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MetWare: metabolomics database project started on SourceForge

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Keywords

Metabolomics, Metware

The Applied Bioinformatics at PRI group where I now work in Wageningen and the group of Steffen Neumann in Halle have started the MetWare project on Sourceforge to develop opensource databases for metabolomics data.

The databases design will be based on and ideally compatible with proposed standards like ArMet (DOI:10.1038/nbt1041) and those recently written up by the Metabolomics Standards Initiative (see the issue around DOI:10.1007/s11306-007-0070-6).

One important design goal is that the project will use BioMart, which will allow easy integration of the database content in data analysis programs like Taverna and R using the biomaRt package (see DOI:10.1093/bioinformatics/bti525).

Though the software will be opensource, it is yet unsure how much data will be open.