Lawrence McKechnie

Identification of Transcription factor binding sites (TFBSs) in enhancers and promoters responsible for activity-regulated gene expression in cortical neurons

In the publication of Kim et al., a large number of enhancer regions were shown to increase in expression upon induction by KCl-mediated neuronal activity in vivo. It was the aim of this study to investigate which transcription factor binding sites (TFBSs) are responsible for such activity-mediated gene expression in enhancers and promoters using ChIP-seq data in the publication mentioned above. Specifically, we found that there are non-overlapping sets of TFBSs significantly enriched in either enhancers or promoters of all genes, regardless of regulatory status. Further, it found that a subset of the set of TFBSs shifted towards enhancers of all genes are also found to be enriched in enhancers associated with those genes that are up-regulated in response to neuronal activity but not enriched in those associated with down-regulated genes, with members of the E-BOX and POU domain family of Transcription factors over-represented. Transcriptional interference is posed as a possible mechanism reflecting the enrichment of TFBSs in promoters of down-regulated genes, relative to those of genes that up-regulated by KCl induction. In addition, sets of TFBSs show differential affinity scores in enhancers and promoters of all genes. There is a correlation between the affinity score and the tendency of matrices to cluster around the position of ChIP-seq peak.