

# **From inert image-based computational biofluid flow model to integrative modeling of the flow in living, reacting conduits**

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Due to high between-subject variability, numerical simulations related to physio/pathophysiological problems are based on medical images. The computational domain is indeed determined by image processing, images being a model of the subject anatomy. 3D reconstruction associated with facetization (crude surface discretization) leads to mesh suitable for computational fluid dynamics. Because anatomical vessels are deformable, fluid dynamics is coupled to vessel wall mechanics. Even though flow simulations in any explored segment of the duct network are carried out in deformable fluid domain, the numerical results remain questionable because : (1) the material constants are most often not known in vivo ; and (2) the vessel wall is assumed to be a more or less passive material. Biological tissues indeed quickly adapt to environmental stimuli, especially to mechanical loads applied on it. In blood flows, the endothelium (interface between blood and wall) is subjected to both chemical cues from neighboring tissues or flowing blood and physical stresses applied by the blood. The endothelium regulates flowing cell extravasation and aggregation, the vasomotor tone of adjoining smooth muscle cells, the substrate transport, and composition of the extracellular matrix. In a point of any blood vessel segment, the endothelial and smooth muscle cells sense the magnitude of amplitude of oscillations in wall shear stress and wall stretch. These cells responds with a short-time scale to adapt the vessel caliber according to the loading, especially when changes exceed the limits of the usual stress range. The size of the computational domain thereby depends on the controled motions of the blood vessel wall.