BIOENGINEERING SEMINAR


Friday – December 12, 2014 – 12:30 p.m.
EPFL – room SV1717a

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host: Prof. Vassily Hatzimanikatis

Abstract:
New technologies now enable a considerably more detailed picture of the state of nucleic acids in organisms, and notably of the DNA methylation and the deep, strand-specific RNome. Here we examined the methylome (state of DNA methylation) of Clostridium acetobutylicum and C. pasterianum under normal and, for C. acetobutylicum, metabolite stress conditions. We also used Illumina-based strand-specific RNAseq to probe the deep RNome of C. acetobutylicum under both normal and stress conditions.

Several strains of C. acetobutylicum and C. pasterianum were sequenced and assembled via Single Molecule Real-Time (SMRT; PacBio) sequencing. The WT C. pasterianum type was assembled into 2 contigs (4.4 Mb) and was compared to the previously published version of the same strain, which exists in 37 contigs with a total length of 4.28 Mb. Mutations introduced to an evolved, more tolerant to crude glycerol C. pasterianum strain were identified by sequence comparison to the WT. DNA methylation patterns identified with SMRT sequencing were used to aid in optimization of transformation efficiency of plasmid DNA. The DNA methylome of C. acetobutylicum under normal versus metabolite stress conditions was also compared aiming to understand the impact of stress on DNA methylation and if this is possibly related to cell survival and gene expression. Strand-specific RNAseq was employed to explore the complex transcriptome of these two organisms, with emphasis on identifying strand-specific expression of small RNAs (both cis and trans), unknown genes, and also transcriptional start sites to probe the impact of culture conditions on the rich RNome of these organisms. The results demonstrate a much richer RNome that could anticipated, to the point in fact that the expected RNome based on the genome is only a small fraction of the experimentally observed strand-specific RNome. The information that can be extracted from such data leads to new ways to solve old problems, and significantly provides a much deeper understanding of the inner workings of the cells.

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