FlyMine

An integrated database for *Drosophila* and *Anopheles* genomics

Richard Smith
Genetics Department
University of Cambridge

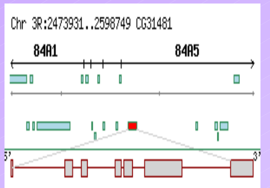
Outline

- What is FlyMine?
- What can you do with it?
- InterMine – generic data warehouse
- FlyMine – integrating biological data
- Data integration examples

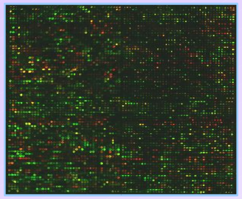
What is FlyMine?

- A data warehouse that integrates several genomic and proteomic data sets in one place.
- Main focus is *Drosophila melanogaster* and *Anopheles gambiae* with cross species comparasons with other organisms
- Website allows users to build arbitrary complex queries across all data.
- Focus is on complex queries in place rather than data access.

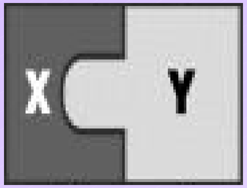
Data Sources



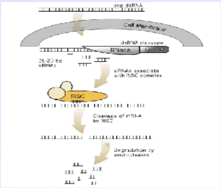
Genome Annotation



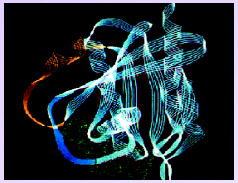
Microarray expression data (soon)



2-hybrid
Protein-Protein
Interactions

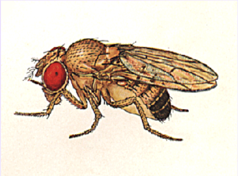
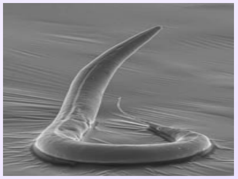


RNAi Phenotypes

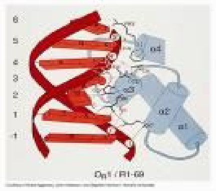


3-D structural
domain predictions

GO Annotation

 ↔ 

Ortholgues/
Paralogues

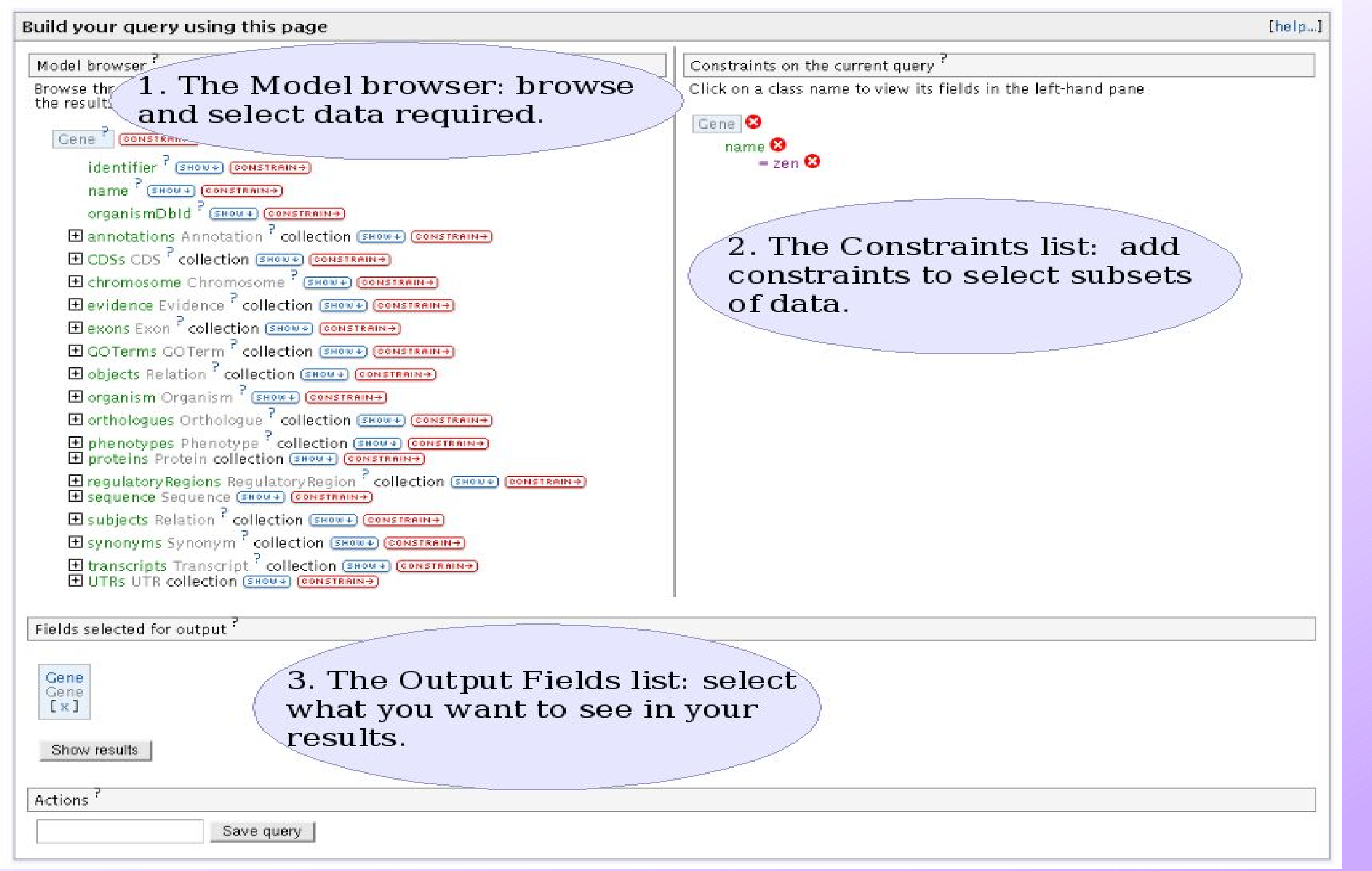


DNAase 1 footprints

Example Queries

- For proteins for which there is evidence that they interact, find whether the orthologues of these proteins also have evidence that they interact (ie search for interologs)
- Search for Drosophila genes associated with a particular transcription factor binding site and show the predicted orthologues for these genes.
- *Determine whether proteins that may interact are also co-expressed under any conditions*

The Query Builder:



Build your query using this page [help...]

Model browser ?

Browse thr
the result

1. The Model browser: browse and select data required.

Gene ? CONSTRAIN→

identifier ? SHOW↓ CONSTRAIN→
name ? SHOW↓ CONSTRAIN→
organismDbId ? SHOW↓ CONSTRAIN→
⊞ annotations Annotation ? collection SHOW↓ CONSTRAIN→
⊞ CDSs CDS ? collection SHOW↓ CONSTRAIN→
⊞ chromosome Chromosome ? SHOW↓ CONSTRAIN→
⊞ evidence Evidence ? collection SHOW↓ CONSTRAIN→
⊞ exons Exon ? collection SHOW↓ CONSTRAIN→
⊞ GOTerms GOTerm ? collection SHOW↓ CONSTRAIN→
⊞ objects Relation ? collection SHOW↓ CONSTRAIN→
⊞ organism Organism ? SHOW↓ CONSTRAIN→
⊞ orthologues Orthologue ? collection SHOW↓ CONSTRAIN→
⊞ phenotypes Phenotype ? collection SHOW↓ CONSTRAIN→
⊞ proteins Protein collection SHOW↓ CONSTRAIN→
⊞ regulatoryRegions RegulatoryRegion ? collection SHOW↓ CONSTRAIN→
⊞ sequence Sequence SHOW↓ CONSTRAIN→
⊞ subjects Relation ? collection SHOW↓ CONSTRAIN→
⊞ synonyms Synonym ? collection SHOW↓ CONSTRAIN→
⊞ transcripts Transcript ? collection SHOW↓ CONSTRAIN→
⊞ UTRs UTR collection SHOW↓ CONSTRAIN→

Constraints on the current query ?

Click on a class name to view its fields in the left-hand pane

Gene ☒
name ☒
= zen ☒

2. The Constraints list: add constraints to select subsets of data.

Fields selected for output ?

Gene
Gene
[x]

Show results

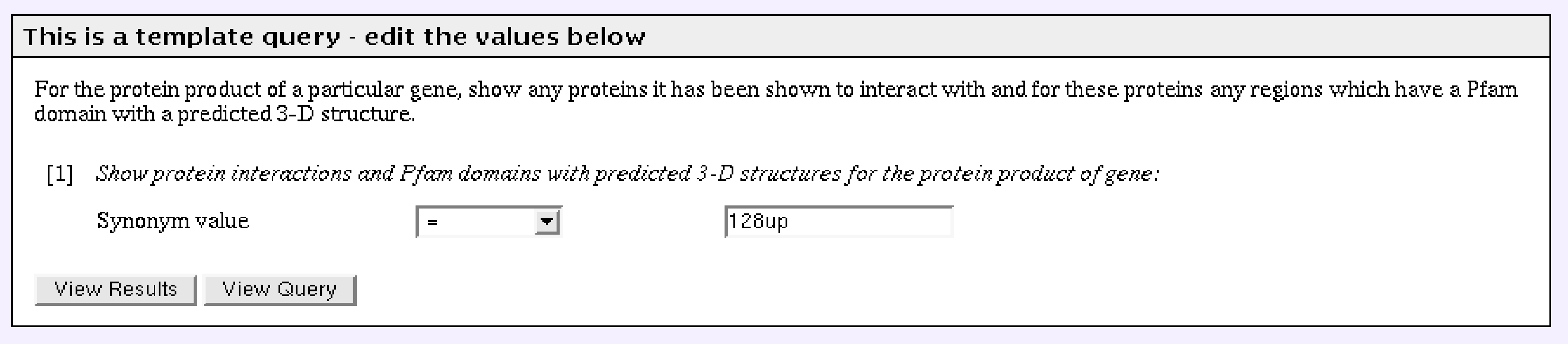
3. The Output Fields list: select what you want to see in your results.

Actions ?

Save query

Template Queries

- For the protein product of a particular gene, show any proteins it has been shown to interact with, the Pfam domains of these proteins and any predicted structure for the domains.



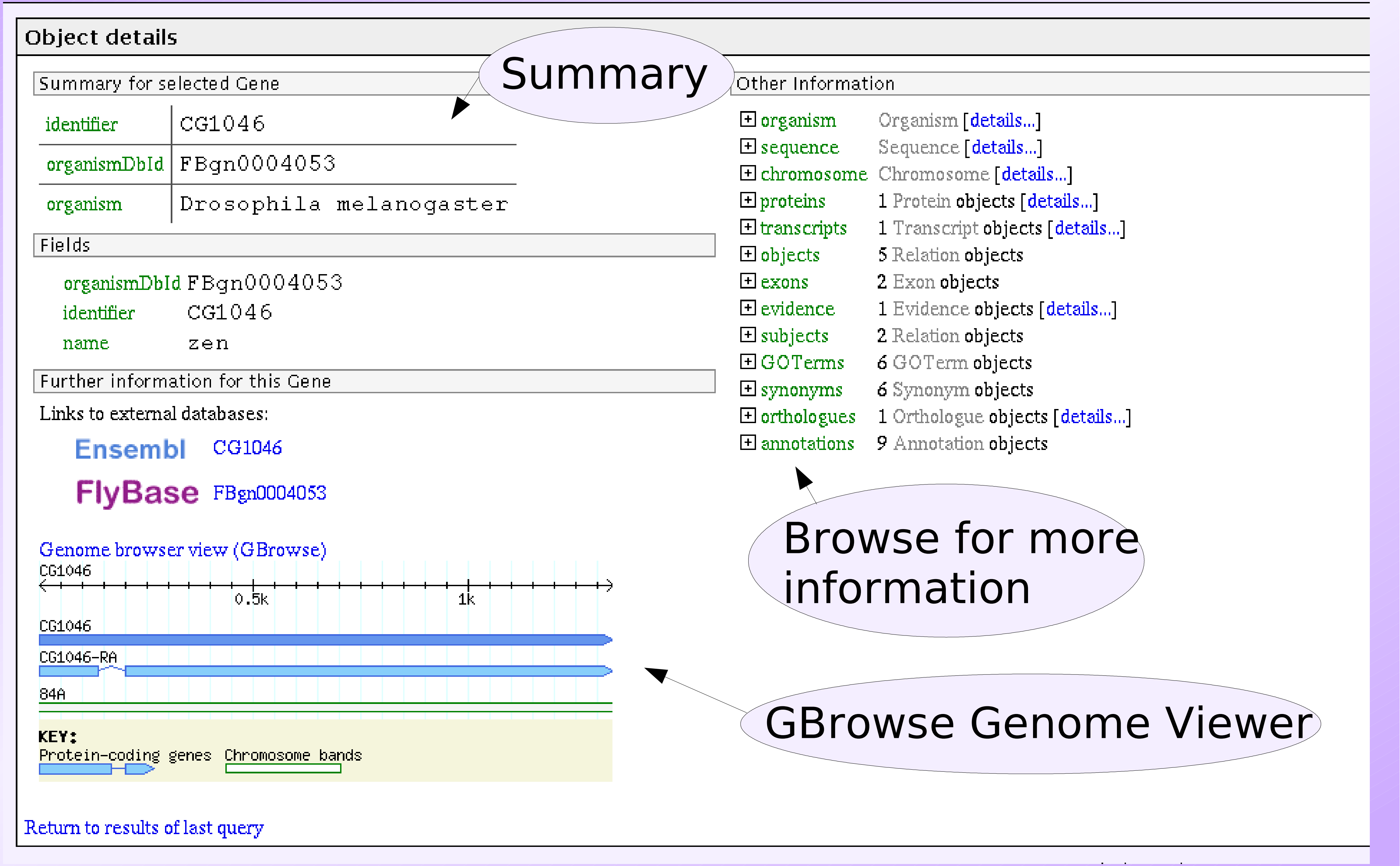
This is a template query - edit the values below

For the protein product of a particular gene, show any proteins it has been shown to interact with and for these proteins any regions which have a Pfam domain with a predicted 3-D structure.

[1] *Show protein interactions and Pfam domains with predicted 3-D structures for the protein product of gene:*

Synonym value = 128up

Browsable Details Page:



Object details

Summary for selected Gene

identifier	CG1046
organismDbId	FBgn0004053
organism	Drosophila melanogaster

Fields

organismDbId	FBgn0004053
identifier	CG1046
name	zen

Further information for this Gene

Links to external databases:

Ensembl	CG1046
FlyBase	FBgn0004053

Genome browser view (GBrowse)

Return to results of last query

Other Information

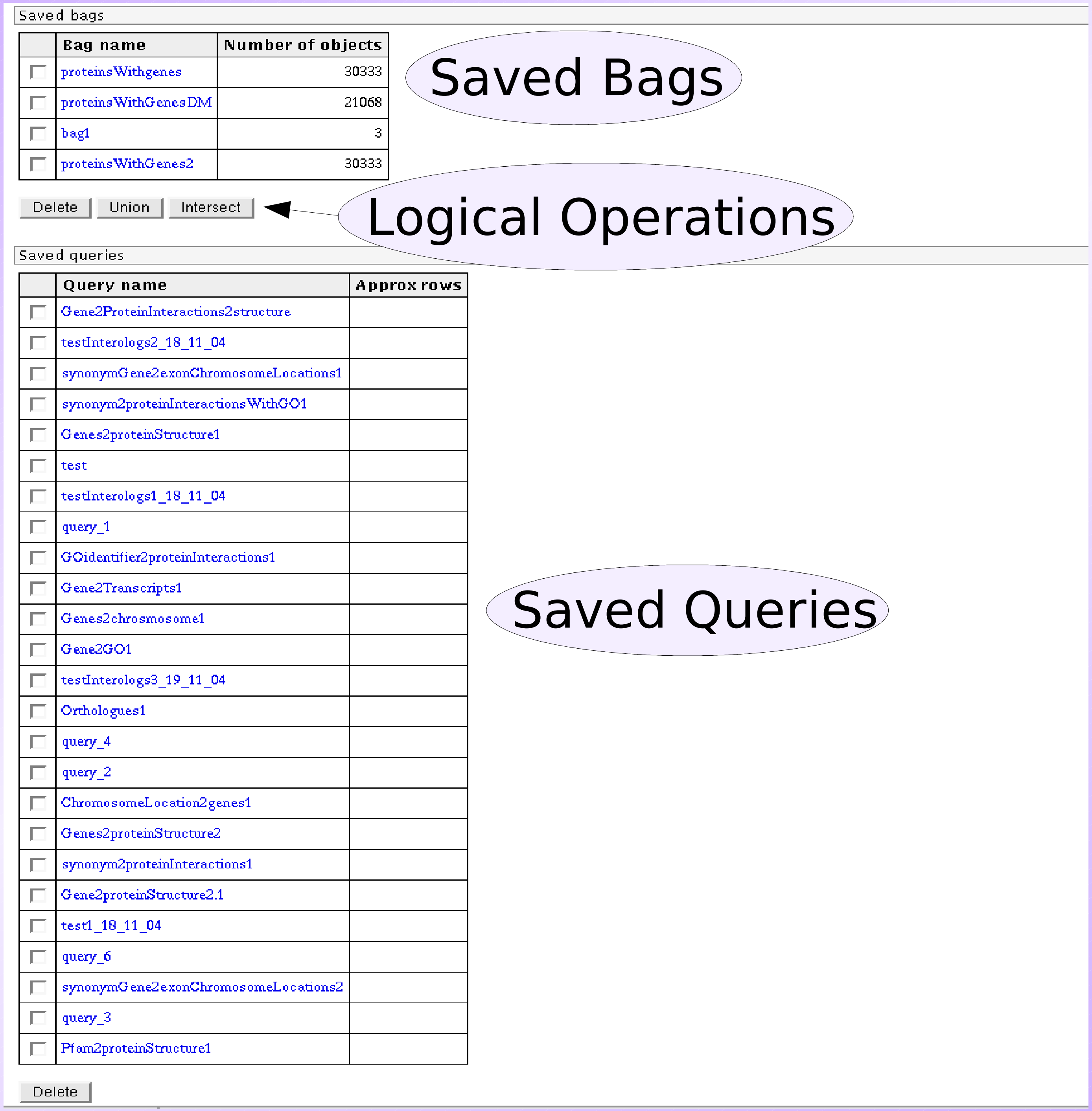
⊞ organism	Organism [details...]
⊞ sequence	Sequence [details...]
⊞ chromosome	Chromosome [details...]
⊞ proteins	1 Protein objects [details...]
⊞ transcripts	1 Transcript objects [details...]
⊞ objects	5 Relation objects
⊞ exons	2 Exon objects
⊞ evidence	1 Evidence objects [details...]
⊞ subjects	2 Relation objects
⊞ GOTerms	6 GOTerm objects
⊞ synonyms	6 Synonym objects
⊞ orthologues	1 Orthologue objects [details...]
⊞ annotations	9 Annotation objects

Summary

Browse for more information

GBrowse Genome Viewer

Other Features:



Saved bags

	Bag name	Number of objects
□	proteinsWithgenes	30333
□	proteinsWithGenesDM	21068
□	bag1	3
□	proteinsWithGenes2	30333

Saved Bags

Logical Operations

Saved queries

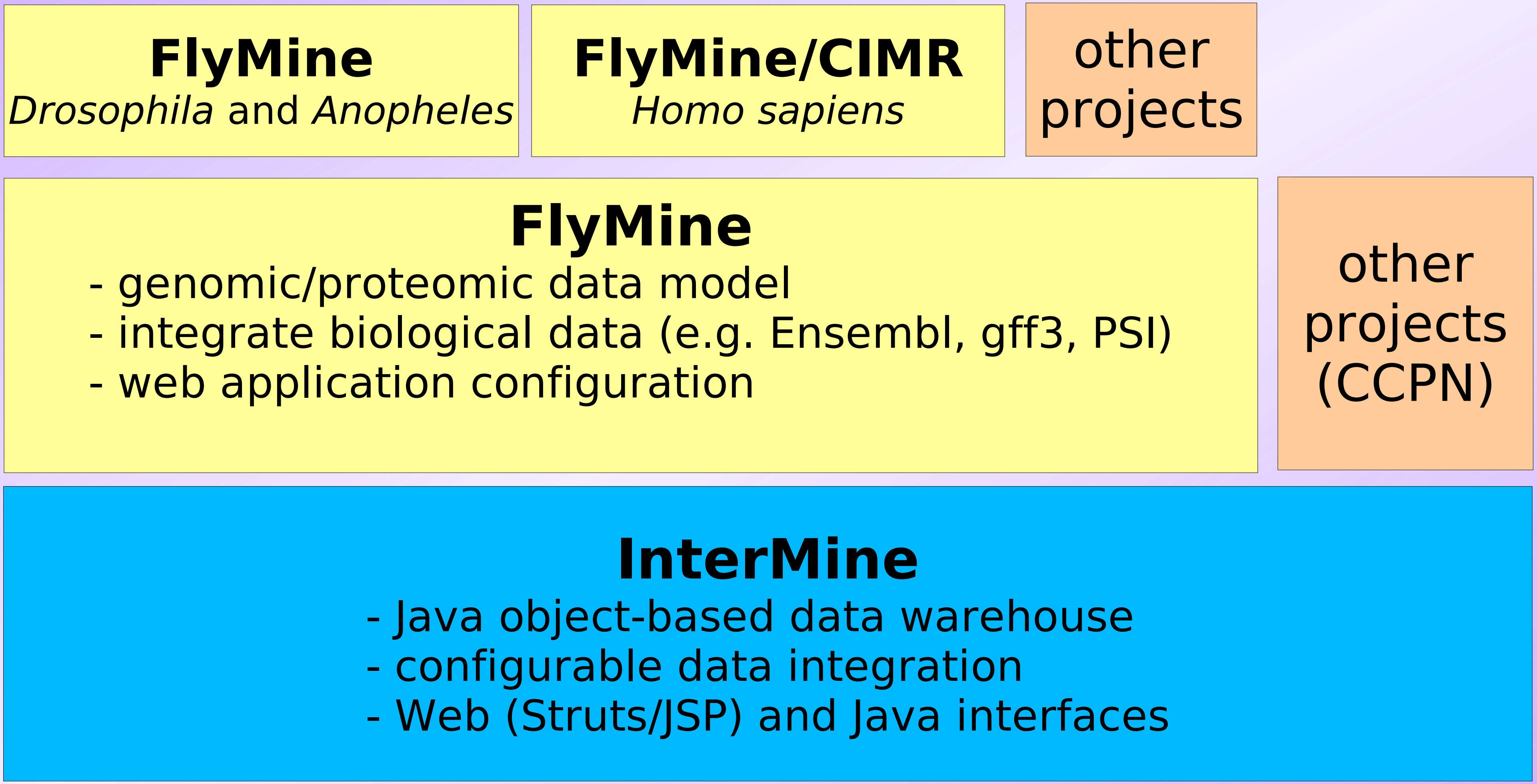
	Query name	Approx rows
□	Gene2ProteinInteractions2structure	
□	testInterologs2_18_11_04	
□	synonymGene2exonChromosomeLocations1	
□	synonym2proteinInteractionsWithGO1	
□	Genes2proteinStructure1	
□	test	
□	testInterologs1_18_11_04	
□	query_1	
□	GOidentifier2proteinInteractions1	
□	Gene2Transcripts1	
□	Genes2chrosmosome1	
□	Gene2GO1	
□	testInterologs3_19_11_04	
□	Orthologues1	
□	query_4	
□	query_2	
□	ChromosomeLocation2genes1	
□	Genes2proteinStructure2	
□	synonym2proteinInteractions1	
□	Gene2proteinStructure2.1	
□	test1_18_11_04	
□	query_6	
□	synonymGene2exonChromosomeLocations2	
□	query_3	
□	Pfam2proteinStructure1	

Saved Queries

Software Goals

- Integrate multiple data sets into a single data warehouse
- Flexible - continual addition of new types of data
- Powerful - allow complex queries not known at design time to run on the data warehouse
- Robust – reject queries that would take too long

FlyMine Software



FlyMine
Drosophila and *Anopheles*

FlyMine/CIMR
Homo sapiens

other projects

FlyMine

- genomic/proteomic data model
- integrate biological data (e.g. Ensembl, gff3, PSI)
- web application configuration

other projects (CCPN)

InterMine

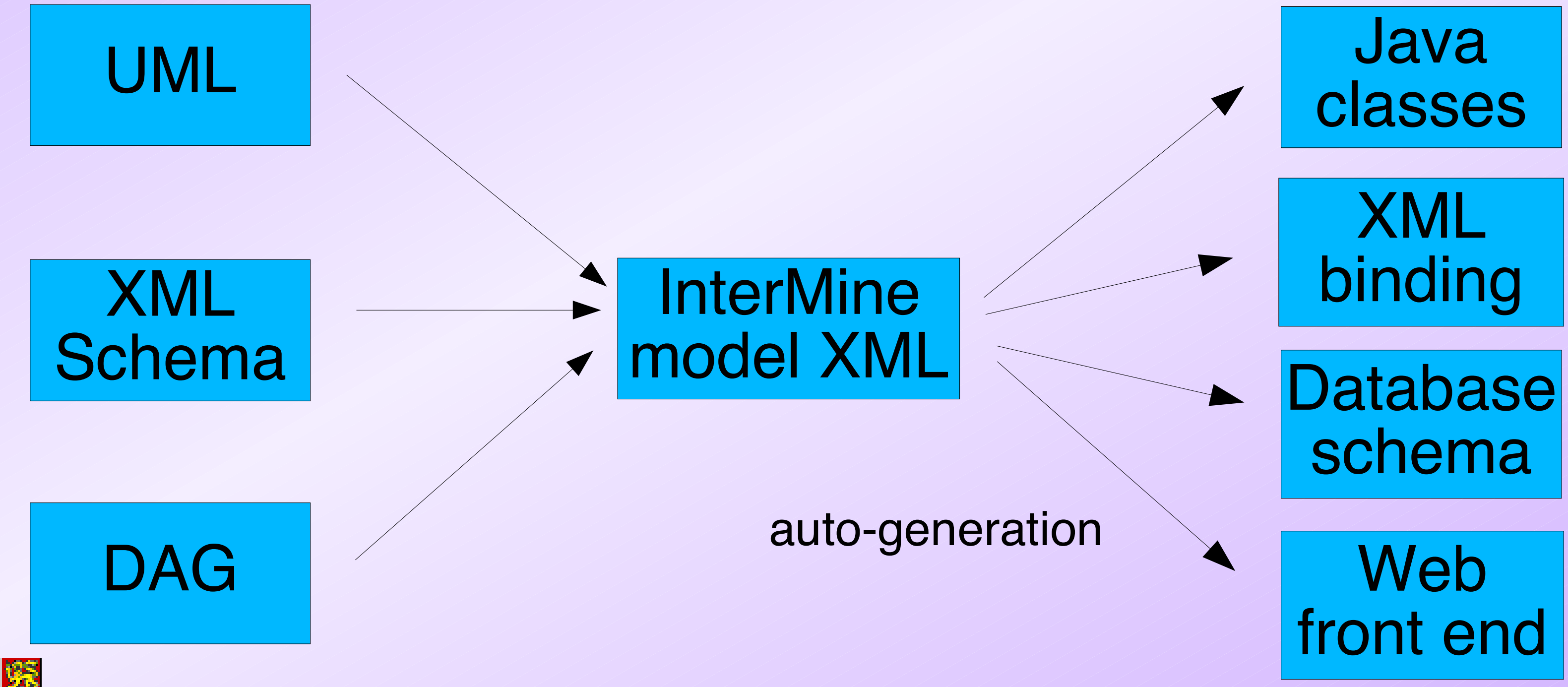
- Java object-based data warehouse
- configurable data integration
- Web (Struts/JSP) and Java interfaces

InterMine

- Object/relational query system
- Data model independent
- Query optmisation system – pre-computed tables/query re-writing
- Flexible data integration
- Retrieve data from RDBMS, XML, flat files
- Web application (Struts/JSP)

InterMine - Model Independent

- auto-generation from XML model definition
- single model or merge multiple



FlyMine

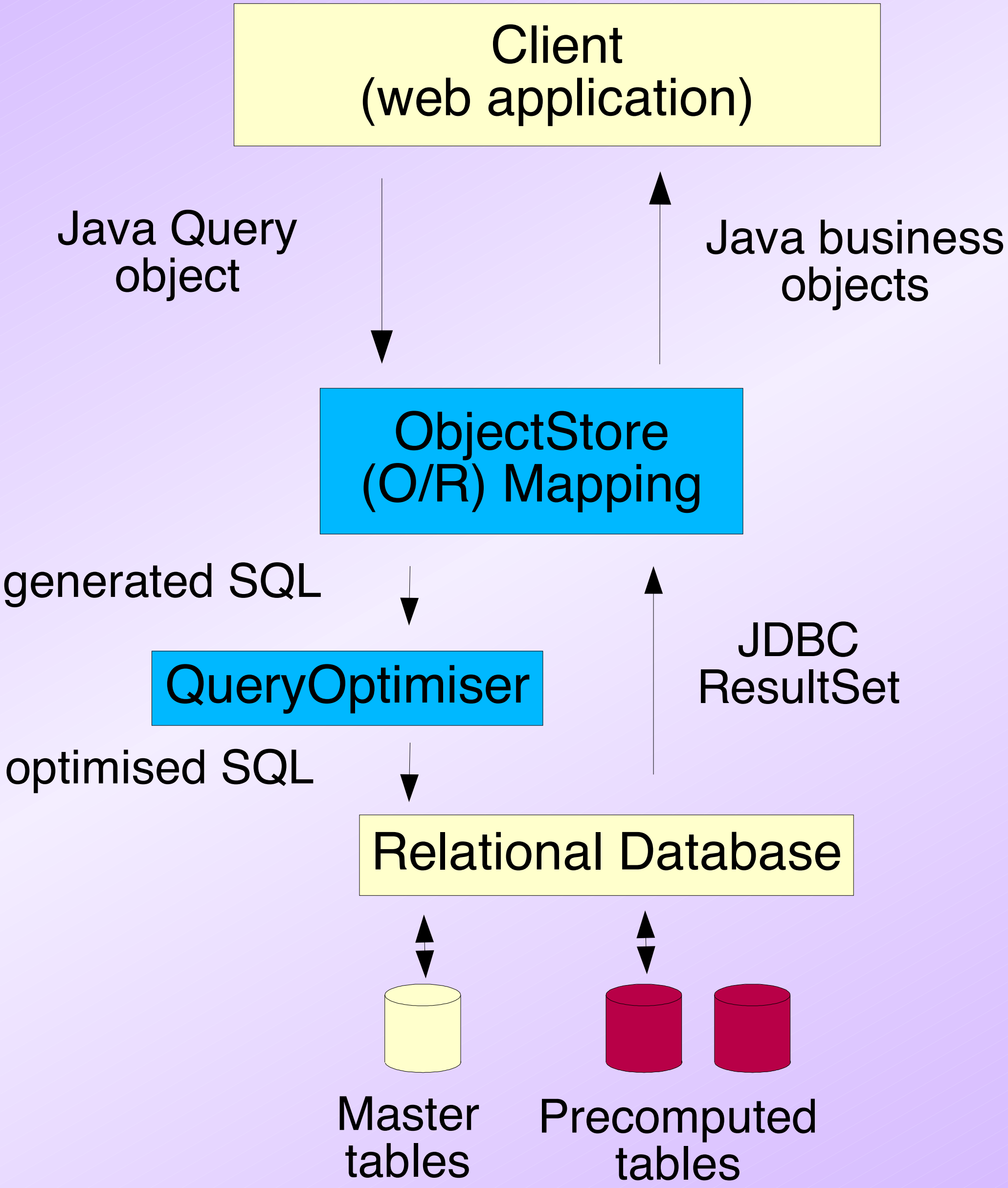
Arbitrary queries – problems

- Badly formed queries may overload database server
- Difficult to optimise database for all queries
  - Which indexes to use?
  - Slow response to complex queries involving multi-table joins

Arbitrary queries – solutions

- Close relationship with database server query planner
  - ask how long a query will take before attempting to run it (~3ms)
  - Disallow queries that will take longer than a certain threshold
- Store data massively redundantly in “precomputed tables” and rewrite incoming queries on-the-fly.

InterMine- Query Optimisation



Client
(web application)

Java Query
object

Java business
objects

ObjectStore
(O/R) Mapping

generated SQL

QueryOptimiser

JDBC
ResultSet

optimised SQL

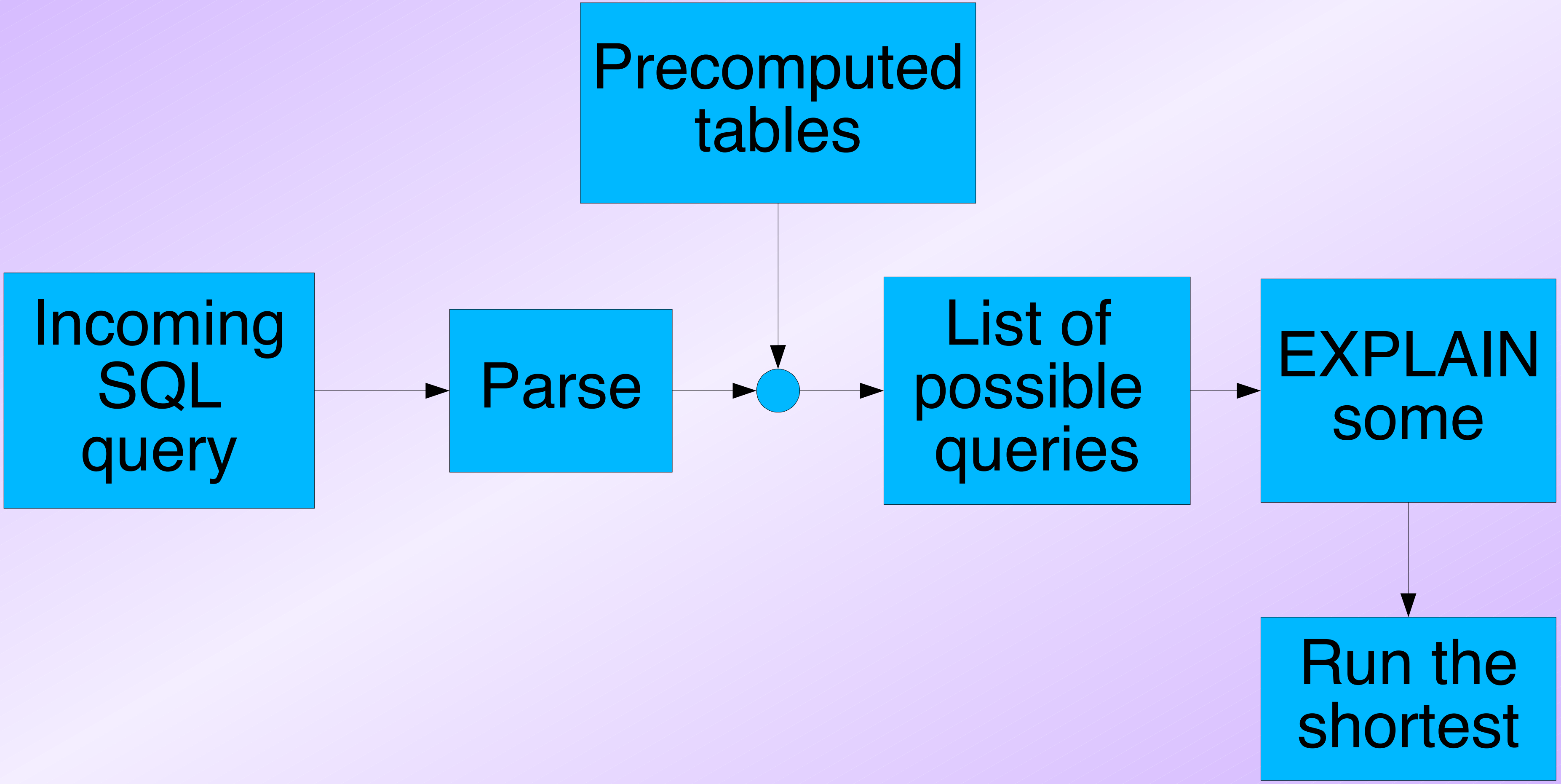
Relational Database

Master
tables

Precomputed
tables

FlyMine

Query optimisation



O/R Data Warehouse

- No need to design a query optimised schema
- Query optimisation moved away from business model
- Pre-computed tables can be added any time after build – **adapt query optimisation to usage**
- Pre-compute template queries

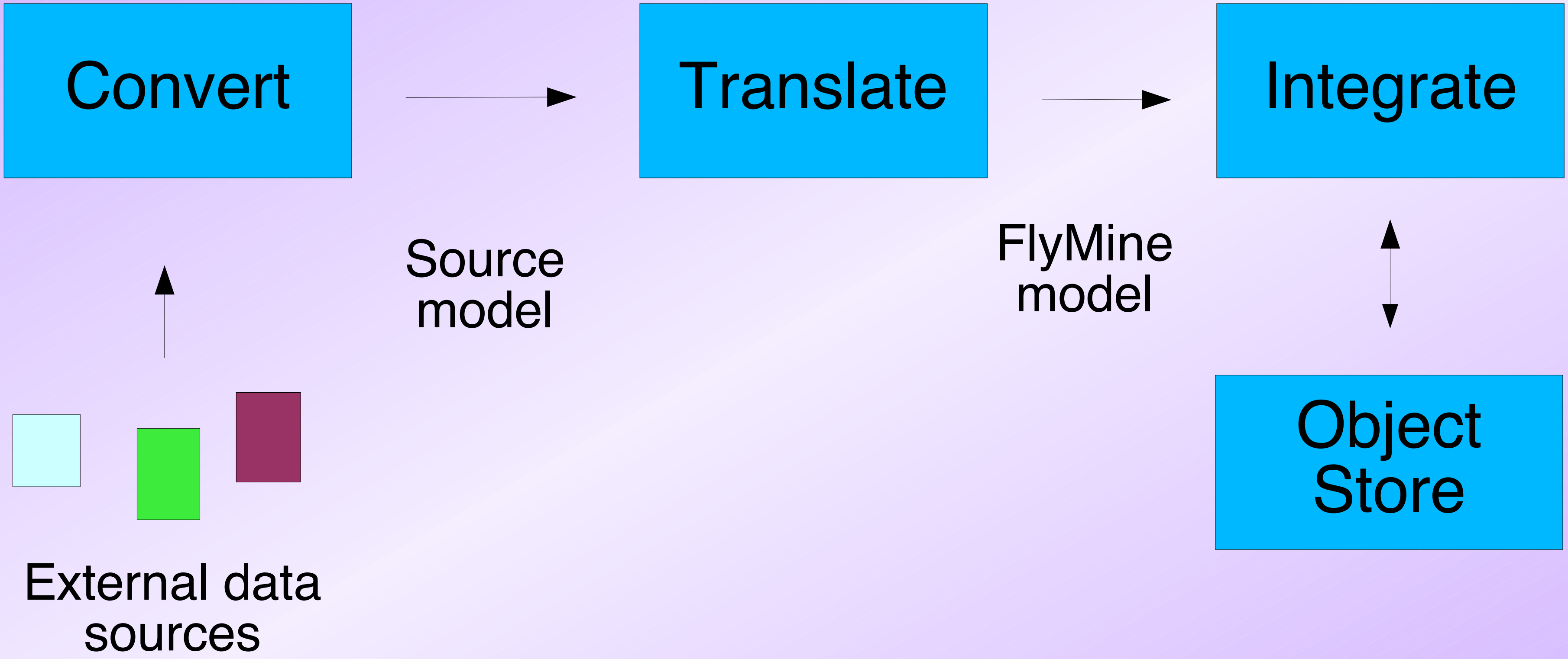
FlyMine – biological model

- Avoid creating a “schema of everything”
- Model based on SOFA
- Data sets add classes to model
  - e.g. orthologue data adds Orthologue/Paralogue classes
- Data sets add fields to model
  - e.g. ensembl adds length field to Contig

FlyMine – data sets

- Based on standards
  - PSI, MAGE, GFF3, DAG
- And common formats
  - Ensembl, Uniprot XML, Inparanoid output
- Configure generic code, handlers
- Very little is organism specific

Data loading pipeline



Convert

Translate

Integrate

Source model

FlyMine model

Object Store

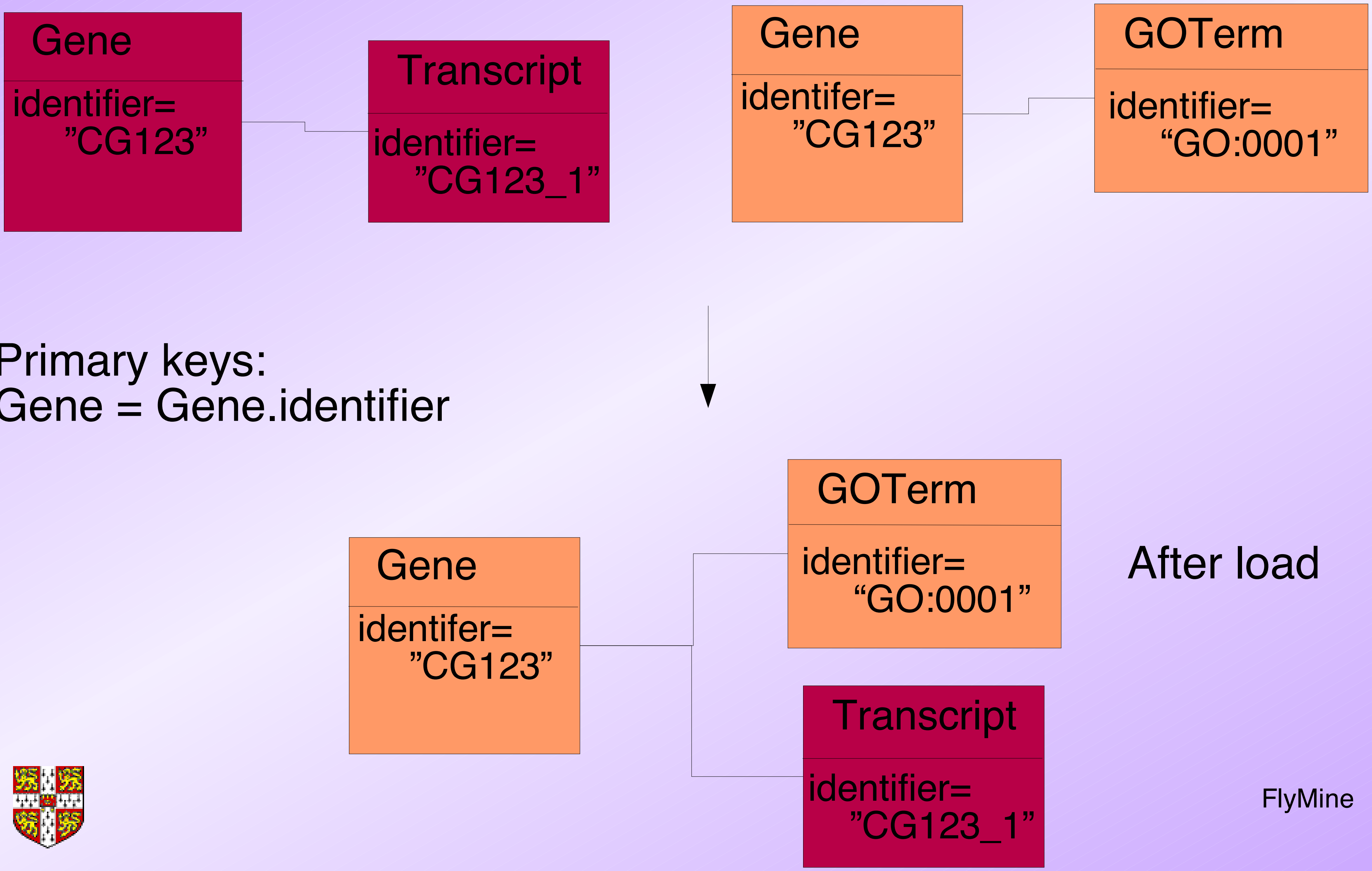
External data sources

Integration

- Define “primary keys” for each class
- Define “primary keys” that each source uses
- Define priorities for fields from different sources
- IntegrationWriter keeps track of originating sources for each field of each object

New objects

Currently in database



Gene

identifier=
”CG123”

Transcript

identifier=
”CG123_1”

Gene

identifer=
”CG123”

GOTerm

identifier=
“GO:0001”

Primary keys:
Gene = Gene.identifier

GOTerm

identifier=
“GO:0001”

Gene

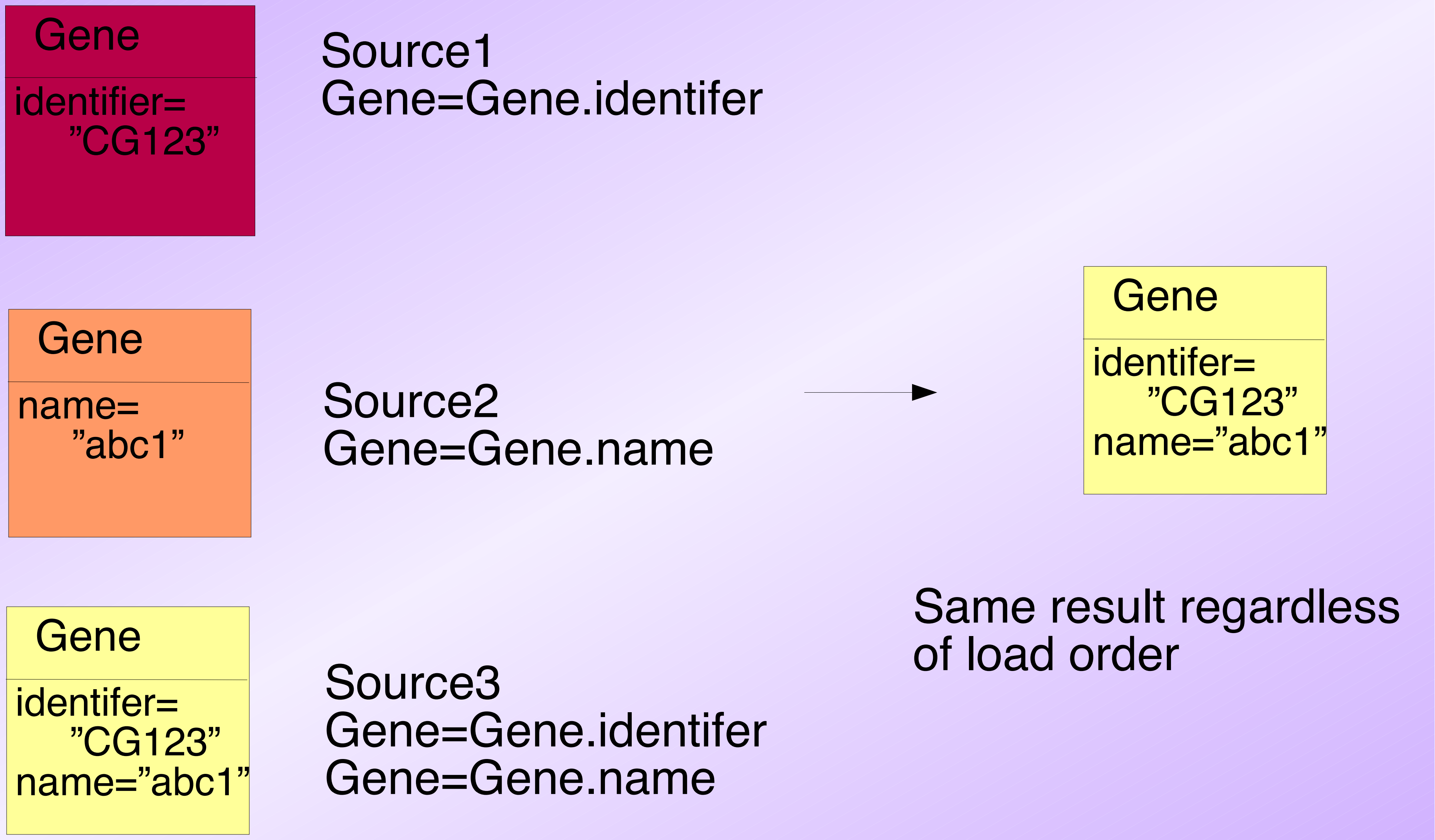
identifer=
”CG123”

Transcript

identifier=
”CG123_1”

After load

FlyMine



Gene

identifier=
"CG123"

Source1
Gene=Gene.identifer

Gene

name=
"abc1"

Source2
Gene=Gene.name

Gene

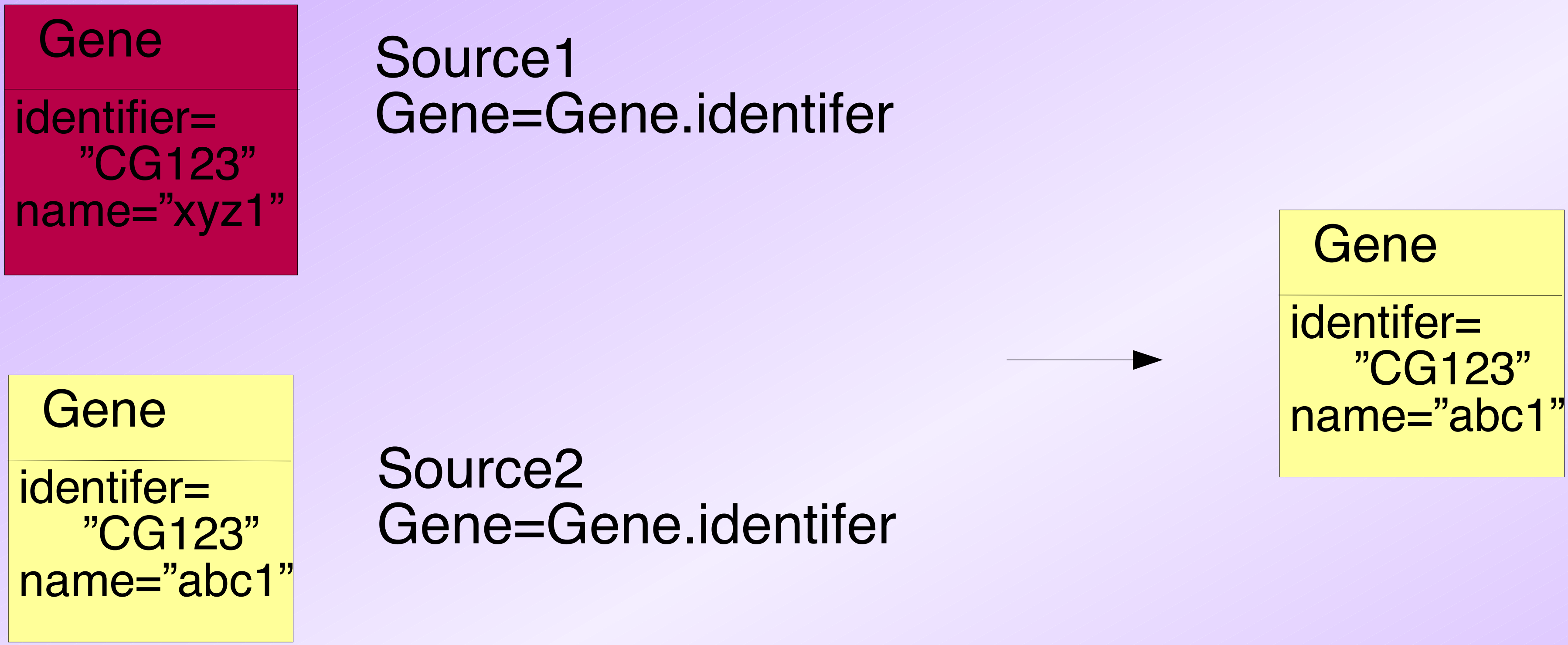
identifer=
"CG123"
name="abc1"

Source3
Gene=Gene.identifer
Gene=Gene.name

Gene

identifer=
"CG123"
name="abc1"

Same result regardless of load order



Gene

identifier=
"CG123"
name="xyz1"

Source1
Gene=Gene.identifer

Gene

identifer=
"CG123"
name="abc1"

Source2
Gene=Gene.identifer

Gene

identifer=
"CG123"
name="abc1"

Same result regardless of load order

Priorities:
Gene.name = Source2, Source1

Acknowledgements

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Gos Micklem

former
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More information at www.flymine.org

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