Special Undergraduate Talk
University of Texas at Arlington - Department of Mathematics
Proudly Presents:

Dr. Nick Hengartner
Los Alamos National Laboratory
Friday, October 26, 2018
12-1:00pm
305 Pickard Hall

Probability in Action

Abstract: This talk will discuss fundamental concepts of probability theory through hands on examples. Specifically, I will show that I can distinguish between true sequences of heads and tail and made-up sequences, give an elegant proof of Buffon's needle using cooked (instead of raw) spaghetti, and share with you a party game that will convince turn you into a mind reader. Finally, I'll present a card game in which will make you rich. While no calculus is needed, some intuition about probability, conditional probability and expectation will be helpful.

Short bio: Dr. Nick Hengartner received his MS in Statistics from the University of Waterloo in 1988 and his Ph.D. in Mathematical Statistics and Probability from the University of California, Berkeley in 1993. Currently, Dr. Hengartner is the Group Leader of the Theoretical Division T-6: Theoretical Biology and Biophysics at Los Alamos National Laboratory. His research interests include statistical modeling, nonparametric smoothing, statistical inverse problems, application of stochastic modeling to epidemics, particle transport, metagenomics and electricity consumption modeling. He is a very well accomplished scholar and has published over 200 peer-reviewed journal articles and technical reports.

The Theoretical Biology and Biophysics group at LANL focuses on the modeling of biological systems and the analysis and informatics of molecular and cellular biological data. It is one of the few research groups in the world devoted to mathematical modeling and computational analysis of problems in cellular and molecular biology. Research efforts include understanding dynamics and treatment of viral diseases such as HIV, influenza, and hepatitis; immune system modeling; receptor-ligand interactions and cell signaling; computational aspects of the human genome initiative; pattern recognition in DNA sequences; characterization and prediction of macromolecular structure; protein function and dynamics; and protein folding. The group has also created, and is responsible for the maintenance of the Influenza Sequence Database and the HCV and HIV sequence, immunology and resistance databases.

Refreshments before the talk and socializing following the talk
http://www.uta.edu/math/seminars