Author's response to reviews

Title: Anticancer drug sensitivity prediction from baseline gene expression by Support Vector Machine via recursive feature selection

Authors:

Zuoli Z Dong (shnu_dzl@sina.com)
Naiqian N Zhang (naiqianwfu@gmail.com)
Haiyun H Wang (wanghaiyun@tongji.edu.cn)
Y F (fanyun0919@shnu.edu.cn)
Xiaoqi X Zheng (zheng.shnu@gmail.com)
Jun Wang (jwang@shnu.edu.cn)

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Author's response to reviews: see over
Dear Editor,

On behalf of my colleagues, who have read and approved the manuscript, I am submitting the enclosed paper entitled “Anticancer drug sensitivity prediction from baseline gene expression by Support Vector Machine via recursive feature selection” for publication in *BMC Cancer* as a regular paper.

Though having quite similar clinical symptoms, different patients may have different responses to the same drug or therapy. So personalized medicine, which makes medical decisions based on the context of a patient’s genetic content, becomes the main direction of the future medical science. Recently, two large-scale pharmacogenomic studies (CCLE and CGP) screened multiple anticancer drugs on over 1000 cell lines. These two datasets provided us an opportunity to systematically identify genomic markers for a huge number of drugs in parallel.

Based on these two datasets, we proposed a robust predictor to predict AZD6244, Erlotinib, PD-0325901 using an SVM model after recursive feature selection. 10-fold cross validation on CCLE dataset showed that our model achieves the accuracy of over 80% for 10 of 22 drugs. Independent test on CGP suggests that only 3 of 11 common drugs between CCLE and CGP get satisfying result, further implying the inconsistency between these two datasets. Although exhibited promising performance by cross-validation test, we still need to assess their clinical relevance by testing them first *ex vivo* on patients’ tumor cells, then in clinical trials.

This paper is a full-length manuscript that has not simultaneously been submitted elsewhere for print or electronic publication.

We have revised our paper in the following aspects. Firstly, we’ve made our manuscript include line and page numbers. Secondly, ethics statement has appeared in the methods section of the manuscript.

We would be very glad to contribute our recent work to *BMC Cancer* and highly appreciate your editorial suggestions for this manuscript.

Yours respectfully,
Dr Xiaoqi Zheng