Dear Editor,

Enclosed please find our substantially revised manuscript “MGRFE: multilayer recursive feature elimination based on embedded genetic algorithm for cancer classification”. In this revised manuscript, we have carefully addressed all the concerns by the eight reviewers. We greatly appreciate the Referee’s comments on our manuscript. The following is our point-by-point response to each comment of the reviewers. Furthermore, I would like to take this opportunity to thank you for handling the review of our manuscript.

*Our responses to the review comments are in blue and italic.*

Sincerely yours,

Ying Li, Ph.D.

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Editor Comments

Associate Editor

Comments to the Author:

This manuscript was reviewed by two experts.

Both of them have concerns on comparison with other methods, ways of computational experiments, and statistical tests.

Furthermore, one reviewer recommends that the type of the paper should be changed to regular one.

And, I agree with this opinion.

(For page length/paper type issue, please do not ask me instead ask to the editorial staff or the editor in chief.)

Based on these points, I recommend the authors to revise the manuscript with taking all reviewers' comments into account.

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Reviewer: 1

Recommendation: Author Should Prepare A Minor Revision

Comments:

A multilayer recursive feature elimination technique based on embedded genetic algorithm for cancer classification has been presented. The authors have proposed a hybrid technique comprising both filter and wrapper methods for gene subset selection. The work is interesting and the manuscript is well organized.

1. In the introduction section author has mentioned the phrase "lack an explicit decline of the feature number". The particular phrase is not clear. Please elaborate and explain clearly the lacuna of swarm intelligence based gene selection approach.

***Response****: Thank you for this comment. We’ve made the suggested changes. The swarm intelligence based gene selection approaches decrease the gene number by .*

* *swarm intelligence based gene selection approach对基因特征的数量没有强制性的控制手段，只是靠迭代，目标函数越高个体越优秀。0-1编码，只是靠个体之间的交叉变异操作来改变特征数量，对每个个体中1的数量即特征数量没有显式的精确控制方式。*
* *在SVM-RFE过程中，每一步都会显式地去除权重低的基因，这样可以对基因特征的数量有准确地控制，而且算法更快。*

2. In algorithm 1, it has been mentioned to sort the optimal gene combination in GC and to preserve the top ranked genes. On what basis the top ranked gene would be sorted? For sorting what procedure is used?

***Response****: Thank you for this comment.*

* *Sorting rule：We sort different GA individuals based on two metrics, F and gene number. The individual with higher F is superior. For two individuals with the same F values, the one with a smaller gene number is superior. MGRFE and GaRFE also use the above-mentioned sorting rule to rank different gene combinations. [这些是文中的话]*
* *Sorting procedure：the default sorting procedure in Python, Timsort. Timsort is a hybrid stable sorting algorithm, derived from merge sort and insertion sort, designed to perform well on many kinds of real-world data.*

3. In the search space reduction stage, it has been mentioned that top 1000 genes have been selected by a threshold of 0.05 in t-test technique and thereafter MIC has been applied on the 1000 genes to re-rank them. Is there any particular reason of selection 0.05 value as threshold? Is there any mathematical reason for selecting particularly this value for threshold in t-test? Or it has been selected experimentally and any other value can also be chosen? Clarify in detail.

***Response****: Thank you for this comment.*

* *Why P=0.05? [http://www.jerrydallal.com/LHSP/p05.htm]*

*[http://www.p-value.info/2013/01/whats-significance-of-005-significance\_6.html]*

*The standard level of significance used to justify a claim of a statistically significant effect is 0.05. For better or worse, the term statistically significant has become synonymous with P≤ 0.05.*

*In the majority of analyses, an alpha of 0.05 is used as the cutoff for significance.*

4. What is the rationale for using particularly t-test first and then MIC? Can any combination of other two filter methods be used in search space reduction task? Clarify in detail. **Use any other combination of two filter methods and compare it to the proposed combination of t-test and MIC-based search space reduction.**

***Response****: Thank you for this comment.*

* *t-test（基于统计）广泛用于gene selection in microarray，MIC（基于信息）也在这个问题上有良好表现。*
* *（其它组合也可以）。前端的filter过程仅筛出差异性表达基因，用来缩小特征搜索空间,（理论上可换别的filter methods）。后端的多层迭代特征选择过程更重要!!！*
* ***更多实验。***

5. The researchers have used t-test and then MIC. The gene selected after MIC is used in the proposed MGRFE algorithm. In table 5, why the t-test-based gene ranking has been compared? **MIC based ranking** should also be compared.

***Response****: Thank you for this comment.*

* *修改****Table 5，添加MIC ranking****，添加说明。*

6. Elaborate the significance of '0' ranked gene in t-test.

***Response****: Thank you for this comment.*

* *程序中一般数组中第一个元素索引为0，所以这里对排在首位的基因标号为0.*
* *->文章中统一改成1？*

7. The comparative results of SRBCT, ALL-AML and ALL have been shown in table 7, 8 and 9. However, the tables are very similar to work in kar et al. [28]. **The similar type of comparison should be given for all the dataset used i.e. 19 dataset in the present work.**

***Response****: Thank you for this comment.*

* *是的，我们在kar et al.的表格上增加了新的条目，kar et al.整理的三个表格很详细，我们可以与之前在这三个数据集上的工作有比较直观的效果比较。*
* ***19个都做好像不太现实****。再整理一两个？*

8. The proposed work has also been compared with Kar et al. [28] in computational performance. Kar et al. have applied a swarm intelligence-based method to the space of all genes. They have not reduced the search space prior to the optimization task. In contrast, the proposed method have applied MGRFE technique on the reduced search space. The reduce search space have been constructed by t-test and then by MIC technique. In my opinion the search space reduction is fixed. It is done once before the application of MGRFE. **In that regard, the comparison of computational time would not significant because it has been computed in the reduced search space. The genes outside the reduced search space could carry valuable information towards classification accuracy.**

***Response****: Thank you for this comment.*

* *首先，Kar et al. 的 KNN+PSO没有使用filter方法来降低其搜索空间是 他们程序运行时间非常高的一个因素。但是，MGRFE中的快速的RFE过程也确实使得程序运行速度大大提高。*

*在数据集SRBCT，ALL\_AML，MLL上，初始基因特征数分别是2308,7129,12582，KNN+PSO分别用时2.7956, 2.7906 and 7.1488 hours。MGRFE对应的在filter过程后剩余的特征数分别是700，500，700，filter+wrapper程序完整用时分别是10.8230, 9.0108 and 8.8739 minutes。处理SRBCT上700个基因MGRFE包含filter过程用了10分钟，而2308个基因KNN+PSO用了2.7956小时，差距还是比较明显的。*

* *在reduced search space (规模500对于二分类，700对于多分类)中已经包含了足够多的差异性表达基因来有效地区分不同疾病种类，因为在多数microarray中最终选出的是10条以内的基因，500已经提供了较大的备选空间。*
* *确实在reduced search space外也有有价值的基因，但此处我们不做考虑。*

9. In the Conclusion section, the authors will need to clearly address the research contributions in theory. The research contributions in theory must be fully stated in at least one paragraph.

***Response****: Thank you for this comment.*

* *在启发式算法GA中引入RFE思路，是首例。而且结果很好。*
* *…*

10. In the Conclusion section, the authors need to fully discuss insightful and practical implications.

***Response****: Thank you for this comment.*

* *看最新的Gene selection in microarray文章最后结尾这里怎么处理的。仿照来写。*

Reviewer: 2

Recommendation: Author Should Prepare A Major Revision For A Second Review

Comments:

First of all, the paper is described as "Survey/Tutorial," but it appears to describe a claimed original contribution by the authors, namely the MGRFE algorithm. The proposed new algorithm is compared against several existing algorithms. Therefore, if at all the paper is to be published, it should be as **a regular research paper, and not as a survey/tutorial paper.**

***Response****: Thank you for this comment.*

* *Yes, you are right. Thanks for your suggestion.*

The paper is a mixture of techniques that are by now standard in the world of computational biology. Given a very large number of features, first use some pre-filtering to eliminate perhaps 90% to 95% of the features, and then use recursive feature elimination (RFE) on the remaining features. I could not find any **compelling evidence that the proposed approach is superior to the existing methods.**

***Response****: Thank you for this comment.*

* *我们把GA和RFE过程结合起来了，效果比两类方法单独时都要好。RFE类的方法找的的基因不够识别准确率高。群智能类的方法晒出的基因子集中往往还有多余的基因，对数量没有控制手段，而且收敛慢。*

*两者结合后可以优势互补，既有群智能算法强大的启发式搜索能力，又有RFE过程强制的显式基因数量下降。使得找到的基因特征子集数量区分能力高，而且数量小。*

The authors claim to compare their method on 17 data sets. But I did not see any evidence that the finally determined feature set is validated on an independent data set of the same form of cancer for example. **All that the authors have done is five-fold cross-validation within the same data set. Without this sort of validation on an independent data set, the claimed performance figures by themselves are not very persuasive.** This is because cross-validation within the same data set does not take into account factors such as batch effect, platform variation, and the like.

***Response****: Thank you for this comment.*

* *修改文中表达，更严密。*
* *对于交叉检验，别的同类文章目前也是这么做的。*
* ***可以的话找独立的另外数据集，用当前筛选出的基因在上面看分类效果。***

The authors' **preferred method of genetic algorithms is known to lack theoretical foundations**, to be very sensitive to various parameters in the algorithm, and to be extremely time consuming. In contrast, the original paper where RFE was proposed, by Isabel Guyon, used the support vector machine (SVM) which is very fast and for which lots of theoretical results are available. This is another reason for my not being overly enthusiastic about the paper.

***Response****: Thank you for this comment. For selecting informative gene features in a microarray, the state-of-the art methods are commonly evolutionary-computation based.*

* *SVM-RFE理论好，但效果没有启发式群智能算法好，当前效果最领先的gene selection in microarray的方法都是第二类的。*
* *时间方面，MGRFE相比于GA收敛速度有很大提升，RFE过程使得算法非常快.*
* *时间在这个问题上重要性居于次位，因为对每个数据集执行一次筛选过程即够了，更重要的是筛选出的基因的区分能力。*

There are several places where the authors do not appear to be **aware of simple statistical facts. For instance, the accuracy is a weighted average of the sensitivity and the specificity.**  But the authors talk as though they are independent parameters. Equation (1) in the right column of page 1 is too wide.

***Response****: Thank you for this comment.*

* *修改文中表达方式，调一下公式格式。*

In Section 2.3.1 the authors use the **T-test and MIC to achieve a first-cut reduction in the feature set. I have found that using the so-called "volcano plot," which combines the T-test with a fold-change criterion, works better than just the T-test alone.**

***Response****: Thank you for this comment.*

* ***多一点实验？***