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Evaluating Closed-Loop Effects from Vasodilator Administration for Pulmonary Hypertension Treatment

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Extended Abstract

Closed-loop data science can facilitate clinical decision-making by addressing a common situation in which acting on predictions from a calibrated model affects the initial assumptions of the model, e.g. the patient's physiology, however the model cannot be re-calibrated. Consider the following, typical scenario. At an initial visit a patient undergoes a number of tests, some of which might be invasive, which allows clinicians to diagnose the patient and administer suitable medication. Monitoring at follow-up visits is typically limited to a reduced number of tests, preferably noninvasive and/or less expensive. The challenge is then to assess the impact the administered medications have had on the patient's health and physiology, i.e. the *closed-loop effects* that occur after human intervention.

In the present paper we focus on evaluating closed-loop effects from vasodilator administration for treating pulmonary hypertension (PH), i.e. high blood pressure in the lungs. PH is a serious and potentially fatal disorder, typically treated by administrating vasodilators, i.e. drugs that dilate pulmonary arteries, thus causing the pulmonary arterial pressure (PAP) to decrease. In our framework we apply a 1D fluid dynamic mathematical model with structured tree boundary condition [1] The model predicts pressure, flow and vessel area for a given pulmonary arterial network and parameters characterising the patient's physiology.

An earlier proof-of-concept study [2] has demonstrated the importance of closed-loop data science in cardio-vascular modelling. In that study, the detailed structure of the vasculature related to small blood vessels was approximated by electrical circuit elements (so-called ``Windkessel elements'') to simplify the mathematical complexity. To make our model physiologically more realistic, we have now relaxed this assumption and replaced the Windkessel elements by a more detailed model of the downstream vasculature, i.e. the structured tree model [1]. This leads to challenging problems related to parameter identifiability and interpretability, and we will discuss how they can be addressed so that the model can be calibrated for clinical decision support applications.

References

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