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DNA Methylation Analysis; A Thorough Comparison of Available Analytic Tools

DNA methylation studies have increased in number recently thanks to recent advances in next-generation sequencing and microarray technology, providing many data sets at high resolution, enabling researchers to understand methylation patterns and their regulatory roles in biological processes and diseases. Diverse methods and software create ample opportunities for researchers to do quantitative analysis, however, this also makes it difficult for practitioners to choose one that is suitable and efficient in analyzing the data. The goal of this talk is to compare the available analytic tools using real and simulated data sets to give insights into their validity, efficiency and utility.