

1. Launch WSL (To be followed by Windows users only)

- Search WSL from Start Menu Search (Press Windows key and start typing).



- Click to Launch

2. Launch macOS Terminal (To be followed by macOS users only)

- Search Terminal using Spotlight (Press Command + Space and start typing).



3. Create class2 environment (git, python, biopython) (Both Windows and MacOS users)

```
conda create -n class2 -c bioconda -c conda-forge -c default python biopython git
```

4. Activating class2 environment (Both Windows and MacOS users)

```
conda activate class2
```

5. Download the genomic.fa and genomic.gff record (Both Windows and MacOS users)

Unix commands used:

- gunzip
- ls
- cp

8. Vibe Coding Practice Tasks (Both Windows and MacOS users)

- ORI signal checker: K-mer enrichment and plotting
 - identifies overrepresented k-mers along a genome by counting their occurrences in sliding windows. The enrichment patterns are visualized as plots to highlight localized sequence signals.
 - Given: k = 8, window size = 5000 and step = 500
- Clump finder: L,k,t clumps
 - detects k-mers that appear at least t times within a window of length L. Such (L, k, t)-clumps indicate regions of local sequence repetition.
 - Given: k = 8, t = 3 and L = 1000
- GC skew calculator

$$\text{GC skew} = \frac{G - C}{G + C}$$

- GC skew across sliding windows of a genome.
- window size = 5000 and step = 500
- ORI (Origin of Replication) finder
 - To find ORI using k-mer enrichment and GC skew in genomic sequence.
 - Given: k = 8, window size = 5000 and step = 500

9. Push on GitHub repo (Both Windows and MacOS users)

Git setup commands (to be done once only):

```
git config --global user.name "username"
```

```
git config --global user.email "email"
```

Linux commands:

- mv
- cp
- mkdir

Git commands:

- clone
- status
- add
- push