Abstract View – SFN submission 05/05

Feasibility of multi-site clinical structural neuroimaging studies of legacy data: Aging & Alzheimer's disease

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The Biomedical Informatics Research Network (BIRN) aims to enable scientists to conduct clinical imaging studies across multiple sites to test new hypotheses on larger cohorts. Given that many research groups have valuable existing (legacy) data, one goal of the Morphometry BIRN Testbed has been to assess the feasibility of pooled analysis of legacy structural imaging data. The present study aims to determine whether such legacy data can be meaningfully reanalyzed as a larger combined data set by using rigorous data curation and image analysis methods; in this case, to test the hypothesis that hippocampal volume decreases with age. Legacy T1-weighted MR and demographic data related to normal aging and Alzheimer's disease have been shared through the BIRN by UCSD (TL Jernigan; L Thal; D Salmon), MGH/BWH (M Albert; D Blacker; R Killiany), and Washington Univ. (R Buckner; J Morris). This preliminary report describes our work with older normal control data: UCSD (n=53/28F), MGH/BWH (n=36/22F), and WashU (n=49/24F). Cohorts from the sites were similar in age, education, and mental status. All MR data were analyzed in an automated manner with atlas-based Freesurfer segmentation software to generate volumetric measures of regions of interest (Fischl et al., 2002). Despite closely matched cohorts, mean hippocampal volumes differed across sites. Controlling for age and sex eliminated this site difference. Across the entire multi-site sample, age-related hippocampal volume loss was highly significant (β=-.42, t=-5.4, p<.001). This result suggests that legacy MR data from multiple sites can be pooled to investigate questions of scientific interest.
Support Contributed By: Morphometry BIRN (http://www.nbirn.net), NCRR U24-RR021382; NIA P50 AG05131; DVA Med Res Svc; NIA PO1 AG 04953; ADRC/Howard Hughes; R01 RR16594-01A1; The MIND Inst; P41-RR14075