

Training the Trainers: ELIXIR workshop “best practices in training on NGS Analysis” 13/01/2015
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Imagine, if you will, a room full of teachers. What do you imagine they will talk about? That's right; students. What to teach them, how to teach it and how to get them to do it!

The ELIXIR workshop “Training the Trainers” was a great opportunity to discuss what topics to cover in various bioinformatics courses, how to best get these topics across to students and swap best practices/war stories. This 2-day event was held in Cambridge, England, and was organised by Gabriella Rustici, a bioinformatics trainer from the Cambridge Systems Biology Centre. As a “meta-goal”, she formulated a vision of a coherent set of topic- and learning-objective ontologies with matching educational materials so that trainers all across Europe could quickly put together a course on any arbitrary topic in bioinformatics. So, the part of the first day was spent in trying to define such an ontology of learning-topics, objectives and outcomes. This turned out to be a pretty daunting task; something of a Russian-doll problem where every concept would *actually* contain sub-concepts and so forth... In addition it was found that however short a course might be, a little bit of educational theory would go a long way in getting the material to “stick” with the student. Unfortunately educational theory is a vast subject of its own and we could make only a small survey of all the techniques one could and should use to structure learning materials.

A bit more lighthearted was the discussion on how to motivate your students to *actually do the work* you set them. I am in a luxury position – I teach undergraduate students who I “motivate” by giving them an “F” grade if they don't turn their work in – but in the context of a 2 or 3 day course for life science professionals this is a serious concern. They shouldn't just replicate what you give them either; you need some indication that the *concepts* of what you're teaching get picked up rather than just the ability to type linux commands. One key factor many trainers could relate to was if the trainee would be analyzing their own data. If they were, often there was no motivational problem whatsoever. A suggestion was to make this a required part of attending a course – BYOD (Bring Your Own Data). Another trick of the trade was to “bribe” the students with sweets or drinks (talk about short-term learning!) to reach an answer or analysis first. Perhaps the nicest idea I heard in terms of motivating students to keep working was to have some attribute of the analysis – a coverage count, say, or a fold-change – be the key value in a URL to unlock the next part of the course. I will be sure to try this out in my own courses!

After this discussion on phylogeny of ideas and motivation, we turned towards the “meat” in the meeting; constructing a new example course based on these ideas and preexisting course materials. The hope is that through members of the ELIXIR network a large portfolio of existing course materials can be organised according to the ontology. The case study I was involved in was in restructuring an existing Variant Calling workshop authored by Chiara Batini of the University of Leicester Core Sequencing Facility. By publishing it in a Git repository, structured in a particular way and with markdown-based annotation, it should be easy for a fellow bioinformatics trainer to first of all find this course and then adapt it into the structure of his or her own course. (Unfortunately, the Git repository of courses is currently a private one hosted at Umeå University; but this should eventually change and be communicated through the ELIXIR framework. Stay tuned!²) While a fair bit of work, this procedure should appeal to trainer's enlightened self-interest; by structuring your materials in this way, it also becomes easier to integrate *other's* material with your own.

The final part of the meeting was spent discussing how to *grade* students' performance in a way useful to them – again assuming professional participants rather than undergraduates. Conversely, methods of evaluating your course and its use to the participants were also discussed. Especially desirable is a way to track your course's impact on your trainee's further career, and various text mining (Google Scholar!) methods were proposed to do so automatically – bioinformaticians will be bioinformaticians!

All in all, a very enjoyable meeting of minds and another step on the road to an open framework of bioinformatics courses taught at all levels and across Europe!

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² NB: An effort related to the one described here, and one in which many participants of the workshop are also active, is the GOBLET repository; <http://www.mygoblet.org/training-portal>.