Pharmacokinetic analysis of dynamic positron emission tomography (PET) imaging data maps the measured time activity curves to a set of model-specific pharmacokinetic parameters. Voxel-based parameter estimation via curve fitting is conventionally performed indirectly on a sequence of independently reconstructed PET images, leading to high variance and bias in the parametric images. We propose a direct parametric reconstruction algorithm with raw projection data as input that leverages high-resolution anatomical information simultaneously obtained from magnetic resonance (MR) imaging in a PET/MRI scanner for regularization. The reconstruction problem is formulated in a flexible Bayesian framework with Gaussian Markov Random field modeling of activity, parameters, or both simultaneously. MR information is incorporated through a Bowsher-like prior function. Optimization transfer using an expectation-maximization surrogate and a new Bowsher-like penalty surrogate is applied to obtain a voxel-separable algorithm that interleaves a reconstruction with a fitting step. An analytical input function model is used. The algorithm is evaluated on simulated [(18)F]FDG and clinical [(18)F]FET brain data acquired with a Biograph mMR. The results indicate that direct and simultaneously regularized parametric reconstruction increases image quality. Anatomical regularization leads to higher contrast than
conventional distance-weighted regularization.