BIOENGINEERING SEMINAR

“Exon/Intron-Split Analysis Quantifies both Transcriptional and Post-Transcriptional Contributions to Differential Expression in RNA-Seq”

Tuesday – June 24, 2014 – 12:15 p.m.
EPFL – room SV1717a

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Abstract

Eukaryotic RNA expression is controlled at multiple regulatory layers including transcription, splicing, nuclear export and RNA decay. The steady-state levels of mature RNAs are the net result of the concerted activity of all of these layers. While these levels can be directly quantified using RNA-seq, obtaining information about the transcriptional layer is experimentally challenging and requires specific experimental procedures. It has recently been shown that primary transcripts are also captured during RNA-seq library preparation, suggesting that intronic reads could be used to infer differences in transcription without the need for specialized experimental approaches.

We can demonstrate in several experimental systems that intronic reads mostly stem from nuclear RNA and that changes in intronic read counts accurately predict changes in transcriptional activity. We also found that the comparison of intronic and exonic levels, which we refer to as "Exon/Intron-split analysis", allows the direct separation of transcriptional and post-transcriptional contributions to mRNA expression changes. Our findings suggest that a standard RNA-seq experiment does not only allow the assessment of transcript levels and structures, but also reveals transcriptional and posttranscriptional responses to cellular perturbations, increasing the value of existing and newly generated RNA-seq data.

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