InterMine
Data Warehouse

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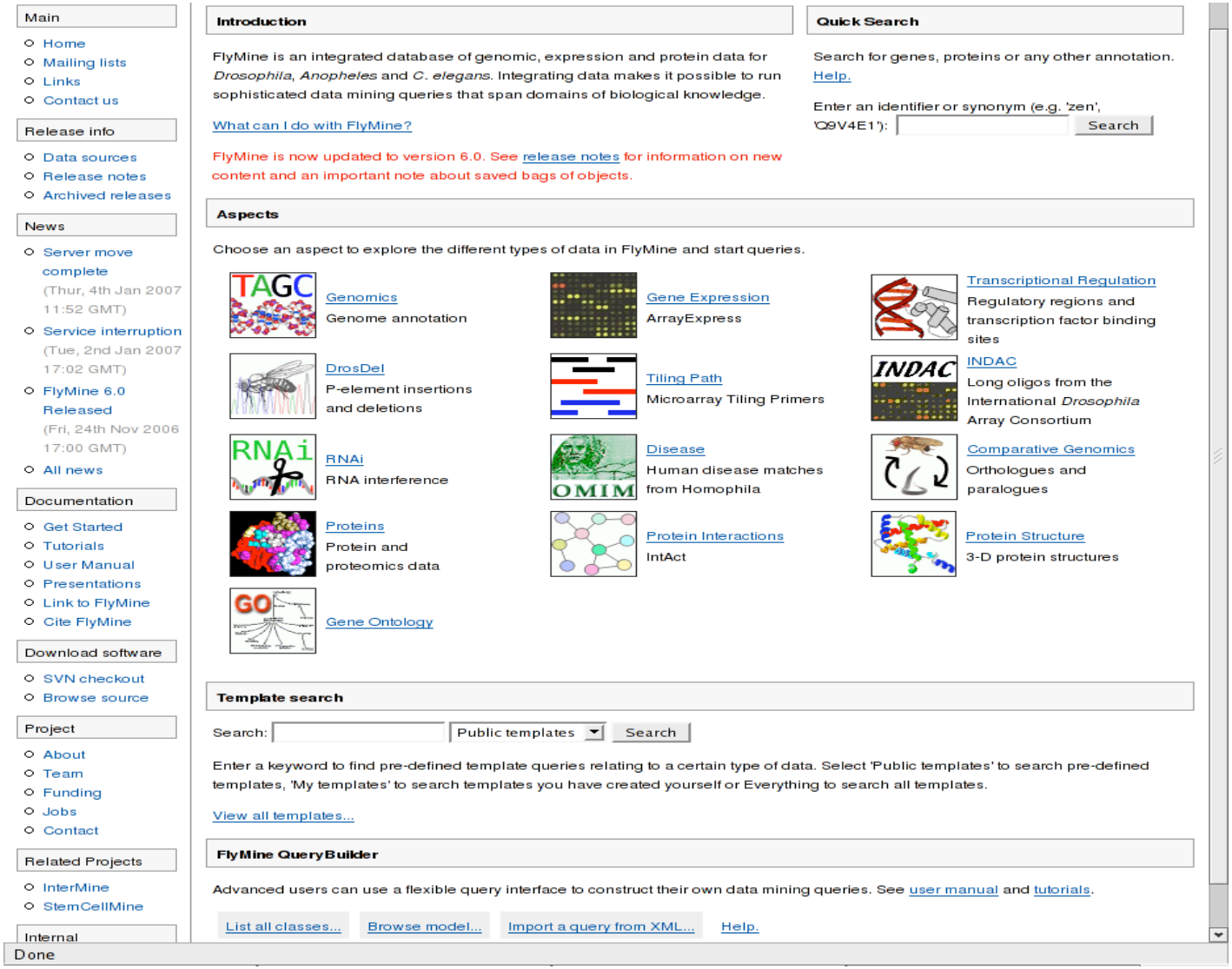
InterMine used to build FlyMine

An integrated database of Drosophila and Anopheles data

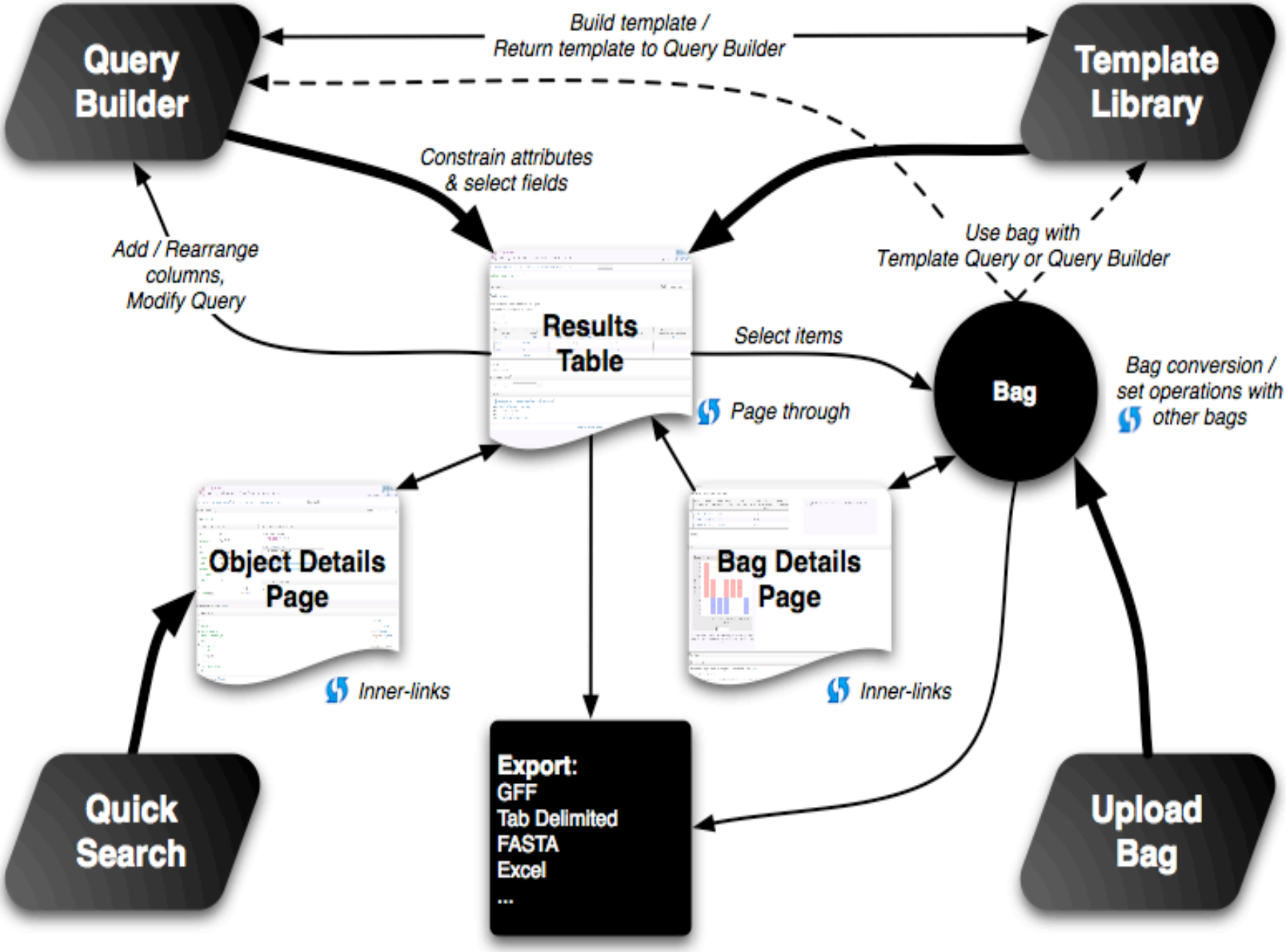


Project Stats

- Team of 7 FTE
  - 5 developers, one sys admin,
  - 1 biologist/ bioinformatician
- Java/ postgreSQL
- SVN: 125,000 lines of code + 57,000 lines of tests
- Started in 2002
- In use by others in Cambridge, Edinburgh, Vienna… + modENCODE DCC if funded
- modENCODE/ Chado

InterMine Guiding Principles

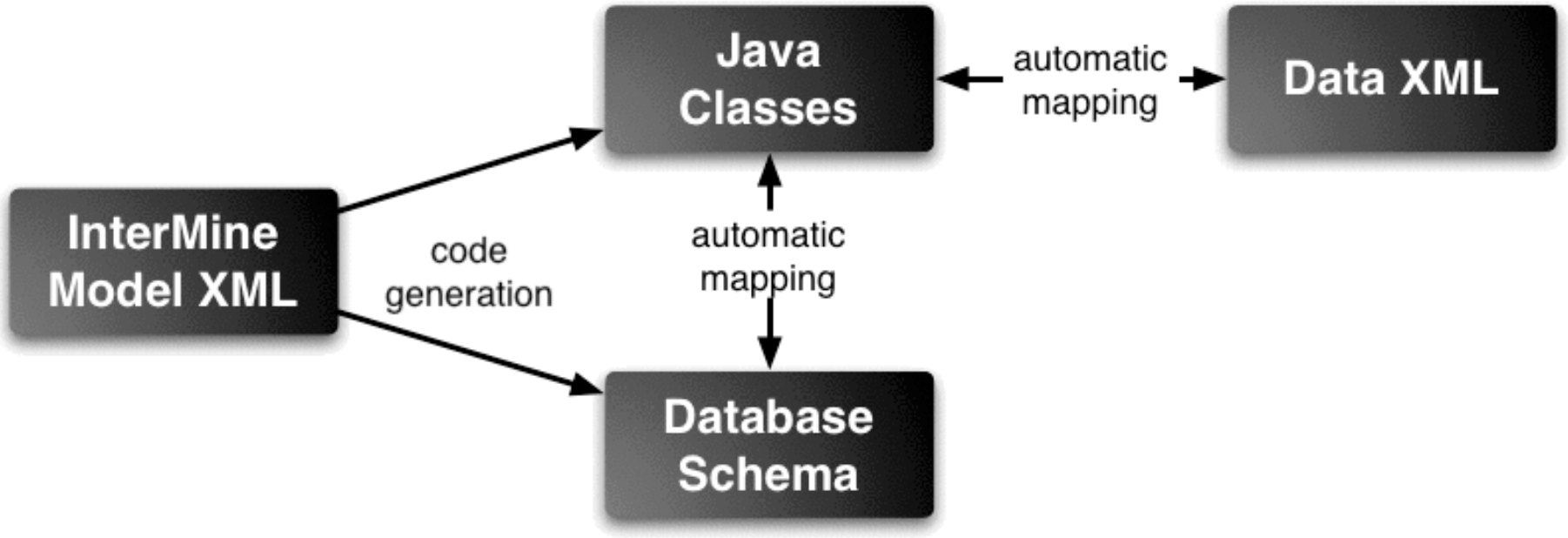
- Open Source
- Generic
- Maximum us of automatic code generation/ testing
- Integrate diverse types of data - standard formats
- Load order independent (fine-grained source priorities)
- Query re-writing: uncouple data model and tuning
- Allow performance tuning of the live database
- Allow domain-specific configuration of the user interface
    - By domain experts not developers
    - Release independently of database
- Scope: small project databases to large scale data warehouses


Query Builder
Build template /
Return template to Query Builder
Template Library
Constrain attributes
& select fields
Add / Rearrange
columns,
Modify Query
Use bag with
Template Query or Query Builder
Results Table
Select items
Page through
Bag
Bag conversion /
set operations with
other bags
Object Details Page
Inner-links
Bag Details Page
Inner-links
Export:
GFF
Tab Delimited
FASTA
Excel
...
Quick Search
Upload Bag

Technical Overview

- Custom Java object/relational system
  - When we started, couldn't select from multiple classes at one time using hibernate.
- Optimised for read-only performance
- Designed for big, complex queries
- Performance optimisation
  - Transparent query re-writing
- Web application - Struts/JSP/Ajax

Code Generation



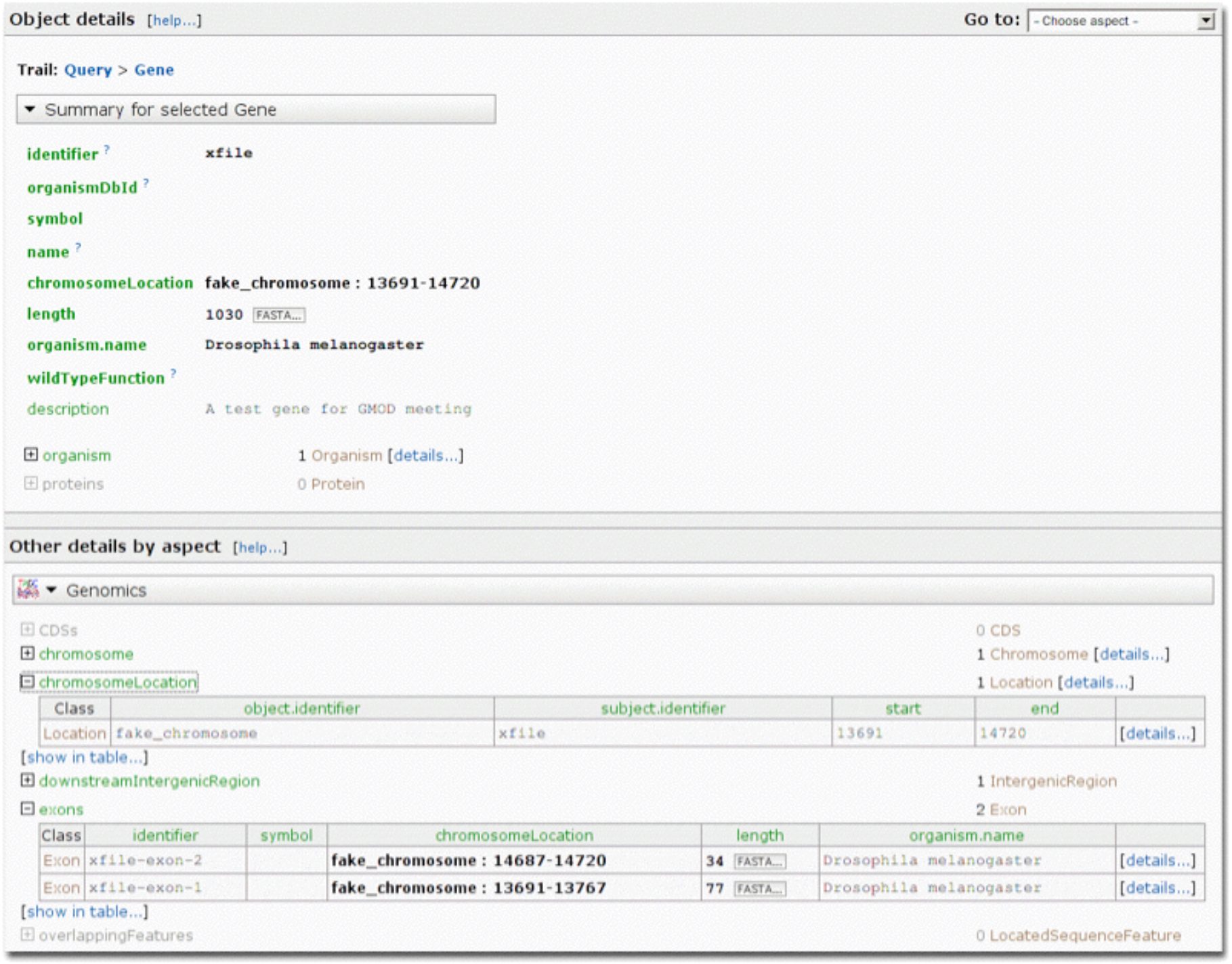
We use SOFA as core data model - similar to Chado.
Added Gene.description, compiled, loaded data (here XML + FASTA), released webapp.

Loading Data

- Read-only in production environment
- Load data from InterMine XML
- Parsers from standard formats
  - e.g. UniProt, GFF3, PSI, FASTA
- Powerful integration system

Example InterMine XML

```
<items>
   <item id="0_3" class=”” 
implements="http://www.flymine.org/model/genomic#Gene">
      <attribute name="identifier" value="xfile" />
      <attribute name="description" value="A test gene for GMOD 
meeting" />
      <reference name="organism" ref_id="0_1" />
      <collection name="transcripts">
         <reference ref_id="0_9" />
      </collection>
   </item>
   <item id="0_1" class="" 
implements="http://www.flymine.org/model/genomic#Organism">
      <attribute name="taxonId" value="7227" />
   </item>
   ...
```



Object details [help...] Go to: - Choose aspect -

Trail: Query > Gene

Summary for selected Gene

identifier ?	xfile
organismDbId ?	
symbol	
name ?	
chromosomeLocation	fake_chromosome : 13691-14720
length	1030 FASTA...
organism.name	Drosophila melanogaster
wildTypeFunction ?	
description	A test gene for GMOD meeting

organism 1 Organism [details...]

proteins 0 Protein

Other details by aspect [help...]

Genomics

CDSs 0 CDS

chromosome 1 Chromosome [details...]

chromosomeLocation 1 Location [details...]

Class	object.identifier	subject.identifier	start	end	
Location	fake_chromosome	xfile	13691	14720	[details...]

[show in table...]

downstreamIntergenicRegion 1 IntergenicRegion

exons 2 Exon

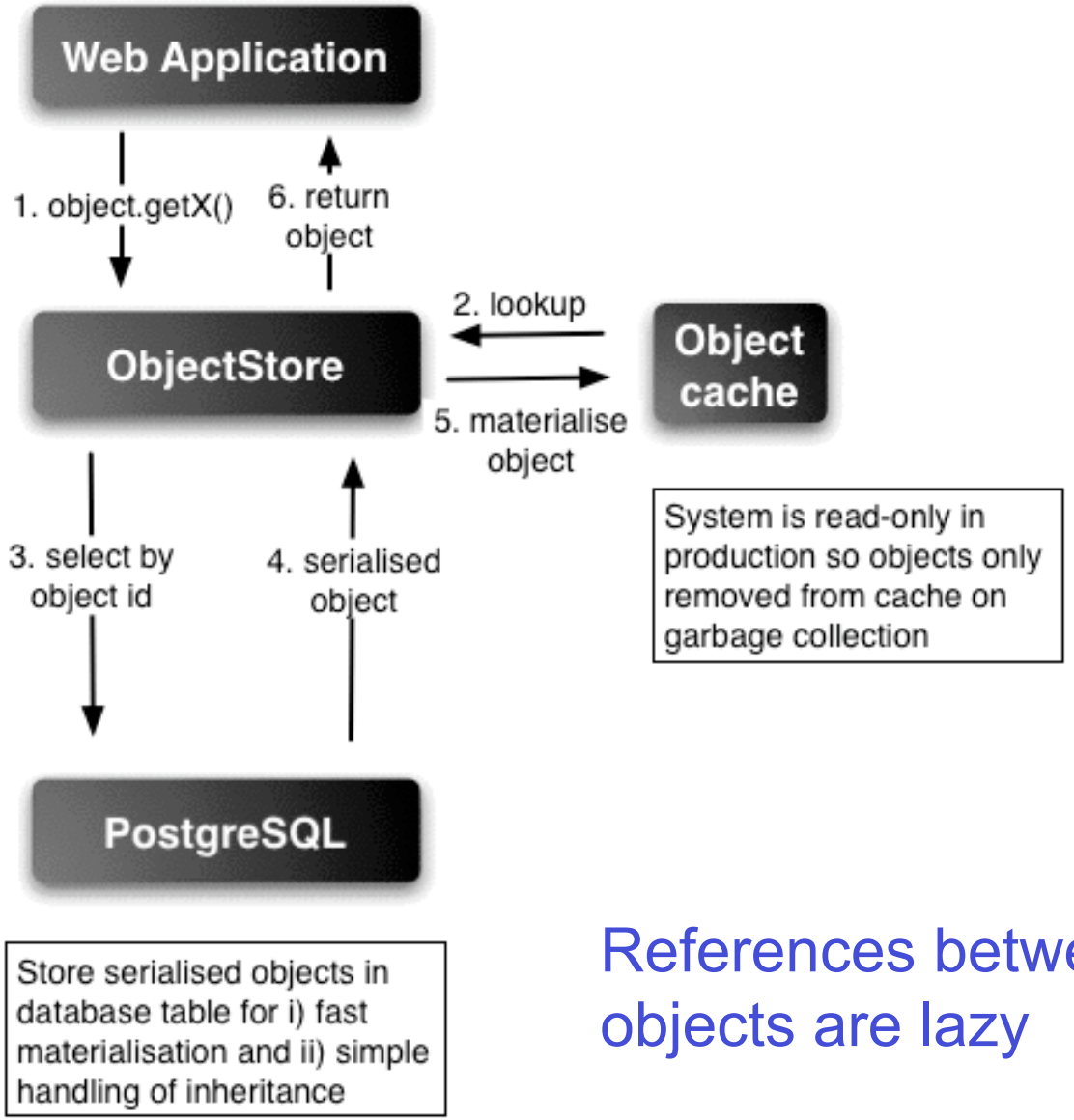
Class	identifier	symbol	chromosomeLocation	length	organism.name	
Exon	xfile-exon-2		fake_chromosome : 14687-14720	34 FASTA...	Drosophila melanogaster	[details...]
Exon	xfile-exon-1		fake_chromosome : 13691-13767	77 FASTA...	Drosophila melanogaster	[details...]

[show in table...]

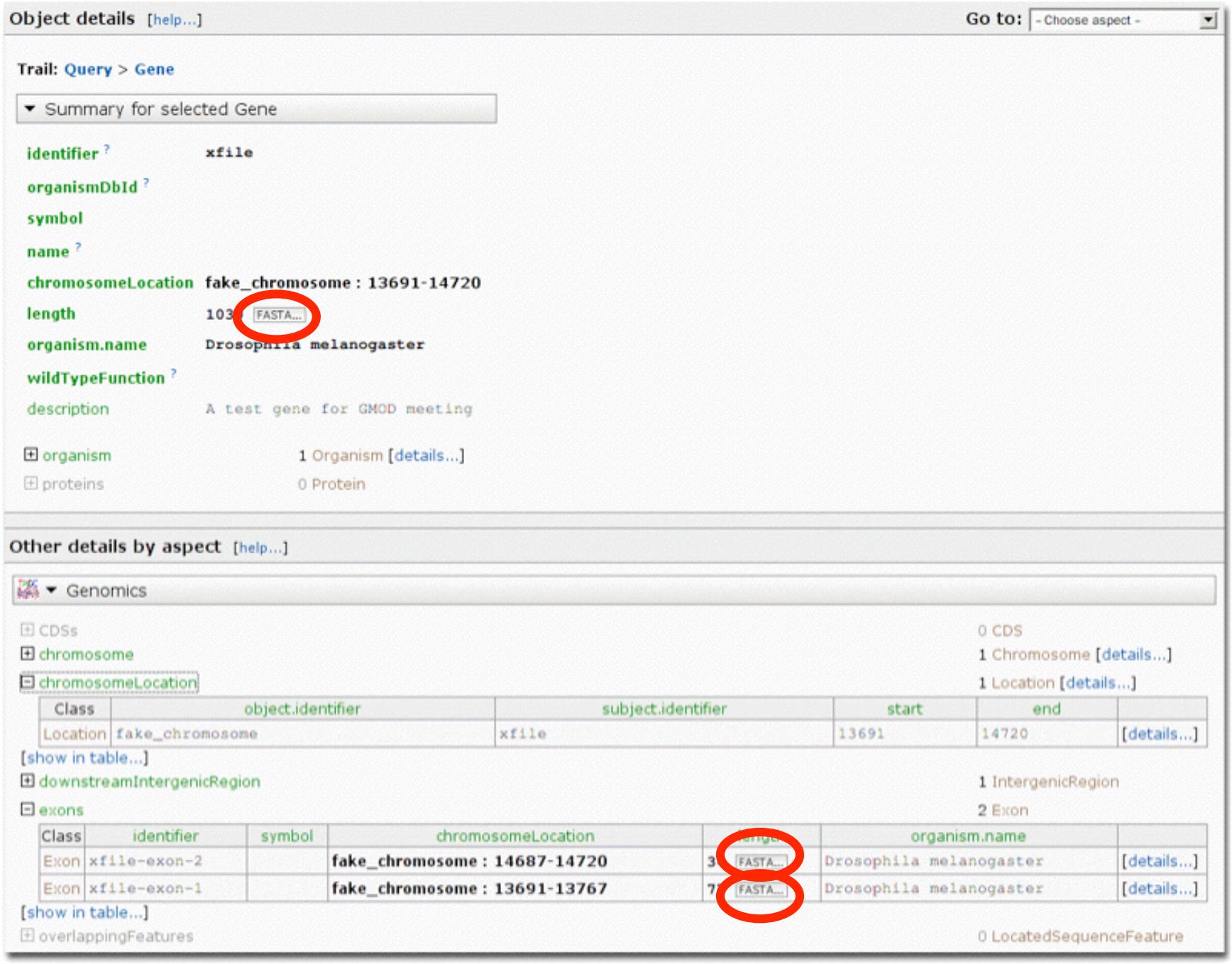
overlappingFeatures 0 LocatedSequenceFeature

Retrieving Objects

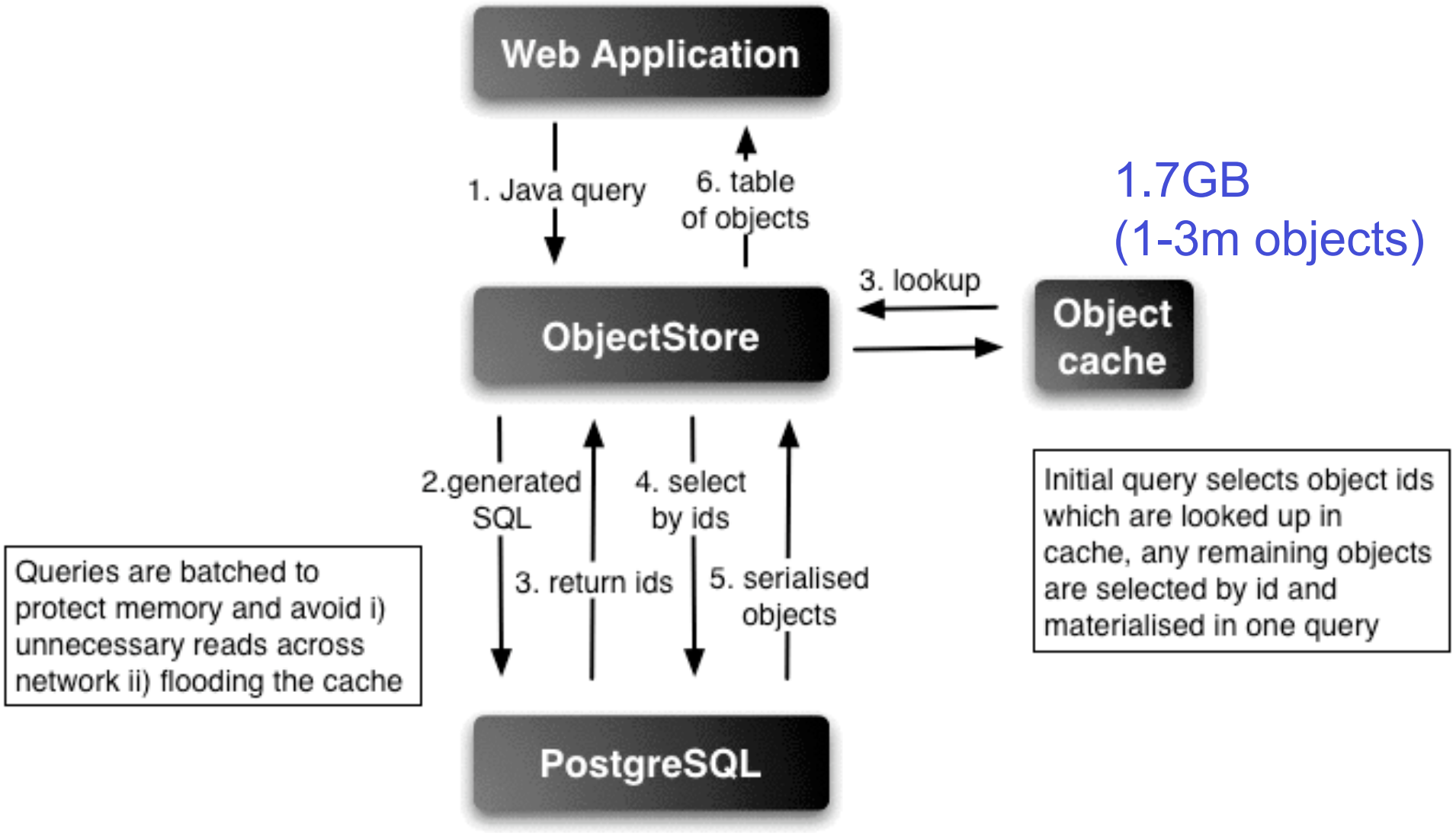
(Unrelated to commercial product)



References between objects are lazy


Object details [help...]
Go to: - Choose aspect -
Trail: Query > Gene
Summary for selected Gene
identifier ? xfile
organismDbId ?
symbol
name ?
chromosomeLocation fake_chromosome : 13691-14720
length 103 FASTA...
organism.name Drosophila melanogaster
wildTypeFunction ?
description A test gene for GMOD meeting
organism 1 Organism [details...]
proteins 0 Protein
Other details by aspect [help...]
Genomics
CDSs 0 CDS
chromosome 1 Chromosome [details...]
chromosomeLocation 1 Location [details...]
Class object.identifier subject.identifier start end
Location fake_chromosome xfile 13691 14720 [details...]
[show in table...]
downstreamIntergenicRegion 1 IntergenicRegion
exons 2 Exon
Class identifier symbol chromosomeLocation organism.name
Exon xfile-exon-2 fake_chromosome : 14687-14720 FASTA... Drosophila melanogaster [details...]
Exon xfile-exon-1 fake_chromosome : 13691-13767 FASTA... Drosophila melanogaster [details...]
[show in table...]
overlappingFeatures 0 LocatedSequenceFeature

Executing a Query



InterMine Queries

Quicksearch

```
Java API:
  Query q = new Query();
  QueryClass qcObj = new QueryClass(Gene.class);
  q.addFrom(qcObj);
  q.addToSelect(qcObj);

  QueryField qf = new QueryField(qcObj, "identifier");

  SimpleConstraint sc = new SimpleConstraint(qf, ConstraintOp.MATCHES, new
        QueryValue("x-%"));
  q.setConstraint(sc);

IQL:
  SELECT DISTINCT a1_.identifier AS a2_ FROM org.flymine.model.genomic.Gene
AS a1_ WHERE a1_.identifier LIKE 'x-%'


Perl API:
  my $genes = InterMine::Gene::Manager->get_genes(query => [
                                identifier => { like => 'x-%' },],);
```

Larger Query

Results for template: **Gene --> Transcripts and exons + chromosomal locations and lengths.**

For a particular gene, list the transcripts and exons and show the chromosomal locations and lengths of the transcripts and exons.

Page size 10

First Previous Next Last

Gene > identifier	Gene > transcripts > identifier	Gene > transcripts > chromosome > identifier	Gene > transcripts > chromosomeLocation > start	Gene > transcripts > chromosomeLocation > end	Gene > transcripts > length	Gene > transcripts > exons > identifier
CG2328	CG2328-RA [MRNA]	2R	5491054	5492592	1468	CG2328:1
CG2328	CG2328-RA [MRNA]	2R	5491054	5492592	1468	CG2328:2

Displaying all 2 rows

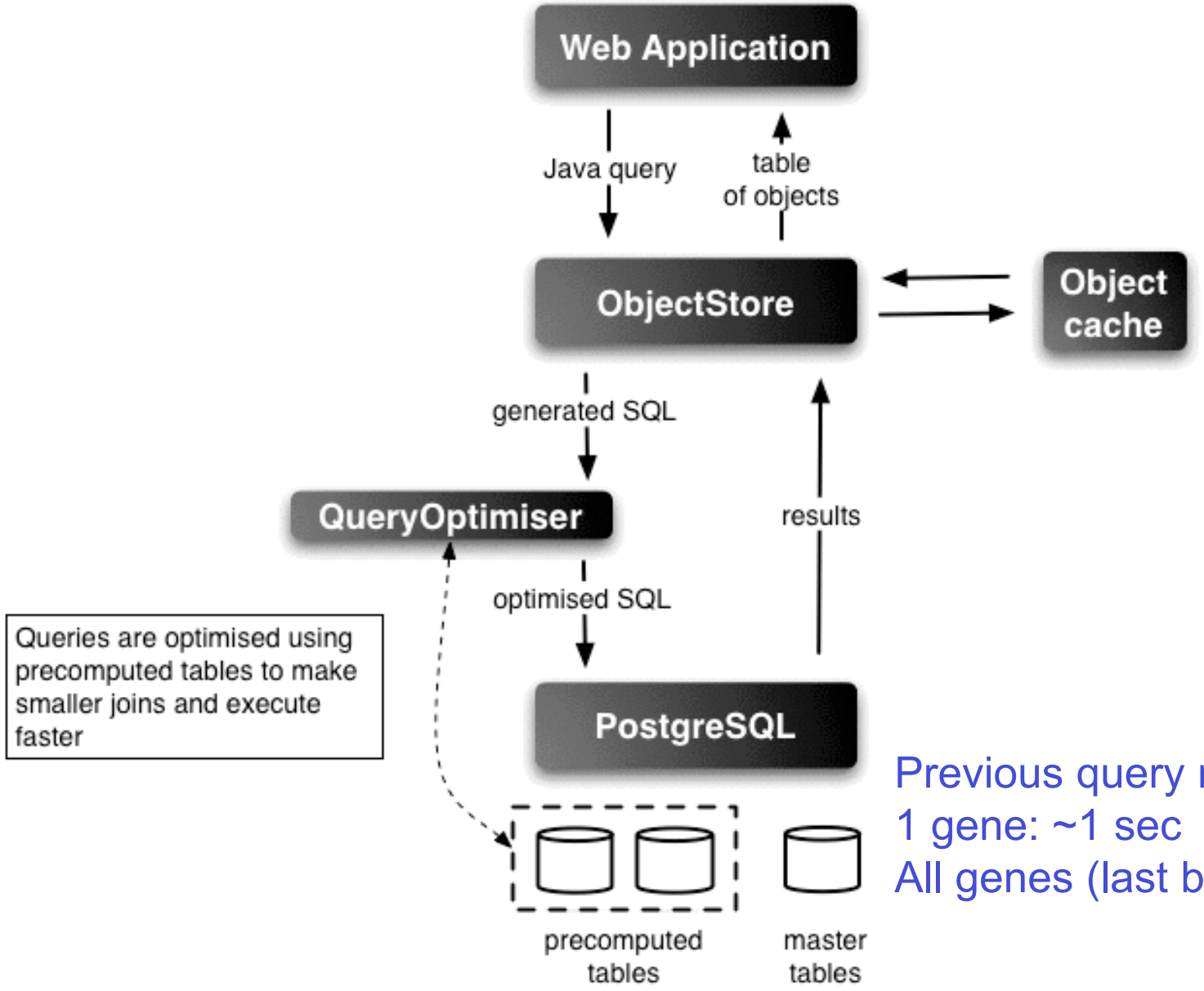
First Previous Next Last

- Joins 7 classes - all are on select list of query
- Here, one gene (two rows) ~2 seconds
- All genes, all organisms ~300,000 rows in 36 sec (not via
- pre-computation)

```
public class BakeOff {
    public static void main(String[] args) throws Exception {
        // code to get the "xfile" gene
        ObjectStore os = ObjectStoreFactory.getObjectStore("os.production");
        Query q = new Query();
        QueryClass qcObj = new QueryClass(Gene.class);
        q.addFrom(qcObj);
        QueryField qf = new QueryField(qcObj, "identifier");
        q.addToSelect(qf);
        SimpleConstraint sc = new SimpleConstraint(qf, ConstraintOp.EQUALS, new QueryValue("xfile"));
        q.setConstraint(sc);
        System.err.println("query: " + q);
        Results res = os.execute(q);

        // a Results object is a List of Lists
        List rr = (List) res.get(0);
        Gene gene = (Gene) rr.get(0);

        System.err.println ("symbol: " + gene.getIdentifier());

        // a BioEntity in FlyMine has a collection of Synonym objects -
        // we need Synonym.value for each Synonym
        System.err.print ("synonyms: ");
        Iterator synIter = gene.getSynonyms().iterator();
        while (synIter.hasNext()) {
            Synonym syn = (Synonym) synIter.next();
            System.err.print (syn.getValue() + ' ');
        }
```

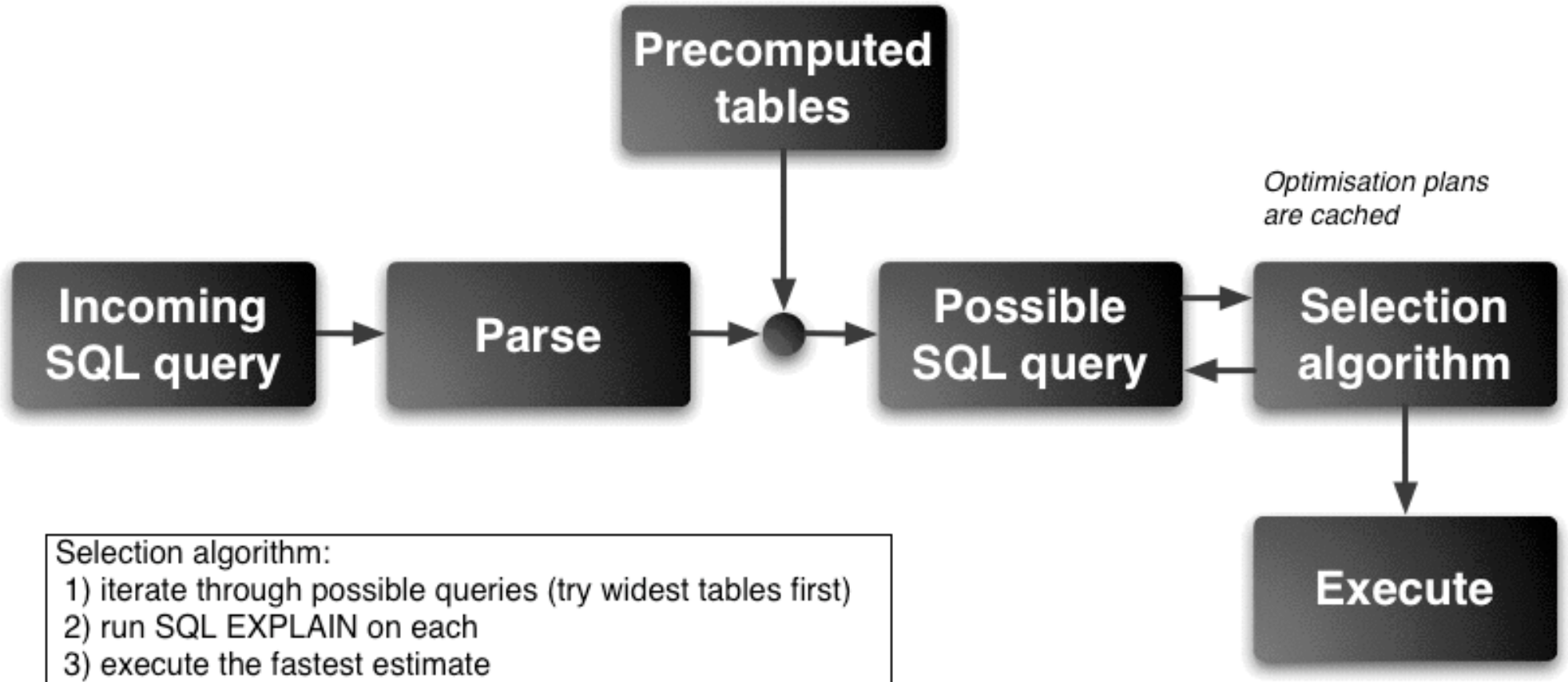
```
System.err.println ("description: " + gene.getDescription());

        // get the class name, but we already know that the gene is a Gene
        System.err.println ("type: " + gene.getClass().getName());

        // make a List from a the Set of exons for this Gene
        List exons = new ArrayList(gene.getExons());
        Exon exon1 = (Exon) exons.get(0);
        Exon exon2 = (Exon) exons.get(1);

        // get the start and end via the Location object
        System.err.println ("exon1 start: " + exon1.getChromosomeLocation().getStart());
        System.err.println ("exon1 end: " + exon1.getChromosomeLocation().getEnd());
        System.err.println ("exon2 start: " + exon2.getChromosomeLocation().getStart());
        System.err.println ("exon2 end: " + exon2.getChromosomeLocation().getEnd());

        // write out the first cds
        List cdss = new ArrayList(gene.getCDSs());
        FlyMineSequence flymineSequence = FlyMineSequenceFactory.make((CDS) cdss.get(0));

        // use BioJava to output the sequence
        Annotation annotation = flymineSequence.getAnnotation();
        annotation.setProperty(FastaFormat.PROPERTY_DESCRIPTIONLINE,
                               gene.getIdentifier() + " cds");
        SeqIOTools.writeFasta(System.err, flymineSequence);
    }
}
```

Query Optimisation



Previous query now:
1 gene: ~1 sec
All genes (last batch): ~1sec

Query Optimisation



Selection algorithm:
1) iterate through possible queries (try widest tables first)
2) run SQL EXPLAIN on each
3) execute the fastest estimate

Heuristics to improve performace:
a) avoid optimising very simple queries
b) run immediately if a one table query found
c) minimise number of EXPLAINs needed
d) avoid EXPLAINs on very large joins
e) bail out if taking too long

Query Optimisation - implications

- Performance optimisation not tied to schema design
- Can adapt performance optimisation to usage
- Template queries pre-computed (40 run per gene details page - renders in seconds)

Future Directions

- Import of any Chado database
- Improvements to build process
- User groups for sharing of templates/ bags
- Public bags/ tagging
- Relative genome coordinate based queries
- REST-style web services from templates
- Elaboration of bag details page:
  - graphical widgets, bag comparison, protein interaction graph functions, gene expression, generalised GoSTAT, chromosome distribution, enriched publications…

Cons

- slow build times (which are getting better)
- lots of disk space but it's a data warehouse and disks are cheap
- configuration is still a bit complicated, but improving fast
- we can't do much with locations yet except query starts and ends, although we do have the overlappingFeatures collections now...
- export is still limited to tab or comma delimited or FASTA
- we don't handle sequence very well:
  e.g. each chromosome sequence is stored in one big text field in PostgreSQL
- we can't do queries involving sizes of collections of things (e.g. find the genes with only 1 transcript)

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www.flymine.org www.intermine.org

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Bioinformatics Position in Berkeley

www.berkeleybop.org/jobs

- Work with Chris Mungall and Gos Micklem on Chado and InterMine
- Gather requirements and design data models for novel, high-throughput, large-scale experiments
- Build a workflow system, a la UCSC, for data submission
- Integrate data from WormBase and FlyBase
- Integrate database with GBrowse, BioMart, and other software
- Applications and questions may be sent to Nicole Washington (nlwashington@lbl.gov)