

that there is an association in at least one study. The discovered SNPs with replicated associations were a subset of the discovered associated SNPs, but their meta-analysis  $p$ -values were not ranked smallest among all meta-analysis  $p$ -values (not shown). Importantly, the discoveries from the meta-analysis could not serve as evidence towards replicability, since while the average fraction of SNPs with no association in both studies among the meta-analysis discoveries was 0.06, the average fraction of SNPs with no replicated association among the meta-analysis discoveries was 0.78.

## 6 A simulation study

The goal of the simulations was threefold. First, to investigate the effect of the choice of  $q_1$  and  $w_1$  on the power of Procedures 3.2 and 4.1. Second, to compare these procedures to the alternative of applying BH on the maximum  $p$ -values, i.e. the partial conjunction approach when exactly two studies are analyzed. Third, to investigate the effect of the selection rule on the power of the procedures.

The procedures compared were (1) the BH procedure at level 0.05 on maximum  $p$ -values; (2) Procedure 4.1 with  $w_1 \in \{0, 0.5, 1\}$ ,  $c = q_1/q \in \{0.1, 0.2, \dots, 0.9\}$ , and  $q = 0.05$ ; and (3) the naive (BH- $i$ , BH- $j$ ) procedure,  $i, j \in \{1, 2\}$ ,  $i \neq j$ , which applies the BH procedure at level 0.05 on the  $p$ -values of study  $i$ , and separately on the  $p$ -values of study  $j$  for the hypotheses that were rejected in study  $i$ , and declares hypotheses rejected in both studies as false no replicability null hypotheses; (4) the oracle Procedure 3.2 with parameters  $(q_1, q) = (q', 2q')$ , where  $q'$  was the solution to  $\frac{|I_{00}|}{m}(q')^2 + \left(\frac{|I_{01}|}{m} + 1\right)q' = 0.05$ . This oracle procedure controls the FDR at level 0.05, see Appendix B for a proof.

The  $p$ -values were generated independently as follows. For  $H_j$ ,  $j = 1, \dots, m$ ,  $P_{1j} = 1 - \Phi\left(\frac{X_{1j}}{\sigma_1}\right)$  and  $P_{2j} = 1 - \Phi\left(\frac{X_{2j}}{\sigma_2}\right)$ , where  $X_{1j} \sim N(\mu_{1j}, \sigma_1^2)$  and  $X_{2j} \sim N(\mu_{2j}, \sigma_2^2)$ .