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Predicting pathogenicity behavior in *escherichia coli* population through a state dependent model and TRS profiling

An important challenge in computational biology is the analysis of genetic molecular data through sophisticated computer science and mathematical methods that are implemented by interdisciplinary research groups. In this study we propose a comprehensive approach for predicting pathogenicity in a population based on a state dependent model and TRS-PCR profiling [1]. This method is based on the Binary State Speciation and Extinction (BiSSE) model that allows the diversification rates to be controlled by a binary trait. Additionally, we have evaluated the possibility of using the BiSSE model for estimating parameters from genetic data. We analyzed a real dataset (from 251 *E. coli* strains) and confirmed previous biological observations demonstrating a prevalence of some virulence traits in specific bacterial sub-groups. Noteworthy, this is a comprehensive approach and it may be used to predict pathogenicity of other bacterial taxa. We believe that our developed software should be useful for biologists that want to use BiSSE models.

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References

- [1] K. Bartoszek, M. Majchrzak, S. Sakowski, A.B. Kubiak-Szeligowska, I. Kaj, P. Parniewski, *Predicting pathogenicity behavior in Escherichia coli population through a state dependent model and TRS profiling*, PLoS Computational Biology 14 (2018), no. 1, e1005931.