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GARD: Gender difference analysis and recognition based on machine learning[✩](#_bookmark7)

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A R T I C L E I N F O A B S T R A C T

*Keywords:*

Gender difference analysis Gender recognition Medical examination data Machine learning

In recent years, intelligent diagnosis and intelligent medical treatment based on big data of medical examina- tions have become the main trend of medical development in the future. In this paper, we propose a method for analyzing the difference between males and females in medical examination items (medical attributes) and find that males and females of different ages have differences in medical attributes. Then, the cluster analysis method is used to further analyze the differences between male and female in medical examination items, such that some common important attributes (CIAs) that can be used for gender recognition are found within a specific age range. Following, we propose two gender recognition models (GRMs) by using the found CIAs to identify the gender. A large number of experimental results are provided to validate the effectiveness of the proposed GRMs. Experimental results show that the medical attributes with a large value of difference really contribute to gender recognition. Within a certain age range, such as 17 to 51 years old, the proposed GRM can reach 92.8% accuracy using only six medical attributes.

# Introduction

With the rapid development of computer technology and hospital information systems, electronic medical record (EMR) has been pop- ularized to replace the traditional handwritten medical records [[1](#_bookmark34)]. Furthermore, the establishment of an advanced EMR system will bring the hospital into a new era of digital hospitals and provide proactive, convenient, and efficient data services for the hospital’s medical, scien- tific research and teaching as well as hospital management. However, during collecting the EMR data, the values of some medical examina- tion items cannot be avoided to lose, such as the value of gender. For EHR analysis, patient ender information plays a very essential role in referring some useful information, and the lack of this information will affect the data quality of EMR. However, in some Chinese EHRs, gender information is either missing [[2](#_bookmark35)], or it is hidden and deleted due to

privacy concerns [[3](#_bookmark36)]. Therefore, it is necessary to investigate the filling miss value algorithm with the non-missing value of medical data, and predict gender from data that does not involve privacy risks.

It is well-known that accurate analysis of medical examination data, which depends on data integrity, is conducive to early disease detection, patient care, and community service. However, the incom- pleteness of medical examination data will reduce the analysis accu- racy. Yoon et al. proposed a generative adversarial imputation network (GAIN) for imputing missing data by adopting the well-known gener- ative adversarial network (GAN) framework [[4](#_bookmark37)]. Yang et al. pointed out that GAIN is not suitable for analyzing medical examination data, because GAN itself adapts to pixel data, so they combined fuzzy coding to adjust the GAIN [[5](#_bookmark38)]. As most of the medical examination data in the intensive care unit are time series, Luo et al. combined GAN

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with the gated recurrent unit to construct the gated recurrent unit for data imputation for filling missing values in time series data [[6](#_bookmark39)]. Similarly, the time dimension information is used to fill missing values by multidirectional recurrent neural network [[7](#_bookmark40)]. Machine learning

EMR. McLean et al. introduced Predictive Mean Matching, *𝐾* Nearest and deep learning are also widely used to fill in missing values in

Neighbors, Iterative Imputer, and MICE to generate values for missing data in EMR centered on oncology [[8](#_bookmark41)]. Farnaz et al. developed a time series medical generative adjunctive network (GANs) for a wound prognosis model that can generate continuous and categorical features from EMR [[9](#_bookmark42)].

When solving the problem of data incompleteness, filling gender information, i.e., gender recognition is also a research hotspot. For gender identification, Li et al. introduced a multiple support vector machine (SVM) gender classifier based on five facial features in addi- tion to human hair and clothes [[10](#_bookmark43)]. The Gabor filter responses of face images were used to identify gender and age [[11](#_bookmark44)]. A RestNet based gender recognizer was developed by detecting and locating the face landmarks on the regression tree set [[12](#_bookmark45)]. In addition to face images, there are studies that use text, mobile phone behaviors, and neural signals to distinguish males and females. Moumita et al. effectively identified the male and female by extracting the Euler Numbers of names [[13](#_bookmark46)]. The gender information of users is predicted by matching the mobile text data of users with the gender representative word set based on Web documents [[14](#_bookmark47)]. Dongxu et al. used reposing behav- iors on social networks to distinguish male and female by combining statistical knowledge and sociological knowledge [[15](#_bookmark48)]. Kaur et al. tried to mine useful information from neural signals, they designed a prediction framework to use neural signals collected by brain wave sensors to identify age and gender [[16](#_bookmark49)]. In the medical field, Jun- mei et al. developed a data management method using convolutional neural network(CNN) to predict missing values of patient gender from EMR [[2](#_bookmark35)]. Serkan et al. proposed a machine learning algorithm based on multidetector computed tomography (MDCT) image measurement of the patella, using a decision tree (DT) method to determine gen- der [[17](#_bookmark50)]. Yuichiro et al. used brain MRI(magnetic resonance imaging) to construct a multichannel 3D-CNN and verified the effect of brain structure image patterns on gender recognition [[18](#_bookmark51)].

In this paper, we first analyze the differences between males and females in medical examination items, and then build two gender recognition models based on the results of the analysis to identify males and females. The main contributions are summarized as follows:

1. An algorithm based on overlapping areas is proposed to analyze the difference between males and females in medical examina- tion;
2. Some common important attributions (CIAs) in a certain age ranges are found to facilitate the recognition of males and females via using cluster analysis, and an age range division algorithm is proposed as a by-product;
3. Two gender recognition models (GRMs), i.e., GRM A for the sample to be identified with known age, and GRM B for the sample to be identified with unknown age, are developed to identify the gender of samples. Experimental results show that in certain age ranges, such as 17 to 51 years old, the proposed GRM A and GRM B can reach 92.8% and 93.8% accuracy, respectively.

The rest of the paper is organized as follows. In Section [2](#_bookmark10), we describe the dataset and analyze the differences between males and females in medical examination. In Section [3](#_bookmark13), we further analyze through cluster analysis and determine the medical examination items that play an important role in gender recognition in each age subrange. In Section [4](#_bookmark24), two gender recognition models are proposed according to whether the age of the examples is known or not. Then, we evaluate the proposed models and the role of data analysis in gender recognition in Section [5](#_bookmark29). Finally, we conclude in Section [6](#_bookmark33).

# Data description and analysis

* 1. *Data description*

To analyze the differences between males and females in medical ex- amination data, we collected 62,072 samples from the Xiangya Medical

the set of samples. Each sample contains *𝑁* = 39 medical examination Big Data System after desensitization. For ease of presentation, let Q be

items (medical attributes) and 2 basic attributes (‘‘AGE’’: Age, ‘‘SEX’’: Sex). In particular, [Table](#_bookmark11) [1](#_bookmark11) lists the medical attribute types, index, attributes, and full name of attributes. The medical attributes include the routine blood test, liver function test, renal function test, and examination of plasma prothrombin time measurements. To grasp the data structure in set Q, we list the common statistics of each attribute, including the mean value (Mean), minimum (MIN), and maximum (MAX). For the basic attributes, the minimum age and the maximum age of samples in set Q are 1 and 70, respectively, i.e., the age range is

f = {1*,* 2*,* … *,* 69*,* 70}. For the male samples, the value of attribute ‘‘SEX’’

is ‘‘0’’, while for the female samples, the value of attribute ‘‘SEX’’ is ‘‘1’’.

* 1. *Difference analysis*

The existing studies have shown that there are differences between males and females in some medical attributes listed in [Table](#_bookmark11) [1](#_bookmark11). For example, the medical attributes RBC, HGB, and HCT have a signifi-

cant differences between males and females after 2 years old [[19](#_bookmark52),[20](#_bookmark53)].

Through the statistical analysis of samples between 1 and 17 years old,

CREA and UA have a significant differences between males and females within 12 to 17 years old [[21](#_bookmark54)]. However, the statistical methods used in the aforementioned literature can only determine whether the distribu-

tions of medical attributes *𝛾* of males and females are the same or not.

mEdical Attribute (DEFEA) *𝛾* is considered significant. However, these If they are not the same, the Difference between malEs and Females in

aforementioned literature has not revealed the change trend of DEFEA

*𝛾*, what we only know is there is the DEFEA *𝛾*. In other words, they do not compare the magnitude of DEFEA *𝛾*. In short, these statistical analysis cannot tell us the specific value of DEFEA *𝛾* [[22](#_bookmark55)]. In what follows, we analyze the DEFEA *𝛾* through the distribution of medical attribute *𝛾* of male and female, respectively.

[Fig.](#_bookmark16) [1](#_bookmark16) shows the numerical distribution of three medical attributes at different ages of males and females. Specifically, [Figs.](#_bookmark17) [1(a)](#_bookmark17), [1(b)](#_bookmark19), and [1(c)](#_bookmark19) illustrate the numerical distribution of medical attributes CREA, HGB, and PT%, respectively. It is not difficult to find that for medical attributes CREA and HGB, the numerical distribution of males and females is almost the same at the age of 5. However, there are large differences between the numerical distribution of males and females over 5 years old. For the medical attribute PT%, the difference between the numerical distribution of males and females is not obvious at these

ages. From the statistical viewpoint, for the medical attribute *𝛾*, the

closer the numerical distribution of males and females is, the larger

DEFEA *𝛾* at age *𝑡* can be evaluated with the overlap area **𝐎** (*𝑡, 𝛾*) of the the overlap area of the numerical distribution is. This implies that the numerical distribution of medical attribute *𝛾* of males and females at age *𝑡*, given by

**𝐃** (*𝑡, 𝑟*) = − ln (**𝐎** (*𝑡, 𝑟*)) *,* (1)

where *𝑟* represents the index of the corresponding medical attribute *𝛾*,

*𝑟* ∈ k = {1*,* 2*,* … *,* 39}, and **𝐎** (*𝑡, 𝛾*) is calculated by

**𝐎** (*𝑡, 𝑟*) = min *𝑃𝑚* (*𝑡, 𝑟, 𝑗*) *, 𝑃𝑓* (*𝑡, 𝑟, 𝑗*) *,* (2)

∑ ( )

*𝑗*∈*𝛬𝛾*

where *𝛬𝛾* is a set of subintervals generated by dividing uniformly the value range of medical attribute *𝛾* into multiple intervals, *𝑃𝑚* (*𝑡, 𝑟, 𝑗*) and *𝑃𝑓* (*𝑡, 𝑟, 𝑗*) represent the frequency of samples of medical attribute

*𝛾* of males and females belonging to the *𝑗*th subinterval at age *𝑡*,

**Table 1**

Data structure.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| Attribute types | Index | Attribute | Full name of attribute | Mean | MIN | MAX | Unit |
| Blood routine | 1 | RBC | Erythrocyte count | 4.46 | 3.27 | 5.60 | 10^12/L |
| examination | 2 | HCT | Hematocrit | 40.05 | 29.40 | 49.00 | % |
|  | 3 | MCV | Erythrocyte mean corpuscular volume | 89.97 | 73.40 | 100.00 | fL |
|  | 4 | MCH | Mean corpuscular hemoglobin | 29.52 | 22.30 | 33.10 | Pg |
|  | 5 | MCHC | Mean corpuscular hemoglobin concentration | 328.27 | 301.00 | 351.00 | g/L |
|  | 6 | RDW-CV | Red blood corpuscular volume distribution width-CV | 12.77 | 11.60 | 17.00 | % |
|  | 7 | WBC | Leukocyte count | 6.29 | 3.54 | 12.63 | 10^9/L |
|  | 8 | LYM# | Lymphocyte count | 2.02 | 0.77 | 5.47 | 10^9/L |
|  | 9 | LYM% | Lymphocyte concentration | 32.80 | 10.50 | 61.70 | % |
|  | 10 | MONO# | Monocyte count | 0.33 | 0.05 | 0.64 | 10^9/L |
|  | 11 | MONO% | Monocyte concentration | 5.27 | 0.70 | 8.30 | % |
|  | 12 | EO | Eosinophil concentration | 2.50 | 0.10 | 9.00 | % |
|  | 13 | BASO | Basophil concentration | 0.40 | 0.00 | 0.90 | % |
|  | 14 | PCT | Plateletcrit | 0.25 | 0.13 | 0.42 | % |
|  | 15 | MPV | Mean platelet volume | 10.96 | 9.00 | 13.50 | fL |
|  | 16 | HGB | Hemoglobin | 131.48 | 92.00 | 164.00 | g/L |
|  | 17 | PLT | Blood platelet count | 231.93 | 111.00 | 425.00 | 10^9/L |
|  | 18 | P\_LCR | Platelet-larger cell ratio | 32.50 | 16.00 | 52.70 | % |
|  | 19 | PDW | Platelet distributionwidth | 13.27 | 9.10 | 20.10 | % |
|  | 20 | EO# | Eosinophil count | 0.15 | 0.01 | 0.62 | 10^9/L |
|  | 21 | BASO# | Basophil count | 0.02 | 0.00 | 0.06 | 10^9/L |
|  | 22 | RDW-SD | Red blood corpuscular volume distribution width-SD | 12.77 | 11.60 | 17.00 | % |
| Liver function test | 23 | TBA | Total bile acid | 4.46 | 0.10 | 15.50 | μmol/L |
|  | 24 | TBIL | Total bilirubin | 10.25 | 3.60 | 24.90 | μmol/L |
|  | 25 | TP | Total Protein | 66.98 | 55.60 | 78.90 | g/L |
|  | 26 | GLO | Globulin | 26.59 | 19.00 | 36.00 | g/L |
|  | 27 | A/G | Albumin globulin ratio | 1.54 | 0.98 | 2.18 |  |
|  | 28 | ALB | Albumin | 40.39 | 30.90 | 47.90 | g/L |
|  | 29 | ALT | Alanine aminotransferase | 16.77 | 3.30 | 52.90 | μ/L |
|  | 30 | AST | Aspartate aminotransferase | 20.03 | 5.30 | 45.00 | μ/L |
|  | 31 | AST/ALT | Aspartate aminotransferase/alanine aminotransferase | 1.38 | 0.52 | 3.24 |  |
|  | 32 | DBIL | Direct Bilirubin | 3.20 | 0.10 | 7.00 | μmol/L |
| Renal function test | 33 | CREA | Creatinine | 61.02 | 22.30 | 113.90 | μmol/L |
|  | 34 | BUN | Urea nitrogen | 4.96 | 2.50 | 9.30 | mmol/L |
|  | 35 | UA | Uric acid | 297.26 | 162.40 | 500.00 | μmol/L |
| Plasma prothrombin | 36 | PT\_sec | Prothrombin time | 11.94 | 10.00 | 14.40 | s |
| time detection | 37 | PT% | Prothrombin time activity | 114.34 | 76.00 | 166.00 | % |
|  | 38 | PT\_Ratio | Prothrombin time ratio | 0.95 | 0.82 | 1.14 |  |
|  | 39 | INR | International normalized ratio | 0.95 | 0.78 | 1.17 |  |
| Personal information | 40 | SEX | Sex | 0.56 | 0 | 1 |  |
|  | 41 | AGE | Age | 41 | 1 | 70 |  |

respectively. Note that **𝐃** (*𝑡, 𝑟*) is negatively correlated with **𝐎** (*𝑡, 𝑟*), and approximates 0 when **𝐎** (*𝑡, 𝑟*) is close to 1. In other words, the overlap

of the two numerical distributions means that there is no difference between females and males in a medial attribute.

[Fig.](#_bookmark18) [2](#_bookmark18) shows the change of the value of DEFEA as age increases. It can be seen that for most medical attributes, the value of DEFEA is smaller than 0.5 at all ages and fluctuates with age. However, with an increasing age, the value of DEFEA has obvious changes for some medical attributes, such as CREA, HGB, HCT, RBC, UA, AST/ALT, and ALT. In particular, one can see that for these medical attributes, the value of DEFEA grows rapidly from the age of 12, and reaches the highest point between the ages of 15 and 50 years old. After 50 years old, the values of DEFEA CREA, HGB, HCT, RBC, and UA are still large, while the values of DEFEA AST/ALT and ALT drop to a lower level

an age subrange C*𝑖*, i.e., ∪*𝑖*C*𝑖* = f . As a result, in the age subrange C*𝑖*, we focus on designing an effective method to divide age range f into

some common medical attributes can be used to distinguish males and females. Note that to reduce the computational complexity and to take into account the fact that the age itself is ordered, the age contained in

age subrange C*𝑖* should be adjacent, such as C*𝑖* = {1*,* 2*,* 3}.

DEFEAs at age *𝑡* as For easy of presentation, we define the mean value of the values of

∑

*𝜋* (*𝑡*) = *𝑟*∈k **𝐃** (*𝑡, 𝑟*) *.* (3)

*𝑁*

If **𝐃** (*𝑡, 𝑟*) is higher than *𝜋* (*𝑡*), the medical attribute *𝛾* is regarded as an important attribute (IA) in distinguishing males and females at age *𝑡*. We introduce a matrix **𝐌** whose element is given by

{1*,* if **𝐃** (*𝑡, 𝑟*) *> 𝜋* (*𝑡*)

compared with other medical attributes, such as MONO#, MCH, and LYM.

**𝐌** (*𝑡, 𝑟*) =

(4)

0*,* other*,*

# Cluster analysis

where *𝑡* ∈ f , *𝑟* ∈ k. The cohesion of IAs in the age subrange C*𝑖* is

defined as

∑

( )

After the aforementioned analysis, one can find that only a few

*𝛷* (*𝑖*) =

*𝑡*1 *,𝑡*2 ∈C*𝑖*

*𝐻* (*𝑡*1*, 𝑡*2) *,* (5)

medical attributes, such as CREA, ALT, have an obvious differences between males and females in a certain age range in terms of the value of DEFEA. The difference between the values of other medical attributes is not obvious at each age. Can we find medical attributes, which play an important role in distinguishing males and females with a higher value of DEFEA at each age? To answer this question, in what follows,

where *𝐻 𝑡*1*, 𝑡*2 is calculated by

*𝐻 𝑡*1*, 𝑡*2 = **𝐌** *𝑡*1*, 𝑟* − **𝐌** *𝑡*2*, 𝑟 .* (6)

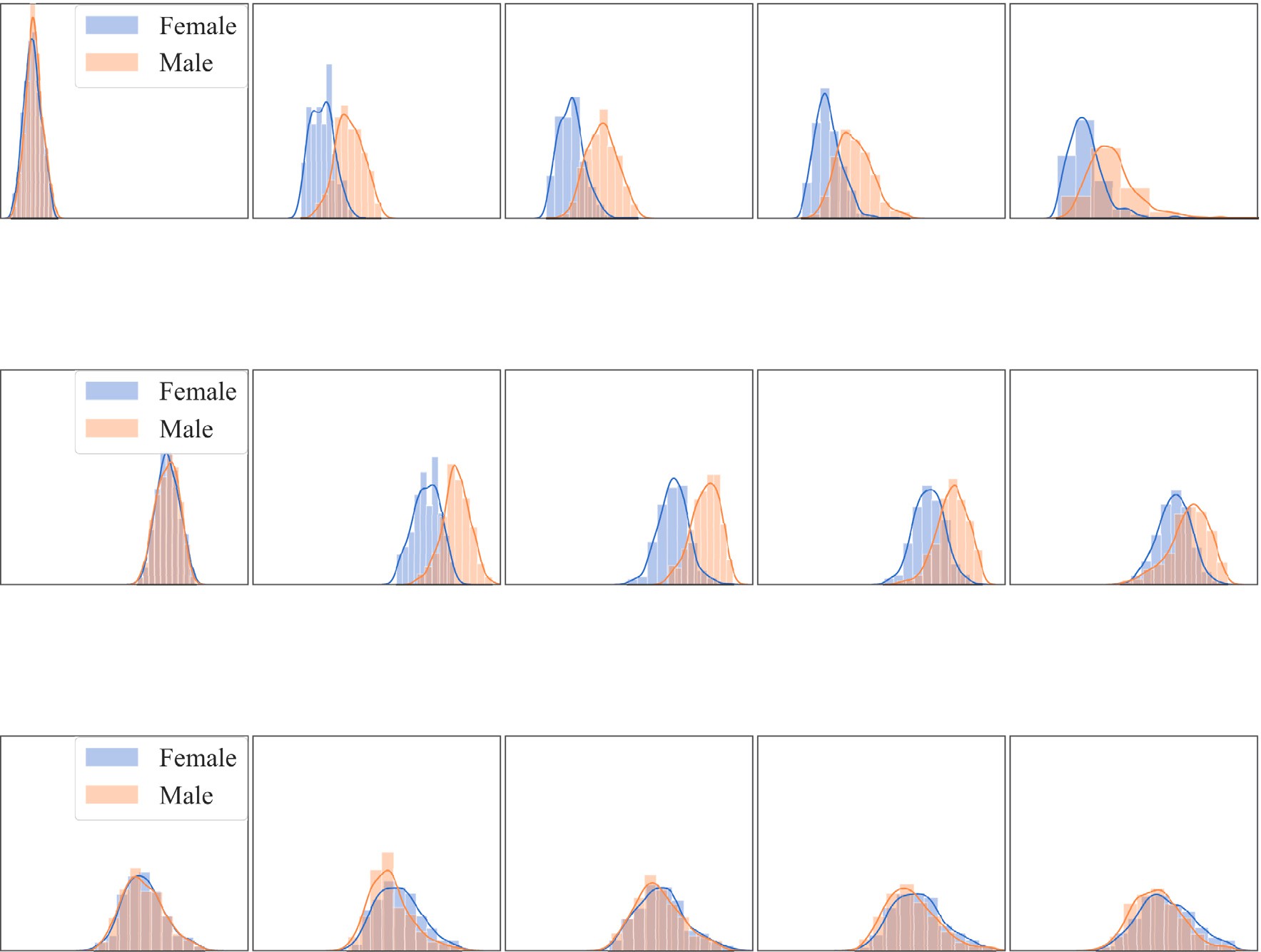
( ) ∑ | ( ) ( )|

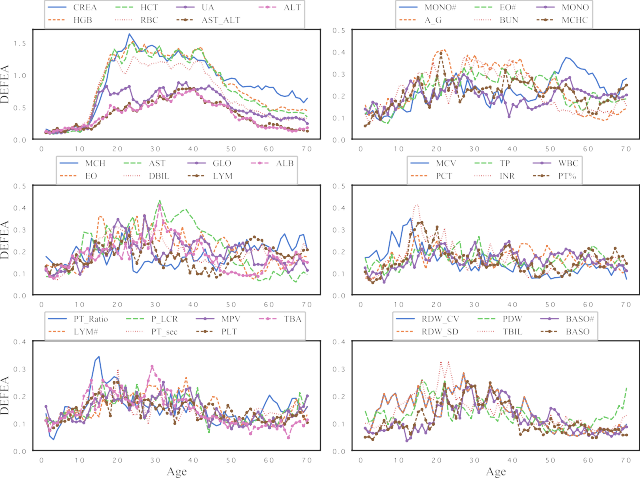
*𝑟*∈k

As can be seen from Eqs. ([5](#_bookmark14)) and ([6](#_bookmark15)), the smaller the cohesion, the larger similarity of IAs in age subrange C*𝑖*.



**/ig. 1.** Numerical distribution of (a) CREA, (b) HGB, (c) PT% in different ages.





**/ig. 2.** The value of DEFEAs.

By using the concept of cohesion, we use division hierarchical clustering (DHC) to divide the age range f into some age subranges with the goal of minimizing the sum of cohesion of age subranges,

such that the IAs between ages in age subrange C*𝑖* is as the same as

possible. The detailed DHC is summarized as Algorithm [1](#_bookmark20). To illustrate

the process of running Algorithm [1](#_bookmark20), [Fig.](#_bookmark23) [3](#_bookmark23) gives out an example of the

age subrange contains a small number of age before the age of 16, and contains more ages after the age of 16. This implies that the common IAs changes frequently between the ages of 1 and 16 years, and tends to be stable after the age of 16. Furthermore, the IAs of different ages within the same age subrange obtained by DHC may also be different.

In the age subrange C*𝑖*, we regard the mean value of DEFEA *𝛾* at all

ages as the value of DEFEA *𝛾*, given by

**𝐕** (*𝑖, 𝑟*) = *𝑡*∈C*𝑖* **𝐃** (*𝑡, 𝑟*) *,* (7)

∑

C*𝑖*

| | | |

where *𝑟* ∈ k, C*𝑖* means the number of ages in the age subrange C*𝑖*. Similarly, for the age subrange C*𝑖*, we define the mean value of the

values of DEFEAs as

*𝛱* (*𝑖*) = *𝑟*∈k **𝐕** (*𝑖, 𝑟*) *.* (8)

∑

*𝑁*

If **𝐕** (*𝑖, 𝑟*) is higher than *𝛱* (*𝑖*), the medical attribute *𝛾* is regarded as a

common important attribute (CIAs) in distinguishing males and females in the age subrange C*𝑖*.

**Algorithm 1** Divisive Hierarchical Clustering

**Input:** *𝑛* (the number of age subranges (*𝑛* ≤ 70));

**Output:** Cell array *𝐶𝑙𝑢𝑠𝑡𝑒𝑟*, *𝑛* cells of *𝐶𝑙𝑢𝑠𝑡𝑒𝑟* represent *𝑛* age subranges;

1: Using Eq. Eq. ([4](#_bookmark12)) to calculate **𝐌**;

⎧⎨⎪ ⎫⎬⎪

2: Initialize cell array *𝐶𝑙𝑢𝑠𝑡𝑒𝑟* = {1*,* 2*,* ⋯ *,* 70} *,* ∅*,* ∅*,* ⋯ *,* ∅ ;

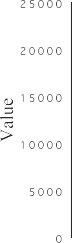
*⏟⏞⏞⏞⏟⏞⏞⏞⏟*

number of age subranges is 10. One can see that when *𝑛* = 10, each

3: **while** *𝐶𝑙𝑢𝑠𝑡𝑒𝑟* {*𝑛*} = ∅ **do** ⎩

*𝑛*−1 ⎭

**/ig. 4.** Change of cohesion and number of CIAs with an increasing number of age subranges.



choice,[1](#_bookmark22) i.e., C1 = {1*,* 2*,* … *,* 7}, C2 = {8*,* 9*,* … *,* 16}, C3 = {17*,* 18*,* … *,* 51},

C4 = {52*,* 53*,* … *,* 70}. [Table](#_bookmark25) [2](#_bookmark25) lists the CIAs in age subrange C*𝑖* and the ratio of DEFEA *𝛾* calculated by

**𝐃** (*𝑖, 𝑟*)

**/ig. 3.** Change of cohesion and number of IAs with division number.

*𝑟* (*𝑖, 𝑟*) =

[∑](#_bookmark25)*𝑘*∈k **𝐃** (*𝑖, 𝑘*)

⋅ 100%*.* (9)

4: Initialize array *𝐿𝐶*, the size of *𝐿𝐶* is *𝑛*, the elements of *𝐿𝐶* are 0;

5: **for** *𝑗* = 1 ∶ *𝑛* **do**

6: **if** *𝐶𝑙𝑢𝑠𝑡𝑒𝑟* {*𝑗*} ≠ ∅ **then**

7: *𝐿𝐶* (*𝑗*) ←the cohesion of *𝐶𝑙𝑢𝑠𝑡𝑒𝑟* {*𝑗*};

8: **end if**

9: **end for**

10: *𝑘* ← arg max *𝐿𝐶*;

11: *𝑎* ← min *𝐶𝑙𝑢𝑠𝑡𝑒𝑟* {*𝑘*};

12: *𝑏* ← max *𝐶𝑙𝑢𝑠𝑡𝑒𝑟* {*𝑘*};

13: Initialize array *𝑆𝐶*, the size of *𝑆𝐶* is (*𝑏* − *𝑎*), the elements of *𝑆𝐶*

are 0;

14: **for** *𝑙* = 1 ∶ *𝑏* − *𝑎* **do**

15: *𝑆𝐶* (*𝑙*) ←the sum of the cohesion of {*𝑎, 𝑎* + 1*,* ⋯ *, 𝑎* + *𝑙* − 1}

and

16: {*𝑎* + *𝑙,* ⋯ *, 𝑏*};

17: **end for**

18: *𝑢* ← arg min *𝑆𝐶* + *𝑎* − 1;

19: **for** *𝑖* = *𝑛* − 1 ∶ −1 ∶ *𝑘* + 1 **do**

20: *𝐶𝑙𝑢𝑠𝑡𝑒𝑟* {*𝑖* + 1} ← *𝐶𝑙𝑢𝑠𝑡𝑒𝑟* {*𝑖*};

In [Table](#_bookmark25) [2](#_bookmark25), there is a total of 27 different medical attributes. The number of CIAs varies greatly across age subranges. Specifically, there

are 18 CIAs in the age subrange C1, which is the most. The number of

CIAs in the age subrange C3 is 7, which is the least. In addition, the number of CIAs in age subrange C2 and C4 are 13 and 11, respectively.

non-CIAs in age subrange C1 are not much different, on the contrary, This implies that the values of DEFEA CIAs and the values of DEFEA the values of DEFEA CIAs in age subrange C3 are much higher than

that of non-CIAs, which is consistent with [Fig.](#_bookmark18) [2](#_bookmark18). For the most medical attributes, the value of DEFEA remains below 0.4 at any age, we can

think that the smaller the number of CIAs in age subrange C*𝑖*, the higher the value of DEFEA of CIAs in age subrange C*𝑖*.

Note that the correlation between CIAs is not considered in Algo- rithm [1](#_bookmark20), therefore, the Pearson correlation method is firstly used to reduce some correlated medical attributes for facilitating the construc- tion of GRMs. Generally speaking, if the absolute value of Pearson

correlation coefficient corr (x, y) is greater than *𝛿* = 0*.*80, the variables

*𝑥* and *𝑦* have a strong correlation. [Table](#_bookmark26) [3](#_bookmark26) lists all medical attributes

with the absolute value of Pearson correlation coefficients larger than

*𝛿*. When corr (x, y) *> 𝛿*, we discard the medical attribute with a low

value of DEFEA. For a more intuitive display, [Table](#_bookmark25) [2](#_bookmark25) shows whether

21: **end for**

the attribute is retained or not, in which ‘‘

*⁓⁓⁓⁓*

’’ means that the

22: *𝐶𝑙𝑢𝑠𝑡𝑒𝑟* {*𝑘*} ← {*𝑎, 𝑎* + 1*,* ⋯ *, 𝑢*};

23: *𝐶𝑙𝑢𝑠𝑡𝑒𝑟* {*𝑘* + 1} ← {*𝑢* + 1*, 𝑢* + 2*,* ⋯ *, 𝑏*};

24: **end while**

25: **return** *𝐶𝑙𝑢𝑠𝑡𝑒𝑟*

Through Algorithm [1](#_bookmark20), the age range f is divided into many age subranges, but excessive division is not necessary. To determine the optimal number of age subranges, two methods are used in this paper. One is to observe the changing trend of the sum of cohesion of all age subranges as the number of age subranges increases. The other is to observe the changing trend of the number of different CIAs in all age subranges as the number of age subranges increases. [Fig.](#_bookmark21) [4](#_bookmark21) illustrates the aforementioned two trends with an increasing number of age subranges. One observes that the total cohesion decreases with the number of age subranges increases and tends to saturation. While, the number of different CIAs in all age subranges increases with an increasing number of age subranges and also tends to saturation. To make the division results as accurate as possible, we need to make trade-offs. On the one hand, it is necessary to avoid unnecessary

medical attribute is discarded, otherwise the medical attribute is used to construct the GRMs.

# Gender recognition

To further assess the effectiveness of CIAs, in this section, according to whether the age is known or not, we construct two GRMs to distin- guish the gender of samples. In particular, we study an effective GRM for case I in which the age is known. While, for the age is not known,

represent the reserved CIAs in the age subrange *𝐶𝑖* as the set *𝜎𝑖*. called case II, we design another GRM. For the sake of explanation, we

**Case I: When the age is known, it is easy to know that the sam- ple belongs to which of the four age subranges.** This implies that we can use the CIAs of each age subrange to construct the corresponding

GRM. Let the samples whose age belongs to age subrange C*𝑖* constitute a sample subset X*𝑖*, *𝑖* ∈ *𝜛* = {1*,* 2*,* 3*,* 4}. It is not difficult to find that

the gender recognition problem belongs to two-classification problem. Therefore, for the age subrange C*𝑖*, the two-classification learning algo- rithm such as Logistic Regression (LR) [[23](#_bookmark56)], Random Forest (RF) [[24](#_bookmark57)],

divisions. On the other hand, it is necessary to ensure that ages within

in what follows, we divide age ranges f into 4 age subranges is a better the same age subrange have similar CIAs. Combining these two factors,

1 The proposed gender recognition can be used in other cases, i.e. other number of age subranges.

**Table 2**

CIAs and their DEFEA ratio.

Age subrange CIAs and the DEFEA ratios

MCV (4*.*00%), MCH (3*.*14%), ALT (3*.*04%), MONO (3*.*01%), A\_G (2*.*95%), RDW-SD (2*.*95%),

C1 = {1*,* 2*,* … *,* 7}

C2 = {8*,* 9*,* … *,* 16}

RDW-CV (2*.*95%), EO (2*.*95%), TP (2*.*93%), AST/ALT (2*.*89%), HGB (2*.*87%), RBC (2*.*83%),

PDW (2*.*82%), LYM (2*.*81%), MPV (2*.*80%), LYM# (2*.*74%), CREA (2*.*68%), BUN (2*.*62%)

*⁓⁓⁓*

*⁓⁓⁓⁓⁓*

RBC (5*.*44%), HGB (5*.*14%), HCT (4*.*53%), UA (4*.*35%), CREA (3*.*94%),

MCV (3*.*34%), INR (3*.*01%), BUN (2*.*85%), ALT (2*.*76%), PT% (2*.*68%),

*⁓⁓*

AST (2*.*62%), PT\_Ratio (2*.*58%), MONO (2*.*56%)

*⁓⁓⁓⁓⁓*

HGB (9*.*79%), CREA (9*.*77%), HCT (9*.*60%), RBC (8*.*26%),

C3 = {17*,* 18*,* … *,* 51}

*⁓⁓*

UA (5*.*51%), AST/ALT (4*.*52%), ALT

(4*.*40%)

CREA (8*.*76%), HGB (6*.*02%), HCT (5*.*40%), RBC (4*.*34%), UA (4*.*11%), MONO# (3*.*50%),

C4 = {52*,* 53*,* … *,* 70}

*⁓⁓*

MONO (3*.*00%), MCH (2*.*86%), DBIL

(2*.*75%), LYM (2*.*74%), MCHC (2*.*58%)

**Table 3**

Correlation coefficient of the removed medical attributes.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| ID | Age subrange | | *𝑥* | | | *𝑦* | corr (*𝑥, 𝑦*) |
|  | C1 | C2 | C3 | C4 |  |  |  |
| 1 | ✓ |  |  |  | PDW | MPV | 0.83 |
| 2 | ✓ |  |  |  | RDW-CV | RDW-SD | 1.00 |
| 3 |  | ✓ |  |  | PT\_Ratio | INR | 0.96 |
| 4 |  | ✓ | ✓ | ✓ | HCT | HGB | 0.82 |

recognition model *𝐵𝑖* is trained using samples at all ages. In particular, to train recognition *𝐵𝑖*, the CIAs in set ∪*𝑖*∈*𝜛 𝜎𝑖* are regarded as features.

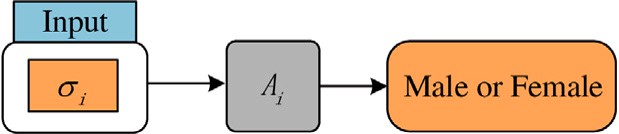
At the same time, the males sample and females sample in sample subset X*𝑖* are labeled as ‘‘m’’ and ‘‘f’’, respectively, and the sample

in set ∪*𝑗*≠*𝑖*X*𝑗* is labeled as ‘‘o’’. Then, the three probabilities of each

age subrange are jointly used to identify the gender of samples via computing the integrated probabilities of males and females, i.e.,

*𝜌* (*𝑚*) = ∑ *𝑝𝑖* (*𝑚*) *,*

*𝑖*∈*𝜛 𝑝𝑖* (*𝑜*)

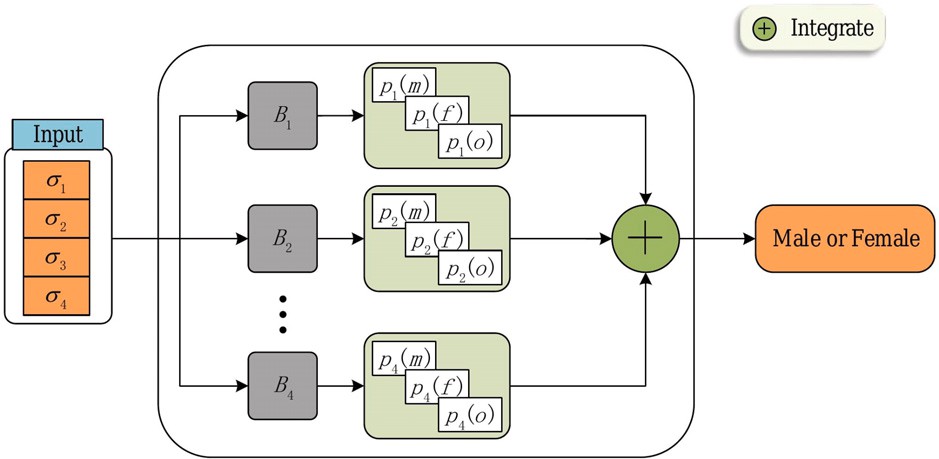
( ) = *𝑝𝑖* (*𝑓* )

*𝜌 𝑓* ∑ *.*

*𝑖*∈*𝜛 𝑝𝑖* (*𝑜*)

(10)

**/ig. 5.** Gender recognition process of GRM A.



**/ig. 6.** GRM B.

can be used to construct the recognition model *𝐴𝑖*. The recognition model *𝐴𝑖* is trained with the samples in sample subset X*𝑖* by regarding the elements in the set *𝜎𝑖* as the features and the basic attribute SEX as the label of samples, respectively. Thus, all recognition models *𝐴𝑖*

constitute GRM A. When using GRM A for gender recognition, if the age

of sample to be identified is within the age subrange C*𝑖*, the sample is identified by the corresponding recognition model *𝐴𝑖* is shown in [Fig.](#_bookmark27) [5](#_bookmark27).

**Case II: When the age is not known, we do not know which age subrange the age of sample to be identified belongs to, it means that the ideas of designing GRM A cannot be directly used.** To effectively exploit the CIAs of each age subranges, in what follows, we design a three-classification learning for each age subrange. Then, the integration learning method is used to construct GRM B to identify the gender of the samples to be identified. Specifically, recognition model

*𝐵𝑖* for age subrange *𝐶𝑖* has the ability of identifying the gender of the

probabilities *𝑝𝑖* (*𝑚*), *𝑝𝑖* (*𝑓* ), and *𝑝𝑖* (*𝑜*). *𝑝𝑖* (*𝑚*) is the probability that the sample and judging the age range of the sample by outputting three

the age subrange C*𝑖*. *𝑝𝑖* (*𝑓* ) is the probability that the age of sample to age of sample to be identified with the gender being males is within be identified with the gender being females is within age subrange C*𝑖*.

*𝑝𝑖* (*𝑜*) is the probability that the age of sample to be identified is not in

age subrange C*𝑖*. Unlike the training process of recognition model *𝐴𝑖*,

If *𝜌* (*𝑚*) *> 𝜌* (*𝑓* ), the gender of sample is males, otherwise is females.

To clearly describe GRM B for case II, the detailed structure of GRM B is

illustrated in [Fig.](#_bookmark28) [6](#_bookmark28). Note that even the age of samples to be identified is known, we also can use GRM B to identify the gender of samples via ignoring the age information. This implies that GRM B has a wider range of applications compared to GRM A.

# Experiment

In this section, we evaluate the performance of the GRMs and discuss further the role of CIAs as well as the important of the division of age range. For each experiment, five learning algorithms, i.e., LR, linear discriminant analysis (LDA) [[25](#_bookmark58)], naive Bayes (NB) [[26](#_bookmark59)], RF, and gradient boosting decision tree (GBDT) [[27](#_bookmark60)], are used. In addition, for

comparison, we also evaluate several simple GRM, i.e., GRM0, GRM1,

and GRM2. In particular, GRM0 directly identifies the gender of the

factor. GRM0 is trained with samples at all ages and uses ∪*𝑖*∈*𝜛 𝜎𝑖* as sample via two-classification method, i.e., without considering the age the training feature. GRM1 and GRM2 regard the CIAs in ∪*𝑖*∈*𝜛 𝜎𝑖* and in

∪*𝑗*≠*𝑖𝜎𝑗* as features to train GRM *𝐴𝑖*, respectively. We take the recognition

result of recognition model *𝐴𝑖* as the result of GRM A (GRM1 and GRM2) in age subrange C*𝑖*. The recognition results of GRM B and GRM0 in age subrange C*𝑖* are computed via the sample whose age belongs to age

subrange C*𝑖*.

[Table](#_bookmark30) [4](#_bookmark30) shows the recognition accuracy of GRM A and GRM B. It can

be seen that when we use the classical learning algorithm such as LR, LDA, and NB, there is a comparable performance difference between

GRM A and GRM B in age subrange C1 and C2. Specifically, GRM A

is a tiny difference between GRM A and GRM B in age subrange C3 and obtains about 6% accuracy gain compared to GRM B. However, there C4. When using learning algorithms with strong learning ability, such

reach the level of GRM A in age subrange C1, and in age subrange C3 as RF and GBDT are adopted, the recognition accuracy of GRM B can and C4, GRM B outperforms GRM A. Experimental results show that the

in age subrange C1 and C2. In addition, no matter GRM A or GRM B, the lack of age information has a more severe impact on gender recognition accuracy of five algorithms is the lowest in age subrange C1, and is the highest in age subrange C3. This is because the smaller the number of

CIAs in age subrange C*𝑖*, the larger the value of DEFEA in age subrange

C*𝑖*. We also find that the smaller the number of CIAs in age subrange C*𝑖*,

Recognition performance of GRM A and GRM B.

Model Age subrange Algorithm (Mean±Std of Accuracy)

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
|  | LR | LDA | NB | RF | GBDT |
| C1 = {1*,* 2*,* … *,* 7} | 0.6069 ± 0.0203 | 0.6254 ± 0.0206 | 0.6152 ± 0.0300 | 0.6134 ± 0.0230 | 0.6192 ± 0.0136 |
| GRM A C2 = {8*,* 9*,* … *,* 16} | 0.6999 ± 0.0356 | 0.7308 ± 0.0337 | 0.6807 ± 0.0287 | 0.7276 ± 0.0192 | 0.7295 ± 0.0273 |
| C3 = {17*,* 18*,* … *,* 51} | 0.9222 ± 0.0060 | 0.9276 ± 0.0049 | 0.9116 ± 0.0072 | 0.9234 ± 0.0059 | 0.9287 ± 0.0058 |
| C4 = {52*,* 53*,* … *,* 70} | 0.8419 ± 0.0117 | 0.8391 ± 0.0124 | 0.8235 ± 0.0108 | 0.8475 ± 0.0087 | 0.8460 ± 0.0077 |
| C1 = {1*,* 2*,* … *,* 7} | 0.5460 ± 0.0217 | 0.5351 ± 0.0159 | 0.5607 ± 0.0204 | 0.6094 ± 0.0222 | 0.5919 ± 0.0199 |
| GRM B C2 = {8*,* 9*,* … *,* 16} | 0.6475 ± 0.0209 | 0.6216 ± 0.0262 | 0.6324 ± 0.0275 | 0.6797 ± 0.0148 | 0.6541 ± 0.0259 |
| C3 = {17*,* 18*,* … *,* 51} | 0.9116 ± 0.0034 | 0.9236 ± 0.0034 | 0.9055 ± 0.0052 | 0.9371 ± 0.0068 | 0.9381 ± 0.0059 |
| C4 = {52*,* 53*,* … *,* 70} | 0.8361 ± 0.0061 | 0.8400 ± 0.0055 | 0.8104 ± 0.0071 | 0.8624 ± 0.0060 | 0.8614 ± 0.0059 |

**Table 5**

Comparison between GRM0 , GRM B and GRM1 .

Age subrange Model Algorithm (Mean±Std of Accuracy (Gain (%)))

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
|  | | LR | LDA | NB | RF | GBDT |
|  |  | 0.5365 ± 0.0205 | 0.5237 ± 0.0174 | 0.5543 ± 0.0234 | 0.5992 ± 0.0237 | 0.5871 ± 0.0190 |
|  | GRM0 | (–) | (–) | (–) | (–) | (–) |
| C1 = {1*,* 2*,* … *,* 7} | GRM B | 0.5460 ± 0.0217 | 0.5351 ± 0.0159 | 0.5607 ± 0.0204 | 0.6094 ± 0.0222 | 0.5919 ± 0.0199 |
|  |  | (1.77%) | (2.18%) | (1.15%) | (1.70%) | (0.82%) |
|  |  | 0.6069 ± 0.0248 | 0.6217 ± 0.0224 | 0.6120 ± 0.0312 | 0.6051 ± 0.0150 | 0.6203 ± 0.0177 |
|  | GRM1 | (13.12%) | (18.71%) | (10.41%) | (0.98%) | (5.65%) |
|  |  | 0.6502 ± 0.0240 | 0.6390 ± 0.0215 | 0.6279 ± 0.0296 | 0.6789 ± 0.0198 | 0.6296 ± 0.0232 |
|  | GRM0 | (–) | (–) | (–) | (–) | (–) |
| C2 = {8*,* 9*,* … *,* 16} | GRM B | 0.6475 ± 0.0209 | 0.6216 ± 0.0262 | 0.6324 ± 0.0275 | 0.6797 ± 0.0148 | 0.6541 ± 0.0259 |
|  |  | (−0.42%) | (−2.72%) | (0.72%) | (0.12%) | (3.89%) |
|  |  | 0.6992 ± 0.0433 | 0.7321 ± 0.0202 | 0.6807 ± 0.0295 | 0.7270 ± 0.0154 | 0.7315 ± 0.0258 |
|  | GRM1 | (7.54%) | (14.57%) | (8.41%) | (7.08%) | (16.18%) |
|  |  | 0.9033 ± 0.0039 | 0.9138 ± 0.0030 | 0.9017 ± 0.0067 | 0.9288 ± 0.0140 | 0.9285 ± 0.0077 |
|  | GRM0 | (–) | (–) | (–) | (–) | (–) |
| C3 = {17*,* 18*,* … *,* 51} | GRM B | 0.9116 ± 0.0034 | 0.9236 ± 0.0034 | 0.9055 ± 0.0052 | 0.9371 ± 0.0068 | 0.9381 ± 0.0059 |
|  |  | (0.92%) | (1.07%) | (0.42%) | (0.89%) | (1.03%) |
|  |  | 0.9390 ± 0.0078 | 0.9428 ± 0.0045 | 0.9155 ± 0.0057 | 0.9377 ± 0.0044 | 0.9413 ± 0.0060 |
|  | GRM1 | (3.95%) | (3.17%) | (1.53%) | (0.96%) | (1.38%) |
|  |  | 0.8211 ± 0.0059 | 0.8244 ± 0.0044 | 0.8028 ± 0.0055 | 0.8627 ± 0.0068 | 0.8561 ± 0.0070 |
|  | GRM0 | (–) | (–) | (–) | (–) | (–) |
| C4 = {52*,* 53*,* … *,* 70} | GRM B | 0.8361 ± 0.0061 | 0.8400 ± 0.0055 | 0.8104 ± 0.0071 | 0.8624 ± 0.0060 | 0.8614 ± 0.0059 |
|  |  | (1.83%) | (1.89%) | (0.95%) | (−0.03%) | (0.62%) |
|  |  | 0.8678 ± 0.0151 | 0.8656 ± 0.0126 | 0.8367 ± 0.0175 | 0.8677 ± 0.0086 | 0.8674 ± 0.0105 |
|  | GRM1 | (5.69%) | (5.00%) | (4.22%) | (0.58%) | (1.32%) |

the better the recognition accuracy of GRMs in age subrange C*𝑖*. This shows that the medical attributes with a large value of DEFEA really

contribute to gender recognition.

[Table](#_bookmark31) [5](#_bookmark31) gives out the comparison between GRM0, GRM B, and GRM1

to further evaluate the effectiveness of GRM B and analyze the role

of age range division. Note that in most age subranges, GRM B with

age subrange C2, GRM B does not show an overwhelming advantage. the five learning algorithms obtains up to 1% gain. However, in the

However, it is worth mentioning that if the learning algorithms NB, RF

that of GRM0 in age subrange C2. This means that GRM B is effective or GBDT are used, the recognition accuracy of GRM B is still higher than even for age subrange C2 which is most affected by the lack of age

information. At the same time, it also shows that if we do not know the age of samples and divide the age range, we can still improve the accuracy of gender recognition. Let us look at the results of another

GRM1 outperforms GRM0 in terms of the recognition accuracy for the group of control experiments, it can be seen that in all age subranges, five learning algorithms. In particular, in age subrange C1 and C2, the average gain is 10.3%, while in age subrange C3 and C4, the average

gain is 2.8%. This means that if we know the age of samples, the age range division will improve the accuracy of gender recognition more, which is much higher than the case of unknown sample age. Furthermore, the division of age range is more helpful for gender

recognition in age subrange C1 and C2. This is because the gender

differences are different in different age subranges, and learning their

gender difference information separately helps improve recognition accuracy. If the age range is not divided, GRM is more inclined to learn the gender difference information of medical attributions in age

subrange C3 and C4 in which the gender difference is obvious.

[Table](#_bookmark32) [6](#_bookmark32) lists the comparison between GRM A, GRM1, and GRM2 to reflect the role of CIAs. We can see that in age subrange C1 and C2, GRM1 has no significant improvement in terms of the recognition accuracy compared to GRM A. This means that for age subranges C1 and C2, the selection of CIAs is appropriate, and we have not left out

age subranges C3 and C4, the participation of more medical attributes any useful medical attributes for distinguishing males and females. For

leads to a small improvement in recognition accuracy. In particular, in age subrange C3 and C4, GRM1 obtains about 2% gain in terms of the recognition accuracy at the cost of large computation complexity. This

distinguishing males and females. For example, in age subrange C3, the means that the CIAs cover the vast majority of useful information for

with only six CIAs. In age subrange C1 and C2, compared to GRM five learning algorithms can achieve about 92% recognition accuracy A, GRM2 has 10% recognition accuracy loss. While, the recognition accuracy loss will be more in age subrange C3 and C4, close to 20%.

subrange C1 and C2 are not much different, on the contrary, the values The values of DEFEA CIAs and the values of DEFEA non-CIAs in age of DEFEA CIAs in age subrange C3 and C4 are much higher than

that of non-CIAs, which leads to the above situation. The above two comparisons show that the CIAs are indeed more conducive to gender

**Table 6**

Controlled experiments on the role of CIAs.

Age subrange Model Algorithm (Mean±Std of Accuracy (Gain (%)))

(Attribute number) LR LDA NB RF GBDT

GRM A 0.6069 ± 0.0203 0.6254 ± 0.0206 0.6152 ± 0.0300 0.6134 ± 0.0230 0.6192 ± 0.0136

(16) (–) (–) (–) (–) (–)

C1 = {1*,* 2*,* … *,* 7}

C2 = {8*,* 9*,* … *,* 16}

C3 = {17*,* 18*,* … *,* 51}

C4 = {52*,* 53*,* … *,* 70}

GRM1 0.6069 ± 0.0248 0.6217 ± 0.0224 0.6120 ± 0.0312 0.6051 ± 0.0150 0.6203 ± 0.0177

(23) (0.00%) (−0.59%) (−0.52%) (−1.35%) (0.18%)

GRM2 0.5138 ± 0.0225 0.5917 ± 0.0278 0.5895 ± 0.0295 0.5536 ± 0.0227 0.5783 ± 0.0259

(7) (−15.34%) (−5.39%) (−4.18%) (−9.75%) (−6.61%)

GRM A 0.6999 ± 0.0356 0.7308 ± 0.0337 0.6807 ± 0.0287 0.7276 ± 0.0192 0.7295 ± 0.0273

(11) (–) (–) (–) (–) (–)

GRM1 0.6992 ± 0.0433 0.7321 ± 0.0202 0.6807 ± 0.0295 0.7270 ± 0.0154 0.7315 ± 0.0258

(23) (−0.10%) (0.18%) (0.00%) (−0.08%) (0.27%)

GRM2 0.5969 ± 0.0522 0.6542 ± 0.0212 0.6420 ± 0.0214 0.6349 ± 0.0212 0.6426 ± 0.0271

(12) (−14.72%) (−10.48%) (−5.69%) (−12.74%) (−11.91%)

GRM A 0.9222 ± 0.0060 0.9276 ± 0.0049 0.9116 ± 0.0072 0.9234 ± 0.0059 0.9287 ± 0.0058

(6) (–) (–) (–) (–) (–)

GRM1 0.9390 ± 0.0078 0.9428 ± 0.0045 0.9155 ± 0.0057 0.9377 ± 0.0044 0.9413 ± 0.0060

(23) (1.82%) (1.64%) (0.43%) (1.55%) (1.35%)

GRM2 0.7444 ± 0.0151 0.7564 ± 0.0130 0.7345 ± 0.0151 0.7521 ± 0.0068 0.7545 ± 0.0086

(17) (−19.28%) (−18.46%) (−19.43%) (−18.55%) (−18.76%)

GRM A 0.8419 ± 0.0117 0.8391 ± 0.0124 0.8235 ± 0.0108 0.8475 ± 0.0087 0.8460 ± 0.0077

(10) (–) (–) (–) (–) (–)

GRM1 0.8678 ± 0.0151 0.8656 ± 0.0126 0.8367 ± 0.0175 0.8677 ± 0.0086 0.8674 ± 0.0105

(23) (3.08%) (3.16%) (1.60%) (2.38%) (2.53%)

GRM2 0.6630 ± 0.0134 0.6683 ± 0.0129 0.6554 ± 0.0136 0.7054 ± 0.0102 0.6724 ± 0.0122

(13) (−21.25%) (−20.36%) (−20.41%) (−16.77%) (−20.52%)

recognition than other attributes and cover most of the information that can be used for gender recognition.

# Conclusion

In this paper, we proposed a method for calculating the difference of medical attributes between males and females at a specified age via the distribution of medical attributes of males and females. We find that only a few medical attributes have an obvious differences between males and females. Then, we further analyzed the differences between males and females by cluster analysis, and found some CIAs in a certain age subrange. In addition, we proposed two GRMs based on the results of data analysis to identify the gender of samples according to whether the age is known or not. Experiment results have shown that in a certain age range, such as 17 to 51 years old, the proposed GRM can reach 92.8% accuracy using only six medical attributes. In addition to evaluating GRM recognition effect, we also verified the effectiveness of GRM B, cluster analysis, and CIAs through comparative experiments.

# Declaration of competing interest

The authors declare that they have no known competing finan- cial interests or personal relationships that could have appeared to influence the work reported in this paper.

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