Author's response to reviews

Title: Computational Cancer Biology: Education is a natural key to many locks

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Author's response to reviews: see over
First of all, we would like to thank the academic editor and the three reviewers for their valuable comments that helped to improve our paper.

Comments from the academic editor:

I believe the diverse comments of the reviewers are a good thing for a debate paper. Like the authors, I am not convinced that all reviewers were aware of the type of submission (debate rather than research) and I judged their comments accordingly. I would like to avoid sending this paper out for re-review, which would take some additional weeks, and I have decided to take it from here myself.

A: Thank you.

Here is an example: You report that 12 out of 92 MRC fellowships were awarded to computational researchers and interpret this as evidence for the lack of appreciation of computational work. When reviewer 1 challenges you, you answer: We agree with the reviewer that the numbers can be seen differently (the glass is half-full or half-empty, depending on your perspective). I cannot accept this as a good response. Even in a debate paper we need to adhere to basic scientific standards, and in this case what you are lacking (and what the reviewer is complaining about) is a control measurement. How many fellowships were awarded to the fields that you would like computational oncology to be coequal with? How often do these fields appear in the MRC, NCI and NIH documents you quote? Without this context the information 12 of 92 is open to speculation and does not proof your point at all.

A: We revised this part and enriched it with more information to show that the presented arguments are not special, but similar patterns can be observed across a range of different examples.

Other examples: You describe results of a summer school you held in Belfast. Here, too, I would like to see more context: Are you the only ones who do summer schools like this? What are other educational opportunities that exist already? In Cambridge, for example, we have a Wellcome Trust PhD program on Mathematical Genomics and Medicine, which shows that at least the WT has an appreciation for computational work in medicine (mostly oncology). Note: The point is NOT to list all of these programs, but to point out what parts of an ideal computational education are still missing from them.

A: The example given in section ‘A naturally induced shifting’ was not to show that Queen’s organizes the only summer program, but that students selected ‘computational biology’ as most important research at the CCRCB. As such we tried to share our experience with the reader.
Missing components: We added a new section ‘Practical implementations’ to provide a discussion about some specific issues that should be addressed in general.

The same holds for your discussion of CASYM. I noticed the words ‘develop strategies’ are in italics and you seem to imply that developing strategies is not yet enough. But you need to explicitly describe what is still missing.

A: We put ‘develop strategies’ in italics to emphasize that the funder of CASYM do not expect a well defined strategy in place, but its development is at the core.

We revised the section correspondingly.

Minor point:

You write on p2 ‘That means, usually, original data are considered as a necessary contribution of an article.’ Again, be more explicit why this is a problem, eg by adding a sentence like ‘even though profound insights are possible from rigorously reanalyzing existing data.’

A: We revised this correspondingly.

Speaking of profound insights: You write ‘Some examples for success stories can be found in the following studies [11,12,13,14,15,16] that demonstrate impressively the power and benefit of computational approaches’ but as a list ‘11,?,16’ these papers are not impressive at all. Please be explicit about what makes these papers so impressive.

A: We revised this and added a more clearer description.

In particular, I noticed that your set of positive examples consists of half data papers without much new methodology (like Sorlie) and half stats methodology without much new biology (like Storey). I think you need to choose your examples better. Can you point to computational papers in major bio journals that did not contain original data and still led to major insights?

My own ideas (but I am completely happy to accept others) are Eran Segal’s module maps http://www.nature.com/ng/journal/v36/n10/abs/ng1434.html
Dana Pe’ter’s Conexic http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3013278/
Lawrence et al http://www.ncbi.nlm.nih.gov/pmc/articles/PMC3919509/
A: These are excellent examples we included at the end of the introduction.

In summary:

I don’t think you are trailblazers pointing out that computational work is central to all areas of genomics, including cancer genomics. (The WT program and CASYM are evidence that many educational programs in this direction are already under way.)

A: We feel it is important to note that we are not trying to argue that there are so far no initiatives at all that support computational cancer biology, but that this support is not coequal. Yes, there are excellent programs, but there extent is not enough to cope with contemporary problems and big cancer data.

We added a paragraph about this to the section ‘Conclusion’.

I think the way to develop your manuscript is to discuss HOW this education should look like and WHAT is missing from current programs.

A: The new section ‘Practical implementations’ discusses some key features of educational programs.

Please go through the original reviewer comments again and I am happy to consider a revised version of the manuscript that includes improvements based on their and my comments.

A: We revised the whole paper by re-considering the original comments by the reviewers.