

GENETICS, BIOINFORMATICS, AND SYSTEMS BIOLOGY COLLOQUIUM

THURSDAY FEBRUARY 23
12:00PM PST
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THE ORCHESTRATION OF GENE EXPRESSION DYNAMICS ACROSS THE CELL

This seminar will explore different areas of our research into the complex processes underlying gene expression. I will discuss our work on how mRNAs move through the cell, with different rates of release, export, loading, and degradation. We found that transcripts with similar functions or targeting similar proteins move across subcellular compartments in similar ways. We also identified molecular features that influence the lifecycle of mammalian mRNAs. I will also discuss another study where we asked how multi-intron splicing order in human cells proceeds across the average of 8 introns per gene. We found that most genes are spliced in one or a few predominant orders, which are conserved across different cell types and differentiation stages. Introns flanking alternatively spliced exons were often excised last, with perturbations to the spliceosomal U2 snRNA altering the preferred splicing order of many genes. We identified cis-regulatory mechanisms that ensure splicing fidelity across long pre-mRNAs. Finally, I will present on our work dissecting the packaging of mitochondrial DNA into nucleoids that occurs without the aid of histones or other nuclear chromatin machinery. We used single-molecule accessibility mapping to observe the compaction of individual nucleoids. We discovered that human mtDNA compacts largely in an all-or-none way, and that the majority of nucleoids exist in an inaccessible, inactive state. We found that the primary nucleoid-associated protein, TFAM, packages nucleoids via a "nucleation and spreading" mechanism. Together, these stories demonstrate the importance of exploring the complex, multifaceted nature of gene expression regulation.