Background:

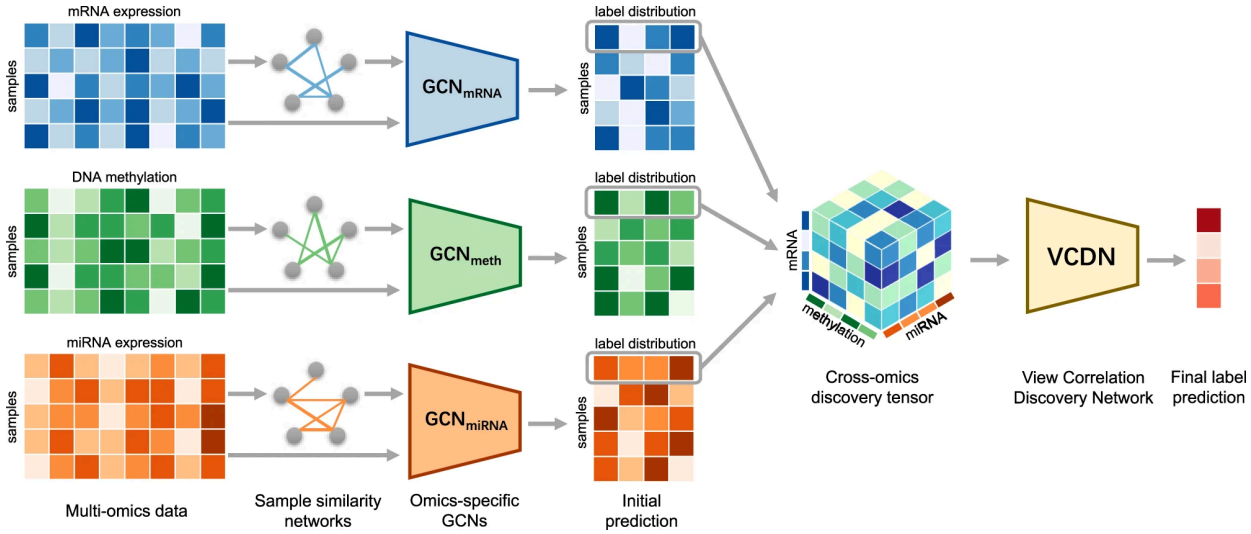
MOGONET is a computational method that integrates multiple types of omics data (like mRNA and DNA methylation) using graph convolutional networks to improve biomedical classification tasks. MOGONET excels in recognizing correlations between different omics datasets and identifying relevant biomarkers, outperforming other state-of-the-art methods in various biomedical applications. This approach is shown to be particularly effective in predicting diseases and analyzing complex biomedical data.

Spiking Neural Networks (SNNs) are a type of artificial neural network that mimics the behavior of biological neurons. Unlike traditional neural networks that process continuous data inputs using simple activation functions, SNNs operate using discrete events called spikes. These spikes are binary events (either firing or not firing) and are used to process and transmit information.

Starting Point:

Here we provide the architecture on which you should base your study and the python library you should use to accomplish the goal. MOGONET integrates multi-omics data using graph convolutional networks allowing patient classification and biomarker identification | Nature Communications

1. MOGONET (this repo holds the code and the dataset necessary to solve the task):
    - https://github.com/txWang/MOGONET
    - https://github.com/txWang/MOGONET/tree/main/BRCA (dataset we what you to focus on)
    - https://github.com/txWang/MOGONET/blob/main/models.py (model you need to convert in
      spiking)



2. snnTorch library (the framework adopted to convert LMU)
    - documentation: https://snntorch.readthedocs.io/en/latest/
    - tutorials: https://snntorch.readthedocs.io/en/latest/tutorials/index.html

Goal:

We want you to convert this model architecture into a spiking one. The idea behind this conversion is based on the fact that all the activation functions can be seen as neurons, so what we would like to implement is an architecture where neurons replace these activation functions.