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Next generation sequencing is revolutionizing molecular biology. Owing to this new technology it is now possible to carry out a panoply of experiments at an unprecedented low cost and high speed. These go from sequencing whole genomes, transcriptomes and small non-coding RNAs to description of methylated regions, identification protein – DNA interaction sites and detection of structural variation. The generation of gigabases of sequence information for each of this huge bandwidth of applications in just a few days makes the development of bioinformatics applications for next generation sequencing data analysis as urgent as challenging.



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