

ID No.	K2101
Project Title	<i>In-silico</i> functional analyses of non-coding regions in genome sequence
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Report	<p>We have tried to use hybrid deep learning framework for enhancer prediction. We found that combining the sequence information with epigenetic information (Dnase-seq data and histone modification data) can slightly improve the performance on different cell lines. We also found that local histone modification signal is informative for enhancer prediction. Furthermore, We tried the use of GCN (Graph Convolutional Network) for enhancer prediction, which takes the enhancer prediction as graph classification. Each enhancer region is a graph, in which each nucleotide is a node and the bond between two nucleotides is an edge. The result showed that GCN can perform better than CNN (Convolutional Neural Network). A paper reporting these results are still in preparation (the paper in the publication list is a kind of by-product). Although we planned to have a conference for the discussion of our current results at IMSUT, the speakers could not come because of the COVID-19 problem. We held an online conference, instead.</p>