Title:	Characterization of distinct epigenomic features associated with Enhancer-like promoters in human cell-lines
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Abstract:	The human genome vastly consists of non-coding DNA, and this portion contains variants associated with diseases, as shown by GWAS studies. Many studies have shown that the SNPs for diseases often lie in the regulatory elements of other genes. This creates a gaping hole in our understanding of how Trans regulation among genes happens inside our genome and how these phenotypes manifest as a result of this regulatory propagation in the genome. Recent studies have shown that certain promoters interact with each other, much like enhancers and promoers interact spatio-temporally. Several other studies have shown that a small proportion of promoters display enhancer activity. This evidence along with studies that blur the classical architectural demarcations between enhancers and promoters indicate that gene regulation is much more complex that earlier thought of, and how these promoter-promoter interactions could amplify in the genome due to network effect. In this thesis, we study the epigenomic markers associated with Enhancer-like promoters, namely Histone modification and Transcription factor marks in two ENCODE human cell lines – K562 and HeLa-S3. We also analyse how Enhancer-like promoters are temporally expressed with respect to regular promoters in the presence of environmental stimuli, and their position in the 3-D genome with respect to CTCF loops. We hypothesize that these promoters with enhancer activity are associated with inducible genes and kick-start the developmental program in the cell. They are enriched within CTCF loops; which constrain the transcriptional induction of ELPs and stop ripple effect.
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