



University
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Department
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Swiss Institute of
Bioinformatics

BIOZENTRUM

The Center for
Molecular Life Sciences

Basel Computational Biology Seminar

21563 Current research in Bioinformatics II



Laurent Duret

Why is selection for translation-optimized codons so rare in metazoans?

Early studies on invertebrate model organisms (*Drosophila melanogaster* and *Caenorhabditis elegans*) clearly demonstrated that their synonymous codon usage is under selective pressure to optimize the efficiency of translation in highly expressed genes (a process called translational selection). In contrast, mammals show very little evidence of selection in favor of translationally optimal codons. To understand this difference, we investigated synonymous codon usage across 223 metazoan species, covering a wide range of animal clades. For each species, we predicted the set of optimal codons based on the pool of tRNA genes present in its genome, and we analyzed how the frequency of optimal codons varies with gene expression, controlling for variation in neutral substitution patterns. Based on these variations, we quantified the intensity of translational selection (S) in each species, and analyzed how it correlates with estimates of effective population size (N_e) or life history traits. Our analyses revealed that surprisingly, few metazoans show clear signs of translational selection. As expected, the highest values of S are observed in species with large N_e . However, overall, N_e appears to be a poor predictor of the intensity of translational selection, which suggests important differences in the fitness effect of synonymous codon usage across taxa. We will discuss several factors that may drive this variation.

Speaker Information

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Event Details

Date: Monday, May 4, 2026
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Host: Samuel Mondal
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