

## Appendix 2

### Query Options for the Download of the Original Versions of the Datasets

#### **Mitochondrial dataset (Nov 16, 2020) :**

We used the software Geneious and the following keywords: *Mitochondrion*, *Mitochondria*, *Vertebrata* and *Complete Genome*.

#### **Bacterial dataset (Jan 18, 2021):**

We downloaded the file `bac120_taxonomy_r95.tsv` directly from GTDB <https://data.gtdb.ecogenomic.org/releases/release95/95.0/> and filtered the families from the complete taxonomy.

#### **Influenza A virus dataset (Oct 14, 2020):**

The sequences were downloaded directly from:

<https://www.ncbi.nlm.nih.gov/genomes/FLU/dataset/nph-select.cgi#mainform>, using the following query options:

- sequence type: Nucleotide
- type: A
- subtypes: H1N1,H2N2, H5N1, H7N3, and H7N9
- segment: 6(NA)
- other options: default
- full length only
- collapse identical

-----Dataset Statistics -----

Total num of classes: 5

Total num of sequences: 13078

Min genome length: 52

Avg genome length: 1392.2

Max genome length: 1544

Data distribution:

H5N1	=>	3095
H2N2	=>	175
H1N1	=>	9189
H7N9	=>	293
H7N3	=>	326

### **Dengue virus dataset (Oct 14, 2020):**

The sequences were downloaded directly from:

<https://www.ncbi.nlm.nih.gov/genomes/VirusVariation/dataset/nph-select.cgi?taxid=12637>, using the following query options:

- sequence type: Nucleotide
- other options: default
- collapse identical
- full-length only

#### -----Dataset Statistics -----

Total num of classes: 5

Total num of samples: 5868

Min genome length: 10161

Avg genome length: 10582.002044989775

Max genome length: 11195

Data distribution:

Subtype-1	=>	2446
Subtype-2	=>	1891
Subtype-3	=>	1121
Subtype-4	=>	407
N/A	=>	3

### **Hepatitis B virus dataset (Oct 14, 2020):**

The whole dataset was downloaded directly from:

<https://hbvdb.lyon.inserm.fr/HBVdb/HBVdbDataset?seqtype=0>.

#### -----Dataset Statistics -----

Total num of classes: 6

Total num of samples: 6493

Min genome length: 3182

Avg genome length: 3209.943015555213

Max genome length: 3254

Data distribution:

A	=>	880
B	=>	1765
C	=>	2194
D	=>	1090
E	=>	306
F	=>	258

**Note:** The curated datasets used to obtain the results in the paper can be found at:

<https://github.com/millanp95/DeLUCS/tree/master/data>