

SIAM/APPLIED AND NUMERICAL ANALYSIS SEMINAR

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Speaker: Khanh Ngoc Dinh

Title: Modeling and simulating cancer evolution with mutations and copy number variants

Abstract:

It is well-known that the evolution of cancer is led by positive selection, fueled by driver events that offer the cancer cells some selective advantage. The theoretical results thus far have largely focused on mutational drivers, namely oncogenes and tumor suppressor genes. However, many experimental studies have shown that copy number events, which affect the overall structure of the genome, can themselves be drivers and interplay with mutational events, resulting in a complex picture of how cancers evolve. Nevertheless, cancer growth models involving copy number are difficult to simulate, and the theory is often intractable.

We present a modeling framework that incorporates both mutational and copy number events. This framework is flexible and can be employed to study many cancer types. Moreover, we developed a simulation algorithm, based on the tau-leaping scheme, that are magnitudes faster than the traditional Gillespie algorithm, and can simulate populations of size observed in real life within minutes. The outcome of our simulation method includes the mutational and copy number landscape, and phylogeny tree of the sample, which are important for down-stream analysis and mathematical theory.