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Novel prediction method for early detection of diabetes mellitus by questionnaire

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Symptoms of Diabetes Mellitus (DM) may develop rapidly in type-1 DM but much more slowly or even absent in type-2 DM. The diagnosis of DM is based on measurements of fasting plasma glucose level, glucose tolerance test or serum glycosylated hemoglobin. The awareness of DM ranges on 36.9-77.6%, increasing with ages. Risk factors of DM include family history, cardiovascular disease, hyperuricemia, obesity, physical inactivity, smoking and Western diet. Life-style is an important cause of DM occurrence. This study aims to develop a fast screening method to identify high-risk DM people by questionnaire, which is closer to life-style change than study using blood sample. Supervised machine learning approach to modeling for predicting DM needs a training cohort consisting of subjects with DM and subjects without DM. However, due to low DM awareness rate in young people, some respondents who already have DM may answer themselves DM-free and were categorized into subjects without DM. This work proposes a novel prediction method (Pred-DM) based on support vector machine and an optimal feature selection method. Pred-DM considers respondents who answer themselves DM-free as uncertain-disease subjects, which include DM subjects and non-DM subjects. This study cohort consists of 3464 subjects and 119 features chosen from a national-wide questionnaire study of the National Health Interview Survey of Taiwan. Pred-DM identified 26 of 119 features, including family history, smoking, hypertension, hyperlipidemia, eye problem, missing teeth, physical activity, eating habits, mental status and seeking medical service. Considering respondents who answer themselves DM-free as uncertain-disease subjects enhanced the screening test sensitivity of DM from 0.71 to 0.93. The questionnaire-based method Pred-DM is helpful to identify high-risk DM patients for early detection.

Biography

Shinn-Ying Ho is a Professor in the College of Biological Science and Technology and Institute of Bioinformatics and Systems Biology at the National Chiao Tung University, Taiwan. His major research fields are bio-inspired optimization methodologies, bioinformatics, computational biology, bio-image informatics and biomedical engineering, especially in the field of machine learning on high-dimensional medical data. He has developed some prediction systems for protein functions, biopsy and liquid biopsy-based disease/cancer and has produced more than 80 papers in peer-reviewed journals as a first author or corresponding author.

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