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Spiking convolutional neural network for brain tumor classification

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Abstract

Medical image analysis has brought a particular interest amongst researchers over the last few years as it exposes challenges to improve the way we diagnose and treat illnesses and diseases. The wide variety of shapes and locations brain tumors can take make diagnoses difficult to establish and automate. Continuously offering more accuracy, Artificial Neural Networks have been widely studied and successfully adapted to solve medical image processing tasks. However, they suffer from their significant memory and energy cost as well as a high dependency to powerful devices, preventing their realistic deployment in the medical field. A recent growth of interest for Spiking Neural Networks (SNN) is leading to the development of faster, lighter and power efficient models proven to tackle the aforementioned challenges in cognitive tasks such as object recognition, speech recognition, image classification and segmentation. In this work, we present the implementation of a single trainable layer Convolutional Spiking Neural Network (C-SNN) for brain tumor classification in order to prove the efficiency of spiking models in medical image analysis.

Keywords: Spiking neural networks, Brain tumor diagnosis, Spike-timing-dependent plasticity, Reward modulated learning, Medical image analysis

1 Introduction

In recent years, studies in the development of computer-aided brain tumor diagnosis systems highlighted the efficiency and rapid growth of deep learning for medical image analysis. This focus induced the creation of a wide variety of methods from which Artificial Neural Networks (ANNs) and more specifically Convolutional Neural Networks (CNNs) emerged as highly efficient solutions to solve brain tumor recognition tasks (Havaei et al (2017); Kumar and Mankame (2020); Dong et al (2017)). While they often proved to outperform the human eye, these neural networks suffer from high computational and energy cost, a dependence to large datasets and GPU-powered devices as well as a lack of transparency and explainability. This does not make their usage realistic in clinical settings where data is protected by privacy and ethics, where the costs of diagnosis has to be kept as low as possible and where being able to properly explain a decision is crucial. Hence, in order to be fully successful, the alteration or complete replacement of these methods have to considered.

Aiming for a drastic reduction in computational and energy costs, several studies have investigated model compression methods to reduce the memory footprint of CNNs and let them be deployed on low-power devices (Niepceron et al (2020); Li et al (2019); Isono et al (2020)). However, if compression can successfully reduce the computational costs of CNNs, it is also causing performance penalties. With the interest to solve these issues, other methods are being investigated to make the most of the opportunities carried by neural computation and bio-plausibility (Niepceron et al (2021); Han and Roy (2020); Tang et al (2019)). The promising results obtained by bio-inspired models is then leading to new ways to perform medical image analysis.

With the aim to simulate biological neurons dynamics and motivated by the efficiency of visual processing performed by the human brain, SNNs are now being developed as strong competitors to ANNs. There has, indeed, been a significant growth in the appearance of such models in the state-of-the-art over the last few years. This came strengthening the assumption that the performance of spike-based models could approach the effectiveness of deep learning methods. In this dynamic, some efforts have been made to transfer the powerful feature extraction performed by CNNs to their spiking counter parts and led to the creation of Convolutional Spiking Neural Networks (C-SNNs). These networks offer the best of both artificial and bio-plausible world and allow to build effective solutions for computer vision (Mozafari et al (2019b); George et al (2020); Ke et al (2020)). However, if they can be used to create efficient recognition systems and solve the computational and energy cost problems of deep neural networks by providing easy hardware implementation, these models are not yet able to really outperform CNNs in most vision tasks. Moreover, if several studies investigated the performance of these methods on simple pattern recognition like MNIST (Mozafari et al (2019b)) or low resolution natural image classification like CIFAR-10 (Sorbaro et al (2020)), their application to complex data like brain images has not been explored. In fact, with a lack of

training methods and the use of encoding schemes that often induces information loss, building effective SNNs for complex computer vision still remains a challenge.

Hence, to investigate the application of neural computation to brain image analysis and prove that SNNs can be used in the medical field as computer-aided diagnosis systems, we propose the implementation of a single trainable layer C-SNN for brain tumor classification. Keeping the size of the model as small as possible, our work does not aim to perform better than state-of-the-art CNNs but rather provides bases to build C-SNNs for medical image analysis.

In this work, we first describe the classification tasks our model aims to solve as well as a pre-processing pipeline designed to ease the extraction of features by the C-SNN. Then, we detail the structure of the network and review the learning mechanism it relies on. Finally, we describe and compare the precision of our method with deep and machine learning methods performing the same tasks in order to demonstrate the promising opportunities of spike-based computation in medical image analysis.

2 Material and methods

If the artificial counterparts of C-SNNs have been widely studied in medical image analysis and proved their efficiency in classification, segmentation or lesion detection, the performances of spiking models when dealing with medical imaging is yet to be investigated. In this section, we first describe two brain tumor classification tasks based on different brain imaging dataset. Then we give details on the pre-processing pipeline used to ease the conversion of raw Magnetic Resonance Imaging (MRI) to spike times. Finally, we describe the architecture of the proposed network and discuss a bio-plausible supervised learning strategy to train it.

2.1 Tumor classification tasks and data processing

In order to provide different proofs of the model's performances in terms of brain tumor classification using medical imaging, we define two different classification tasks based on different datasets. The first task (CT1) aims to analyze tumors from the 2015 version of the BraTS dataset in order to label them as high- (HGG) or low-grade (LGG) gliomas. Only the FLAIR scans of this dataset were used for training and evaluation as they show higher pixel intensities around tumorous regions. The second task (CT2) exploits the dataset presented in the work of Cheng et al. (Cheng et al (2015)) which is composed of 3064 MRI slices taken from 233 patients and showing 3 different types of tumor cases namely glioma, pituitary tumors and meningioma.

Using pre-processing operations before feeding data to SNNs can be crucial to ease the time encoding process performed in their input layer. In the case of MRI, removing bone structures and anomalies caused by potential artifacts can for example reduce the number of firing neurons and facilitate the extraction of meaningful features. In this work, MRI slices from both datasets were

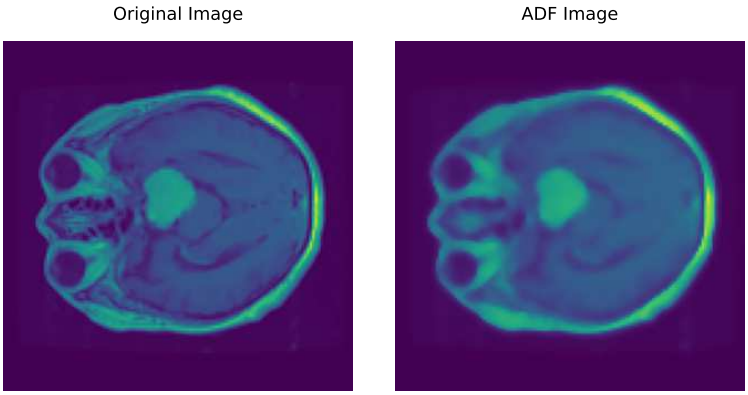

Fig. 1 Anisotropic Diffusion Filtering applied to an MRI slice.

altered using the same pre-processing pipeline. First, skull-stripping was performed when needed and was done following the method proposed by Shattuck et al. (Shattuck et al (2001)). This method relies on several operations that include edge Marr-Hildreth edge detection and morphological operations that split bone structures and brain regions up. Secondly, to match the intensity levels of both datasets, we then took a FLAIR scan from the BraTS dataset as a template to perform histogram matching. Then, each MRI slice was converted to a grayscale image and normalized. Moreover, in search for a low computational workload when running our experiments, the slices were downsized to 128x128 images. Finally, since artifacts are inherent to MRI and since brain images are often noisy, the last step of our pre-processing pipeline performs an Anisotropic Diffusion Filtering (ADF) (Perona and Malik (1990)). This method has widely been explored for the processing of medical images (Gerig et al (1992); Krissian and Aja-Fernández (2009); Palma et al (2014)) as it allows to keep edges intact while smoothing images in order to remove outlier pixels (See Fig. 1). This last processing step is described by :

$$I_{p_1}^{t+1} \approx I_{p_1}^{t} + \frac{\lambda}{\mid \eta_{p_1} \mid} \sum_{p_2 \in \eta_{p_1}} f(\mid \nabla I_{p_1,p_2}^{t} \mid, \gamma) \nabla I_{p_1,p_2}^{t} \tag{1}$$

Where $I_{p_1}^{t}$ is the intensity of pixel p_1 at time t from image I, η_{p1} corresponds to a set of neighboring pixels from pixel p_1, γ is a positive constant that regulates the smoothing level of the filter, λ is a scalar associated to the diffusion rate, f is an the edge-stopping function that is responsible for the smoothing process and $\nabla I_{p_1,p_2}^{t}$ indicates the magnitude of the directional gradient from pixel p_1 to p_2. This complete pre-processing pipeline was performed on all MRI slices before they entered the network and is illustrated in Fig. 2.

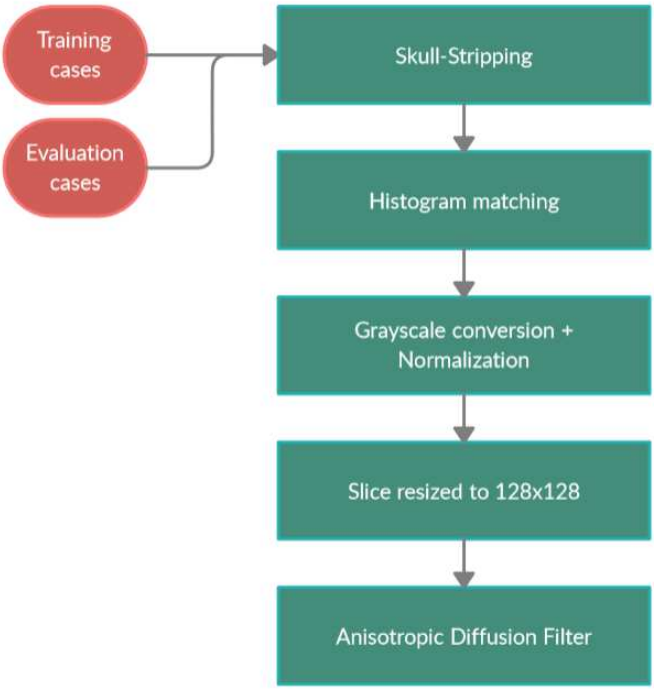

Fig. 2 Pre-processing pipeline performed on the MRI datasets.

2.2 Network's structure

The ability of extracting relevant features in data is at the core of CNNs efficiency in computer vision and is why they were studied in a wide range of domains to build efficient visual decision making systems. Similarly, the recent success of SNNs for pattern recognition showed the efficiency of neural computation for the processing of data with temporal dependencies. However, SNNs were not shown to be as efficient as CNNs when it came to perform complex feature extraction, what explains the gap in their performance in computer vision. Being the spiking counterparts of CNNs, C-SNNs aims to provide the feature extraction methods brought by CNNs while exploiting the computational cost reduction and low-latency of spike-based computation. Such network mostly consists of three layers performing data encoding, feature extraction and decision making respectively. The first layer often aims to simulate the biological pathway between the retina and the visual cortex by applying a set of filters on the original data and converting visual stimuli to spike times or rates. The second layer employs the operations commonly found in CNNs such as pooling and convolution to perform the feature extraction. During this step, a new

Fig. 3 Output example from the S1 layer for one MRI slice.

representation of the data is created and propagated under the form of temporal codes obtained by a set of spiking neurons that convert the features into spike times. In such model, the learning process takes place between the two previous layers and often relies on plastic synaptic connections. The last layer of a simple C-SNN is composed of sets of neurons which activities, driven by the activity of neurons in the previous layer, determine the decision made by the system. In a classification task, a common method to define which label to attach to an input data is thus to attribute classes to output neurons and label the input regarding the timing of spikes of each neuron so that the neuron that spikes the earliest defines the class to apply. In this section, we thus detail the structure and development of such model. The network proposed in this work follows the structure of the HMAX (Riesenhuber and Poggio (1999)) model. Originally designed for object recognition, this model can simulate the complex feature selectivity and invariance observed in the ventral stream by the mean of simple and complex cells respectively.

2.2.1 V1 Simple Layer 1 - S1

The S1 layer marks the input of the network and receives the pre-processed MRI slices. In this layer, the encoding performed by the lateral geniculate nucleus is simulated using Difference-of-Gaussian filters applied to the images. This operation is followed by a V1 simple-cells encoding modeled as Gabor filters known to perform edge detection. Four different filters with a 45 degrees shift were thus used in our experiments to extract all oriented edges. The stimuli are then converted to spike times using the time-to-first-spike encoding defined as :

$$T(p) = \frac{T_{max}}{1 + exp(-\sigma(128 - p)} \tag{2}$$

Where p is the current pixel intensity being encoded and σ is a non-linear coding variable set to 0.05. T_{max} is the maximum firing time. This encoding process leads to the creation of one feature map one the same size as the input for each Gabor orientation. In these feature maps, each position thus corresponds to neuron firing time. This type of encoding allows neurons representing salient edges to have a stronger effect on later neurons by spiking earlier than others. Fig. 3 illustrates the output of this layer for one MRI slice.

2.2.2 V1 Complex Layer 1 - C1

Complex cells are responsible for the robust spatial phase invariance properties of human perception. They come extending the work done by simple cells by reacting to oriented grating stimuli with a variety of spatial phases. To obtain this invariance, the first layer of complex cells in our network performs pooling operations on all feature maps propagated from the previous layer. Additionally to the invariance it introduces to the system, the pooling operation also allows to drastically reduce computational cost by downsizing the incoming feature maps and only keeping the earliest spikes. Lateral inhibition was also used in this layer to provide sparse feature representations. This is firstly done by using an inhibition kernel in each feature map that increases the spike timing of the earliest neurons' neighbours. Secondly, a spike in one feature map induces inhibition on the neurons at the same positions in all other maps. This allows to prevent feature redundancy by insuring that each feature map gives a distinct representation of the input data.

2.2.3 V1 Simple Layer 2 - S2

This next layer of simple cells is the only trainable layer and is in charge of the majority of the processing happening in the network. It comprises groups of integrate-and-fire neurons which membrane potentials are driven by kernels of C1 neurons and release a spike when these potentials reach a certain threshold. These neurons are only allowed to fire once per input image by respecting a refractory period after each spike. The connections between S2 and the previous layer are plastic and are responsible for the network's learning process which depends on the chosen learning rule. Taking a simple Spike-Timing-Dependent Plasticity (STDP) rule, the potentiation or depression of weights between the layer is driven by the order of pre- and post-synaptic spikes. Each spike in this layer also triggers a winner-takes-all mechanism to insure that only meaningful features get propagated further.

2.2.4 V1 Complex Layer 2 - C2

The last layer of the model is another complex cell group of neurons that performs the classification process. In this layer, all neurons are connected to one distinct set of neurons from the previous layer and only propagate the first spike from it. The C2 neuron groups are assigned to labels and the input data is then classified according to the group of neurons that fired the first.

2.3 Learning with R-STDP

A large amount of research works have looked at the significance of the reward system in the human brain and found that the process of decision-making was significantly influenced by it. In a typical reward system, rewards are sent to stimulate a condition or behavior to repeat itself. Penalty signals, on the other hand, can be used to prevent certain behaviors from occurring. In

biological settings, when the brain receives these signals, it often responds by increasing the generation of dopamine, a neurotransmitter that has been shown to promote positive actions. Neurotransmitters such as dopamine have been demonstrated to influence synaptic plasticity in learning. As a result, this system may be thought of as a reinforcement learning method.

A commonly used method to reproduce this system is the Reward-Modulated STDP (R-STDP) (Frémaux and Gerstner (2016)), an extension of the STDP rule that make use of the reward system to train SNNs in a supervised way. In this learning rule, the effect on synaptic weight changes does not only rely on the order of spikes, it is positively or negatively modulated by reward or punishment signals according to the stimuli transmitted to the network. The timing of these signals is also important in biological settings. In fact, while a signal received in a short time after it has been triggered by a positive activity will be understood as a reward or punishment for that particular trigger, a signal sent long after will not have any use as other events could occur in the meantime. This issue was discussed in the work of Izhikevich (Izhikevich (2007)). To prevent the reward and punishment signals to come in too late, synaptic traces that store the outcome of STDP can be used so that the signals can be consumed and induce the weight changes at the proper time. Under a reward signal, the weight changes ΔW_{ij} between pre-synaptic neuron j and post-synaptic neuron i in layers l_1 and l_2 respectively induced by the R-STDP rule can be defined as :

$$\Delta W_{ij} = \begin{cases} A_+ W_{ij} \cdot (1 - W_{ij}) & t_{l1}(j) - t_{l2}(i) > 0, \\ A_- W_{ij} \cdot (1 - W_{ij}) & t_{l1}(j) - t_{l2}(i) \leq 0 \end{cases} \tag{3}$$

Where t is the firing time of a neuron and A is the magnitude of weight change. Our proposed model thus employs the reward mechanism to induce a positive weight change when the output of the network corresponded to the label of the input data propagated through it.

3 Experiments and results

3.1 Implementation details

The model proposed in this work was implemented using the SpykeTorch simulator (Mozafari et al (2019a)). SpykeTorch was specifically designed to build C-SNNs with at most one spike per neuron and offers the required tools to train them in supervised and unsupervised ways utilizing synaptic plasticity rules, as opposed to other SNN simulators. It is based on the PyTorch framework and has the ability to make use of GPU resources while providing a user-friendly interface for deep learning developers. While the framework aims to make the implementation of C-SNN easy, building models for different tasks or network with more than 2 layers can become tedious as the forward passes have to be implemented for each layer in a conditional way for both training and testing. Since the training of a C-SNN under SpykeTorch is done layer wise,

the training loops also have to be defined individually and their computation was not automated regarding the structure of the network and the learning method employed. To facilitate the implementation of our experiments, we thus extended the framework to let the definition and the training of C-SNNs be more user friendly. Our extended interface is inspired by the Keras library and allows to create C-SNN in a sequential way. We also solved the hard definition of the training loops by providing an automation of the learning process so that training could be ran using only one function call. Our contribution to the framework along with the implementation of our experiments can thus be found at : https://github.com/bniepce/csnn-brain-tumor-classification.

We trained our model on both classification task for 500 epochs and all images from the datasets were used and propagated through the network by batch of 64 samples. To evaluate the classification performances, testing samples were used to compute the average accuracy at the end of each iteration. Although GPU support is available on the SpykeTorch simulator, we ran our experiments on an Intel Xeon Bronze 3106 CPU to prove the efficiency of spike-based computation and the ability of C-SNN to be trained without GPU resources. Training the network for CT1 and CT2 thus took roughly 20 and 45 minutes respectively.

3.2 Results

Our proposed network could successfully be trained to classify the different types of tumors found in the dataset used for both classification tasks while being competitive with state-of-the-art methods. The model obtained average accuracy scores 0.868 and 0.828 for CT1 and CT2 respectively. We compared these performances with machine and deep learning tumor classification methods found in the literature as seen in Table 1 and 2. Both tables demonstrate that our model performed moderately worse than other works, but that it still produces acceptable results regarding the fact it only has one trainable layer and uses considerably less computing power than the approaches we compared it to. These findings also show that complex features like those found in brain scans may be learned using basic bio-plausible learning principles.

Also, while Polly and Cui's machine learning models exposed in Table 1 outperformed ours, the size of the data set they employed was limited, and their results do not demonstrate the algorithm's efficiency over a large number of cases or its capacity to generalize and be less influenced by data variances. The CNN models proposed by Banerjee et al. and Díaz-Pernas et al. outperformed all other methods, demonstrating the superiority of deep learning models in general. However, one being a deep CNN and the other one being made up of multiple pathways, unlike our method, both models do not fulfill the cost-effectiveness requirements set by health-care providers. Furthermore, in CT2, our proposed method came near the performances of the CNN presented by Abiwinanda et al. and surpassed the one proposed by Pashaei et al's work. This demontrates SNNs' potential to be viable alternatives to deep learning models.

Table 1 Comparative results on the CT1 task

Authors	Methods	Total classification accuracy
Banerjee et al (2019)	Deep CNN	0.971
Polly et al (2018)	DWT + SVM	0.914
Mzoughi et al (2020)	Deep CNN	0.96
Cui et al (2019)	Random Forest	0.913
Proposed model	**Single layer C-SNN**	**0.868**

Table 2 Comparative results on the CT2 task

Authors	Methods	Total classification accuracy
Díaz-Pernas et al (2021)	Multiscale CNN	0.973
Anaraki et al (2019)	CNN + Genetic algorithm	0.942
Abiwinanda et al (2019)	CNN	0.841
Proposed model	**Single layer C-SNN**	**0.828**
Pashaei et al (2018)	CNN	0.810

4 Conclusion

In this study, the implementation of a C-SNN for brain tumor classification was discussed in order to demonstrate the efficiency and effectiveness of SNNs in medical image analysis. Our work yielded encouraging findings, highlighting the advantages of bio-plausible models in computer vision. We introduced two different brain tumor classification tasks along with the datasets they relied on. A data pre-processing pipeline was then introduced to enhance feature extraction and ease the time encoding performed by the C-SNN. The network's design was then broken down layer by layer, and the use of R-STDP as a reinforcement learning rule was explored. To make the developement of our experiments easier, we developed an extended version of the SpykeTorch framework, and we successfully trained the C-SNN without GPU support in relatively fast times. Our results showed the opportunities carried by spike-based models to tackle the issues brought by deep learning and its application to the medical field. By comparing our C-SNN to state-of-the-art brain tumor classification methods, we built confidence regarding the promising performances SNNs can offer to develop efficient computer-aided brain tumor diagnosis systems while meeting clinical settings requirements.

Compliance with ethical standards

Conflict of interest

The authors of the paper declare that they have no conflict of interest.

Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

Authorship contributions

All authors contributed to the study conception and design. Material preparation, data collection and analysis were performed by Brad Niepceron. The first draft of the manuscript was written by Brad Niepceron and all authors commented on previous versions of the manuscript. All authors read and approved the final manuscript.

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Competing Interests

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Data availability

The datasets analysed during the current study are available at https://www.smir.ch/BRATS/Start2015 and https://doi.org/10.6084/m9.figshare.1512427.v5.