

**MATHEMATICAL OPTIMIZATION FOR LIPOSOMAL
DOXORUBICIN IN TUMOR****RAFAL HRYNYK^{1*} and MAREK LANGNER^{1,2}**

¹Laboratory for Biophysics of Supramolecular Aggregates, Institute of Physics,
Wrocław University of Technology, Wyb. Wyspiańskiego 27,
50-370 Wrocław, Poland, ²Academic Center for Biotechnology of Lipid
Aggregates, Przybyszewskiego 63/77, 51-148 Wrocław, Poland

Liposomes are particulate drug formulation intended to modify drug efficiency by improving its performance. It has been shown that liposomes accumulate preferentially in tumors due to the elevated blood vessel permeability. Since liposomes are then intratumoral drug depot therefore their properties will determine the drug pharmacokinetics at the location. The objective of presented works is to construct a theoretical model capable to predict the effect of liposomal formulation properties on free drug pharmacokinetics in the tumor tissue. Biodistribution and pharmacokinetic specification of free and encapsulated drug was simulated with the improved PK/PD model proposed by Tsuchihashi [Tsuchihashi, M. *et al.* **J. Control. Release** 61 (1999) 9] and later by Fung's [Fung, V.W.H. *et al.* **Biochim. Biophys. Acta** 1611 (2003) 63] concerning dictated liposomal accumulation as well as characteristic of influx and efflux parameters at different time points after accumulation. It was shown that there is a set of liposome's properties which allow optimalization of the intratumoral concentration drug profile. Proposed analysis is needed to improve the understanding of drug-target interaction and the ability to translate the theoretical findings to practical application. Such approach may greatly assist the design and development process of liposomal drug formulations.

* E-mail: rafal.hrynyk@pwr.wroc.pl