DAY 1

Download reference files:

!wget

https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/005/845/GCF_000005845.2_ASM584v2/GCF_000005845.2_ASM584v2_genomic.fna.gz

reference sequence of the parental (unevolved, not resistant to antibiotics) E. coli strain

wget

https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/005/845/GCF_000005845.2_ASM584v2/GCF_000005845.2_ASM584v2_genomic.gff.gz

wget https://figshare.com/ndownloader/files/23769692
wget https://figshare.com/ndownloader/files/23769689

zcat 23769689 | head -20

Managing environments:

micromamba install -c bioconda trimmomatic fastqc bwa samtools igv varscan snpeff

```
zcat reads1.fa.gz | wc -l \\ 1823504 /4 = 455876 reads zcat reads2.fa.gz | wc -l \\ 1823504 /4 = 455876 reads
```

fastqc -o . reads1.fa.gz reads2.fa.gz

Trimming reads by 20 quality:

https://datacarpentry.org/wrangling-genomics/03-trimming.html

```
gunzip reads1.fa.gz > rreads1.fastq
gunzip reads1.fa.gz > rreads2.fastq
```

trimmomatic PE -threads 4 -phred33 rreads1.fastq rreads2.fastq trimmed1.fastq untrimmed1.fastq trimmed2.fastq untrimmed2.fastq LEADING:20 TRAILING:20 SLIDINGWINDOW:10:20 MINLEN:20

fastqc -o . trimmed1.fastq trimmed2.fastq

Trimming reads by 30 quality:

mkdir trimmed 30

trimmomatic PE -threads 4 -phred33 rreads1.fastq rreads2.fastq \ trimmed 30/R1.trimmed.fastq trimmed 30/R1 un.trimmed.fastq \

 $trimmed_30/R2.trimmed.fastq\ trimmed_30/R2_un.trimmed.fastq\ \backslash$

LEADING:30 TRAILING:30 SLIDINGWINDOW:10:30 MINLEN:20

!mkdir fastqc_trimmed_30 !fastqc trimmed 30/* -o fastqc trimmed 30

DAY 2

Aligning sequences to reference

Index the reference file bwa index ref/GCF*fna.gz

Align your reads

bwa mem ref/GCF_000005845.2_ASM584v2_genomic.fna.gz trimmed/R1.trimmed.fastq trimmed/R2.trimmed.fastq > align/GCF_000005845.2_ASM584v2_genomic.sam

Compress SAM file

samtools view -S -b align/*.sam > align/GCF_000005845.2_ASM584v2_genomic.bam

samtools flagstat align/*bam # 99.87 % of reads were mapped

Sort and index BAM file

samtools sort align/*bam -o align/GCF_000005845.2_ASM584v2_genomic.sorted.bam samtools index align/*sorted.bam

Variant calling

samtools mpileup -f ref/GCF_000005845.2_ASM584v2_genomic.fna align/GCF_000005845.2_ASM584v2_genomic.sorted.bam > var_call/GCF_000005845.2_ASM584v2_genomic.mpileup

varscan mpileup2snp var_call/*mpileup --min-var-freq 0.4 --variants --output-vcf 1 > var_call/vs_results.vcf

Automatic SNP annotation

```
wget
```

```
https://ftp.ncbi.nlm.nih.gov/genomes/all/GCF/000/005/845/GCF_000005845.

2_ASM584v2/GCF_000005845.2_ASM584v2_genomic.gbff.gz
echo "k12.genome : ecoli_K12" > snpEff.config
mkdir -p db/k12
gunzip *gbff.gz
ls
cp *gbff db/k12/genes.gbff
snpEff build -genbank -v k12
```

GENES FROM IGV

1. ftsl

Loc 93,043 Ref C Alt G

544 aminoacid from Ala(hydrophobic) to Gly

Inhibited by beta-lactam antibiotics such as penicillin, moenomycin, macarbomycin, furazlocillin and piperacillin. Antibiotics inhibit the activity by binding to the catalytic serine https://www.ncbi.nlm.nih.gov/pmc/articles/PMC305773/

FtsI (also called PBP3) of Escherichia coli is a transpeptidase required for synthesis of peptidoglycan in the division septum and is one of several proteins that localize to the septal ring.

Ampicillin acts as an irreversible inhibitor of the enzyme transpeptidase, which is needed by bacteria to make the cell wall.

https://www.rcsb.org/structure/7ONN

https://pubmed.ncbi.nlm.nih.gov/34356681/

2.acrB (for discussion)

569 aninoacid Gln (polar uncharged) to Leu(hydrophobic) Acroflavine resistance family https://pubmed.ncbi.nlm.nih.gov/15155734/

https://pubmed.ncbi.nlm.nih.gov/18781920/

The E. coli AcrB protein is a transporter that is energized by proton-motive force and that shows the widest substrate specificity among all known multidrug pumps, ranging from most of the currently used antibiotics, disinfectants, dyes, and detergents to simple solvents

https://www.rcsb.org/structure/2HQC

Unimportant:

rsgA - s30 mitochondrial

EnvZ functions as a membrane-associated protein kinase that phosphorylates OmpR in response to environmental signals

glnH - glutamine transport

DAY 3 TASKS

- Figure out what mutations do
- Classify mechanism of resistance
- Make recommendations for alternative treatment

Github page - https://github.com/Aryunaa/bioPrac_p1