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An Investigation of Classification Algorithms for Predicting HIV Drug Resistance without Genotype Resistance Testing

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Abstract

The development of drug resistance is a major factor impeding the efficacy of antiretroviral treatment of South Africa’s HIV infected population. While genotype resistance testing is the standard method to determine resistance, access to these tests is limited in low-resource settings. In this paper we investigate machine learning techniques for drug resistance prediction from routine treatment and laboratory data to help clinicians select patients for confirmatory genotype testing. The techniques, including binary relevance, HOMER, MLkNN, predictive clustering trees (PCT), RAkEL and ensemble of classifier chains were tested on a dataset of 252 medical records of patients enrolled in an HIV treatment failure clinic in rural KwaZulu-Natal in South Africa. The PCT method performed best with a discriminant power of 1.56 for two drugs, above 1.0 for three others and a mean true positive rate of 0.68. These methods show potential for application where access to genotyping is limited.