INTRODUCTION
Relaxation times are important for quantitation of metabolite concentrations, especially in long-TE MRS methods [1]. While the signal from uncoupled spins is governed by the relaxation only, the spectral pattern and signal intensity of coupled resonances are also determined by the scalar coupling effects. Therefore, the J evolution effects have to be accounted for in measuring the transverse relaxation times of coupled resonances. Here, we report measurement of coupled-spin metabolites by point-resolved spectroscopy (PRESS) using optimized echo times. Preliminary in vivo results from the human brain are presented.

METHODS
A PRESS sequence was employed to measure the apparent transverse relaxation times ($T_2^*$) of brain metabolites at 3T. The first and second subecho times were optimized, with computer simulations, for glutamate (Glu) and glutamine (Gln) separation. Four pairs of subecho times were selected; $(T_{E1}, T_{E2}) = (32, 22), (32, 80), (32, 214), \text{and} (36, 338)$ ms. The $(32, 22)$ ms pair was the shortest possible echo times for given RF and gradient pulses. In vivo experiments were conducted on a whole-body 3T scanner (Philips Medical Systems). A body coil was used for RF transmission and an 8-channel phased-array coil for reception. Data were acquired in the steady-state conditions ($TR = 3 – 3.4$ s). Number of averages was 16, 32, 64, and 128 for the four TEs, respectively. LCMoModel software [2] was employed to analyze the in vivo data, using numerically calculated model spectra as basis functions.

RESULTS AND DISCUSSION
Figure 1 shows simulated spectra of Glu, Gln, GSH (glutathione), NAA, and Cr (creatine) at the four selected $T_{E1}$-$T_{E2}$ pairs. The C4-proton multiplets of Glu and Gln are well preserved at the echo times. Figure 2 presents in vivo spectra from the human occipital cortex, obtained with adjusted $TR$ to maintain constant initial longitudinal magnetization prior to the $90^\circ$ excitation RF pulse for various echo times and with $TR = 8$ s to obtain fully-recovered signal strengths (at $TE = T_{E1} + T_{E2} = 112$ ms). The spectra are well reproduced by the fits. The spectral pattern in 2 – 3 ppm is in good agreement with Fig. 1. Myo-inositol (m-Ins) is well differentiated from neighboring resonances in the spectra at $TR = 112$ and 246. The lactate (Lac) 1.31 ppm resonance appears inverted at $TE = 112$ ms, but positive at $TE = 246$ ms. In $T_2$ fitting with a monoexponential function, the data at $TE = 54$ ms were excluded because of uncertainty of the fits due to the effects of macromolecule signals. Figure 3 presents $T_2$ values of metabolites included in spectral fitting. The $T_2$’s of Cr, NAA, and GPCP+PC agree with published values [4]. The metabolite concentrations were estimated such a way that the fully-recovered signals at $TE = 112$ ms, obtained with $TR = 8$ s, were extrapolated to zero TE using the $T_2$ values from the fitting, as shown in Fig. 4. The concentration ratio with respect to Cr was estimated to be $8.2\pm1.3, 4.6\pm0.6, 9.5\pm0.8, \text{and} 1.1\pm0.1$ (mean$\pm$SD, $N = 5$) for Glu, m-Ins, NAA, and GPCP+PC, respectively.

REFERENCES