DANIEL ZENKLUSEN, Université de Montréal

Imaging Single Transcripts Resolves Kinetics of Gene Expression Processes

Many cellular processes involve a small number of molecules and undergo stochastic fluctuations in their levels of activity; consequentially, biological processes are probably not executed with the precision often assumed. Hence, expression levels of proteins and mRNAs can vary considerably over time and between individual cells, limiting considerably the value of experimental datasets acquired through ensemble measurements that rely in pooling thousands of cells, as these datasets will only reflect an average behavior of a particular process. This underlines that cells should not be studied as 'the average cell' but as individual entities. Truly understanding 'cellular biochemistry' therefore requires the ability to study the behavior of individual cells, and ideally, individual molecules, only this results in datasets that represent the whole range of possible scenarios that can occur within a cell. We will summarize recent advances in single molecule RNA imaging approaches that have facilitated single molecule studies in cells and illustrate how we apply these techniques to determine how cells execute different processes along the gene expression pathway, in particular transcription.