The Edinburgh Mouse Atlas and Gene-Expression Database:
A Spatio-Temporal Database for Biological Research

Albert Burger[*†], Richard Baldock[*], Yiya Yang[*],
Andrew Waterhouse[*], Derek Houghton[*], Nick Burton[*], Duncan Davidson[*]
Human Genetics Unit, Medical Research Council, Edinburgh

Abstract

The Edinburgh Mouse Atlas Project (EMAP) has developed a digital atlas of mouse development which provides a bioinformatics framework to spatially reference biological data. The EMAP core database contains 3D grey-level reconstructions of the mouse embryo at various stages of development [3], a systematic nomenclature of the embryo anatomy, and defined 3D regions (domains) of the embryo.

The reconstructions define a spatial framework for mapping data. Software has been developed to re-align serial sections and create a 3D voxel model of a mouse embryo which can be resectioned at any arbitrary 3D orientation and position so that experimental data can be mapped onto it [2]. The anatomical nomenclature is used as a controlled vocabulary for annotating and describing gene-expression patterns and is currently organised as a "part-of" hierarchy. The notion of groups *of anatomical terms is used to support alternative structuring of the hierarchy. Anatomical domains are defined 3D regions and provide the mapping between the voxel model and the anatomical terms in the nomenclature.*

Data from an in-situ *gene-expression database is spatially mapped onto the atlas allowing the users to query gene-expression patterns using the 3D embryo model as a reference. The mouse atlas and gene-expression databases are publicly accessible through a set of Web-based tools, which also provide some level of integration with other bioinformatics resources on the Internet, such as the Mouse Genome Informatics (MGI) database at the Jackson Laboratory, USA.*

The system consists of a set of tools and databases, some of which reside locally on the Mouse Atlas hosts, others are remote. The development of tools has been separated from the database side through a layered software architecture approach. The middleware layer is primarily CORBA-based, but also makes use of Java servlets. Data is primarily stored in an object-oriented database system (ObjectStore), though the anatomical nomenclature is also exported in XML and GO formats. The voxel models and the underlying anatomy data are fairly static, therefore users can obtain a version of it on CD, thus reducing much of the network overhead required when accessing the voxel models and the anatomical data. The Proxy design pattern [1] has been used in the design of remote client software access to local and centrally stored data.

As a public bioinformatics resource, the Mouse Atlas system must be easily accessible to researchers all over the world, both for submission of data, e.g. gene-expression patterns, and for querying data. Hence, interoperability is a key issue. At the tools level this is achieved through the use of Web-based technology, e.g. Web pages with embedded Java applets and Java applications that can be deployed through the Web using Java Web Start technology. At the data level, the project makes increasingly use of XML. The project team are also closely monitoring activities relating to the Grid, Semantic Web and formal ontologies (using DAML+OIL), as these technologies may be incorporated into the Mouse Atlas to further develop its interoperability with other resources.

The Mouse Atlas is an on-going research and development project at the Medical Research Council, Human Genetics Unit, in Edinburgh. Access to its databases and further information is available through its Web site (see genex.hgu.mrc.ac.uk).

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[*] Human Genetics Unit, Medical Research Council, Edinburgh

[†] Dept. of Computing and Elec. Eng., Heriot-Watt University, Edinburgh

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