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Abstract

It is intended to support a unique design of a primer. To calculate an indication showing the occurrence frequency of a sequence in a genome sequence, the occurrence frequencies of partial sequences having a definite length in the genome sequences are calculated. Then the occurrence of frequency of each partial sequence of the definite length is stored in an incidence/isolation degree table (16). Concerning each partial sequence of the definite length, a degree of isolation i, which means that j mutation indicating the conversion of j bases (j=<i-1) does not occur in the genome sequence but i mutation indicating the conversion of i bases occurs in the genome sequence, is calculated. Then the degrees of isolation of the partial sequences of the definite length are stored in the incidence/isolation degree table (16). In a visualization processing portion (18), respective bases are clolored in a definite manner based on the occurrence of frequency and/or the degree of isolation of each base to give an image showing the genome sequence.

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