BIOENGINEERING SANDWICH SEMINAR

“Origins and Regulation of Gene Expression Heterogeneity”

Monday – March 31, 2014 – 12:15 p.m.
EPFL – room SV1717a

Prof. Jonathan Chubb
MRC Laboratory for Molecular Cell Biology,
University College London, London (UK)

host: Prof. D. Suter

Abstract

Despite the generation of transcriptional differences between nearby related cells being the basis of most differentiation and disease, our standard measures of RNA synthesis do not register the origins of these differences. Although useful for a preliminary rough sorting of genes to context, the widespread techniques of Northern blotting, microarrays, RT-PCR and RNA-Seq measure bulk RNA levels from homogenous population extracts. These approaches lose dynamic information from individual cells, and give the impression transcription is a continuous smooth process. The reality is that transcription is irregular, with strong variable duration periods of activity, interspersed by variable duration periods of inactivity. Averaged over millions of cells, this appears continuous. But at the individual cell level, there is considerable variability, and for most genes, very little activity at any one time. Transcription of genes, the process which transforms the stable code written in DNA into the mobile RNA message can occur in “bursts” or “pulses”. These phenomena have recently come to light with the advent of new technologies, to detect RNA in single cells, allowing precise measurements of RNA number, or RNA emergence at a gene. We would like to understand the mechanistic basis of pulsing, and how it is responsive to signals, developmental and chromatin context. And we are testing the implications of noisy transcription on the generation of diversity between cells in developmental and clinical contexts.

Sandwiches will be provided

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