Penerapan metode pengelompokan regularized markov clustering (R-MCL) untuk menganalisa kekerabatan virus dengue = Implementation regularized markov clustering (R-MCL) algortihm to analyze family of dengue virus / Darno Raharjo

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Abstrak

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Virus dengue terdiri atas 10 protein penyusun yang berbeda dan diklasifikasikan menjadi empat serotipe utama (DEN 1 ? DEN 4). Penelitian ini dirancang untuk melakukan pengelompokan terhadap 30 sekuens protein virus dengue yang diambil dari Virus Pathogen Database and Analysis Resource (ViPR) menggunakan metode Regularized Markov Clustering (R?MCL) dan untuk menganalisis hasilnya. Dengan menggunakan program Python 3.4, algoritma R-MCL diimplementasikan dan menghasilkan 8 kelompok dengan pusat kelompok lebih dari satu di beberapa kelompok. Banyaknya pusat kelompok menunjukkan tingkat kepadatan interaksi. Interaksi protein ? protein yang terhubung padat dalam jaringan cenderung membentuk kompleks protein yang berfungsi sebagai unit proses biologi tertentu. Hasil analisis menunjukkan hasil pengelompokan dengan R-MCL menghasilkan kelompok ? kelompok kekerabatan virus dengue berdasarkan peran yang sama dari protein penyusunnya, tanpa memperhatikan serotipenya.
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ABSTRACT
Dengue virus consists 10 different constituent proteins and are classified into four major serotypes (DEN 1 - DEN 4). This study was designed to perform clustering against 30 protein sequences of dengue virus taken from Virus Pathogen Database and Analysis Resource (VIPR) using Regularized Markov Clustering (R-MCL) algorithm and tp analyze the result. By using Python program 3.4, R-MCL algorithm produces 8 clusters with more than one centroid in several clusters. The number of centroid shows the density level of interaction. The density of interactions protein - protein connected in a network tend to form a protein complex that serves as the unit of specific biological processes. The analyzing result shows the R-MCL clustering produces clusters of dengue virus family based on the similirity role of their constituent protein, regardless serotypes;Dengue virus consists 10 different constituent proteins and are classified into four major serotypes (DEN 1 - DEN 4). This study was designed to perform clustering against 30 protein sequences of dengue virus taken from Virus Pathogen Database and Analysis Resource (VIPR) using Regularized Markov Clustering (R-MCL) algorithm and tp analyze the result. By using Python program 3.4, R-MCL

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