Exon Sequencing Mutation Detection Algorithm Based on PCR Matching

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Abstract

Background: With the development of second-generation sequencing technology, more and more DNA sequence variations have been detected. Exon sequencing is the first choice for sequencing many cancer genes, and it can be better used to identify disease status by detecting gene variants. PCR sequence is an effective method to capture that sequence of an exon in the process of sequencing. Exon sequencing sequence contains PCR primer sequence, the correct position of the sequence can be determined by PCR primer sequence, which can be found in SNP, Indel mutation point by comparing the sequence of PCR primer sequence.

Results: In this paper, a matching algorithm based on the PCR primer sequence is proposed, which can effectively sequence the position of PCR primer sequence and find out the key position sequence. Then the sequencing sequence is sorted and the number of the same sequence is counted to reduce the matching times. Then, the sequenced sequence was matched with PCR primer sequence, so that the DNA position could be accurately matched and the variation in the sequenced sequence could be found more quickly.

Conclusions: Compared with the traditional sequence matching method, PCR primer sequence matching method can match many sequences and find more variation. It also showed a high recall rate in the recall rate.

Full Text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the manuscript can be downloaded and accessed as a PDF.

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DNA target sequencing original data structure

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Four kinds of software Indel recall rate