Summary of Discussion for:

Agile methods in biomedical software development: a multi-site experience report David W Kane, Moses M Hohman, Ethan G Cerami, Michael W McCormick, Karl F Kuhlmman and Jeff A Byrd.

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This week's discussion focused on how agile software development methods have been implemented in a handful of bioinformatics projects. In their article, Kane et al briefly lay out what agile development is (philosophically) and proceed to discuss their study in which they used a convenience sample of six agile-related projects to develop an idea of how agile processes are being used in bioinformatics research. Their survey consisted of a lengthy questionnaire (36 open-ended questions) along with follow-up interviews when necessary.

The results of the survey indicated that all these agile "teams" were fairly small (1-6 people), exclusively using Java, and mostly only concentrating on one project at a time. Unfortunately, the survey also discovered that there was no dedicated quality assurance (QA) team for any of these projects, and that these projects were rather complex and thus difficult to manage. Still, the agile model did foster a close(r) working relationship between the biologists and developers (though often an *information asymmetry* resulted, requiring a terminology translation step between the two parties). Other noted benefits included collaborative decision-making, independence of semi-collocated parties, and therefore a further team-level investment in the process.

The projects interviewed also used some standard agile practices to complete their tasks, including capturing requirements, automated acceptance testing, open workspaces, a feature backlog which drives future iterations, and project planning/prioritization (highly influenced by the short iteration cycles of agile development—in this case ranging from 1 to 8 weeks). The latter two agile tools also allow the development team to better calculate the "velocity" of work (i.e. features completed divided by time). The agile teams were aware of *pair programming* where two team members work together programming the same feature, but none of the teams used it.

In our discussion of the article there was initial debate about what exactly agile development is and why this is different from other models (e.g. waterfall). Unfortunately we came to the conclusion that while it is relatively clear what agile is when you see it, a definition is more difficult to come up with, because agile blends many disparate aspects of other programming techniques. We would have appreciated being offered more detail about agile in the article, with perhaps examples of other agile projects outside of bioinformatics. There are examples of agile methods given (XP, Scrum) but they don't

get to the heart of the uniqueness of agile and therefore make it difficult to evaluate this paper and its goals.

We had a few problems with the survey itself as well as how far the authors decided to take the project. While the survey is rich, its open-endedness makes it very difficult for people to give quantifiable answers and thus much is left up to the authors' interpretation. This survey looks ideal as a preliminary step, from which a more directed, quantifiable survey might be built. It should be pointed out that we did not disagree with the authors use of open-ended questioning in general; this is a very good means of getting an idea of what's going on in the bigger picture. It was just disappointing to see this project not taken to a greater fruition. In the end the paper is only one small piece of a larger puzzle, offering only a qualitative, somewhat subjective sample of just six projects and what they're doing with agile. It lacks a clear picture of where agile fits into bioinformatics more broadly, nor does this article even offer a clearer picture of what agile development is, as each project approaches the technique slightly differently. As a result, there is no way to evaluate agile against the more established practices in the field. This would prove a very useful tool, as larger companies (who do the bulk of private sector bioinformatics development) are slower to change and would not be able to evaluate much for their purposes based on this article.

Thus, while the article largely accomplishes what it set out to do ("a multi-site experience report"), we found that we were left wanting more: more clarity and definition, more subjects, more data, and ultimately more useful results.