The Challenge of Uniqueness in the Application of Dynamic SPECT

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Abstract

Dynamic single photon emission computed tomography (SPECT) imaging involves studying the kinetics of biochemical processes in living organisms. This entails following the uptake of radiopharmaceuticals, its potential metabolism or catabolism, and the eventual washout of tagged products from organs of interest. The greatest challenge for dynamic SPECT imaging is to measure the blood tracer concentration as a function of time where input to the organ of interest often changes faster than the systems ability to obtain consistent tomographic projections. For years dynamic imaging has been realized with positron emission tomography (PET). It has been used to study physiological processes to better understand organ function in health and disease because of a geometric detector sensitivity that allows for rapid measurement of consistent projections. Dynamic sequences of fully 3D reconstructions can be obtained from which time activity curves are generated for the purpose of estimating kinetic parameters of multicompartment pharmacokinetic models. The development of SPECT clinical systems has moved away from providing sufficient fast acquisition of fully 3D reconstructed dynamic sequences. Time activity curves of blood input and organ uptake and washout or even kinetic model parameters must be estimated directly from projection measurements. Even though this involves the challenge of determining unique solutions to large inverse problems, the effort has lead to the

realization that this is the correct way to process SPECT and even PET dynamic data because the estimation of parameters directly from projections provides more efficient estimates of parameters than those estimated from time activity curves generated from reconstructed regions of interest.