BIOCHEMISTRY SEMINAR SERIES

Midstream Presentation - Fall 2020

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Wollman Group

“Phenotypic Consequences of Gene Expression Variability”

The concept of cell states is often used to explain differences among apparently homogenous cells in their responses to drugs, environmental cues, and more. These states usually give rise to persistent, specific phenotypes that are maintained by many layers of regulation from environment down to gene expression. Despite the fundamental importance of this persistence, it is yet unknown which regulatory level maintains a given cell state and to what degree. To address this question, we developed a tool using information theory and deep learning to quantify the dependency between any paired measurements in single cells. First, we measured information content in Ca^{2+} signaling dynamic state during repeated stimulations calculated as the mutual information between responses. Interestingly, we found that this number is significantly higher than the information Ca^{2+} response has about a ligand. We next asked where this extra information is encoded. We found that Ca^{2+} phenotypic persistence is encoded primarily at the gene expression level with ~85% of the total gene expression variance conserved in Ca^{2+} signaling dynamics. Our results quantitatively demonstrate that cell state is regulated at the level of mRNA abundances.

Tuesday, October 27, 2020

via Zoom

4:00 pm

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