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Implementation of CNV-CH Algorithm Using Map-Reduce Approach

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Abstract : We have developed an algorithm to detect the abnormal segment/"structural variation in the genome across a number of samples. We have worked on simulated as well as real data from the BAM Files and have designed a segmentation algorithm where abnormal segments are detected. This algorithm aims to improve the accuracy and performance of the existing CNV-CH algorithm. The next-generation sequencing (NGS) approach is very fast and can generate large sequences in a reasonable time. So the huge volume of sequence information gives rise to the need for Big Data and parallel approaches of segmentation. Therefore, we have designed a map-reduce approach for the existing CNV-CH algorithm where a large amount of sequence data can be segmented and structural variations in the human genome can be detected. We have compared the efficiency of the traditional and map-reduce algorithms with respect to precision, sensitivity, and F-Score. The advantages of using our algorithm are that it is fast and has better accuracy. This algorithm can be applied to detect structural variations within a genome, which in turn can be used to detect various genetic disorders such as cancer, etc. The defects may be caused by new mutations or changes to the DNA and generally result in abnormally high or low base coverage and quantification values.

Keywords : cancer detection, convex hull segmentation, map reduce, next generation sequencing
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