Prediction of Disease Causing Non-Synonymous SNPs by the Artificial Neural Network Predictor NetDiseaseSNP.

We have developed a sequence conservation-based artificial neural network predictor called NetDiseaseSNP which classifies nsSNPs as disease-causing or neutral. Our method uses the excellent alignment generation algorithm of SIFT to identify related sequences and a combination of 31 features assessing sequence conservation and the predicted surface accessibility to produce a single score which can be used to rank nsSNPs based on their potential to cause disease. NetDiseaseSNP classifies successfully disease-causing and neutral mutations. In addition, we show that NetDiseaseSNP discriminates cancer driver and passenger mutations satisfactorily. Our method outperforms other state-of-the-art methods on several disease/neutral datasets as well as on cancer driver/passenger mutation datasets and can thus be used to pinpoint and prioritize plausible disease candidates among nsSNPs for further investigation. NetDiseaseSNP is publicly available as an online tool as well as a web service: http://www.cbs.dtu.dk/services/NetDiseaseSNP.

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