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A comparative study of Bisulphite-seq analysis pipeline

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Abstract

Recent advances in next generation sequencing (NGS) technology provide the opportunity to rapidly understand whole genome methylation profile. However, there are challenges in handling and interpretation of the methylation sequence data because of its large volume and the consequences of bisulphite modification. Most of the current pipelines include a specific aligner to decode and quantify the fraction of methylated cytosine per base; further this quantitative data is studied for differential methylation and annotated for genomic features. We have examined the performance of three pipelines for alignment and differential methylation profiling using the published data from plant and animals. We compared the consistency across these tools and explored various visualization features. We also illustrate our *in-house* visualization based analytic tool for a higher quality comprehension of whole genome methylation profile. Our comparative study showcases the performance of the widely accepted tools and can guide the scientific community in choosing the appropriate method for their methylation data analysis.

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