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Applications Note

Data and text mining

mHapTk: a comprehensive toolkit for the analysis of DNA methylation haplotypes

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Abstract

Summary: Bisulfite sequencing remains the gold standard technique to detect DNA methylation profiles at single-nucleotide resolution. The DNA methylation status of CpG sites on the same fragment represents a discrete methylation haplotype (mHap). The mHap-level metrics were demonstrated to be promising cancer biomarkers and explain more gene expression variation than average methylation. However, most existing tools focus on average methylation and neglect mHap patterns. Here, we present mHapTk, a comprehensive python toolkit for the analysis of DNA mHap. It calculates eight mHap-level summary statistics in predefined regions or across individual CpG in a genome-wide manner. It identifies methylation haplotype blocks, in which methylations of pairwise CpGs are tightly correlated. Furthermore, mHap patterns can be visualized with the built-in functions in mHapTk or external tools such as IGV and deepTools.

Availability and implementation: https://jiantaoshi.github.io/mhaptk/index.html.

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Supplementary information: Supplementary data are available at *Bioinformatics* online.

1 Introduction

DNA methylation is an essential epigenetic regulatory mechanism that plays critical role in many biological processes, including embryonic development (Greenberg and Bourc'his, 2019), tumorigenesis (Blewitt *et al.*, 2019) and aging (Unnikrishnan *et al.*, 2019). Mammalian DNA methylation predominantly occurs at CpG sites. Bisulfite sequencing (BS-seq), including whole genome bisulfite sequencing (WGBS) and reduced representation bisulfite sequencing, is the gold standard technique to detect DNA methylation profiles at single-nucleotide resolution. The DNA methylation status of CpG sites on the same fragment represents a discrete methylation haplotypes (mHap) (Shoemaker *et al.*, 2010). The mHap-level metrics characterize DNA methylation patterns rather than average methylation. Based on mHap-level patterns, methylation entropy was defined to assess the variability of DNA methylation (Xie *et al.*, 2011). The Proportion of Discordant Reads (PDR) was proposed to measure intra-sample heterogeneity (Landau *et al.*, 2014). Recently, Cellular Heterogeneity-Adjusted cLonal Methylation (CHALM) (Xu *et al.*, 2021) and methylation concurrence ratio (MCR) (Shi *et al.*, 2021) were demonstrated to explain gene expression variation better than average methylation. Furthermore, the mHap-level patterns show promising translational potentials. For example, DNA methylations of adjacent CpG sites were found to be co-methylated and form methylation haplotype blocks (MHBs) (Guo *et al.*, 2017). This co-methylation pattern can be quantified by methylated haplotype load (MHL) and methylation block score (MBS) (Liang *et al.*, 2021), both of which preserve a higher signal-to-noise ratio than average methylation in early cancer detection.

However, the tools for analyzing DNA methylation haplotypes are limited. One tool of this kind is RLM, but it only calculates PDR and entropy, and does not support a plot interface. Besides, it takes aligned BAM/SAM files as input, which is prohibitively large in size for large-scale BS-seq analysis (Hetzel *et al.*, 2021). Previously, we have developed a novel mHap format, which reduces the size of a BAM file by up to 140-fold while keeps all mHap-level information (Zhang *et al.*, 2021). It is also compatible with the Tabix tool for random and fast access (Li, 2011). Furthermore, the mHap format file contains no genetic information and can be shared as the CpG-level mean methylation file, which poses minimal risk to an

individual's privacy. Here, we further developed mHapTk, a comprehensive toolkit for the analysis of DNA methylation haplotypes based on mHap format.

2 mHapTk description

mHapTk takes mHap files as standard input, which can be converted from BAM files using mHapTools (Zhang *et al.*, 2021). Functions in mHapTk can be assigned into three categories, visualization, MHB discovery and calculation of mHap-level summary metrics (Fig. 1, Supplementary Fig. S1).

For a given region, mHapTk visualizes the read-level methylation statuses as a tanghulu plot (Guo *et al.*, 2018) (Supplementary Fig. S2A). Reads with the same methylation pattern can be optionally stacked with its occurrence number shown beside (Supplementary Fig. S2B). For a region with large number of reads, a given number (20 by default) of mHaps can be simulated to maximize the likelihood given the observed sequencing reads (Supplementary Fig. S2C). Alternatively, mHap-level information can be shown as a heatmap (Supplementary Fig. S2D, upper panel). The co-methylation levels of pairwise CpGs are measured by linkage disequilibrium (LD) R^2, calculated from individual reads rather than mean methylation (Guo *et al.*, 2017). Note that we used signed R^2 to distinguish positive and negative correlations (Supplementary Fig. S2D, lower panel). The combination of these two plots is termed mHapView in mHapTk. It also implemented a *de novo* MHB discovery tool that identifies locally co-methylated regions across the genome. Using a public dataset of esophageal squamous cell carcinoma as an example (Cao *et al.*, 2020), mHapTk identified 11 112 MHBs, which can be potentially used for non-invasive cancer detection (Supplementary Fig. S3). For a set of regions, typically defined by a BED file, mHapTk calculates eight mHap-level summary statistics, i.e. average methylation, CHALM, PDR, MHL, MCR, Entropy, MBS and signed LD R^2 (Supplementary Table S1). Furthermore, the above mHap-level metrics can also be calculated in terms of individual CpG sites across the genome, resulting in files in bedGraph format, which can be used in combination with IGV (Thorvaldsdottir *et al.*, 2013), pyGenomeTracks (Lopez-Delisle *et al.*, 2021) and WashU browser (Li *et al.*, 2022) for visualization. For instance, CASC9 is upregulated in esophageal cancer, which is potentially explained by decreased CHALM PDR, and MBS, as well as the presence of MHBs in the promoter region (Supplementary Fig. S4). The bedGraph files generated by mHapTk can be converted to bigWig files and used by deepTools (Ramirez *et al.*, 2014) for visualization (Supplementary Fig. S5). Example outputs of mHapTk have been described with more details in Supplementary Table S1–S6.

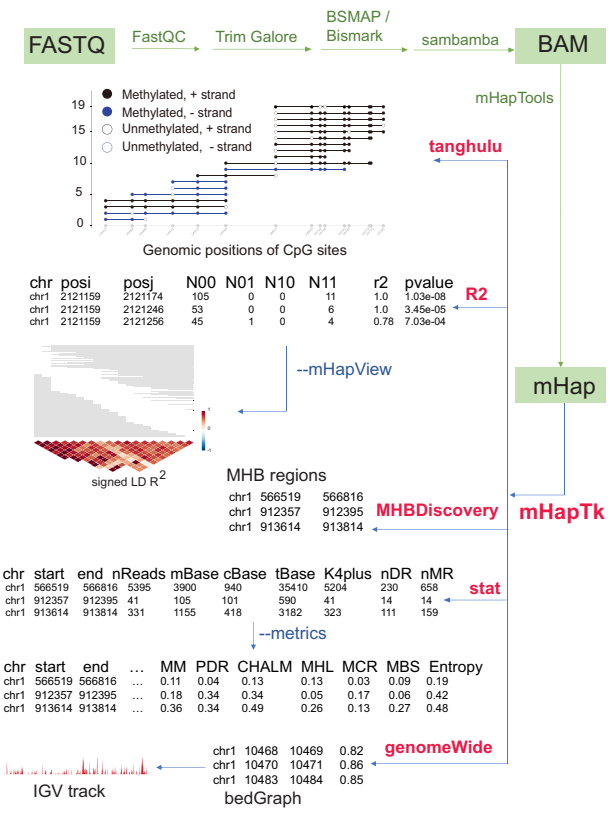

Fig. 1. A schematic diagram of mHapTk. The pre-processing steps output mHap files that are used as standard input in mHapTk. There are five sub-commands in mHapTk, including 'tanghulu', 'R2', 'MHBDiscovery', 'stat' and 'genomeWide'. The example outputs of each command are shown in a concise way

3 Application to real datasets

We used mHapTk to explore the potential association between DNA methylation patterns and gene expression in lung cancer cell lines from the CCLE dataset. We focused on promoters with significant changes only in mHap-level metrics but not mean methylation. For instance, promoters were assigned into different groups according to changes in mean methylation and changes in DNA methylation entropy between two subtypes of lung cancer, i.e. non-small cell lung cancer and small cell lung cancer (Supplementary Fig. S6). Specifically, four groups were defined: gene promoters with significant changes in both mean methylation and entropy (Supplementary Fig. S6A), significant changes in entropy only (Supplementary Fig. S6B), significant changes in mean methylation only (Supplementary Fig. S6C) and those with no significant changes in either mean methylation or entropy (Supplementary Fig. S6D). Interestingly, the association between DNA methylation entropy and gene expression is statistically significant regardless of the change in mean methylation (odds ratio = 610.64, p-value $< 2.2e{-}16$). Besides entropy, PDR, CHALM and MBS also explain gene expression variation independent of mean methylation (Supplementary Fig. S7–12). These results demonstrate that mHapTk has the potential to uncover a novel association between DNA methylation patterns and gene expression. Finally, we benchmarked the running time of mHapTk and showed that it was computationally efficient for typical WGBS samples (Supplementary Fig. S13).

4 Conclusion

Here, we present mHapTk, a novel software for manipulating mHap data. Using mHap format data as standard inputs, it separates the steps of pre-processing and data mining when dealing with BS-seq data. Coupled with mHapTools, it streamlines the analysis of DNA methylation haplotypes. Given the tools in mHapTk, it will have broad application in the fields of gene regulation and biomarker discovery.

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Conflict of Interest: none declared.

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