The Brain Architecture Management System

Mihail Bota, Larry W. Swanson, & Hong-Wei Dong
The NIBS Neuroscience Program, University of Southern California, 3641 Watt Way, Los Angeles, California 90089-2520, USA

The Brain Architecture Management System (BAMS) (http://brancusi.usc.edu/bkms) is an online informatics environment for retrieval and processing of data related to brain regions, neuronal cell types, and fiber tracts interconnecting them.

BAMS is organized in three main modules: brain regions, neuronal cell types, and connections between regions. The object-relationship (OR) structure of BAMS is centered on the object "Brain Region" as defined in different nomenclatures and uniquely identified by name, species, atlas (nomenclature scheme), and version of atlas. The design of the brain region nomenclatures module distinguishes between neural cell masses (grisea), major fiber tracts, and ventricles. The structure of BAMS allows the hierarchical organization of neuroanatomical nomenclatures and the association of the criteria used for construction. Users are able to view the existent brain nomenclatures hierarchically organized, and inspect the criteria used for brain regions by different sources or collators.

The cell type module is constructed in an m:n relation with "Brain Regions" because a neuronal cell type may distribute in many brain regions and a brain region typically has many cell types. The OR structure of BAMS allows the insertion of qualitative and numerical data related to a given cell type. Any neuronal cell type associated with a brain region can be described in terms of pattern of appearance, density, localization, and extension within the region; as well as in terms of absolute numbers or percentage of labeled neurons.

Neural connections are viewed in BAMS as relations between different brain regions defined in a given nomenclature. The module of connections between regions allows the insertion of reports of neuroanatomical connections collated from the literature, and experimental results of tract tracing experiments before they are published. The allowed types of connectivity data that can be inserted, processed, and retrieved from BAMS range from qualitative information to quantitative data. The connectivity module of BAMS describes a report of a neuroanatomical projection in more than 40 parameters, allowing users to inspect information about the positions and extensions of the injection site and of terminal fields relative to the target structures, respectively; the density of the connection in qualitative or numerical terms; association of connectivity reports with major fiber tracts; the description of the projection as found in the associated reference; and data about each of the animals used. Each connectivity report that is recorded in the knowledge base of BAMS can be associated to a set of images presented in the related reference.

Because the OR structure of the connectivity module of BAMS allows the insertion of numerical data, any reference used to collate tract tracing results can be converted into histograms of labeled cells at different neuroanatomical levels. An important aspect of the connectivity module of BAMS is that it allows the association of a connectivity report

with records of cell types specific to the efferent and afferent regions defined in a given nomenclature.

The BAMS web interface allows users to query the system in different ways (search for information by structure names, species, and references), to relate nomenclature and connectivity information, and to insert prepublished experimental neuroanatomical data.

BAMS inference engines relate information stored in the system's knowledge base about brain region nomenclature, neuronal cell types, and connections. A hierarchically organized, internally consistent brain nomenclature allows construction of dynamical trees of brain regions and inferences about projections to and from a region from the information related to the sets of substructures. A similar inference type is used to reconstruct the profile of cell types in a particular brain region if the required nomenclature is hierarchically organized.

Users may construct customized connection matrices, by choosing regions from the list of all structures recorded in an internally consistent nomenclature system. These matrices can be evaluated in terms of information in individual references, and when data is available, in terms of connection strengths.

BAMS also includes an inference engine for constructing possible networks of brain regions defined in a specific nomenclature from the available connectivity data inserted in the knowledge base of the system. This inference engine evaluates the sets of intermediary stations that are possibly connected with two regions specified by users. The maximal number of intermediary stations between any two regions is three.

To relate different parcelling schemes for the same brain regions we adapted a qualitative inference algorithm that uses topological relations between brain regions (specified in the literature, or inferred by collators). If a pair of brain structures defined in two nomenclatures has more than one topological relation (i.e., both structures are present in more than one pair of levels from the compared atlases), then the system infers a general spatial relation between the considered regions, by taking into account the set of all topological relations across all associated pairs of levels.

Another inference type implemented in BAMS concerns the set of references associated with a particular nomenclature in the system. This inference engine answers queries about references common to multiple nomenclatures, and brain regions defined in a particular reference and allows users to compare any number of brain nomenclature systems in terms of common references and brain regions.

BAMS contains an additional module designed for inserting and processing results of tract tracing experiments. This module allows registered users to store their experimental results in personal accounts where they can organize, perform statistical analysis of data, and group different cases in complex tables. The statistical tools that are implemented in BAMS manipulate qualitative data: evaluation of the maximum connection strength across atlas levels, and the mode of distribution of data. Registered users of BAMS are also allowed to give personal assessments of the pool of qualitative data associated with a given projection and across atlas levels. Users have the option of grouping the processed cases and the resulting tables can be further arranged if the used neuroanatomical nomenclature is hierarchically organized, and saved in an Excel format in the personal computers of registered users.

BAMS is therefore a web based system that stores, systematizes, and processes data across three levels of organization of the central nervous system: cell types, brain regions

defined in different nomenclatures, and networks of structures related by neuroanatomical projections. It provides a powerful and versatile framework for structuring neuroanatomical data in different ways, inferring efferent and afferent matrices of projections and cellular profiles of regions of interest from unrelated information, and inferring spatial relations between brain regions defined in different nomenclatures.

BAMS was created in MySql and uses PHP as scripting language. It contains to date more than 5000 brain region names from 9 nomenclatures dealing with the human, monkey, cat, and rat brain, and more than 10,000 reports of neuroanatomical connections in the rat.