

A-MADMAN: Annotation-based MicroArray Data Meta-Analysis tool

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Motivation

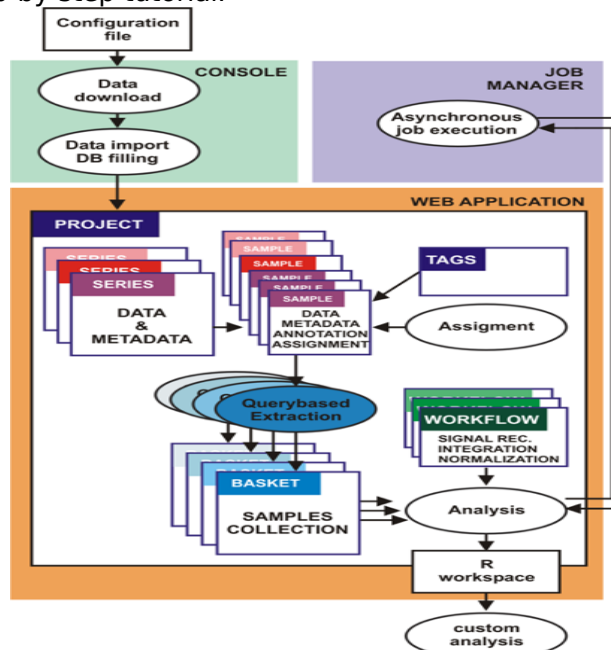
Publicly available datasets of microarray gene expression signals represent an unprecedented opportunity for extracting genomic relevant information and validating biological hypotheses. However, the exploitation of this exceptionally rich mine of information is still hampered by the lack of appropriate computational tools, which are able to overcome the critical issues raised by meta-analysis.

Results

We developed A-MADMAN, an open source web application which allows the retrieval, annotation, organization and meta-analysis of gene expression datasets obtained from Gene Expression Omnibus. A-MADMAN addresses and resolves several open issues in the meta-analysis of gene expression data. In particular, A-MADMAN allows

- i) the batch retrieval from Gene Expression Omnibus and the local organization of raw data files and of any related meta-information,
- ii) the re-annotation of samples to fix incomplete, or otherwise inadequate, metadata or to create user-defined batches of data,
- iii) the integrative analysis of data obtained from different Affymetrix platforms through custom chip definition files and meta-normalization.

The software, written in python, is based on the popular Django web framework and uses R as a backend. A-MADMAN supports a collaborative working style for local or geographically dispersed teams through LAN or Internet deployment options, but can be used also by a single researcher on his Windows Personal Computer installing an all-in-one package that bundles all required dependencies except R. The software comes with supporting material: program description, installation instructions and step-by-step tutorial.



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