Machine Learning in Applications
Bio-inspired Spatial Data Project Report

Gabriele Quaranta, Giulio Maselli, Mattia Pecce, Alperen Bitirgen
Politecnico di Torino

CONTENTS

LIST OF FIGURES

LIST OF TABLES

Machine Learning in Applications Bio-inspired Spatial Data Project Report

***Abstract*—In this study, we introduce SMOGONET, a Spiking Neural Network (SNN) adaptation of MOGONET, designed for the integration and classification of multi-omics data in biomedical applications. SMOGONET leverages the energy-efficient, spike-based computations of SNNs to enhance the performance in breast cancer diagnosis using the Breast Invasive Carcinoma (BRCA) dataset from The Cancer Genome Atlas (TCGA).**

By converting the Graph Convolutional Networks (GCNs) and the View Correlation Discovery Network (VCDN) components of MOGONET into their spiking equivalents, SMOGONET effectively captures both intra- and cross-omics correlations while provinding an increase in performance compared to the original mode.

Our findings suggest that SMOGONET offers a promising avenue for efficient and accurate multi-omics data integration

I. Introduction

In recent years, the integration of multi-omics data has emerged as a powerful approach for enhancing our understanding of complex biological systems and improving disease classification. One such application is in breast cancer, where the integration of diverse molecular data types can potentially lead to more accurate diagnosis and prognosis.

Among the various methods developed for multi-omics integration, MOGONET (Multi-Omics Graph cOnvolutional NETwork) [1] has shown promising results in biomedical classification tasks. MOGONET exploits of both sample-wise correlations within each omics type and label-space correlations across different omics data types. However like many deep learning models, it faces challenges in terms of computational efficiency and energy consumption, particularly when dealing with large-scale datasets.

To address these challenges, we propose SMOGONET (Spiking Multi-Omics Graph cOnvolutional NETwork), an adaptation of MOGONET that incorporates principles from spiking neural networks (SNNs).

SNNs, inspired by the biological functioning of the human brain, have gained attention for their potential to reduce energy consumption and improve computational efficiency in neural network models. By converting MOGONET to a spiking version, we aim to enhance its classification performance while reducing computational overhead.

We present SMOGONET as a spiking neural network-based framework for multi-omics data integration and classification, with a specific focus on breast cancer diagnosis. We detail the architecture of SMOGONET, explaining how it adapts the GCN and VCDN components of MOGONET to work with spike-based computations. We evaluate the performance of SMOGONET on breast cancer multi-omics datasets, comparing its performance against the original MOGONET and other state-of-the-art multi-omics integration methods.

II. Background

A. Spiking Neural Networks

Spiking neural networks (SNNs) are biologically inspired artificial neural networks that mimic the behavior of biological neurons more closely than traditional artificial neural networks. In SNNs, neurons communicate through discrete spikes or action potentials, rather than continuous values.

The membrane potential V(t) of a spiking neuron can be modeled using the leaky integrate-and-fire (LIF) equation:

$$\tau \frac{dV}{dt} = -V(t) + RI(t)$$

Where τ is the membrane time constant, R is the membrane resistance, and $I(t)$ is the input current. When $V(t)$ reaches a threshold V_{th}, the neuron fires a spike and its potential is reset to a resting value.

SNNs have gained attention for their potential energy efficiency and ability to process spatiotemporal data. Various learning algorithms have been developed for SNNs, including spike-timing-dependent plasticity (STDP) and variants of backpropagation adapted for spiking neurons (Tavanaei et al., 2019).

B. Spiking Convolutional Networks

The SpikingGCN [2] approach combines Graph Neural Networks (GNNs) and Spiking Neural Networks (SNNs) to address the challenge of semi-supervised node classification in graphs. This novel method aims to perform biologically interpretable reasoning on graph structures in an energy-efficient manner, representing graphs as sets of nodes and their relationships.

The SpikingGCN architecture consists of several key components. It employs a graph convolution technique inspired by GCN and SGC to incorporate both topological information and node attributes. This is followed by a representation encoding step, which transforms continuous node representations into discrete spike signals using a probability-based Bernoulli encoding scheme. The spike encoder extracts information from the graph and outputs hidden states of each node as spike trains.

The key idea behind SpikingGCN is to incorporate topological information of the graph into the node representations. This is achieved by normalizing the weights using the adjacency

relationship, allowing nodes to selectively aggregate attributes from their neighbors.

The update rule for the node representation $\mathbf{h}_i$ is given by:

$$\mathbf{h}_i \leftarrow \frac{1}{d_i+1}\mathbf{x}_i + \sum_{j=1}^{N} \frac{a_{ij}}{\sqrt{(d_i+1)(d_j+1)}}\mathbf{x}_j$$

where:

- $\mathbf{h}_i$ is the new representation of node v_i.
- $\mathbf{x}_i$ is the original attribute (feature) of node v_i.
- d_i is the degree of node v_i.
- a_{ij} is the element of the adjacency matrix A, indicating whether there is an edge between node i and node j.
- N is the total number of nodes in the graph.

This update rule means that each node's new representation is a weighted combination of its own attribute and the attributes of its neighbors. The weights are normalized by the degrees of the nodes to ensure that the representation is balanced across the graph.

C. Dataset: BRCA Multi-Omics Data

We focus on the Breast Invasive Carcinoma (BRCA) dataset from The Cancer Genome Atlas (TCGA) program. This comprehensive dataset provides a rich source of multi-omics data for breast cancer research, enabling in-depth analysis and classification of breast cancer subtypes.
The BRCA dataset encompasses multiple types of omics data collected from breast cancer patients, including:

- Gene Expression (GE) data: This consists of RNA sequencing data, providing information about gene expression levels across the genome.
- DNA Methylation (ME) data: This data type represents the epigenetic modifications of DNA, which can influence gene expression without altering the DNA sequence.
- miRNA Expression (MI) data: This includes expression levels of microRNAs, small non-coding RNA molecules that play crucial roles in gene regulation.

For our study, we focus on these three omics data types (due to their complementary nature and potential to provide a comprehensive molecular profile of breast cancer. The dataset includes samples from 891 patients, each with matched data across all three omics types.

D. MOGONET

MOGONET is a novel supervised multi-omics integration framework designed for biomedical classification tasks. The approach begins with preprocessing and feature pre-selection to reduce noise and redundancy in the data. It employs Graph Convolutional Networks (GCNs) to learn classification tasks for each omics data type individually. This is achieved by constructing weighted sample similarity networks using cosine similarity for each omics type, allowing the GCNs to leverage information from both the omics data and sample correlations for improved prediction.

The framework utilizes the initial predictions from each omics-specific GCN to construct a cross-omics discovery tensor, which captures cross-omics label correlations. This tensor is reshaped into a vector and fed into a Variation-based Cross-Domain Network (VCDN) for final label prediction. The VCDN effectively integrates the initial predictions by exploring latent correlations across different omics data types in a higher-level label space.

The key innovation of MOGONET lies in its ability to combine effective omics-specific predictions from GCNs with learned cross-omics label correlation knowledge from VCDN. This makes it the first method to exploit both GCNs and cross-omics relationships in the label space for multi-omics integration in biomedical data classification tasks.

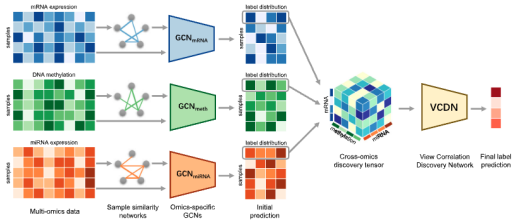

Fig. 1. **MOGONET Architecture:** MOGONET combines GCN for multi-omics-specific learning and VCDN for multi-omics integration.

I

III. SMOGONET

MOGONET operates by first preprocessing omics data and using Graph Convolutional Networks (GCNs) to learn from each omics type separately, constructing a sample similarity network. Initial predictions from these GCNs are combined into a cross-omics discovery tensor, capturing correlations across different omics types. This tensor is then processed by a View Correlation Discovery Network (VCDN) to refine the final predictions.

In our approach to converting MOGONET to a Spiking Neural Network (SNN), we draw inspiration from Spiking GCNs, as described by Zhu et al. (2022). During the preprocessing step for each omics view, we incorporate the topological structure of the data by applying the update rule prior to converting the data to rate encoding.

This method enables us to restructure the three GCNs as simple spiking neural networks, allowing for faster training while maintaining an equivalent level of information aggregation as achieved by conventional convolutional networks.

The outputs from the three SGCNs are then utilized directly to construct a cross-omics discovery tensor, following a strategy similar to that outlined in the original MOGONET framework. This tensor is subsequently reshaped and fed into a spiking equivalent of the VCDN (SVCDN) from MOGONET. The SVCDN facilitates the integration of information from each omics-specific network by leveraging the correlations across different omics data types.

Consistent with the original model, our proposed SMOGONET is trained end-to-end, involving an initial

pretraining of the individual SGCNs followed by the training of the entire architecture.

In addition to following the training procedure outlined in the original paper, we implemented an evolutionary algorithm for parameter selection. Details on this approach will be further discussed in the Ablation Studies section.

IV. Results and discussion

We compare the classification performance of SMOGONET with the original MOGONET model and other existing supervised multi-omics integration algorithms. I

Model	Acc	F1	F1 Macro
SMOGONET (ours)	0.840	0.843	0.802
SMOGONET_EA (ours)	0.847	0.851	0.813
MOGONET	0.829	0.825	0.774
NN_VCDN	0.792	0.781	0.721
KNN	0.742	0.730	0.682
SVM	0.729	0.702	0.640
Lasso	0.732	0.698	0.642
XGBoost	0.781	0.764	0.701

TABLE I
CLASSIFICATION RESULTS ON BRCA DATASET.

The results indicate that our proposed model, SMOGONET, outperforms several established methods in terms of accuracy, F1 score, and F1 macro for multi-omics integration in biomedical classification tasks.

SMOGONET achieved an accuracy of 0.840, an F1 score of 0.843, and an F1 macro of 0.802, surpassing the performance of MOGONET (0.829, 0.825, 0.774) and other traditional models such as NN_VCDN, KNN, SVM, Lasso, and XGBoost.

Additionally, the enhanced version, SMOGONET_EA, which utilizes an evolutionary algorithm for parameter selection, further improves performance with an accuracy of 0.847, an F1 score of 0.851, and an F1 macro of 0.813.

These results highlight the effectiveness of our approach, particularly the evolutionary algorithm, in optimizing the model's parameters and achieving superior predictive performance compared to existing methods.

The higher F1 and F1 macro scores achieved by SMOGONET and SMOGONET_EA indicate that our models not only performs well in overall accuracy but also perform consistently well across all classes. This suggests that our models are more effective at identifying both majority and minority classes, reducing biases and leading to more reliable predictions in biomedical classification tasks.

V. Ablation Studies

A. Rate VS Latency Encoding

In rate encoding, information is represented by the frequency of spikes over a given period; a higher firing rate (more spikes) corresponds to a stronger stimulus. In contrast, latency encoding conveys information through the timing of a neuron's first spike, with stronger stimuli causing earlier spikes.

The preprocessing of data and the algebraic operations required to compute node representations can be performed independently of the encoding method used to convert the data into spike trains. However, using latency encoding results in a performance decrease of approximately 30

The Leaky Integrate-and-Fire (LIF) neurons in our model integrate incoming spikes over time and fire when the accumulated membrane potential reaches a threshold. This mechanism is inherently compatible with rate encoding, where information is encoded by spike frequency over time.

Batch normalization is also more suited to rate encoding, as it normalizes outputs based on data batches. In latency encoding, the precise timing of the first spike is important, and normalization could disrupt this timing information, leading to a significant reduction in performance.

Model	Acc	F1	F1 Macro
$SMOGONET$	0.840	0.843	0.802
$SMOGONET_{latency}$	0.627	0.577	0.434
$SMOGONET_{no\ batch\ norm}$	0.498	0.331	0.132
$SMOGONET_{no\ L2\ reg}$	0.833	0.838	0.803
$SMOGONET_{SGD}$	0.311	0.305	0.297
$SMOGONET_{Adamax}$	0.836	0.839	0.786

TABLE II
ABLATION STUDIES

B. Batch Normalization

Batch normalization plays a crucial role in stabilizing and accelerating the training of neural networks, including spiking neural networks (SNNs) such as SMOGONET. It helps maintain a stable distribution of neuron activations, preventing them from becoming too large or too small during training. This stabilization is particularly important in spiking neural networks, where the timing and frequency of spikes are critical for effective learning. Batch normalization ensures consistent spiking behavior across layers, which promotes more reliable and efficient learning.

The results clearly demonstrate the significant impact of batch normalization on performance: models with batch normalization achieve substantially higher accuracy, F1 score, and F1 macro compared to those without it.

C. L2 Regularization

L2 regularization plays an important role in preventing overfitting by penalizing large weights in neural networks, including spiking neural networks (SNNs) like SMOGONET. L2 regularization encourages the model to maintain smaller, more stable weights, which helps in generalizing better to unseen data.In the context of SNNs, L2 regularization helps avoid over-reliance on specific weights, leading to more robust learning dynamics.

However, our results show that omitting L2 regularization results in only a minor decrease in performance. This minor performance drop indicates that the primary benefits of L2 regularization in this case are marginal, perhaps due to the

model's inherent ability to generalize well across the dataset.

D. Optimizers

We experimented with three different optimizers: Adam, SGD, and Adamax, to assess their impact on the performance of SMOGONET.

Adam, which was also used in the original MOGONET framework, consistently outperformed the other optimizers in terms of both accuracy and convergence speed. It efficiently balanced the adaptive learning rate, making it well-suited for the complex multi-omics integration tasks and spiking neural network dynamics.

SGD, on the other hand, performed very poorly, likely due to its inability to dynamically adjust the learning rate, leading to slower convergence and poorer generalization, especially on a high-dimensional dataset like BRCA.

Adamax, a variant of Adam, performed reasonably well, but its performance was slightly inferior to Adam, as it tended to converge more slowly and with less precision.

Adam remained the best choice for SMOGONET, offering the highest performance and most stable results across experiments.

E. Evolutionary Approach for Hyperparameter Selection

To fine-tune the SMOGONET model's hyperparameters, we employed an evolutionary algorithm (EA) following our ablation studies. We optimized parameters such as learning rate, hidden layer size, beta values, step size, and gamma values for both the Spiking Graph Convolutional Network (SGCN) layers and the Virtual Convolutional Decision Network (VCDN).

The EA began with a randomly generated population of candidates, each representing a unique hyperparameter configuration. In each generation, candidates were evaluated measuring model performance through pre-training and training epochs. The highest-performing individuals became "parents" for the next generation. Offspring were generated via crossover, with mutation applied to introduce variation. An adaptive mutation rate was used, gradually increasing if convergence was detected to prevent stagnation.

The EA-produced configurations outperformed the manually selected baseline as shown previously in table I.

VI. Conclusions and future works

By leveraging the energy-efficient computations of spiking neural networks, SMOGONET not only enhances predictive performance but also addresses the computational challenges associated with large-scale omics datasets. The results of our study indicate that SMOGONET outperforms traditional methods, including the original MOGONET, showing its potential as a more efficient and robust alternative for multi-omics data analysis.

Looking forward, future research should explore further enhancements to the SMOGONET framework, such as integrating additional types of omics data, incorporating more sophisticated spiking neuron models to capture more complex data interactions as well as employing more sophisticate evolutionary strategies for further automatic tuning of the models parameter.

Additionally, extending the application of SMOGONET to other diseases beyond breast cancer and developing domain-specific optimizations could further demonstrate its versatility and effectiveness. Finally, exploring hybrid approaches that combine spiking and non-spiking neural networks may offer additional performance gains and open new possibilities for energy-efficient, high-performance biomedical data analysis.

References

[1] T. Wang, W. Shao, Z. Huang, H. Tang, J. Zhang, Z. Ding, and K. Huang, "Mogonet integrates multi-omics data using graph convolutional networks allowing patient classification and biomarker identification," 2021.

[2] Z. Zhu, J. Peng, J. Li, L. Chen, Q. Yu, and S. Luo, "Spiking graph convolutional networks," 2022.