# FlyMine 4.0



Genomics Genome annotation



Gene Expression ArrayExpress



Binding Sites
Protein binding sites



Dros Del
P-element
Insertions and
Deletions



<u>Tiling Path</u> Microarray Tiling Primers



INDAC Long Oligos



RNAi RNA interference



<u>Disease</u> Human disease matches from Homophila



Comparative Genomics
Orthologues
and Paralogues



Proteins
Protein and proteomics data



Protein Interactions IntAct



Protein Structure
3-D protein
structures



Gene Ontology

An integrated database for Drosophila and Anopheles



## Outline

- What is FlyMine?
- Release 4.0 data sources
- Demonstration



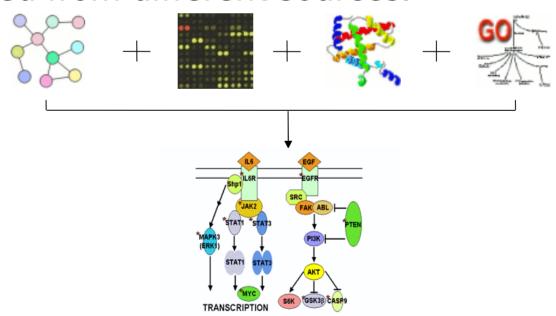
# What is FlyMine?

- A generic database allowing complex and arbitrary queries across diverse data sets
- Main focus: Drosophila, Anopheles and other insects (+ yeast, C. elegans)
- A genomics/proteomics focus
- Operates on lists
- Integrated viewing and analysis tools



#### Motivation

- Massive amounts of experimental data (microarray, proteomics) being produced.
- Data quality can vary significantly: high-throughput datasets tend to be noisy.
- Stronger inferences can be made when data are combined from different sources.

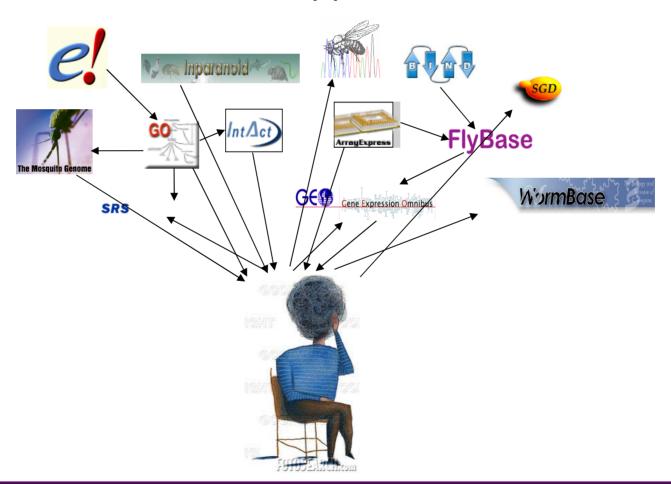






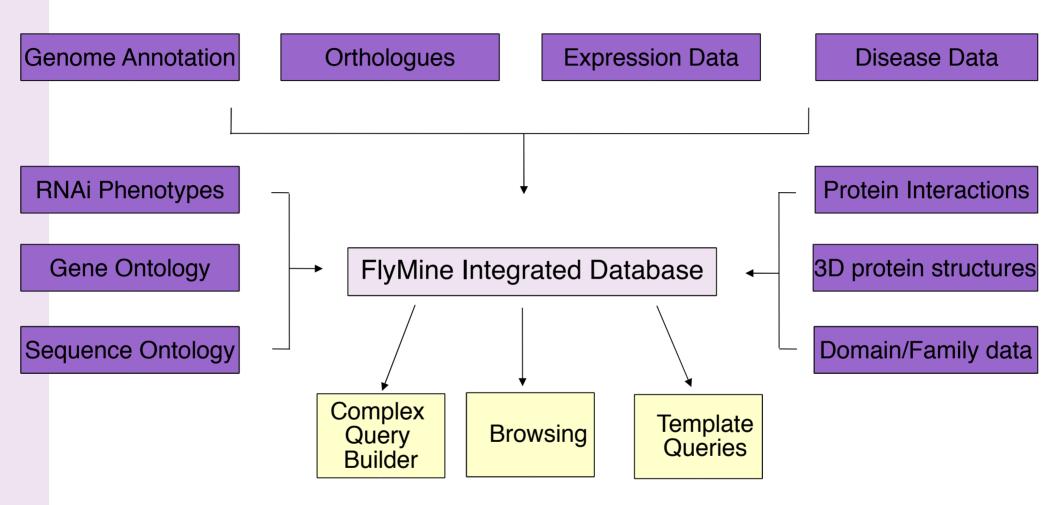
# The Challenge of Integration

- Lots of databases
- Lots of different formats
- Need bioinformatics support





## Creating an Integrated database



Easy to configure, easy to add more data





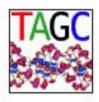
## Release 4.0 Data Sources

- D. melanogaster genome annotation FlyBase
- A. gambiae genome annotation **Ensembl**
- InParanoid orthologues between multiple organisms
- UniProt protein data for multiple organisms
- Protein-protein interactions (multiple experiments) for D. melanogaster and C. elegans IntAct
- Protein Family and Domain data for D. melanogaster, A. gambiae and C. elegans InterPro
- D. melanogaster protein domain 3-D structure predictions Kenji Mizuguchi, University of Cambridge
- RNAi phenotypes for *C. elegans* genes **WormBase**
- GO annotations for D. melanogaster, A. gambiae and C. elegans
- DNase I footprint data for D. melanogaster FlyReg
- Microarray gene expression data, including Arbeitman et al (2002) *D. melanogaster* time course experiment
- D. melanogaster **DrosDel** P-element insertion and deletion locations
- Homophila human disease to *Drosophila* gene data set
- INDAC microarray oligo set for *D. melanogaster* **INDAC Consortium**
- D. melanogaster whole genome tiling amplimer set





## Aspects



Genomics Genome annotation



DrosDel
P-element
Insertions and
Deletions



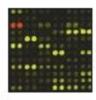
RNAi RNA interference



Proteins
Protein and proteomics data



Gene Ontology



Gene Expression ArrayExpress



Tiling Path Microarray Tiling Primers



Disease
Human disease matches from
Homophila



Protein Interactions IntAct



Binding Sites Protein binding sites



INDAC Long Oligos



Comparative Genomics
Orthologues
and Paralogues



Protein Structure 3-D protein structures



## Aspects

- Links to source databases and publications
- Access to bulk datasets
- Query start points
- Template queries
  - for simpler access to the data
  - For a set of genes, search for the C. elegans orthologues and their RNAi phenotypes.
  - adapt to make new queries
  - easy to add more suggestions welcome





#### Releases

- Release cycle (content, functionality)
- Release 5.0 (Easter 2006)
  - D. pseudoobscura FlyBase, UniProt
  - A. mellifera Ensembl, UniProt,
  - InParanoid orthologues and GO annotation for more organisms
- Future development input welcome



# Help and Feedback

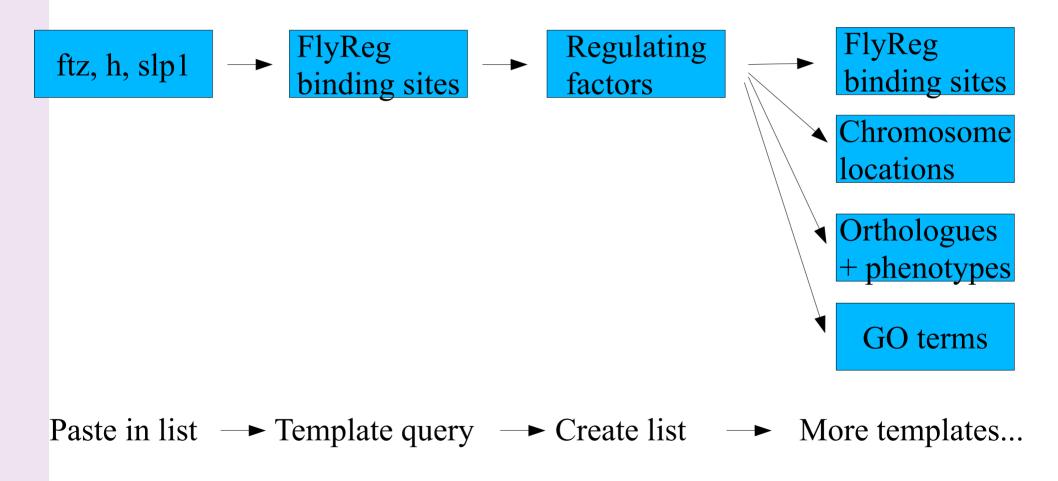
Quick-start guide + Tutorials

Mailing lists (sign up sheets)

Support/ suggestions/ feedback welcome:

- Email: support@flymine.org
- Feedback links on every FlyMine page
- Call us: +44 (0)1223 333 377

# Demonstation Example





# Acknowledgements

Richard Smith
Kim Rutherford
Matthew Wakeling
Tom Riley
Peter McLaren
Wenyan Ji

Rachel Lyne
Hilde Janssens
Florian Reisinger
François Guillier
Debashis Rana
Gos Micklem

#### More information at www.flymine.org



FlyMine is funded by the Wellcome Trust (grant no. 067205), awarded to M. Ashburner, G. Micklem, S. Russell, K. Lilley and K. Mizuguchi.



