



Data integration for analyzing gene expression data

Hong-Hai Do¹, Toralf Kirsten¹, Erhard Rahm^{1,2}
¹Interdisciplinary Centre for Bioinformatics ²Department of Computer Science
http://www.izbi.de http://dbs.uni-leipzig.de

1. Motivation

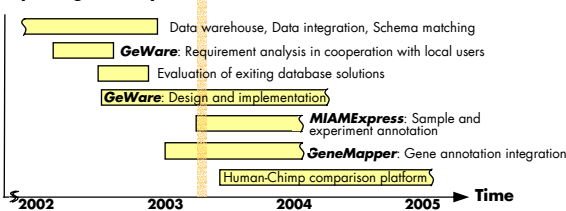
- Microarrays: High-throughput method to monitor the expression of thousands of genes in a single experiment
 - Promising, however high requirements to a supporting data management and analysis solution
- Various user groups at University of Leipzig with different research focus, requiring gene expression analysis
 - Comparative genomics for different primates
 - Change detection in signal transduction in thyroid pathologies
 - Gene expression profiling of brain tumors
- Current capacity: about 300-500 experiments per year using Affymetrix microarrays

2. Gene Expression Warehousing: Goals and Objectives

- Data warehouse: Central data management and analysis platform supporting special local requirements
- Integration of annotation data with expression data
 - Experiment annotations: documenting the specific biological focus of an experiment and the technical process of conducting it
 - Gene annotations: describing all known aspects about the gene sequences on the microarray chips; to be exploited from public sources
- Integration of existing software and tools with the database for flexible data analysis

3. Project Context: A Chronology

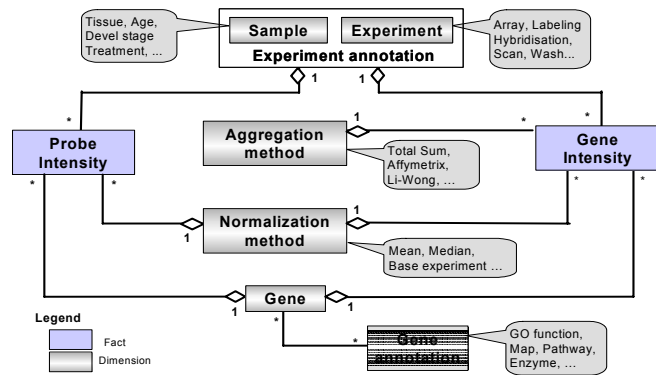
Work packages / Projects



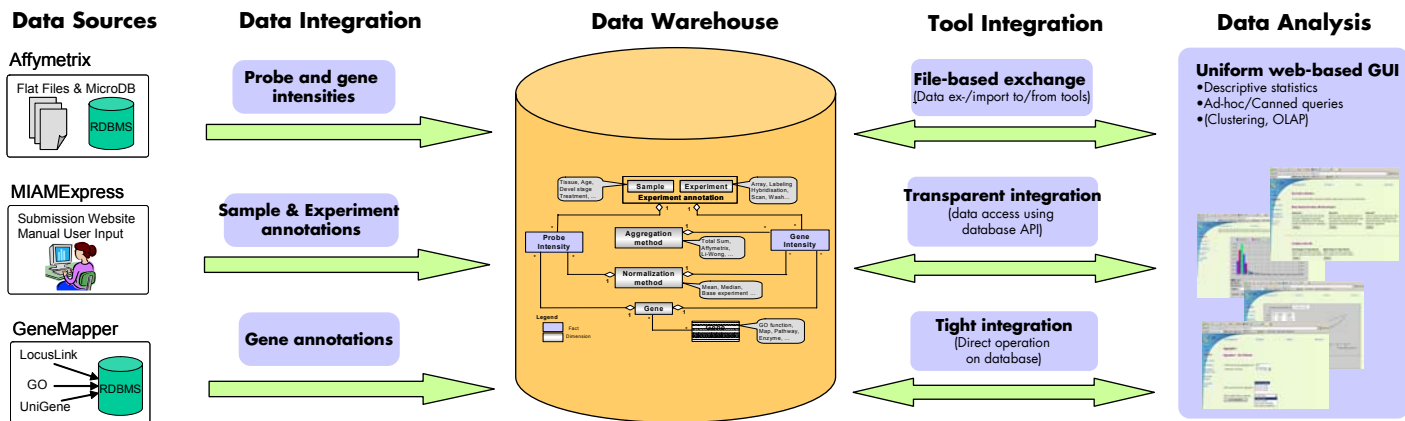
4. Evaluation of Existing Solutions [2]

- Comparison of 8 published microarray databases:
 - ArrayDB (NHGRI), ExpressDB (Harvard Univ.), GeneX (NCGR), GIMS (Univ. Manchester), M-CHIPS (DKZF), RAD2 (Univ. Pennsylvania), SMD (Stanford Univ.), YMD (Yale Univ.)
- Major evaluation criteria
 - Data storage and management: Image and expression data, annotation data
 - Data integration: Integration of annotation data, especially gene annotations, with expression data
 - Tool integration: Integration of tools/algorithms for interactive and iterative data analysis
- State of the art
 - Sample and experiment annotations: Mostly free-text fields, no controlled vocabularies used
 - Gene annotations: Mostly not locally integrated but linked through web links, not sufficient for analysis
 - Data analysis and tool integration: Large variety of data mining approaches available, however advanced analysis outside of database by means of stand-alone tools

5. GeWare Data Model



6. GeWare Overall Architecture



7. Contributing/Built-upon Projects

Integrating gene annotations with GeneMapper

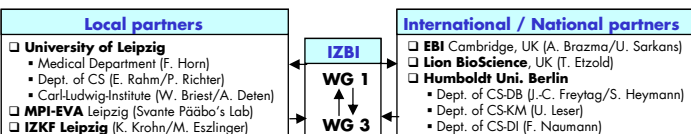
- Various public sources with different annotations, however related to different gene representations, i.e. identifiers
 - Public sources: LocusLink (NCBI), Human Genome Browser (UCSC) and Ensembl (EBI-Sanger), UniGene, Tigr, GeneCards, Genelynx, ...
 - Vendor-based sources, e.g. NetAffx (Affymetrix): annotations of proprietary genes, i.e. probesets
- Project goals: Finding gene-oriented views on annotations by means of matching between different gene representations



Human-Chimpanzee Comparison Platform (in cooperation with MPI-EVA)

- Recent availability of draft versions of the human and chimpanzee genomes: first example of two closely related mammalian genomes
- Project goals: Design and implementation of an integrated platform for comparative analysis between humans and chimpanzees [3]
 - Genome-wide comparisons at both sequence and expression levels
 - Determining genes with expression drastically changed during human evolution: Identification of traits specific to humans
- Collecting data at the MPI-EVA in cooperation with Charite Berlin
 - Application of various techniques: Microarray, mass spectrometry, gel electrophoresis
 - High volume of data expected: currently ca. 3TB data available stored in flat files associated with ca. 800 microarray-based experiments

8. Cooperation Partners



9. References

- Brazma, A. et al.: *Minimum Information about a Microarray Experiment (MIAME) – Toward Standards for Microarray Data*. *Nature Genetics* **29**, 2001
- Do, H.-H., Kirsten, T., Rahm, E.: *Comparative Evaluation of Microarray-based Gene Expression Databases*. Proc. **10. Conf. Database Systems for Business, Technology and Web (BTW)**, Leipzig, Feb. 2003
- Enard, W. et al.: *Intra- and Interspecific Variation in Primate Gene Expression Patterns*. *Science* **296**, 2002
- Kirsten, T., Do, H.-H., Rahm, E.: *GeWare: A Data Warehouse for Integrated Gene Expression Analysis*, Work in progress, 2003