MPI-NAT SEMINAR SERIES

Tuğçe Aktaş

MPI for Molecular Genetics, Berlin

RNA processing across evolution

RNA splicing is a eukaryotic innovation and even though the spliceosome machinery is mostly conserved from yeast to humans, the number, length and distribution of introns is highly variable and can rapidly change during evolution. One of the contributing factors to this diversity is the expansion of transposable elements (TEs) that make up 47% of human introns.

During mRNA synthesis, intronic TEs are transcribed along with their host genes but rarely contribute to the final mRNA product because they are spliced out and degraded. Interestingly, TEs are an abundant source of RNA-processing signals through which they can create new introns and chimeric transcripts. We work on several aspects of transposon-host interactions and their impact on the evolution and wiring of post-transcriptional RNA processing networks.

We take candidate-approach to study RNA binding proteins (RBPs) that are implicated in exon and intron selection for a mechanistic understanding of the exclusion of TEs from the final mRNA. In addition, we take unbiased approaches and study RBP hubs, such as Nuclear Speckles, to investigate how strategies that suppress, delay or neutralize transcribed transposons/viruses shape our transcriptomes and through evolution, our genomes. Results from our most recent work will be presented.

Thursday, 3 April 2025, 1:00 pm

Host: Kristina Žumer

Faßberg Campus
Manfred Eigen Hall

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