1176-92-245 **Yasaman Moghadamnia*** (ymoghad@udel.edu), **Sasan Paryad-Zanjani**, **Aditya Jagarapu**, **Michael Donzanti**, **Elias P Rosen**, **Michael J Piovoso**, **Jason P Gleghorn** and **Ryan Zurakowski**. *Mathematical modeling of ARVs diffusion into the lymph nodes to investigate drug transport mechanisms.*

Direct imaging of anti-retroviral (ARV) distribution in rhesus macaque (RM) lymph nodes (LNs) show concentration variation of 10-30-fold within the same LN. Barriers between the blood, sinus, and lobule may hinder free drug transport; therefore, cell-mediated ARV transport may dominate despite being much slower. We evaluate this hypothesis using a predictive model of drug distribution within a lymph node lobule. This model solves PK reaction and spatial diffusion dynamics on a fully reconstructed 3D geometry of a murine LN, reproducing observed spatial patterns of ARV distribution. To construct the 3D model high resolution confocal imaging, segmentation, and volumetric anatomical reconstruction were used. Blood and sinus compartments were treated as boundary conditions. Transport within the LN lobule is assumed to be heterogeneous diffusion. PK kinetics for each ARV were adapted from previously published PK models. Numerical solutions were computed using Finite Volume Methods. A steady-state reduction of the model was used to fit IR-MALDESI data of ARV distribution in RM LNs. Estimated ARV diffusivity matches lymphocyte transport but is an order-of-magnitude too slow for free-drug transport. This strongly implies exclusive cell-associated transport for ATZ within the LN lobule. (Received January 24, 2022)