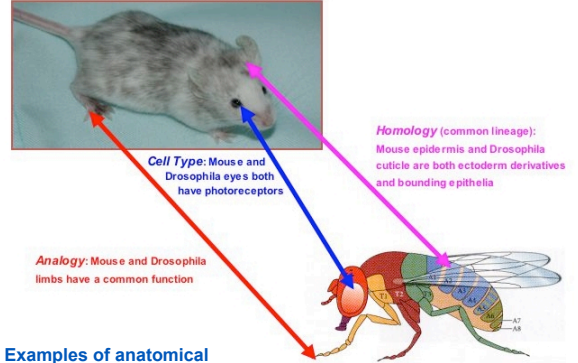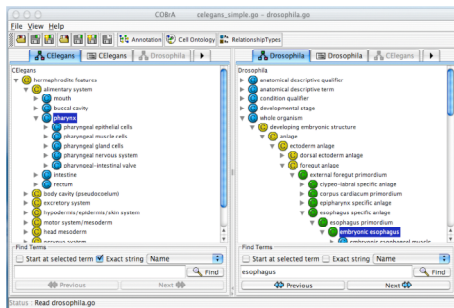# XSPAN
A Cross Species Anatomy Network

Introduction

One surprising fact to emerge from the molecular revolution is that organisms are far more similar at the genetic level than previously thought. This means that we can use knowledge about one organism to understand another. XSPAN aims to provide this knowledge.

The project aims to link the detailed anatomies of the main model animals (human, mouse, Drosophila, C elegans, zebra fish). Tissues will be linked on the basis of:

- analogy and homology (evolutional, lineage and functional data)
- common cell-types (using a new cell-type ontology)
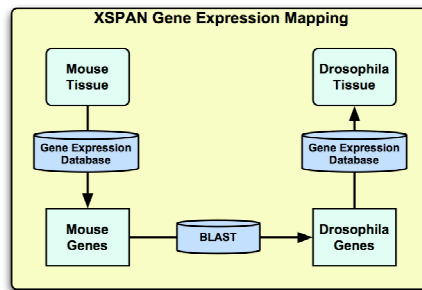- molecular similarities (based on common gene-expression patterns)
- terminology

Cell Type: Mouse and Drosophila eyes both have photoreceptors

Homology (common lineage): Mouse epidermis and Drosophila cuticle are both ectoderm derivatives and bounding epithelia

Analogy: Mouse and Drosophila limbs have a common function

Examples of anatomical relationships between mouse and Drosophila

Expert based mapping
Using COBrA to make the link between the pharynx of C elegans with the Drosophila embryonic esophagus.

XSPAN Gene Expression Mapping

Mouse Tissue → Gene Expression Database → Mouse Genes → BLAST → Drosophila Genes → Gene Expression Database → Drosophila Tissue

Gene expression based mapping
A user will, for example, be able to find those genes that a tissue of interest expresses (from the relevant database). This information can then be used to suggest novel genes that linked tissues in other organisms might express.
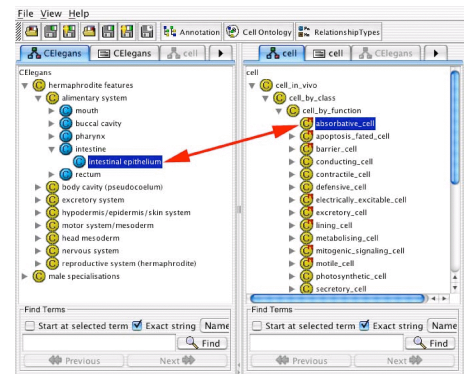

Cell-type based mapping
COBrA being used to make the link between the intestinal epithelium of C elegans anatomy ontology with the absorptive epithelium of the cell-type ontology.

Producing this system requires us to confront a series of problems in ontologies, data warehousing, anatomical relations and data formats.

Overview

Diagram showing a conceptual view of proposed system.
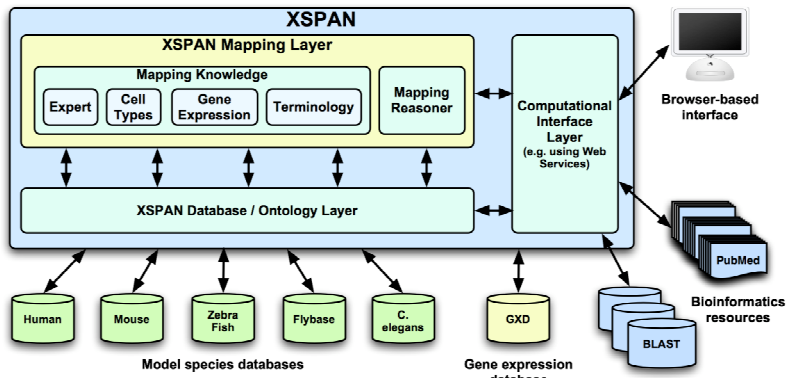
The system will:

- import existing community anatomy databases into the XSPAN data / knowledge base
- include additional mapping knowledge (from domain experts)
- incorporate domain knowledge consisting of explicit cross-species tissue mappings and mapping roles based on tissue names and tissue properties
- support a data warehouse approach for database integration
- be built around user friendly interfaces (e.g. GUIs, Web Services)

XSPAN Project Team

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XSPAN
## A Cross Species Anatomy Network
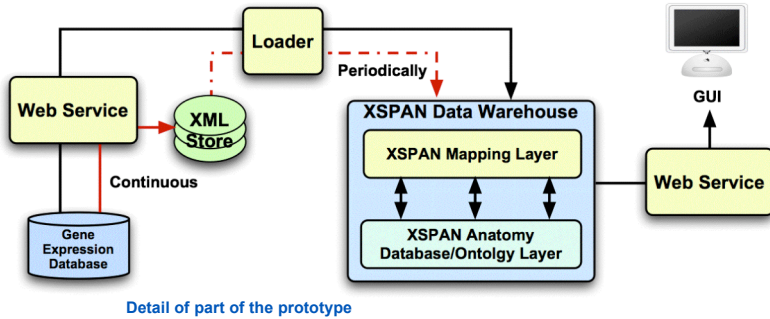
Prototyping

Detail of part of the prototype

An initial prototype, using Java and a IBM's DB2 relational database, has been developed and successfully tested.

- XML store allows computation of incremental changes (deltas)
- the deltas are used for efficient maintenance in the XSPAN data warehouse

Other points relating to the prototype:

- producing a data warehouse to integrate the anatomy databases
- establishing the concept of equivalence classes with the DB
- establishing access to the literature via PubMed
- developing GUIs using Java as a separate layer
- developing middleware to communicate with the databases and the data warehouse
- ensuring that other users will be able to adapt existing GUIs/develop new GUIs for specialist applications in future
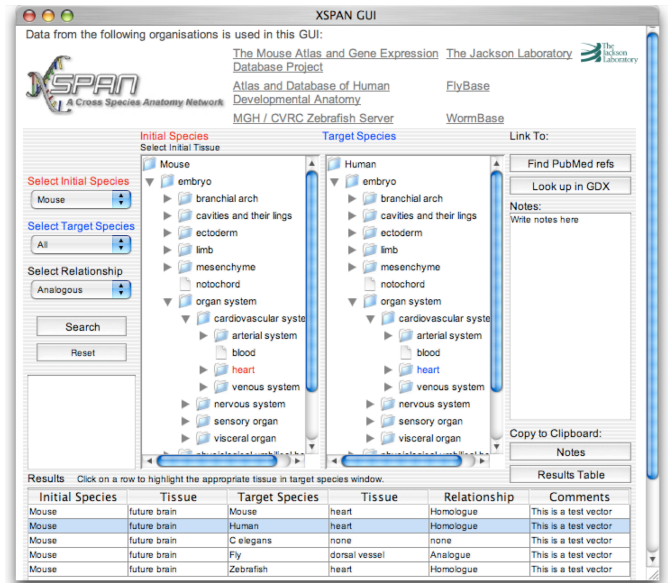
XSPAN GUI Applet
Allows anatomy hierarchies from different species to be compared. Tissues in one species can be selected, and related tissues in another species identified.
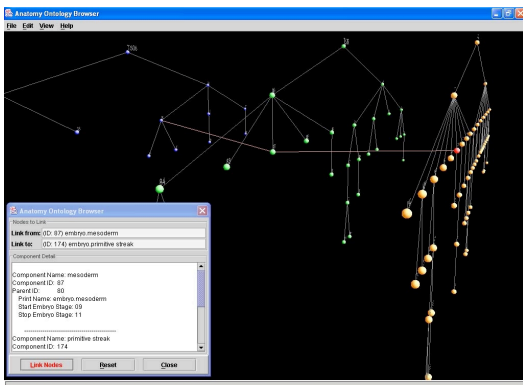
3-D plots
Anatomy Ontology Browser can plot tissue hierarchies as 3D, radial and other plots. Use of such visualisations is undergoing evaluation.

In addition, other ways of visualising the anatomy data are being evaluated, including the use of 3D trees and radial plots.

Ontologies

"Part-of" relations are central to anatomy, but the definition, formalisation and use of "part-of" in anatomy ontologies is problematic. A survey of existing formal approaches and use of part-of in the Open Biological Ontologies (OBO) anatomies of model species has been undertaken. Based on this analysis, we have proposed a minimal ontology for anatomy which is expressed in the Semantic Web languages - RDFS and OWL-Full.

An Example: the definition of partOf in OWL

```
<gowl:PartOfProperty rdf:ID="partOf">
<rdfs:domain rdf:resource="http://www.aiai.ed.ac.uk/resources/go/go-owl-full#ObjectClass"/>
<rdfs:range rdf:resource="http://www.aiai.ed.ac.uk/resources/go/go-owl-full#ObjectClass"/>
<rdfs:subPropertyOf rdf:resource="http://www.aiai.ed.ac.uk/resources/go/go-owl-full#parts"/>
<rdfs:comment>
partOf is a class-level relation between the Part-Class and the Whole-Class.
The intended interpretation is defined by the following KIF axiom:
(<=> (and (partOf Part-Class Whole-Class) (classDefinition Part-Class Whole-Class)) (forall(?w)
(implies (type ?w ?Whole-Class) (exists(?p) (and(type ?p ?Part-Class) (isProperPartOf ?p ?w))))))
```

Ongoing and Future Work

- access to multiple gene expression databases
- anatomy based access to PubMed
- exploit formal ontology languages (OWL-Full) and reasoners in establishing matches
- terminology-based mapping
- text mining for tissue mapping
- evaluation of different visualisation models
- further user testing

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