

METHOD FOR PREDICTION OF SINGLE NUCLEOTIDE POLYMORPHISMS

ABSTRACT

There are disclosed methods that utilize learning machine algorithms for predicting of single nucleotide polymorphisms in polynucleotide sequences. The methods comprise steps of: generating training sets of positive and negative SNPs; calculating one or more parameters of each member of the training sets of positive and negative SNPs; training a learning machine algorithm with the one or more parameters of members of the training sets of positive and negative SNPs; and testing the trained learning machine algorithm with test sets of positive and negative SNPs; thereby the best prediction results are recorded by using any of the one or more parameters. The parameters of positive and negative SNPs used for the learning machine algorithms include free energy change (ΔG), entropy (ΔS), enthalpy (ΔH), melting temperature, GC content, SNP distribution score information, sequence information, gene information, intron information and exon information; wherein each parameter is calculated by its own rules.