Decoding transcript efficiency and its cellular impact: bridging from model to experiments

Back in the 1950s, scientists began investigating the connections between cell physiology and cellular composition by looking at quantitative relationships among growth rates and cellular components. These "growth laws" are traditionally translation-centric, governed by ribosome allocation changes across conditions.

In this perspective, ribosome usage and allocation is believed to be one of the primary factors governing cellular physiology. However, identifying how coding sequence features affect the rate of translation, and therefore the overall biomass production, remains one of the greatest challenges in developing biophysical models.

In my talk I will first introduce a ribosome traffic model -based on the exclusion process- which will allow me to provide a model-inspired definition of single-transcript translation efficiency. By integrating models and experimental data of ribosome profiling (S. cerevisiae), we infer biophysical parameters of the translation process and show how both translation initiation and the first codons are the main determinants of protein production rate. Then, I will discuss how growth laws can emerge from basic principles of ribosome allocation using the same class of models.


Date: Monday, November 27, 2023
Time: 16:15h - 17:15h
Location: 02.073, Biozentrum
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