**Assignment**

You are a member of a team investigating a recent Salmonella outbreak in a local community. The outbreak has been traced back to a local pork restaurant, but the source of the contamination is not yet clear. Your team has collected samples from various sources including the pork meat served at the restaurant, the restaurant's drinking water, and some of the affected individuals. Your task is to use WGS and genomic analysis to identify the source of contamination.

**Questions:**

1. Explain the principles of genomic sequencing and describe the main types of sequencing technologies used in pathogen genomics.

2. Describe the steps involved in the genomic characterization of a foodborne epidemic from sample collection to interpretation of results.

3. Your team has obtained genomic sequencing data. These sequences are provided in the following link in fasta format, i.e., an already assembled genome file: [https://figshare.com/s/d6e7df4a555478a38aa6](https://figshare.com/s/d6e7df4a555478a38aa6](https://figshare.com/s/d6e7df4a555478a38aa6%5d(https://figshare.com/s/d6e7df4a555478a38aa6)

The Salmonella samples in this link are:

* From fish samples ID:18 to 54
* Water samples ID: 164 to 181
* Sick Patient stool samples: ID 185 to 376.

Proceed with genomic characterization including confirmation of the serovar, MLST, and statistical data on the quality of sequences at your disposal. You can present these results in tabular form.

4. Discuss the likely source of the epidemic at this stage.

5. Using Resfinder and PlasmidFinder, determine the resistance genes and the genetic mechanisms underlying antimicrobial resistance (e.g., mobile elements like plasmids) present in the strains and discuss the implications of your findings for the epidemic.

6. You are informed that the reference strain corresponding to the sequences you have is the strain with the accession number CP028357. Find this reference strain in NCBI and download it in fasta format.

7. Use the reference strain and other provided strains (pork, water, and patients) to produce a phylogenomic analysis. This can be done online with the CSIPhylogeny tool.

Display and interpret the phylogenetic tree.

8. Discuss the limitations and challenges associated with using genomics for outbreak investigations. Include in your answer a discussion on the limitations of genomics to identify the source of contamination in situations where there is cross-transmission between different locations or complex environmental contamination.