

Final impressions of Vienna: time to go with the (work)flow...

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So that's [ISMB](#) over for another year. The worlds computational biologists are now sleeping off their Austrian wine and Sacher Torte hangovers on flights back home, hopefully inspired and brimming with fresh ideas for the next year. On the whole it seemed a productive and positive meeting, and whilst personal perspectives always differ depending on the tracks attended, there did seem to be several recurring themes.

After [attending](#) the Bio-Ontologies SIG, many of the same topics and issues did seem to follow into the main meeting, particularly in the Bio-resource descriptor ([BioCoreDB](#) and [Biosharing](#)) workshop, and culminating in [Michael Ashburners](#) closing (and typically acerbic) keynote highlighting the genesis of [Gene Ontologies](#).

As we enter the era of [next-next generation sequencing](#), with desktop sequencers likely to become as ubiquitous as PCR machines, Bioinformaticians feel secure in their jobs knowing that the user base for their services is likely to explode. Massive challenges lie ahead, and the large number of talks on new tools, workflows, and ways of making the cloud more accessible for the data-driven researcher shows that there is a growing community anticipating these developments. The [Galaxy Team](#) were out in force at ISMB, with best-practice talks and demos of its current functionality by Jeremy Goecks and Dan Blackenberg, as well as case-studies by external users such as [Marc Bras](#) and Peter Cock, even demonstrating it's utility with non-NGS data.

Despite the proliferation of similar systems, with new ones launched at the meeting such as [YABI](#), there fortunately seems to be moves to make these more interoperable. Kostas Karasavvas presented work on combining [Galaxy](#) and [Taverna](#) – allowing the use each of others tools and workflows. Bringing together two already well established communities massively widens the user base and functionality of them both, and the [MyExperiment](#) portal widens this even further by combining and listing nearly 2000 workflows spanning all of science.

The ability to use these systems in the cloud takes this usability and reproducibility even further, allowing completely configured clusters to be deployed in a matter of minutes and opening up high-performance computing capabilities to users without the infrastructure or programming experience. This was demonstrated very well by Paul Foster with an [example](#) of Taverna in the cloud, and by Enis Afgan presenting [Galaxy Cloudman](#), which by enabling instant access to the >100 tools from [CloudBiolinux](#) plus the entire suite of tools and reference datasets of Galaxy has

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great potential to provide killer functionality. Much is still in the pipeline, but with momentum building and the user base growing, it will be interesting to see how things have developed by the next [ISMB](#) in Long Beach. GigaScience hopes to see many of you then!

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