chem-bla-ics

Taverna Workshop, Hinxton, UK

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I arrived at the EBI last night for the Taverna workshop, during which the design of Taverna2 is presented and workflow examples are discussed. Several ‘colleagues’ from Wageningen and the SARA computing center in Amsterdam are present, along with many other interesting people. This afternoon is my presentation.

Paul Fisher just presented his PhD work on using workflows to improve the throughput of QTL matching against pathway information and phenotype. One interesting note was its function to make biological informational studies more reproducible. He had getting the versions of online databases explicitly in the workflow, so that it gets stored in workflow output.