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The virtual rat brain: software environment for integration of 3d cellular data of the rat brain

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We have developed a software environment to integrate and store 3D cellular anatomical data of the rat brain. The collected vectorial data represents point loci of cell populations of different neurochemical phenotype and fully reconstructed, electrophysiologically identified neurons. The program can be downloaded from <http://www.ratbrain.org>. The software tools are developed in JAVA programming language with cross platform support (Windows, Mac, Unix). A special XML format (MorphML) is used for data modeling. The analytical tools in its present form include the investigation of density information (clusters), as well as, the topological association pattern of different cell populations using the 'overlapping analysis tool'. The overlapping analysis method was designed to compare density and overlap between two or more cell populations. The program divides the brain volume occupied by the datasets into boxes (voxels, bins) of a given size and counts the objects (cells, fibers, etc) within each box. If the cell number of each population within a box is equal or above a certain threshold, the program shows this box in a different color to indicate spatial segregation or overlap. There are several outputs of the program including visualization of bin distribution and summarized cell and bin numbers in Excel format. This program is re-implementation of an algorithm used in the Micro3D (Oslo Research Park) environment.

In many brain systems neuronal populations show non-homogeneous distribution and neurons form cell aggregates or clusters. Neuronal clusters have been suggested as sites of integrative operations. The cluster algorithm determines the number of cell bodies within a spherical volume around each neuron and if this number increases linearly with the volume of the sphere, the cell population is considered to be homogeneously distributed. In contrast, local deviations from the linear function (critical density) indicate clusters. Applying the critical density as a threshold the program is able to select and visualize neurons which are part of a putative cluster.

The usefulness of this software environment has been demonstrated on various experimental datasets related to the basal forebrain cholinergic and non-cholinergic neurons of the rat brain. The development of generic and open-source systems will provide neuroscientists with powerful tools for sharing, comparing and integrating multidimensional quantitative anatomical data. These analytical tools may facilitate to look the structure-function relationship in the brain from a new perspective.

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