Reviewer's report

Title: Weighted Multiple Testing Procedures for Genomic Studies

Version: 1 Date: 29 February 2012

Reviewer: Todd L Edwards

Reviewer's report:

This paper is articulate and well written, but as a review of multiplicity control for genetic studies this paper is incomplete.

Major revisions:
There are several methods that control the FWER by deriving the effective number of independent tests from correlated SNP data, and then using this quantity in either a Bonferroni or Sidak equation to discover the appropriate point-wise threshold for significance. These methods vary in formulation, and generally fall into the basic categories of PCA-based (Gao et al, genetic epidemiol, 2011; Nyholt et al, am j hum genet, 2004; Li and Ji, heredity, 2005) numerical integration-based (Conneely and Boehnke, Am J hum genet, 2007) and (Han et al, PloS Genet, 2009), and permutation testing. Also see (Dudbridge and Gusnanto, Genet Epidemiol, 2008), and (Hoggart et al., Genet Epidemiol, 2008), for discussions of this topic. The FDR-based methods described in this paper do not handle the correlated tests issue, and this is a major concern for most genetic epidemiologists.

Minor revisions
Figure I is not very useful, and could be dropped

The plural of stratum is strata

“Equation (2) can be further simplified” on page 4, but I think it should say Equation (1)

Level of interest: An article of limited interest

Quality of written English: Acceptable

Statistical review: Yes, and I have assessed the statistics in my report.

Declaration of competing interests:
I declare that I have no competing interests