# FINAL GENOME ANALYSIS

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BIOL 4810 — Bioinformatics

# Introduction

| | |
|---|---|
| **Bacteria**: | *Vibrio cholerae* |
| **Sample Description**: | O1 |
| **SRR**: | SRR33049458 |
| **Background**: | Two specific serogroups of *Vibrio cholerae* are associated with causing cholera—O1 and O139. |
| **Question**: | Will pathogenic *Vibrio* species have higher Average Nucleotide Identity (ANI) results with my *V. cholerae* sample than non-pathogenic *Vibrio* species? |

# Methods ( ⅓)

1. Genome Assembly with SPAdes (v4.1.0) and ABySS (v2.3.7)
2. Quality Check with QUAST (v5.3.0)

## SPAdes QUAST Report

| Assembly | scaffolds |
|---|---|
| # contigs (>= 0 bp) | 837 |
| # contigs (>= 1000 bp) | 55 |
| # contigs (>= 5000 bp) | 25 |
| # contigs (>= 10000 bp) | 19 |
| # contigs (>= 25000 bp) | 17 |
| # contigs (>= 50000 bp) | 17 |
| Total length (>= 0 bp) | 4456675 |
| Total length (>= 1000 bp) | 4034084 |
| Total length (>= 5000 bp) | 3972412 |
| Total length (>= 10000 bp) | 3925738 |
| Total length (>= 25000 bp) | 3901578 |
| Total length (>= 50000 bp) | 3901578 |
| # contigs | 476 |
| Largest contig | 638239 |
| Total length | 4295388 |
| GC (%) | 47.69 |
| N50 | 246717 |
| N90 | 72121 |
| auN | 325175.3 |
| L50 | 5 |
| L90 | 17 |
| # N's per 100 kbp | 6.98 |

## ABySS QUAST Report

| Assembly | assembly-scaffolds |
|---|---|
| # contigs (>= 0 bp) | 1001 |
| # contigs (>= 1000 bp) | 149 |
| # contigs (>= 5000 bp) | 113 |
| # contigs (>= 10000 bp) | 85 |
| # contigs (>= 25000 bp) | 51 |
| # contigs (>= 50000 bp) | 26 |
| Total length (>= 0 bp) | 4166685 |
| Total length (>= 1000 bp) | 4008622 |
| Total length (>= 5000 bp) | 3900163 |
| Total length (>= 10000 bp) | 3697469 |
| Total length (>= 25000 bp) | 3169209 |
| Total length (>= 50000 bp) | 2250260 |
| # contigs | 170 |
| Largest contig | 172801 |
| Total length | 4021995 |
| GC (%) | 47.50 |
| N50 | 57580 |
| N90 | 12537 |
| auN | 65738.4 |
| L50 | 22 |
| L90 | 79 |
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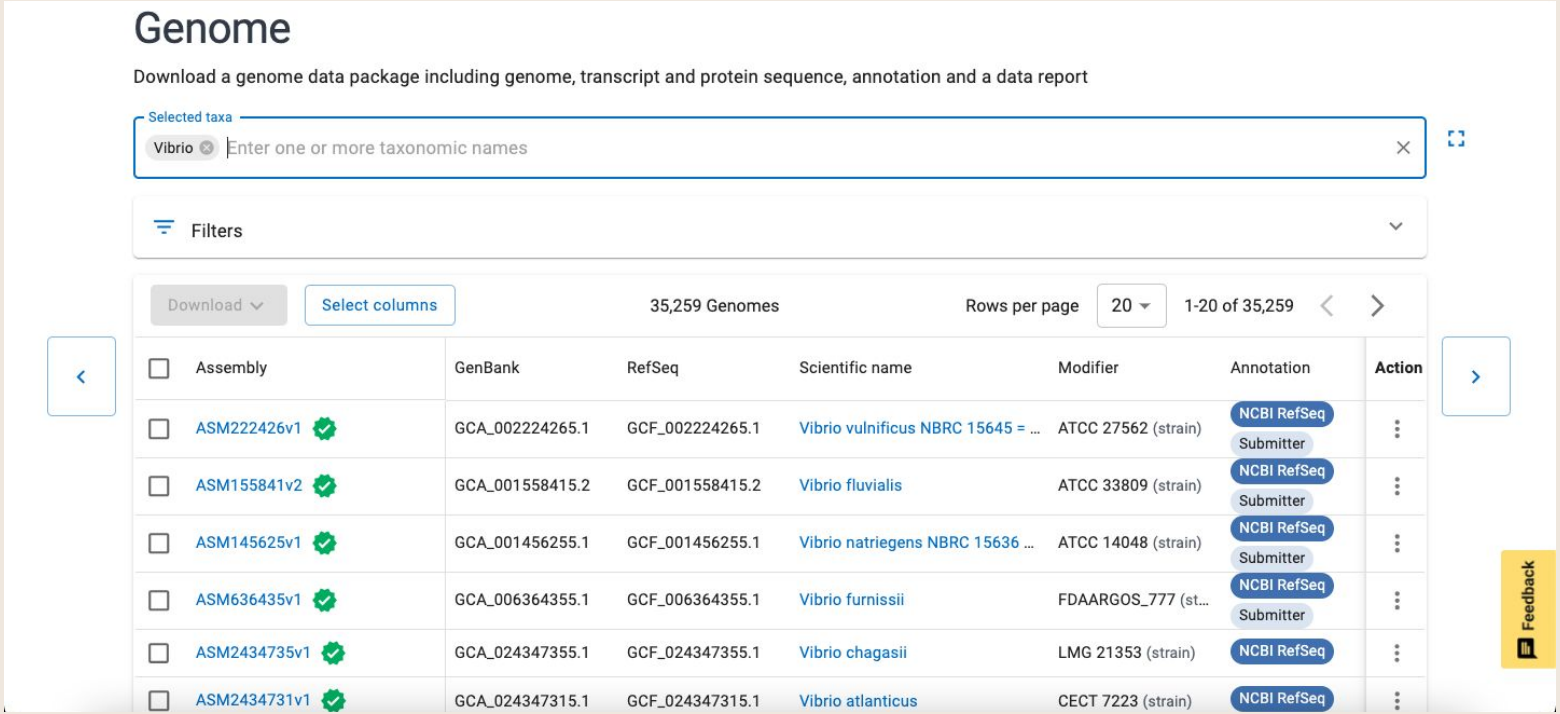
# Methods ( ⅔)

## 3. Use NCBI to download *Vibrio* spp. files.



# Methods (3/3)

## 4. Determine Pathogenicity with PathogenFinder2 (v0.4.1)

| ***Vibrio* spp.** | **PathogenFinder2 Results** | **Categorization** |
|---|---|---|
| *V. vulnificus* | 0.9501 | Human Pathogenic |
| *V. diazotrophicus* | 0.7999 | Human Pathogenic |
| *V. ponticus* | 0.7405 | Human Pathogenic |
| *V. tritonius* | 0.6404 | Human Pathogenic |
| *V. tasmaniensis* | 0.4500 | Human Non Pathogenic |
| *V. rumoiensis* | 0.3899 | Human Non Pathogenic |
| *V. penaeicida* | 0.3347 | Human Non Pathogenic |
| *V. atlanticus* | 0.2794 | Human Non Pathogenic |
| *V. cholerae* | 0.9765 | Human Pathogenic |

# Results

## 5. Measure Overall Similarity Between Genomes with fastANI (v1.34)

vibrioneighbors.txt — Edited

```
spadesout/scaffolds.fastavulnificus.fasta        78.912     414     1320
spadesout/scaffolds.fastadiazotrophicus.fasta    78.8503    378     1320
spadesout/scaffolds.fastaponticus.fasta          78.7645    337     1320
spadesout/scaffolds.fastatritonius.fasta         78.6619    309     1320
spadesout/scaffolds.fastaatlanticus.fasta        78.1464    269     1320
```

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|---|---|---|---|
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# Conclusion

The fastANI algorithm is designed to remove distant genomes (Jain et al., 2018).

Given that 3/4 of the non-pathogenic *Vibrio* spp. were removed from the fastANI results, it is likely they share less similarity to the *V. cholerae* sample than the pathogenic *Vibrio* spp.

# References

Ferrer Florensa, A., Almagro Armenteros, J. J., Kaas, R. S., Clausen, P. T., Nielsen, H., Rost, B., Aarestrup, F. M. (2025). Whole-genome prediction of bacterial pathogenic capacity on novel bacteria using protein language models, with PathogenFinder2. bioRxiv, 2025-04.

Jain, C., Rodriguez-R, L.M., Phillippy, A.M. *et al.* High throughput ANI analysis of 90K prokaryotic genomes reveals clear species boundaries. *Nat Commun* 9, 5114 (2018). https://doi.org/10.1038/s41467-018-07641-9