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UNIVERSITY OF CALIFORNIA, BERKELEY

MATHAMATICS COLLOQUIUM
JOINT WITH BIOPHYSICS &
SYSTEMS BIOLOGY SEMINAR

"Towards a multi-scale analysis of translation dynamics: Integrating theory, sequencing and structural data"

Abstract: The translation of mRNA into protein is a fundamental biological process, mediated by the flow of ribosomes. As these dynamics can be locally regulated by many biophysical factors and mechanisms, analytical tools are needed to find the determinants of translation speed. In this talk, I will present recent methods to study translation across different scales, encompassing molecular, cellular and evolutionary aspects. These methods importantly rely on a stochastic model that generalizes the totally asymmetric simple exclusion process (TASEP). Analyzing this model led us to characterize the different regimes of transport and find the key parameters that govern translation efficiency. In the context of recent advances in deep sequencing, we also used the generalized TASEP model to infer gene- and position-specific translation rates for a large set of genes in yeast, and analyzed the contribution of traffic jams, codon specificity, and other biophysical parameters in explaining the inferred rates. In particular, our results highlight the impact of electrostatic interactions between the nascent polypeptide chain and the ribosome, which we confirmed by closely analyzing cryo-EM data structures. Altogether, these completing approaches shed light on key parameters and mechanisms that regulate translation, emphasizing the major role played by the ribosome in gene expression.

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