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Phylogetic Tree from the Tangled Nature Model and Its Community Structure¹ OSMAN CANKO, FERHAT TASKIN, KAMIL ARGIN, Erciyes University — In the evolutionary biology, taxonomy and origination of species are a widely emphasized subject. An estimation of the evolutionary tree can be done via available DNA sequence data. The calculation of tree are made by well-known and frequently used methods such as maximum likelihood and neighbor-joining. In order to inquire the results of these methods, an evolutionary tree is pursued computationally by a mathematical model, called Tangled Nature. A relatively small genome space is investigated due to computational burden and it is found that actual and predicted tree are in a reasonably good agreement in terms of shape. Moreover, speciation and emerged community structure of food-web are investigated by modularity.

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