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Basel Computational Biology Seminar

21563 Current research in Bioinformatics II

Marco Cosentino-Lagomarsino

Coordinated biosynthetic fluxes drive yeast growth rate

Cell growth requires supporting the core processes of gene expression under finite resources, yet how eukaryotic cells tune these processes to control growth rate remains unclear. In budding yeast, available models assume that growth is primarily regulated by ribosome abundance, with translation and protein turnover kinetics largely fixed. Here, we challenge this view by combining new reporters of translation elongation with quantitative run-off proteomics, amino-acid metabolomics, and global RNA and protein measurements, supported by mathematical modeling and validation experiments. We find that faster- growing cells not only increase ribosome content, but also accelerate translation elongation, enhance protein degradation, increase mRNA pools, and deplete intracellular amino-acid pools. These coordinated changes point to a “flux-centric” growth-control strategy in which multiple interconnected processes are coordinated, rather than a single rate-limiting step. A minimal mathematical model captures this behavior and provides a predictive framework for eukaryotic growth regulation, highlighting general principles that may extend across diverse systems.

Speaker Information

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Event Details

Date: Monday, May 11, 2026
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Location: Biozentrum, U1.197
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