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MODULAR FULL-HEAD FNIRS SIMULATOR FOR HEMODYNAMIC RESPONSE MODELING

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ABSTRACT

Functional near-infrared spectroscopy (fNIRS) is a noninvasive neuroimaging modality that has shown promising results as a tool for clinical neuroimaging and brain-computer interfaces (BCI). Due to the shortcomings of heuristic denoising and expert-dependent postprocessing, data-driven approaches (e.g., deep learning) to fNIRS analysis are becoming increasingly popular. To accommodate for the associated demand for large, labeled fNIRS datasets, we develop a modular 3D fNIRS simulator. Our simulator can generate spatiotemporal distributions of a variety of hemodynamic response functions (HRFs), allowing for high-fidelity modeling of experiment-specific cortical activity. We describe the model used for generating synthetic data, and compare several HRF basis functions used to model cortical hemodynamic activity.

1 INTRODUCTION

Functional near-infrared spectroscopy (fNIRS) is a noninvasive neuroimaging technique that is gaining popularity for its low cost, unobtrusive setup, and comparatively high spatial and temporal resolution (Yücel, Selb, Huppert, Franceschini, and Boas 2017). As a result, fNIRS has seen increased use in neuroimaging studies such as clinical monitoring (Rahman, Siddik, Ghosh, Khanam, and Ahmad 2020) and brain-computer interfaces (BCI) (Naseer and Hong 2015). However, current data processing practices, which rely on lengthy post-hoc denoising and heuristic analyses, can hinder many real-world applications (Dans, Foglia, and Nelson 2021). To overcome these limitations, data-driven methods (e.g., deep learning) have been widely employed in fNIRS research (Eastmond, Subedi, De, and Intes 2022). While such methods have shown promising results across different tasks, their reliance on large labeled datasets can make training impractical in many cases. To address this challenge, we develop a novel synthetic data generator that models full-head hemodynamics and leverages multiple hemodynamic response function (HRFs) to reduce potential simulation gaps due to a single HRF (Lindquist, Loh, Atlas, and Wager 2009).

2 MESH-BASED MONTE CARLO SIMULATIONS

To simulate neural time series, we register an experimental fNIRS montage on a tetrahedral full head mesh that is segmented into tissue types. Using the MATLAB-based toolbox Mesh-Based Monte Carlo (MMC) (Tran, Yan, and Fang 2020), photon propagation through the mesh is simulated in order to construct the sensitivity matrix (i.e., Jacobian) of the registered probe to the full head ($\mathbf{J}$).

By manipulating the change in absorption ($\delta\mu_{at}$ where μ_a is the absorption coefficient) at each time point t, we can use the Jacobian to model synthetic fNIRS time series via the equation: $\mathbf{J}\,\delta\mu_{at} = \mathbf{b}_t$ where the Rytov-normalized measurement vector $\mathbf{b}_t$ relates the simulated baseline measurement ϕ_0 with the simulated intensity measurement vector ϕ_{1t} using $\mathbf{b}_t = \log\phi_0 - \log\phi_{1t}$. By manipulating $\delta\mu_{at}$, we can generate a series of measurement vectors which are dependent on the spatial sensitivity profile $\mathbf{J}$ (see Figure 1**A**) and a set of physiological parameters θ which are used to model $\delta\mu_{at}$.

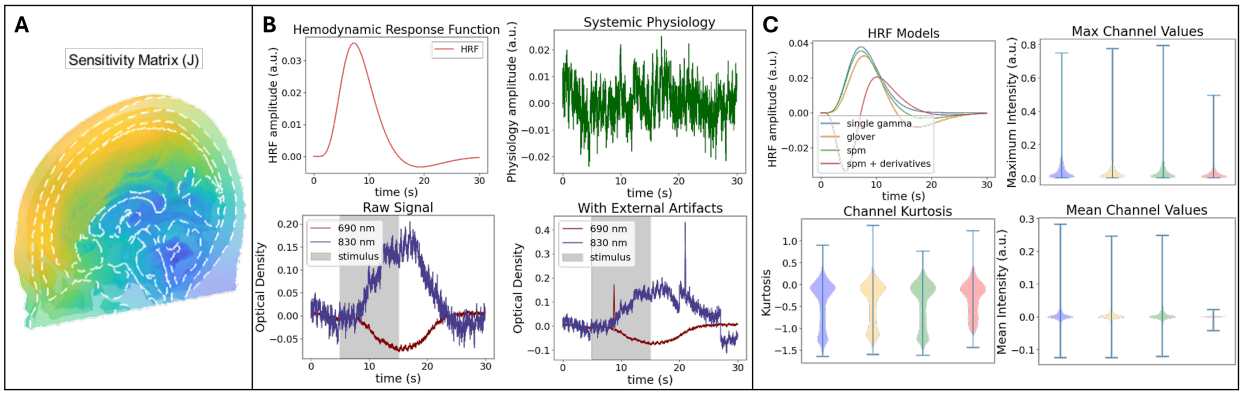

Figure 1: A graphical overview of our simulation toolkit including the full-head sensitivity matrix (Panel **A**), modeled signal components and example signals (Panel **B**), as well as a comparison of example HRF models and associated high-level signal statistics over an ensemble of simulations (Panel **C**).

3 CORTICAL ACTIVITY

To model local cortical activity, we convolve a parametric HRF with an experimental stimulus vector to simulate fNIRS signals obtained in a block experiment design. To mitigate potential simulation gaps associated with reliance on a single HRF model (Lindquist, Loh, Atlas, and Wager 2009), we have implemented the HRF models shown in Figure 1**C** to account for various phenomena, such as increased delay in the hemodynamic response or uncertainty in response timing.

4 SYSTEMIC PHYSIOLOGY AND EXTERNAL ARTIFACTS

Since systemic physiological contributors to fNIRS data are defined by characteristic frequency bands (Dans, Foglia, and Nelson 2021), we can model contributions to systemic physiology in the frequency domain via the relative power and central frequency of the following components: Mayer waves, respiratory oscillations and cardiac oscillations, along with a $1/f^{\alpha}$ exponential frequency component (see Figure 1**B**). These systemic physiological components are spatially distributed throughout the head and summed with the modeled localized change in absorption due to cortical activity to model $\delta\mu_{at}$ for every time point t. Finally, we model motion artifacts as spike and baseline shift events, which are directly added to simulated intensity values. Further, we model channel dropout as measurement channel replacement with Gaussian white noise with random amplitudes.

Significance: The proposed simulation pipeline provides a method for modeling the complex spatiotemporal information present in fNIRS data, with greater flexibility in modeling cortical activity than any current method, allowing for the generation of large, labeled, high-fidelity fNIRS datasets

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