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Patterns of Correlated DNA Methylation.

Genome-scale assessments of DNA methylation have been used to identify disease-contributing loci in variety of human diseases, cancers, and traits. Mainly focusing upon identifying differences in methylation level between disease and non-disease states. Methylation sites in close proximity of each other are known to have sustainable correlation structures (CSs). Very little is known about CSs consistency across individuals and tissues, genomic context, and relevance to disease. Here, we develop a novel Image Clustering Method (ICM) that leverages image conversion and correlation matrices, to assess patterns of correlated methylation sites. We apply our method to 31 publicly-available datasets, spanning 27 tissues and >11,000 individuals. We identify 207 clusters of contiguous correlation between adjacent sites. We also observe significant positive and negative correlation between contiguous clusters extending as far as 250kb. These non-contiguous clusters are bound within topology-associated domains (TADs) and suggest coordinated methylation between CpG sites at gene-clusters, as well as across gene bodies. Finally, we identify significant differences in cluster correlation between diseased and non-disease states, including cancer, with disease-specific patterns of disruption. (Received August 05, 2020)