SUBJECT SELECTION FRAMEWORK TO IMPROVE PERSONALISED MODELS FOR MOTOR-IMAGERY BCIS VIA WAVELETS AND GRAPH DIFFUSION

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ABSTRACT

Personalized electroencephalogram (EEG) decoders hold a distinct preference in healthcare applications, especially in the context of Motor-Imagery (MI) Brain-Computer Interfaces (BCIs), owing to their inherent capability to effectively tackle inter-subject variability. This study introduces a novel subject selection framework that blends ideas from discriminative learning (based on continuous wavelet transform) and graph-signal processing (over the sensor array). Through experimentation with a publicly available MI dataset, we showcase enhanced personalized performance for MI-BCIs. Notably, it proves particularly advantageous for subjects who initially demonstrated suboptimal personalized performance.

1 INTRODUCTION

Brain-Computer Interface (BCI) technology represents a cutting-edge frontier in the field of human-computer interaction, seeking to establish seamless communication and control between the human brain and computers. Motor-Imagery (MI) stands out as a pioneering paradigm. MI-BCIs harness the power of cognitive processes, allowing individuals to mentally simulate motor actions, such as hand or foot movements, without the need for actual physical execution (Decety & Ingvar (1990)). By decoding and interpreting the intricate patterns of brainwaves captured through EEG signal recordings using signal processing and machine learning techniques, MI-BCIs hold immense promise in revolutionizing the way we interface with technology, offering various medical applications ranging from rehabilitation (e.g. Mane et al. (2020), Robinson et al. (2021), (Sebastián-Romagosa et al. (2020)) to neuroprosthetics (e.g. Ofner & Müller-Putz (2012), Pascual et al. (2012), (Wang et al. (2022)).

The advent of deep learning has significantly enhanced the performance of MI-BCIs (Schirrmeister et al. (2017), Lawhern et al. (2018), Santamaría-Vázquez et al. (2020)) by allowing the automatic extraction of intricate patterns from EEG signals and alleviating the need for manual feature extraction, a process which usually requires significant neurological expertise and experience. In addition, deep learning's ability to adapt and generalize across diverse datasets has paved the way for more universally applicable MI-BCI systems, opening new possibilities for real-world applications. Despite deep learning's success, a fundamental obstacle confronting MI-BCIs lies in adapting to variations in data distributions among different subjects (Saha & Baumert (2020), Barmpas et al. (2022)). The distinctive brain anatomy and functionality inherent to each individual pose a significant challenge in identifying and utilizing shared invariant features. Therefore, modern deep learning-based MI-BCIs often struggle to effectively generalize to unseen subjects primarily due to this type of data distribution shift.

Although several methods have been proposed to tackle inter-subject variability (e.g. He & Wu (2020), Özdenizci et al. (2020), Wei et al. (2022), Barmpas et al. (2023b)), personalized models are favored in MI-BCIs within healthcare applications due to their inherent advantage in effectively handling inter-subject variability. By adopting personalized models, MI-BCIs can tailor their algorithms to the specific characteristics and the intricacies of an individual's brain activity, resulting in enhanced performance. Historically, personalized MI-BCI models relied on manual features. However, in more recent developments, deep learning architectures have emerged for MI-BCIs that enable the training of efficient personalized models without succumbing to overfitting.

In this work, we introduce a subject selection framework for augmenting the data available to craft a personalized model, by incorporating additional signals from subjects with similar brain activations. The overall framework utilizes brain signal analytics to compare responses at individual sensor levels and employs a graph-based approach to analyze discriminative patterns across subjects, resulting in a semantic map facilitating the identification of relevant data for training personalized models. Our framework demonstrates enhanced performance for personalized MI-BCIs, particularly benefiting subjects who initially exhibited low personalized performance. In our experiments, we use mainly BrainWave-Scattering Net (Barmpas et al. (2023a)), as a state-of-the-art lightweight deep learning architecture for personalised MI-BCI decoders.

2 BACKGROUND

BrainWave-Scattering Net (Barmpas et al. (2023a)) is a lightweight neural network architecture employing trainable Gabor wavelets to disperse EEG signal information into scattering decomposition paths across frequency and slow-varying temporal modulations. It utilizes a joint time-frequency wavelet scattering transform (Anden et al. (2019)), comprising a first-order time scattering transform followed by independent two-dimensional wavelet analysis in the time and frequency domains using one-dimensional wavelets.

$$Sx = ||x(t) * \psi_\lambda(t)| * \Psi(t, \lambda)| * \phi(t) \tag{1}$$

where $\Psi(t, \lambda) = \psi(t)\psi(\lambda)$ is the product of two one-dimensional wavelets functions in time and frequency. Equation 1 captures the joint variability of $|x(t) * \psi_\lambda(t)|$ at frequency and time, while the modulus and time-averaging operation $\phi(t)$ ensures time-shift invariance and time-warping stability. Equation 1 is implemented in BrainWave-Scattering Net via a series of depthwise convolutions, various kernel sizes, striding and non-linearity operations.

3 METHOD

We denote vectors as $\boldsymbol{x}$, matrices as $\boldsymbol{X}$ and tensors of order ≥ 3 as $\mathbf{X}$. Let $\boldsymbol{X}_i(c, t) \in \mathbb{R}^{C \times T}$ denote each single-trial EEG signal recorded with C channels that comes with the label y_i.

3.1 GRAPH DIFFUSION DISTANCES

Enhancing the efficacy of personalized deep learning-based MI-BCI decoders through targeted subject selection during training necessitates the adoption of an appropriate metric to assess subject similarities. Our proposed framework leverages continuous wavelet transform (CWT) and graph diffusion distances.

For each subject in the dataset, and for each sensor independently, we first derive all the single-trial scalograms, using CWT based on analytic Morse wavelet. We then statistically compare the distribution of moduli at each point in the time-frequency domain using two-sample unpaired Wilcoxon test. The resulting discriminability scores $\mathbf{S}(c, f, t) \in \mathbb{R}^{C \times F \times T}$ express the differences between the contrasted conditions (e.g. left vs right hand MI) for each sensor. Integration over the frequency-time dimensions yields a discriminability profile $\boldsymbol{p}(c) \in \mathbb{R}^C$ for each subject.

To systematically compare the discriminability profiles across subjects, we adopted the following graph-theoretic perspective so as to accommodate for the fact that these are patterns over a irregular domain (i.e. the sensor array). To this end, we consider each profile as a graph signal (Laskaris et al. (2020)) and employ graph-diffusion distance as a means to express their pairwise similarity

relationships. Using the Euclidean distance of spatial coordinates of the sensors, the adjacency matrix $\boldsymbol{A} \in \mathbb{R}^{C\times C}$ of the graph as well as its corresponding Laplacian $\boldsymbol{L} \in \mathbb{R}^{C\times C}$ are computed. Then we obtain the pseudo-inverse of the graph Laplacian $\boldsymbol{Q} = (\boldsymbol{I} + \boldsymbol{L})^{-1} \in \mathbb{R}^{C\times C}$ where $\boldsymbol{I}$ is the identity matrix. The graph diffusion distance between two subjects is computed using the equation:

$$d(s_1, s_2) = ||\boldsymbol{Q} \times (\boldsymbol{p}_{s_1} - \boldsymbol{p}_{s_2})||_2 = ||(\boldsymbol{I} + \boldsymbol{L})^{-1}(\boldsymbol{p}_{s_1} - \boldsymbol{p}_{s_2})||_2 \tag{2}$$

$(\boldsymbol{I}+\boldsymbol{L})^{-1}$ can be interpreted as the solution to a diffusion equation on the graph, formed by the EEG sensors, starting with an initial condition of $(\boldsymbol{p}_{s_1} - \boldsymbol{p}_{s_2})$. While the norm operation measures the magnitude or "spread" of this diffusion process. It provides a way to quantify how much the initial difference between $\boldsymbol{p}_{s_1}$ and $\boldsymbol{p}_{s_2}$ has diffused across the graph after applying the pseudo-inverse of the graph Laplacian. The rationale behind this computation is to counteract the spatial jitter in these profiles that reflect possible inter-subject anatomical variabilities. For a dataset with K unique subjects, applying our method yields a symmetric matrix $\boldsymbol{D} \in \mathbb{R}^{K\times K}$

3.2 Subject Selection

To represent the (dis)similarities conveyed in the symmetric matrix $\boldsymbol{D} \in \mathbb{R}^{K\times K}$ in an intelligible way, we perform classical multidimensional scaling (MDS). This results in a semantic map (Laskaris & Ioannides (2002)), in which each subject is mapped on a two-dimensional space in which the distances between points (subjects) approximate the (dis)similarities in matrix $\boldsymbol{D}$. For the subject selection step, we calculate the Euclidean distance between the subjects in this two-dimensional space and choose the N (where N acts as a hyper-parameter) neighbours to include in the training phase of the personalized deep learning-based MI-BCI decoder.

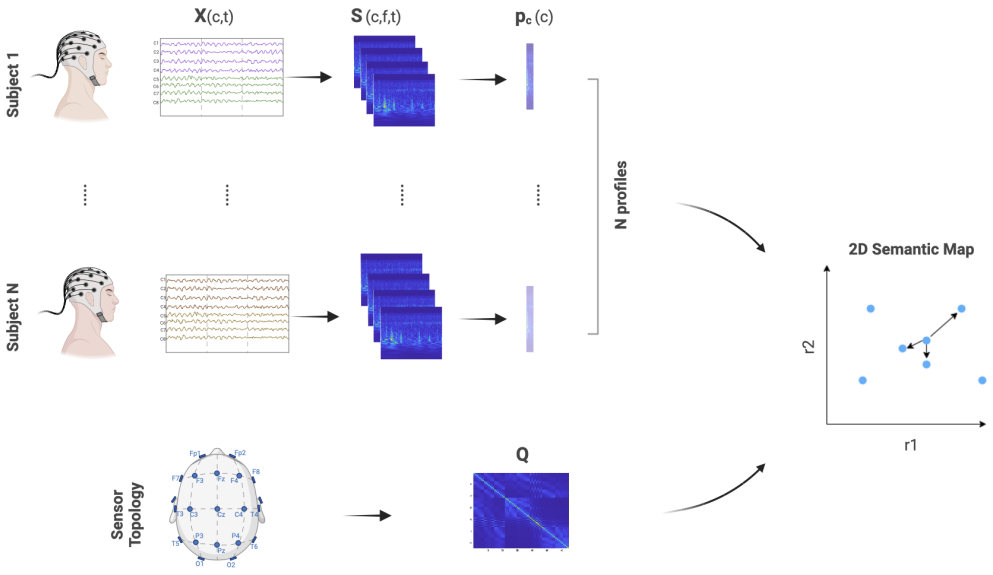

Figure 1: Our proposed subject selection framework using wavelet transform and graph diffusion. For each subject, the discriminability scores **S** are calculated. Integration over the frequency-time dimensions yields discriminability profile $\boldsymbol{p}$ for each subject. From the sensor topology, the pseudo-inverse of the graph Laplacian $\boldsymbol{Q}$ is calculated. Using the $\boldsymbol{p}$ profiles and $\boldsymbol{Q}$, the symmetric matrix $\boldsymbol{D}$ is computed that contains the graph diffusion distances. Finally, the $\boldsymbol{D}$ is mapped onto a two-dimensional space and neighbouring subjects are selected.

4 EXPERIMENTS

We tested our proposed subject selection framework using BrainWave-Scattering Net (Barmpas et al. (2023a)), a state-of-the-art architecture for both personalized and generalized MI-BCI decoders, in a binary classification task (MI Left vs Right Hand), formed based on the publicly available MI dataset Physionet (Goldberger et al. (2000)). The Physionet dataset was chosen due to its handful data sampled per subject. The initial Physionet dataset comprises brain recordings obtained from 109 healthy individuals, recorded using 64 EEG sensors with a sampling frequency of 160 Hz during the execution of a set of pseudo-randomized cue-triggered Motor-Imagery (MI) tasks. In our study, we omitted data from 6 participants (subjects 88, 89, 92, 100, 104, and 106) due to variations in either the sampling frequency or the duration of the tasks performed. We extracted trials (45 trials per subject) corresponding to MI hand movements in the form of segments starting with the visual cue and lasting for 4.1 seconds.

Using the proposed framework in Section 3, we computed the symmetric matrix $\mathbf{D} \in \mathbb{R}^{103\times103}$ (excluding the 6 bad subjects) and generated the two-dimensional discriminability map displayed in Figure 2. We evaluated the personalised performance of the subjects on leave-one-trial-out cross-validation scheme. We noticed that the subjects on the right-hand side of the discriminability map demonstrated higher personalised performance compared to the ones on the left-hand side.

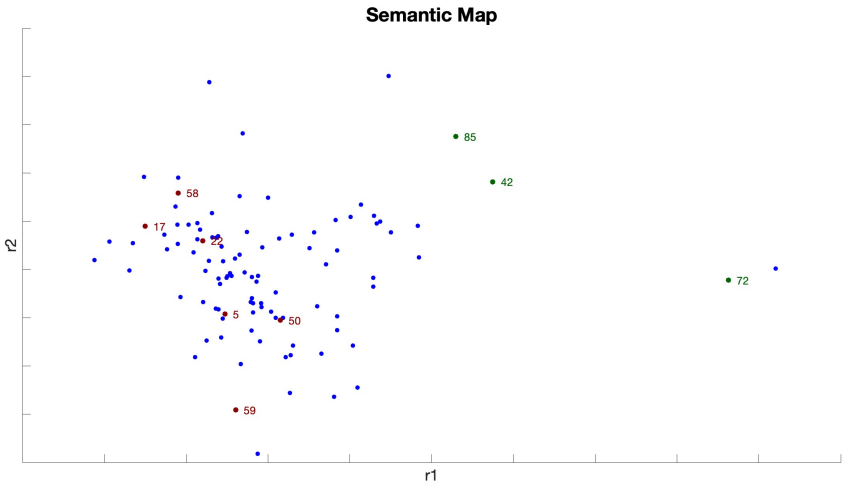

Figure 2: Two-dimensional semantic map for the 103 Physionet subject based on graph diffusion distances of our proposed subject selection framework. Green subjects have personalised performance $> 70\%$ while red subjects have personalised performance $< 70\%$.

Our objective with the proposed subject selection framework is to investigate whether the personalized performance of bad performing subjects can be improved. To assess this hypothesis, we identified 6 subjects exhibiting performance close to random levels during leave-one-trial-out cross-validation. For each of these subjects, we opted to incorporate 5 neighboring subjects ($N = 5$) in the training phase of their respective personalized models. To mitigate concerns regarding any potential performance enhancement being solely attributed to the increase in training data samples, we conducted the same personalized training using five randomly-selected non-neighboring subjects. Subsequently, we compared the performance of these personalized models with that of generic models trained on the remaining 102 subjects. As it is shown in Table 1, the models trained with our proposed subject selection framework demonstrate increased personalised performance while in most cases outperforming their respective generic models.

Subject	Only Subject's Samples	With Neighbours	With Random	Generic
17	64.4%	**91.1%**	68.8%	86.6%
22	57.7%	**84.4%**	66.6%	73.3%
58	66.6%	**75.5%**	68.8%	64.4%
5	60%	**75.5%**	60%	**75.5%**
59	60%	**80%**	62.2%	73.3%
50	53.3%	**80%**	66.6%	**80%**

Table 1: Performance of personalised (trained and evaluated in a leave-one trial-out fashion) models of MI-classification (Left / Right hand) tasks in Physionet for BrainWave-Scattering Net using i) only subject's samples, ii) extra neighbours selected using our proposed framework, iii) extra randomly selected subjects and iv) comparing with a generic model.

5 CONCLUSION

In this work, we proposed a subject selection framework, harnessing wavelet transform and graph diffusion distances. Through experimentation, we showcased that our proposed framework achieves increased personalised performances of subjects who initially exhibited poor performance. This advancement holds particular significance in medical applications, where personalized models play a pivotal role in achieving tailored and effective interventions. Future work will include evaluation on more MI datasets and MI tasks, training with other deep learning-based MI decoders (that allow training of personalised models with limited training data) as well as an ablation study of the influence of neighboring-selected subjects (N) in our results.

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