Virtual Pharmacokinetic Model of the Human Eye

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Abstract

There is a great need for an effective drug treatment of the posterior eye, as the major reason for visual disability in industrial countries is Age-related Macular Degeneration (AMD). In USA alone, there are almost 2 million people affected by AMD [1]. A virtual pharmacokinetic 3D model of the human eye is built to address this problem, using COMSOL Multiphysics® software, based on the Finite Element Method (FEM) [Fig.1]. The model considers drug release from a polymer patch placed on sclera. The model concentrates on the posterior part of the eye, retina being the target tissue, and comprises choroidal blood flow, partitioning of the drug between different tissues and active transport at the Retina Pigment Epithelium (RPE)-choroid boundary. In order to check the mass balance, no protein binding or metabolism is yet included. It appeared that the most important issue in obtaining reliable simulation results is the finite element mesh, while time stepping has hardly any significance. Simulations were extended to 100,000s. The concentration of a drug is shown as a function of time at various points of retina, as well as its average value, varying several parameters in the model [Fig.2]. This work demonstrates how anybody with the basic knowledge of calculus is able to build physically meaningful models of quite complex biological systems.

Reference

D.S. Friedman, B.J. O'Colmain, B. Munoz, S.C. Tomany, C. McCarty, R.T. De Jong, B. Nemesure, P. Mitchell, J. Kempen, Prevalence of age-related macular degeneration in the United States, Arch. Ophthalmol. 122 (2004) 564-572.

Figures used in the abstract

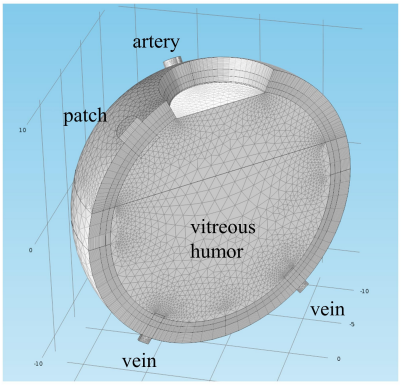

Figure 1: COMSOL drawing of an eye.

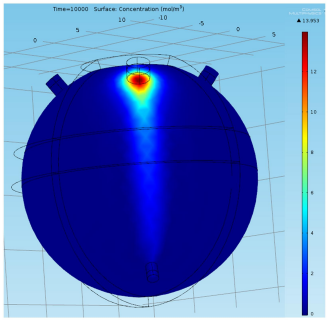

Figure 2: Concentration.