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### ***Delineation of epigenetic landscape in human cells***

The concept of epigenetic landscape is widely appreciated in description of how cell fate is decided. With the fast accumulation of genomic and epigenomic data, it is tempting to fill biological details into this abstract framework and delineate the epigenetic landscape at the systems level. Two perspectives on delineating the epigenetic landscape in human cells will be discussed. The first aspect is to depict the epigenetic states by genome-wide measurements of chromatin states and DNA methylation across diverse human cells, which paints a global view of the relationship between epigenetic modifications and cell type specificity. Comparative annotation of these epigenomes is able to reveal the regulatory elements responsible for specifying cell functions. The second perspective is to determine the cell states based on genetic network and delineate the potential landscape of cell states that defines the cell specificity. Recent progress on developing efficient computational methods to overcome the hurdles of modeling complex genetic network will be reported. The applications of such a systems biology approach in phenotype prediction will be discussed.