# Comparing multiple testing correction methods between two softwares for single nucleotide polymorphisms association analyses.
# Using *OPRD1* and diastolic blood pressure in methadone maintenance patients as an example

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## Abstract

Multi-testing correction methods are usually applied in more than one single nucleotide polymorphisms (SNPs) of association analyses to determine the significance of results in the face of testing multiple hypotheses. One of the statistical methods applied in these analyses is called false discovery rate (FDR) procedure. In this study, we compared the FDR theories behind the statistical software of Statistical Analysis Software (SAS) and Golden Helix using a database obtained from a methadone maintenance treatment cohort in Taiwan. The association analyses were performed between the delta opioid receptor (OPRD1) of seven SNPs from rs2236861 to rs760588, or four SNPs from rs2236861 to rs419335, and the diastolic blood pressure (DBP) in both genotypes and allele types. In general linear model (GLM) of association analyses, SNP rs797397 had the most significant association with DBP among seven or four SNPs of both genotype ($p$ = 0.0012) and allele type ($p$ = 0.0004) using SAS and Golden Helix programs. The calculated values of FDR in genotype and allele type of this SNP were 0.0039 and 0.0018 after using Benjamini and Hochberg (BH) procedure in SAS program, and were 0.0083 and 0.0027 after adopting the positive false discovery rate (pFDR) in Golden Helix program in analyses of seven SNPs. In analyses of four SNPs, the FDR values in genotype and allele type of this SNP were 0.0022 and 0.0015 after using BH procedure and were 0.0047 and 0.0015 after adopting the pFDR. In summary, the pFDR had less significant level than BH procedure in the most significant GLM associations SNP in

both genotypes and allele types at seven and four numbers of SNPs. The FDR values were the same in both BH and pFDR multiple corrections in the allele type of four SNPs. The BH procedure in SAS provided a more consistent FDR in both genotype and allele type of multiple correction analyses despite the number of SNPs.