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SÉMINAIRE

Genome-scale transcriptional activity of *Bacillus subtilis* cells under various life styles.

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Microorganisms rely largely on changes of the transcriptional activity to adapt to the variations of the environment. However, it has not been possible until recently to obtain a knowledge of the transcriptional activity that could compare with the completeness of the genome sequences. Ideally the data should be unbiased with respect to the set of conditions, as well as with respect to the segments of chromosome whose transcription is assessed. The oligonucleotide tiling array technology provides this opportunity and was used in this work to quantify the transcriptional activity of *B. subtilis*. A set of 97 conditions (240 hybridizations) were explored to provide the broadest coverage of the biology of the bacterium. As a validation of our experimental design, we observed that most known genes belonged to the highly expressed ones in at least one condition. The data allowed the precise and systematic mapping of the transcribed regions and of the changes in transcriptional activity of *B. subtilis*. Here we will present our main findings concerning the architecture of transcriptional control in this versatile bacterium. We will also present two distinct statistical models motivated by the analysis of this data. The purpose of the first model is to improve the processing of the hybridization signal with a hidden-Markov model. The second model intends to relate the expression data to the presence of sequence motifs in the genome with a transdimensional MCMC algorithm. <http://genome.jouy.inra.fr/~pnicolas/> A Basysbio/Bacell SysMO collaborative work.