# Discovery and Characterization of Chromatin States for Systematic Annotation of the Human Genome

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A plethora of epigenetic modifications have been described in the human genome and shown to play diverse roles in gene regulation, cellular differentiation and the onset of disease. Although individual modifications have been linked to the activity levels of various genetic functional elements, their combinatorial patterns are still unresolved and their potential for systematic de novo genome annotation remains untapped. Here, we use a multivariate Hidden Markov Model to reveal chromatin states in human T cells, based on recurrent and spatially coherent combinations of chromatin marks. We define 51 distinct chromatin states, including promoter-associated, transcription-associated, active intergenic, large-scale repressed and repeat-associated states. Each chromatin state shows specific enrichments in functional annotations, sequence motifs and specific experimentally observed characteristics, suggesting distinct biological roles. This approach provides a complementary functional annotation of the human genome that reveals the genome-wide locations of diverse classes of epigenetic function.

V. Bafna and S.C. Sahinalp (Eds.): RECOMB 2011, LNBI 6577, p. 53, 2011.