Time Domain Integral Equation –Based Analysis of Light Scattering from Biological Cells

Pei-Lin Jiang* (1) and Eric Michielssen (2)
(1) University of Illinois at Urbana-Champaign, IL 61801
(2) University of Michigan, Ann Arbor, MI 48109

Interactions of (polarized) light with biological cells provide a means for controlling cell movement (optical trapping/tweezers) and assessing cell morphological and biochemical composition (noninvasive sensing/imaging). Modeling efforts in support of these applications often rely on full-wave electromagnetic simulators based on finite difference time domain [CG Liu *et al*., *J Biom Opt*, **10,** Art No.014007, 2005], frequency domain integral equation (FDIE) [TW Lloyd *et al*., *IEEE Antennas Propagat Lett*, **4**, 482-485, 2005], or discrete dipole approximation methods [A Karlsson *et al*., *IEEE Trans Biom Eng*, **52**, 13-18, 2005]. To date, time domain integral equation (TDIE)-based schemes have not been applied to the analysis of light scattering from cells. Were it not for their high computational complexity, TDIE-based methods would be ideally suited for this purpose, however. Indeed, they automatically impose the radiation condition and conveniently model curved surfaces bounding homogeneous volumes (as FDIE methods do); this feature is important especially for applications that involve moving cells. Furthermore, they generate broadband results with one code execution and are applicable to nonlinear problems (as FDTD schemes do); this feature is attractive when accounting for effects from nonlinear control systems for manipulating cells.

Here, light scattering from biological cells is simulated using a fast TDIE-based marching-on-in-time (MOT) solver. The solver models a cell as a closed dielectric volume with inclusions (nucleus, organelles, and cytoplasm) of varying refractive index. Leveraging the surface equivalence principle, electric and magnetic field TDIEs in terms of the surface electric and magnetic currents are formulated. These equations account for the lossy nature of the cell background and interior media; considering that the refractive indices of these media exhibit low contrast, the time domain extension of the frequency domain N-Müller formulation [P Yla-Oijala and M Taskinen, *IEEE Trans Antennas Propagat*, **53**, 3316-3323, 2005] is used to form a set of well-conditioned combined field TDIEs and eliminate the possibility of internal resonances. Unfortunately, if the resulting TDIEs are solved using the classical MOT scheme, the computational complexity scales as $O(N_s^2 N_t^2)$, where N_s and N_t denote the number of spatial and temporal degrees of freedom of the cell surface currents. Here the plane wave time domain (PWTD) method [PL Jiang *et al*., submitted to *J Comput Phys*] is used to evaluate the contributions from far-field interactions. Moreover, a Prony series-based recursive convolution method [PL Jiang and E Michielssen, *Microw Opt Tech Lett*, **44**, 223-230, 2005] is used to speed up the evaluation of the temporal convolutions in the computation of near-field interactions. Consequently, the computational cost of the MOT scheme is reduced to $O(N_s N_t \log^{\alpha} N_s \log^{\beta} N_t)$ ($\alpha, \beta = 1 \sim 2$ depending on implementation choices). Using this fast algorithm, the fields near red blood cells immersed in dissipative fluids are calculated, and their scattering cross sections are computed.