

POPULATION-BASED AND PATIENT-STRATIFICATION APPROACHES APPLIED TO A HUMAN CARDIAC MODEL OF ELECTROPHYSIOLOGY

Giulia Simoni^{1,2}, Corrado Priami^{1,3}, Luca Marchetti^{*1} and Eric Sobie⁴

¹Fondazione the Microsoft Research-University
of Trento Centre for Computational and Systems Biology (COSBI),
Rovereto, Italy

²Department of Mathematics,
University of Trento, Trento, Italy

³Department of Computer Science,
University of Pisa, Pisa, Italy

⁴Department of Pharmacology and Systems Therapeutics,
Mount Sinai School of Medicine, New York, USA

marchetti@cosbi.eu (*corresponding author), simoni@cosbi.eu

Mathematical models of cardiac electrophysiology are usually defined to represent average data from voltage-clamp experiments of ionic membrane current [1]. It is only recently, with the advancement of the computational capabilities, that new modeling techniques have been developed to account for the individual variability that typically affects these biological processes. Among these techniques, the most common is the population-based approach that identifies a set of key model parameters that can be varied to address the scientific question in different phenotypical conditions. In parallel with the development of this population approach, several computational strategies have emerged with the purpose to elucidate the role of each model parameter for specific physiological behaviors. This could be addressed with a parameter sensitivity analysis that, in the context of electrophysiology, is usually performed with multivariate regression methods [2]. The combination of these two approaches with clustering techniques allows an integrative understanding of the individual variability of disease progression, as well as the response to drug actions, thus could play an essential role in the advancement of precision medicine [3].

We used the population-based approach to generate a group of virtual patients, representing the healthy and the heart failure (HF) phenotypes [4, 5], by considering a human cardiac model of electrophysiology [6]. We employed a novel-defined computational pipeline for patient stratification to identify the key mechanisms responsible for the stratification and highlight the importance of including additional phenomenological functions in the mathematical model to better represent the variability of the disease phenotypes. Besides, we compared the results of a global sensitivity analysis (GSA) [7], performed by coupling a sampling algorithm [8] with a logarithmic sensitivity approach [9], with the results of two linear-regression sensitivity algorithms [10, 11]. Both the two regression approaches proved to work well even with a com-

plex non-linear system, providing similar results to the ones computed with GSA, but with considerable advantages in terms of computational cost.

References

- [1] Mayourian J., Sobie E.A., Costa K.D. (2018). *An Introduction to Computational Modeling of Cardiac Electrophysiology and Arrhythmogenicity*. In: Ishikawa K. (eds) *Experimental Models of Cardiovascular Diseases*. Methods in Molecular Biology, vol 1816. Humana Press, New York, NY
- [2] Sobie E. (2009). *Parameter sensitivity analysis in electrophysiological models using multivariable regression*. Biophysical Journal, 96(4):12641274. doi: 10.1016/j.bpj.2008.10.056.
- [3] Collins F.S. and Varmus H. (2015). *A new initiative on precision medicine*. New England Journal of Medicine, 372(9):793-795, doi: 10.1056/NEJMp1500523.
- [4] Gong J. and Sobie E. (2018). *Population-based mechanistic modeling allows for quantitative predictions of drug responses across cell types*. npj Systems Biology and Applications, 4(1), doi: 10.1038/s41540-018-0047-2.
- [5] Gomez J., Cardona K., Romero L., Ferreo J. and Trenor B. (2014). *Electrophysiological and structural remodeling in heart failure modulate arrhythmogenesis. 1d simulation study*. PLoS ONE, 9(9), e106602.
- [6] OHara T., Virag L., Varro A. and Rudy Y. (2011). *Simulation of the undiseased human cardiac ventricular action potential: Model formulation and experimental validation*. PLOS Computational Biology, 7(5):129. doi: 10.1371/journal.pcbi.1002061.
- [7] Zi Z. (2011). *Sensitivity analysis approaches applied to systems biology models*. IET Systems Biology, 5(6):336346. doi: 10.1049/iet-syb.2011.0015.
- [8] McKay M.D. (1992). *Latin hypercube sampling as a tool in uncertainty analysis of computer models*. In Proceedings of the 24th Conference on Winter Simulation, WSC 92, pages 557-564, New York, NY, USA, doi: 10.1145/167293.167637.
- [9] Nagaraja S., Wallqvist A., Reifman J., and Mitrophanov A.Y. (2014) *Computational Approach To Characterize Causative Factors and Molecular Indicators of Chronic Wound Inflammation*. The Journal of Immunology, 192(4):18241834, doi: 10.4049/jimmunol.1302481.
- [10] Abdi H. (2010). *Partial least squares regression and projection on latent structure regression (PLS Regression)*. Wiley Interdisciplinary Reviews: Computational Statistics, 2(1):97106, doi: 10.1002/wics.51.
- [11] Tibshirani R. (1996). *Regression Shrinkage and Selection via the Lasso*. Journal of the Royal Statistical Society. Series B, 58(1):267288.