

---

**Abstract**

Cancer is a world-famous deadly disease. Prostate cancer is one of the most common types of cancer in men. In 2018 it was estimated that around 1.3 million men worldwide had prostate cancer. During the last 8 years, the number of prostate cancer patients in three Indonesian teaching hospitals, namely Jakarta, Surabaya and Bandung, was 1,102 patients with an average age of 67.8 years. To detect prostate cancer requires clinical trials conducted in specialist hospitals and takes a long time. One alternative way to predict prostate cancer is by utilizing machine learning technology on microarray data. Microarrays are able to predict certain tissues in humans. This study aims to build a classification model for prostate cancer detection based on microarray data. The methods built in this research are Genetic Algorithm (GA) as feature selection and Support Vector Machine (SVM) as classification. This study proves that the use of GA feature selection has succeeded in increasing SVM performance for the three kernels. The best model is obtained using a linear kernel with 250 features that produce accuracy evaluation values and F1-scores of 80.8% and 85.3%, respectively, where accuracy is the overall correct prediction ratio, while the F1-score is a weighted comparison of the average precision and recall.

**Keywords:** Prostate Cancer, Microarray, GA, SVM