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The Brain Architecture Management System: a mature neuroinformatics workbench for neurobiology

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The Brain Architecture Management System (BAMS; http://brancusi.usc.edu/bkms/) is an online neuroinformatics system that handles data related to brain parts defined in neuroanatomical nomenclatures, and across four levels of organization of the mammalian central nervous system. BAMS contains four interrelated modules: *Brain Parts*, *Molecules*, *Cell Types*, and *Connections*.

The *Brain Parts* module contains structure denominations as identified in referenced atlases, hierarchically organized. The brain parts hierarchies inserted in BAMS are relations of the type '*part-of*', are checked for consistency, and are fully referenced.
The *Molecules* module of BAMS stores information about the chemoarchitectonic makeup of brain regions, and presence of chemicals in different cell types. It allows insertion of data ranging from qualitative assessments to quantitative measurements. The *Molecules* module also allows insertion of coexpression, time-dependent, and concentration-dependent experimental data, and includes a comprehensive set of experimental and neuroanatomical mapping metadata that can be used for data comparison across different experiments.

The *Cell Types* module allows complex neuronal cell type descriptions, and it includes a web accessible *Neuron Ontology*. *BAMS's Neuron Ontology* includes terms and their definitions, classification criteria, hierarchies, and relations—with annotations documenting each ontology entry. Relations allowed in *BAMS's Neuron Ontology* include "is-a" and semantic relations between terms defined by different authors. Users can query online the *Neuron Ontology* for terms and their relationships.
The *Connections* module contains information related to axonal projections between *Brain Parts* and *Cell Types*, and in BAMS they can be described in terms of more than 50 attributes.

The inference engines implemented in BAMS allow online manipulation of experimental data, or data inserted by collators. Thus, users construct connection matrices of different complexities, infer networks of brain regions (displaying results in tabular or image formats), reconstruct chemical profiles of brain regions of interest, group experiments of interest in complex tables, run online queries for mining the effects of different types of perturbations (e.g., structural lesions, or injection of specific drugs), and query for chemical makeup and patterns of connections of different neuron classes.

BAMS is also a data provider to several other neuroinformatics systems, using backend MySQL connections, various web services protocols, and XML files.

We will present the structure of BAMS, describe its interfaces and inference engines, and demonstrate its main functionalities to the neuroscience community. Supported by NINDS/NIMH/NIBIB/NLM Grant NS050792-01.