

Spatio-temporal Modeling to Measure the Effects of Mutations and Selections

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The innovation of biotechnology and medical sciences makes significant role to improve the quality of life in modern society. At the same time, the ecosystem experiences an unprecedented strength of selection pressure. We will present some spatio-temporal statistical modeling approach to measure the adaptive mutations that may be related with human society. We predict adaptive mutations in a viral population using a model of population dynamics of virus, antibodies, and normal and infected cells in a host. It includes two key parameters: the binding affinities of the viral particles with the host cell-receptors and with the antibodies. The binding affinity is estimated by comparing the likelihood of protein sequences under two structural environments. When the protein-tertiary structure as well as sequence information is available, it is possible to estimate the region under diversifying selection by a Bayesian hierarchical model. Commercial breeding introduces directional selection on the target traits of the species, whereas seed production processes in stock enhancement and conservation-programs may relax natural selection pressure. Escapees from breeding cages and released animals therefore may affect the fitness of the wild populations. Graphical modeling of gene expression and phenotypes makes it possible to investigate the effect on endocrine system, immune system, and behaviors that are related with the fitness such as reproductive success. The information of chronological order and biological databases determine the constraints on the graph space. Using the information criteria, we estimate the maximal connected graph that includes the nodes of target phenotypes. The estimated correlation structure may be used to test the substantial equivalence.

Key Words: Spatio-temporal modeling, graphical modeling, adaptive mutation, substantial equivalence