

Pengelompokan sekuens protein virus herpes menggunakan tribe markov clustering (tribe-MCL) = Clustering of protein sequences herpes virus using tribe markov clustering (tribe-MCL) / Nurlaili Lisma Febriyani

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Abstrak

[ABSTRAK

Berdasarkan data World Health Organization (WHO) diketahui prevalensi herpes di negara-negara berkembang lebih tinggi dibandingkan dengan di negara maju. Virus herpes dapat ditemukan dimana saja dan salah satu ciri penting adalah kemampuannya yang dapat menimbulkan infeksi akut dan kronik pada waktu-waktu tertentu. Akibat infeksi tersebut memungkinkan terjadi komplikasi yang lebih berat. Virus herpes terdiri atas genome DNA tertutup inti yang mengandung protein dan dibungkus oleh glikoprotein. Dengan mempelajari ekspresi gen (sekuen DNA/protein) dan didukung oleh kemajuan di bidang bioinformatika, dapat ditemukan sub-sub bagian penting dan kelompok gen. Virus-virus ini dapat dikelompokkan dengan menganalisa sekuens protein dari virus herpes dengan menggunakan algoritma Tribe Markov Clustering (Tribe-MCL). Tribe-MCL merupakan metode clustering efisien berdasarkan teori rantai Markov chain, untuk mengelompokkan barisan keluarga protein. Data sekuens protein virus herpes diperoleh di GenBank yang dapat diakses pada situs National Center for Biotechnology Information (NCBI), kemudian disejajarkan menggunakan program BLASTp. Hasil pengelompokan sekuens protein virus herpes menggunakan algoritma Tribe-MCL dengan program R diperoleh enam kelompok. Semua kelompok menunjukkan jenis protein yang sama, dalam hal ini jenis protein yang digunakan adalah glikoprotein B, M, dan H pada delapan jenis virus herpes yang terjangkit pada manusia.

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ABSTRACT

Based on World Health Organization (WHO) data, the prevalence of herpes in developing countries is higher than in developed countries. The herpes virus can be found anywhere and one of the important characteristics is its ability to cause acute and chronic infection at certain times. Due to infections enables more severe complications occur. The herpes virus is composed of DNA containing protein and wrapped by glycoproteins. By studying the expression of genes (sequences of DNA / protein) and is supported by advances in bioinformatics, can be found an important sub-sections and groups of genes. These viruses can be classified by analyzing the sequence of the protein-sequence of the herpes virus using algorithm Tribe Markov Clustering (Tribe-MCL). Tribe-MCL is an efficient

clustering method based on the theory of Markov chains, to classify sequences of protein families. Herpes virus protein sequence data obtained in GenBank which can be accessed on the website National Center for Biotechnology Information (NCBI), then aligned using BLASTp program. The results of clustering protein sequences herpes virus using algorithms (Tribe-MCL) with a program of R obtained six cluster. All clusters showed the same type of protein, in this case the type of protein used is a glycoprotein B, F, and H in eight types of herpes virus that infected humans, Based on World Health Organization (WHO) data, the prevalence of herpes in developing countries is higher than in developed countries. The herpes virus can be found anywhere and one of the important characteristics is its ability to cause acute and chronic infection at certain times. Due to infections enables more severe complications occur. The herpes virus is composed of DNA containing protein and wrapped by glycoproteins. By studying the expression of genes (sequences of DNA / protein) and is supported by advances in bioinformatics, can be found an important sub-sections and groups of genes. These viruses can be classified by analyzing the sequence of the protein-sequence of the herpes virus using algorithm Tribe Markov Clustering (Tribe-MCL). Tribe-MCL is an efficient clustering method based on the theory of Markov chains, to classify sequences of protein families. Herpes virus protein sequence data obtained in GenBank which can be accessed on the website National Center for Biotechnology Information (NCBI), then aligned using BLASTp program. The results of clustering protein sequences herpes virus using algorithms (Tribe-MCL) with a program of R obtained six cluster. All clusters showed the same type of protein, in this case the type of protein used is a glycoprotein B, F, and H in eight types of herpes virus that infected humans]