Reviewer's report

Title: Spatially Uniform ReliefF (SURF) for Computationally-Efficient Filtering of Gene-Gene Interactions

Version: 2 Date: 20 July 2009

Reviewer: Brett McKinney

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I believe the discussion in the “Relief and SURF” section would be clearer if it was pointed out that SURF is being motivated by a toy example and not really describing the full algorithm. This section focuses on the situation of two “relevant” SNPs with a known penetrance function. However, in practice more than two SNPs are considered by Relief, and it is not known a priori which SNPs are relevant nor is the penetrance function known. I also agree with previous reviews that a lot is assumed about the reader’s understanding of the Relief algorithm.

I am sometimes confused by the use of the term “relevant.” I assume it means relevance of a SNP to the phenotype; however, it sometimes seems to be used in a more generic sense, which I find confusing. For example the authors state, “… Relief adjusts weights only for pairs of individuals having differing genotypes at relevant SNPs.” First, how does Relief know what is a relevant SNP and second, Relief looks at differences between individuals at all SNPs.

The fixed radius used in the application to simulated data is determined by the mean distance between all pairs of individuals in the data set. On average, how many nearest neighbors does this result in? Is it more or less than the standard k=10, and does the average differ between hit and miss groups?

Level of interest: An article of importance in its field

Quality of written English: Acceptable

Statistical review: No, the manuscript does not need to be seen by a statistician.

Declaration of competing interests:

I declare that I have no competing interests.