

CDK-Taverna paper published

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It took a while, but the [CDK-Taverna paper](#) (doi:10.1186/1471-2105-11-159) which has been in preparation for a while [in the CDK subversion repository](#), is now published. Christoph already wrote up [a brief explanation in his blog](#):

The workflow paradigm allows scientists to flexibly create generic workflows using different kinds of data sources, filters and algorithms, which can later be adapted to changing needs. In order to achieve this, library methods are encapsulated in Lego(TM)-like building blocks which can be manipulated with a mouse or any pointing device in a graphical environment, relieving the scientist from the need to learn a programming language. Building blocks, so-called workers, are connected by data pipelines to enable data flow between them, which is why pipelining is often used interchangeably for workflow.

[Taverna](#) is not the only open source workflow environment, but certainly gotten a lot of visibility in the eScience communities in at least The Netherlands and the UK. There exists other workflow environments too with CDK nodes, including [KNIME](#) which is [since version 2.1.0](#) licensed GPL3.

[Thomas](#) uploaded some [17 example workflows](#) to [MyExperiment.org](#), to give you further idea what the system can do. Development has gone down considerably, since Thomas finished his thesis, and if you like to work on the CDK-Taverna project, and be [the next Dr Who](#), please contact me, [Achim](#) or Christoph. I started experimenting with CDK nodes for Taverna in 2005 (see [CDK-Taverna fully recognized](#)), and would love to see it live on. Andreas and I made an attempt last December to port things to Taverna 2.1, and the code we worked on can be found in [this GitHub repository](#).