

To get more information about tissue perfusion from T1-weighted dynamic contrast enhanced magnetic resonance imaging, more complex models than the commonly accepted Kety model have to be used. However using adiabatic approximation to the tissue homogeneity model (ATH) brings serious convergence problems, caused mainly by discontinuities in the criterion curve-fitting function. A solution to these issues is presented by using the distributed-capillary adiabatic tissue homogeneity model (DCATH) and continuous estimation of bolus arrival time in the Fourier domain. Comparison of the criterion curve-fitting functions for ATH and DCATH, which are to be minimized, is presented as well as perfusion maps obtained by this algorithm for an animal model.