

Inferring Molecular Networks

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With the increasing quantities of high throughput data, it is possible to infer biological networks from these measurements. For example, recent high throughput technologies, such as 'ChIP-chip' and 'ChIP-seq', have generated high resolution maps for many histone modifications on the human genome. Different modifications may combine to form complex 'histone codes'. To infer these codes, we used the Bayesian network framework to find causal and combinatorial relationships among histone modifications and gene expression. Our unbiased network model not only confirmed already known relationships, such as those of H3K27me3 to gene silencing, H3K4me3 to gene activation, and the effect of bivalent modification of both H3K4me3 and H3K27me3, but also identified many other relationships that may predict new epigenetic interactions important in epigenetic gene regulation. We also developed and applied network structure inference methods to computationally predict various molecular networks during other biological or pathological processes.