Poster presentation

The HoneyBee Standard Brain (HSB) – a versatile atlas tool for integrating data and data exchange in the neuroscience community

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The HoneyBee Standard Brain (HSB) serves as an interactive tool for comparing morphologies of bee brain neurons and relates it to functional as well as biological properties [1]. Recent efforts by several labs have accumulated confocal image stacks from extra- and intracellular stained neurons in the bee central nervous system [2]. We present a pipeline through which confocal images of neurons can be traced and presented in a common space (Figure 1). The first step is an automatic extraction of the neuron's skeleton based on threshold segmentation. In a second step this skeleton can be edited using semi-automatic and interactive tools within Amira's Filament Editor. Hereby, the user is assisted by displaying maximum intensity projections and 3D representations in two separate viewers. Next the skeletonized neuron can be labeled (i.e. annotated) by using multiple sets of hierarchically organized label attributes (Figure 2). Finally, the neuron's topological and metric features can be visualized, statistically analyzed and/or exported to a simulation package such as Neuron.

The neuronal anatomy of the bee brain can be visualized through 3D reconstructions using an ontology those surface-based reconstructions are organized hierarchically into structures and substructures. The ontology also contains relations between the structures and is further linked to our surfaces. By means of the structured and information enhanced data we are able to create semi-automatic
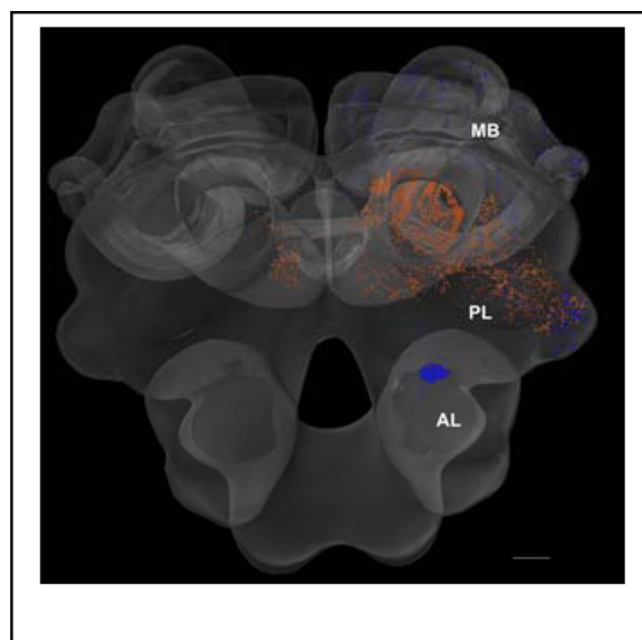
Figure 1
Olfactory (blue) and central (orange) neurons registered into the HSB. MB: mushroom body, AL: antennal lobe, scale: 100 μm.

effective visualizations [3]. In cooperation with the German Neuroinformatics Node (G-Node, http://www.g-node.org) the HSB will be integrated into a new honeybee brain platform for sharing data, models and tools in order to spur scientific productivity across experimental and theoretical disciplines. The future challenge will be to integrate anatomical reference and morphological reconstructions with electrophysiological, imaging and molecular (e.g. gene expression) data in a meaningful and flexible manner. The currently developed ontology tools will play a central role in achieving our goals. Ultimately, this will allow the user to specify a certain cell type in order to retrieve morphologies along with a physiological characterization and related models. In the ideal situation different types of physical data, morphology and physiological recordings, exist for the very same neuron [4].
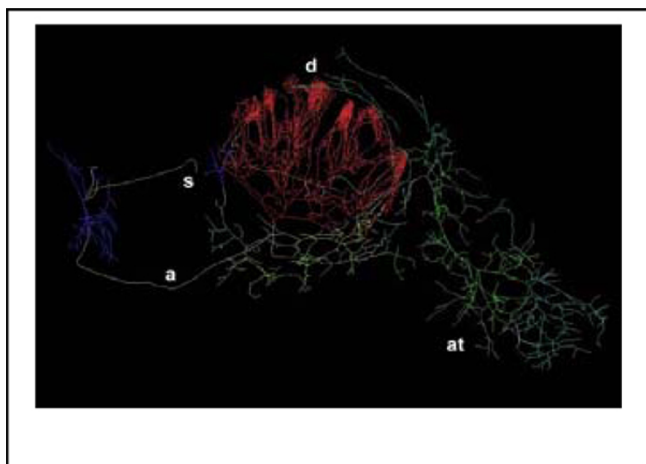
Figure 2
The Pe1 neuron of the central bee brain. Multi-coloring represents different brain regions. s: soma, a: axon, d; dendrite, at; axon terminals.

References
1. Brandt R, Rohlfing T, Rybak J, Krofczik S, Maye A, Westerhoff M, Hege HC, Menzel R: **Three-dimensional average-shape atlas of the honeybee brain and its applications.** *J Comp Neurol* 2005, **492**:1-19.
2. **Honeybee brain atlas** [http://www.neurobiologie.fu-berlin.de/beebrain/]
3. Kuß A, Prohaska S, Meyer B, Rybak J, Hege HC: **Ontology-based visualisation of hierarchical neuro-anatomical structures.** *Proc Visual Computing for Biomedicine* 2008:177-184.
4. Krofczik S, Menzel R, Nawrot MP: **Rapid odor processing in the honeybee antennal lobe network.** *Front Comput Neurosci* 2008, **2**:9. doi:10.3389/neuro.10.009.2008