

BME Seminar Series

Edward M. Marcotte, PhD

Professor

Institute for Cellular and Molecular Biology

College of Natural Sciences

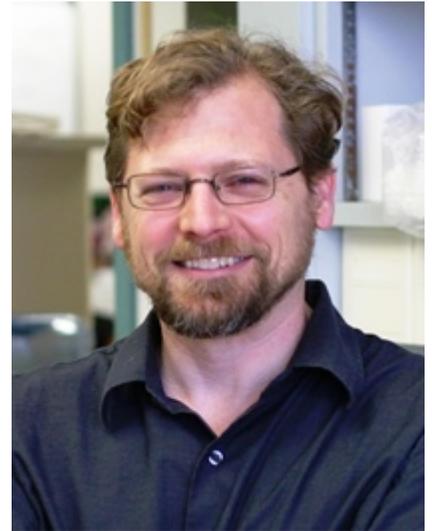
The University of Texas at Austin

Date: Monday, October 7, 2019

Time: 1:30 pm

Location: Traylor 709, Talbot Room, East Baltimore
Video-conferenced, Clark Hall 110, Homewood

Faculty Host: Winston Timp



Single-Molecule Protein Sequencing

Abstract: The identification and quantification of proteins lags behind DNA sequencing methods in scale, sensitivity and dynamic range. Currently, mass spectrometry is the method of choice for large-scale protein identification, but it is limited in its ability to analyze low-abundance samples and map rare amino acid variants. These limitations can in principle be addressed by highly parallel single-molecule protein sequencing, a concept analogous to nucleic acid technologies that sequence millions to billions of oligonucleotides in complex mixtures in parallel. I'll describe our development of such an approach, termed fluorosequencing, for directly visualizing individual fluorescently labeled peptide or protein molecules as they are sequenced by step-wise chemical degradation. This required developing instrumentation and methods, extensive testing of fluorophores, microfluidic design, chemistry of peptide immobilization and sequential degradation, image processing algorithms for monitoring individual peptide's fluorescent intensities, and classifying and modeling the sources of errors. Using fluorosequencing, we show that sparse amino acid sequence information can be obtained for individual protein molecules for thousands to millions of molecules in parallel. Single-molecule protein sequencing combines aspects from DNA sequencing, mass spectrometry proteomics, and classic peptide chemistry, and can potentially improve the sensitivity and throughput of proteomics experiments by orders of magnitude, as well as offering digital quantification, by counting molecules.

Bio: Dr. Edward Marcotte is a Professor in the Department of Molecular Biosciences at the University of Texas, where he holds the Mr. and Mrs. Corbin J. Robertson, Sr. Regents Chair in Molecular Biology and co-directs the UT Center for Systems and Synthetic Biology. His research falls in the general areas of proteomics, bioinformatics, and systems and synthetic biology, with current work focused on the interactions, dynamics, and evolution of proteins across the tree of life. Marcotte has authored 200 journal publications and 16 issued/in process patents, received a National Institutes of Health Director's Pioneer Award, is a Fellow of the Royal Society of Chemistry, the American Academy of Microbiology, and the American Association for the Advancement of Science, and co-founded the single molecule protein sequencing company Erisyon, Inc.