

MADMAX

Management and Analysis Database for Multi-platform microArray eXperiments

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Version : 1.2
Date : 23 September 2008
Author : Philip de Groot (Philip.deGroot@wur.nl)

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Introduction

MADMAX: Management and Analysis Database for Multi-platform MicroArray eXperiments. URL: <https://madmax.bioinformatics.nl>.

MADMAX is a universal and easy-accessible bioinformatics facility to store and analyze microarray data independent from the vendor. After researchers have executed a microarray experiment, MADMAX assists in storage and analysis of their valuable data.

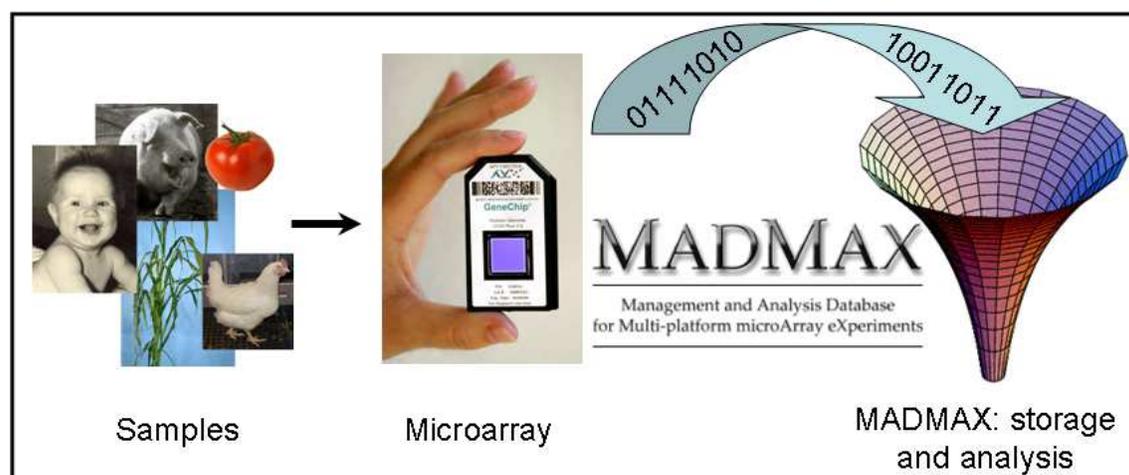


Figure 1: Schematic overview demonstrating where MADMAX gets involved during a microarray analysis.

MADMAX in a nutshell	
Easy accessible via browser	✓
Secured internet access	✓
Ease of use (tailored towards biologists)	✓
Tools that biologists asked for	✓
Multi-platform raw microarray data storage	✓
MIAMI compliant Laboratory Information and Management System (LIMS) [1]	✓
Controlled vocabulary in the LIMS (“scientists speak the same language”)	✓
Sophisticated tools analyze the raw data independently from the database	✓
Quality control pipeline (did the experiment work as expected?)	✓
Statistical analysis pipeline (extract biologically relevant information)	✓
Fast (automated) biologically relevant analysis is fully supported	✓
Tools are based on R/Bioconductor [2-3]	✓
Easy addition of new analysis strategies	✓
New microarray platforms can be (relatively) easily supported	✓
Flexible: fast anticipation on (changing) market demands	✓
Will support metabolomics in the (nearby) future	✓
Will support proteomics in the (nearby) future	✓
Will support high throughput sequencing in the future	✓

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Why MADMAX?

Usually, a biologist has a question which should be (partly) answered via microarray analysis. Unfortunately, performing a microarray experiment is a tedious, expensive, difficult, error-sensitive, and time-consuming task. Additionally, multiple microarray suppliers provide their own solutions for performing, storing, and analyzing a microarray experiment. In the scientific community, new and improved analysis methods are continuously being created and published at such a fast rate that the commercial microarray vendors cannot incorporate all these developments in their analysis packages in time. Most published methods can be used by anyone whom knows how to work in R and Bioconductor, but these methods are still tailored towards a single microarray manufacturer [2-3]. This fact makes it extremely hard to switch to another microarray vendor. This is where MADMAX helps the biologists: we can store and analyze microarrays from different vendors utilizing the most state-of-the-art and scientifically well-accepted tools. For the biologist, this saves an enormous amount of time and effort: biologically relevant results can already be obtained within a few hours instead of (at least) several months!

“Biologists like to focus on advanced levels of analysis and don’t want to be bothered with the preliminary analysis of the data”

Our MADMAX offer

Reduce the microarray analysis time considerably:

“Utilizing the statistical tools in MADMAX on my microarray experiment reduced the analysis time from 3 months to a couple of hours”

We provide access to the infrastructure (hardware and software) to store and analyse microarray data.

MADMAX in more detail

- Industry standard Oracle database
- Vendor independent
- Standardization of analysis
- Outstanding Affymetrix quality control pipeline
- Outstanding Affymetrix statistical analysis pipeline
- Supports custom CDFs (up-to-date gene annotations for the microarrays)
- MIAMI compliant LIMS
- Controlled vocabulary
- Extensive plants support, e.g. Arabidopsis, tomato, Medicago
- Supports follow-up analysis in other software packages, e.g. ermineJ, GSEA, and Spotfire
- MAGE-TAB import and export (easy and standardized exchange of microarray data)
- MADMAX reduces microarray analysis time considerably
- MADMAX is in production for over 2 years now
- If you wish: verify the MADMAX results in Bioconductor yourself

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References

- [1] Alvis Brazma et al., Minimum information about a microarray experiment (MIAME)—toward standards for microarray data, *Nature Genetics* 29, 365 - 371 (2001). Url: <http://www.mged.org/Workgroups/MIAME/miame.html>.
- [2] R: A Language and Environment for Statistical Computing, R Foundation for Statistical Computing, Vienna, Austria, 2007, url: <http://www.R-project.org>.
- [3] Bioconductor: Open software development for computational biology and bioinformatics, Robert C Gentleman, Vincent J. Carey, Douglas M. Bates, Ben Bolstad, Marcel Dettling, Sandrine Dudoit, Byron Ellis, Laurent Gautier, Yongchao Ge, Jeff Gentry, Kurt Hornik, Torsten Hothorn, Wolfgang Huber, Stefano Iacus, Rafael Irizarry, Friedrich Leisch, Cheng Li, Martin Maechler, Anthony J. Rossini, Gunther Sawitzki, Colin Smith, Gordon Smyth, Luke Tierney, Jean Y. H. Yang, and Jianhua Zhang, *Genome Biology*, 5, 2004, p. R80, url1: <http://genomebiology.com/2004/5/10/R80>, url2: <http://www.bioconductor.org>.

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