Connections between evolution algebras and graphical model of hereditary disease

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ABSTRACT

In Biology, genes interactions are usually described in terms of graphs. Certain of those genes dispose in bi-functional modules within the graph according to their (anti)correlation to a state of functioning (e.g., permittivity to a genetic disorder of codominant traits) [1]. A disease may be characterised by a finite number of those modules. For a given module, there exist some allelic variants at risk (i.e., genetics risk factor) leading to a permissive state what eventually would cause disease in an individual if the other modules were also in the same permissive state. At present, the effective modelling of all these inherited genetics factors is impossible in biomedicine. However, within the framework of evolution algebras, it can be possible. In this work, we will explore connections between random walks on disease graphs [2-3] and the evolution algebra determined by the same graph.

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[2] Jianjun Tian & Xiao-Song Lin, Continuous time Markov processes on graphs, Stochastic Analysis and Applications, Vol. 24(2006), no. 5, 953-972.

[3] Jianjun Paul Tian & Zhenqiu Liu, Coalescent random walks on graphs, Journal of Computational and Applied Mathematics, 202(2007), no. 1, 144-154.