

Klasifikasi Risiko Human Immunodeficiency Virus (HIV) Menggunakan Parameter CD4 dengan Metode Support Vector Machine

Erica Nursanti¹, Yuliant Sibaroni, S.Si., M.T.²

^{1,2}Prodi S1 Informatika, Fakultas Informatika, Universitas Telkom, Bandung

¹ericanursanti@students.telkomuniversity.ac.id, ²yuliant@telkomuniversity.ac.id

Abstract

Based on data from UNAIDS, in 2019 38 million people worldwide are estimated to suffer from Human Immunodeficiency Virus (HIV). Whereas until now there is still no cure for HIV. However, there are types of drugs that can retard the progression of the virus that is antiretroviral (ARV). ARVs work by eliminating the elements needed by the HIV virus to multiply, and preventing the HIV virus from destroying cell clusters of differentiation 4 (CD4).

Stigma towards people living with HIV / AIDS (PLWHA) pose a major obstacle to HIV / AIDS prevention, treatment, care and support. Stigma and discrimination are spread in the society, causing anxiety and prejudice against PLWHA so people are reluctant to carry out HIV testing or do not disclose HIV status to partners. All of these cause delays or denial of care and non-compliance with HIV treatment.

In this final project, a system design has been carried out to classify immunodeficiency as HIV risk using CD4 parameters. The method used is Support Vector Machine (SVM) as a classifier. Classification using the SVM method with the right measurements can provide help to prevent the spread of the virus in the body of HIV sufferers. Machine learning has been used as a prediction tool in many fields of medicine, including predicting ARV drugs. Machine learning can also be used to classify risk from CD4 cell information. SVM is a machine learning method that works with the aim of getting the best hyperplane that separates classes in the input space.

The results obtained in this Final Project are Python-based applications that can process data for HIV risk classification. The number of data samples used in this Final Project research is still limited to 16 test data and 500 training data. The resulting performance of the system is the average accuracy of the 68.75% Linear Kernel, the 87.5% Kernel RBF accuracy with the parameter values on the SVM sequential training.

Keywords: Immunodeficiency, HIV, SVM, CD4
