INTRODUCTION

Tumors are cells that can grow abnormally in any part of the body [1]. Tumors are classified into two types, benign and malignant [2]. Malignant tumors are the same as cancer that can spread and invade other important organs in the body. According to The Global Cancer Observatory (2020), there are 19,2 million cancer cases that occur in 2020 while the number of deaths caused by cancer in 2020 was 9,9 million [3]. One type of cancer with high mortality rates is brain and central nervous system cancer with a percentage of deaths reaching 81%. Brain and central nervous system cancer is one of the most deadly and life-threatening types of cancer [4].

The most common malignant tumour in the brain and central nervous system is glioma. It represents around 30% of all primary tumors originating in this system [5]. WHO has classified glioma into four levels based on its malig- nancy (from I to IV). Grade I and II is referred to as low-grade glioma (LGG) while The Cancer Genome Atlas

(TCGA) classifies grades II and III as low-grade glioma [6]. Low-grade glioma also can develop into WHO grade IV glioblastoma multiforme (GBM), which exhibits extremely high malignancy levels and a worse prognosis [7]. Most patients diagnosed with glioblastoma multiforme die within less than a year and almost none can survive in the long term. The median survival period for adult patients is usually around 10 months and can be up to 14 months for pa- tients undergoing combined treatment with radiotherapy [8]. Meanwhile, patients diagnosed with low-grade glioma have a median survival time of about 5 years despite having a high recurrence rate as well as having high radiation resistance and drug resistance [6].

Brain tumor detection is done through Magnetic Reso- nance Imaging (MRI) examination [9]. Other methods used by doctors are biopsy and direct observation. However, these methods take a long time and there is a risk of error [10]. In the case of Glioma, rapid and accurate assessment of glioma grade is necessary for diagnosis and treatment op- tions, especially in distinguishing between low-grade glioma and glioblastoma [11]. As it is known that glioma has a short life expectancy, it is necessary to analyze it early so that it can be diagnosed and treated appropriately. Therefore, a classification method that can be processed quickly and has a fairly high level of accuracy is needed, one of which is a machine-learning approach

Previous research conducted glioma grade classification using ensemble learning techniques with the application of voting-based feature selection [12]. The machine learning models used were Logistic Regression, Support Vector Ma- chine, K-Nearest Neighbor, Random Forest, and AdaBoost. There are 3, 4, and 5 combinations of the five models so there are a total of 16 different ensemble model combina- tions. This study used The Cancer Genome Atlas (TCGA) and Chinese Glioma Genome Atlas (CGGA) datasets. The researchers performed experiments on each dataset with all ensemble model combinations. They compared the results on each dataset based on the feature selection methods used, namely voting-based, LASSO (Least Absolute Shrinkage and Selection Operator), and no feature selection process. The best accuracy on TCGA and CGGA datasets comes from a

combination of models that use voting-based feature selection methods. On the TCGA dataset, the best accuracy result is

87.6% with the Support Vector Machine, Random Forest, and AdaBoost model combination. While on the CGGA dataset, the best accuracy result is 79.7% with a combination of Support Vector Machine, K-Nearest Neighbor, Random Forest, and AdaBoost models.

In the following study, Research [13] conducted a com- parison between glioma grade classification using the Deep Convolutional Neural Network method and glioma classification using the Random Forest, Support Vector Machine, and Gradient Booster methods. The study used data in the form of MRI images of 660 images from a total of 237 glioma patients to train the Deep Convolutional Network model. While RF, SVM, and GB models use radiomic data as their datasets. From this study, the classification results using the Deep Convolutional Network method were obtained with an accuracy rate of 87%. While the classification results using RF, SVM, and GB methods are 58%, 56%, 64% respectively. Based on this research, it can be concluded that the neural network method provides results with greater accuracy than traditional methods.

Another research [14] conducted feature extraction from MRI images using Convolutional Neural Network using various classifier methods for glioma grade classification. Some of the methods used are Random Forest, Na¨ıve Bayes, Support Vector Machine, and Multilayer Perceptron. There are 4430 tumor images and 4250 non-tumor images. The author divides the dataset into four modalities based on the characteristics of the images in the dataset. Based on the research conducted, the Support Vector Machine method produces the highest accuracy which is around 95.02% to 96.19%. While the Multilayer Perceptron method produces an accuracy of around 89.93% to 94.85%.

It is known that the Multilayer Perceptron algorithm can produce higher accuracy by optimizing. One of them is using Genetic Algorithm as an optimization algorithm. As in the research [15], Multilayer Perceptron optimized by Genetic Algorithm as an optimization algorithm. The author per- forms arrhythmia disease classification using the Multilayer Perceptron method optimized with Genetic Algorithms. The research tested the effectiveness of optimization by compar- ing the accuracy results between the Multilayer Perceptron model optimized with Genetic Algorithm with the Multilayer Perceptron model without optimization. The results prove that Genetic Algorithm optimization of Multilayer Perceptron can increase the accuracy of the model from 92.7% to 94.2%.

This study will optimize the Multilayer Perceptron (MLP) algorithm using Genetic Algorithm (GA) to classify glioma grade. The dataset used is tabular data related to molecular features in genes. The model will be evaluated using the Confusion Matrix method to determine the level of accuracy produced. In this study, a comparison will be made between MLP optimized with Genetic Algorithm and MLP that is not optimized to determine the comparison of accuracy and effectiveness of optimization.