Analysis of Omics Data - Homework 2 Part 1

By R. Urdiales Muñoz, M. A. Grela Hernandez, J. R. Alonso Fernandez.

Preamble and objectives

With the worldwide spread of SARS-CoV-2 the concern about natural reservoirs of virus has increased. On this proposal, we will take a look on the use of omic data analysis on identifying potential species which could act as a reservoir for viruses. Proposed viruses:

```
Virus:          Sars-CoV        MERS-CoV        Measles
Protein:        ACE2            DDP4 (CD26)     SLAM (CD150)
```

Analysis Proposal

Part 1: look for similar receptors in other species

We will take a set of human proteins known to be bind by viroids, and we will align their sequences to multiple different species in order to retrieve the most similar. We will use the the NCBI tool and database for that purpose.

Part 2: find evidence for known transmission

For each of the species we will research scientific literature for evidence of the transmission of those virus, and split the previous result based on that. This part will need to be done manually, which shows the importance and potential benefits of publishing biologic research following the FAIR principles.

Part 3: compare and search for specific regions

We will align the proteins from species known to be affected by the virus and search for the conserved regions. Then, we will compare to the rest of the proteins in search for differences. We will use the provided Galaxy server for that purpose.

We will then use those patterns to search again for new proteins and repeat the process in hope of discovery for potential new species. In case the molecular interactions have been already described in the literature, we will also compare the results with the known facts.