A computational approach to characterizing nucleosome dynamics

Ngoc Tu Le (850803)

School of Knowledge Science,
Japan Advanced Institute of Science and Technology

February 2010

Keywords: nucleosome dynamics, epigenetics, histone modifications, rule induction.

The ability of the cells in living organisms to grow, replicate, repair themselves and even evolve under the stimuli of environment depends much on how genetic information kept inside the cell nucleus is expressed through diverse biological processes, such as protein synthesis, DNA replication, DNA repair and genetic recombination. By controlling these processes, the cell can decide most of its functions.

Genomes of eukaryotic organisms are packaged into chromatin, a compact structure containing fundamental units of nucleosomes. The mobility of nucleosomes is known to play important roles in many DNA-related processes by regulating the accessibility of regulatory elements to biological machineries. Although it has been known that various factors, such as DNA sequences, histone modifications and histone variants, chromatin remodeling complexes, could affect nucleosome stability, the mechanisms of how they regulate this stability are still unclear.

The work here proposed a computational method based on rule induction learning for characterizing nucleosome dynamics using both genomic and histone modification information. Our results on *S.cerevisiae* showed

that, some DNA motifs and post-translational modifications of histone proteins play significant roles in regulating nucleosome stability. Interestingly, these DNA motifs are strong determinants for nucleosome forming and inhibiting, and these histone modifications have strong relation with transcriptional activation and repression. We also found some new patterns which may reflect the cooperation between these two factors in regulating the stability of nucleosomes. These results led to the conclusion that DNA motifs and histone modifications can independently and, in some cases, cooperatively regulate nucleosome stability. This suggests additional insights into mechanisms by which cells control important biological processes, such as transcription, replication and DNA repair.