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Title: MACHINE LEARNING APPROACHES UNMASK CHROMATIN STATE REPROGRAMMING EVENTS IN TUNE WITH NEURAL CREST SPECIFICATION ACROSS EARLY ZEBRAFISH DEVELOPMENT

Abstract:

A UMAP re-analysis of publicly available chromatin accessibility data (ATAC-seq) across two studies from 3-12hpf (fertilization to gastrulation) in Zebrafish NC progenitors shows that genome-wide chromatin accessibility scores group by replicate and by stage. Further parsing and analysis elucidates the regional chromatin accessibility patterns that underlie this separation, which are predominantly increasing or decreasing across time. Upon investigation of parsed regions, we find that H2A.Z is enriched in increasingly accessible regions and depleted in decreasingly accessible regions at 6, 24, and 36hpf. ANP32E signal is low in increasingly accessible regions that are high in H2A.Z, and ANP32E is high in decreasingly accessible regions that are low in H2A.Z. Increasingly accessible regions in cluster 1 are enriched for Gene Ontology (GO) terms associated with the differentiation of Neural Crest (NC) and are also enriched for Sox10 motifs (Sox10 is widely held as the master TF for NC lineages). Taken together, this supports a role of H2A.Z-ANP32E antagonism in NC specification and differentiation where H2A.Z and ANP32E distributions match with expected trends in chromatin accessibility.