

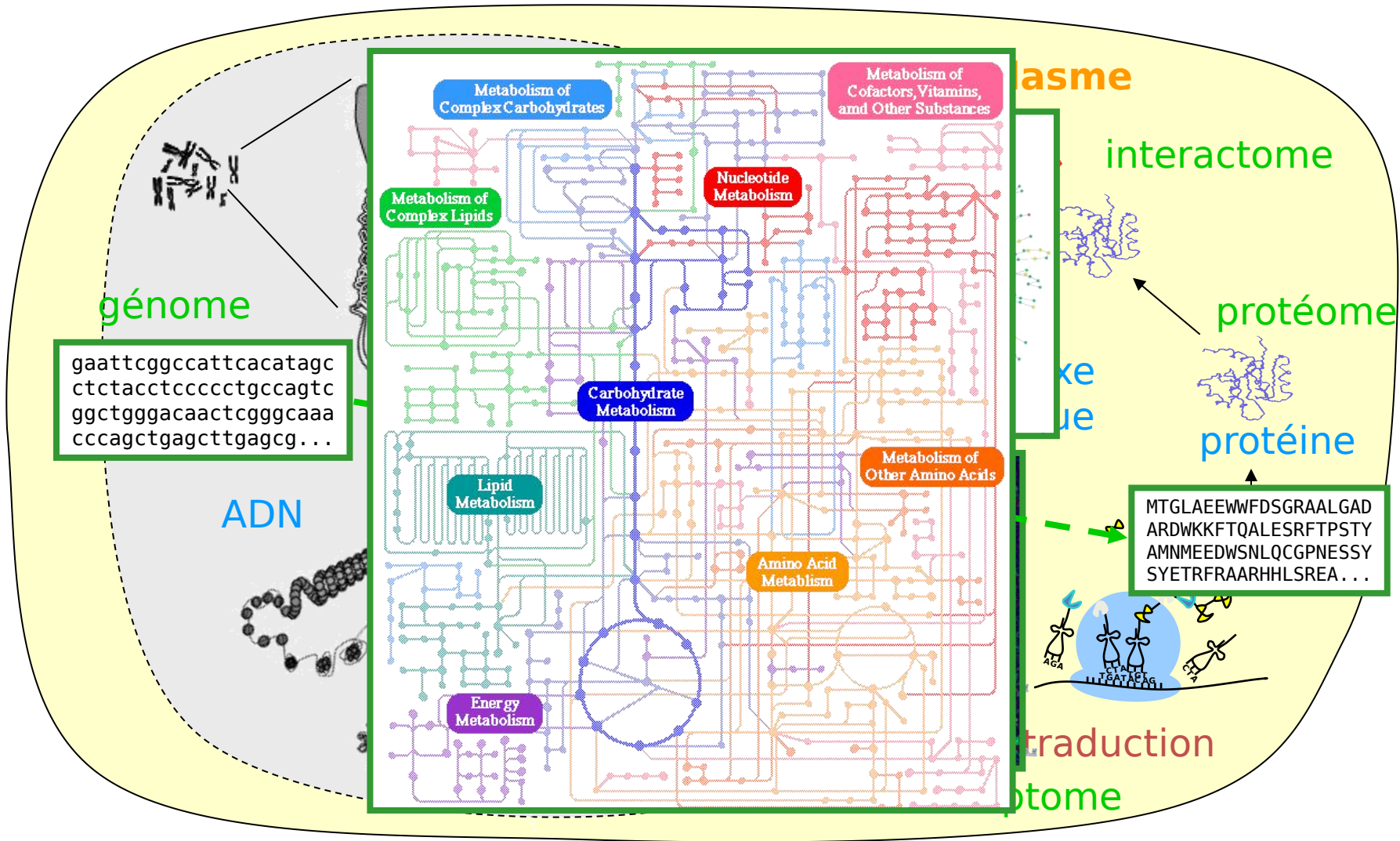
Intégration de données hétérogènes Approches

Master 2

Bioinformatique et Biologie des Systèmes

- Pourquoi ?
- Qu'est-ce que l'intégration ?
 - Interconnexion
 - Fusion
 - Médiation
 - Modélisation
 - Confrontation
 - Recoupement

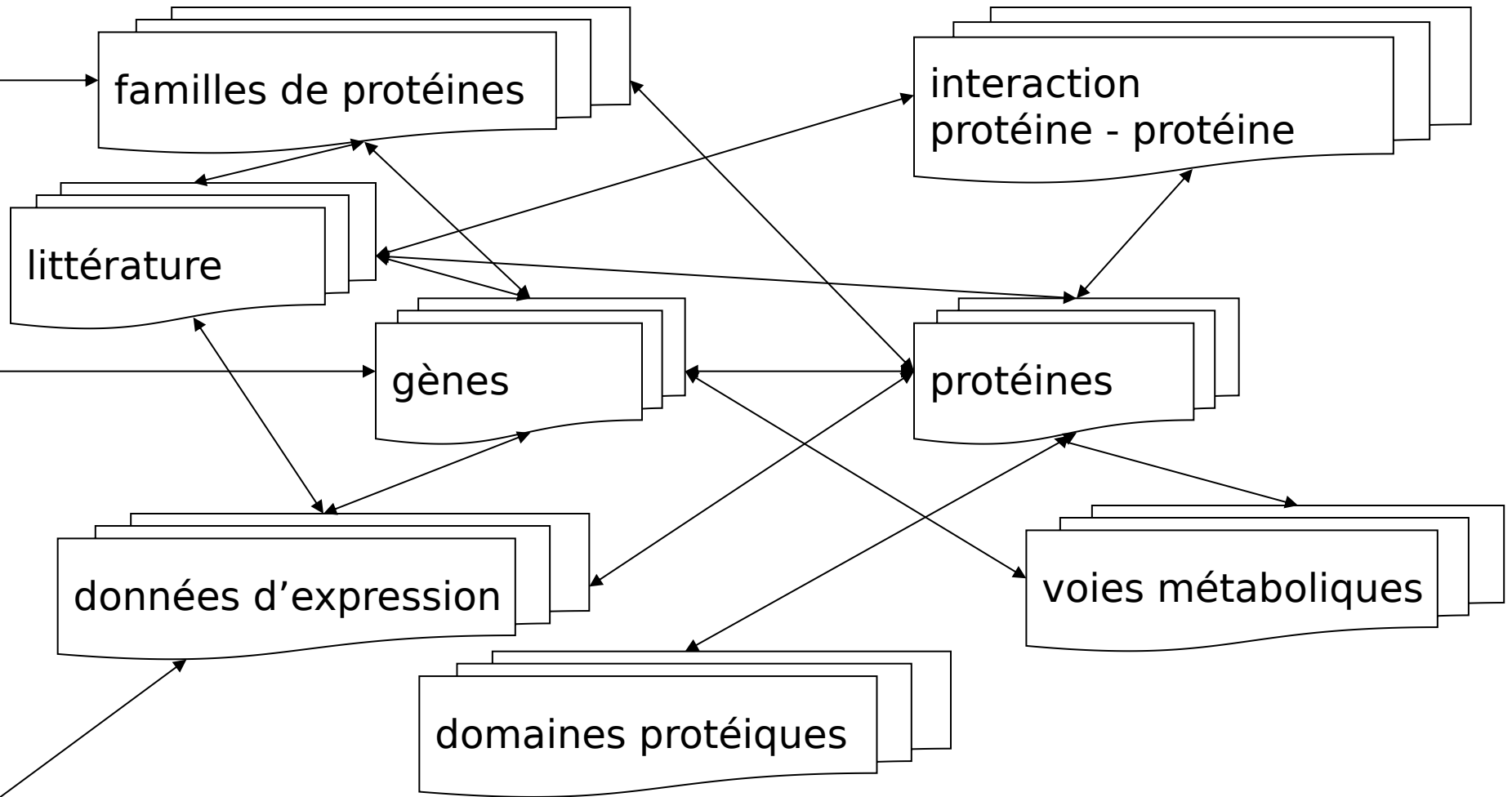
Biologie, mesures, données et connaissances



Cellule eucaryote

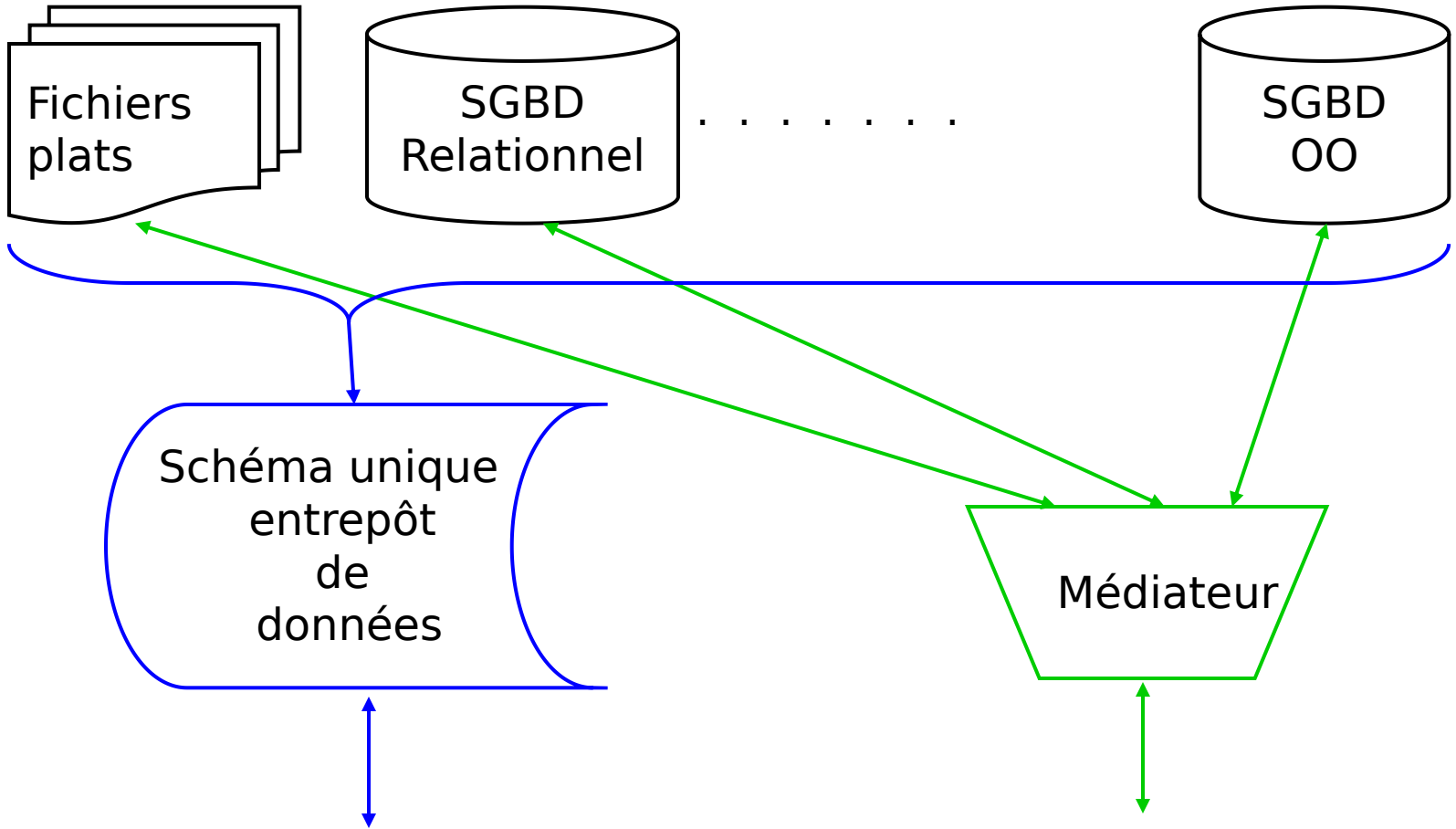
- Exploitation des références (croisées)
 - interconnexion
 - schéma unifié matérialisé : entrepôt
 - schéma unifié virtuel : médiateur
- Modélisation
- Statistiques
- Confrontation visuelle, exploratoire
- Exploitation de la notion de voisinage
 - exploration
 - recoupement
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 - fusion

Intégration par interconnexion : principe



SRS [Etzold *et al.*, 1996], Entrez [Schuler *et al.*, 1996], ...

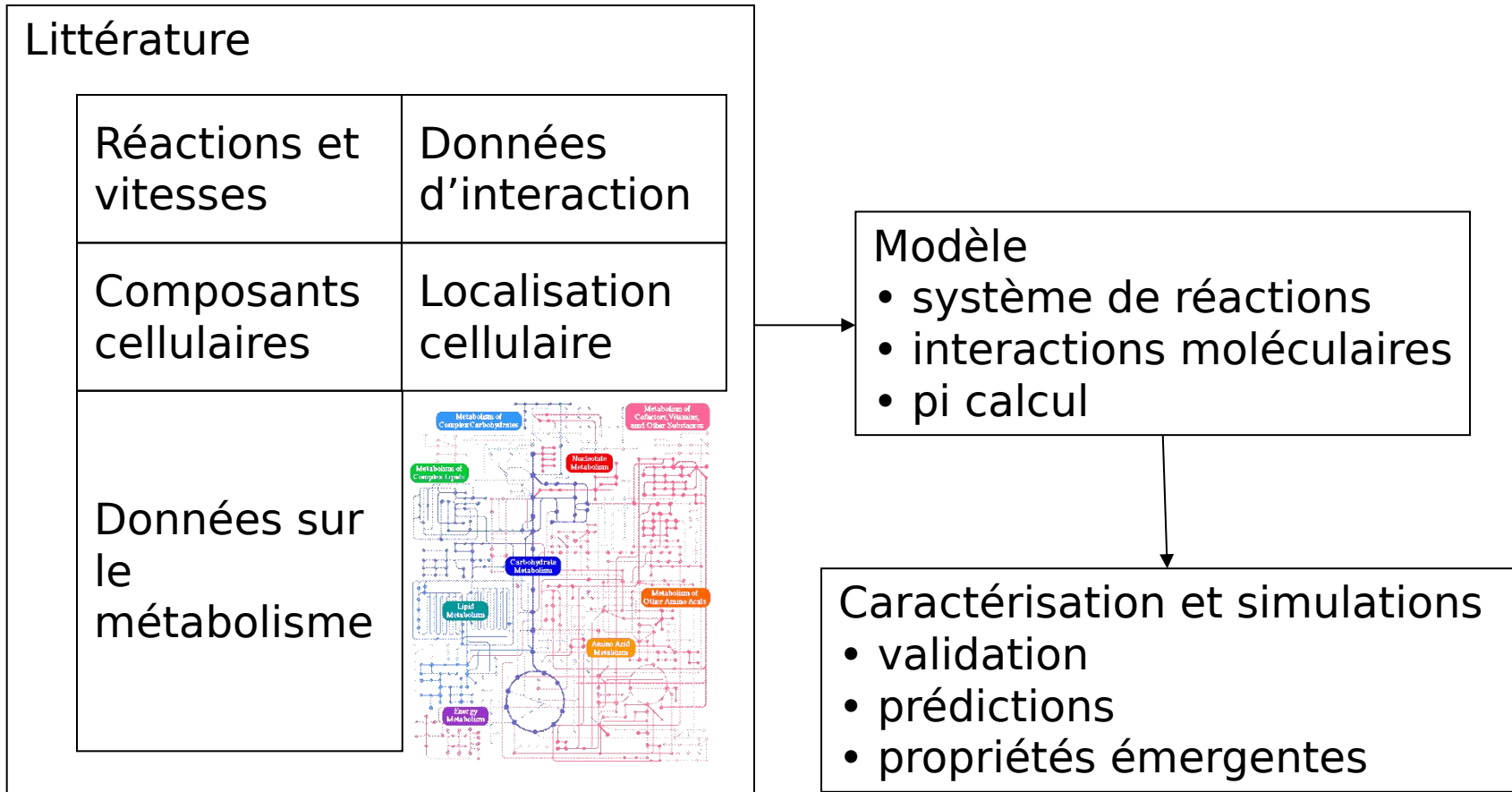
Intégration par fusion ou par médiateurs



Integr8 [Kersey *et al.*, 2005], BioMart [Kasprzyk *et al.*, 2004],
WInGS [Abergel *et al.*, 2004], BioKleisli [Davidson *et al.*, 1997], ...

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Intégration par la modélisation : vers la cellule virtuelle



Virtual Cell [Loew et Schaff, 2001], E-CELL [Tomita *et al.*, 1999],
 Cellerator [Shapiro *et al.*, 2003],
 MetExplore [Cottret *et al.*, 2010], ...

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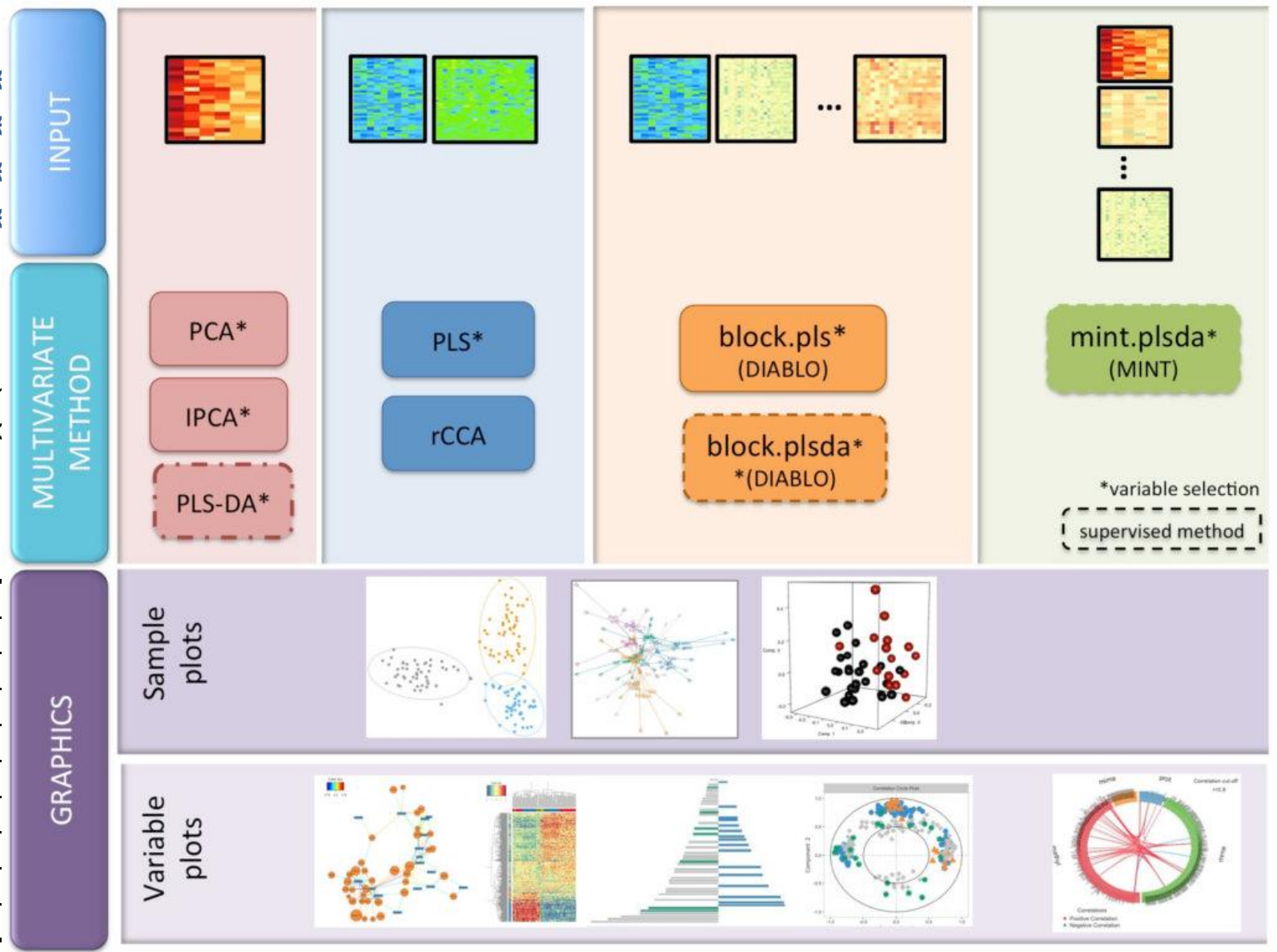
Statistiques

- Analyse
- Analyse
- Analyse
- Analyse
- ...

integrOr
MixOmic

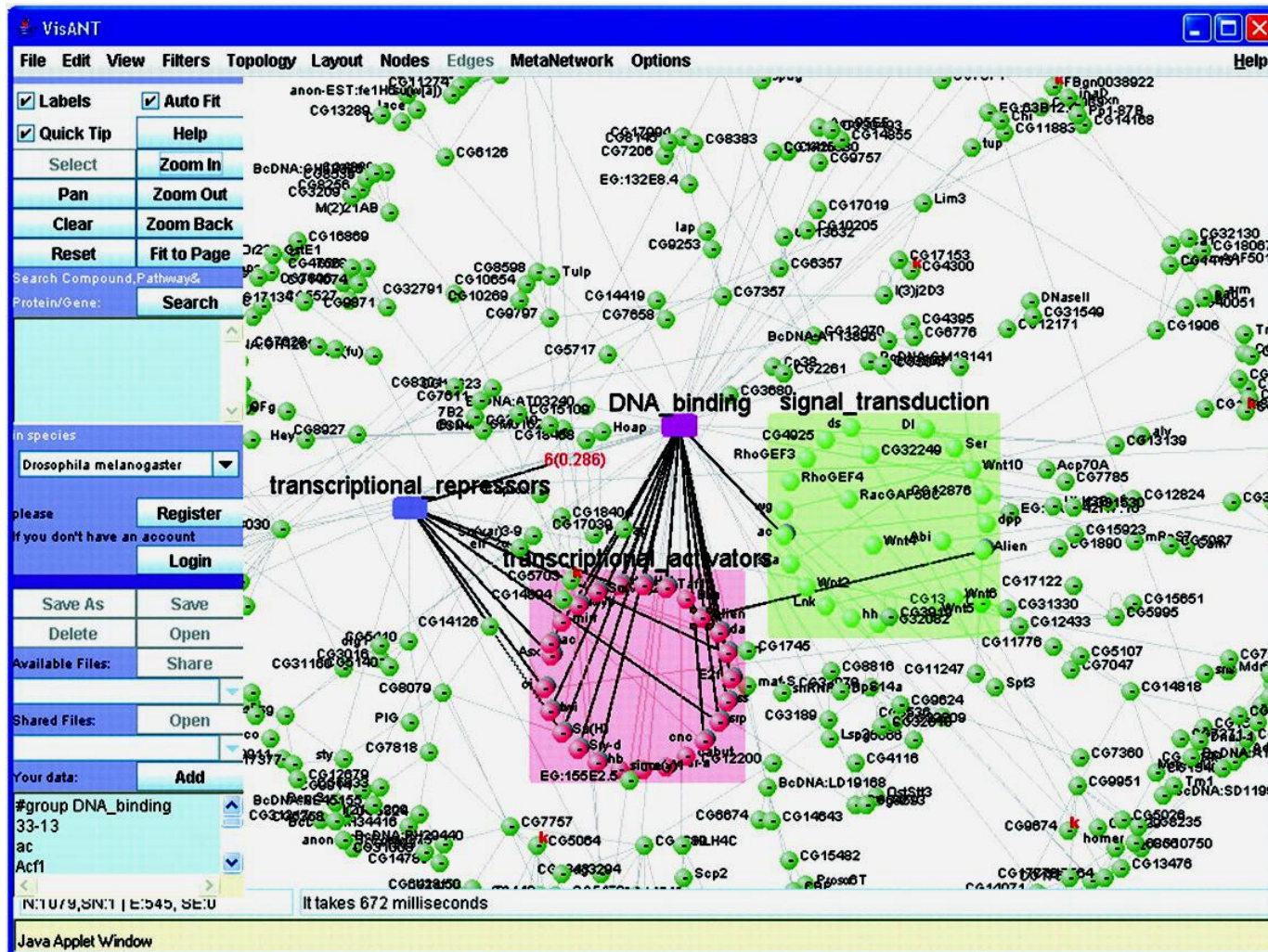
a

gènes



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Confrontation visuelle

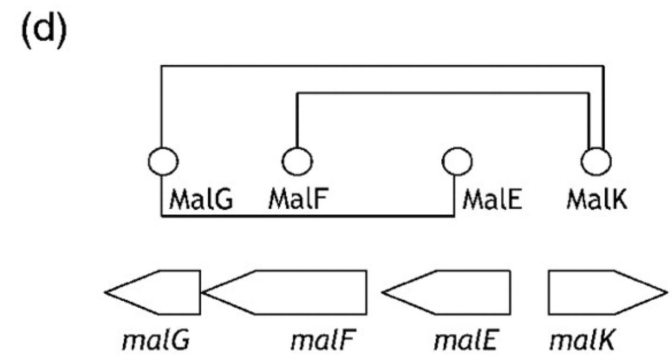
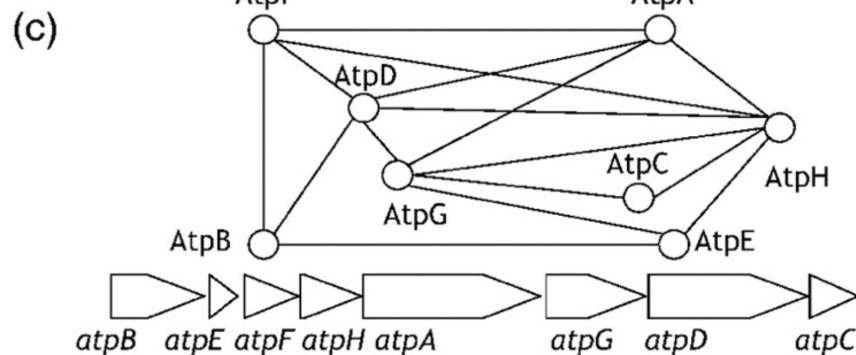
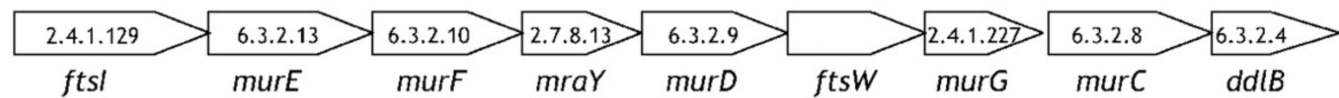
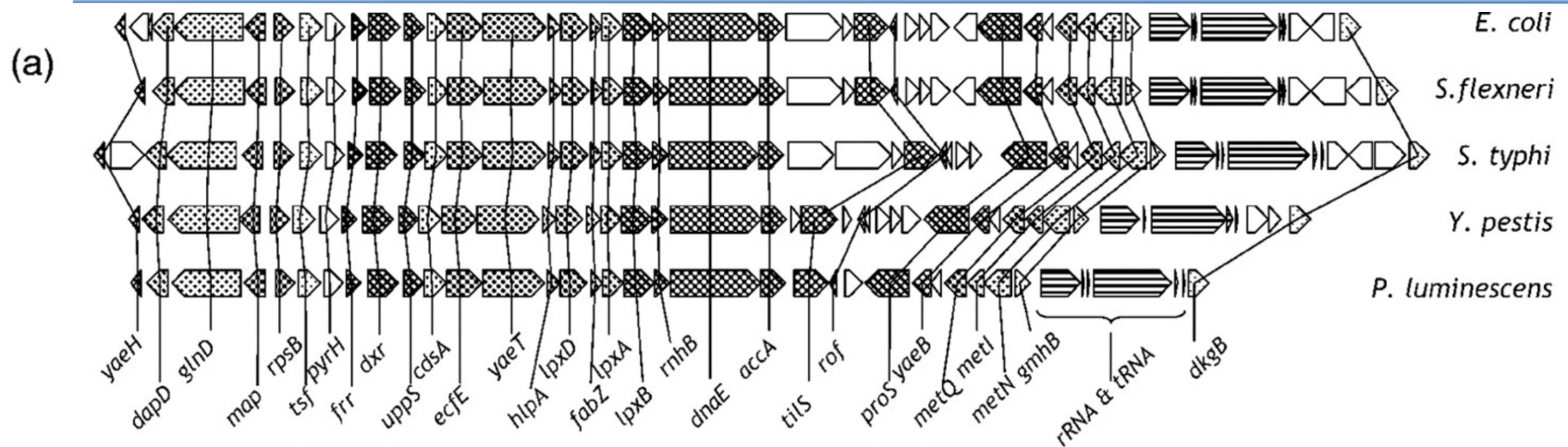


Visant [Hu *et al.*, 2005]

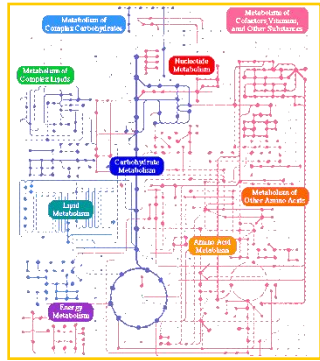
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The image displays two overlapping Java applet windows. The left window, titled "argB neighbours", features a navigation menu with buttons for "Swiss Prot", "Classification", "Codons", "Bibliography", "pI", and "Save / Print". Below the menu is a scatter plot showing a cluster of points. At the bottom, a "Neighbor genes" list includes `argA`, `ybjD`, `ybbB`, and `yeiE`. The right window, titled "argH neighbours", has a similar menu but includes a "Pathway" button. Its main content area is titled "Bibliography" and contains a list of references, including "Escherichia coli and Salmonella typhimurium cellular and molecular biology" and "Variations on a Theme by Escherichia". It also lists "Biosynthesis of Arginine and Polyamines" and "Arginine Biosynthetic Enzymes" with sub-items like "N-Acetylglutamokinase" and "Arginine Reulon". A "Neighbor genes" list is present but empty. A "Delete" button is located at the bottom right of the interface.

Recoupement de voisinages : approche basée sur les graphes



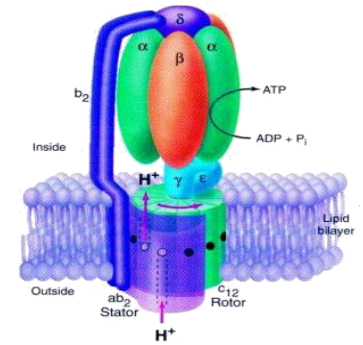
Recoupement de voisinages : approche ensembliste



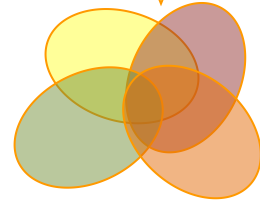
voies métaboliques



localisation chromosomique



complexes protéiques



ensembles de gènes

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ENDEAVOUR update: a web resource for gene prioritization in multiple species

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ABSTRACT
Endeavour (<http://www.esat.kuleuven.be/endeavour>); this web site is free and open to all users and there is no login requirement) is a web resource for the prioritization of candidate genes. Using a training set of genes known to be involved in a biological process of interest, our approach consists of (i) inferring several models (based on various genomic data sources), (ii) applying each model to the candidate genes to rank those candidates against the profile of the known genes and (iii) merging the several rankings into a global ranking of the candidate genes. In the present

BACKGROUND
With the recent improvements in high-throughput technologies, many organisms have seen their genomes sequenced and, more importantly, annotated. This process leads to the generation of a large amount of genomic data and the creation and maintenance of corresponding databases. However, covering genomic data into biological knowledge to identify genes involved in a particular process or disease remains a major challenge. Nevertheless, there is much evidence to suggest that functionally related genes often cause similar phenotypes (1-3). To identify which genes are responsible for which phenotype, association studies and linkage analyses are often used, resulting in large lists of candidate genes. In

co-citation

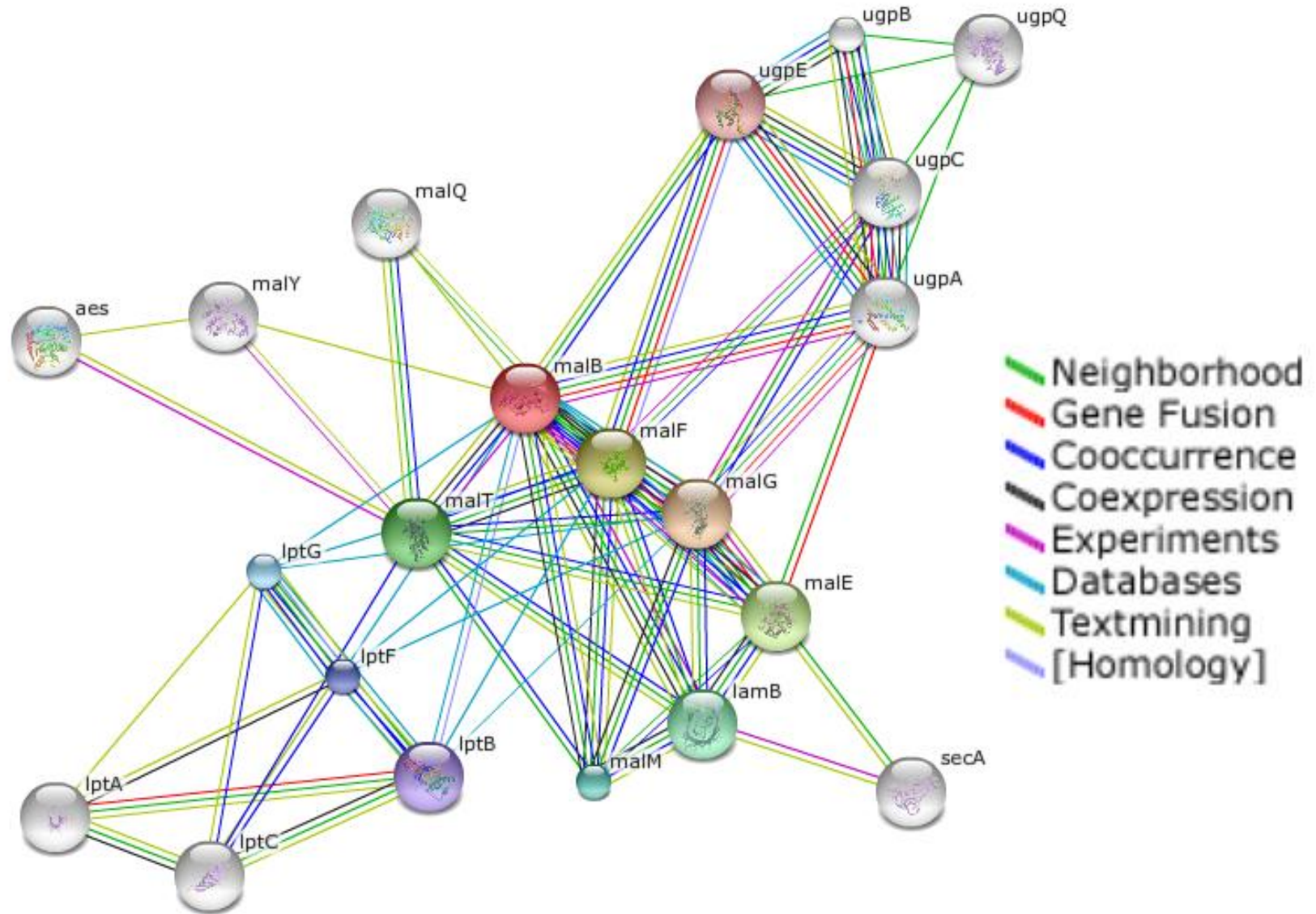


domaines protéiques



Gene Ontology

Fusion : approche basée sur les graphes



STRINGdb [von Mering *et al.*, 2003]

