



A. Moghaddas Gholami (1), C. Schmitt (2), M. Visvanathan (1), N.C. Hauser (2), S. Rupp (2), J. Hoheisel (1), K. Fellenberg (1)

Deutsches Krebsforschungszentrum (DKFZ), Dept. Functional Genome Analysis, Heidelberg, Germany (1)  
Fraunhofer Institut für Grenzflächen- und Bioverfahrenstechnik (IGB), Dept. Molecular Biotechnology, Stuttgart, Germany (2)

## Motivation

The Multi-Conditional Hybridization Intensity Processing System (M-CHiPS), provides a common platform for integrated analysis of microarray data along with supplementary information - like GO terms and clinical data. For the biologist, it integrates all major platforms such as Affymetrix-, two-color microarrays, or 2D gels, providing a guided tour through the data's variance by mouse click. On the developer's side, it integrates Perl, Matlab, and R, providing the convenient programming environments for various tasks.

## Background

- M-CHiPS ([www.mchips.org](http://www.mchips.org)) is in use since 1999
- Fields of research: Cancer, Yeast (*S.cerevisiae*, *Candida albicans*, *N.crassa*), *Arabidopsis*, *Antirrhinum*, *Drosophila*, *Trypanosoma*, *Aspergillus*, *P.putida*, *H.echinata*, Mouse etc.
- Application: statistical analysis of a microarray database's entire content including the experiment annotations [1, 2]
- Advantages:
  - Flexibility allows the use of one and the same system for different fields of microarray research where different experimental factors are relevant.
  - Allows to add experiment annotations and/or allowed values within seconds on the fly i.e. without altering the database structure

## Results

### New functionalities concerning biologists:

- Menu/GUI re-organization for intuitive use
- Figures and text results
- Export function to GenMAPP
- Integration of AIDA-Analysis Output
- normalization methods:

- The non-linear LOWESS (locally weighted scatterplot smoothing) and LOESS as well as VSN (Variance Stabilization Normalization)
- P-values can be computed by SAM (Significance Analysis of Microarray data) using Empirical Bayes methods (eBayes from the limma package)

### New functionalities concerning bioinformaticians and statisticians:

- Matlab-R Interface
- Detailed meta data recording everything that has been done to the data during M-CHiPS workflow

## Conclusion

Being applied by an increasing number of users since 1999, M-CHiPS has been grown a communication platform, bridging between biologists and statisticians / bioinformaticians. While providing well-established and seamless data analysis by mouse click to the former it allows to apply and/or write any R package or Matlab function on top of the existing functionality to the latter.

## References

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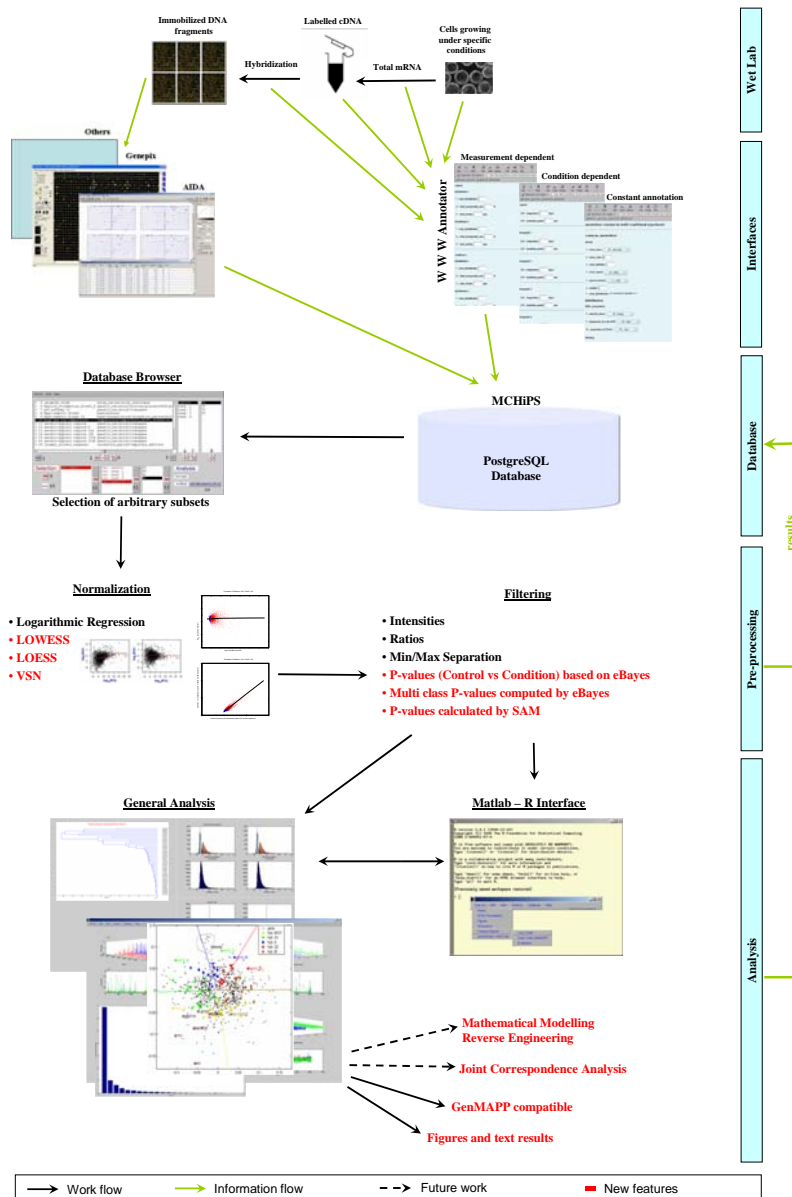
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## Contact:

Amin Moghaddas Gholami  
Deutsches Krebsforschungszentrum (DKFZ)  
Dept. Functional Genome Analysis  
Im Neuenheimer Feld 580, 69120 Heidelberg, Germany  
Phone: +49 (0)6221 422718 Email: a.moghaddas@dkfz.de



Dipl. Inf. (Bioinf.) Corinna Schmitt  
Fraunhofer Institut für Grenzflächen- und Bioverfahrenstechnik (IGB)  
Dept. Molecular Biotechnology  
Nobelstraße 12, 70569 Stuttgart, Germany  
Phone: +49 (0)711 970 4044 Email: corinna.schmitt@igb.fraunhofer.de



## Contact: