THE UNIVERSITY   OF HONG KONG

Department of Mathematics

Numerical Mathematics and Applied Analysis Group Seminar (NMAA)

Transcriptional Regulatory Network Discovery via Information Mining Approach in Rett Syndromes Study

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on Friday, August 6, 2010 at 11:00am
in Room 206, Run Run Shaw Bldg., HKU

Abstract

Methyl-CpG binding protein 2 (MeCP2) was identified as both activator and repressor in Rett syndrome. Numerous genes in the hypothalamus expressed differentially under the regulation of MeCP2. Experimental results indicated that only a small fraction of genes were directly bound by MeCP2. The transcriptional regulatory networks from the source MeCP2 to its downstream genes were built to reveal the mechanism of molecular processes and signal transduction. Information mining approaches, including database search, literature mining, interaction prediction, and computational inference were integrated to maximize the discovery due to the limitation of prior knowledge of MeCP2. Hub cofactors, whose binding sites were enriched in the MeCP2 activated and repressed groups, comparing with that of the whole genome, were finally identified by using novel linear programming algorithm. The network topology analysis results proved the hub cofactors were important for network structure.

All are welcome