Biomedical information systems are developed in order to navigate, search, structurally represent, and graphically display biological systems (1). By means of biomedical information systems researchers are able to integrate and combine a variety of biological data, analyze relationships between data, plan experiments, and furthermore model biological processes. They are also used in medical therapy planning and in education in biology and medicine. For example there are information systems that support the exploration of biochemical connections and relations such as genome sequence assemblies (2) or differences of genomes of species (3). Another type of information systems represents spatial and spatial-temporal relations, facilitating the analysis of morphology and sometimes also physiology. Here 3d and 4d digital atlases come into play.

Those atlases serve as common spatio-temporal reference systems in which data from different experiments, imaging modalities and scales are integrated. Furthermore, semantic information is linked to the atlas data. This semantic linking requires the registration of the data with an ontology or controlled vocabulary (4). Ontologies increase the potential use and reusability of digital atlases by forming a standardized approach to annotating, analyzing, and querying data (4) (5).

So far, digital atlas generation concentrates on modeling neural structures, such as brains or nerve cords of mammals and invertebrates (4). In order to support the understanding and analysis of structural and functional characteristics of brain structures, ontologies need to fulfil several requirements. An ideal brain ontology would include a complete set of structural parts and nerve types. It would further contain axonal projections between regions and nerve types and it would include morphological, connectional, and electrophysiological properties of neurons. An ideal ontology also would be species-specific (5). Ontologies that describe brain parts, nerves and neural connections have for example been developed for the rat brain (5), the mouse brain (6), and the fly brain (7).

We started to build an ontology of the structures of the honeybee brain in which parts of the bee brain are modeled from wholemounts down to synaptic swellings (boutons) of nerves. We linked our ontology to the surface reconstructions of the honeybee standard atlas (HSB) (8) by assigning the reconstruction’s ID and file name to appropriate parts of the ontology. This step actually enables an ontology-based browsing of the atlas. In a first usage approach of the ontology-linked HSB we addressed the automatic creation of meaningful visualizations. Often the process of creating meaningful and expressive visualizations is time consuming and requires good knowledge of the used visualization software. In our approach all the user has to do is to select a structure to be visualized and to select a predefined query, such as "Show overview". An algorithm then automatically creates a visualization that contains the selected structure highlighted as a focus object and further structures forming the context (9).

In the next steps we want to develop an ontology-based atlas browsing that includes not only reconstructions but also the original data the reconstructions are based on. Further we would like to provide a more visual approach for browsing the ontology. We want to integrate a graph based ontology representation the user can interact with and which presents interesting information in an intuitive way.
References


