**You are cordially invited to a** **Computational Genomics Seminar**

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*"In sickness and in health – Roles of RNA modifications in human disease and across evolution"*

Wednesday **October 20** at **11:15**

**Check Point** building, room **420**

**Abstract:** The field of epitranscriptomics defines the landscape of >150 types of RNA modifications that regulate the life cycle of RNA, and act as instrumental players in modulating cellular outputs. Emergence of mRNA-based therapies, such as the SARS-CoV-2 vaccines, emphasizes a crucial role that distinct RNA modifications play in stabilizing RNA and allowing it to fulfil various functions. A pivotal milestone in elucidating the mechanisms of action of RNA modifications is the development of high-resolution maps, which allow for detection and quantification of modifications in various RNA types. Here I describe novel high-throughput methods we developed for mapping various RNA modifications across the tree of life, and discuss the computational challenges that accompanied their development. Using these methods we have identified RNA acetylation (N4-acetylcytidine; ac4C) as a dynamic heat-responsive modification accumulating on archaeal ribosomes at high temperatures and facilitating organismal thermoresistance. I will also discuss our work in the context of human disease, where we profiled modification patterns in mitochondria-encoded RNA, and identified disease-related enzymes that catalyze them. Overall, these studies quantitatively define the landscape of various RNA modifications, providing a technical and conceptual foundation for elucidating their role in biology and disease.

Host: [Prof. Ron Shamir](mailto:rshamir@tau.ac.il), School of Computer Science, TAU