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# ASSIGNMENT | Application of Bioinformatics in Metagenomics

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Applied Bioinformatics

ESTIMATED WORD COUNT (EXCLUDING FIGURES AND QUESTIONS):

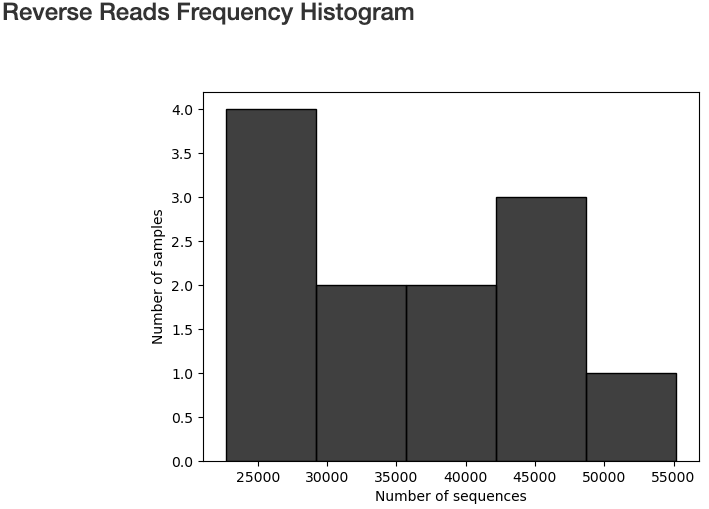
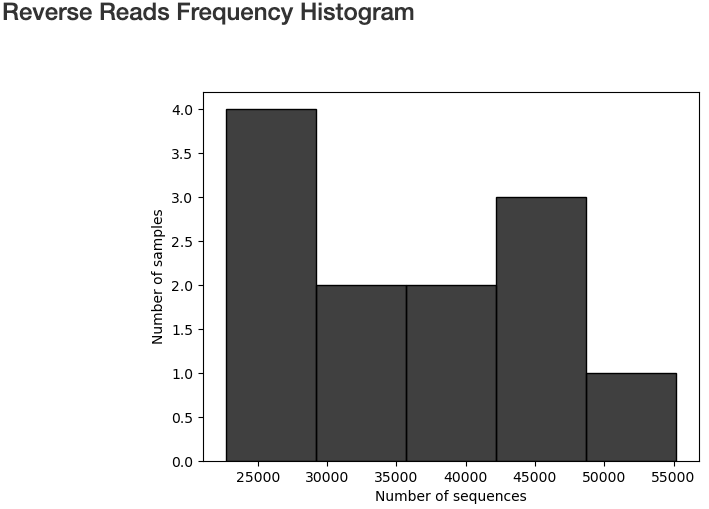
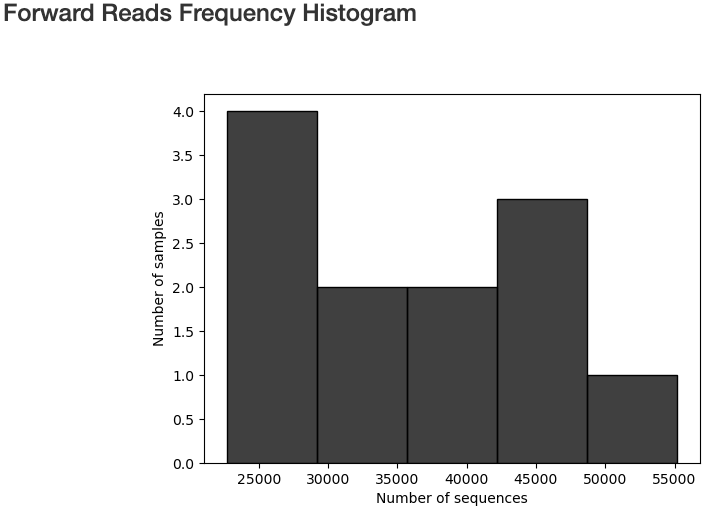
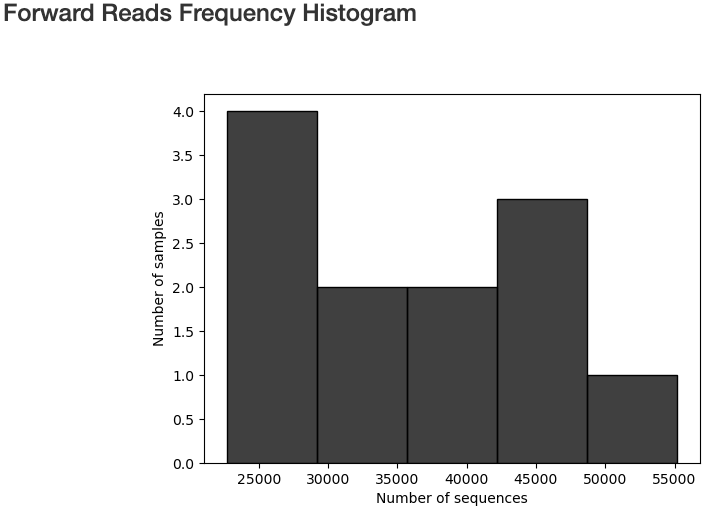
## Download FASTQ files, which correspond to the given twelve SRA IDs

### PASS

## Check quality of the source data using FastQC and MultiQC

### PASS

## Import FASTQ files into QIIME2 file format, pre-process and QC the data with QIIME2 tools



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## Make ASVs feature table using DADA2 algorithm

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## Evaluate phylogeny of identified microbial sequences

### PASS

## Make rarefaction plots, select an appropriate rarefaction threshold

### PASS

## Evaluate and interpret Alpha and Beta diversity in the dataset

### PASS

## Evaluate the taxonomy of the soil microbial communities in the studied grassland sites

### PASS