(base) eilyin@frontend-2-2-13:~$ mkdir /homeworks/hw\_12

(base) eilyin@frontend-2-2-13:~$ ls

(base) eilyin@frontend-2-2-13:~$ cd homeworks

(base) eilyin@frontend-2-2-13:~/homeworks$ ls

(base) eilyin@frontend-2-2-13:~/homeworks$ mkdir hw\_12

(base) eilyin@frontend-2-2-13:~/homeworks$ mkdir ~/homeworks/hw\_12/fastqc

(base) eilyin@frontend-2-2-13:~/homeworks$ mkdir ~/homeworks/hw\_12/trimmed

(base) eilyin@frontend-2-2-13:~/homeworks$ mkdir ~/homeworks/hw\_12/trimmed/fastqc

(base) eilyin@frontend-2-2-13:~/homeworks$ mkdir ~/homeworks/hw\_12/align

(base) eilyin@frontend-2-2-13:~/homeworks$ mkdir ~/homeworks/hw\_12/variant\_calling

(base) eilyin@frontend-2-2-13:~/homeworks$ mkdir ~/homeworks/hw\_12/sam

(base) eilyin@frontend-2-2-13:~/homeworks$ vim ~/homeworks/hw\_12/fastqc/fastqc.sh

(base) eilyin@frontend-2-2-13:~/homeworks$ mkdir ~/homeworks/hw\_12/raw

(base) eilyin@frontend-2-2-13:~/homeworks$ cd ../../

(base) eilyin@frontend-2-2-13:/home$ cd ../

(base) eilyin@frontend-2-2-13:/$ ls

(base) eilyin@frontend-2-2-13:/$ cd projects

(base) eilyin@frontend-2-2-13:/projects$ ls

(base) eilyin@frontend-2-2-13:/projects$ cd mipt\_dbmp\_biotechnology

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology$ ls

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology$ cd genome\_raw

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology$ cd genome\_de\_novo

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genome\_de\_novo$ ls

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genome\_de\_novo$ cd ../

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology$ cd genome

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genome$ ls

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genome$ cd ../

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology$ cd genomics

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genomics$ ls

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genomics$ cd raw

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genomics/raw$ ls

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genomics/raw$ cd

(base) eilyin@frontend-2-2-13:~/homeworks/hw\_12$ ls

(base) eilyin@frontend-2-2-13:~/homeworks/hw\_12$ rmdir raw

(base) eilyin@frontend-2-2-13:~/homeworks/hw\_12$ ls

(base) eilyin@frontend-2-2-13:~/homeworks/hw\_12$ cd ../../

(base) eilyin@frontend-2-2-13:~$ cd ../../

(base) eilyin@frontend-2-2-13:/$ cd projects

(base) eilyin@frontend-2-2-13:/projects$ cd mipt\_dbmp\_biotechnology

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology$ cd genomics

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genomics$ cp raw

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genomics$ cp -r raw ~/homeworks/hw\_12

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genomics$ ls

(base) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/genomics$ cd ~/homeworks/hw\_12

(base) eilyin@frontend-2-2-13:~/homeworks/hw\_12$ cd fastqc

(base) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ ls

(base) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda env list

(base) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda create -n ngs

(base) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda activate ngs

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda install fastqc

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda install multiqc

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda install -c bioconda multiqc

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda install -c bioconda fastqc

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda install -c bioconda multiqc

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda install -c bioconda trimmomatic

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda update -n base -c defaults conda

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda install -c bioconda fastp

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ sbatch fastqc.sh

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ vim fastqc.sh

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ sbatch fastqc.sh

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ vim fastqc.sh

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ sbatch fastqc.sh

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ conda activate sra\_tutorial

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/fastqc$ cd ../

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12$ cd raw

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/raw$ multiqc WGSB\_46\_01\_PTV291209\_325278\_\*\_\*.fq.gz

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/raw$ fastqc WGSB\_46\_01\_PTV291209\_325278\_\*\_\*.fq.gz

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/raw$ multiqc

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/raw$ multiqc

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/raw$ cd ../

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12$ cd trimmed

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ vim fastp.sh

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ sbatch fastp.sh

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ conda activate ngs

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ sbatch fastp.sh

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ vim fastq.sh

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ sbatch fastq.sh

(ngs) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ conda activate sra\_tutorial

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ multiqc ~/homeworks/hw\_12/trimmed

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ multiqc ~/homeworks/hw\_12/trimmed/fastqc

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ multiqc ~/homeworks/hw\_12/trimmed/fastqc

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ cd fastqc

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed/fastqc$ multiqc ~/homeworks/hw\_12/trimmed/fastqc

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed/fastqc$ cd ../

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ ls

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/trimmed$ cd ../

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12$ cd align

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ vim bwa\_wgn.sh

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ sbatch bwa\_wgn.sh

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ vim bwa\_wgn.sh

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ sbatch bwa\_wgn.sh

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ vim bwa\_wgn.sh

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ sbatch bwa\_wgn.sh

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ conda create -n genome

(sra\_tutorial) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ conda activate genome

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ conda install -c bioconda bwa

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ conda install -c bioconda samtools

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ conda install -c bioconda bcftools

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ conda install -c bioconda gatk

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ vim bwa\_wgn.sh

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ sbatch bwa\_wgn.sh

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ cd ../../

(genome) eilyin@frontend-2-2-13:~/homeworks$ cd ../../

(genome) eilyin@frontend-2-2-13:/home$ cd ../

(genome) eilyin@frontend-2-2-13:/$ cd projects

(genome) eilyin@frontend-2-2-13:/projects$ ls

(genome) eilyin@frontend-2-2-13:/projects$ cd mipt\_dbmp\_biotechnology

(genome) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology$ ls

(genome) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology$ ^C

(genome) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology$ cd GRCh38

(genome) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/GRCh38$ ls

(genome) eilyin@frontend-2-2-13:/projects/mipt\_dbmp\_biotechnology/GRCh38$ cd ../../

(genome) eilyin@frontend-2-2-13:/projects$ cd ../

(genome) eilyin@frontend-2-2-13:/$ cd ~/homeworks/hw\_12/align

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12/align$ cd ../

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12$ ls

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12$ cd sam

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12/sam$ vim sam.sh

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12/sam$ sbatch sam.sh

(genome) eilyin@frontend-2-2-13:~/homeworks/hw\_12/sam$