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The ChipYard Framework For Microarray Data Analysis

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One of the major tasks in DNA-chip based experiments is to handle the large amount of data generated. The ChipYard Framework addresses this by providing a solution for tracking, analysis and visualization of microarray data (i.e. expression profiling data, matrix CGH data).

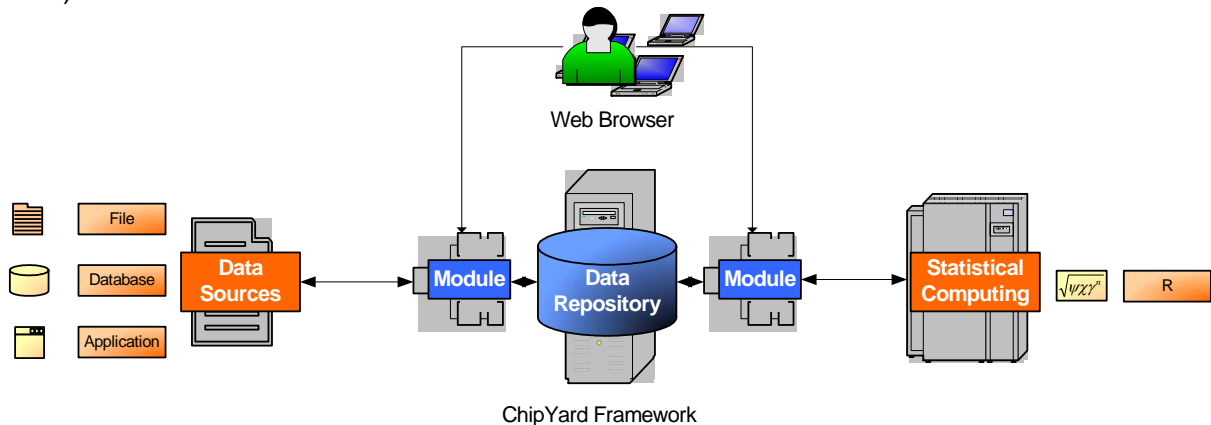


Figure 1. Overview of the ChipYard Framework.

The core component of that framework is a database scheme to store data from many experiments in a well ordered and MIAME (*minimum information about a microarray experiment*, Brazma *et al.*) compliant form.

Access to the framework is handled by a web browser based PHP-interface. After login the user can use different modules to upload data, analyse it and export the results, while all actions are recorded in the background to achieve consistent documentation of analysis. With the generic interface provided for upload modules it is possible to use different datasources, such as files, databases and other applications. In our laboratory ChipYard uses an existing *laboratory information and management system* (LIMS) as datasource, providing technical details about the microarrays used (QuickLIMS, Kokocinski *et al.*).

The same modular approach is employed to obtain high flexibility on the statistical side of the framework. On this basis a variety of analysis techniques as well as several kinds of statistical languages can be included. This was considered critical, since different algorithms have different strengths depending on the type of dataset and experimental design. The modular approach also ensures that novel algorithms and existing codebases from the microarray community can be easily integrated.

The modular interface to the open source language R (R. Ihaka & R. Gentleman) is already implemented in the ChipYard Framework. Different analysis modules for microarray experiments have been made available.

References:

Brazma et al. (2001) *Minimum information about a microarray experiment (MIAME)-toward standards for microarray data*, Nat Genet. Dec;29(4):373.

Kokocinski et al. (2003) *QuickLIMS: facilitating the data management for DNA-microarray fabrication*. Bioinformatics. Jan;19(2):283-4.

Ihaka and Gentleman (1996) *R: A Language for Data Analysis and Graphics*. Journal of Computational and Graphical Statistics, 5(3): 299