

Estimating the Receiver Operating Characteristic Curve from Clustered Data and Case-Control Studies

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Abstract : Receiver operating characteristic (ROC) curves have been widely used in medical research to illustrate the performance of the biomarker in correctly distinguishing the diseased and non-diseased groups. Correlated biomarker data arises in study designs that include subjects that contain same genetic or environmental factors. The information about correlation might help to identify family members at increased risk of disease development, and may lead to initiating treatment to slow or stop the progression to disease. Approaches appropriate to a case-control design matched by family identification, must be able to accommodate both the correlation inherent in the design in correctly estimating the biomarker's ability to differentiate between cases and controls, as well as to handle estimation from a matched case control design. This talk will review some developed methods for ROC curve estimation in settings with correlated data from case control design and will discuss the limitations of current methods for analyzing correlated familial paired data. An alternative approach using Conditional ROC curves will be demonstrated, to provide appropriate ROC curves for correlated paired data. The proposed approach will use the information about the correlation among biomarker values, producing conditional ROC curves that evaluate the ability of a biomarker to discriminate between diseased and non-diseased subjects in a familial paired design.

Keywords : biomarker, correlation, familial paired design, ROC curve

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