics
https://genome.ucsc.edu/goldenPath/help/bed.html	Genomic data structured using the UCSC BED
https://re3data.org	Launched2012
https://re3data.org/search	Registry of Research Data Repositories (re3data.org)
https://www.nature.com/scitable/topicpage/alternative-splicing-in-the-control-of-gene-999/	Types of Gene Splicing
https://github.com/ncbi/sra-tools https://www.ebi.ac.uk/ena/browser/faq#download	SRA , ENA
https://www.htslib.org/doc/samtools.html https://genome.ucsc.edu/FAQ/FAQformat.html#format1 https://broadinstitute.github.io/picard/ https://www.gnu.org/software/sed/manual/sed.html https://www.gnu.org/software/gawk/manual/gawk.html https://spark.apache.org/docs/latest/ https://www.apache.org/	SAM, BED, PANDA,SED,PICARD,APACHE SPARK,SQL,DPLYR,AWK