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DMRL: Differentially Methylated Region Locator

A versatile Python tool to quantify DNA methylation difference and identify DMRs

DNA methylation plays critical roles in transcriptional regulation, development, X-chromosome inactivation, chromatin remodelling. Sodium bisulfite converts unmethylated cytosines to uracils, but 5-methylcytosines remain unconverted. After PCR amplification, unmethylated cytosines appear as thymines and methylated cytosines appear as cytosines. Coupled with high-throughput DNA sequencing technologies, it's now available to perform genome-wide measurements of DNA methylation at single-base resolution. Analysis of genome-wide methylation data starts with alignment of bisulfite-converted reads. After alignment, statistical methods are employed to identify differentially methylated regions (DMRs) between samples. Extensive work has been dedicated to alignment (such as BS-Seeker2, Bismark, BSMAP, etc.) but methods for post-alignment analysis are limited. However, DMRs have important implications for gene regulation. Therefore, genome-wide mapping of DMRs across various temporal and spatial samples is important in revealing the impact of epigenetic modifications on heritable phenotypic variation. Here we present a versatile Python tool, differentially methylated region locator (DMRL), to quantify methylation difference and identify DMRs from genome-wide methylation profiles.