

Membangun tricluster data ekspresi gen human immunodeficiency virus-1 melalui multi slope measure dengan algoritma triclustering genetic based = Generating tricluster gene expression data of human immunodeficiency virus-1 through multi slope measure with triclustering genetic based algorithm

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Abstrak

Tantangan komputasi dibutuhkan pada analisis data microarray dikarenakan karakteristik data tersebut yang memiliki ukuran yang sangat besar dan memiliki ekspresi gen yang bervariasi di setiap kondisi, seperti contohnya data microarray Human Immunodeficiency Virus-1. Penelitian sebelumnya telah menggunakan ukuran Multi Slope Measure pada algoritma Triclustering Genetic Based tetapi algoritma tersebut belum tersedia secara luas dan belum dapat digunakan semua orang. Penelitian ini bertujuan untuk membangun program Multi Slope Measure pada algoritma Triclustering Genetic Based menggunakan perangkat lunak R berbasis open source pada data microarray ekspresi gen Human Immunodeficiency Virus-1. Pada simulasi program yang dibangun digunakan pada data microarray ekspresi gen untuk melihat kesuksesan program yang telah dibangun. Teknik triclustering diperlukan untuk mengelompokkan data 3 Dimensi berdasarkan data yang memiliki kesamaan pola. Algoritma Triclustering Genetic Based merupakan algoritma yang berdasarkan teori evolusi yang dapat mengelompokkan data dengan ukuran kualitas yang maksimum. Penelitian ini menargetkan mencari 10 tricluster dan berhasil didapatkan semua 10 tricluster nya. Dari 10 tricluster tersebut didapatkan 6 gen yang berkaitan dengan Human Immunodeficiency Virus-1 yaitu HLA-C, JUN, CCR5, ELF1, CX3CR1, dan GATA-3.

.....Computational challenges are needed in microarray data analysis because the characteristics of the data are very large and have gene expressions that vary in each condition, such as the microarray data for Human Immunodeficiency Virus-1 disease. Previous research used the Multi Slope Measure on the Genetic Based Triclustering algorithm, but the algorithm is not yet globally available and cannot be used by everyone. This study aims to build a Multi Slope Measure program on the Triclustering Genetic Based algorithm using open source-based R software on the microarray data of Human Immunodeficiency Virus-1 disease gene expression. In the simulation of the program that has been built, the program is tested on gene expression microarray data to see its success. The triclustering technique is needed to group 3-dimensional data based on data that has the same pattern. Genetic Based Triclustering Algorithm is an algorithm based on the theory of evolution that can classify data with maximum quality measure. This study aimed to find 10 triclusters and has successfully obtained all 10 triclusters. From the 10 triclusters, 6 genes were found related to Human Immunodeficiency Virus-1, namely HLA-C, JUN, CCR5, ELF1, CX3CR1, and GATA-3.