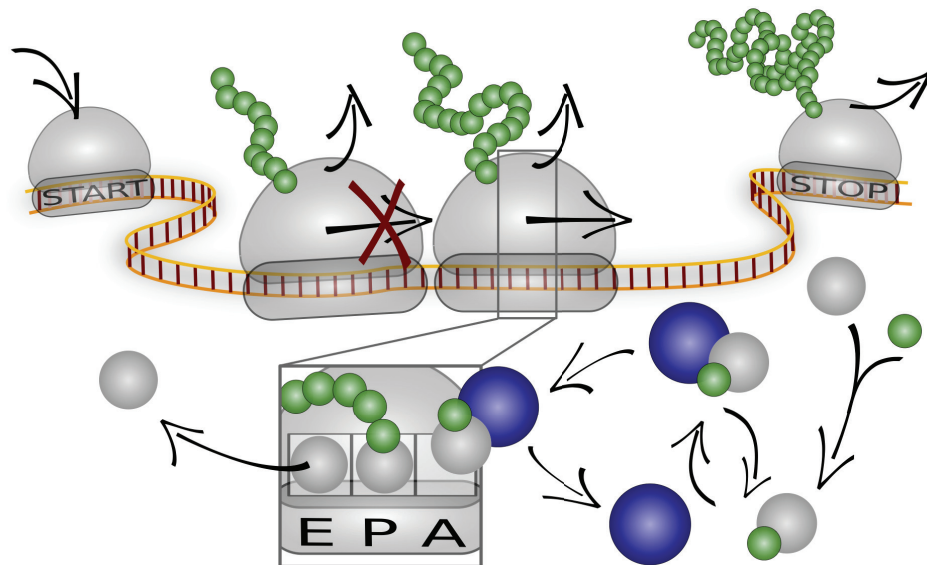


<https://uni-due.zoom-x.de/j/64228670246?pwd=RjVQeFNIUkRKRkpiNVpKYXhJaFNLdz09> (gilt für alle Vorträge)

Decoding mRNA translation: Computational and experimental approaches to understanding gene expression

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Our research explores advanced computational and experimental approaches to understanding mRNA translation dynamics and optimizing gene expression. In the first approach that I will present, a Markov model of translation was employed to decompose fluorescent signals from in-vitro ensemble experiments, revealing hidden kinetic information on early mRNA translation. The study highlights the challenges in signal decomposition, particularly when ribosomes translate mRNAs with more than five codons, and demonstrates that regularization can resolve these issues to extract translation state-specific data. The second approach utilizes a computational framework implemented in our research software OCTOPOS, designed to optimize mRNA sequences for enhanced protein expression. By combining OCTOPOS with Live Imaging on Single Cell Arrays, the study tracks translation kinetics and links ribosome dynamics with mRNA lifespans in lung tissue cells. It reveals that mRNAs with slow-codon windows have shorter lifespans but greater stability in the presence of siRNA. Our findings demonstrate that manipulating translation dynamics through the selection of synonymous codons can provide an effective means to control mRNA stability under RNA interference.