

Implementasi Minimum Redudansi Maksimum Relevansi (MRMR) dan Genetic Algorithm (GA) untuk Klasifikasi Data Microarray dengan C4.5 Decision Tree

Irne Mabarti¹, Adiwijaya², Annisa Aditsania³

^{1;2;3}Fakultas Informatika, Universitas Telkom, Bandung
¹irnemabarti@students.telkomuniversity.ac.id, ²adiwijaya@telkomuniversity.ac.id,

³aaditsania@telkomuniversity.com

Abstract

Cancer is one of the highest causes of death in various countries, even an increase in mortality rates happens every year. On the other hand, bioinformatics technology will be very helpful in predicting cancer, one of the methods that can be considered in predicting cancer is the classification of microarrays data. Microarray data is data containing many gene expressions that describe DNA cells. Microarray data has large dimensions. The dimension reduction method used in this study is the Minimum Redundancy Maximum Relevance (MRMR), the optimization method used is the Genetic Algorithm (GA) method, and the last method is C4.5 aimed at classifying gene data. In this study there were two trials. The first trial used the Minimum Redundancy Maximum Relevance (MRMR) method combined with Genetic Algorithm (GA) as an optimization method and the C4.5 classification method, the trial resulted in an average accuracy of 79%. While the second trial using the Genetic Algorithm (GA) method for feature selection and the C4.5 classification method produces an average accuracy of 78%.

Keywords: Cancer, Microarray, *Minimum Redundancy Maximum Relevance (MRMR)*, *Genetic Algorithm (GA)*, C4.5.

¹ Irne Mabarti

² Adiwijaya

³ Annisa Aditsania