# Incorporating Endophenotypes into Family-based Allelic Association Studies

Wen-Chang Wang, I-Shou Chang, Chin-Hao Chang, Chao A. Hsiung*

*Division of Biostatistics and Bioinformatics, National Health Research Institutes

**Abstract**

For a genetic study in which there are concordant and discordant sibpairs for a complex disease trait and there are also available the measurements of other endophenotypes for each of the individuals, we describe a test for association that utilizes nonparametrically the additional endophenotypes. The usefulness of this method is evaluated in simulation studies, which show that the gain in power is influenced by not only the endophenotypic value but also the correlation between the diagnosis-based phenotype and the endophenotype. Comparison with multivariate FBAT in terms of power will be presented. An additional benefit of our approach is that it provides a method to evaluate the usefulness of endophenotypes. This study is partly motivated by the Stanford Asian Pacific Program in Hypertension and Insulin Resistance (SAPPHIRe) study, which included both concordant sibpairs (both sibs being hypertensives or hypotensives) and discordant sibpairs (one hypertensive and one hypotensive sib) and collected several biochemical assay data on metabolic variables. Data from the SAPPHIRe study are used to illustrate the method.