

# Game theoretic models in molecular biology

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**Abstract.** There are many challenges in computational modeling of biological processes. Few processes such as signaling pathways operate independently of others but rather involve substantial coordination and shared resources. The level of abstraction appropriate for understanding different processes, e.g, viewing a pathway as a filter or a molecular cascade, varies by context and the type of predictions sought. Moreover, we would like to derive valid predictions about responses to experimental interventions even when the level of biological detail available about the system of interest varies widely. Some of these challenges can be resolved by casting models in game theoretic terms. I will exemplify this broader line of inquiry by discussing our recent work on modeling coordinate operation of DNA binding regulators. Our game theoretic model allocates proteins to neighborhoods of sites, and to sites themselves, in a resource constrained manner, while explicitly capturing coordinate and competitive relations among proteins with affinity to the site or region. I will provide examples of biological subsystems that are naturally translated into our framework, illustrate predictions that can be derived from the model, and highlight areas where we envision using game theoretic models more broadly.

The talk is based on joint work with Luis Perez-Breva, Luis Ortiz, and Chen-Hsiang Yeang.