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# From whole-organ imaging to in-silico blood flow modeling : a new multi-scale network analysis for revisiting tissue functional anatomy[1]

FRANCK PLOURABOUE, Fluid Mechanics Institute of Toulouse UMR CNRS-UPS-INPT, J. COLOMBELLI COLLABORATION, C. BARREAU, C. GUISSARD, L. TEYSSEDRE, J. ROUQUETTE, A. LORSIGNOL, LOUIS CASTEILLA COLLABORATION, P. KENNEL, J. DICHAMP TEAM — We present a multidisciplinary image-based blood flow perfusion modeling of a whole organ vascular network for analyzing both its structural and functional properties. We show how the use of Light-Sheet Fluorescence Microscopy (LSFM) permits whole organ micro-vascular imaging, analysis and modelling. By using adapted image post-treatments workflow, we could segment, vectorize and reconstruct the entire micro-vascular network composed of 1.7 millions vessels, from the tissue-scale, inside a $\sim 25 \times 5 \times 1 = 125\text{mm}^3$ volume of mouse fat pad, hundred time larger than previous studies, down to the cellular scale at micron resolution, with the entire blood perfusion is modeled. Adapted network analysis revealed the structural and functional organization of meso-scale tissue as strongly connected communities of vessels. These communities share out a distinct heterogeneous core region and a more homogeneous peripheral region, consistently with known biological functions of fat tissue. Graph clustering analysis also revealed two distinct robust meso-scale typical sizes (from 10 to several hundred times the cellular size), revealing, for the first time, strongly connected functional vascular communities. These communities networks support

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