M-CHiPS:
Universal platform for Microarray Data Interpretation

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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) 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:
  1. Flexibility allows the use of one and the same system for different fields of microarray research where different experimental factors are relevant.
  2. 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 statistcans:
- 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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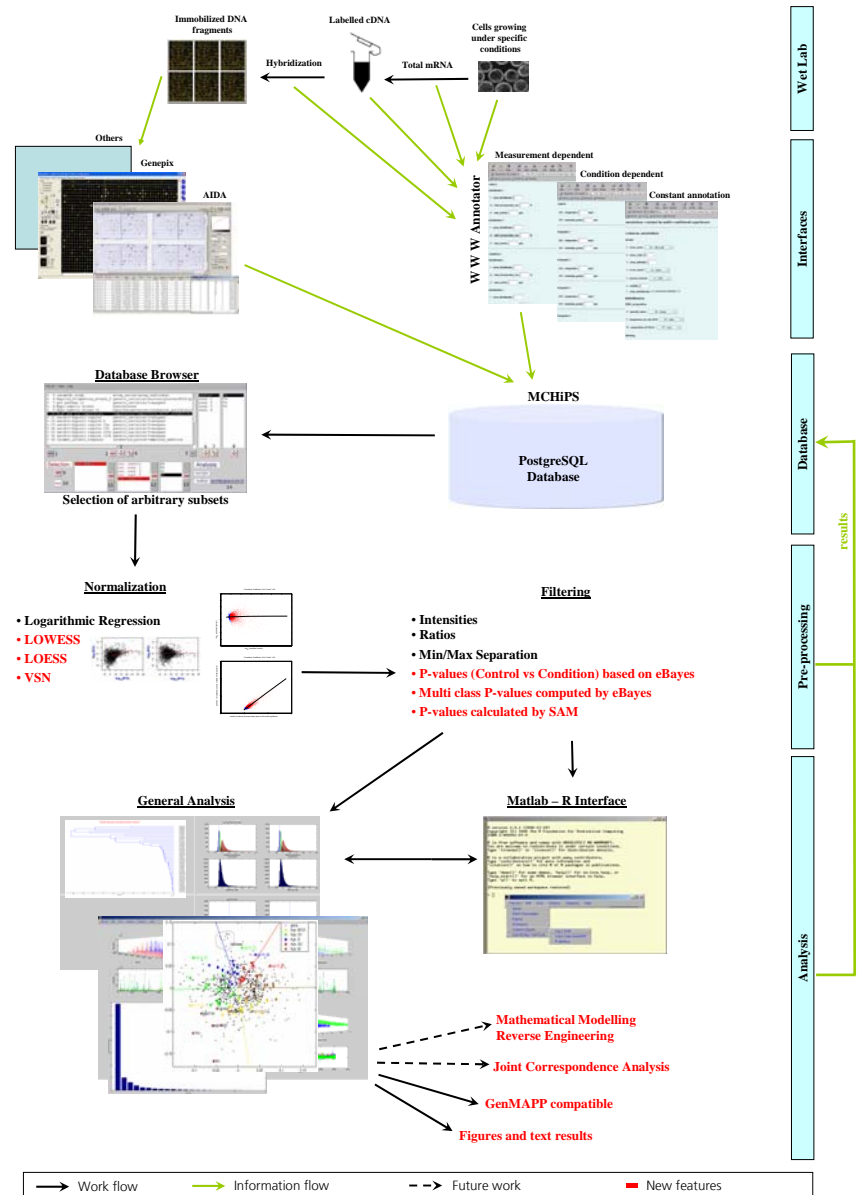
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