

MetWare: metabolomics database project started on SourceForge

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Metabolomics, Metware

Abstract

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.

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chem-bla-ics

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.