Enhancing Classification Performance of Convolutional Neural Networks for Prostate Cancer Detection on Magnetic Resonance Images: a Study with the Semantic Learning Machine

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ABSTRACT

Prostate cancer (PCa) is the most common oncological disease in Western men. Even though a significant effort has been carried out by the scientific community, accurate and reliable automated PCa detection methods are still a compelling issue. In this clinical scenario, high-resolution multiparametric Magnetic Resonance Imaging (MRI) is becoming the most used modality, also enabling quantitative studies. Recently, deep learning techniques have achieved outstanding results in prostate MRI analysis tasks, in particular with regard to image classification. This paper studies the feasibility of using the Semantic Learning Machine (SLM) neuroevolution algorithm to replace the fully-connected architecture commonly used in the last layers of Convolutional Neural Networks (CNNs). The experimental phase considered the PROSTATEx dataset composed of multispectral MRI sequences. The achieved results show that, on the same non-contrast-enhanced MRI series, SLM outperforms with statistical significance a state-of-the-art CNN trained with backpropagation. The SLM performance is achieved without pre-training the underlying CNN with backpropagation. Furthermore, on average the SLM training time is approximately 14 times faster than the backpropagation-based approach.

CCS CONCEPTS

• **Computing methodologies** → **Neural networks**; **Bio-inspired approaches**; *Search methodologies*; *Learning settings*;

KEYWORDS

Semantic Learning Machine, Neuroevolution, Convolutional Neural Networks, Classification, Prostate cancer detection, Multiparametric Magnetic Resonance Imaging

1 INTRODUCTION

In 2019 the Prostate Cancer (PCa) is going to be the most common one in Western men [9]. Nowadays, high-resolution multiparametric Magnetic Resonance Imaging (MRI) is acquiring clinical and scientific interest, also enabling quantitative studies [10]. Therefore, computer-assisted MR image analysis approaches are mandatory for improving results repeatability in large-scale clinical studies [8].

The idea explored in this work is to improve the performance of a Convolutional Neural Network (CNN) by replacing the fully connected layers (used to perform the classification tasks based on the image features extracted from the previous convolutional layers) with a network constructed by a neuroevolution algorithm on high-level image features. Two different approaches are considered: (1) a regular CNN training process in which backpropagation is used to train a given CNN architecture, and (2) a neuroevolution-based approach where the outputs from the convolutional layers of a given CNN are passed as inputs (without pre-training) to a neuroevolution algorithm. To achieve the challenging objective previously described, this work relies on a recently defined neuroevolution algorithm called Semantic Learning Machine (SLM) [2, 3, 5].

Even though several CNN architectures networks were used in medical imaging, they have to be specifically adapted for the medical imaging application at hand. In this work, we considered the XmasNet architecture [6] as deep feature extractor and for the prediction between benign and malignant PCa.

XmasNet [6] was developed *ad hoc* for the PROSTATEx 2017 challenge. Despite the simple architecture (four convolutional and two fully-connected layers), it achieved state-of-the-art performance in the challenge. Because of this, XmasNet we selected as an end-to-end trainable deep model for the PROSTATEx dataset.

2 SEMANTIC LEARNING MACHINE

The SLM neuroevolution algorithm proposed by Gonçalves et al. [2] was created by deriving, for Neural Networks (NNs), a mutation operator from Geometric Semantic Genetic Programming (GSGP) [7]. In GSGP, Moraglio et al. [7] showed that any supervised learning problem where the error is measured as a distance to the known targets has a unimodal error landscape that can be effectively explored by constructing specific variation operators. These operators are known as geometric semantic operators. In this context, the term semantics is used to refer to the outputs of any supervised learning model (e.g., an NN) over a set of data instances. The reasoning behind these geometric semantic operators can be used to create equivalent operators for other representations or computational models. The SLM was created by defining a geometric semantic mutation for NNs, allowing the SLM to explore unimodal error landscapes and to effectively explore the space of NNs.

3 DATASET AND EXPERIMENTAL SETTINGS

In this work, we consider the non-contrast-enhanced MRI sequences included in the dataset provided by the PROSTATEx Challenge [1].

To estimate the best performing configuration of the considered CNN, random search was performed. The original data set was divided into three parts: training, validation and test. In particular, 60% was used for training purpose, 20% for validation, and 20% for testing the performance of the model over unseen instances. 30 random configurations were tested and for each configuration the model was trained on the training and validation sets 30 times, by averaging the achieved results.

For SLM the following parameters were tuned: (1) in the initial population each NN is generated with a random number of hidden layers selected between 1 and 5; (2) in the initial population each NN randomly selects the number of neurons for each hidden layer between 1 and 5; (3) each hidden neuron randomly selects its activation function from the following options: logistic, Rectified Linear Unit (ReLU), and tanh; (4) each hidden neuron randomly selects the weight of each incoming connection from values in the interval $[-mncw, mncw]$, where $mncw$ represents the maximum neuron connection weight parameter (subject to parameter tuning); (5) each hidden neuron randomly selects the weight of its bias from values in the interval $[-mbw, mbw]$, where mbw represents the maximum bias weight parameter; (6) every time a new NN is created by the mutation operator, the number of new neurons to be added to each layer is randomly selected between 1 and 3; (7) the weights of connections from the new neurons in the last hidden layer to the output neuron are selected from values in the interval $[-mls, mls]$, where mls represents the maximum learning step parameter (subject to parameter tuning); and (8) the training stopping point is determined by one of the two semantic stopping criteria proposed by Gonçalves et al. [4]: the error deviation variation criterion and the training improvement effectiveness criterion.

4 MAIN RESULTS AND DISCUSSION

To analyze the classification performance, the Area Under the Receiver Operating Characteristic (AUROC) curve was taken into account, considering that the dataset is not balanced. According to the results obtained, it is possible to state that the SLM outperforms XmasNet in classifying unseen PCa images. Considering a significance level (α) of 0.05, the differences observed are statistically significant as the p-value returned by the Mann-Whitney U-test is 0.016.

With respect to the time required to perform the training process of the two approaches, the experimental results show that SLM is significantly more efficient than the backpropagation-based approach (the p-value returned by the Mann-Whitney test is smaller than 10^{-10}). The average speed-up (calculated as $\frac{\text{CNN}_{\text{time}}}{\text{SLM}_{\text{time}}}$) is 14.008.

In conclusion, these encouraging results point out that the SLM neuroevolution algorithm can be properly applied to the biomedical imaging domain. As a future direction, we aim at designing a novel version of the SLM to evolve the whole topology of deep neural networks.

REFERENCES

[1] Samuel G Armato, Henkjan Huisman, Karen Drukker, Lubomir Hadjiiski, Justin S Kirby, Nicholas Petrick, George Redmond, Maryellen L Giger, Kenny Cha, Artem Mamonov, et al. 2018. PROSTATEx Challenges for computerized classification of prostate lesions from multiparametric magnetic resonance images. *J. Med. Imaging* 5, 4 (2018), 044501. https://doi.org/10.1117/1.JMI.5.4.044501

[2] Ivo Gonçalves, Sara Silva, and Carlos M. Fonseca. 2015. Semantic learning machine: a feedforward neural network construction algorithm inspired by geometric semantic genetic programming. In *Progress in Artificial Intelligence*. Lecture Notes in Computer Science, Vol. 9273. Springer, 280–285. https://doi.org/10.1007/978-3-319-23485-4_28

[3] Ivo Gonçalves. 2017. *An Exploration of Generalization and Overfitting in Genetic Programming: Standard and Geometric Semantic Approaches*. Ph.D. Dissertation. Department of Informatics Engineering, University of Coimbra, Portugal.

[4] Ivo Gonçalves, Sara Silva, Carlos M. Fonseca, and Mauro Castelli. 2017. Unsure when to Stop? Ask Your Semantic Neighbors. In *Proceedings of the Genetic and Evolutionary Computation Conference (GECCO)*. ACM, New York, NY, USA, 929–936. https://doi.org/10.1145/3071178.3071328

[5] Jan-Benedikt Jagusch, Ivo Gonçalves, and Mauro Castelli. 2018. Neuroevolution under unimodal error landscapes: an exploration of the semantic learning machine algorithm. In *Proceedings of the Genetic and Evolutionary Computation Conference (GECCO) Companion*. ACM, New York, NY, USA, 159–160.

[6] Saifeng Liu, Huaixiu Zheng, Yesu Feng, and Wei Li. 2017. Prostate cancer diagnosis using deep learning with 3D multiparametric MRI. In *Medical Imaging 2017: Computer-Aided Diagnosis (Proceedings SPIE)*, Vol. 10134. International Society for Optics and Photonics, 1013428. https://doi.org/10.1117/12.2277121

[7] Alberto Moraglio, Krzysztof Krawiec, and Colin G Johnson. 2012. Geometric semantic genetic programming. In *Parallel Problem Solving from Nature-PPSN XII*. Springer, 21–31. https://doi.org/10.1007/978-3-642-32937-1_3

[8] Leonardo Rundo, Carmelo Militello, Giorgio Russo, Antonio Garufi, Salvatore Vitabile, Maria Carla Gilardi, and Giancarlo Mauri. 2017. Automated prostate gland segmentation based on an unsupervised fuzzy c-means clustering technique using multispectral T1w and T2w MR imaging. *Information* 8, 2 (2017), 49.

[9] Rebecca L Siegel, Kimberly D Miller, and Ahmedin Jemal. 2019. Cancer statistics, 2019. *CA Cancer J. Clin.* 69, 1 (2019), 7–34. https://doi.org/10.3322/caac.21551

[10] Radka Stoyanova, Mandeep Takhar, Yohann Tschudi, John C Ford, Gabriel Solórzano, Nicholas Erho, Yoganand Balagurunathan, Sanoj Punnen, Elai Davicioni, Robert J Gillies, et al. 2016. Prostate cancer radiomics and the promise of radiogenomics. *Transl. Cancer Res.* 5, 4 (2016), 432.