生命科学研究科 附属生命情報解析教育センター セミナー

数理モデル駆動型のリボソーム動態解析

Model-driven investigation of ribosome dynamics

Illustrated by Hiroko Uchida

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京都大学医学・生命科学総合研究棟(G 棟) セミナー室 A

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Translation, the decoding of mRNA to synthesize proteins, is fundamental to cellular homeostasis and function. Ribosome profiling (Ribo-seq), which measures ribosome-protected footprints genome-wide, has revealed that ribosomes traverse mRNAs at highly heterogeneous speeds; they pause at specific positions and can even collide after prolonged stalling. However, Ribo-seq is a static snapshot of ribosome occupancy rather than direct decoding speeds, and gene-level read counts can be inflated by pausing, obscuring true protein output. These features hinder our understanding of complex ribosome behaviors and our ability to link ribosome behavior to protein synthesis.

In this talk, I will present mathematical and computational models that quantitatively connect codon sequences, ribosome densities, elongation kinetics, and protein production rates. I developed a TASEP-grounded deep learning framework that infers position-specific elongation speeds from Ribo-seq-derived density. A stochastic simulation converts these speeds into actionable metrics such as protein production rates and collision propensity, which could be used for codon optimization. To extend analysis to mRNAs lacking Ribo-seq, I fine-tuned a codon language model to predict ribosome density from sequences only.

Together, the proposed framework of a sequence-density-speed-output mapping improves the interpretability of Ribo-seq, laying a foundation for rational, ribosome-aware codon optimization.

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