NGS data analysis: the user POV

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Bioinformaticians working in NGS are used to in-depth involvement in difficult problems and developing ingenious solutions to solve each and every specific user need. The users' point of view (POV) however tends to drift from their initially specific plans into fuzzier forays.

When used in the wet lab, NGS data opens a hoard of potential studies to carry out, empowering users to address several complex problems at once. This broad potential compels users to aim towards exhaustive mining of their NGS data in a multidimensional approach in an attempt to extract maximum information from their experimental results (e. g. deep sequencing for theoretical model validation may help characterise novel strains, identify mutations, understand evolutive events and do genome reconstruction as well). However, data analysis is still a difficult task requiring strong bioinformatics support, and while attractive, post hoc multidirectional analysis entails major challenges that may some times be better served by careful planning in close collaboration with a bioinformatician or a bioinformatics community.

Deeper understanding of users' initial expectations and how they evolve after data has been collected, their demands, analysis patterns, and requirements provides useful insight on the major problems faced and to be addressed by bioinformaticians and software developers involved in SEQAHEAD.

In this talk we draw on our experience working in close collaboration with users and applications at CNB to present the users' point of view on NGS data analysis, its inherently polifacetic approach to laboratory problems and raise some concerns with the way NGS is currently being considered by users vs. developers, suggesting possible approaches to deal with this post hoc complexity by exploiting SEQAHEAD collaborative infrastructure.

Relevant Web sites

1. http://www.es.embnet.org/
2. http://www.cnb.csic.es/
3. http://www.cnb.uam.es/content/research/microbial/stress/