

Semi-automated shape analysis of dendrite spines from animal models of FragileX and Parkinson's disease using Large Deformation Diffeomorphic Metric Mapping

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The discipline of Computational Anatomy focuses on shape analysis of anatomical structures obtained in biomedical imaging. Under the auspices of the Mouse Morphometry Biomedical Informatics Research Network (www.nbirn.net), a processing pipeline has been developed to enable processing of morphometry data obtained from the Cell Centered DataBase. As a testbed, the pipeline was used to analyze dendrite spines obtained from wildtype and knockout animal models of FragileX and Parkinson's disease. The data consisted of segmented spines and associated shafts in the form of triangulated graphs. The spines were checked for topological defects, scaled and aligned with respect to a wildtype spine in a standard coordinate system, and converted into binary images. Shape analysis of the spines was conducted using the Large Deformation Diffeomorphic Metric Mapping (LDDMM) tool on the TeraGrid. Briefly, LDDMM computes the velocity vectors that transform one binary image I_0 to another I_1 giving the metric distance $d(I_0, I_1)$ connecting the images in the space of velocity vector fields that are generated by the group of infinite dimensional diffeomorphisms (which is the generalization of the rotation, translation and scale group), the necessary group for studying shape. These distances give a precise mathematical description of what shapes are similar and different. Preliminary statistical analysis of the metric distances distinguishing between wildtype and knockout dendrite spines is presented.

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