DEEP LEARNING APPROACH FOR IN-STENT RESTENOSIS USING BIOLOGICALLY-INFORMED NEURAL NETWORKS

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Introduction

Coronary artery disease (CAD) is one of the largest causes of death worldwide. Percutaneous coronary intervention (PCI) is one of the minimally invasive procedures used to overcome CAD by restoring blood flow in clogged coronary arteries. Unfortunately, PCI is associated with several risk factors including in-stent restenosis and stent thrombosis. Drug-eluting stents were developed to counteract the severe restenosis observed after bare-metal stent implantation. The risk of restenosis still prevailed due to the inhibitory effect of the drug on endothelial healing.

The current work focuses on developing a multiphysics-based model using a **deep learning** framework to include the effect of anti-inflammatory drugs embedded in the drug-eluting stents. An additional advection-reaction-diffusion equation governing the drug transport is introduced herein. Additionally, the effect of drugs, specifically rapamycin-based ones, on the proliferation of smooth muscle cells (SMC) is captured.

Methods

The highly resolved multiphysics model is based on a set of coupled partial differential equations (PDEs), which govern the mechanism of neointimal hyperplasia by capturing the effects of platelet aggregation, growth-factor release, cellular motility, endothelial barrier function and drug deposition [1]. This framework is intended to aid in individualizing the PCI parameters that include stent geometry, balloon overexpansion, and the level of drug embedment. Also, they assist in personalizing the post-operative therapeutic regimens.

Biologically-informed neural networks (BINNs), an extension of the physic-informed neural network (PINNs), are applied to solve the underlying dynamics of biological systems.

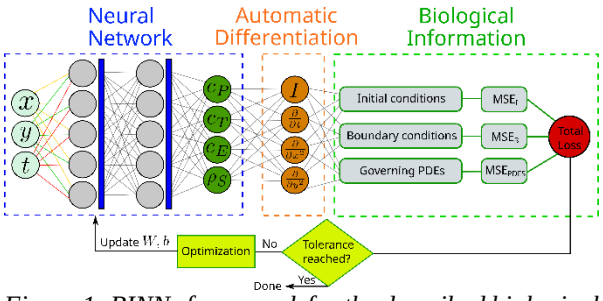

Figure 1: BINNs framework for the described biological system.

Results

Fig. 2 shows the normalized extracellular matrix (ECM) concentration and SMC density 100 days after PCI.

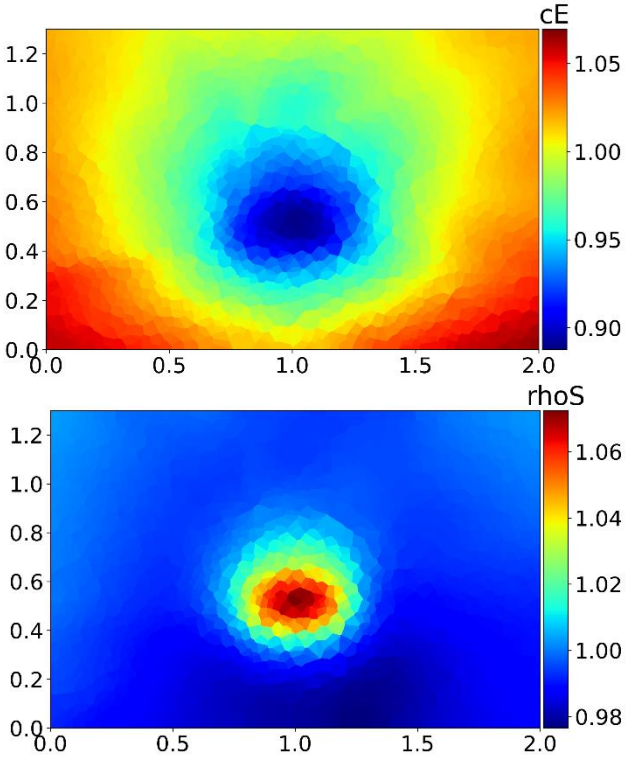

Figure 2: Normalized extracellular matrix (ECM) concentration and the smooth muscle cells (SMC) density 100 days after balloon angioplasty.

Discussion

The coupled PDEs have been successfully solved using BINNs, where the deep learning results are evaluated and verified by comparing the simulation results of classical finite element methods. Hence, deep learning based on BINNs can be regarded as a reliable methodology for modeling biological systems.

References

1. Manjunatha et al., Comput. Biol. Med., 150:106166, 2022.

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