Support vector machine in construction of personal treatment rules

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Abstract: One central task of personalized medicine is to establish individualized treatment rules (ITRs) for patients with heterogeneous responses to different treatments. Motivated from a diabetes clinical trial, we consider a problem of great relevance to translational medicine, where many biomarkers are potentially useful to improve an existing ITR. This calls for a screening procedure to assess added values of new biomarkers to derive an improved ITR. We propose net benefit index (NBI) that quantifies gain or loss of treatment benefit due to reclassification in which the optimal labels are obtained by support vector machine (SVM) in the context of outcome weighted learning (OWL). We calculate p-value of the proposed NBI-based test using the bootstrap null distribution generated by stratified permutations on individual treatment arm. The performance of the proposed method is evaluated by simulations and the motivating clinical trial. Our results show that the NBI-based test controls false discovery rate well and achieves high sensitivity. In addition, this screening method demonstrates an improved correct classification rate when ITR is expanded by including selected biomarkers. This is a joint work with Yiwang Zhou and Haodo Fu.