



## Introduction

The overall objective of XSPAN is to support cross-species access to tissue-based genetic information through the development of an internet-based cross-species anatomy network, i.e. a cross-species anatomy ontology system.

The system will provide interoperability between anatomy databases of key model embryos which will, in turn, facilitate access to gene expression and other tissue-based data across species, and to other genomic and proteomics resources.

XSPAN is a joint project between the *School of Mathematical and Computer Sciences at Heriot-Watt University*, and the *Divisions of Biomedical Sciences and Informatics at the University of Edinburgh*.

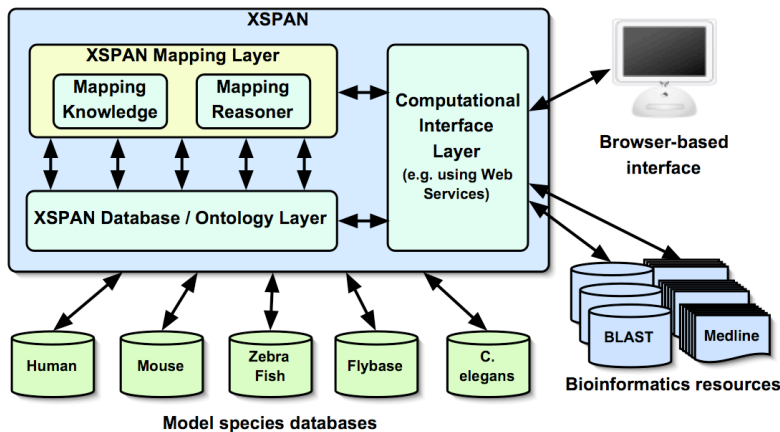
## Motivation

The close relationship between gene homologues from even distantly related species has been known for some time. There are also similarities in the expression pattern of gene homologues during development.

Computational tools exist for suggesting sequence homologies, and they can be used in querying genetic databases. However it is not yet possible to query gene expression databases on the basis of tissue homologies as there are currently no ontologies incorporating knowledge of structural and tissue-based anatomical relationships among the core model species.

## Overview

Diagram showing 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
- explore use of formal ontology languages (DAML+OIL) and reasoners (FaCT)
- involve study of terminology issues
- support a data warehouse approach for database integration
- be built around user friendly interfaces (e.g. GUIs, Web Services)

## Funded by:



biotechnology and biological sciences  
research council

### XSPAN Project Team

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## Requirements Analysis

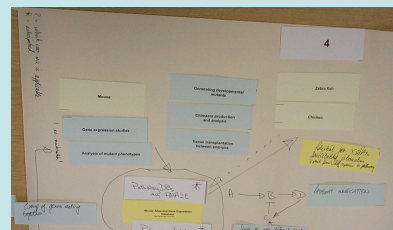
Extensive User Requirements Analysis for the proposed system is being undertaken by the project team.

Techniques being used to elicit the nature of the tasks and the ways they are carried out by users include:

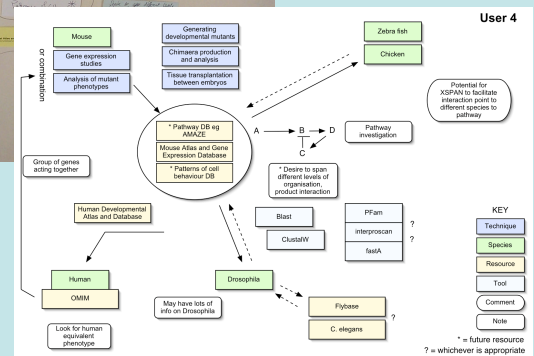
- expert review by biologists, bioinformatics, database and HCI specialists
- cognitive walkthroughs by users and experts
- user questionnaires
- card sorting - with biologists and bioinformatics experts

An example of results from a card sorting exercise:

### Typical card sort result



... rendered as a diagram

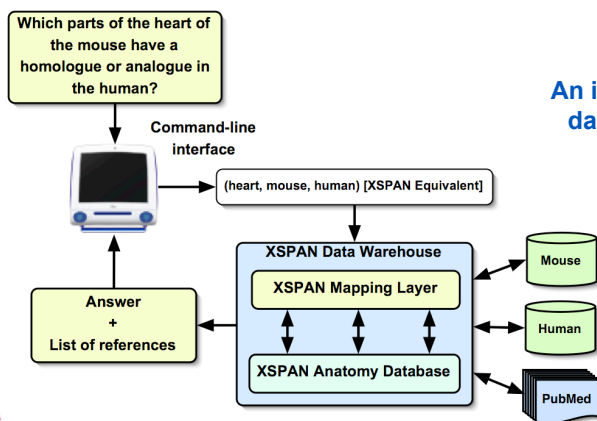


### Key Objectives

- identification of user groups and their requirements
- interoperability requirements with other bioinformatics systems
- definition of tissue equivalence across species, e.g. based on homology and analogy

## Early Prototyping

Outline of early prototype:



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

- data warehouse integrating anatomy databases
- abstract concept of equivalence classes implemented in DB
- linked with PubMed
- queries in extension of PubMed query syntax
- hierarchical nature of anatomy data leads to transitive closure queries in relational database

The prototype is being further developed by the addition of a Graphical User Interface, and expansion of the bioinformatics resources linked to.



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