Reviewer’s report

Title: Virtual CGH: an Integrative Approach to Predict Genetic Abnormalities from Gene Expression Microarray Data Applied in Lymphoma

Version: 1 Date: 8 September 2010

Reviewer: Jindan Yu

Reviewer’s report:

- Major Compulsory Revisions
  1. The source code and the program need to be made available to the research community.

- Minor Essential Revisions
  2. Current analysis showed very high concordance between CGH and vCGH at the cytoband level. The authors mentioned about gene level analysis. As GEP is regulated by many other mechanisms besides genomic gain or loss, it is expected to see much less concordance at the gene level. It will be interesting to see this data.
  3. Genomic gain and loss derived from vCGH are presumably functional subsets. This is, however, not readily perceivable from current results.

- Discretionary Revisions
  4. It seems that the performance of rGEP and sGEP is much inferior to that of vCGH. However, there are not too many samples with paired GEP and CGH data out there that will allow vCGH to work, which was the original impetus for the development of this algorithm. Therefore, sGEP and rGEP will most likely be used in reality. However, they do not seem to perform well enough. As an alternative approach, it may be interesting to examine whether the parameters in vCGH can be trained in one small dataset (which has paired GEP and CGH data) and be used to predict vCGH in another GEP dataset of the same sample type. Cross-data validation will enhance the application of this method.

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

Quality of written English: Acceptable

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.