

AbstractID: 1984 Title: Phantom Comparison of Standard Clinical Spectroscopy Packages

In-vivo H-1 spectroscopy of brain abnormalities has become a more common imaging tool in recent years as vendors have greatly improved the ease of use of their clinical spectroscopy packages, and have included it in their advanced neuroimaging software packages. Although the basic acquisition and analysis methods are well described in the literature, and are reasonably similarly implemented, both the interactive technologist-driven acquisition methods and the final clinical presentation of the result are still very highly vendor-specific. At a facility which utilizes MR systems from multiple vendors, we are particularly interested in variability of results due to system-dependent factors. As the initial step in our evaluation of this variability, we have analyzed the single-voxel and multi-voxel spectra for three vendor's phantoms on all three systems, using both the on-line clinical package provided for each system, and an off-line research spectroscopy software. There were no significant differences between systems in shim quality obtainable using the automatic shim routines. During this testing, it was discovered that the standard analysis routines use different references for baseline correction, leading to inaccurate automatic analysis of other vendor's phantoms due to variations in their composition. However, manual analysis demonstrated that variations between the systems was not significant for single-voxel spectra on the same phantom (standard clinical PRESS sequences; TE=30/35; 135/144; 270/288ms). Variability between the multi-voxel data was much greater, with significant differences occurring in the outermost spectra.