Institute of Molecular Biology

IMB TechTalk

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"Whole-genome DNA Methylation Profiling by Bisulfite-Sequencing"

15 May 2012, 11:00 (*s.t.*)

Venue: 2nd Floor Seminar Room
Institute of Molecular Biology (IMB)
Johannes Gutenberg University Campus Mainz

All are welcome to attend

Host: Dr. Bernhard Korn, Director CF & Technology, IMB
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Abstract:

DNA methylation can be measured by a variety of different techniques, such as affinity-based methods that enrich for 5-methyl-cytosines using antibodies (MeDIP) or methyl-binding domain proteins (MBD), microarray based approaches (e.g. Illumina Infinium BeadChip) or treatment of DNA with bisulfite and sequencing (Bis-seq).
While all of these methods have distinct advantages and disadvantages, Bis-seq is considered the “gold standard” because of its single nucleotide resolution and unambiguous absolute readout of methylation status. Through recent technological advances that have tremendously reduced the cost of DNA sequencing, genome-wide Bis-seq experiment have become feasible.
The computational challenges of genome-wide Bis-seq experiments are illustrated in this talk, from the coverage requirements that are a major determinant of cost, over processing and interpretation of these large data sets, up to the identification of regions with low methylation levels.

I will show why it is important to know the single nucleotide polymorphisms (SNPs) for the interpretation of methylation status, and what can be learned from low methylated regions about the binding of transcription factors.