## The Taverna Workbench: Integrating and analysing biological and clinical data with computerised workflows



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Katy Wolstencroft is a Research Fellow in the School of Computer Science, University of Manchester and a visiting researcher in the Molecular Cell Physiology group at the Vrije Universiteit, Amsterdam. She has a PhD and MSc in Bioinformatics from the University of Manchester, and a BSc in Biochemistry from the University of Leeds.

Katy's work is primarily in the area of data and related techn and knowledge integration, where she leads the bioinformatics research activities in the myGrid to consortium. myGrid is a UK e-Science initiative that has produced, amongst other things, the Taverna workflows workbench (http://www. taverna.org.uk/), the myExperiment workflow repository (http://www.myexperiment.org) and the BioCatalogue service catalogue (http://www. biocatalogue.org). Currently, her main focus is on the BBSRC funded SysMO SEEK project, to develop a data exchange and modelling envioant and related techn summer schools the world. In this to troduction to design high-throughput be ing Taverna and related techn summer schools the world. In this to troduction to design high-throughput be ing Taverna and related techn summer schools the world. In this to troduction to design high-throughput be ing Taverna and related techn summer schools the world. In this to troduction to design high-throughput be ing Taverna and related techn summer schools the world. In this to troduction to design high-throughput be ing Taverna and related techn summer schools the world. In this to troduction to design high-throughput be ing Taverna and related techn summer schools the world. In this to troduction to design high-throughput be ing Taverna and related techn summer schools.

(http://www.sysmo-db.org/). It was designed for the SysMO consortium, (Systems Biology of Micro-Organisms), but it has now been adopted by many other consortia, providing a common platform for hundreds of research labs in Europe.

Katy also coordinates the training and outreach activities in myGrid. As such, she has been involved in teaching scientific workflows and related technologies in over 50 workshops, summer schools and conferences throughout the world. In this tutorial, she will provide an introduction to designing and reusing workflows for high-throughput bioinformatics data analysis, using Taverna and myExperiment. Scientific workflows enable the chaining together of distributed analysis resources and databases to construct complex analysis pipelines that are ideal for high throughput omics data analysis. These workflows are reusable experimental methods that can be shared and rerun for other data, or for experimental validation.