

# How cells deal with uncertainty

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Researchers at McGill University have found that cells respond to their ever-changing environment in a way that mimics the optimal mathematical approach to doing so, also known as Bayes' rule; an application of probability theory. Their findings are published in the April 17 issue of PNAS, the *Proceedings of the National Academy of Sciences*.

“Biology is seeing a re-birth,” said Dr. Peter Swain, an assistant professor in the Department of Physiology and a Canada Research Chair in Systems Biology, as more researchers are “thinking about the cell using schemes that we know work from engineering and computer science.”

The study was carried out at McGill's Centre for Nonlinear Dynamics in Physiology and Medicine (CND). Eric Libby, PhD candidate at the CND and lead author on the paper, Dr. Ted Perkins, assistant professor in the School of Computer Science, and Dr. Swain simulated data on a biochemical response mechanism in a strain of *E. coli* bacteria.

“The ideal mathematical model and the simulation meshed perfectly with Bayes' rule,” remarked Swain. The bacteria's collection of genes and proteins that responded to changing environmental conditions acted as a successful Bayesian ‘inference module’, which takes noisy, uncertain information and interprets what it means for the cell.

There are many known schemes for inference that exist in mathematics. This study suggests that cells may have evolved to incorporate the most

efficient decision-making abilities into their biochemical pathways.

Quick, accurate cell responses to signals are necessary for survival. When we sense danger, our bodies can tell if the signal is real and trigger the production of adrenaline immediately. However, modeling the effects of a signal on one part of a cell, even in isolation from body tissues and organs, is complicated. “With many drugs, we don’t know how they work or exactly what they are targeting in a cell,” noted Swain. He explained that further study of inference modules could allow us to model more sophisticated cellular behavior, which could one day lead to computerized drug experiments and trials.

Source: McGill University

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