Molecular Imaging through Optimized Magnetic Resonance Spectroscopy for Personalized Cancer Medicine

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**Computationally fast, with robust noise suppression, the high-resolution derivative fast Padé transform, dFPT, is poised to be implemented in clinical MR scanners, with more effective patient care & enhanced cost-effectiveness**

- The long sought hope of radiologists would be realized: to visualize the entire clinical MRS information by seeing clearly disentangled overlapping peaks and inspecting the displayed concentrations of all diagnostically-relevant metabolites.

- Optimized MRS could thereby become a standard, clinically reliable part of cancer diagnostics.

Via high-resolution data analysis, magnetic resonance spectroscopy (MRS) can improve the specificity of magnetic resonance imaging (MRI) for timely and accurate cancer diagnosis. The sensitivity of MRI excellent, but its specificity is often insufficient. By going beyond morphology, MRS assesses the biochemical content of tissue. This requires advanced signal processing.

Key milestones have been achieved with the high-resolution processor, the parametric fast Padé transform (FPT) for in vivo encoded magnetic resonance time signals from tumorous tissues.

The previously unexplored properties of the non-parametric derivative FPT (dFPT) are benchmarked for robust detection and quantification of phosphocholine (PC), a key biomarker of breast cancer and other malignancies.

The figure shows the noise suppression capabilities of the dFPT, while the derivative FFT (dFFT) markedly amplifies noise. The higher order dFPT identifies & exactly quantifies PC despite its close overlap with phosphoethanolamine (PE).