Using controlled language to query atlas space

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Abstract. Specifying regions of interest to search 3D anatomical space can be difficult. Ontology-based queries are often imprecise and return extra (unwanted) data. Drawing regions of interest in graphical 3D representations of a model organism in principle allows for high precision, but user interfaces can be awkward to use and time consuming. In this poster we promote the use of spatial descriptions as an alternative approach. Spatial descriptions take advantage of existing ontological spatial information, such as in anatomy ontologies and spatial relations ontologies, e.g. BSPO, on the one side and the spatial information embedded in voxel-based representations of anatomy and other spatio-temporal data, e.g. in-situ gene expression patterns, on the other.

Keywords: spatial ontologies, biomedical atlases, spatial reasoning, biomedical images

1 Introduction

Many types of biomedical data have a spatial dimension, e.g., tumours, gene expression patterns and phenotypes can all be associated with a location within a particular organism. The spatial dimension can be described at a coarse-grained level by using an anatomy or more precisely with a biomedical atlas [1].

Biomedical atlases provide a geometric model of an organism's space to which data can be mapped. For example, the eMouseAtlas (EMA) [2] provides a series of 3D models for the developmental mouse, with each model tied into a particular developmental stage. The EMAGE embryonic mouse *in situ* hybridisation gene expression database maps the results of experimental procedures onto the appropriate EMA model, describing the space in which a gene is expressed [2]. A user can query EMAGE in a variety of ways: (s)he can ask where a gene is expressed, which genes are expressed in a particular EMAP term or (s)he can draw a space and ask which genes are expressed there.

Querying via the anatomy alone is imprecise as the granularity is restricted by the level of detail in the anatomy. If the intended search space cuts across multiple named regions, every region must be included within the query and thus the space searched is larger than the intended space. Querying by a 2D drawing is imprecise because there is no way of restricting the 3^{rd} axis. Searching via a 3D drawing can be precise, but it is often awkward so it is not used frequently.

An alternative is to use a controlled language description of space as the query. This is more precise than using anatomy terms or a 2D drawing and is easier than drawing in 3D.

2 Spatial Descriptions

A description will define the boundary the of the query space. Descriptions are constructed from a series of statements that include *anatomical_features* and *spatial_relationships*. *anatomical_features* are based on anatomy ontology terms and can be a single structure, a landmark point (e.g., apex of liver) or a fiducial line (line between 2 landmarks). *spatial_relationship*s need to be biologically meaningful, e.g., based on the biological axes. A potential source is BSPO the Biological SPatial Ontology [3]. An example statement: heart is cranial_to the query space. Therefore the query space is caudal_to the heart and all space cranial_to the heart is ruled out.

3 The journey from letters to pixels

For spatial descriptions to be used as a mechanism to query a biomedical atlas there must be a bridge between a textual representation of space and a geometric one; Figure 1 summarises this. Atlases provide a 2D/3D visualisation of (geometric) atlas space and a mechanism to map from the visualisation into the underlying spatial framework. Each pixel/voxel (voxel is a 3D pixel) represents a particular location within atlas space. We require the mapping from a controlled language (i.e., spatial description) into the visual representation of the atlas.

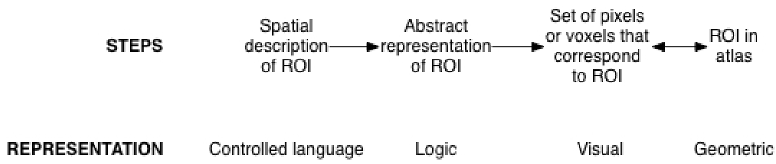

Fig. 1. From controlled language to atlas space.

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