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Advances in computational neuroanatomy

Accepted: 21 September 2001

Structure is the basis for function. At the level of single neurons, the morphology of axonal and dendritic processes plays a fundamental role in supporting and shaping function. At the level of systems and brain regions, the detailed topographical organization, e.g., spatial relationships among ensembles of neurons, influences functional properties in brain networks. The classical field of quantitative neuroanatomy covers a range of methods and approaches. Traditional and manual approaches typically generate figures, tables, and numbers representing some feature of the brain. At a more advanced level, computerized approaches typically produce larger and more complex data sets, allowing multidimensional analysis. The term computational neuroanatomy is here used to describe computationally demanding quantitative neuroanatomic analyses, and computational modeling of brain structure and spatial organization based on such quantitative data. This emerging field is likely to play also a pivotal role in future modeling of brain function. Functional modelers, usually referred to as computational neuroscientists, increasingly make use of detailed, quantitative neuroanatomic data at multiple levels to produce more advanced and realistic simulations of brain functions (Jennings and Aamodt 2000; De Schutter 2000).

This special issue of *Anatomy and Embryology* presents seven articles that highlight the field of computational neuroanatomy. The emphasis is on tools and methods. Multiple levels of investigation, from single neurons to brain regions, are covered. The authors are developers of new technology as well as investigators seeking answers to important scientific questions.

The two review papers (van Pelt et al. 2001; Toga et al. 2001) represent extremes on a scale from single-

neuron to brain-region analyses. Van Pelt et al. (2001) review recent developments in reconstruction and morphological quantification of single neurons, modeling of neuronal morphology and function, and databasing. Global initiatives in brain databasing are also discussed. Toga et al. (2001) review methods for brain atlas of normal and disease-specific human brains. The authors demonstrate the usefulness of these methods for detecting regional pathology and variability, e.g., in patients with Alzheimer's disease and schizophrenia.

The original articles (Ascoli et al. 2001; Nadasdy and Zaborszky 2001; Brevik et al. 2001; Kötter et al. 2001; Geyer et al. 2001) also cover a wide range of analytical approaches. Ascoli et al. (2001) demonstrate the powerful use of computational methods for generating large amounts of virtual neurons (with dendritic trees), based on a limited amount of reconstructed real neurons. These efforts may turn out to be essential in future modeling of large ensembles of neurons. Nadasdy and Zaborszky (2001) take the step from single neurons to neuronal populations, applying new methods for visualization and analyses of neuronal density distributions. Another approach for studying the distribution of large ensembles of neurons within limited brain regions is provided by Brevik et al. (2001). They introduce internal coordinate systems for individual brain stem nuclei, which are important in the context of databasing and comparison of data from different laboratories.

While Ascoli et al. (2001), Nadasdy and Zaborszky (2001), and Brevik et al. (2001) use rodent material, Kötter et al. (2001) and Geyer et al. (2001) deal with the monkey and human brain. The two latter contributions focus on location of cortical areas. Kötter et al. (2001) describe a methodological framework for the characterization and classification of cortical areas. The framework is used to analyze receptor binding and connectivity data in motor and visual areas of macaque monkeys. Geyer et al. (2001) combine cytoarchitectonic mapping of post-mortem brains with computerized brain atlas, and apply their methods to localize regional blood flow changes.

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Across the diversity of approaches and species used in the articles, several issues in common are discussed. These include aspects of three-dimensional (3-D) reconstruction and visualization (van Pelt et al. 2001; Toga et al. 2001; Ascoli et al. 2001; Nadasdy and Zaborszky 2001; Brevik et al. 2001; Geyer et al. 2001), databasing of neuroanatomic data (van Pelt et al. 2001; Nadasdy and Zaborszky 2001; Brevik et al. 2001; Kötter et al. 2001) and multidimensional scaling, 3-D data comparison, and coordinate systems (Toga et al. 2001; Brevik et al. 2001; Kötter et al. 2001; Geyer et al. 2001). Several other examples of computational neuroanatomy projects have been collected recently by Ascoli (2001). These and other activities demonstrate a rapid evolution in neuroanatomy that is likely to have a strong impact on neuroscience.

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