We study how cells process information using a combination of experiments, mathematics and computation. We have a tradition of recruiting undergraduate students to our lab: over the last 10 years, 6 students have been first authors on published papers arising from their undergraduate work and 2 others have received Harvard's Thomas Hoopes Prize. This poster gives an overview of some of our research, with a focus on mathematical and computational problems, which are easier to accomplish within an internship or rotation. The photographs show some of the students who have worked in the lab over the years.

We have developed a mathematical framework for doing time-scale separation in biochemical systems. It is based on graph theory and polynomial algebra. The framework allows us to eliminate the overwhelming molecular complexity found in cellular mechanisms like allostery, post-translational modification and gene regulation and construct mathematical representations of how these mechanisms process information. We are applying this framework to several biological problems and especially to gene regulation in eukaryotes, in collaboration with Angela DePace’s lab.

If a network of molecular reactions obeys mass-action kinetics, which is usually the case in biology, it yields a polynomial dynamical system, whose steady states form a real algebraic variety. By using methods of computational algebraic geometry, such as Gröbner bases, as well as the linear framework, we can often summarise the steady-state variety in a polynomial expression that we call an “invariant”. We have found that invariants can tell us a great deal about network behaviour.