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Computational Systems Biology: Discrete Models of Gene Regulatory Networks

In this talk we will describe a hands-on project in computational systems biology for students and that can be used in a variety of settings, from high school to college, with a particular focus on the use of discrete mathematics. The biological focus is the *Escherichia coli* lactose operon, one of the first known intracellular regulatory networks. The modeling approach uses the framework of Boolean networks and tools from discrete mathematics for model simulation and analysis.

The talk is based on materials from a workshop for high school teachers described in Martins et al. [1] and conducted as a collaboration between the Virginia Bioinformatics Institute (VBI) at Virginia Tech and the Institute for Advanced Learning & Research (IALR) in Danville, VA. The workshop structure simulated the team science approach common in today practice in computational molecular biology and thus represents a social case study in collaborative research.

During the workshop the participants were provided with all the necessary background in molecular biology and discrete mathematics required to complete the project, and developed activities intended to show students the value of mathematical modeling in understanding biochemical network mechanisms and dynamics.

REFERENCES

- [1] A. Martins, P. Vera Licona, R. Laubenbacher. Computational systems biology: Discrete models of gene regulation networks. To appear in MAA Notes volume: Undergraduate Mathematics for the Life Sciences: Processes, Models, Assessment, and Directions. 2011.