Comparing models and biological data using computational algebra and topology

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Many biological problems, such as tumor-induced angiogenesis (the growth of blood vessels to provide nutrients to a tumor), or signaling pathways involved in the dysfunction of cancer (sets of molecules that interact that turn genes on/off and ultimately determine whether a cell lives or dies), can be modeled using differential equations. There are many challenges with analyzing these types of mathematical models, for example, rate constants, often referred to as parameter values, are difficult to measure or estimate from available data.

I will present mathematical methods we have developed to enable us to compare mathematical models with experimental data. Depending on the type of data available, and the type of model constructed, we have combined techniques from computational algebraic geometry and topology, with statistics, networks and optimization to compare and classify models without necessarily estimating parameters. Specifically, I will introduce our methods that use computational algebraic geometry (e.g., Gröbner bases) and computational algebraic topology (e.g., persistent homology). I will present applications of our methodology on datasets involving cancer. Time permitting, I will conclude with our current work for analyzing spatio-temporal datasets with multiple parameters using computational algebraic topology. Mathematically, this is studying a module over a multivariate polynomial ring, and finding discriminating and computable invariants.