Non-readily identifiable data collaboration analysis for multiple datasets including personal information

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Abstract

Multi-source data fusion, in which multiple data sources are jointly analyzed to obtain improved information, has considerable research attention. For the datasets of multiple medical institutions, data confidentiality and cross-institutional communication are critical. In such cases, data collaboration (DC) analysis by sharing dimensionality-reduced intermediate representations without iterative cross-institutional communications may be appropriate. Identifiability of the shared data is essential when analyzing data including personal information. In this study, the identifiability of the DC analysis is investigated. The results reveals that the shared intermediate representations are readily identifiable to the original data for supervised learning. This study then proposes a non-readily identifiable DC analysis only sharing non-readily identifiable data for multiple medical datasets including personal information. The proposed method solves identifiability concerns based on a random sample permutation, the concept of interpretable DC analysis, and usage of functions that cannot be reconstructed. In numerical experiments on medical datasets, the proposed method exhibits a non-readily identifiability while maintaining a high recognition performance of the conventional DC analysis. For a hospital dataset, the proposed method exhibits a nine percentage point improvement regarding the recognition performance over the local analysis that uses only local dataset.

1 Introduction

1.1 Background

Multi-source data fusion, in which multiple data sources are jointly analyzed to obtain improved information or refined data with lower cost, higher quality, and more relevant information have attracted considerable research attention [1, 29, 30, 34, 35]. For example, in medical data analysis for rare diseases, it was reported that when the analysis is conducted using only data from a single institution, the accuracy is insufficient because of the small sample size [22]. On the other hand, in some real-world applications, such as medical, financial, and manufacturing data analyses, sharing the original data for analysis is difficult because of

¹This is a definition introduced in [35]. Because “data fusion” is a broad concept, diverse definitions exist.
Objective:
• Multiple medical data sources are jointly analyzed to obtain improved information with only sharing non-identifiable data.

Method:
• Non-identifiable data collaboration (DC) analysis in which the shared intermediate reps. are non-readily identifiable to the original data.

Contributions:
• We introduce a mathematical definition of the identifiability of the data.
• We reveal that the shared intermediate reps. of the conventional DC analysis are readily identifiable to the original data for supervised learning.
• The proposed method realizes privacy-preserving analysis of multiple medical datasets only sharing non-readily identifiable intermediate reps. without iterative cross-institutional communications.

Figure 1: Outline of the proposed method. The proposed method realizes privacy-preserving analysis of multiple medical datasets sharing only non-readily identifiable intermediate representations without iterative cross-institutional communications.

data confidentiality. Furthermore, privacy-preserving analysis methods, in which datasets are collaboratively analyzed without sharing the original data, are essential.

Federated learning [5,17,18,23,31] is a typical technology for this topic. In multi-source data fusion on multiple medical institutions, cross-institutional communication is a major concern for social implementation. In such cases, instead of the federated learnings based on iterative model updating with cross-institutional communications, data collaboration (DC) analysis [13,14] by sharing intermediate representations constructed by some dimensionality reduction method such as principal component analysis (PCA) [27] without iterative cross-institutional communications is preferred.

Identifiability of the shared data is essential for analyzing data including personal information. In the general data protection regulation (GDPR) of EU, California consumer privacy act (CCPA) of USA, and amended act on the protection of personal information (APPI) of Japan, data that can indirectly identify individuals are defined as personal information.

In this study, a mathematical definition of the identifiability of the data is introduced; see Definition 1 in Section 3. The shared data should be non-readily identifiable in privacy-preserving machine learning.

1.2 Motivation and contributions

In this study, we focus on supervised machine learning for classification problems of medical data held by multiple medical institutions and investigate the identifiability of the DC analysis. We analyze the identifiability of the shared intermediate representations and reveal that the shared intermediate representations are readily identifiable to the original data for supervised learning even with a random sample permutation. Next, we propose a non-readily identifiable DC analysis only sharing non-readily identifiable data based on strategies: a random sample permutation, the concept of interpretable DC analysis [11], and usage of functions that cannot be reconstructed (Figure 1).

The main contributions are as follows:
This study introduces a mathematical definition of the identifiability of the data (Definition 1 in Section 3), which is based on whether or not someone hold a key to collate non-personal information with personal information.

This study reveals that the shared intermediate representations of the conventional DC analysis are readily identifiable to the original data for supervised learning even with a random sample permutation (Section 4.2).

This study proposes a non-readily identifiable DC analysis that realizes privacy-preserving analysis of multiple medical datasets sharing only non-readily identifiable intermediate representations without iterative cross-institutional communications (Section 5).

In numerical experiments in Section 6 on medical datasets, the proposed non-readily identifiable DC analysis exhibits a non-readily identifiability while maintaining a high recognition performance of the conventional DC analysis for medical datasets (Section 6). The numerical experiments also demonstrates that the recognition performance of the proposed method is comparable to the centralized analysis that shares the raw datasets.

2 Related works

2.1 Federated Learning

Federated learning systems have been developed for privacy-preserving analysis on multiple datasets. The concept of federated learning was first proposed by Google [17] typically for Android phone model updates [23]. Federated learning is primarily based on (deep) neural network and updates the model iteratively [17, 18, 23, 31].

To update the model, federated stochastic gradient descent (FedSGD) and federated averaging (FedAvg) are typical strategies [23]. Federated learning including more recent methods, such as FedProx [19] and FedCodl [26], requires cross-institutional communication in each iteration. This requirement is a major concern for social implementation specifically for data owned by multiple medical institutions. For more details, we refer to [18, 31] and references therein.

2.2 DC analysis

As an approach for privacy-preserving analysis on multiple datasets, non-model share-type federated learning called DC analysis has been proposed for supervised learning [11, 13, 14, 24], novelty detection [15], and feature selection [32]. In DC analysis, the dimensionality-reduced intermediate representations are centralized instead of sharing the model. The centralized intermediate representations are transformed to incorporable forms called collaboration representations. For constructing the incorporable collaboration representations, all the parties generate a shareable anchor dataset and centralize its intermediate representation. Next, the collaborative representation is analyzed as a single dataset.

DC analysis preserves the privacy of the original data by allowing each party to use individual functions to generate the intermediate representation and not sharing them [10]. The DC analysis does not require iterative communications between parties.
2.3 Homomorphic encryption computation

Cryptographic computation is one of the most well-known methods used for ensuring privacy preservation [4, 8, 16]. Cryptographic methods can compute a function over distributed data while retaining the privacy of the data. Any given function can be computed by applying fully homomorphic encryption [7]. However, this method is not feasible for large datasets because of the large computational cost even with the latest implementations [3, 33].

3 Identifiability of the data

3.1 Importance of identifiability

When analyzing data including personal information, various privacy and data protection laws, professional duties, and custodial obligations are applied. If the analysis is outsourced to another organization, the analysis organization is subject to the same obligations. In addition to directly personally identifiable data, similar obligations could be imposed on data that can be linked with personal information and thereby indirectly identify individuals.

For example, in laws regarding personal information in countries such as the general data protection regulation (GDPR) of EU, California consumer privacy act (CCPA) of USA, and amended act on the protection of personal information (APPI) of Japan, data that indirectly identifies individuals are defined as personal information as follows:

- **Article 4(1) of GDPR:**
  “Personal data” means any information relating to an identified or identifiable natural person (‘data subject’); an identifiable natural person is one who can be identified, directly or indirectly.

- **1798.140(o) of CCPA:**
  “Personal information” means information that identifies, relates to, describes, is capable of being associated with, or could reasonably be linked, directly or indirectly, with a particular consumer or household.

- **Article 2 of Amended APPI:**
  “Personal information” in this Act means that information relating to a living individual . . . (including those which can be readily collated with other information and thereby identify a specific individual).

Therefore, the identifiability of the shared information is essential for privacy-preserving analysis. Because readily identifiable data are treated in the same manner as personal information data, the shared data should be non-readily identifiable to the original data for privacy-preserving analysis on multiple datasets including personal information.

3.2 Definition and property of identifiability

In this study, we define identifiability of the data as the data readily collated with the original data including personal information. Here, we introduce the following mathematical definition of readily identifiable data.
**Definition 1.** Let \( x^p_i \) and \( x^{np}_i \) be a pair of the data including and not including personal information that can directly identify a specific individual for the \( i \)-th person, respectively. We let \( X^p = \{ x^p_1, x^p_2, \ldots, x^p_n \} \) and \( X^{np} = \{ x^{np}_1, x^{np}_2, \ldots, x^{np}_n \} \) be personal and non-personal information datasets for the same \( n \) persons, respectively.

For non-personal information \( x^{np} \in X^{np} \), if and only if someone else holds a key to correctly collate the corresponding personal information \( x^p \in X^p \) or can generate the key by their own, then the non-personal dataset \( X^{np} \) is defined as “readily identifiable” to personal dataset \( X^p \).

Examples of the key to collate the data are unique common IDs and features. In addition, excellent approximations of the features can be a key to correctly collate the data. Here, we have the following property.

**Proposition 1.** If either of the followings:

- The data holder of \( X^p \) holds the function \( v \) such that \( x^{np}_i = v(x^p_i) \) or can generate the function by their own,

- The data holder of \( X^{np} \) holds the function \( w \) such that \( x^p_i = w(x^{np}_i) \) or can generate the function by their own,

then \( X^{np} \) is readily identifiable to \( X^p \).

**Proof.** In case, the data holder of \( X^p \) holds the function \( v \) such that \( x^{np}_i = v(x^p_i) \) or can generate the function by their own, they can obtain pairs of \( (x^p_i, x^{np}_i) \) corresponding to any \( x^p_i \in X^p \) using the function \( v \). Therefore, using \( x^{np}_i \) as a key, for non-personal information \( x^{np} \in X^{np} \), the corresponding personal information \( x^p \in X^p \) can be collated accurately.

In the same manner, for the case that the data holder of \( X^{np} \) holds the function \( w \) such that \( x^p_i = w(x^{np}_i) \) or can generate the function by their own, they can obtain pairs of \( (x^{np}_i, x^p_i) \) corresponding to any \( x^{np}_i \in X^{np} \) using the function \( w \). Therefore, using \( x^p_i \) as a key, for non-personal information \( x^{np} \in X^{np} \), the corresponding personal information \( x^p \in X^p \) can be collated accurately.

Proposition 1 indicates that encrypted datasets shared in homomorphic encryption computation are readily identifiable to the original data because someone holds encryption and decryption functions. Retention of excellent approximations of functions \( v \) and \( w \) can result in readily identifiable.

## 4 Identifiability of DC analysis

In this study, we focus on supervised machine learning for classification problems, which aims to construct a prediction or classification model by labeled training datasets [2], of medical data of multiple medial institutions.

Let \( m \) and \( n \) denote the numbers of features (dimensionality of each data) and training data samples. Let \( X = [x_1, x_2, \ldots, x_n]^T \in \mathbb{R}^{n \times m} \) and \( Y = [y_1, y_2, \ldots, y_n]^T \in \mathbb{R}^{n \times \ell} \) be the training dataset and the corresponding ground truth or label. In this study, for privacy-preserving analysis on multiple parties, we consider horizontal data partitioning, that is, data
samples are partitioned into \( c \) parties as follows:

\[
X = \begin{bmatrix}
X_1 \\
X_2 \\
\vdots \\
X_c
\end{bmatrix}, \quad Y = \begin{bmatrix}
Y_1 \\
Y_2 \\
\vdots \\
Y_c
\end{bmatrix}.
\]

(1)

Then, the \( i \)-th party has a partial dataset and the corresponding ground truth,

\[
X_i \in \mathbb{R}^{n_i \times m}, \quad Y_i \in \mathbb{R}^{n_i \times \ell},
\]

where \( n = \sum_{i=1}^c n_i \).

Here, we introduce the algorithm of the DC analysis for supervised learning of horizontal partitioned data (1) and analyze its identifiability. DC analysis is applicable to the datasets with partially common features [24] and horizontal and vertical partitioned data [14].

### 4.1 DC analysis

In the practical operation strategy, the DC analysis is operated by two roles, namely worker and master. The workers have the private dataset \( X_i \) and the corresponding ground truth \( Y_i \) and want to analyze them without sharing \( X_i \). The master supports to collaborative analysis.

First, all workers generate the same anchor data \( X_{\text{anc}} \in \mathbb{R}^{r \times m} \), which is shareable data consisting of public data or dummy data that are randomly constructed. A random matrix works well in general [13–15]. Then, each worker constructs intermediate representations,

\[
\tilde{X}_i = f_i(X_i) \in \mathbb{R}^{n_i \times \tilde{m}_i}, \quad \tilde{X}_{\text{anc}} = f_i(X_{\text{anc}}) \in \mathbb{R}^{r \times \tilde{m}_i},
\]

with a linear or nonlinear row-wise mapping function \( f_i \) such as dimensionality reduction, with \( \tilde{m}_i < m \), including unsupervised methods [9, 21, 27] and supervised methods [6, 12, 20, 28]. For privacy and confidentiality concerns, the function \( f_i \) should be set such that the original data \( X_i \) and its intermediate representation \( \tilde{X}_i \) do not have (approximately) the same features. Then, the intermediate representations are send to the master.

At the master side, mapping function \( g_i \) for the collaboration representation is constructed satisfying \( g_i(\tilde{X}_{\text{anc}}) \approx g_{i'}(\tilde{X}_{\text{anc}}) \) \( (i, i' = 1, 2, \ldots, c) \) in some sense. In practice, \( g_i \) is set as a linear function \( g_i(\tilde{X}_{\text{anc}}) = \tilde{X}_{\text{anc}} G_i \) with \( G_i \in \mathbb{R}^{\tilde{m}_i \times \tilde{m}} \) and is constructed using the following minimal perturbation problem:

\[
\min_{E_i, G_i} \sum_{i=1}^c \| E_i \|_F^2 \quad \text{s.t.} \quad (\tilde{X}_{\text{anc}} + E_i) G_i = Z.
\]

where \( \| \cdot \|_F \) denotes the Frobenius-norm of a matrix. This can be solved by a singular value decomposition (SVD)-based algorithm for total least squares problems. Let

\[
[\tilde{X}_{\text{anc}}^{\text{anc}}, \tilde{X}_{\text{anc}}^{\text{anc}}, \ldots, \tilde{X}_{\text{anc}}^{\text{anc}}] \approx U_{\tilde{m}} \Sigma_{\tilde{m}} V_{\tilde{m}}^T
\]

be the rank \( \tilde{m} \) approximation based on SVD. Then, the target matrix \( G_i \) is obtained as follows:

\[
G_i = (\tilde{X}_{\text{anc}}^{\text{anc}})^\dagger U_{\tilde{m}} C.
\]
where $\dagger$ denotes the Moore–Penrose inverse and $C \in \mathbb{R}^{\hat{m} \times \hat{m}}$ is a nonsingular matrix, for example, $C = I$ and $C = \Sigma_{\hat{m}}$ are used in practice. The collaboration representations are analyzed as a single dataset, that is,

$$Y \approx h(\hat{X}), \quad \hat{X} = [\hat{x}_1, \hat{x}_2, \ldots, \hat{x}_n]^T = \begin{bmatrix} \hat{X}_1 \\ \hat{X}_2 \\ \vdots \\ \hat{X}_c \end{bmatrix} = \begin{bmatrix} \hat{X}_1G_1 \\ \hat{X}_2G_2 \\ \vdots \\ \hat{X}_cG_c \end{bmatrix} \in \mathbb{R}^{n \times \hat{m}}$$

with the shared ground truth $Y_i$ using some supervised machine learning or the deep learning methods for constructing the model function $h$ of the collaboration representation $\hat{X}$.

Functions $g_i$ and $h$ are returned to the $i$-th worker.

Let $X_{i_{\text{test}}} \in \mathbb{R}^{s_i \times m}$ be a test dataset of the $i$-th party. For the prediction phase, the prediction result $Y_{i_{\text{pred}}}^i$ of $X_{i_{\text{test}}}^i$ is obtained by the following equation:

$$Y_{i_{\text{pred}}}^i = h(g_i(f_i(X_{i_{\text{test}}}^i))) \quad (4)$$

through the intermediate and collaboration representations.

The algorithm of the DC analysis is summarized in Algorithm 1, where $g_i$ is set by (3). The DC analysis requires only three cross-institutional communications, Steps 1, 4, and 9 in Algorithm 1. A major advantage is observed over federated learnings. The most time-consuming parts of Algorithm 1 are computing intermediate representations in each worker (Steps 2, 3), generating $G_i$ by (2) and (3) in the master (Step 6), and analyzing the collaboration representation in the master (Step 8). Because the costs of computing intermediate representations and analyzing the collaboration representation are almost the same as that of the centralized analysis sharing the raw datasets, the main increase in computational complexity of the DC analysis relative to the centralized analysis is for generating $G_i$ by (2) and (3).

The DC analysis has the following double privacy layer for the protection of private data $X_i$:

- No one can possess private data $X_i$ because $f_i$ is private under the protocol;
- Even if $f_i$ is stolen, private data $X_i$ is still protected regarding $\varepsilon$-DR privacy [25] because $f_i$ is a dimensionality reduction function ($\bar{m}_i < m$), see [10] for more details.

4.2 Analysis on identifiability of the intermediate representations

Based on Definition 1, we analyze the identifiability of the intermediate representation $\hat{X}_i$ stored in the master.

In DC analysis, for privacy and confidentiality concerns, function $f_i$ is constructed such that the original data $X_i$ and its intermediate representation $\hat{X}_i$ do not have (approximately) the same features. Therefore, no identical features exist that are key to collate $\hat{X}_i$ with $X_i$. By contrast, in the naive implementation (Algorithm 1), $\hat{X}_i$ and $X_i$ share the row index, that is the $k$-th row of $\hat{X}_i$ is collated with the $k$-th row of $X_i$, because $f_i$ is a row-wise function. This difficulty can be simply solved by using a random permutation matrix $P_i \in \mathbb{R}^{n_i \times n_i}$ such
Algorithm 1 DC analysis

Input (for worker-side): $X_i \in \mathbb{R}^{n_i \times m}$, $Y_i \in \mathbb{R}^{n_i \times \ell}$, and $X_i^{\text{test}}$ individually

Output (for worker-side): $Y_i^{\text{pred}}$ ($i = 1, 2, \ldots, c$).

Worker-side ($i = 1, 2, \ldots, c$)
1: Generate $X^{\text{anc}}$ and share to all workers
2: Generate $f_i$
3: Compute $\tilde{X}_i = f_i(X_i)$ and $\tilde{X}^{\text{anc}}_i = f_i(X^{\text{anc}})$
4: Share $\tilde{X}_i$, $\tilde{X}^{\text{anc}}_i$, and $Y_i$ to master

Master-side
5: $\triangledown$ Obtain $\tilde{X}_i$, $\tilde{X}^{\text{anc}}_i$, and $Y_i$ for all $i$
6: Compute $G_i$ from $\tilde{X}^{\text{anc}}_i$ for all $i$ by (2) and (3)
7: Compute $\tilde{X}_i = \tilde{X}_i G_i$ for all $i$, and set $\tilde{X}$
8: Analyze $\tilde{X}$ to obtain $h$ such that $Y \approx h(\tilde{X})$
9: $\checkmark$ Return $G_i$ and $h$ to each worker

Worker-side ($i = 1, 2, \ldots, c$)
10: Obtain $G_i$ and $h$
11: Compute $Y_i^{\text{pred}} = h(f_i(X_i^{\text{test}}) G_i)$

that each worker computes $\tilde{X}'_i = P_i f_i(X_i)$ and $Y'_i = P_i Y_i$ and erase $P_i$ before sharing $\tilde{X}'_i$ and $Y'_i$ to the master. Here, $P_i$ does not change the machine learning model.

However, $\tilde{X}'_i$ is still readily identifiable to $X_i$ for supervised learning. Because intermediate representation is constructed by $\tilde{x}_k = f_i(x_k)$ and function $f_i$ should be stored in the worker for prediction phase [4]. Therefore, based on Proposition 1, $\tilde{X}'_i$ is readily identifiable to $X_i$.

5 Non-readily identifiable DC analysis

In Section 4.2, we revealed that the shared intermediate representations of the conventional DC analysis are readily identifiable to the original data for supervised learning even with a random sample permutation. Identifiability of the shared data is essential for analyzing data including personal information.

To solve this difficulty, we propose a non-readily identifiable DC analysis to realize privacy-preserving analysis of horizontal partitioned multiple medical datasets sharing only non-readily identifiable intermediate representations without iterative cross-institutional communications. Note that the proposed non-readily identifiable DC analysis is naturally extendable to the datasets with partially common features and horizontal and vertical partitioned data in the same manner as [24] and [14] for the conventional DC analysis, respectively.

5.1 Basic concept

In this study, we propose a non-readily identifiable DC analysis in which the intermediate representations are non-readily identifiable to the original data based on the following strate-
gies:

- The proposed method uses a random permutation for the sample index in each worker.
- The proposed method makes functions $f_i$ erasable based on the concept of interpretable DC analysis [11].
- The proposed method uses functions $f_i$ that cannot be reconstructed.

5.2 Practical algorithm

Each worker constructs a dimensionality-reduced function $f'_i$ that cannot be reconstructed. Simple examples of $f'_i$ are as follows:

- $f'_i$ is constructed as a dimensionality reduction function constructed from the raw data with a small perturbation $X_i + E_i$, where $E_i \in \mathbb{R}^{n_i \times m}$,
- $f'_i$ is constructed as $f'_i(X) = f_i(X)E_i$ with a dimensionality reduction function $f_i$ constructed from the raw data $X_i$ and a random matrix $E_i \in \mathbb{R}^{\tilde{m}_i \times \tilde{m}_i}$, where entries of $E_i$ are generated by the hardware random number generator or pseudo random number generator with the CPU time as the seed. Each worker constructs a permutation matrix $P_i$ as well as $E_i$ and subsequently computes the intermediate representation as follows:

$$
\tilde{X}'_i = P_if'_i(X_i), \quad \tilde{X}^{\text{anc}}_i = f'_i(X^{\text{anc}}_i), \quad Y'_i = P_iY_i.
$$

Next, each worker erases $P_i$ and $f'_i$ and share $\tilde{X}_i, \tilde{X}^{\text{anc}}_i$ and $Y'_i$ to the master. Function $f'_i$ and the matrix $P_i$ cannot be reconstructed even using the same program code. In the case for classification problems, $P_i$ cannot be reconstructed from $Y_i$ and $Y'_i$ because each row of $Y_i$ and $Y'_i$ are not unique.

At the master side, shared intermediate representations are transformed to the collaboration representations $\hat{X}'_i$ in the same manner as the conventional DC analysis written in Section 3.1.1 and analyzed as a single dataset as follows:

$$
Y' \approx h(\hat{X}').
$$

To realize prediction without $f'_i$, based on the concept of the interpretable DC analysis, a prediction result $Y^{\text{anc}}_i$ of the anchor data $X^{\text{anc}}_i$ is computed as follows:

$$
Y^{\text{anc}}_i = h(\hat{X}^{\text{anc}}_i), \quad \hat{X}^{\text{anc}}_i = \tilde{X}_iG_i \in \mathbb{R}^{r \times \tilde{m}}.
$$

The prediction result $Y^{\text{anc}}_i$ of $X^{\text{anc}}_i$ is returned to the $i$-th worker. The prediction model $t_i$ is then constructed by some supervised machine learning or the deep learning methods from $X^{\text{anc}}_i$ and $Y^{\text{anc}}_i$, that is,

$$
Y^{\text{anc}}_i \approx t_i(X^{\text{anc}}_i),
$$

in each worker. For the prediction phase, the prediction result $Y^{\text{pred}}_i$ of $X^{\text{test}}_i$ is obtained by

$$
Y^{\text{pred}}_i = t_i(X^{\text{test}}_i).
$$
Figure 2: The overview of non-readily identifiable DC analysis with $c = 2$.

Algorithm 2 Non-readily identifiable DC analysis

Input (for worker-side): $X_i \in \mathbb{R}^{n_i \times m}, Y_i \in \mathbb{R}^{n_i \times \ell}$, and $X_i^\text{test}$ individually

Output (for worker-side): $Y_i^\text{pred} (i = 1, 2, \ldots, c)$.

Worker-side ($i = 1, 2, \ldots, c$)

1: Generate $X_i^\text{anc}$ and share to all workers
2: Generate $f_i'$ and $P_i$ that cannot be reconstructed
3: Compute $\hat{X}_i = P_i f_i'(X_i), \hat{X}_i^\text{anc} = f_i'(X_i^\text{anc}),$ and $Y_i' = P_i Y_i$
4: Erase $f_i'$ and $P_i$
5: Share $\hat{X}_i', \hat{X}_i^\text{anc}$, and $Y_i'$ to master and erase them

Master-side

6: Obtain $\hat{X}_i', \hat{X}_i^\text{anc}$, and $Y_i'$ for all $i$
7: Compute $G_i$ from $\hat{X}_i^\text{anc}$ for all $i$ by (3)
8: Compute $\hat{X}_i' = \hat{X}_i' G_i$ for all $i$, and set $\hat{X}'$
9: Analyze $\hat{X}'$ to obtain $h$ such that $Y' \approx h(\hat{X}')$
10: Compute $Y_i^\text{anc} = h(\hat{X}_i^\text{anc} G_i)$
11: Return $Y_i^\text{anc}$ to each worker

Worker-side ($i = 1, 2, \ldots, c$)

12: Obtain $Y_i^\text{anc}$
13: Analyze $X_i^\text{anc}$ to obtain $t_i$ such that $Y_i^\text{anc} \approx t_i(X_i^\text{anc})$
14: Compute $Y_i^\text{pred} = t_i(X_i^\text{test})$

The algorithm of the non-readily identifiable DC analysis is summarized in Algorithm 2 and Figure 2. The proposed non-readily identifiable DC analysis requires only three cross-institutional communications, namely Steps 1, 5, and 11 in Algorithm 2 and has a double privacy layer for protection of private data $X_i$ as well as the conventional DC analysis described in Section 4.1. Regarding computational complexity, the proposed non-readily identifiable DC analysis is more computationally intensive than the conventional DC analysis for analyzing anchor data $\hat{X}$ to obtain the model $t_i$ (Step 13 in Algorithm 2).
5.3 Analysis on the identifiability of intermediate representations

Based on the protocol of the proposed non-readily identifiable DC analysis (Algorithm 2), we have the following expression:

- No common features to collate $X_i$ and $\tilde{X}_i'$, based on the property of the function $f'_i$.
- No common sample ID to collate $X_i$ and $\tilde{X}_i'$, based on using a random permutation $P_i$ that cannot be reconstructed.
- No function $f'_i$ because $f'_i$ cannot be constructed and is erased before sharing $\tilde{X}_i'$. Function $f'_i$ can be re-generated only by solving the optimization problem $\tilde{X}_i^{\text{anc}} = f'_i(X^{\text{anc}})$ for $f'_i$ by the cooperation of $i$-th worker and master.
- No function $(f'_i)^{-1}$ such that $x_k = (f'_i)^{-1}(\tilde{x}'_k)$ because $f'_i$ is a dimensionality-reduced function.

Therefore, from Definition 1, the intermediate representation $\tilde{X}_i'$ is non-readily identifiable to original data $X_i$.

6 Experiments

In this section, the efficiency of the proposed non-readily identifiable DC analysis in Algorithm 2 (DC-proposed) is evaluated and compared with the conventional DC analysis in Algorithm 1 (DC-naive). We compared with the centralized analysis that shares the raw datasets (Centralized) and the local analysis that uses only local dataset $X_i$ (Local). Centralized are considered as an ideal case because the raw data cannot be shared in our target situation.

6.1 General settings

As dimensionality reduction method in the worker-side of DC analyses, DC-naive used the principal component analysis (PCA) [27] and DC-proposed used

$$f'_i(X_i) = X_i F_i, \quad F_i = B_i E_i^{(1)},$$

where $B_i \in \mathbb{R}^{m \times \tilde{m}_i}$ is a projection matrix of PCA for $X_i$ and $E_i^{(1)} \in \mathbb{R}^{\tilde{m}_i \times \tilde{m}_i}$ is a random matrix whose entries are normal random numbers that cannot be reconstructed. We set $\tilde{m} = \tilde{m}_i$. We used the ridge regression for analyzing the collaboration representation (Step 8 in Algorithm 1 and Step 9 in Algorithm 2) and for prediction model (Step 13 in Algorithm 2).

The anchor data $X^{\text{anc}}_i$ is constructed based on a low-rank approximation-based approach introduced in [11] as follows: In each worker, the local anchor data $X^{\text{approx}}_i$ is constructed by using a low-rank approximation of $X_i$ with random perturbation, that is,

$$X^{\text{approx}}_i = X^{\text{TSDV}}_i + \delta E_i^{(2)},$$

where $X^{\text{TSDV}}_i \in \mathbb{R}^{n_i \times m}$ is a low-rank approximation based on the truncated SVD of $X_i$, $\delta = 0.05$ is a perturbation parameter, and $E_i^{(2)} \in \mathbb{R}^{n_i \times m}$ is a random matrix whose entries are uniform random numbers in $[-1, 1]$. Sharing $X^{\text{approx}}_i$ with all users, $n$ samples of anchor
data are generated as $X^{\text{approx}} = [(X_1^{\text{approx}})^T, (X_2^{\text{approx}})^T, \ldots, (X_c^{\text{approx}})^T]^T \in \mathbb{R}^{n \times m}$. Next, to generate $r$ samples of anchor data $X^{\text{anc}}$, we applied an augmentation technique by linear combination if $r > n$, and we select $r$ samples randomly otherwise (that is, $r \leq n$). We set $r = 2,000$ as the number of anchor data. These settings are based on our preliminary experiments and not always the best choice in terms of performance.

We used the ridge regression for Centralized and Local. We set the ground truth $Y$ as a binary matrix whose $(i, j)$-th entry is $1$ if the training data $x_i$ are in class $j$ and $0$ otherwise. This ground truth has been applied to various classification algorithms, including ridge regression and deep neural networks [2].

All numerical experiments were performed using MATLAB\(^2\).

### 6.2 Experiment I: proof-of-concept

As a proof of concept of the proposed method, we used a simulated hospital dataset “hospital.mat” from the MATLAB Statistics and Machine Learning Toolbox. The dataset contains 100 samples with six features: sex (male or female), age, weight, smoker (true or false), systolic blood pressure (SBP), and diastolic blood pressure (DBP). We generate a data matrix $X \in \mathbb{R}^{100 \times 4}$ with sex, age, weight, and smoker and set a label $y = [y_1, y_2, \ldots, y_{100}]^T \in \mathbb{R}^{100}$ for high blood pressure as follows:

$$
y_i = \begin{cases} 
  1 & \text{SBP} \geq 140 \text{ or DBP} \geq 80, \\
  0 & \text{otherwise.}
\end{cases}
$$

#### 6.2.1 Identifiability

We discuss the identifiability of the proposed method. We set two parties with randomly selected 10 samples as presented in Table 1. According to the algorithm of the proposed method (Algorithm 2) with $\tilde{m}_i = \hat{m}_i = 3$, each party constructs and shares the intermediate representation $\tilde{X}'_i$ to the master. Table 2 reveals the shared intermediate representations $\tilde{X}'_1$ and $\tilde{X}'_2$ with sample IDs. We note that the sample IDs are not stored in actual operation. Next, the intermediate representations are transformed to the collaboration representations $\hat{X}'_i$ as presented in Table 3.

From the comparison of Tables 1 and 2, the columns of the intermediate representations are uncorrelated or weakly correlated with the features of the raw data (the Pearson correlation coefficients are less than 0.4), which indicates the columns of the intermediate representations cannot be a key to collate $X_i$. Similarly, from the comparison of Tables 1 and 3, the columns of the collaboration representations cannot be a key to collate $X_i$.

On the other hand, according to the algorithm, function $f'_i$ has been erased. Even if the same program code is used to reconstruct $f'_i$, it will not be the same function because random matrix $E_i^{(1)}$ differs completely. In Table 4, the columns of the original and reconstructed $f'_i(X_1)$ for the same data $X_1$ are presented. The reconstructed $f'_i(X_1)$ differs completely from the original and cannot be a key to collate $X_i$.

Thus, from Definition 1, the intermediate and collaboration representations, $\tilde{X}'_i$ and $\hat{X}'_i$, are non-readily identifiable to original data $X_i$.

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\(^2\)Program codes are available from the corresponding author by reasonable request.
Table 1: Raw data $X_1$ and $X_2$ with sample IDs.

| IDs | Sex | Age | Weight | Smoke |
|-----|-----|-----|--------|-------|
| 1   | 1   | 32  | 183    | 0     |
| 2   | 1   | 39  | 188    | 0     |
| 3   | 1   | 43  | 163    | 0     |
| 4   | 0   | 38  | 124    | 0     |
| 5   | 1   | 45  | 181    | 0     |
| 6   | 0   | 32  | 136    | 0     |
| 7   | 0   | 39  | 117    | 0     |
| 8   | 1   | 45  | 170    | 1     |
| 9   | 1   | 50  | 172    | 0     |
| 10  | 0   | 44  | 136    | 1     |

| IDs | Sex | Age | Weight | Smoke |
|-----|-----|-----|--------|-------|
| 1   | 0   | 44  | 146    | 1     |
| 2   | 0   | 25  | 114    | 0     |
| 3   | 0   | 37  | 129    | 0     |
| 4   | 0   | 28  | 123    | 1     |
| 5   | 1   | 25  | 174    | 0     |
| 6   | 1   | 33  | 180    | 1     |
| 7   | 0   | 28  | 111    | 0     |
| 8   | 1   | 45  | 172    | 1     |
| 9   | 0   | 36  | 129    | 0     |
| 10  | 0   | 40  | 137    | 0     |

Table 2: Intermediate representations $\tilde{X}_1'$ and $\tilde{X}_2'$ with sample IDs. Sample IDs are not stored in actual operation.

**Remark:** The columns of the intermediate representations cannot be a key to collate raw data.

| From Party 1 | From Party 2 |
|--------------|--------------|
| IDs | $\tilde{X}_1'(:, 1)$ | $\tilde{X}_1'(:, 2)$ | $\tilde{X}_1'(:, 3)$ |
| 5   | $-220.48$     | $281.54$      | $-132.47$|
| 7   | $-145.23$     | $192.60$      | $-76.83$ |
| 1   | $-219.27$     | $270.20$      | $-145.82$|
| 2   | $-226.92$     | $284.14$      | $-144.41$|
| 4   | $-153.01$     | $200.55$      | $-84.36$ |
| 10  | $-168.93$     | $222.65$      | $-89.66$ |
| 3   | $-199.22$     | $256.20$      | $-117.13$|
| 6   | $-165.21$     | $209.60$      | $-101.05$|
| 9   | $-211.47$     | $275.30$      | $-119.52$|
| 8   | $-208.30$     | $267.56$      | $-121.20$|

| IDs | $\tilde{X}_2'(:, 1)$ | $\tilde{X}_2'(:, 2)$ | $\tilde{X}_2'(:, 3)$ |
|-----|----------------------|----------------------|----------------------|
| 6   | $163.34$             | $-145.69$            | $-139.68$            |
| 8   | $164.24$             | $-140.06$            | $-133.82$            |
| 9   | $124.30$             | $-104.44$            | $-101.18$            |
| 4   | $115.00$             | $-100.18$            | $-95.27$             |
| 2   | $105.73$             | $-91.89$             | $-89.22$             |
| 1   | $142.96$             | $-119.37$            | $-113.59$            |
| 5   | $153.42$             | $-139.48$            | $-135.81$            |
| 10  | $133.08$             | $-111.02$            | $-107.51$            |
| 7   | $105.16$             | $-89.69$             | $-86.98$             |
| 3   | $124.91$             | $-104.50$            | $-101.21$            |

6.2.2 Recognition performance

The recognition performance of the proposed method was evaluated. We set 1–8 parties with randomly selected 10 samples for the training dataset. We also set test dataset $X^\text{test}$ with 20 samples.

Recognition performance was evaluated by the area under the curve (AUC) of the receiver operating characteristic, and its average and standard error of 20 trials for each method are detailed in Figure 3. The results reveal that the recognition performance of Centralized, DC-naive and DC-proposed increase with the increase in the number of parties. DC-proposed reveals almost the same high values as that of DC-naive with the exception of one party and is comparable to that of Centralized. For eight parties, Centralized, DC-naive, and DC-proposed achieves 12 percentage point, 10 percentage point, and 9 percentage point performance improvements in the average AUC over Local, respectively.
Table 3: Collaboration representations \( \hat{X}_1 \) and \( \hat{X}_2 \) with sample ID. Sample IDs are not stored in actual operation.

**Remark:** The columns of the collaboration representations cannot be a key to collate raw data.

| From Party 1 | From Party 2 |
|--------------|--------------|
| IDs          | \( \hat{X}_1(1) \) | \( \hat{X}_1(2) \) | \( \hat{X}_1(3) \) | IDs          | \( \hat{X}_2(1) \) | \( \hat{X}_2(2) \) | \( \hat{X}_2(3) \) |
| 5            | -464.96      | 0.26          | 0.97          | 6            | -453.51      | -14.49        | -0.72        |
| 7            | -308.22      | 13.40         | 0.56          | 8            | -443.80      | 4.08          | -0.64        |
| 1            | -459.64      | -17.67        | 0.88          | 9            | -334.40      | 5.44          | 0.66         |
| 2            | -476.94      | -10.01        | 0.94          | 4            | -314.17      | -2.38         | -0.92        |
| 4            | -324.08      | 9.77          | 0.57          | 2            | -290.24      | -4.24         | 0.53         |
| 10           | -357.47      | 14.64         | -0.85         | 1            | -381.22      | 11.32         | -0.73        |
| 3            | -420.64      | 3.51          | 0.91          | 5            | -432.83      | -23.98        | 0.71         |
| 6            | -347.94      | -2.14         | 0.55          | 10           | -356.51      | 8.13          | 0.72         |
| 9            | -447.45      | 9.86          | 0.98          | 7            | -285.44      | 0.73          | 0.55         |
| 8            | -439.05      | 4.71          | -0.55         | 3            | -335.18      | 6.77          | 0.67         |

Table 4: The 1st, 2nd, and 3rd columns of original and reconstructed \( f_1'(X_1) \) for the same \( X_1 \) with sample IDs.

**Remark:** Reconstructed \( f_1'(X_1) \) differs completely from original \( f_1'(X_1) \).

| Original \( f_1'(X_1) \) | Reconstructed \( f_1'(X_1) \) |
|--------------------------|-----------------------------|
| IDs          | 1st | 2nd | 3rd | IDs          | 1st | 2nd | 3rd |
| 1            | -219.27      | 270.20 | -145.82 | 1            | -3.12          | 105.89 | 38.18  |
| 2            | -226.92      | 284.14 | -144.41 | 2            | 3.35          | 107.70 | 53.41  |
| 3            | -199.22      | 256.20 | -117.13 | 3            | 8.00          | 91.75  | 67.59  |
| 4            | -153.01      | 200.55 | -84.36  | 4            | 10.02         | 68.93  | 63.63  |
| 5            | -220.48      | 281.54 | -132.47 | 5            | 6.84          | 102.37 | 68.68  |
| 6            | -165.21      | 209.60 | -101.05 | 6            | 3.79          | 77.31  | 47.37  |
| 7            | -145.23      | 192.60 | -76.83  | 7            | 11.80         | 64.49  | 67.32  |
| 8            | -208.30      | 267.56 | -121.20 | 8            | 8.54          | 96.37  | 70.78  |
| 9            | -211.47      | 275.30 | -119.52 | 9            | 11.89         | 96.00  | 82.03  |
| 10           | -168.93      | 222.65 | -89.66  | 10           | 12.80         | 75.90  | 75.10  |

6.3 Experiment II: performance evaluation for real-world datasets

Here, the recognition performance for five datasets was evaluated as presented in Table 5 obtained from the survival package of the R language. For each dataset, a label \( y = [y_1, y_2, \ldots, y_n]^T \in \mathbb{R}^n \) was set using a survival time \( t_i \) as presented in Table 6. We set four parties with randomly selected 10 samples for the training dataset and set test dataset \( X^{\text{test}} \) with 20 samples.

Average recognition performance (AUC) and standard error in 20 trials of methods are presented in Table 7. The results demonstrated that the recognition performance of **DC-proposed** reveals almost the same high values as that of **DC-naive** and is comparable to that of **Centralized**. In some cases, **DC-naive** and **DC-proposed** outperform **Centralized**, which may be derived from a performance improvement because of a dimensionality reduction method and a model reconstruction with a large number of anchor dataset \( X^{\text{anc}} \). This will be investigated in the future.
Remark: DC-proposed reveals almost the same high values as that of DC-naive and is comparable to that of Centralized.

Table 5: Datasets obtained from the survival package of the R language for Experiment II.

| Name of dataset | n  | m  | Description                                           |
|-----------------|----|----|------------------------------------------------------|
| colon           | 888| 13 | Chemotherapy for Stage B/C colon cancer data         |
| kidney          | 76 | 6  | Kidney Catheter Data                                 |
| lung            | 167| 7  | NCCTG Lung Catheter Data                             |
| pbc             | 276| 17 | Mayo Clinic Primary Biliary Cholangitis Data         |
| veteran         | 137| 4  | Veterans’ Administration Lung Cancer Study Data      |

Table 6: Label setting for Experiment II.

| Name of dataset | condition for \( y_i = 1 \) | rate of \( y_i = 1 \) |
|-----------------|-------------------------------|----------------------|
| colon           | \( t_i \geq 1500 \)         | 0.50                 |
| kidney          | \( t_i \geq 100 \)          | 0.36                 |
| lung            | \( t_i \geq 400 \)          | 0.26                 |
| pbc             | \( t_i \geq 2000 \)         | 0.44                 |
| veteran         | \( t_i \geq 100 \)          | 0.39                 |

7 Discussion

Multi-source data fusion, in which multiple data sources are jointly analyzed to obtain improved information, has considerable research attention. In case of multi-source data fusion on multiple medical institutions, data confidentiality and cross-institutional communication are major concerns for social implementation. For analysis of data including personal information, identifiability of the shared data is also essential.

Although DC analysis may be a suitable choice regarding data confidentiality and cross-institutional communication concerns, this study revealed that it is difficult to solve the identifiability concern based on the conventional DC framework. This study then proposed the non-identifiable DC analysis that solves the identifiability concern while maintaining the strength of DC analysis. The proposed method could become a breakthrough technology for future multi-source data fusion on multiple medical institutions.
Table 7: Recognition performance (AUC) for real-world datasets.

**Remark:** DC-proposed reveals almost the same high values as that of DC-naive and is comparable to that of Centralized.

| Name of dataset | Local   | Centralized | DC-naive | DC-Proposed |
|-----------------|---------|-------------|----------|-------------|
| colon           | 0.51 ± 0.03 | 0.63 ± 0.02 | 0.64 ± 0.03 | 0.63 ± 0.03 |
| kidney          | 0.66 ± 0.04 | 0.72 ± 0.02 | 0.74 ± 0.02 | 0.74 ± 0.02 |
| lung            | 0.50 ± 0.04 | 0.56 ± 0.05 | 0.53 ± 0.04 | 0.53 ± 0.04 |
| pbc             | 0.61 ± 0.03 | 0.66 ± 0.03 | 0.71 ± 0.02 | 0.71 ± 0.03 |
| veteran         | 0.65 ± 0.03 | 0.69 ± 0.02 | 0.72 ± 0.02 | 0.72 ± 0.02 |

However, this study is based on the mathematical definition of identifiability (Definition 1 in Section 3). The legal justification should be examined separately.

8 Conclusions

This study addressed challenges, such as data confidentiality, cross-institutional communication, and identifiability, of the multi-source data fusion of multiple medical datasets including personal information. A recent DC framework was used to address the data confidentiality and cross-institutional communication concerns. This study investigated the identifiability of DC analysis.

A mathematical definition of the identifiability of the data (Definition 1 in Section 3) was introduced. The results revealed that the shared intermediate representations of the conventional DC analysis are readily identifiable to the original data for supervised learning (Section 4.2). Next, we proposed a non-readily identifiable DC analysis based on a random sample permutation, the concept of interpretable DC analysis, and usage of functions that cannot be reconstructed. In this method, the shared intermediate representations are non-readily identifiable to the original data (Section 5).

The proposed non-readily identifiable DC analysis exhibited a non-readily identifiability while maintaining a high recognition performance of the conventional DC analysis for medical datasets (Section 6). For a hospital dataset, the proposed method exhibited a nine percentage point improvement regarding the recognition performance (AUC) over the local analysis. The numerical experiments also demonstrated that the recognition performance of the proposed method was comparable to the centralized analysis that shares the raw datasets.

In the future, we will further develop the algorithm and software for social implementation.

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References

[1] E. Acar, E. E. Papalexakis, G. Gürdeniz, M. A. Rasmussen, A. J. Lawaetz, M. Nilsson, R. Bro, Structure-revealing data fusion, BMC bioinformatics 15 (1) (2014) 1–17.

[2] C. M. Bishop, Pattern Recognition and Machine Learning (Information Science and Statistics), Springer-Verlag Berlin, Heidelberg, 2006.

[3] I. Chillotti, N. Gama, M. Georgieva, M. Izabachene, Faster fully homomorphic encryption: Bootstrapping in less than 0.1 seconds, in: International Conference on the Theory and Application of Cryptology and Information Security, Springer, 2016.

[4] H. Cho, D. J. Wu, B. Berger, Secure genome-wide association analysis using multiparty computation, Nature biotechnology 36 (6) (2018) 547.

[5] M. F. Criado, F. E. Casado, R. Iglesias, C. V. Regueiro, S. Barro, Non-IID data and continual learning processes in federated learning: A long road ahead, Information Fusion 88 (2022) 263–280.

[6] R. A. Fisher, The use of multiple measurements in taxonomic problems, Annals of human genetics 7 (2) (1936) 179–188.

[7] C. Gentry, Fully homomorphic encryption using ideal lattices, in: Stoc, vol. 9, 2009.

[8] R. Gilad-Bachrach, N. Dowlin, K. Laine, K. Lauter, M. Naehrig, J. Wernsing, Cryptonets: Applying neural networks to encrypted data with high throughput and accuracy, in: International Conference on Machine Learning, 2016.

[9] X. He, P. Niyogi, Locality preserving projections, in: Advances in neural information processing systems, 2004.

[10] A. Imakura, A. Bogdanova, T. Yamazoe, K. Omote, T. Sakurai, Accuracy and privacy evaluations of collaborative data analysis, in: Proceedings of The Second AAAI Workshop on Privacy-Preserving Artificial Intelligence (PPAI-21), 2021.

[11] A. Imakura, H. Inaba, Y. Okada, T. Sakurai, Interpretable collaborative data analysis on distributed data, Expert Systems with Applications 177 (2021) 114891.

[12] A. Imakura, M. Matsuda, X. Ye, T. Sakurai, Complex moment-based supervised eigenmap for dimensionality reduction, in: Proceedings of the AAAI Conference on Artificial Intelligence, vol. 33, 2019.

[13] A. Imakura, T. Sakurai, Data collaboration analysis framework using centralization of individual intermediate representations for distributed data sets, ASCE-ASME Journal of Risk and Uncertainty in Engineering Systems, Part A: Civil Engineering 6 (2020) 04020018.

[14] A. Imakura, X. Ye, T. Sakurai, Collaborative data analysis: Non-model sharing-type machine learning for distributed data, in: Uehara H., Yamaguchi T., Bai Q. (eds) Knowledge Management and Acquisition for Intelligent Systems. PKAW 2021. Lecture Notes in Computer Science, vol. 12280, 2021.
[15] A. Imakura, X. Ye, T. Sakurai, Collaborative novelty detection for distributed data by a probabilistic method, in: Proceedings of The 13th Asian Conference on Machine Learning (ACML 2021), 2021.

[16] S. Jha, L. Kruger, P. McDaniel, Privacy preserving clustering, in: European Symposium on Research in Computer Security, Springer, 2005.

[17] J. Konečný, H. B. McMahan, F. X. Yu, P. Richtarik, A. T. Suresh, D. Bacon, Federated learning: Strategies for improving communication efficiency, in: NIPS Workshop on Private Multi-Party Machine Learning, 2016.

[18] Q. Li, Z. Wen, Z. Wu, S. Hu, N. Wang, B. He, A survey on federated learning systems: Vision, hype and reality for data privacy and protection, arXiv preprint (2019) arXiv:1907.09693.

[19] T. Li, A. K. Sahu, M. Zaheer, M. Sanjabi, A. Talwalkar, V. Smith, Federated optimization in heterogeneous networks, Proceedings of Machine Learning and Systems 2 (2020) 429–450.

[20] X. Li, M. Chen, F. Nie, Q. Wang, Locality adaptive discriminant analysis, in: Proceedings of the 26th International Joint Conference on Artificial Intelligence, AAAI Press, 2017.

[21] L. v. d. Maaten, G. Hinton, Visualizing data using t-SNE, Journal of machine learning research 9 (2008) 2579–2605.

[22] D. Mascalzoni, A. Paradiso, M. Hansson, Rare disease research: Breaking the privacy barrier, Applied & Translational Genomics 3 (2) (2014) 23–29.

[23] H. B. McMahan, E. Moore, D. Ramage, S. Hampson, et al., Communication-efficient learning of deep networks from decentralized data, arXiv preprint (2016) arXiv:1602.05629.

[24] A. Mizoguchi, A. Imakura, T. Sakurai, Application of data collaboration analysis to distributed data with misaligned features, Informatics in Medicine Unlocked 32 (2022) 101013.

[25] H. Nguyen, D. Zhuang, P.-Y. Wu, M. Chang, Autogan-based dimension reduction for privacy preservation, Neurocomputing 384 (2020) 94–103.

[26] X. Ni, X. Shen, H. Zhao, Federated optimization via knowledge codistillation, Expert Systems with Applications 191 (2022) 116310.

[27] K. Pearson, LIII. On lines and planes of closest fit to systems of points in space, The London, Edinburgh, and Dublin Philosophical Magazine and Journal of Science 2 (11) (1901) 559–572.

[28] M. Sugiyama, Dimensionality reduction of multimodal labeled data by local Fisher discriminant analysis, Journal of machine learning research 8 (May) (2007) 1027–1061.
[29] L. Wan, R. Liu, L. Sun, H. Nie, X. Wang, UAV swarm based radar signal sorting via multi-source data fusion: A deep transfer learning framework, Information Fusion 78 (2022) 90–101.

[30] P. Wang, L. T. Yang, J. Li, J. Chen, S. Hu, Data fusion in cyber-physical-social systems: State-of-the-art and perspectives, Information Fusion 51 (2019) 42–57.

[31] Q. Yang, Y. Liu, T. Chen, Y. Tong, Federated machine learning: Concept and applications, ACM Transactions on Intelligent Systems and Technology 10 (2) (2019) Article 12.

[32] X. Ye, H. Li, A. Imakura, T. Sakurai, Distributed collaborative feature selection based on intermediate representation, in: The 28th International Joint Conference on Artificial Intelligence (IJCAI-19), 2019.

[33] J. Zalonis, F. Armknecht, B. Grohmann, M. Koch, Report: State of the art solutions for privacy preserving machine learning in the medical context, arXiv preprint arXiv:2201.11406.

[34] P. Zhang, T. Li, Z. Yuan, C. Luo, G. Wang, J. Liu, S. Du, A data-level fusion model for unsupervised attribute selection in multi-source homogeneous data, Information Fusion 80 (2022) 87–103.

[35] S. Zhang, L. T. Yang, J. Feng, W. Wei, Z. Cui, X. Xie, P. Yan, A tensor-network-based big data fusion framework for Cyber–Physical–Social Systems (CPSS), Information Fusion 76 (2021) 337–354.