Abstract—Federated learning is an emerging paradigm allowing large-scale decentralized learning without sharing data across different data owners, which helps address the concern of data privacy in medical image analysis. However, the requirement for label consistency across clients by the existing methods largely narrows its application scope. In practice, each clinical site may only annotate certain organs of interest with partial or no overlap with other sites. Incorporating such partially labeled data into a unified federation is an unexplored problem with clinical significance and urgency. This work tackles the challenge by using a novel federated multi-encoding U-Net (Fed-MENU) method for multi-organ segmentation. In our method, a multi-encoding U-Net (MENU-Net) is proposed to extract organ-specific features through different encoding sub-networks. Each sub-network can be seen as an expert of a specific organ and trained for that client. Moreover, to encourage the organ-specific features extracted by different sub-networks to be informative and distinctive, we regularize the training of the MENU-Net by designing an auxiliary generic decoder (AGD). Extensive experiments on four public datasets show that our Fed-MENU method can effectively obtain a federated learning model using the partially labeled datasets with superior performance to other models trained by either localized or centralized learning methods. Source code will be made publicly available at the time of paper publication.

Index Terms—Federated learning, Deep learning, Medical image segmentation, Partial label.

I. INTRODUCTION

CONVOLUTIONAL neural network (CNN) based deep learning (DL) as a data-driven methodology has demonstrated unparalleled performance in various segmentation tasks, providing that the model can train on large-scale data with sufficient diversity. To suffice the large appetite of CNNs, researchers often collect data from multiple sources to jointly train a model for improved performance. However, in the healthcare domain, such centralized learning paradigm is often impractical because the clinical data cannot be easily shared across different institutions due to the regulations, such as Health Insurance Portability and Accountability Act (HIPAA). To overcome the barrier of data privacy and realize large-scale DL on isolated data, federated learning (FL) [1], an emerging decentralized learning paradigm, has been adopted in the medical image analysis, solving various clinical problems such as prostate segmentation [2], [3] and COVID-19 diagnosis [4], [5].

FL allows different data-owners to collaboratively train one global DL model without sharing the data. The model training is completed by iterating over a server node and several client nodes. Each client individually trains a copy of the global model using their local data after the server updates the global model by aggregating the locally trained models. By repeating this process, the global model can effectively absorb the knowledge contained in the client datasets without data sharing. As data privacy has become a critical issue concerned by healthcare stakeholders, FL attracts a growing attention from both the research and clinical communities in recent years.

Although the capability of FL for medical image analysis has been demonstrated by the prior studies, it comes with limitations. A critical issue is about the strict requirement for the label consistency. Specifically, in an FL system, all the participating sites need to have identical regions-of-interest (ROIs) annotated on their local data, so the FL model can be optimized following the same objective across different clients. However, in practical scenarios, different clinical sites often have different expertise and thus follow different protocols for data annotation. This leads to inconsistent ROI labels across different sites. The requirement for labeling consistency hinders the FL methods from large-scale deployment in practice. Therefore, a more flexible FL framework supporting the training with inconsistently labeled client data is highly desired. From a technical point of view, this is an FL problem with partial labels since each client merely has a partially labeled dataset with respect to the whole set of ROIs in the federation. To the best of our knowledge, this is a new problem that has not yet been explored before, but at the same time is of great clinical significance and technical urgency to tackle.

In this paper, we propose a novel method, called federated multi-encoding U-Net (Fed-MENU), to address the above challenge. We then demonstrate its performance on a representative task, i.e., multiple abdominal organ segmentation from computed tomography (CT) images. The underlying assumption of our design is that, although the data from different clients show disparities in terms of the labeled ROIs, they share the same or similar image contents and thus can provide complementary information to facilitate the learning of robust features in a unified FL system. Since the client datasets are partially labeled with different ROIs, they can be seen as a set of experts with different expertise. Each expert focuses on learning the features within its expertise (labeled ROIs) while avoiding introducing the unreliable or noisy information from the non-expertise (unlabeled ROIs). To achieve this goal, we design a multi-encoding U-Net (MENU-Net) to decompose the multi-organ feature learning task into a series of individual sub-tasks of organ-specific

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The contributions of this paper are three-fold. First, learning model trained by combining all the datasets. The main advantage of the trained model is superior to the localized learning approach. Second, it utilizes the isolated datasets with different partial labels to train a global model for multi-organ segmentation. The performance of the trained model is superior to the localized learning model trained by any single dataset and also the centralized learning model trained by combining all the datasets. The main contributions of this paper are three-fold.

- We addressed a new problem in FL to enable collaboratively training a global model using isolated datasets with inconsistent labels.
- We proposed a novel Fed-MENU method to deal with this challenging problem. In our method, organ-specific features are individually extracted by different sub-networks of the MENU-Net and further enhanced by the accompanied AGD.
- We evaluated the performance of our Fed-MENU method for multi-organ segmentation using four public abdominal CT datasets. Our experimental results on both in-federation and out-of-federation testing sets demonstrated the effectiveness and superior performance of our design.

The rest of this paper is organized as follows. Section II gives a brief review of the previous literature related to this work. Section III illustrates the details of the proposed method. Section IV presents the experiments and results on four public datasets. Finally, we conclude this work in Section V.

II. RELATED WORKS

Since our study involves both FL-based medical image analysis and DL-based image segmentation with partially labeled data, we review the related works in these two areas before presenting our proposed method.

A. Federated learning for medical image analysis

In recent years, FL has been widely applied in various medical image analysis tasks to address the conflict between large-scale DL model training and healthcare data privacy. For example, Dayan et al. [3] trained a FL model for COVID-19 clinical outcome prediction using chest X-rays images from 20 institutes across the globe. The experimental results showed that the FL model provided a 16% improvement in the average area under the curve (AUC) measured across all participating sites. Xia et al. [6] derived an auto-FedAvg method from FedAvg [1] for medical image segmentation using data that are not independently and identically distributed (non-iid). Their method automatically learns the aggregation weights of each client based on the client data distribution. Roth et al. [2] combined FL with neural architecture search strategy to develop a super-network with a self-learned structure for whole prostate segmentation from multi-institute magnetic resonance imaging (MRI) data. Recently, Yang et al. [4] extended FL to semi-supervised learning paradigm and applied it to COVID region segmentation using chest CT data from three nations.

The prior studies [2, 4–11] have demonstrated the feasibility and effectiveness of FL in solving the problem of large-scale DL model training without data sharing in the healthcare community. However, all these successes are built upon a prerequisite that the participating sites have consistent labels so that they can contribute to the same training objective of one global model. However, such a strong requirement may not be met in the real scenarios, where different clinical sites often follow different protocols to annotate their local data. The gap caused by the label inconsistency largely narrows the application scope of the FL-based methods for medical image analysis and thus motivates our study in this work.

B. Medical image segmentation with partial labels

Due to the high cost of data annotation, medical images are often partially labeled with different ROIs or labels, even though they may share the same imaging field. This created a barrier for the DL-based medical image analysis methods when the model is trained on the partially labeled data. To solve this problem, Yan et al. [12] developed a universal lesion detection algorithm trained by CT images labeled with different lesion types. In their method, the missing labels were mined by exploiting clinical prior knowledge and cross-dataset knowledge transfer. Recently, Petit et al. [13] proposed to conduct partially labeled DL training through an iterative confidence relabeling method, in which a self-supervised scheme was employed to iteratively relabel the missing organs by introducing pseudo labels into the training set. For the partial label problem in segmentation tasks, Fang and Yan [14] proposed a pyramid-input-pyramid-output feature abstraction network (PIPO-FAN) for multi-organ segmentation, in which a target adaptive loss is integrated with a unified training strategy to enable image segmentation over multiple partially labeled datasets with a single model. Shi et al. [15] designed two types of loss functions, namely marginal loss and exclusion loss, to train a multi-organ segmentation network using a set of partially labeled datasets.

Although the problem of training DL models using partially labeled data [12–17] had been studied in the context of centralized learning, it is still an unexplored area for the field of FL. In this paper, we present the Fed-MENU method, which can learn from partially labeled data distributed on different sites.
Fig. 1: Scheme of the proposed Fed-MENU method. For better understanding, the method is presented using an example scenario where three clinical sites with partially labeled abdominal CT images collaboratively train an FL model for segmentation of the liver, kidney, and pancreas. The left panel of the figure shows the federation structure. The right panel details the local training procedure on Client node 3, where the pancreas is the only labeled organ.

### III. Method

Fig. 1 gives an overview of the proposed Fed-MENU method. For a better understanding, it is presented in a specific scenario where the federation contains three client nodes and each node possesses a CT dataset partially labeled with one of the abdominal organs (liver, kidney, and pancreas). We then describe the FL framework adopted by our method in Section III-A. The technical innovation of this work resides in the MENU-Net designed for organ-specific feature extraction (Section III-B) and the AGD designed for organ-specific feature enhancement (Section III-C). The training configurations and other technical details of the proposed method are provided in Section III-D.

#### A. Federated learning framework

Our method inherits the framework of the federated averaging (FedAvg) [1] algorithm, which is a commonly adopted benchmark in FL. It consists of one server node and $K$ client nodes. The server takes the responsibility of coordinating the communication and computation across different clients, while the clients focus on model training using their local data and devices. Given the universal label set of $M$ organs, each of the client nodes has a local dataset $D_k$ partially labeled with a subset of $N_k(\leq M)$ organs. Our goal is to train a $M$-organ segmentation network $F(\cdot, \theta)$ using the partially labeled datasets $\{D_k\}_{k=1}^K$, which reside in different client nodes and cannot be shared or gathered for centralized training.

The training process of the FL framework consists of $T$ rounds of communication between the server and the client nodes. Specifically, in the $t$-th communication round, each client node $k$ will first download the parameters of the current segmentation network $F(\cdot, \theta^t)$ on server (denoted as global model), resulting in a local copy of $F(\cdot, \theta^t)$ (denoted as local model). The client node then trains the local model using its local dataset $D_k$ and device for $E$ epochs. After the local training, the server collects the trained local models $F(\cdot, \theta^t_k)$ from all the $K$ client nodes and aggregates them into a new global model through a parameter-wise averaging:

$$
\theta^{t+1} = \frac{1}{\sum_k |D_k|} \sum_k \frac{|D_k|}{|D_j|} \cdot \theta^t_k,
$$

where $|D_k|$ indicates the sample size of dataset $D_k$. The whole FL procedure is accomplished by repeating the above process until the global model $F(\cdot, \theta)$ converges.

Because the local models are individually trained on the client nodes, the server node only needs to transfer the model parameters instead of the raw data from the clients. That helps the FL model obtain knowledge contained in the decentralized client datasets without violating the data privacy. However, since the original FedAvg framework is designed for FL with fully labeled data, there is a technical gap to bridge before we can deploy it to the case of partially labeled data. Therefore, we propose the following MENU-Net with AGD to meet the need.

#### B. MENU-Net for organ-specific feature extraction

A straightforward way to train a multi-organ segmentation network using the partial labels is to calculate the training loss merely using the labeled organs while ignoring the unlabeled ones. However, in the case of FL with partial labels, different organs are labeled in the client datasets, focusing on different expertise for image segmentation. As a consequence, the segmentation performance of the trained local models would be biased to the labeled organs. Intuitively, a uniform aggregation of all local models (see Eq. 1) may weaken the expert client models. A more reasonable way may be to promote the strength of the local models on segmenting the labeled organs and avoid the interference from their weaknesses with the unlabeled organs.
To achieve the above goal, we designed the MENU-Net to explicitly decompose multi-organ feature extraction into several individual processes of organ-specific feature extraction. As illustrated in the right panel of Fig. 1, the MENU-Net consists of $M$ sub-encoders $\{g_m(\cdot | \theta_{gm})\}_{m=1}^M$ followed by a shared decoder $f(\cdot | \theta_f)$ as well as the skip connections between them. Fig. 1 shows an example with $M=3$. Each sub-encoder $g_m(\cdot | \theta_{gm})$ serves as an organ-specific feature extractor for the $m$-th organ. An input image $x$ is fed to all the sub-encoders to get the features of all the organs in parallel. The extracted features are then concatenated into one stream and fed to the shared decoder $f(\cdot | \theta_f)$, which is used to interpret the organ-specific features into the multi-organ segmentation masks. This process is formally defined as

$$F(x) = f((g_1(x) \oplus g_2(x) \cdots \oplus g_M(x)))$$

where $\oplus$ denotes channel-wise concatenation.

Given a client node with partial labels on the $m$-th organ, the local model training only tunes the parameters in the sub-encoder $g_m(\cdot | \theta_{gm})$ and the shared decoder $f(\cdot | \theta_f)$, which can be expressed as:

$$\arg \min_{\theta_f, \theta_{gm} < \theta} L_{sup}[F_m(x | \theta), \hat{y}_m],$$

where $F_m(x)$ and $\hat{y}_m$ are the predicted and ground-truth segmentation of the $m$-th organ, respectively. $L_{sup}$ denotes the supervised loss measuring the similarity between the prediction and ground truth, which can be in any form of pixel-wise loss functions (e.g., Cross-entropy loss and Dice loss [18]) or their combinations.

### C. AGD for organ-specific feature enhancement

Benefitting from the decomposed feature extraction in MENU-Net, organ-specific knowledge from the labeled clients (experts) can be individually learned by different sub-encoders with less interference from other unlabeled clients (non-experts). However, since each local model can only see the images from one client dataset, the organ-specific features learned by the sub-encoders may also include some domain-specific information. This is unfavorable for the subsequent shared decoder. Ideally, the sub-encoder should focus on the structural information of the corresponding organ, which is invariant across domains. In addition, the extracted organ-specific features should be distinctive enough from that of other organs, making the subsequent shared decoder easier to interpret them into different organs’ segmentation.

Motivated by the above idea, we design the AGD shared across different sub-encoders to help regularize the training of our MENU-Net, aiming to enhance the extracted organ-specific features. Specifically, as illustrated in the mid-bottom of Fig. 1, given the organ-specific features $g_m(x)$ extracted by an arbitrary sub-encoder $g_m(\cdot | \theta_{gm})$, we feed them to a set of AGDs to perform an organ-agnostic (binary) segmentation of the $m$-th organ:

$$G_m(x) = h(g_m(x)).$$

Here, we denote the collection of all AGDs as $h(\cdot | \theta_h)$ parameterized by $\theta_h$. The AGD has a lite structure consisting of three convolutional layers. The first two convolutional layers contain $3 \times 3$ kernels followed by instance normalization [19] and LeakyReLU activation [20]. The last convolutional layer has $1 \times 1$ kernels with two output channels followed by a softmax activation. Due to the shallow structure of AGD, it has limited representation ability and thus enforces the preceding sub-encoder layers to extract more discriminative features to approach the organ segmentation. On the other hand, since the AGD is working as a generic decoder for different organs when combined with different sub-encoders, the sub-encoders are encouraged to extract features distinctive enough from each other so that the following AGD can interpret them into the corresponding organ’s segmentation without extra information.

During the local training stage, the AGDs are tuned together with different sub-encoders over all client nodes by minimizing the segmentation error between the output $G_m(x)$ and the corresponding ground truth $\hat{y}_m$. This process can be expressed as:

$$\arg \min_{\theta_h, \theta_{gm}} L_{aux}[G_m(x | \theta_h, \theta_{gm}), \hat{y}_m],$$

where $L_{aux}$ denotes the auxiliary loss quantifying the binary segmentation error between the AGDs’ output and the corresponding ground truth. We calculate $L_{aux}$ as a sum of the Cross-entropy loss and Dice loss [18]. Note that, since the AGDs are connected to the multi-scale levels of the sub-encoder, they have multiple outputs in different scales. All these outputs will be resampled to the original size of the ground-truth segmentation $\hat{y}_m$ and counted in the auxiliary loss in Eq. 5. After the local training, the tuned parameters of AGDs from all clients are aggregated through the FedAvg algorithm as shown in Eq. 1 which is the same as that of the shared decoder $f(\cdot | \theta_f)$.

### D. Implementation details

The proposed method is implemented for 3D segmentation using PyTorch. Model parameters in the segmentation network are initialized using the Xavier algorithm [21] and optimized by an SGD optimizer. The learning rate is initialized to be 0.01 and decayed throughout the training following a poly learning rate policy [22] with a momentum factor of 0.99. We train the model for $T=400$ rounds of communication ($E=1$ epoch of local training per round) and evaluate its performance on the validation set every epoch using Dice similarity coefficient (DSC) as the metric. The model achieving the highest DSC on the validation set is selected as the final model to be evaluated on the testing set. The training batch size is set to 16 on four NVIDIA A100 GPUs. The input CT images are cut into stacks along z-axis. Each stack has a uniform pixel size of $128 \times 128 \times 32$ with a spacing of $3.0 \times 3.0 \times 5.0 \text{mm}^3$. The image intensities are normalized from [-200.0, 400.0] Hounsfield units (HU) to [0.0, 1.0] for a good soft-tissue contrast. Random translation (-20,20)[mm] and rotation (-0.1,0.1)[rad] are used to augment the training samples. Unless otherwise noted, all the competing methods and ablation models in our experiments are trained and evaluated using the same configuration.
TABLE I: Detailed information of liver, kidney, pancreas, and BTCV datasets.

| Datasets           | Image info. | Label info. |
|--------------------|-------------|-------------|
|                    | # of CT images (training/validation/testing) | Slice size [in pixel] | # of slice [per image] | Spacing [mm] | Slice thickness [mm] | Liver | Kidney | Pancreas |
| Liver (Client #1)  | 131 (79 / 13 / 39) | 512 | 74~987 | 0.56~1.00 | 0.70~5.00 | ✓ | ✓ | × |
| Kidney (Client #2) | 210 (126 / 21 / 63) | 512,796 | 29~1059 | 0.44~1.04 | 0.50~5.00 | × | ✓ | ✓ |
| Pancreas (Client #3)| 281 (169 / 28 / 84) | 512 | 37~751 | 0.61~0.98 | 0.70~7.50 | × | × | ✓ |
| BTCV (Test only)  | 30 (0 / 0 / 30) | 512 | 85~198 | 0.59~0.98 | 2.50~5.00 | ✓ | ✓ | ✓ |

as our method. For better reproducibility, the source code will be released at the time of paper publication.

IV. EXPERIMENTS

A. Datasets

We conducted experiments using four public abdominal CT image datasets, including 1) liver tumor segmentation challenge (LiTIS) dataset \[23\], 2) kidney tumor segmentation challenge (KiTS) dataset \[24\], [25\], 3) medical segmentation decathlon dataset (Task #7) \[26\] and 4) multi-atlas labeling beyond the cranial vault challenge (BTCV) dataset \[27\].

For brevity, we denote the four datasets as the liver, kidney, pancreas, and BTCV, respectively, in the rest of the paper. Table I shows the details of these four datasets.

Liver dataset contains 131 images, whose sizes range between [74~987]×[512]×[512] (in D×H×W pixels). The in-plane spacing of these CT slices varies from 0.56mm to 1.00mm and the slice thickness varies from 0.70mm to 5.00mm. Each CT image has a pixel-wise annotation of liver and tumor segmentation stored in the same size as the corresponding image. We treat the liver tumor regions as part of the liver in our experiments.

Kidney dataset contains 210 images, whose sizes range between [29~1059]×[512]×[512] (in D×H×W pixels). The in-plane spacing of CT slices varies from 0.44mm to 1.04mm and the slice thickness varies from 0.50mm to 5.00mm. Each CT image has a pixel-wise annotation of kidney and tumor segmentation stored in the same size as the corresponding image. We treat the kidney tumor regions as part of the kidney in our experiments.

Pancreas dataset contains 281 images, whose sizes range between [37~751]×[512]×[512] (in D×H×W pixels). The in-plane spacing of these CT slices varies from 0.61mm to 0.98mm and the slice thickness varies from 0.70mm to 7.50mm. Each CT image has a pixel-wise annotation of pancreas and tumor segmentation stored in the same size as the corresponding image. We treat the pancreas tumor regions as part of the pancreas in our experiments.

BTCV dataset contains 30 images, whose sizes range between [85~198]×[512]×[512] (in D×H×W pixels). The in-plane spacing of these CT slices varies from 0.59mm to 0.98mm and the slice thickness varies from 2.50mm to 5.00mm. Each CT image has a pixel-wise annotation of liver, kidney, and pancreas segmentation stored in the same size as the corresponding image.

For the liver, kidney, and pancreas datasets, we randomly split each of them into training/validation/testing sets with a fixed ratio of 60%:10%:30%. The experimental results on the three testing sets are used for in-federation evaluation, which indicates the model performance when the testing data follows the same distribution as the training and validation data. For the BTCV dataset, we reserve it as an out-of-federation testing set, which is completely unseen to the model during training and validation. The performance on the BTCV dataset gives a good indication of the model’s generalization ability.

B. Metrics

We calculated the mean and standard deviation of Dice similarity coefficient (DSC) and average symmetric surface distance (ASD) for each organ to quantitatively evaluate the segmentation results yielded by different methods. The average of the three target organs’ mean values was used as the indices of global performance. Instead of performing an overall case-wise averaging, this strategy was to avoid the bias from unbalanced sample numbers among the datasets, ensuring the global DSC and ASD calculated from each dataset with different sizes play an equal role. We also conducted paired t-tests on the above metrics to check the statistical significance between different groups of results.

C. Comparison with benchmarks

1) Benchmarks: We compared our method with three benchmarks to demonstrate its effectiveness. The benchmarks include:

   **Localized learning model**: Three single-organ segmentation networks were individually trained using the liver, kidney, and pancreas datasets, respectively. Given an unseen testing CT image, the three trained models were successively applied to segment the target organs. This benchmark simulated the scenario where the clinical sites cannot share their data with each other and no techniques are adopted to deal with the data privacy issue during the model training.

   **Centralized learning model**: A multi-organ segmentation network was trained using the combination of the liver, kidney, and pancreas datasets. This benchmark simulated an ideal scenario where the clinical sites can freely share their data without any concern on the data privacy during the model training.

   **Federated learning model**: A multi-organ segmentation network was trained using the FedAvg \[1\] algorithm with the

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1https://competitions.codalab.org/competitions/17094
2https://kits19.grand-challenge.org/home/
3http://medicaldecathlon.com/
4https://www.synapse.org/#!Synapse:syn3193805/wiki/89480
TABLE II: Quantitative performance evaluation of different methods when tested on the in-federation data. Best results are marked in bold. The underlined results indicate a statistically significant difference with our result ($p<0.05$).

| Models                        | Liver [DSC [Mean(SD) %]] | Kidney [DSC [Mean(SD) %]] | Pancreas [DSC [Mean(SD) %]] | Average [DSC [Mean(SD) %]] | Liver [ASD [Mean(SD) mm]] | Kidney [ASD [Mean(SD) mm]] | Pancreas [ASD [Mean(SD) mm]] | Average [ASD [Mean(SD) mm]] |
|-------------------------------|---------------------------|----------------------------|-------------------------------|----------------------------|----------------------------|----------------------------|-------------------------------|----------------------------|
| Localized learning (liver)    | 93.11(2.28)               | -                          | -                             | 84.86                      | 2.46(1.90)                 | -                          | -                             | 2.54                       |
| Localized learning (kidney)   | -                         | 92.27(6.63)                | -                             | 84.10                      | 2.60(2.83)                 | -                          | -                             | 2.70                       |
| Localized learning (pancreas) | -                         | -                          | 69.18(15.15)                  | 84.86                      | 2.46(1.90)                 | -                          | -                             | 2.54                       |
| Centralized learning          | 92.63(3.23)               | 91.11(6.44)                | 69.03(12.44)                  | 84.26                      | 2.60(2.60)                 | 2.05(2.74)                 | 3.44(2.76)                   | 2.70                       |
| Federated learning (U-Net)    | 92.79(3.03)               | 91.32(7.98)                | 69.16(13.78)                  | 84.42                      | 3.20(3.23)                 | 2.04(2.69)                 | 3.50(3.39)                   | 2.91                       |
| Federated learning (ours)     | 93.34(2.27)               | 92.50(5.95)                | 71.11(14.54)                  | 85.65                      | 2.52(1.81)                 | 1.46(1.63)                 | 3.23(3.62)                   | 2.40                       |

TABLE III: Quantitative performance evaluation of different methods when tested on the out-of-federation data. Best results are marked in bold. The underlined results indicate a statistically significant difference with our result ($p<0.05$).

| Models                        | Liver [DSC [Mean(SD) %]] | Kidney [DSC [Mean(SD) %]] | Pancreas [DSC [Mean(SD) %]] | Average [DSC [Mean(SD) %]] | Liver [ASD [Mean(SD) mm]] | Kidney [ASD [Mean(SD) mm]] | Pancreas [ASD [Mean(SD) mm]] | Average [ASD [Mean(SD) mm]] |
|-------------------------------|---------------------------|----------------------------|-------------------------------|----------------------------|----------------------------|----------------------------|-------------------------------|----------------------------|
| Localized learning (liver)    | 92.53(3.89)               | -                          | -                             | 79.67                      | 2.76(3.93)                 | -                          | -                             | 4.49                       |
| Localized learning (kidney)   | -                         | 83,91(16.27)               | -                             | 79.67                      | 3.88(3.17)                 | -                          | -                             | 4.49                       |
| Localized learning (pancreas) | -                         | -                          | 62.57(16.75)                  | 79.67                      | -                          | 6.84(10.14)                | -                             | 4.60                       |
| Centralized learning          | 93.10(2.42)               | 82.20(17.46)               | 69.03(12.46)                  | 78.74                      | 2.20(1.57)                 | 5.53(11.54)                | 6.00(5.54)                   | 4.60                       |
| Federated learning (U-Net)    | 93.28(2.69)               | 82.81(16.94)               | 62.84(16.45)                  | 79.65                      | 3.83(3.70)                 | 4.04(6.90)                 | 6.95(9.01)                   | 4.95                       |
| Federated learning (ours)     | 93.41(3.85)               | 83.60(16.38)               | 70.41(9.13)                   | 82.47                      | 3.23(5.88)                 | 5.47(17.03)                | 3.55(3.93)                   | 4.08                       |

liver, kidney, and pancreas datasets distributed on three client nodes. This benchmark simulated a practical scenario where the clinical sites cannot share their data with each other and a naive FL solution is adopted to deal with the data privacy issue during the model training.

We adopted U-Net [28] as the segmentation network for the above models. The training configuration of all the methods followed the recommended settings by nnU-Net [22]. For the FL model, we employed the marginal loss and exclusion loss [15] as the training objective to supervise the segmentation network with partial labels on different clients. For the sake of fairness, the same objective was also used as the supervised loss $L_{sup}$ in our method.

2) In-federation performance: Table II shows the quantitative results of the in-federation evaluation. Overall, our method obtained the highest accuracy over other competing models, which demonstrated the feasibility of using different partially labeled datasets to collaboratively train a model through FL. Our method achieved significant improvements in most of the cases. It is worth noting that our method showed a significant improvement over the localized learning benchmark on the pancreas segmentation. The boundary of pancreas exhibits more variable shapes and lower contrast than the other two organs. Our method can efficiently learn the knowledge in different datasets and thus obtained larger improvement in this case. Another interesting observation was that, in our experiment, the three benchmarking models showed similar performance. The centralized learning model did not lead to a higher accuracy than the federated learning model or the localized learning models. This result was different from that in the conventional FL scenario, where all the client datasets have the identical set of ROIs fully labeled. In that case, the centralized learning often represented the upper-bound performance of the FL models. We attribute this phenomenon to the fact that the mixture of the partially labeled data could confuse the deep models during training, if the expertise of different ROIs is not well-decomposed. This result can also serve as an endorsement of our method that the organ-specific feature learning is necessary for the FL model when dealing with the partial labels.

3) Out-of-federation performance: Table III shows the quantitative results of the out-of-federation evaluation. Our method achieved the best performance in terms of the average accuracy over the three organs. When compared with the in-federation segmentation, the out-of-federation segmentation showed a global performance drop, which is caused by the data distribution shift from the training domain (the liver, kidney, and pancreas datasets) to an unseen testing domain (the BTCV dataset). It was worth noting that, among all the competing models, our method suffered the least from the domain shift issue. Our segmentation DSC on the pancreas slightly decreased from 71.11% to 70.41% for only 0.70%, while other competing models dropped over 6%. This result demonstrated the good generalizability of our method, which is brought by the MENU-Net and AGD designs for robust organ-specific feature learning. In Fig. 2 and Fig. 3, we visualize some cases of the segmentation results in 2D and 3D views, respectively.

D. Ablation study

In this section, we conducted ablation studies on the proposed method to evaluate the effectiveness of the two key designs, including 1) the MENU-Net for organ-specific feature extraction and 2) the AGD for organ-specific feature enhancement. A U-Net [28] trained using the FedAvg algorithm [1] was used as the baseline method, on which the MENU-Net
and AGD components are sequentially imposed. In addition, we also tried to replace the AGD with a non-generic version, i.e., the auxiliary decoders are locally trained on the client nodes without parameter fusion (see Eq. 1) through the server node. We denote it as auxiliary localized decoder (ALD) in the following contents. This ablation model is used to justify the necessity of parameter sharing in learning the organ-specific features.

The quantitative results of the ablation studies are listed in Table IV. The observations are three-fold. 1) Compared with the baseline, the design of the MENU-Net (Table IV, "+MENU-Net") mainly improved the pancreas segmentation in the out-of-federation evaluation, which indicated a positive effect of the task decomposition in learning domain-invariant features, especially for the organ with variable shape and blurring boundary. 2) Based on the MENU-Net, either the AGD (Table IV, "+MENU-Net+AGD") or the ALD (Table IV, "+MENU-Net+ALD") can further boost the segmentation accuracy for both in-federation and out-of-federation evaluation. This result suggested that the auxiliary supervisions on the intermediate layers can facilitate the learning of more discriminative features, and thus, benefit the subsequent shared

| Models                  | In-federation DSC [Mean(SD) %] | Out-of-federation DSC [Mean(SD) %] |
|-------------------------|-------------------------------|-----------------------------------|
|                         | Liver | Kidney | Pancreas | Average | Liver | Kidney | Pancreas | Average |
| Baseline                | 92.79(3.03) | 91.32(7.98) | 69.16(13.78) | 84.42 | 93.28(2.69) | 82.81(16.94) | 62.84(16.45) | 79.65 |
| + MENU-Net              | 92.82(2.88) | 91.02(8.34) | 69.51(14.46) | 84.45 | 92.93(3.45) | 82.53(16.89) | 64.59(15.92) | 80.02 |
| + MENU-Net + ALD        | 93.09(2.46) | 92.45(6.10) | 71.93(13.45) | **85.82** | 93.26(3.84) | **83.90**(16.25) | 67.84(12.71) | 81.67 |
| + MENU-Net + DeepSup    | 92.96(2.68) | **92.80**(4.53) | 71.60(12.26) | 85.78 | 93.16(3.71) | 83.78(16.13) | 65.79(16.59) | 80.75 |
| + MENU-Net + AGD        | **93.34**(2.27) | 92.50(5.95) | 71.11(14.54) | 85.65 | **93.41**(3.85) | 83.60(16.38) | **70.41**(9.13) | **82.47** |

Fig. 2: 2D Visualization of segmentation results yielded by different methods. Each row shows the results and ground truth of one case. For better comparison, the ground-truth contours are also superimposed on the segmentation results as yellow dashed lines. The yellow arrows highlight the false positive regions wrongly segmented by the centralized learning method and the conventional FL method.

TABLE IV: Experimental results of ablation studies on the proposed method. Best results are marked in bold. The underlined results indicate a statistically significant difference with the bottom row ($p<0.05$).
Fig. 3: 3D Visualization of segmentation results by different methods. Each row shows the results and ground truth of one case. The segmentation of the unlabeled organs is represented by transparent meshes.

Fig. 4: Gradient-weighted class activation maps (Grad-CAMs) [29] generated by the MENU-Net trained without AGD (left), with ALD (middle), and with AGD (right). Yellow dashed lines indicate ground-truth contours. We use the activation (output) of the second convolutional block in the sub-encoders to calculate the Grad-CAMs.

decoder for accurate segmentation. 3) The AGD outperformed the ALD on the out-of-federation pancreas segmentation by a significant margin from a DSC of 67.84% to 70.41% (p<0.05). The resulting performance (DSC=70.41%) is also comparable to that of the in-federation segmentation (DSC=71.11%). This result demonstrated the importance of parameter sharing in our AGD since the auxiliary decoder shared across the clients enforced the preceding sub-encoders to extract discriminative features for different organs.

Fig. 4 visualized the gradient-weighted class activation maps (Grad-CAMs) [29] produced by our MENU-Net (extracted from the second convolutional block in the sub-encoders) when it is trained without AGD, with ALD, and with AGD, respectively. The model trained with AGD generated activation maps with more accurate shapes and fewer false positive regions than the other two models, which indicated that the AGD can effectively enhance the organ-specific features extracted by the sub-encoders in our MENU-Net.

We also tried to replace the AGD in our method with the conventional deep supervision mechanism [30] since it is another way often used to enhance the intermediate features of deep networks. Specifically, we added an output layer (which is a 1×1 convolutional layer with two output channels followed by softmax activation) to each convolutional block in the shared decoder of the MENU-Net and supervised the output segmentations with the partial labels during training. This model is denoted as “+MENU-Net+DeepSup” in Table. IV which showed similar accuracy as our method in the
TABLE V: Quantitative performance evaluation of the proposed method trained with different communication frequencies. Best results are marked in bold. The underlined results indicate a statistically significant difference with the bottom row (p<0.05).

| Communication frequency | In-federation DSC [Mean(SD) %] | Out-of-federation DSC [Mean(SD) %] |
|-------------------------|---------------------------------|-----------------------------------|
|                         | Liver  | Kidney | Pancreas | Average | Liver | Kidney | Pancreas | Average |
| 25 × 16                 | 92.62(2.54) | 92.34(5.38) | 70.70(14.09) | 85.22 | 92.19(5.03) | 84.35(16.45) | 67.37(11.55) | 81.31 |
| 50 × 8                  | 93.78(2.39) | 92.51(5.28) | 71.33(14.76) | 85.67 | 92.37(4.55) | 83.24(16.64) | 67.21(10.77) | 81.12 |
| 100 × 4                 | 93.28(2.31) | 92.82(4.20) | 71.28(13.71) | 85.79 | 93.62(4.12) | 82.82(17.38) | 67.26(11.18) | 81.26 |
| 200 × 2                 | 93.29(2.43) | 92.62(4.74) | 71.57(13.94) | 85.83 | 93.45(3.73) | 83.52(15.99) | 67.70(10.93) | 81.58 |
| 400 × 1                 | 93.34(2.27) | 92.50(5.95) | 71.11(14.54) | 85.65 | 93.41(3.85) | 83.60(16.38) | 70.41(9.13) | 82.47 |

Fig. 5: Average DSC of FL models trained with different communication frequency. Red dashed line indicates the average DSC achieved by a U-Net trained through centralized learning.

E. Effects of communication frequency

Communication frequency is a key factor affecting the performance of the FL methods in practice. In the proposed method, the communication frequency is jointly controlled by the number of communication round $T$ and the number of local training epochs $E$. We successively trained our method with different combinations of $T \times E$ to investigate the effects of communication frequency. For the sake of fairness, the product of these two parameters are fixed to 400, which means all models are optimized with the same number of training batches (iterations).

The experimental results are shown in Table V and Fig. 5. It can be seen that higher communication frequency generally brought better performance to the trained model, which is in line with observations in other FL-based methods [1], [4], [6], [31], and our method consistently outperformed the baseline FL U-Net model. Considering our method is designed for the cross-silo FL [32] scenario, where the clients (clinical sites) have stable internet connections with sufficient bandwidth, we finally choose $T=1$ in our method to achieve higher accuracy.

V. DISCUSSION AND CONCLUSION

In this paper, we revealed and defined a new problem of FL with partially labeled data in the context of medical image segmentation, which is of great clinical significance and technical urgency to solve. Subsequently, a novel Fed-MENU method was proposed to tackle this challenging problem. Compared with the conventional FL framework that worked on the fully-labeled data, our Fed-MENU method had two key designs to adapt to the partially labeled client datasets, 1) the MENU-Net for organ-specific feature extraction and 2) the AGD for organ-specific feature enhancement. Extensive experiments were conducted using four public abdominal CT image datasets. The experimental results comprehensively demonstrated the feasibility and effectiveness of our method in solving the partial label problem in the context of FL.

A potential limitation of this work is that the experiments are conducted in a relatively simplified setting to clearly illustrate the critical problem. In our experiments, each client dataset has only one labeled organ. There are no overlapping labels with other datasets. A more general and practical scenario could be that the datasets owned by different clinical sites may have some labeled ROIs overlapped with other clients. Although the impacts of these overlapped partial labels remain to be investigated in our future work, the framework of our Fed-MENU method is general and we can easily adapt it to such potential scenarios.

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