

MULTISCALE MODELING OF VASCULAR GROWTH AND REMODELING

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ANNA CORTI^{*}, STÉPHANE AVRIL[†]
AND CLAUDIO CHIASTRA[‡]

^{*} Politecnico di Milano
Piazza Leonardo da Vinci, 32, 20133 Milan, Italy
anna.corti@polimi.it - <https://test.deib.polimi.it/eng/people/details/988202>

[†] Mines Saint-Etienne
cours Fauriel 42023 Saint-Étienne Cedex 2 France
avril@emse.fr - emse.fr/~avril/

[‡] Politecnico di Torino
Corso Duca degli Abruzzi 24, 10129 Turin, Italy
claudio.chiastra@polito.it - <https://www.polito.it/en/staff?p=claudio.chiastra>

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ABSTRACT

Vascular adaptation is a crucial process implicated in major cardiovascular diseases, encompassing atherosclerosis, aneurysm formation, and responses to therapeutic interventions like endovascular or surgical procedures. Vascular adaptation processes are governed by multifactorial and multiscale networks of events, involving intricate feedback mechanisms, cause-and-effect relationships and mutual interactions of components across multiple spatial (ranging from molecules to cells and tissues/organs) and temporal (ranging from seconds to days and years) scales [1]. Despite significant progress, a comprehensive understanding of these events remains elusive, posing a significant challenge to advancing our ability to manage cardiovascular diseases. It is clear that moving forward in the understanding and prediction of vascular adaptation processes requires a comprehensive capture of the complex, multiphysic and multiscale nature of the phenomenon. To address this challenge, multiscale mechanobiological computational models have recently emerged as promising tools to investigate arterial growth and remodelling in different vascular regions, such as aorta, coronary arteries and peripheral arteries. By providing a comprehensive framework to capture the complex interplay between biomechanical forces, cellular behaviour, and molecular pathways, these models hold great potential for advancing our understanding of vascular adaptation processes. Various modeling strategies, including continuum, discrete and hybrid (e.g., integrating continuum and discrete methods) have been proposed for investigating vascular adaptation processes, ranging from simulations in idealized vessel geometries to patient-

specific ones [1], [2]. Moreover, the integration of multi-omics data in multiscale models of vascular adaptation, allowing the identification of patient-specific pathophysiological pathways, can provide a remarkable contribution to the understanding of cardiovascular diseases (e.g., through the discovering of disease biomarkers). Consequently, it can contribute to disease prevention, diagnosis and treatment, aligning with the emerging field of personalized medicine. However, as the complexity of the computational models increases, aspects such as verification, uncertainty quantification, calibration and validation of the model, as well as the computational time, become challenging priorities that need to be addressed for their clinical translation. In this context, this mini-symposium will cover recent advancements in the multiscale modeling of vascular growth and remodeling, which are expected to address some of the major challenges currently facing these models.

REFERENCES

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