



BIOINFORMATICS SEMINAR

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GENE EXPRESSION VARIABILITY – FROM SINGLE CELLS TO POPULATIONS

The intrinsic stochasticity of gene expression leads to cell-to-cell variations, noise, in protein abundance. Several processes, including transcription, translation, and degradation of mRNA and proteins, can contribute to these variations. Single cell analyses of gene expression in yeast have uncovered a general trend where expression noise scales with protein abundance. This trend is consistent with a stochastic model of gene expression where mRNA copy number follows the random birth and death process. However, some deviations from this basic trend have also been observed, prompting questions about the contribution of gene-specific features to such deviations. In this talk, I will first describe our approach to untangle transcription and translation related contributors to expression noise. Next, I will describe our studies of expression variations on organismal level. Here we systematically examined the impact of *Drosophila melanogaster* deletions on gene expression profiles to ask whether increased expression variability owing to reduced gene dose might underlie heterogeneity of gene expression. Indeed, we found that, even on organismal level, one-dose genes have higher gene expression variability relative to two-dose genes. Finally, I will briefly discuss our approach to identify cell subpopulations and mapping of such subpopulation between single cell experiments that are subject to experimental and biological noise.

BIOGRAPHY

Teresa Przytycka is a Senior Principal Investigator at the National Center for Biotechnology Information (NCBI), National Institutes of Health. The research in her group focuses on computational methods advancing the understanding of biomolecular systems and the emergence of complex phenotypes, such as cancer. Her group also develops new approaches to study gene regulation both on the global network level focusing on methods to reconstruct Gene Regulator Networks, and on the local gene level where focusing on properties of DNA binding and the role of alternative, non B-DNA, structures. In addition to genome-wide systems level analysis, her group develops algorithms that help to utilize HT-SELEX technology for the identification of RNA binding motifs and drug design. She serves as an editor of several computational biology journals including PloS Computational Biology, Bioinformatics, BMC Algorithms for Molecular Biology, among other journals. She is also a member of the steering committee of RECOMB – one of the most prestigious algorithmic computational biology conferences bridging the areas of computational, mathematical, statistical and biological sciences.

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