Toward Clinically-Inspired Validation of ML-Driven Source Localization in Molecular Communication

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***Abstract*—Accurate localization of tumor sources in the human circulatory system is essential for precision oncology. In prior work, we developed a machine learning (ML) framework to localize anomaly sources using temporal biomarker profiles measured at receiver sites. However, the dataset was generated in a generic source-receiver setting, limiting physiological realism. This work-in-progress paper extends the framework by validating the ML model on a clinically-inspired dataset that emulates endocrine signaling in a controlled synthetic environment. The model is retrained and evaluated using a stratified held-out split with 25 % reserved for testing. Preliminary results show an accuracy of ∼90 %, indicating the potential of ML-driven approaches for tumor source localization in clinically relevant molecular communication settings.**

***Index Terms*—Molecular communication, localization, machine learning, tumor, endocrine signaling, human circulatory system**

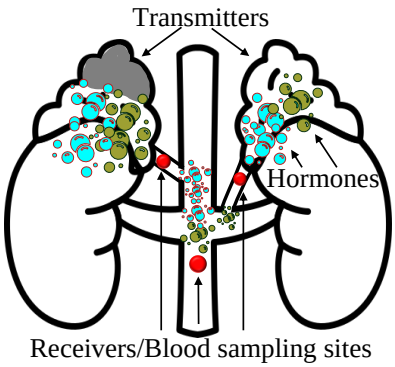


Fig. 1: MC-inspired endocrine signaling model.

I. Introduction

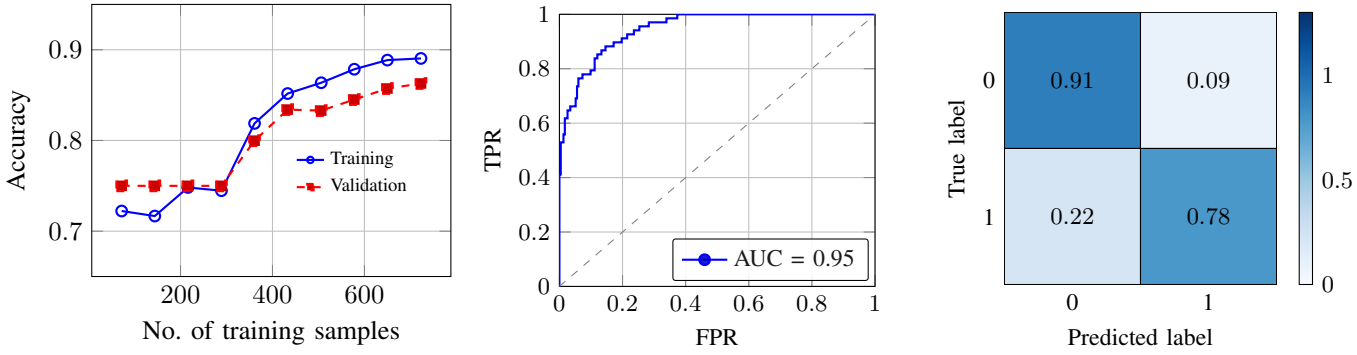
Localizing tumor sources within the human body is a fundamental yet challenging problem for diagnosis and treatment [1]. During disease progression, tumor sites release biochemical signals, or biomarkers, into the human circulatory system (HCS) [2]. As these biomarkers propagate through biological fluids such as blood, their concentration profiles are altered by advection, diffusion, degradation, and dilution. Consequently, wearable receiver sites observe distorted, time-varying signals rather than direct signatures of the tumor origin. Understanding molecular communication (MC) in realistic biological fluids is therefore an important step toward clinically relevant in-body modeling [3]. Within this framework, tumor source localization becomes a challenging inverse problem in which the tumor origin is inferred from stochastic molecular signals measured at the receiver.

Machine learning (ML)-based models offer a data-driven approach to this inverse problem by learning spatiotemporal patterns in receiver-side biomarker time-series signals and inferring source locations from the observed molecular dynamics. This approach is especially relevant from a clinical perspective, where biomarker measurements are typically sparse in both space and time due to limited blood draws or infrequent sampling. Building on this motivation, in our prior work [4], we proposed an ML-based framework for localizing infection sources in the HCS using simulated biomarker time-series data.

However, the previous framework relied on a generic source-receiver setup and lacked physiological realism. This work-in-progress paper explores validating the prior ML framework in a clinically-inspired endocrine signaling scenario involving aldosterone and cortisol secretion by the adrenal glands. To emulate clinically relevant molecular dynamics, we use the MEHLISSA simulator [5] and generate physiology-aware dataset based on adrenal venous sampling (AVS) settings.

II. System Model

Following our previous framework [4], we adopt a biologically grounded model of endocrine signaling, as shown in Fig. 1. The adrenal glands are modeled as hormone-secreting transmitters, the HCS acts as the communication channel, and venous blood sampling sites serve as receivers analogous to clinical AVS. Specifically, the right adrenal vein, left adrenal vein, and inferior vena cava (IVC) are represented as passive receivers that measure hormone concentrations. We implement this setup using the MEHLISSA simulation framework [5], [6], which models the human vascular system as a directed 3D network of blood vessels. The framework is extended with separate left and right adrenal glands and veins to enable continuous secretion of aldosterone and cortisol into the vascular network. The hormones propagate through the vessels via diffusion and advection governed by vessel-specific blood flow and are passively observed at the receivers. At each receiver, hormone arrival times and concentrations are recorded, producing time-series signals that serve as input features for the ML-based localization model.



(a) Accuracy (b) ROC curve (c) Normalized confusion matrix

Fig. 2: Performance of the ML model on the held-out test set.

III. Clinically-Inspired Dataset and Validation

In the AVS-derived clinical measurement, the highest hormone concentration is observed at the right adrenal vein, followed by the IVC and the left adrenal vein. We calibrate the simulator to reproduce key AVS-derived metrics, including the selectivity index and lateralization index [7]. The simulated values closely match the clinical reference measurements, with deviations ranging from $\sim$2 % to $\sim$7 %.

Using this configuration, we generate a dataset from 1205 simulations, each with duration 100 s. Hormone concentrations and arrival times are recorded at three receiver sites. From the resulting time-series data, statistical and temporal features such as peak concentration, time-to-peak, and arrival delay are extracted. Since the clinical measurements served only as calibration references, pseudo-labels were assigned by thresholding the mean concentration per sample at the 75 $^{\text{th}}$ percentile, labeling samples as elevated or normal concentration. To evaluate the adaptability of the prior ensemble model [4], we retrain it on the MEHLISSA-generated dataset. The data are split using an 80/20 stratified train-test split to preserve class balance, and performance is evaluated using standard classification metrics on the held-out test set.

Preliminary results shown in Fig. 2a indicate that the model achieves $\sim$90 % accuracy on the held-out test set. The receiver operating characteristic (ROC) curve in Fig. 2b shows an area under the curve (AUC) of about 0.95, demonstrating strong discriminative performance. The confusion matrix in Fig. 2c further depicts reliable separation between normal and elevated hormone secretion patterns. All associated data and code are publicly available in [8] under CC BY and MIT licenses. These early results suggest the feasibility of ML-based localization in clinically inspired MC scenarios. However, the evaluation is limited to synthetic simulations and a simplified endocrine signaling setup and should therefore be interpreted as a methodological proof-of-concept.

IV. Conclusion

In this work-in-progress paper, we validate our prior ML-based source localization framework using a clinically-inspired endocrine signaling dataset generated with the MEHLISSA simulator. The model achieves around 90% classification accuracy and generalizes well, supporting the potential of ML-driven source localization in clinically relevant settings. In practice, however, background molecular signals, patient-specific variability, and time-varying secretion rates may influence the observed signals and thereby affect localization performance. Future work will extend the framework to incorporate these factors.

Acknowledgments

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