

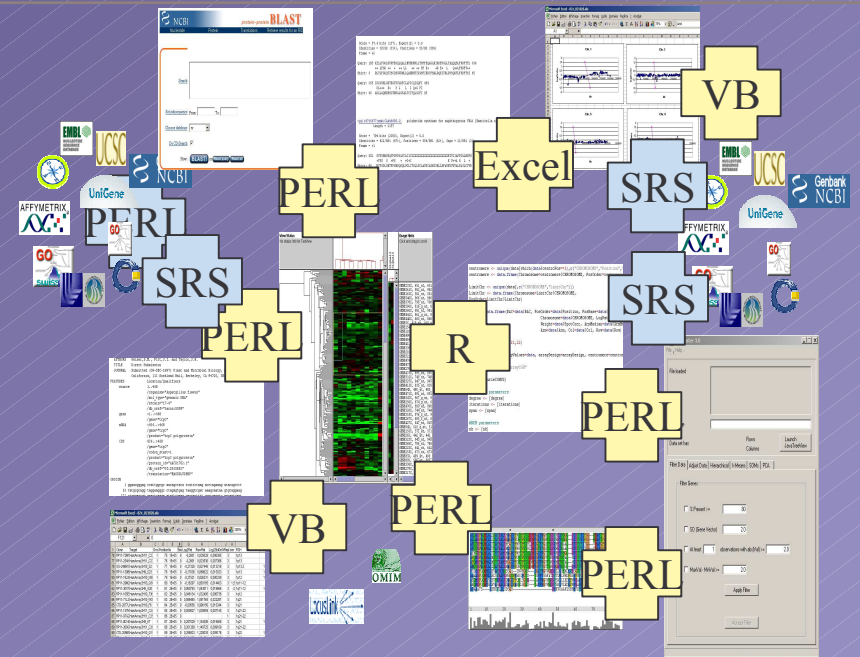
Easy and user-friendly workflow management based on the data- morphing concept

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Integration in Biology

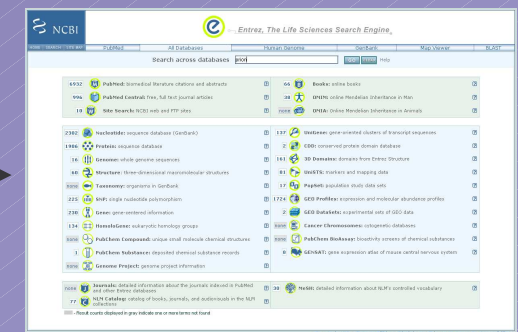
Data-morphing: an innovative approach for:

- **Data integration**
 - Very large volume
 - Heterogeneous data (Nature, format, access)
 - Concepts in constant evolution
- **Tools integration**
 - Heterogeneous formats
 - Different languages and environments
- **Experimental methodology**
 - From lab bench to web
- **Evolutivity - Reactivity**
 - New data
 - New analyses



1 gene →

25000 gene ?



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Easy pipeline definition

A "biologist" speaking tool

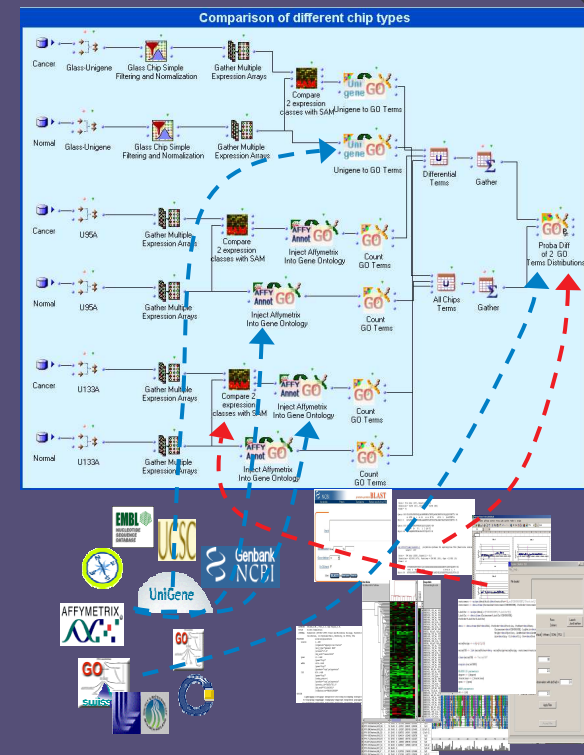
- Definition of pipelines in an homogeneous environment
 - Focus on biological issues
 - **Real-time** →
 - Gain in:
 - Quality
 - Productivity
 - Methodology
 - Execution time
 - **Dramatically shorten experimentation cycles**

Features:

- Instantaneous connexion to any biological data sources
- Intelligent linking of any data source to any other
- Important panels of biological data analysis tools
- Library mechanism for easy non-programmatic extension

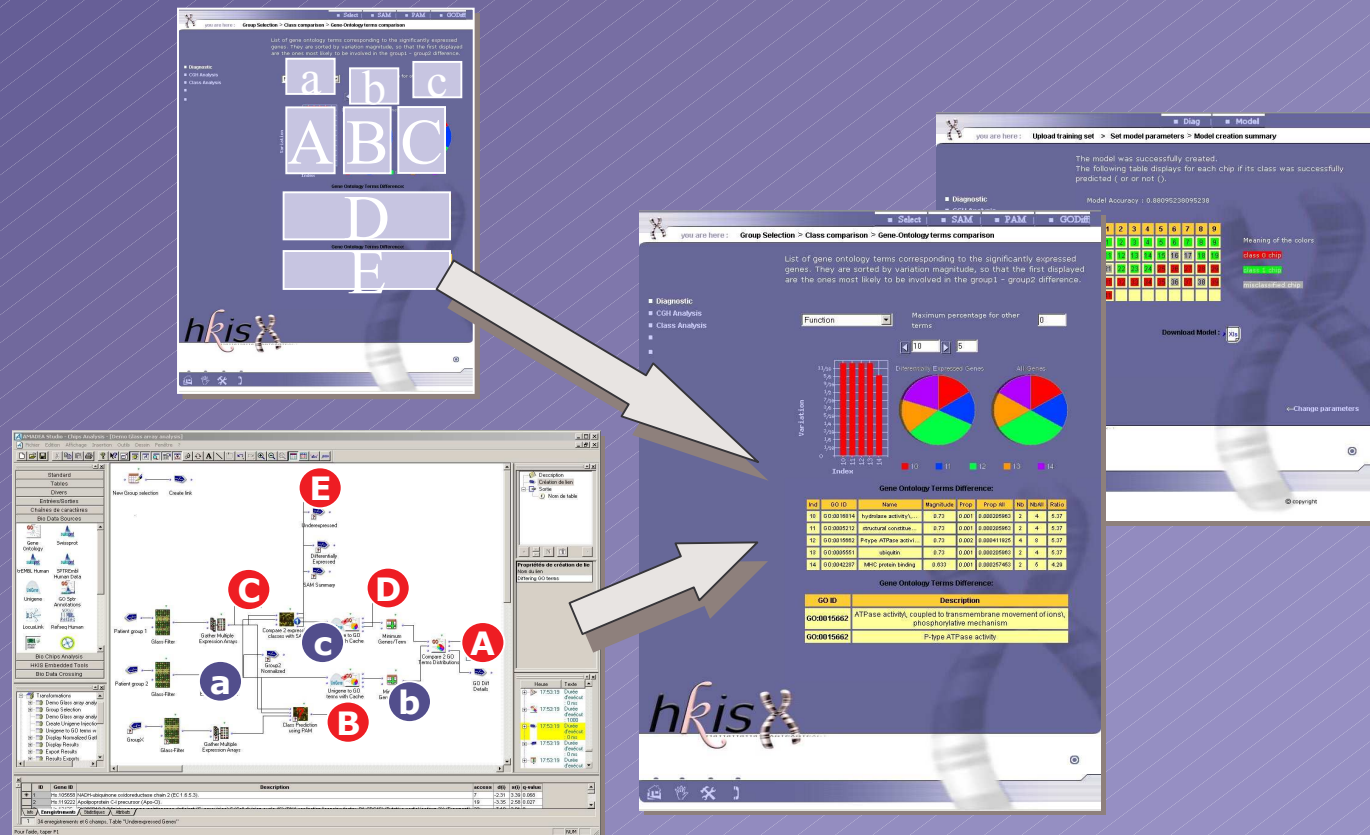
Real-time

- Access to data
- Data linking
- Data analysis
- Parameter tests
- Hypotheses tests



Data-morphing provides the right data at the right place at the right moment

- Immediate publication of applications through the web
 - Interactive graphical interfaces for the end user



Demonstration

- *Quick overview of the platform*
- *How to develop an analysis pipe-line*
 - *Example : Starting from raw DNA chips data, normalize these data, and compare two classes of samples. From the differentially expressed genes, obtain:*
 - *A table showing per gene, with which disease it can be linked*
 - *The list of differentially distributed metabolic functions and the associated bibliography.*
 - *Steps:*
 - *Connexion to chips data*
 - *Normalization and construction of a summary table*
 - *Link to Refseq to obtain Gene information, including link to OMIM diseases*
 - *Link to OMIM to get disease title, and creation of a crossed table*
 - *Class comparison using SAM -> List of differentially expressed genes*
 - *Injection into the Gene Ontology Graph*
 - *Comparison with functions in the whole chip to get differentially distributed functions*