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Publication date
1997

Published in
Progress in Electromagnetics Research Symposium 1997

[Link to publication](#)

Citation for published version (APA):

Hoekstra, A. G., & Sloot, P. M. A. (1997). Elastic light scattering from single biological cells. In J. A. Kong (Ed.), *Progress in Electromagnetics Research Symposium 1997* (pp. 583)

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Elastic Light Scattering from Single Biological Cells

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Single Biological Cells share three properties which determine the approach towards calculating their elastic light scattering:

1. irregularly shaped, usually with internal structure,
2. biological variability,
3. small refractive indices (relative to water).

The consequences of these properties will be discussed by considering cases of light scattering from human white - and red blood cells. First, approximate theories such as RDG and Anomalous Diffraction are considered. The case of RDG calculations of sideward scattering of swelling lymphocytes, and of Anomalous Diffraction calculations of near forward scattering of deformed red blood cells will be discussed. In both examples the calculations and experiments are in good agreement. Experimental evidence however suggests that approximate theories are not able to predict the full scattering matrix. For instance, it is shown that granulocytes show depolarization, and lymphocytes have a non-zero S_{34} element. To calculate such effects requires more involved methods. We apply a reformulation of the so-called Discrete Dipole Approximation (DDA) to simulate elastic light scattering. Currently we are able to simulate scattering from biological cells with diameters up to 8 micrometer on high performance computer systems. The current status of the method and results of simulations on blood cells will be presented. Finally, in view of the three properties formulated above, the role of brute force methods like the DDA in simulating elastic light scattering from biological cells will be discussed.

Abstract: In this paper we discuss the use of the Discrete Dipole Approximation (DDA) to calculate the scattering matrix of biological cells. We compare the results of DDA with those of the Rayleigh Discrete Gradient (RDG) and Anomalous Diffraction (AD) theories. The DDA method is shown to be more accurate than the other two methods, especially in the case of irregularly shaped cells and cells with internal structure. The DDA method is also shown to be more efficient than the other two methods, especially in the case of large cells and cells with internal structure.