Quantitative evaluation of spectral deconvolution technique
in Magnetic Resonance Spectroscopy: Computer simulation

김형중[1], 정광우[1,2], 강형근[2], 백한수[1], 김태훈[1], 김광원[1]
전남대학교 대학원 의공학협동과정[1], 전남대학교 의과대학 진단방사선과학교실[2]

Purpose: In this study, a spectral deconvolution technique was applied to the computer-simulated MR spectra to evaluate the accuracy and precision of peak area quantification under various condition, such as low SNR, peak overlaps, and baseline distortion combined with lipid and macromolecular broad peaks.

Materials and Methods: For the computer simulation study, various types of simulation data consisting of single-peak group, double-peak group and *in vivo* simulation spectra were synthesized from the free induction decay (FID) signals associated with a variety of spectral parameters. Subsequently, spectral deconvolution technique was applied to the clinical spectra obtained from patients with brain diseases to evaluate the concentration changes of brain metabolites.

Results: In the simulation data consisting of single-peak group, the measurement errors of peak width and peak areas increased rapidly as the exponential function when SNR becomes low. In the simulation data involving double-peak group, the measurement errors of peak width and peak areas increased as the peak interval and SNR become low. In the *in vivo* simulation spectra, the measurement error of peak areas that represent metabolites concentration increased as SNR becomes low. In the *in vivo* simulation spectra associated with baseline distortion and Gaussian random noise, the measurement errors of Cho, NAA-1, Cr-1, mI-1, α-Glx, $\beta \cdot \gamma$-Glx, Lac and Lip were 1.94%, 2.2%, 3.95%, 9.14%, 30.36%, 32.3%, 62.75% and 96%, respectively.

Conclusion: Application of the spectral deconvolution technique to the MR spectra yields contract-enhanced spectral patterns with simultaneous noise suppression and resolution improvement, relative to the conventional MR spectra. In particular, these features are outstanding by reduction of baseline distortion to lead to a simpler interpretation of the resonance frequencies of overlapping peak with low SNR as well as to a more accurate peak quantification in complex MR spectra.