Perbandingan Ekstraksi Ciri K-Mers dan Spaced K-Mers pada Klasifikasi Fragmen Metagenome dengan Naïve Bayes Classifier

Metagenome is a genetic material obtained from a simple which is taken directly from the environment such as soil, marine, or human entrails. These metagenome fragments contain a variety of organism, so that a binning process required to classify them before conducting genome assembly. This research employs naïve Bayes classifier (NBC) and spaced k-mers as a feature extraction to classify these fragments into genus level. The results will be compared to those of method which uses NBC and k-mers feature extraction. K-mers feature is a common feature in the DNA fragments classification problem. The comparison results show that the accuracy of classifier using NBC and spaced k-mers is higher than that of classifier using NBC and k-mers

sumber: http://repository.ipb.ac.id/handle/123456789/65920