Dynamic single molecule force spectroscopy provides a powerful approach for probing the underlying energy landscape that governs how molecules fold into complex 3D architectures, bind to each other, and undergo conformational transitions. These sophisticated experiments operate by imposing gradually increasing forces on single molecules (or complexes) and recording their force-extension behavior until eventual rupture. An outstanding question in this field is how to recover the intrinsic energy landscape of the molecule from such force measurements. In this talk I will describe the development of new theoretical models [1,2] for extracting the height and location of activation energy barriers and intrinsic transition rates from single-molecule force measurements. The models go beyond the current state-of-the-art by accounting for both the finite stiffness of the pulling device and the non-linear stretching of the molecular handles often used for connecting the molecule of interest to the device. I will end the talk by discussing our recent efforts in combining such theoretical models with steered molecular dynamics simulations for drug design applications [3].

**Biosketch:** Gaurav Arya is currently an Assistant Professor in the NanoEngineering Department at UCSD. He obtained a Bachelors degree in Chemical Engineering from IIT Bombay in 1998 and a PhD degree in Chemical Engineering from the University of Notre Dame in 2003. He held two brief postdoctoral positions at Princeton University and New York University prior to joining UCSD in 2007. His research interests are in the areas of statistical mechanics, molecular modeling and simulations, chromatin biophysics, single molecule force spectroscopy, and colloidal and polymer physics. He has published over 30 peer-reviewed papers, several of which have been published in Advanced Functional Materials, Annual Review of Biophysics, Biomaterials, PNAS, and PRL. He was a recipient of the Hellman Fellowship in 2008.