Reviewer’s report

Title: A Towards-Multidimensional Screening Approach to Predict Candidate Genes of Rheumatoid Arthritis based on SNP, Structural and Functional Annotations

Version: 3 Date: 12 May 2010

Reviewer: Nora L Nock

Reviewer’s report:

Major Essentional Revisions:

1) The specific research question posed by the authors is still not well defined. The Abstract, in particular, still does not adequately describe the authors’ approach and exactly how this approach improves upon current approaches. The authors actually do a very good job of explaining their approach and how their results compare to conventional GWAS results in their rebuttal letter (predominantly under Reviewer #1, Issue #1 and Reviewer #2, Issue #1); however, they need to concisely summarize the important points and include these in the Abstract. For example, the authors state in the rebuttal letter that they “…found that 273(86.4%) risk SNPs out of GWAS are included in our Bayesian screening result set.” – yet, this critical information is not included in the Abstract. The authors should emphasize in the Results of the Abstract the number of SNPs/genes that their multidimensional Bayesian method identified which were missed by conventional GWAS and Gene Ontology only approaches.

2) The Conclusion section of the manuscript should also highlight the important differences between the authors’ new multidimensional Bayesian screening approach to conventional GWAS approaches (Note: No revisions to this section were made in the revised manuscript submitted).

Minor Essential Revisions

1) Supplemental Table 1: This should be modified so that there is a separate column for the rs#, p-value using conventional GWAS approach and ‘p-value’/Bayes Factor for their new multidimensional Bayesian screening approach.

2) Supplemental Figure 1, 2 and 3: These figures should be combined into one figure with 3 panels and should be included in the main manuscript since the information conveyed by these figures is helpful in understanding how the authors’ new method compares to conventional GWAS and Gene Ontology approaches.

3) The Acknowledgement statement for the GAW 16 data seems incorrect. The authors should contact GAW representative, Vanessa Olmo, to get the appropriate language for the Acknowledgement.
4) Figure 4: Perhaps, this should be identified as a Table. Nonetheless, the authors added a column of new information; however, the lines outlining the new column are missing making the new information seem disjuncted from the rest of the information.

**Level of interest:** An article whose findings are important to those with closely related research interests

**Quality of written English:** Needs some language corrections before being published

**Statistical review:** Yes, but I do not feel adequately qualified to assess the statistics.

**Declaration of competing interests:**

I declare that I have no competing interests