BIODIVERSITY **PSOW** **A3.1 DIVERSITY OF ORGANISMS**

Genome Databases

Introduction

A genome is the totality of genetic information present in every cell within an organism – this includes all genes as well as non-coding DNA sequences. Genomes will vary in both size (total amount of DNA) and organisation (total number of chromosomes). Due to the significant diversity, genome size is not a valid indicator of genetic complexity. Online databases are commonly used to compare genome sizes.

Aim

To use an online database (National Centre for Biotechnology Information) to compare genome sizes

Method

1. Go to the genome database in the NCBI website: https://www.ncbi.nlm.nih.gov/datasets/genome/
2. Enter a species name into the search bar (scientific names are likely to yield more specific results)
3. Click on the link underneath the Assembly filter (it should not matter which modifier is selected)
4. Scroll down to Assembly statistics and record the genome size (should be the first statistic listed)
5. Find the genome size for at least two different viruses, two bacteria, two plants and two animals
    - Examples from syllabus: HIV, JEV, *E. coli*, *V. fischeri*, Orchidaceae, Fabaceae, *Homo sapiens*

Results

	Viruses		**Bacteria**	
Organism				
Genome Size				

	Plants		**Animals**	
Organism				
Genome Size				

Discussion

1. Describe the pattern seen in the comparative genome sizes of viruses, prokaryotes and eukaryotes

2. Suggest reasons for the differences in genome sizes between prokaryotic vs eukaryotic organisms

3. Provide an example of the extreme variation in genome sizes seen within eukaryotic organisms

4. Compare the dinoflagellates *Prorocentrum cordatum* and *Pyrocystis lunula* and explain what these two species suggests about the relationship between the genome size and the genetic complexity of species