Domain Adaptation and Generalization of Functional Medical Data: A Systematic Survey of Brain Data

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Despite the excellent capabilities of machine learning algorithms, their performance deteriorates when the distribution of test data differs from the distribution of training data. In medical data research, this problem is exacerbated by its connection to human health, expensive equipment, and meticulous setups. Consequently, achieving domain generalizations and domain adaptations under distribution shifts is an essential step in the analysis of medical data. As the first systematic review of domain generalization and domain adaptation on functional brain signals, the article discusses and categorizes various methods, tasks, and datasets in this field. Moreover, it discusses relevant directions for future research.

CCS Concepts: • **Computing methodologies** → **Transfer learning**; • **General and reference** → *Surveys and overviews;*

Additional Key Words and Phrases: Domain adaptation, domain generalization, functional medical data

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1 INTRODUCTION

Machine Learning (ML) is the process of guiding a computer system on how to make accurate predictions for a specific task when fed with data. Given the popularity of previous ML approaches, the main challenge in using them is how to choose features that fit more information and overlap less before learning. **Deep Learning (DL)** is a subset of ML techniques that achieve accurate performance and flexibility in several learning tasks, such as medical data analysis, without the

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need to specify features before the learning process; in these models, the data used for both training and testing is assumed to come from the same distribution, known as identically and independently distributed. In other words, the training and testing data behave similarly [153]. The identically and independently distributed assumption, together with the fact that there are various datasets in every ML task, makes it difficult for a model trained on the data from one domain to perform well on the data from another domain. The lack of **domain generalization (DG)**, which is the ability of the model to work well on new data samples from different domains, makes many deep neural networks and traditional ML models impractical and unusable for real-world applications.

The generalization issue is even more apparent in medical data analysis. On the one hand, it is often not practical for the model to work on data measured in a different situation or from a different subject because of the wide range of conditions, priors, and factors affecting each data sample. On the other hand, considering that the study of medical data directly concerns people's health, even small mistakes are unacceptable and can lead to severe consequences. Hence, in these tasks, the ability to adapt the model trained on source domains into a new target domain, known as **domain adaptation (DA)**, and train generalizable models, known as DG, is crucial.

This work presents the first comprehensive review of methods establishing DG/DA for medical data, focusing on functional brain data. Each model is categorized by *Approach*, the main idea for DG/DA, *Domain*, the type of domain defined in the generalization/adaptation task, *Task*, the main task that the model is required to solve in a DG/DA fashion, and *Multi-/single source*, whether the work tackles the situation in which we have multiple sources (multi-source) or not (single source). We also collect the popular and mainly used datasets in the literature and provide a brief explanation of each and a comparison by different properties, such as the number of subjects and size of the dataset. Extra content, tables, and figures are available at http://git.dml.ir/behnamnia.a/DG_DA_fMedical_Survey.

There are several review papers on DG/DA methods in the general concept [33, 99, 153, 183], and one survey paper specialty on DA in medical data [41] which mainly focuses on models built for structural brain data such as **Magnetic Resonance Imaging (MRI)**. Nevertheless, this work focuses on functional brain data, which is more inclusive and vital, and it also investigates recent models more thoroughly and systematically.

In conducting this review, we have systematically gathered, categorized, and explained recent methods pertinent to DG/DA in EEG and fMRI data, which are two of the most prevalent modalities in functional brain data studies. The focus is primarily on research papers published on these modalities between 2019 and the end of 2022. The selection process involved filtering papers based on their performance, novelty, and scientific value. To establish a standardized approach for method selection and presentation to the audience, papers exclusively relying on private datasets have been omitted from this study. These criteria include 98 papers on EEG data and 24 papers on fMRI data, as detailed in Section 4. Subsequently, Section 5 delves into categorizing and discussing popular publicly available datasets in this field featured in the papers mentioned previously.

This article is organized as follows. In Section 2, we briefly review the concepts, notations, and fields related to DG/DA and medical data analysis. Section 3 describes the applications and studied tasks of DA and DG in medical data analysis. Next, Section 4 reviews remarkable recent DA and DG methods used to process medical data. This section provides a comprehensive hierarchy of the approaches followed in the literature that semantically categorizes recent studies in this field. In Section 5, we go through the popular public datasets used as benchmarks for DG/DA of medical data. Last, in Section 6, we propose potential future works that are suggested to be followed according to our studies, and in Section 7, we conclude the article.

2 BACKGROUND

This section briefly describes issues, notations, and categories in DA and DG. In addition, we describe tasks and problems associated with medical data analysis.

2.1 DA and DG

With increasing data, DL models are being pushed to get the most accurate results in many fields. However, a significant portion of the available data is unlabeled, and preparing and labeling proper data for deep neural networks is costly and time consuming [159]. Furthermore, in some fields, like medical data analysis, acquiring data is challenging, and tagging the data requires the collaboration of several experts. Deep models may be trained using labeled datasets and used directly on the target dataset for inference to address this problem. However, this does not effectively transfer knowledge between datasets. It has been demonstrated by Zhao et al. [177] that direct transfer fails in digit recognition and semantic segmentation as well as traditional supervised learning methods. Performance deterioration occurs due to the domain shift between the source and target datasets. Alternatively, transfer learning can resolve the problem by transferring a well-trained model on a dataset with many labeled samples to a target dataset with fewer labels. Figure 1(a) illustrates the different subcategories of transfer learning. DA is referred to a group of ML methods that can transform learned information from one or several fully labeled source datasets to a target dataset defined on the same task, considering the existence of domain shift, which refers to the change in the marginal distribution of the data.

In DG, however, no information about the domain of the target sample is known. So the goal is to develop models that work well on new data without prior knowledge about its domain.

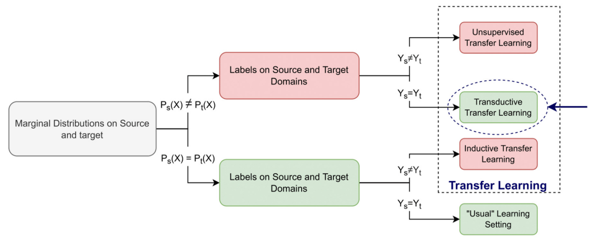
2.1.1 *Notation.*

To define the DA problem, we should explain the source and target domains. Suppose that a shared space $\mathcal{X} \times \mathcal{Y} = \{(x, y) | x \in \mathcal{X}, y \in \mathcal{Y}\}$, where $\mathcal{X}$ is the space of feature values and $\mathcal{Y}$ is the space of label values. A domain $D \subset \mathcal{X} \times \mathcal{Y}$ is a collection of paired data and labels. Training or test data samples come from their corresponding domains. Assume that $D_s = \{(\mathbf{x}_s^{(i)}, y_s^{(i)})\}_{i=1}^{N_s}$ is a domain where $(\mathbf{x}_s^{(i)}, y_s^{(i)})$ is sampled from joint distribution $P_{X_s Y_s}$ defined on $\mathcal{X} \times \mathcal{Y}$.

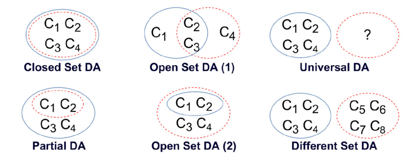
Consider that there are N source domains S_i, where $N \geq 1$, and one target domain T. Note that in some scenarios, we can have several target domains, but for simplicity, we consider a single-target domain problem. Each source domain is denoted by $D_{s_i} = \{(\mathbf{x}_{s_i}^{(j)}, y_{s_i}^{(j)})\}_{j=1}^{N_{s_i}}$, where $(\mathbf{x}_{s_i}^{(j)}, y_{s_i}^{(j)})$ is drawn from the joint distribution $P_{X_{s_i} Y_{s_i}}$ on $\mathcal{X} \times \mathcal{Y}$. We consider the target domain denoted as $D_t = \{(\mathbf{x}_t^{(i)}, y_t^{(i)})\}_{i=1}^{N_t}$, drawn from distribution $P_{X_t Y_t}$ on $\mathcal{X} \times \mathcal{Y}$. For the task of unsupervised DA, which is the focus of this study, we only have the unlabeled target domain $D_t^u = \{\mathbf{x}_t^{(i)}\}_{i=1}^{N_t}$.

In the DA problem, unlike other categories of transfer learning, the conditional distribution of the source and target domain is the same (i.e., $P(Y_{s_i} | X_{s_i}) = P(Y_t | X_t)$) but the marginal distribution ($P_{X_{s_i}}$ for $i \in \{1, 2, \ldots, N\}$ and P_{X_t}) is different—in other words, $P(X_{s_i}) \neq P(X_t)$. This discrepancy is known as domain shift. Note that this discrepancy also exists among each pair of source domains: $P(X_{s_i}) \neq P(X_{s_j})$ for $i, j \in \{1, 2, \ldots, N\}$ and $i \neq j$.

The goal of DA is to reduce the negative effects caused by domain shifts between source and target domains. In other words, given $D_{DA} = \{D_t^u, D_{s_1}, D_{s_2}, \ldots, D_{s_N}\}$, a domain adaption algorithm $\mathcal{L}_{DA} : D_{DA} \rightarrow \mathcal{Y}^{\mathcal{X}}$, where $\mathcal{Y}^{\mathcal{X}}$ is the space of functions from $\mathcal{X}$ to $\mathcal{Y}$, proposes a generalizable and robust function $f : \mathcal{X} \rightarrow \mathcal{Y}$ that gets the minimum prediction error on unseen samples which are drawn from the target domain, which can be shown as $\min_f \mathbb{E}_{(x,y) \in D_t} [l(f(x), y)]$, where l is a loss function that measures the error in the prediction.



(a) Different types of ML methods based on marginal distributions and tasks of source and target domains [117].



(b) Different DA scenarios based on label distributions. The straight blue line represents the source domain label set, and the dotted red line represents the target domain label set [49].

Fig. 1. Definition and categorization of DA.

The same notation applies to DG. The only difference is that the target domain is unknown and can be drawn from an arbitrary distribution on $\mathcal{X} \times \mathcal{Y}$. So here the DG algorithm $\mathcal{L}_{DG} : D_{DG} \rightarrow \mathcal{Y}^{\mathcal{X}}$ uses only the set of source domains $D_{DG} = \{D_{s_1}, D_{s_2}, \ldots, D_{s_N}\} = D_{DA} - \{D_t^u\}$ to estimate a generalizable robust function $f : \mathcal{X} \rightarrow \mathcal{Y}$ which minimizes the prediction error on any arbitrary target domain, denoted by $\min_f \max_{D_t} \mathbb{E}_{(x,y) \in D_t} [l(f(x), y)]$.

2.2 DA and DG Categories

DG/DA methods can be categorized based on several factors, scenarios, limitations, and algorithms. Based on three different settings—labeled data availability, source domain number and distribution, and label space distribution—we discuss the most significant categories related to our issue.

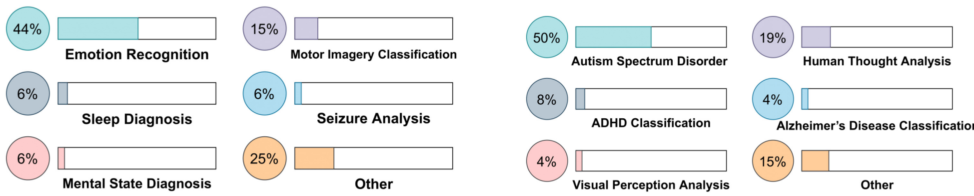
2.2.1 Labeled Data Availability. According to the availability of labeled target data, we can have three classes of DG/DA methods: supervised DG/DA, semi-supervised DG/DA, and unsupervised DG/DA. This article refers to DG/DA as *unsupervised* DG/DA, where there is no labeled data in the target domain.

2.2.2 Number of Source Domains. DG/DA methods can be divided into two varieties based on the number of source domains: single source and multi-source. In single source, only one source domain is available. In contrast, a multi-source context involves multiple distinct source domains that consist of data with different distributions, so considering them as a single domain will decrease the model's performance.

2.2.3 Label Distribution. Based on He and Wu [49], labels of source and target domains can consist of the same or different classes. As illustrated in Figure 1(b), the variability of this difference creates several scenarios for DG/DA methods. In *closed set DG/DA*, labels of source and target domains come from the same classes. *Partial DG/DA* describes the situation where the target domain's classes are a subset of the source domains' classes, which means that all labels in the target domain are available in the source domain. In *open set DG/DA*, the target domain has labels that the source domain does not [118]. It is called *universal DG/DA* when the target domain's label set is unknown and might have several common classes with the source domains' label set [166]. Last, *different set DG/DA* deals with the situation where the domain classes between the source and target are entirely different.

2.3 Medical Data Analysis

Medical data analysis is carried out to diagnose various medical conditions intelligently. Due to the development of systems based on artificial intelligence and the rapid increase in computational



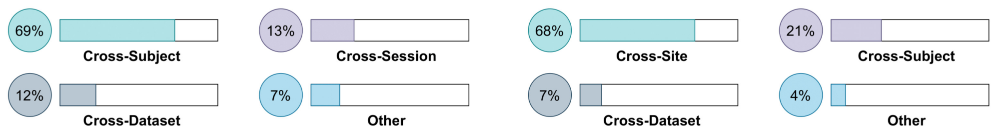
(a) EEG (b) fMRI

Fig. 2. Distributions of recent DG and DA studies based on tasks.

power, it has become more common to process high-resolution medical data intelligently. Medical data can be analyzed faster and more accurately using ML systems trained on large datasets of medical recordings. Doctors can use these models when they are unsure about their diagnosis or miss a critical clue.

There are two types of medical data: structural and functional. Structural medical data are the ones that only record the state of the body in a single unit of time. They focus on the spatial structure of the body part. They include computed tomography, MRI, pathology, endoscopy, colonoscopy, automated breast volume scan, gastroscopy, cytology, and x-ray images. Functional medical data contain both spatial and temporal information, capturing measurements of body processes rather than body states. Most of these measures are captured from the brain, such as EEG, fMRI, MEG, and fNIRS. Some functional medical signals are not measured from the brain, such as ECG (electrocardiogram) (from the heart) and EOG (from the eyes). Structural medical data have been used to diagnose cancers and abnormalities in body organs, including brain tumors, breast tumors, and lung, liver, and kidney diseases. This review focuses on *functional* medical data.

Brain-Computer Interface (BCI) models are the systems that analyze and use brain-related medical data, which constitute the majority of models based on functional medical data. We have categorized different tasks in brain signal analysis. **Motor Imagery (MI)** is a mental process in which the patient imagines moving a part of their body (e.g., imagines moving their hand or finger without actually moving them. Brain-related disease diagnosis involves the detection of brain-related diseases and conditions such as Parkinson's disease, Alzheimer's disease, schizophrenia, **Autism Spectrum Disorder (ASD)**, **Attention Deficit Hyperactivity Disorder (ADHD)**, and motion sickness. **Emotion Recognition (ER)** is also one of the most popular tasks on functional medical data, as well as **Seizure Analysis (SA)** and **Mental State Diagnosis (MSD)**, utilized in seizure and epilepsy prediction and detection, mental workload classification and assessment, mental state prediction, and diagnosis of some mental diseases such as tinnitus. **Awareness Monitoring (AM)** includes driver awareness validation, fatigue and drowsiness detection, and vigilance estimation. In **Sleep Diagnosis (SD)**, brain signals are utilized to recognize different sleep stages or events or detect sleep disorders. The studies in **Visual Perception Analysis (VPA)**, which is the analysis of human visual imagination and understanding of the surroundings, are focused on the study of **Steady-State Visual-Evoked Potential (SSVEP)** and visual recognition. Behavioral state estimation, neural decoding, working memory analysis, and subject variability modeling are among the least common tasks studied in this field. There are also interesting ongoing studies based on **Human Thought Analysis (HTA)**, such as creative drawing and imagined speech recognition. However, these areas of study are still at a very primitive stage. The distribution of the most frequently used tasks in recent DG/DA-related EEG and fMRI papers is shown in Figure 2(a) and (b), respectively.



(a) EEG (b) fMRI

Fig. 3. Distributions of recent DG and DA studies based on domains.

3 DA AND DG FOR MEDICAL DATA ANALYSIS

ML techniques in medical field analysis usually suffer from domain shift. Different centers, devices, subject populations, or experimental conditions can cause this problem. Moreover, gathering considerable medical data can be very time consuming and expensive. Some medical signals require costly measurement devices (e.g., MEG), whereas others need a meticulous and stable experimentation setup (e.g., EEG). Hence, gathering a reasonable amount of data on every new site or subject is not usually affordable. Thus, the challenge of domain shift is unavoidable in the case of medical data analysis. Medical diagnoses directly affected by this problem make DA an undisputed necessity. ML models should also perform well on newly collected data, which is a common challenge. This will be more relevant in the medical field due to the frequency of encountering data from new domains. As a result, DG is also crucial.

3.1 DG and DA Tasks in Medical Data Analysis

Different DA or DG tasks can be defined among different domains, such as subjects, datasets, and sessions. The cross-subject task is the most common in DG/DA on medical data, which considers the variability of data across subjects and tries to eliminate discrepancies between different subjects. The cross-dataset is another common DG/DA task on the medical data addressing domain shifts between datasets. This task aims to learn various aspects of these differences across medical datasets. The cross-session task is also frequent in medical data analysis. It is defined when the goal of DA or DG is to consider intra-subject data variabilities emerging during different experimental circumstances.

There are other less common DA or DG tasks—for instance, the cross-day task is analogous to the cross-session task. Additionally, it is worth noting that the cross-device task may also be studied, which considers the data variability caused by different devices used to measure the subject's signals. Figure 3(a) and (b) show the distribution of the most frequently used medical domains in recent DG/DA-related EEG and fMRI studies, respectively.

3.2 DG vs. DA in Medical Data Analysis

There are fundamental differences between DA and DG, which cause different applications. As mentioned before, high performance for unseen medical data is almost vital, as it is very time consuming to learn a different model for a new subject or patient. Nevertheless, generalization is not always the desired goal in the medical field; sometimes we face specific domains, such as data from the same organ acquired by different devices or from different subjects. The key to minimizing domain shifts between these related but different domains is DA in these situations, either with all target data being unknown or with a few seen samples available. To conclude, the main difference between adaptation and generalization is access to target data during the training process. In other words, in adaptation, we take advantage of our current knowledge of source data and the structure of target data for the analysis of related target data. In contrast, in generalization, we can only use our knowledge of the source data and extend it to propose a model that works well on *any* domain with an arbitrary structure.

Research in medical data analysis is often driven by the desire to generalize models. As mentioned, the better our model performs on new and unseen data, the more reliable it is, and it will become more valuable and practical. Hence, the importance of generalization is inevitable, even when the main task is adaptation. To handle this, some papers with the main task of adaptation also exploit generalization ideas. Therefore, we will explain both their adaptation task and the different ideas used for generalization.

4 METHODS

The most recent methods used to adapt and generalize tasks on functional medical data are categorized and introduced in this section. The case studies covered in these methods are as follows. In each of them, one specific task (e.g., the ones introduced in Section 2.3) is considered, which are all practical tasks inspired by real-world applications and medical procedures. As pointed out in Section 3, depending on the nature of the task, the dataset, and the problem under study, the "domain" is defined, such as subjects, sessions, or other characteristics causing distribution shifts in the practically gathered data samples. Then, the proposed DG/DA idea and the approach used for the downstream task are applied. Subsequently, the performance of the downstream task is analyzed when the proposed method is used on unseen samples with noticeable domain shifts from train samples. This performance is usually shown to have improved compared to cases where no DG/DA ideas are considered. As a result, the decline in performance under domain shift on medical applications is tackled in the literature on this topic, which is a significant and valuable benefit for using ML in real-world situations. These methods are explained based on two perspectives, DA and DG, in the following.

4.1 DA Approaches

We have studied the latest research seeking DA in the context of functional medical data. Based on their design ideas, these methods are classified as in the hierarchy depicted in Figure 4, including alignment, data manipulation, feature disentanglement, and pseudo-label training. Summarized information about the methods discussed in this section can be found in Tables 1 and 2, where Table 1 contains papers related to DA and DG methods on EEG modality and Table 2 summarizes mentioned methods in the fMRI modality. In this section, these approaches and works following their ideas are described.

4.1.1 Alignment. One of the most common DA strategies arises from aligning the model's input at test time with previously seen data or features. A majority of approaches rely on these techniques so that the inputs (or secondary features) to the model are kept aligned with a fixed network architecture. Consequently, the same architecture can yield relatively similar performance for source and target data. Alignment-based methods consist of adversarial alignment (alignment using an adversarial objective), domain alignment (aligning the distribution of target and source data), instance alignment (aligning source and target sample by sample), and classifier alignment (adapting the classifier model to the target domain).

4.1.1.1 Adversarial Feature Alignment. This approach is implemented in a substantial number of papers focusing on aligning source and target domain features. The objective of these methods is to extract features that are similar between target and source data using an adversarial training setup. Inspired by the **Domain Adversarial Neural Network (DANN)** [37], in most of them, a common feature encoder is trained in a min-max game with a domain classifier. Essentially, the feature encoder learns to extract features such that the domain classifier is unable to distinguish

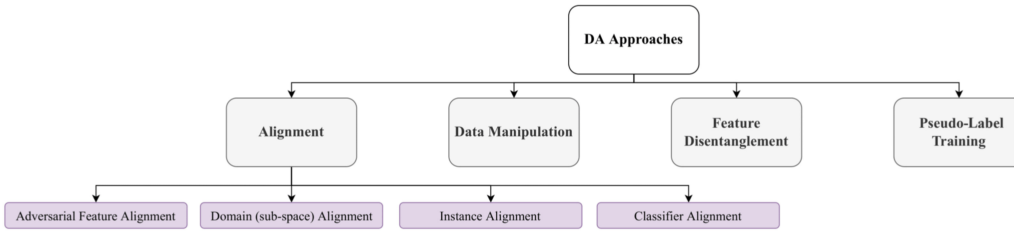


Fig. 4. Hierarchy of DA approaches in functional medical data analysis.

between source and target data. This procedure results in achieving a common feature space between data from different domains.

In the work of Zhao et al. [175] and Lebedeva [75], the idea of DANN is applied by training a domain classifier whose loss is inverted by a **Gradient Reversal Layer (GRL)** [36] and forcing the feature extractor to remove domain-variant features while improving the classification accuracy of the main task. Likewise, the idea of the GRL as a domain adversary was practiced in the work of Xueqi et al. [161], where the proposed architecture predicts the domain by each channel and uses the entropy of prediction as an attention weight to discard domain-dependent channels from the target task prediction. Su et al. [144] employ an adversarial discriminator that is trained to be challenged by a pre-trained feature extraction for brain anomaly detection on fMRI data. Heremans et al. [53] adopt an akin approach to enhance the performance of common neural networks used for sleep stage classification by using an adversarial domain classifier on the feature extraction backbone. In the work of Zhao et al. [179], multi-view features are extracted in the time and frequency domain and then, combined with the original data, are used in an adversarial learning module with two generators for separating patient and seizure features alongside discriminators ensuring this separation. Additionally, in the work of He et al. [51], an Adversarial Discriminative Temporal Convolutional Network (AD-TCN) is proposed, where initially an encoder and a classification layer are trained on the source data. As well, the adversarial loss is employed via a domain classifier applied to the source encoded features and a distinct target encoder, making the target encoder able to be combined with this new classifier for target inference. In the work of Liu et al. [102], in one branch, features obtained from a pure-info encoder are fed into a classifier and an adversarial-side discriminator so that data from the two ears are aligned and processed efficiently together in the classifier. In another branch, after applying a domain-variance encoder, the resulting features plus the ones from the first branch are combined to reconstruct the data, where a domain discriminator is further adversarially trained. Wang et al. [151] propose adversarial adaptation in a multi-source setup by first selecting the source samples most correlated with the target sample and then mapping their corresponding features in a common space, with the aid of a discriminator intended not to be able to differentiate domains. In the work of Pominova et al. [122], the Fader network method is used for DA and removing task-irrelevant features in fMRI data. In this method, an auto-encoder is utilized whose output encoding is used for the final classification task, as well as the domain classification in an adversarial manner. Furthermore, Li et al. [91] use an adversarial subject classifier to ensure the subject independence of the extracted features for ER. Moreover, two different **Recurrent Neural Networks (RNNs)** are also employed for the right and left brain hemispheres in each of the two vertical and horizontal streams over the electrodes to maintain structural information. Eldele et al. [32] utilize adversarial training along with self-attention and self-training in their method, where the extracted features are passed through unshared attention-based modules to retain domain-specific features as well as task-related ones, as domain-specific features may also be helpful for label prediction. The adversarial domain classifier may further encourage data alignment while preserving domain-related features. Bao et al. [7], in addition to **Maximum Mean Discrepancy (MMD)** [39] minimization, further use a domain classifier so that it fails to separate source and target domains, as they mention that merely MMD will not guarantee multi-source DA. Wang et al. [157] use two different modalities, which are the EEG signal and the eye movement, to find a shared feature representation in both source and target domains, and further align the representations through separate discriminators for each modality. In their work, the common features in each domain are obtained using cycle-consistency loss (measured by the distance of the encoder-decoder output given the original and the reconstructed data) and assuming that the multiplication of their prior Gaussian distribution is also Gaussian. Additionally, in the work of Avramidis et al. [4], separate branches are designed for extracting features from EEG data and the music used for data collection. The representation from these two branches is further aligned by a modality classifier inserted with a GRL, enabling adversarial alignment among modalities as in DANN. Rayatdoost et al. [126] also introduces a domain and a subject classifier implemented with GRLs that perform domain and subject classification and are trained adversarially so that features extracted from topological maps obtained from **Power Spectral Density (PSD)** features are free of dataset or subject priors.

Multiple works have further added modifications to DANN to make it more applicable for their purpose. Ding et al. [29] extend DANN by designing two label predictors instead of one. Using pre-trained label predictors on the source data, the two fully connected classifiers are tuned by the **Maximum Classifier Discrepancy (MCD)** criterion [131]. First, target outliers are detected, and MCD is maximized to achieve broader classification boundaries. After relocating target samples to new boundaries, MCD is minimized for better adaptation. Tang and Zhang [146] extend the concept of DANN by applying the domain discriminator to the conditional features (i.e., multiplying the features by the softmax output), thereby capturing a 2D matrix (outer product) that can be inputted into a GRL and a domain discriminator. A similar approach is taken in the work of Hong et al. [55], where both global (marginal) and local (conditional) domain discriminators are adversarially trained against the main classifier, with a dynamic weight ω adjusting their importance. Some works also perform DANN on the shallower representation of the data. In the work of Cai et al. [13], features from shallow layers are used for domain discrimination, which is trained adversarially to align the marginal distributions, while deeper features are fed into two different classifiers whose prediction difference is aimed to be maximized to detect target samples close to the decision boundary. Similarly, the work of Li et al. [85] benefits from an adversarial adaptation by feeding shallower representations to a domain discriminator, as earlier layers typically produce more task-invariant features that reflect the difference in data domains. Additionally, the association strategy computes the probability of transition between the source and target domain based on their features in each batch and introduces a loss in these transitions to encourage them to return to the same class. Li et al. [92] employ a domain classifier in an adversarial scheme after extracting horizontal and vertical flows between channels in horizontal and vertical directions using separate RNNs. Here, also, a loss function is introduced, simulating the similarity between the source and target features by encouraging a hypothetical walk from one domain to the other and then back to the initial domain, alongside a regularizer that guarantees each target sample is visited in these transitions. Ye et al. [165] integrate the idea of a DANN with an attention mechanism. A **Graph Convolutional Neural Network (GCNN)** is exploited with numerous stacked **Convolutional Neural Network (CNN)** layers, creating multi-level features from the GCNN and CNNs. The concatenated representations are inputs to separate adversarial domain classifiers, which help extract more domain-invariant features. For the final label predictor, the feature regions are multiplied by attention weights indicating how difficult it was for the classifier to classify the domains in each region. Zeng et al. [168] combine a GAN with a DANN to seek DA. First, a GAN is trained to achieve a robust target data generator and an accurate target data discriminator. Then, the closest source samples to the target distribution, as specified by the discriminator, are further augmented with fake target data and are used in the DANN to adversarially train the final fatigue prediction network against a domain classifier. In the work of Li et al. [90], the idea of the adversarial domain discriminator is integrated into a federated learning framework that has pre-trained site-specific feature generators that are further trained to confuse the discriminator.

In some cases, a min-max game is performed to separate features in the data. Zhu et al. [186] adversarially train two classifiers on features from an auto-encoder. After training the auto-encoder and classifiers, their prediction discrepancy is maximized. Following that, in a min-max game, the auto-encoder is optimized to decrease this discrepancy. Jeon et al. [60] design a common point-wise convolutional encoder producing class-relevant and class-irrelevant features and a network estimating the mutual information of these two features that are optimized in a min-max manner to guarantee the omission of subject-specific features from the input of the classification network.

An adversarial scheme may also be used to fit the data to certain priors or prototypes. In the work of Peng et al. [120], a Manifold Adversarial Auto-Encoder (MAAE) is developed to fit a manifold prior distribution to the distribution of the auto-encoder latent space. Peng et al. [119] also discard the data specific to patients by presuming a Laplace prior distribution on different patients and considering them as real data. Inspired by GANs, the VAE outputs are regarded as fake data and are fed alongside the real data to a discriminator, aiming to deceive the discriminator. Wang et al. [158] create source and target prototypes and classify samples based on distance from these prototypes using a domain classifier trained in a min-max game with the generator (the symmetric and positive definite matrix network applied to the data covariance matrix).

Some works consider private encoders per domain in adversarial domain alignment. Luo and Lu [105] propose two variants of Wasserstein-distance-based **Multi-source Adversarial Domain Adaptation (wMADA)** for DA in vigilance estimation and ER. The first variant, wMADA-α, adversarially trains k different private discriminators on the Wasserstein distance between source and target outputs. In the second variant, wMADA-β, source features are inputs to a public discriminator as well. Additionally, Qu et al. [125] utilize private and common feature extractors in source and target domains plus a domain classifier (with a GRL unit) to separate sleep-related features from unrelated ones for insomnia detection. A difference loss also forces the two networks to obtain orthogonal features. To improve accuracy, reconstruction losses are embedded in the network, and the target common classifier's features are fed into an LSTM and then the final classifier.

Adversarial training may also be applied to transform source data into the target distribution. Huang et al. [57] propose a generator network that attempts to generate samples similar to target data from source samples by using an adversarial domain discriminator, as in GANs. Overall, the sample data is first transformed to have the target distribution. Finally, an emotion classifier is trained on this data, allowing the target data to be used directly at test time.

Adversarial domain alignment is broadly used in a great number of works due to its general framework that can be combined with various feature encoding modules, making the backbone feature encoding model more robust. Moreover, another benefit that adversarial methods bring about is that they may be applied to unlabeled source data as well, in an unsupervised manner. Despite the numerous improvements adversarial approaches bring about, using them can also be challenging. First of all, training them can be unstable, as finding an equilibrium between the two modules adversarially trained against each other may not be practical. In other words, these two modules may end up with a suboptimal solution where their performance is not satisfying for the final task. The performance of an adversarial model might be limited by the mode collapse issue—that is, if there is no proper alignment between features and classes in different domains, the separate design of the task classifier and domain discriminator may degrade the model's performance [48]. Additionally, adversarial scenarios demand a larger number of data samples to provide meaningful results in comparison with other methodologies. This issue can be problematic in medical data analysis, where the volume of data and providing neat data is labor intensive and expensive. Additionally, adversarial methods have the problem of being time consuming at the training stage.

4.1.1.2 Domain Alignment. A non-adversarial source and target features alignment can be achieved using domain alignment techniques. In this regard, subspace alignment is one of the most straightforward methods. In the context of subspace alignment, the initial concept is to learn a common intermediate representation shared between domains. It has been found that most adaptation approaches in this category start by creating a low-dimensional representation of original data using a variety of deep or non-deep methods and then use distinct objectives such as Kullback–Leibler divergence, Bregman matrix divergence [127], and MMD to reduce the discrepancy between marginal and conditional distributions in a new subspace, as in other works [7, 38, 135]. Ju and Guan [67] also followed this approach by minimizing the mean of the conditional and marginal distributions of target and source data on the SPD space created by the channel covariance matrix of the EEG data. To find the shared space, various deep neural network models are used. For example, Chen et al. [17] proposed a model consisting of an ANN-based common feature extractor and multiple domain-specific feature extractors, with one network per pair of source and target, which is designed to minimize MMD to transform each pair into a different subspace. Likewise, Zhao et al. [178] provide domain-invariant feature extraction modules built on a **Common EEGNet-based Network (C-EEGNet)** [74] as well as domain-specific feature extraction in each pair of sources and targets by using N CNN-based subnets (S-CNNs). A novel alignment algorithm called *Local Label-based MMD* (LLMMD) is proposed in this work to diminish the discrepancy between source and target domains, which explores local label-based fine-grained structure information across all domains and extracts label-based domain-invariant features. In the work of Liu et al. [98], MMD is applied to align source and target features produced using a CNN backbone, where frequency filters are learned using 1D convolution and applied over time, convolutions over timestamps are performed on the resulting features, and, finally, features are extracted using point-wise convolution plus average pooling and softmax weights. To extract discriminative features from EEG signals, Li et al. [93] introduced an ANN-based **Dynamic Domain Adaptation (DDA)** to minimize the local subdomain and global domain shift. Unlike previous methods, DDA reduces local discrepancy by considering each category domain as a local domain in unsupervised and semi-supervised settings. Additionally, Yang et al. [163] use a CNN network that receives connectivity features as an input to align multiple source domain sites and the target domain data into the latent feature space and minimize their Wasserstein distance to reduce their distribution differences. In the work of Shi et al. [139], the Dempster-Shafer [26] evidence theory and rough adjoint inconsistency are applied to derive weight coefficients for each domain. Afterward, the target domain class proportion and optimal coupling distribution set are solved iteratively. Last, each source domain is aligned with the target domain and is used to train the final classifier. As well, Han et al. [44] utilize a DeepConvNet as a feature extractor that constrains learning to a shared space between the subject's motion sickness state and resting-state features, and by doing so, they better make use of distance-based techniques in a well-represented embedding space.

To extract features, Lee et al. [79] use a single-layer gated recurrent unit embedded in a semantic manifold and used **Multi-Kernel MMD (MK-MMD)** as a divergence metric. Moreover, Peng et al. [119] use an auto-encoder and MMD on time-frequency images for the mentioned purpose.

Feature extraction can also be conducted using tensors. Shen et al. [137] proposed a tensor-based alignment model in their work. This model uses Tucker decomposition to tensorize EEG channel data. As a result of tensor network summation, features of training and testing tensor samples are derived from corresponding subspace matrices. A Deep Domain Adaptation Network (DDAN) is proposed by Hang et al. [46] that employs a CNN to automatically detect features, MMD to minimize distribution discrepancy, and a Center-based Discriminative Feature Learning (CDFL) method to force the deep features closer to their respective class centers and to make the inter-class centers more distinguishable. As well, in the work of Meng et al. [109], a novel method, Deep Subdomain Associate Adaptation Network (DSAAN), is described that combines the advantages of both subdomain adaptation and associate loop calculation. This model uses ResNet [50] to extract features. Additionally, in the work of Xu and Li [123], the features are extracted using ResNet50 for each source domain, and they are weighted by assigning the normalized mutual information, which is obtained with the informative samples of the target domain, and at the next step, the weighted source domain is transferred to the training set of the target domain to form the aligned source domain. Third, domain-specific distribution alignment is achieved via MMD.

It is also possible to extract meaning from EEG signals by using GNNs. Kuang et al. [73] offer a **Multi-Spatial Domain Adaptive Network (MSDAN)**. Through MSDAN, the original EEG data is mapped into multiple graph-based spaces, and the distribution of the source and target domains in those spaces is narrowed by the use of MMD. Furthermore, Chu et al. [21] used a GCN as a feature extractor and the node attention mechanism to explore the contribution weight of nodes/ROIs automatically. In their model, the differences in data distribution between sites are adapted through the constraint of mean absolute error and covariance.

Attention mechanisms can also be useful in solving excessive alignment problems. As an example, in the work of Ning et al. [112], a CBAM-based module was designed to extract the common features of the source and target. The MMD in RKHS is also used to align the two domain distributions. In this work, to overcome the excessive alignment problem in which the samples of the two domains are mixed, and the categories within each domain cannot be distinguished well, the few-shot learning module is introduced to retain the domain-specific information. Moreover, Chen et al. [18] suggest CS-DASA, which learns the common features from multi-frame EEG images using the convLSTM. Additionally, the model uses a subject-specific module using 2D-CNN with MK-MMD loss in the RKHS to perform adaptation. Furthermore, a subject-to-subject spatial attention mechanism focused on the discriminative spatial features from the target data is used.

Other classic ML techniques are similarly useful for reducing dimension and finding shared subspaces. As a dimensionality reduction technique, **Transfer Component Analysis (TCA)** [116] aims to minimize distribution discrepancies by learning a set of transfer components. In the work of Liu et al. [100], a transfer learning-enabled classifier consisting of a TCA is implemented to mitigate the mismatch among distributions. It anticipates a projection to a latent subspace where the projected source and target data achieve a reduced MMD in RKHS. Similarly, Zhou et al. [185] use TCA, **Joint Distribution Adaptation (JDA)** [103], Balanced Domain Adaptation (BDA) [152], and Transfer Joint Matching (TJM) [104] with an MMD distance measure to adapt the domains. Wang et al. [156] use a JDA-based adaptation module that joints the marginal distribution alignment and conditional distribution alignment to minimize the data distance between the source and the target domains with an MMD measure. Very similarly, Transport-Based Joint Distribution Alignment (T-JDA) blocks are proposed in the work of Zhang et al. [170] that can propagate features or labels from source to target by minimizing the global transportation cost between the empirical joint distribution of a pair of source and target domains. An independent component analysis [22] method is employed to determine the independent components of unlabeled and labeled EEG signals in the work of Qu et al. [124]. In this work, the energy features of independent components are extracted as the source and target domains. As a final step, the marginal distributions of the source subspace base vectors are aligned with the base vectors of the target subspace using linear mappings.

Alternatively, another category of methods assumes that there exists a manifold of transformations between the source and target domains which consists of a space of parameters where each point generates a possible domain. For instance, Zhang and Wu [173] proposed a Manifold Embedded Knowledge Transfer (MEKT) approach by aligning the covariance matrices of the EEG trials in the Riemannian manifold, extracting tangent features, and then performing DA by minimizing the joint probability distribution shift between the source and target domains. Moreover, Liu et al. [97] align source and target domains in the Riemannian manifold by minimizing the Bregman matrix divergence. In the work of Ye et al. [164], an improved version of class centroid matching is presented. This model consists of three main steps in the Riemannian manifold: cluster the target data to find a proto-class center, minimize the discrepancy between two domains using class centroid matching, and learn discriminant information from source class labels. Jiang et al. [62] have also proposed a kernel-based Riemannian Manifold Domain Adaptation technique (KMDA) in which the covariance matrices are aligned in the Riemannian manifold and then mapped to a high-dimensional space by a log-Euclidean metric Gaussian kernel, which is then reduced by MMD. Additionally, Liu et al. [101] utilize the Sample Covariance Matrix (SCM) with a Riemannian-based kernel to obtain the common feature space, which is invariant to all subjects.

Despite the fact that domain alignment techniques are powerful and widely used for DA issues, these techniques need a significant amount of parameters for adaption, and the constraints they are subject to could cause a distortion of semantic feature structures and a loss of class discriminability.

4.1.1.3 Instance Alignment. Target domains can also be aligned with source domains at the instance level. In some studies, pairs of source and target data samples are directly guided to become closer to each other.

Optimal transport has been used to find the least costly alignment between source and target domain samples (e.g., [16, 107, 163]). For cross-subject alignment, Lyu et al. [107] first aligned the samples within the source domain based on their session, then aligned them with the samples of each session in the target domain separately.

From a representation learning aspect, Lee et al. [77] and Wang et al. [154] represent each sample of every source domain by a low-rank transformation of target samples. A shared transformation further generates a new representation for target samples. Similarly, Lee et al. [80] follow a contrastive approach by decreasing the distance between pairs of samples in the same class and different subjects compared to samples with different classes and the same subject.

It is also common to represent target samples or predictions based on their similarity to source samples. For instance, in the work of Zhao et al. [176], after training source-shared and source-specific encoders and decoders and a target-specific encoder, the final prediction on target data results as a combination of target model prediction and source model predictions, weighted by their feature similarity to the target sample. Likewise, Li et al. [87] duplicate the batch normalization layer for each source. In the test phase, for new target samples, the average of batch normalization branches is computed and further weighted by layer statistics similarities of the target and each one of the source domains. From a slightly different viewpoint, Lin et al. [94] train task and subject predictor networks, and select samples from the most similar subjects to train the model on a new domain. Moreover, Wang et al. [151], using direct transfer accuracy, select only related source domains to be used for the main adaptation module.

There are also studies conducted on aligning source and target samples based on their discriminative statistics. For example, Tao and Dan [147] align kernel-based classifiers for each domain to match the label structure of the samples and match the distribution of source and target domains.

In a similar manner, Shen et al. [136] learn a transformation on samples for each source domain so that their covariance matrix becomes as close as possible to the covariance matrix of the target domain samples. Santana et al. [132] proposed a multi-objective optimization method based on genetic programming. This method scores instances in source domains based on their similarity to target samples. Moreover, they introduced metrics to measure the model's adaptability.

As a more general form of domain alignment, instance alignment aligns domains at the sample level. This extension allows for more accurate adaptation when it is successful, but it also fails more often. Instance alignment requires the target domain data to be represented by the source domain or vice versa and can be adversely affected by outliers. Additionally, via these approaches, similarity-based methods cannot adapt to target spaces significantly different from source spaces.

4.1.1.4 Classifier Alignment. Classifiers trained on features extracted from different sources may result in misaligned predictions for target samples close to the domain boundaries in a multi-source setting. By minimizing specific classifier costs, the classifiers are better aligned, resulting in more accurate and generalized models. As an example, Zhang et al. [170] adapt multi-source domains to a single target and penalize decision inconsistency among diverse classifiers trained on paired joint distribution aligned features by minimizing the consistency loss between classifiers trained on source-target domain pairs. In addition, in the work of Chen et al. [17], a discrepancy loss is introduced to achieve convergence of predictions from N classifiers trained on N domain-adapted sources. Moreover, Zhao et al. [178] integrate the probability distribution from N classifiers by a weighted mechanism. Each classifier's prediction probability distribution is used to calculate the weights; the employed global optimization strategy also removes the negative impact of significant individual differences.

Unlike the described methods, classifier alignment is used with a different purpose by Xia et al. [160]. In their presented model, to have a more robust target classifier, different perturbation of target data is fed into some auxiliary classifiers, which are aligned to each other and to the fixed source classifier using consistency regularization loss.

Classifier alignment methods are useful, especially when the target domain samples are at the decision boundary. In this case, the variance of predictions will be high, significantly affecting the results. While these techniques can provide high-accuracy results, they require the extraction of source and target common features for the classifier's input.

4.1.2 Data Manipulation. In this group of methods, data is changed and manipulated for adaptation purposes. The major subtype in these approaches is preprocessing, given that solutions to DA can be injected into data preprocessing steps.

For example, Albuquerque et al. [2] show that feature normalization has a relevant effect on the conditional shift, and by performing z-score normalization, the conditional and marginal shifts can be reduced. Another approach that can be categorized as preprocessing is subject clustering. Concerning this, Liu et al. [96] propose Domain Adaptation with the Subject Clustering (DASC), which clusters the subjects according to their inter-subject similarity of emotion-specific EEG activities and only uses the source cluster that matched the target better for adaptation to the target. Apicella et al. [3] investigated the effects of different normalization methods on EEG data to achieve DA in the emotion classification task.

Applying this approach as a data manipulation method provides independence from the necessity of training and makes it directly applicable. Additionally, preprocessing is integrable with other DA methods. On the contrary, information loss and error propagation through the whole pipeline are disadvantages of this approach.

4.1.3 Feature Disentanglement. One of the recently popular techniques in DA is to disentangle input data into domain-specific and domain-invariant features. By defining appropriate objectives for each part, domain-specific information can be removed from the data, and thus, domain-invariant feature extraction can be used in a new domain for prediction.

Jeon et al. [60] force class-invariant and class-relevant features to contain the least common information by minimizing their mutual information. Liu et al. [102], aside from guiding each part to predict its own information, use adversarial training to prevent them from estimating each other's information. Furthermore, the separated parts are used to reconstruct the original data to ensure that there is a minimum loss of information during disentanglement.

In the context of multi-source DA, Zhao et al. [176] disentangle data from each source into domain-private and shared features and then reconstruct the original data via a shared decoder. The new target domain uses a private encoder that is trained with the reconstruction objective. During the inference phase, data from the target domain can be classified using both private and shared encoders.

When data samples are inherently a combination of multiple parts mixed together, the disentanglement technique is useful. Brain signals are a complex mixture of the brain's response to various stimuli in the environment. Usually, only one of them (class-relevant response) is intended to be analyzed in DA for medical analyses. Hence, disentanglement is a very intuitive and natural way of dealing with complex brain data. Nonetheless, it is important to note that disentanglement requires a significant amount of data to work well due to the need to extract irrelevant features as well.

4.1.4 Pseudo-Label Training. The generation of pseudo-labels from the source model is a common DA approach in medical data analysis. In this approach, a model is trained on source domain data, then its predictions on target domain data are considered pseudo-labels for the model, are exploited to adjust the model to the target domain.

Since pseudo-labels are noisy and not completely accurate, some studies apply them iteratively, and as the model produces better predictions, it uses its more accurate pseudo-labels from the previous iteration. This strategy can be used to transform any transfer learning method that uses the target labels into an unsupervised DA one.

Some examples of this type of iterative self-supervision are the works of Zhang and Wu [173], Eldele et al. [32], Shi et al. [140], Jiang et al. [62], Shen et al. [135], and Wang et al. [156]. While aligning source and target samples, these works iteratively generate pseudo-labels for use in the next step. Additionally, Edele et al. [32] ignore target classification loss in early iterations to tackle the cold start problem. Shi et al. [140] perform JDA iteratively and enhance pseudo-labels using the label propagation algorithm (e.g., [174]). The idea to enhance the pseudo-labels is also proposed by Han et al. [45], where they apply a single step of the k-means algorithm to the extracted features to form more coherent and less uncertain labels.

In some studies, pseudo-labels are directly treated as target data labels, along with other objectives imposed to guide the model in the correct direction. Jiménez-Guarneros and Gómez-Gil [64] retrain their source model on target data using pseudo-labels with an additional loss term controlling the uncertainty and increasing the diversity of predictions. Zoumpourlis and Patras [188], Zhao et al. [175], and Heremans et al. [53] use pseudo-labels for target domain classification alongside their generalization objective. Tao and Dan [147] also generate pseudo-labels and consider the target domain as one of the sources and adapt all of them together.

Pseudo-labels may also be used indirectly, primarily for an objective other than classification. Hong et al. [55] use pseudo-labels to approximate the class probability of target samples for conditional discrimination between samples of source and target domains. Additionally, Zhou

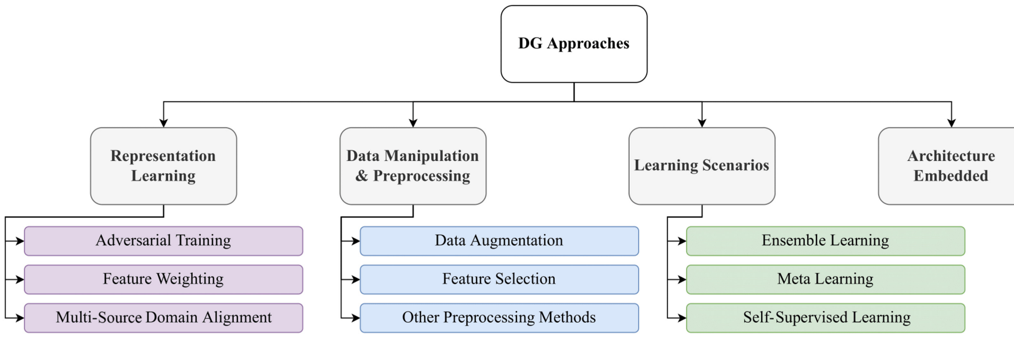


Fig. 5. Hierarchy of DG approaches in functional medical data analysis.

et al. [185] utilize JDA as one of their experimented methods which requires target data labels, derived from pseudo-labels, to calculate class conditional distributions. Moreover, Meng et al. [109] use pseudo-labels to partition target domain samples into subdomains and estimate the similarity of samples in source and target domains.

As a result of pseudo-label-based DA, useful information held by the source model is retained during the transition to the target domain. Despite its ability to prevent the forgetting of source domain information, it may not be able to eliminate domain bias. In particular, the performance of this approach is relatively weak when the difference between the source and target domains is very significant that iterative fine-tuning or additional objectives are not effective. Moreover, convergence is a critical concern when using iterative methods, since negative feedback in the self-supervision process may prevent the model from eventually reaching its optimal state.

4.1.5 Hybrid Methods. Some studies combine multiple DA approaches. In particular, as pseudo-labeling can be conducted independently, it can be easily integrated with other adaptation methods. Thus, as discovered in this study, the most common combination is pseudo-labeling and domain alignment (e.g., [45, 62, 64, 109, 135, 156, 173, 185]). Pseudo-labeling is also used alongside adversarial feature alignment (e.g., [32, 53, 55, 175]).

Furthermore, classifier alignment is mostly accompanied by domain alignment (e.g., [17, 170, 178]). There are also other combinations in the literature. Bao et al. [7] and Peng et al. [119] try to adapt their model using adversarial feature alignment and domain distribution alignment together. Liu et al. [102] use adversarial training to train their feature disentanglement model. Zhao et al. [176] incorporate disentanglement along with instance alignment. Wang et al. [151] utilize adversarial training in conjunction with instance alignment. Additionally, in the work of Tao and Dan [147], pseudo-labels are used to employ instance alignment.

4.2 DG Approaches

Various DG methods have been suggested to process functional brain signals. These approaches include representation learning, data manipulation and preprocessing, learning scenarios, and embedded architectures, which can also be merged to enhance performance on various tasks. Our design hierarchy for these methods and the motivations behind it is shown in Figure 5. In the remainder of this section, we explain DG-specific approaches and techniques presented as part of a DA method where adaptation techniques are improved via generalization ideas. A precise summary of these explanations is also provided in Tables 1 and 2; as mentioned before, Table 1 consists of DG/DA papers on the EEG modality and Table 2 summarizes DG/DA methods concerning the fMRI modality.

4.2.1 Representation Learning. An overall strategy for DG is representation learning, aiming to ensure that the learned representations are domain invariant, meaning that they do not contain much knowledge about the domain from which they originate. In other words, feature extraction is guaranteed to be generalizable to all domains as long as they include similar semantics about the studied task. In the following, the representation learning methods are grouped into adversarial training, domain alignment, and feature weighting. Most of these ideas are designed for multi-source DG scenarios.

4.2.1.1 Adversarial Training. Learning a generalizable representation needed for DG may be achieved through adversarial training. It should be noted that most methods that use an adversarial setting for such a purpose have multi-source setups. Derived from DANN, in most of these methods, common feature extraction is applied to different sources; afterward, a domain classifier, as a discriminator, tries to distinguish domains. By min-max training, the discriminator will fail to identify the domain from the extracted features, meaning that features are global among different source domains. Hence, these features can make the main model generalizable.

Many works employ variations of the preceding strategy for gaining a domain-generalizable feature extraction model. Bethge et al. [10] and Özdenizci et al. [114] propose an adversary network that tries to output the source domain identity (i.e., the given dataset or subject) from the encoded features. Training this domain discriminator adversarially with the main classifier results in a generalized pipeline where the learned features are domain invariant and, hence, accurately classifiable. Similarly, in the work of Jia et al. [61], a domain discriminator is used and is designed to fail at distinguishing the incoming domain while maintaining task-relevant parts in the extracted features obtained via spatial and temporal graph convolutions. Hagad et al. [42] employ a DANN, consisting of a domain and emotion classifier, alongside a beta-VAE [54], treating each of the multiple sources as a single domain and feeding the DANN with outputs of bilateral convolution on the concatenated VAE outputs of the two hemispheres. Albuquerque et al. [1] propose a generalization approach that theoretically guarantees a generalization bound on unseen domains. From a practical viewpoint, they implement this method by using one-vs.-all classifiers, each of which is responsible for computing a divergence score between every source and all other sources. By adversarially training these classifiers with a feature encoder and a task classifier, they demonstrate the generalizability of their given method for EEG ER. In the work of Han et al. [43], a domain classifier is used to force encoders in two different branches to extract features that diminish the distinguishability of domains. Ma et al. [108] suggest that biased network weights in source feature extractors can be regarded as domain-relevant clues and therefore incorporate separate encoders for each domain, having shared unbiased weights and specific biased weights for each domain. They further use the encoded features as inputs to a label predictor and an adversarial domain classifier.

Adversarial training may also be useful for enforcing a low-dimensional distribution of the data. Inspired by GANs, Ming et al. [110] propose an adversarial scheme to align multiple sources with an artificial empirical distribution in low dimensions. To this end, they design a discriminator considering samples from the artificial domain as "real" data and the encoder's output as "fake." These two networks are further adversarially trained so that eventually data from all sources is mapped in a coherent low-dimensional representation space. To avoid a lack of information for further classification tasks due to the artificial distribution, the generator is split into an adapter and a mapper, and the intermediate output from the adapter is used for the final task.

Although adversarial training can remarkably help generalize the representation learning step and may be implemented in integration with various feature encoding methods, they still face challenges such as time-consuming training and mode collapse, as pointed out in Section 4.1.

Additionally, most notably, being data hungry, it may be hard for these methods to obtain their best performance, especially in DG in medical use cases, where data collection is tricky.

4.2.1.2 Feature Weighting. Some works apply feature weighting to obtain domain-invariant features from different sources. These methods' features are associated with some learnable weights during representation learning. Fusing the features concerning these weights will result in a more general representation of features. It is critical to keep in mind that some features might be weighted to zero during the learning process, resulting in some features being omitted. As an example of this category, Cui et al. [24] present Feature Weighted Episodic Training (FWET), which consists of feature weighting to determine the importance of various features and episodic training for DG. Feature weighting, regarding the different significance of various brain areas, assigns a weight to each feature. Feature weighting provides the ability to determine different levels of importance for various features. By doing so, we can improve the value of more generalizable features. However, in some cases, it might be better to use a combination of features instead of setting different weights for features.

4.2.1.3 Multi-Source Domain Alignment. Similar to feature alignment in DA, extracted features from multiple source domains can be aligned to remove the shift between them, thereby generalizing the final model.

To reach a shared space, some works apply TCA algorithms, RKHS-based approaches, or MMD-based losses. For example, Ayodele et al. [5] utilize a modified version of the multi-TCA algorithm based on an RKHS approach to extract a common subspace of the datasets. Moreover, Bethge et al. [9] design a multi-source learning framework for domain-invariant representation learning, including a private feature encoder per domain and a cross-domain shared classifier, for which an MMD-based domain alignment loss is leveraged across private feature encoders to decrease domain-specific deficiency within the learned representations.

In the work of Musellim et al. [111], a prototype-based framework is proposed that forces cross-instance style invariance in each domain.

Zhang et al. [169] present a novel Convolutional Recurrent Attention Model (CRAM) that encodes timepieces extracting the spatio-temporal information. They apply a recurrent-attention network to explore the temporal dynamics among various time portions and focus on the most discriminative ones.

Common feature extraction may also be done in two steps to align source features. For example, Yousefnezhad et al. [167] propose a Shared Space Transfer Learning (SSTL) that first finds common features for all subjects in each site and maps them to a site-independent shared space. Next, it uses a scalable optimization procedure that uses a single iteration multi-view approach to extract the common features for each site and then maps them to the site-independent shared space. There are also some ideas in this arena that take advantage of graph structures to align sources. For instance, Li et al. [89] propose a graph decoding model in which a cross-subject graph showing the similarities across subjects is used. By further regularization, developing a kernel-based optimization, which enables the extraction of non-linear features, would be possible.

In the work of Wang et al. [155], a similarity-driven multi-view linear reconstruction model is designed to learn latent representations and perform subject clustering within each label. Next, a nested singular value decomposition method is used to mitigate inter-site heterogeneity and extract features by learning local cluster-shared features across sites within each label and global category-shared features across classes.

In this category, some models extract features from the intermediate space that can be reconstructed from the original data. It is pertinent to note that in this intermediate space, no information is removed. Accordingly, Huang et al. [58] present the **Manifold-Regularized Multiple Decoder,**

AutoEncoder (MRMD-AE) network, which extracts common latent space representations from multiple sources while respecting the individual data geometry by a pre-computed PHATE embedding while maintaining the ability to decode individual raw fMRI signals. Additionally, Zhang et al. [171] have proposed a low-rank subspace built on low-rank representation theory on fMRI data. They initially encode all domains in a common lower-dimension space. The graph-based data is then loaded into the graph convolution network module, followed by a classification head for ASD diagnosis. Peng et al. [120] adopt the auto-encoder approach to align the mean of the covariance matrix of the latent features of the domains together.

Although multi-source domain alignment is an approach that increases model generalization by concentrating on more common features between various sources and constructing shared subspaces, it could also cause a scarcity of discriminative features among different classes.

4.2.2 Learning Scenarios. Some methods use learning-based approaches for DG. These methods are categorized into ensemble learning, meta-learning, and self-supervised learning.

4.2.2.1 Ensemble Learning. One learning-based idea for generalization is ensemble learning, boosting the final model's performance and accuracy by combining various networks and specifying the main output by majority voting. For example, Li et al. [86] propose a novel decomposition-based ensemble CNN framework. The outputs are integrated with an ensemble architecture employed in two modes, Train CNNs Together (TT) and Output Fusion (OF). Moreover, in the test phase of Zhao et al. [176], predictions of the shared classifier integrated with those of individual classifiers are ensembled after modulation by similarity weights. Additionally, a two-stage ensemble architecture was proposed in the work of Zoumpourlis and Patras [188] with K ($K > 2$) models; at the first stage, they specify a subset of subjects for each model, and at the other stage, they try to control diversity by utilizing an intra-ensemble loss.

However, Zhu et al. [187] first evaluate the feasibility of utilizing EEGNet models [74] with various kernel numbers to decode SSVEP in ear-EEG signals. Then, due to the difficulty of separating useful information from background noise caused by weak SSVEP in ear-EEG, they employ ensemble learning to combine EEGNet models with different kernel numbers to enhance ear-EEG signals classification. Roots et al. [129] propose a model called *EEGNet Fusion*, a multi-branch 2D CNN utilizing various hyperparameters for each branch, which is more flexible across subjects.

As multiple networks are capable of extracting a wider range of features and processing them in a more varied manner, ensemble learning can significantly improve domain-invariant results. However, this approach cannot reveal the unknown differences between various samples and populations. Additionally, such models are not easy to interpret.

4.2.2.2 Meta-Learning. The main goal of meta-learning is learning to learn, meaning that the model observes how different ML methods perform various tasks and uses their metadata to learn how the learning procedure is performed. For example, Luo et al. [106] propose Pseudo Domain Adaptation via Meta-Learning (PDAML) to reduce the time, cost, and storage usage of their emotion predictor model in the test phase.

Some works utilize the **Model-Agnostic Meta-Learning (MAML)** [35] framework. For instance, Lemkhenter and Favaro [82] introduce a meta-learning method for sleep scoring built on top of MAML. Additionally, Duan et al. [31] propose Meta-Learning on Constrained transfer Learning (MLCL). They utilize the MAML algorithm under a novel constrained setting, which preserves adequate flexibility to adapt to a new subject where the number of must-transfer parameters is decreased substantially. In addition, Li et al. [88] propose Multi-Domain MAML (MDMAML) to meta-learn DA process across multiple source subjects. Furthermore, Lee et al. [77] try to learn the adaptation of feature representations within a meta-learning framework by using an episodic-learning strategy.

Using meta-learning leads to more generalization in the model, together with a faster and cheaper training process, because fewer experiments are used in learning. However, the rule set utilized in this approach may be incomplete; additionally, in some of its approaches, there is a limit to the volume of information that meta-features can capture.

4.2.2.3 Self-Supervised Learning. Self-supervised learning is an ML method used to extract useful information from data that has not been labeled. Therefore, it is reasonable to address the lack of sufficient labeled data in medical domains using this method. In this area, two general types of self-supervised methods are contrastive and non-contrastive methods. In contrastive methods, the similarity between two augmented versions of a data sample is maximized in a positive pair, whereas the difference between each of these two samples and samples in negative pairs is minimized. However, in non-contrastive methods, there are no negative pairs, and self-supervised learning is performed only within positive pairs [148].

Self-supervised contrastive learning can be used to solve domain shift problems, and several novel works have been proposed to perform DG. Shen et al. [138] propose **Contrastive Learning for Inter-Subject Alignment (CLISA)**, a self-supervised contrastive learning method to address the issue of inter-subject variability. CLISA is grounded on a neuroscientific inspection which assumes that the neural activity state of subjects is similar when they receive indistinguishable stimuli.

Cheng et al. [19] present a subject-aware learning method, which combines adversarial training with self-supervised contrastive learning to reduce the inter-subject variability in bio-signals such as EEG and ECG. With this method, they manage to achieve competitive results in varied kinds of downstream tasks. Wagh et al. [150] propose three novel self-supervised pre-text tasks, which exploit known patterns in scalp EEG signals and enable the learning of features that could be transferred to other domains and tasks. In their method, pre-text tasks are designed to examine the spatial similarities between the left and right hemispheres of the brain, the behavior of the brain, and changes related to brain activity. In the work of Banluesombatkul et al. [6], sleep stage classification (sleep scoring) is performed using MAML, a meta-learning method based on few-shot DAs. The MAML model, however, is vulnerable to overfitting even on datasets with many samples. A self-supervised stage was introduced to MAML by Lemkhenter and Favaro [82] to solve the overfitting problem without using newly labeled target data (zero-shot learning).

A similar idea to contrastive self-supervised learning is applied in the work of Xia et al. [160], where features extracted by an encoder from unlabeled target data were perturbed and then were used as input of a number of classifiers to train a robust and adaptable model for MI classification task in the cross-subject setting. The proposed approach is different from other mentioned self-supervised DG methods, as the pre-training is applied on target data instead of source data.

Self-supervised learning methods have the advantage of reducing the need for labeled data. These types of methods have also shown considerably high performance in different areas. One of the limitations of this method is that it takes time to prepare a proper pre-trained model, and the model also might need additional data sources for pre-training.

4.2.3 Data Manipulation. By manipulating the input data, a number of studies have been able to increase the generalizability of their models. Some attempt to augment the input data, mostly through adversarial approaches, whereas others try to eliminate unimportant or redundant data. Furthermore, data normalization has been shown to reduce domain bias in some studies.

4.2.3.1 Data Augmentation. In general, more data results in more generalizability because the model can explore a greater proportion of the data space. Consequently, adding new data samples to the available dataset can enhance the generalization capability of the model.

Heremans et al. [52] extend their previous work [53] to empower their model's adaptability using different data augmentation techniques, such as temporal/frequency cutout, adding Gaussian noise, signal mixing, frequency warping, and temporal/frequency recombination. Cheng et al. [19] define augmentations such as channel dropout and temporal cutout and extract features based on contrastive learning. Similarly, Xia et al. [160] enhance the generalization of the source model by using channel dropout during the training. Kim et al. [70] employ a data augmentation technique by perturbing the style information of EEG signals of instances from multiple domains to improve the performance of their model. Additionally, Han et al. [43] equip their model with a set of augmentation functions. Aside from Gaussian noise, scaling, and temporal cutout, they shift the signal's amplitude, roll it in time, and upsample intervals in the signal.

One of the common methods to add new data samples is through adversarial training. In the work of Song et al. [143], adding new data samples to the dataset is accomplished this way. Additionally, they add constraints, such as covariance matrix alignment, to the training objective to ensure that generated data is similar to the original ones.

A consistency-diversity tradeoff always exists in the context of data augmentation. On one hand, there is a risk that the augmented samples will be inconsistent with the real distribution of the data. On the other hand, if the augmented data are too similar to the original ones, it will not allow the model to explore much more of the data space, therefore making them ineffective. Even though appropriate augmentation methods can increase diversity while maintaining consistency, the evaluation of such methods is not straightforward, as the actual data space is unknown.

4.2.3.2 Feature Selection. Prior to the advent of DL, selecting important and essential features from data was one of the most common strategies. This approach is useful even when there are deep models present, as it prevents the model from overfitting to the data. In some studies, feature selection is applied as a preprocessing step. In the work of Pan et al. [115], graph pooling is used to select important nodes in the brain network. Graph pooling reduces redundancy by discarding nodes close to the average of their neighbors. To preserve only the important brain regions, Subah et al. [145] used standard brain atlases and reduced the number of features by averaging values in these important brain regions.

Statistical selection of important features has also been addressed in the literature. Yang et al. [162] calculate a statistical comparison between the distribution of the values for each of the features, separately for positive and negative data (binary classification), and only retain the features with significant differences.

Manual feature selection has the ability to insert prior or expert knowledge into the system, although in many cases it is not available or is very limited. Contrary to this, automatic (learning-based or statistical) feature selection methods can be used in most cases, but their associated criteria are very simple and can only be applied to discard obviously useless features. Information redundancy and sharing are two of the major challenges in feature selection, as all of the features may contain some useful information.

4.2.3.3 Other Preprocessing Methods. As another data-driven approach for DG, the normalization of data values can help reduce domain biases in the data. Every successful medical data analysis study includes a series of preprocessing steps, so here we only focus on those which are directly aimed at DG.

In the work of Fdez et al. [34] and Liu et al. [102], each subject's data values were normalized into the $[0, 1]$ interval to remove subject-specific information that affected the scale and position of the data. Chen et al. [18] use the preprocessing proposed in EEGNet to start with generalizable features, considering the good generalization power of EEGNet.

Numerous preprocessing methods have been employed to remove data noise and various artifacts available in functional brain signals. When it comes to EEG signals, preprocessing becomes more important since they have a low signal-to-noise ratio, meaning that there is a lot of trial-specific, unwanted information. Preprocessing is essential for any kind of adaptation model since the datasets in this field are typically too small for the model to detect and remove data artifacts by itself. Although preprocessing is essential, its performance is always dependent on the prediction model and usually needs other methods to perform well.

4.2.4 Architecture Embedded. Some methods exploit architectures that are naturally capable of more generalizable learning of the task. Additionally, using particular layers inside the network, such as batch normalization layers, can help reduce the unwanted variability of data within the network. Such ideas have been investigated in multiple works. In this category, some methods try to bring extra values to conventional CNNs used for feature extraction. Two different CNN architectures were proposed by Dissanayake et al. [30] for predicting epileptic seizures from EEG signals. As a result of the use of a customized convolutional architecture, it is possible to learn major features from data much more efficiently and robustly. On the CHB-MIT-EEG [141] dataset, the proposed models performed well when compared to the existing models. Additionally, they use interpretability methods to understand how these models work. Cui et al. [23] developed InterpretableCNN, a CNN architecture for driver drowsiness recognition in cross-subject settings, and an interpretation technique to uncover what happens inside the model. Compared with other models, the model achieved competitive results by incorporating separable convolutions to process the spatio-temporal aspects of EEG signals. Additionally, the proposed interpretation technique can provide meaningful insights into the model and input data. Zhang et al. [172] take advantage of the generalizability of a novel Separated Channel Attention Convolutional Neural network (SC-CNN-attention), which enables good performance in the leave-one-site-out scenario. To this end, a separated channel CNN yields temporal features of brain regions, followed by an attention-based network learning temporal dependencies and a fully connected classifier for ADHD diagnosis. Jiang et al. [63] proposed 4DResNet, an architecture that combines 4D convolution with 3D attention modules to extract temporo-spatial information from fMRI signals. The attention mechanism improved the framework's ability to recognize distinct features and enhanced its performance. They used their proposed model in different settings, including cross-task and cross-dataset.

In a study published by Jana et al. [59], the capsule network [130] is utilized to recognize emotional states across subjects by exploiting spatial and temporal information from EEG signals. To create a spatio-temporal frame group for EEG recordings, spatial frames were stacked with time frames (temporal frames). A particular data-splitting method was also used to make the model perform better on unseen data.

Some methods exploit graph structures to provide a generalizable representation. Self-Organizing Graph Neural Networks (SOGNNs) were introduced by Li et al. [84] for cross-subject ER on EEG signals. With the help of a self-organized graph construction module, their proposed architecture can dynamically generate specific graph structures for each signal. Cross-subject performance of the model is enhanced by aggregating connections between channels and temporal features. In another work, Cao et al. [14] introduced a framework consisting of a 16-layer deep graph convolutional neural network (DeepGCN) with ResNet and DropEdge [128] units for the task of ASD diagnosis in a cross-site scenario on the **Autism Brain Imaging Data Exchange (ABIDE)** I dataset. Based on their experiments, their proposed method is robust to vanishing gradients, overfitting, and oversmoothing.

In the work of Joshi et al. [66], several machine learning methods are trained with a cross-dataset scenario on SEED, DEAP, and IDEA [65] datasets, using different types of EEG signal features like PSD, Hjorth parameters, and **Linear Formulation of Differential Entropy (LF-DE)**. They conclude that the bidirectional LSTM with LF-DE features performs best in inter-dataset mode.

The **Sub-Epoch-wise Feature Encoder (SEFE)**, developed by Lee et al. [76], can be added to well-known deep models for EEG signals to extract temporal information from input data. By using SEFE in DeepConvNet [133], ShallowConvNet [133], and EEGNet, the performance of the model improves in the task of visual imagery classification in a subject-independent setting.

Some works benefit from the generalization obtained by combining multiple known structures. To detect emotion in Parkinson's disease patients, Dar et al. [25] combined a 1D **Convolutional Recurrent Neural Network (CRNN)** with an Extreme Learning Machine (ELM) classifier and used several preprocessing methods. They demonstrated that their proposed framework is reliable in cross-subject and cross-dataset scenarios by testing it on cross-dataset data. In the work of Lin et al. [95], a CRNN is proposed that is applied in subject-level cross-validation. First, BOLD signals, calculated from covariance and standard deviation from fMRI time series, are calculated and further passed through a network with spatial and temporal convolutions followed by an LSTM, which captures relations between consecutive neighboring windows. Giving this output to the final classifier leads to a generalizable model for Alzheimer's disease classification.

To reduce inter-subject variability in EEG signals, Li et al. [86] employ the Component-Specific Batch Normalization (CSBN) layer in their proposed ensemble model. Kobler et al. [71], after extracting features as a SPD matrix from EEG signals, apply multi-source batch normalization directly on the space of SPD matrices, and model the whole pipeline as an end-to-end neural network. Jiménez-Guarneros and Gómez-Gil [64] use Adaptive Batch Normalization (AdaBN) to reduce cross-subject variability and normalize extracted features from different domains. To improve generalization in cross-subject settings, Kim et al. [70] used alignment loss to reduce the distance between the intra-class labels as a regularization term in the loss function.

Huang et al. [58] propose MRMD-AE), which can extract shared features from a number of different subjects' fMRI data and reconstruct specific data for each subject with its numerous decoders. Furthermore, a special kind of regularization and penalties have been used to extract more precise shared representations. Harrison et al. [47] proposed the PROFUMO framework, which can be used to model rfMRI properties in spatial and temporal domains. Furthermore, it can capture differences in levels of activity and generate additional summaries of this kind of data.

DG methods based on an architecture-embedded approach perform well on specific tasks and datasets because of their specialized structure and architecture. However, one of their disadvantages is that they cannot be used for multiple downstream tasks and settings. In the case of having a single specified task for the final performance of the model is the goal, these types of methods are optimal. However, if a general framework is needed for several tasks and datasets, it might be better to use another approach.

4.2.5 Hybrid Methods. DG approaches can be fused together to produce a more generalizable model. Among different combinations, data augmentation and self-supervised learning have been tried together (e.g., [19, 160]). Additionally, Huang et al. [58] not only attempt to match source domain distributions but also account for DG when training their models through regularization. As well, Li et al. [86] carry out ensemble learning while embedding adaptive batch normalization layers in their model architecture, and Lemkhenter and Favaro [82] integrate meta-learning with self-supervised learning. Moreover, Zoumpourlis and Patras [188] utilized pseudo-labeling alongside ensemble learning.

5 DATASETS

This section provides general information about the most common datasets used in the papers, including attributes and experimental procedures.

5.1 Main EEG Datasets

This section introduces the most commonly used EEG datasets, which are organized according to their tasks. In Table 3, a summary of these datasets is presented. Additionally, it is worth mentioning that for the most frequent ones, the state-of-the-art papers are presented in Table 1.

5.1.1 Emotion Recognition. *DEAP* [72] is a multi-modal ER dataset consisting of 32 subjects (16 males and 16 females, between 19 and 37 years old, with an average of 26.9 years). This dataset includes 32-channel EEG signals alongside 13 peripheral physiological signals. Participants rated several music video clips from five aspects: arousal, valence, like/dislike, dominance, and familiarity.

DREAMER [68] is a multi-modal dataset including EEG and ECG signals from 23 healthy participants. Each subject watched 18 emotional film clips and rated their emotional response based on valence, arousal, and dominance. Participants were between 23 and 33 years old (the mean age is 26.6 years).

SEED [181] is a dataset consisting of two main sections: SEED_EEG, which includes EEG data, and SEED_Multimodal, which consists of EEG and eye movement data. The EEG signals were recorded as 62-channel samples. Generally, there are 15 Chinese subjects in this dataset consisting of seven males and eight females who are 23.27 years old on average. All subjects underwent three recording sessions with 2-week breaks between successive sessions. There were 15 trials per subject in each session, and during each of the trials, 4-minute movie excerpts were used to induce positive, negative, and neutral emotions.

SEED-IV [180], which expands the original SEED dataset, has four emotion classes: happy, neutral, sad, and fear. The dataset's subject population is almost identical to the original SEED. Each subject participated in three recording sessions held on different days. There were 24 trials per subject in each session, and during each of these trials, the subject watched a 2-minute clip, and their 62-channel EEG signals and eye movement data were collected.

5.1.2 Motor Imagery. *BCI Competition IV*[1] provides five datasets, two of which are used frequently in the papers: dataset 2a [12], and dataset 2b [81]. In *dataset 2a*, 22-channel EEG signals were recorded from nine subjects in two sessions on different days. This dataset has four classes, including the imagination of movement of the left hand, right hand, both feet, and tongue. *Dataset 2b* contains three bipolar-channel EEG signals gathered from nine subjects with two classes: left hand and right hand.

5.1.3 Awareness Monitoring. *SEED-VIG* [182] is a multi-modal dataset consisting of 12- and 6-channel EEG, 4-channel forehead EEG, and EOG signals of 23 subjects made up of 11 males and 12 females with an average age of 23.3 years old. A four-lane highway was shown to subjects controlling the wheel and the gas pedal of a vehicle in front of an LCD screen. Most experiments were conducted immediately after lunch. The simulated road was straight and monotonous, and the experiment duration was about 2 hours. Finally, from eye tracking data, they acquired labels ranging from 0 for drowsy to 1 for wakeful.

[1] https://www.bbci.de/competition/iv/

Table 1. Summary of Papers Related to DA and DG Methods on the EEG Modality

			DA Approaches							DG Approaches										Dataset							Architecture													
			Alignment							Representation Learning			Data Manipulation			Learning Scenarios											Deep								Non-Deep					
Reference	Year	Code	Adversarial Feature Alignment	Domain Alignment	Instance Alignment	Classifier Alignment	Data Manipulation	Feature Disentanglement	Pseudo-Label Training	Adversarial Training	Feature Weighting	MS Domain Alignment	Augmentation	Feature Selection	Other Preprocessing Methods	Ensemble Learning	Meta Learning	Self-Supervised Learning	Architecture Emb.	SEED	DEAP	SEED IV	SEED VIG	DREAMER	BCI	Others	ANN	CNN	RNN	Attention	Graph	GAN	Auto-Encoder	Capsule Net	SVM	Tensor Net	Others	Multi-/Single Source	Task Categories	Domain (Cross-X)
[3]	2022	-					×																				×								×			SS	ER	Subject
[93]	2022	-		×																×		×					×											SS	ER	Subject/Session
[70]	2022	-											×						×							×		×										MS	ER	Subject
[44]	2022	-		×																						×		×										MS	MoSD	Subject
[188]	2022	link							×							×										×		×										MS	MI	Subject
[161]	2022	-	×																							×					×							SS	AM	Subject
[71]	2022	-																	×							×												MS	MSD	Subject/Session
[67]	2022	-		×																																		MS	MI	Session
[98]	2022	-		×																					×			×										SS	MI	Subject
[123]	2022	-		×																					×			×										MS	MI	Subject/Dataset
[52]	2022	-	×										×													×		×										SS	SD	Dataset
[157]	2022	-	×																														×					SS	ER	Modality
[92]	2022	-	×																	×									×									SS	ER	Subject
[88]	2022	-															×									×		×										MS	MI	Subject
[23]	2022	link																	×							×		×										SS	AM	Subject
[9]	2022	-										×								×	×	×		×			×											MS	ER	Subject
[59]	2022	-																	×		×							×										SS	AM	Subject
[160]	2022	link				×							×					×									×											SS	MI	Subject
[66]	2022	-																	×	×	×					×			×									SS	ER	Dataset
[80]	2022	link			×																					×	×											MS	VPA	Subject
[62]	2022	-		×					×																×												×	SS	MI	Subject
[25]	2022	-																	×			×				×		×	×								×	MS	ER	Dataset
[120]	2022	-	×									×														×	×						×					MS	SA	Subject
[102]	2022	-						×							×											×							×					MS	MSD	Dataset
[10]	2022	link								×										×	×	×		×			×	×										MS	MSD	Dataset
[57]	2022	-	×																		×											×						SS	ER	Subject
[86]	2022	-														×			×							×		×										SS	AM	Subject
[109]	2022	-		×					×											×								×										SS	ER	Subject/Session
[124]	2022	-		×																						×									×			MS	MSD	Session
[82]	2022	-															×	×								×		×										SS	SD	Subject/Dataset
[53]	2022	-	×						×																	×			×									SS	SD	Dataset
[111]	2022	-										×														×		×										SS	MI	Subject
[4]	2022	link	×																		×								×									SS	ER	Subject
[185]	2022	-		×					×																	×									×			SS	MSD	Task/Subject
[186]	2022	-	×																	×								×										SS	ER	Session
[179]	2022	-								×																×	×					×						SS	SA	Subject
[34]	2021	-													×					×							×											MS	ER	Subject
[61]	2021	link								×																×				×	×							SS	SD	Subject
[158]	2021	-	×																		×			×				×				×						MS	ER	Subject
[30]	2021	-																	×							×		×										SS	SA	Subject
[176]	2021	-			×			×								×				×									×	×								MS	ER	Subject
[7]	2021	-	×	×																×								×										MS	ER	Day/Subject
[84]	2021	link																	×	×		×									×							SS	ER	Subject
[64]	2021	-		×					×										×							×			×									SS	HTA	Subject
[168]	2021	-	×																							×	×											SS	FAM	Subject
[187]	2021	-														×										×		×										SS	VPA	Session
[55]	2021	-	×						×																×			×										SS	MI	Session
[126]	2021	link	×																							×		×										SS	ER	Subject/Dataset
[17]	2021	link		×		×														×		×					×											MS	ER	Subject/Session
[87]	2021	-			×																					×		×										SS	AM	Subject
[151]	2021	-	×		×															×								×										SS	ER	Subject
[147]	2021	-			×				×											×	×						×											MS	ER	Subject/Dataset
[178]	2021	-		×		×																				×	×										×	MS	MSD	Subject
[136]	2021	link			×																					×										×		MS	AM	Subject
[51]	2021	-	×																		×			×				×										SS	ER	Subject/Dataset
[96]	2021	-					×														×						×											MS	ER	Subject
[43]	2021	-								×			×												×			×										SS	MI	Subject/Session
[42]	2021	-								×										×	×												×					SS	ER	Subject
[29]	2021	-	×																	×							×											SS	ER	Subject/Phase
[138]	2021	-																×		×						×		×										MS	ER	Subject
[156]	2021	-		×					×				×		×							×																SS	ER	Session
[79]	2021	link		×																						×			×									MS	VPA	Subject
[73]	2021	-		×																						×					×							SS	ER	Subject/Device
[119]	2021	-	×	×																						×									×			SS	SA	Subject
[112]	2021	-		×																×	×							×		×								SS	ER	Subject
[165]	2021	-	×																	×										×	×							MS	ER	Subject
[13]	2021	-	×																	×												×						SS	ER	Subject/Session
[76]	2021	-																	×							×		×										SS	ND	Subject
[150]	2021	-																×								×		×										SS	BSE	Subject/Session/Dataset
[143]	2021	-											×												×							×						MS	MI	Subject
[125]	2021	-	×																							×			×									MS	SD	Dataset
[32]	2021	link	×						×																	×		×		×								SS	SD	Dataset
[94]	2021	-			×															×								×										SS	ER	Subject
[135]	2021	-		×					×													×															×	SS	ER	Session/Trial
[106]	2021	-															×			×									×									SS	ER	Subject
[105]	2021	-	×																	×			×															SS	AM	Subject
[18]	2021	-		×											×											×		×		×								SS	MSD	Subject
[114]	2020	-								×																×		×										SS	MI	Subject
[19]	2020	-											×					×								×							×				×	SS	ND	Subject
[129]	2020	-														×										×		×										SS	MI	Subject
[175]	2020	-	×						×																×	×		×										SS	MI	Subject
[146]	2020	-	×																							×		×										SS	MI	Subject
[31]	2020	-															×			×	×				×													MS	MI	Subject
[5]	2020	-										×														×		×	×									MS	SA	Dataset
[137]	2020	-		×											×											×										×		SS	AM	Session
[75]	2020	-	×																		×														×		×	SS	ER	Subject/Session/Dataset
[85]	2019	-	×																	×	×						×											SS	ER	Subject/Session
[169]	2019	link										×													×			×		×								SS	MI	Subject
[1]	2019	link								×										×																		MS	ER	Subject
[91]	2019	-	×																	×		×				×			×									SS	ER	Subject
[162]	2019	-												×						×	×														×			SS	ER	Subject
[173]	2019	link		×					×																	×												SS	MI	Subject
[24]	2019	-									×															×	×											MS	AM	Subject
[46]	2019	-		×																					×			×										SS	MI	Subject
[108]	2019	-								×										×			×				×											MS	ER	Subject
[100]	2019	-		×																						×		×										SS	AM	Subject
[110]	2019	-								×																×						×						SS	AM	Subject/Session
[60]	2019	link						×																		×	×											SS	MI	Subject
[2]	2019	-					×																			×												MS	MSD	Subject

SS, single source; MS, multi-source; ND, neural decoding; BSE, behavioral state estimation; MoSD, motion sickness diagnosis. The state-of-the-art papers in cross-subject and cross-session settings are shown by red and blue crosses in the dataset columns, respectively.

Table 2. Summary of Papers Related to DA and DG Methods on the fMRI Modality

Reference	Year	Code	DA Approaches					DG Approaches				Dataset							Architecture									Task	Domain (Cross-X)
			Alignment					Representation Learning	Preprocessing	Learning Scenarios									Deep							Non-Deep			
			Adversarial Feature Alignment	Domain Alignment	Instance Alignment	Classifier Alignment	Pseudo Label Training	MS Domain Alignment	Feature Selection	Meta Learning	Architecture Emb.	ABIDE	HCP	ADHD-200	OpenfMRI	ADNI	ABCD	Others	ANN	CNN	RNN	Attention	Graph	GAN	Auto-Encoder	SVM	kNN		
[21]	2022	-		×				×				×											×					ASD-D	Site
[163]	2022	-		×	×							×							×									ASD-D	Site
[155]	2022	-						×				×							×									ASD-D	Site
[139]	2022	-		×								×														×	×	ASD-D	Site
[45]	2022	-		×			×					×						×	×									ASD-D	Site
[14]	2021	-									×	×											×					ASD-D	Site
[145]	2021	-							×			×							×									ASD-D	Site
[122]	2021	link	×									×								×				×	×			ASD-D	Site
[115]	2021	link							×			×											×					ASD-D	Site
[140]	2021	-					×					×														×		ASD-D	Site
[58]	2021	-						×			×							×	×									VPA	Subject
[144]	2021	-	×										×					×	×									AD	Site
[63]	2021	-									×		×							×		×						HTA	Subject/Task/Dataset
[171]	2021	-						×				×											×					ASD-D	Site
[95]	2021	-									×					×				×	×							AD-D	Subject
[77]	2021	-								×		×																ASD-D	Site
[90]	2020	link	×									×							×									ASD-D	Site
[154]	2020	-			×							×																ASD-D	Site
[47]	2020	link									×		×															MSV	Subject
[172]	2020	-									×			×						×		×						ADHD-D	Site
[170]	2020	-		×		×						×							×									ASD-D	Site
[167]	2020	-						×										×								×		HTA	Site
[38]	2020	-		×									×							×								WM / HTA	Subject
[89]	2020	-						×							×													HTA	Subject

ASD-D, autism spectrum disorder diagnosis; AD, anomaly detection; AD-D, Alzheimer's disease diagnosis; ADHD-D, attention deficit hyperactivity disorder diagnosis; MSV, modeling subject variability; WM, working memory; Sc-D, schizophrenia diagnosis. The state-of-the-art papers in cross-subject and cross-site settings are shown by red and green crosses in the dataset columns, respectively.

5.2 Main fMRI Datasets

Some of the most commonly used fMRI datasets are categorized by their usage in different tasks. These datasets are overviewed in Table 4. Additionally, the state-of-the-art papers are marked in Table 2 for the most frequent ones.

5.2.1 ASD Diagnosis. ABIDE[2] contains two main groups: ABIDE I [28] and ABIDE II [27]. Each group involves several sites sharing datasets with R-fMRI (resting-state functional magnetic resonance imaging, anatomical, and phenotypic data types. These datasets have the same labels, including ASD and **Typical Controls (TCs)**; it is worth noting that the scanning procedure is almost identical in two groups of ABIDE across different sites. While ABIDE I is gathered from 17 international sites and yields a 1,112-member dataset comprising 539 subjects with ASD and 573 subjects with TC problems aged from 7 to 64 years and 14.7 years old as the median, ABIDE II is assembled from 19 sites and yields a 1,114-member dataset including 521 subjects with ASD and 593 subjects with TC problems aged between 5 and 64 years old.

5.2.2 Human Thought Analysis. The **Human Connectome Project (HCP)** [149] is a dataset consisting of 1,206 adult subjects who are healthy and aged between 22 and 35 years from families with and without siblings. This dataset has five data types: structural MRI, R-fMRI, T-fMRI (task fMRI, dMRI (diffusion MRI, and MEG. During the experiments, participants were asked to follow these instructions: first, process different types of information like words, images, voices, or letters; second, utilize various thinking skills like memory, language generation, and decision making; and finally, respond in various ways, such as shouting the answer or pressing some buttons.

[2]https://fcon_1000.projects.nitrc.org/indi/abide/

Table 3. Most Common EEG Datasets

Dataset Name	Subject #	Total Sample Count	Channel #	Task	Class #	Link + Availability	Article References
SEED [181]	15	675	62	ER	3	Access Request	[1, 7, 9, 10, 13, 17, 29, 31, 34, 40, 42, 66, 83–85, 91, 94, 105, 106, 108, 109, 112, 138, 147, 151, 162, 165, 176, 186]
DEAP [72]	32	1,280	32	ER	5	Access Request	[4, 9, 10, 31, 40, 42, 51, 57, 59, 66, 75, 85, 96, 112, 147, 158, 162]
DREAMER [68]	32	414	14	ER	3	Access Request	[9, 10, 51, 158]
SEED-IV [180]	15	1,080	62	ER	4	Access Request	[9, 10, 17, 25, 84, 91, 135, 156]
CHB-MIT [141]	22	664	Mostly 23 or 24–26	SA	4	Available	[5, 30, 119, 120, 179]
ISRUC-Sleep [69]	100, 8, 10	126	6	SD	3	Available	[61, 82]
MASS [113]	200	200	4, 17, 19, 20	SD	5	Access Request	[16, 53, 61, 125]
Taiwan Driving Dataset [15]	27	81,576	32	AM	3	Raw Preprocessed	[23, 86, 87]
BCI Competition IV: 2a [12]	9	5,184	22	MI	4	Available	[31, 43, 46, 55, 62, 143, 169, 175]
BCI Competition IV: 2b [81]	9	6,480	3 bipolar	MI	2	Available	[55, 175]
THU-EP [56]	80	2,240	32	ER	9	Available	[138]
MAHNOB-HCI [142]	27	540	32	ER	2	Access Request	[126]
SEED-VIG [182]	23	885	6, 12	AM	2	Access Request	[105, 108]
KU [78]	54	5,400	62	MI	2	Access Request	[60]
GIST [20]	52	5,200 ≤≤ 6,240	62	MI	2	Available	[60]

Note that for each dataset, information like the reference to the paper in which the dataset was first published, the number of subjects whose data is available in the dataset, the number of all sample trials that are provided in the dataset, the number of EEG channels used for signal acquisition, the type of task that the dataset is used for, the number of different classes covered by the dataset, the availability state of the dataset, and the references to articles that utilize the dataset are provided.

The *OpenfMRI*[3] database is a repository for human brain imaging data gathered using MRI and EEG techniques. This database provides several datasets, one of which is used frequently in the papers: the balloon analog risk-taking task dataset [134]. The balloon analog risk-taking task dataset contains fMRI data from 16 right-handed and healthy subjects. During the experiment, subjects must inflate simulated balloons, and for each successive pump during a particular trial, monetary rewards were assigned to them. The number of trials in this experiment varied for each subject because the task was self-paced. There were 10-minute scanning runs unless the subject ran out of balloons.

5.2.3 ADHD Diagnosis. *ADHD-200* [11] is a dataset with the R-fMRI type of data acquired from eight independent sites and composed of 973 subjects, including 176 participants as the test dataset and 776 participants as the training dataset, which includes 491 ordinary individuals and 285 participants with ADHD aged between 7 and 21 years. This dataset has some adjoining phenotypic data, including diagnostic status, dimensional ADHD symptom measures, age, sex, intelligence quotient, and lifetime medication status.

[3]https://openfmri.org/

Table 4. Most Common fMRI Datasets

Dataset Name	Subject #	Task	Class #	Link + Availability	Extra Information	Article References
ABIDE I [28]	1,112	ASD-D	2	Access Request	Site #: 17	[14, 45, 77, 90, 115, 139, 140, 145, 154, 155, 170, 171]
ABIDE II [27]	1,114	ASD-D	2	Access Request	Site #: 19	[122, 155]
HCP [149]	1,206	HTA	2	Available	–	[38, 47, 63, 144]
OpenfMRI: Balloon Analog Risk-Taking Task [134]	16	HTA	2	Available	–	[89, 184]
ADHD-200 [11]	973	ADHD-D	3	Access Request	Site #: 8	[172]
ADNI1 [121]	819	AD-D	3	Access Request	–	[95]
ADNI2 [8]	1,601	AD-D	4	Access Request	–	[95]

ASD-D, autism spectrum disorder diagnosis; ADHD-D, attention deficit hyperactivity disorder diagnosis; AD-D, Alzheimer's disease diagnosis.
Note that in this table, for each dataset, information like the reference to the paper in which the dataset was first published, the number of subjects whose data is available in the dataset, the type of task that the dataset is used for, the number of different classes covered by the dataset, the availability state of the dataset, some extra information like the number of sites from which data was gathered or the number of total sample counts, and the references to articles that utilize the dataset is provided.

5.2.4 Alzheimer's Disease Diagnosis. The **Alzheimer's Disease Neuroimaging Initiative (ADNI)**[4] provides two primary datasets: ADNI1 [121] and ADNI2 [8]. In ADNI1, 1.5T T1-weighted structural MRI data were acquired from 819 subjects, including 192 with Alzheimer's disease, 229 who were cognitively normal, and 398 MCI participants. However, ADNI2 added 782 participants to the 819 recruited by ADNI1. Additionally, ADNI2 added a cohort clinically evaluated as cognitively normal but with subjective memory complaints.

6 FUTURE DIRECTIONS

In this section, we address the attention-worthy tracks that deserve to be investigated more deeply in the literature on DA and DG in functional medical data in the future. These topics are presented as follows.

6.1 Interpretation

Interpretability of deep neural networks, specifically in the health and medical domains, has always been a limiting factor for use cases requiring trust in the obtained results. This has attracted experts' attention to unknown factors and causalities. Interpretability and visualization play a critical role in the generalization and adaptation of methods for health-related data analysis. Even though only a few interpretable DG/DA models have been proposed to analyze medical data, most existing approaches remain black boxes. By making a DG/DA model interpretable, it may be possible to determine each domain's influential aspects and features, select common elements, eliminate noise, and improve its reliability for health professionals. Hence, developing effective strategies in this field is essential, as they have significant real-world implications.

6.2 Incremental and Online Learning

A limited number of data sources are available during the training process for real-world issues, which means that when a new source, sample, or target becomes available over time, the model

[4] https://adni.loni.usc.edu/

needs to be trained based on limited data and then be improved accordingly; as an example, brain data processing can take on data from a new subject, a new center, or a new trial. As a result, if the planned model can learn from consistently added data over time, the model will be more accurate and provide significant benefits, such as the ability to adapt to time-related changes. Taking these observations into account in practical use cases, it is necessary to establish online and incremental strategies to address the mentioned scenario promptly.

6.3 Privacy

Many recent works have focused on DG/DA in deep neural networks, where the network is adapted or generalized without access to the source domain data. In such cases, only the architecture of the network (or, in a more extreme case, only a black-box) is available, so many common DG/DA approaches that rely on moderating data from the source domains fail. Although privacy-preserving ideas have been widely applied to the fields like computer vision and natural language processing, they have not yet been used in medical data analysis to their full potential. Privacy is an undeniable factor in medical fields of study. Patients' information is confidential, so keeping their signals private is necessary. Furthermore, many medical centers might not be willing to share their data with others to keep their methodologies and sources safe from potential rivals. Hence, developing methods to exclude data from DG/DA approaches without affecting performance becomes essential. Still, to the best of our knowledge, so far, only three works, one on EEG data (i.e., [160]) and two on fMRI data (i.e., [45, 90]), have studied source-free DA on EEG data. Thus, there is a growing demand for DG/DA research that preserves privacy.

6.4 Disentangled Representation Learning

Disentangled representation learning is the process of learning narrowly separable features, often supervised by specific semantics within the data. Extensive research on image and video feature disentanglement proves this approach useful for medical data, in which many clues relating to the subjects and tasks are interwoven. The disentanglement of features in brain data is more complex than images or videos, which are relatively understandable and easy to visualize. Additionally, our knowledge about functional brain data is limited, making the decomposition even harder. In this study, we have noted several works that address disentanglement for DG/DA on functional medical data (i.e., [60, 102, 176]). Nevertheless, a more profound investigation of disentanglement for functional medical data remains a challenging problem.

6.5 Multi-Modal Medical Data Processing

Each type of brain signal has its own properties. Hence, a more substantial amount of information is extracted if we process multiple types of brain signals at the same time. For instance, EEG signals have a high temporal resolution but lack spatial resolution, whereas fMRI signals have a high spatial resolution but cannot accurately determine the timestamp of observations. Thus, processing EEG/fMRI data simultaneously makes better use of EEG's spatial and fMRI's temporal resolution. This is useful in HTA tasks, where immediate detection and local information are vital for reliable predictions. Furthermore, different types of signals are produced by different biological processes. Unlike some modalities like image and text, which have much more common information, medical data can offer more information together, which also makes an efficient fusion of these signals more difficult. In addition, multi-modal data incurs combined measurement costs, as each signal has limitations and costs, causing challenges for multi-modal studies. For example, in contrast to fMRI data, EEG signals can be measured while moving under controlled conditions, like driving, whereas fMRI signals can only be measured in steady-state ones.

6.6 Federated Learning of Medical Data

Numerous medical datasets are available for research, but the amount of data generated by medical institutions and hospitals are well beyond what academics can access. In addition to privacy issues, the amount of resources required to process, store, maintain, and update the dataset makes it impractical to gather all data that are continuously measured at medical sites. A high-performance system that works well in real-world applications can be obtained by processing this data in a federated learning framework. Local sources (e.g., hospitals) will not be concerned about their private patient information or statistics being exposed. Furthermore, each source can train and prepare its model using a relatively cheap computer system, update its data and model according to its schedule, and use a high-performing model trained based on information from multiple sources at no extra cost.

7 CONCLUSION

Several methods covering various applications have been developed in the literature to allow medical data analysis models trained on one or more source domains to adapt to unidentified **Out-Of-Distribution (OOD)** target data and train generalizable models. This area of research has recently received considerable attention and is an essential component of deploying many ML algorithms. We presented a systematic and comprehensive review of DA and DG methods for functional medical data, particularly functional brain data. In addition to OOD generalization and adaptation fundamentals, we presented the major approaches, architectures, and essential datasets used in medical data analysis. In this study, we have collected and summarized 98 papers on EEG and 24 papers on fMRI data. Furthermore, a systematic categorization for the collected papers is introduced, providing a comprehensive and detailed description of numerous approaches in the recent literature. Additionally, details about well-known and publicly available datasets in this research field are presented. These datasets include 15 EEG and 7 fMRI datasets, covering various applications such as ER, SD, and MI. Our analysis eventually addresses several potential outstanding issues like interpretation and privacy, and some promising directions such as federated learning, multi-modal data processing, and online learning in Section 6, for future research to further expand this field of study and make it more consistent with real-world applications and trends.

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