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Convalescent-plasma-transfusion intelligent framework for rescuing COVID-19 patients across centralised/decentralised telemedicine hospitals based on AHP-group TOPSIS and matching component

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Abstract

As coronavirus disease 2019 (COVID-19) spreads across the world, the transfusion of efficient convalescent plasma (CP) to the most critical patients can be the primary approach to preventing the virus spread and treating the disease, and this strategy is considered as an intelligent computing concern. In providing an automated intelligent computing solution to select the appropriate CP for the most critical patients with COVID-19, two challenges aspects are bound to be faced: (1) distributed hospital management aspects (including scalability and management issues for prioritising COVID-19 patients and donors simultaneously), and (2) technical aspects (including the lack of COVID-19 dataset availability of patients and donors and an accurate matching process amongst them considering all blood types). Based on previous reports, no study has provided a solution for CP-transfusion-rescue intelligent framework during this pandemic that has addressed said challenges and issues. This study aimed to propose a novel CP-transfusion intelligent framework for rescuing COVID-19 patients across centralised/decentralised telemedicine hospitals based on the matching component process to provide an efficient CP from eligible donors to the most critical patients using multicriteria decision-making (MCDM) methods. A dataset, including COVID-19 patients/donors that have met the important criteria in the virology field, must be augmented to improve the developed framework. Four consecutive phases conclude the methodology. In the first phase, a new COVID-19 dataset is generated on the basis of medical-reference ranges by specialised experts in the virology field. The simulation data are classified into 80 patients and 80 donors on the basis of the five biomarker criteria with four blood types (i.e., A, B, AB, and O) and produced for COVID-19 case study. In the second phase, the identification scenario of patient/donor distributions across four centralised/decentralised telemedicine hospitals is identified 'as a proof of concept'. In the third phase, three stages are conducted to develop a CP-transfusion-rescue framework. In the first stage, two decision matrices are adopted and developed on the basis of the five 'serological/protein biomarker' criteria for the prioritisation of patient/donor lists. In the second stage, MCDM techniques are analysed to adopt individual and group decision making based on integrated AHP-TOPSIS as suitable methods. In the third stage, the intelligent matching components amongst patients/donors are developed on the basis of four distinct rules. In the final phase, the guideline of the objective validation steps is reported. The intelligent framework implies the benefits and strength weights of biomarker criteria to the priority configuration results and can obtain efficient CPs for the most critical patients. The execution of matching components possesses the scalability and balancing presentation within centralised/decentralised hospitals. The objective validation results indicate that the ranking is valid.

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1 Introduction

In December 2019, a cluster of patients with a novel coronavirus was identified in Wuhan, China. Initially named as 2019 novel coronavirus, the virus has now been named as SARS-CoV-2 by the International Committee of Taxonomy of Viruses [1–3]. This virus can cause the disease known as coronavirus disease 2019 (COVID-19) [4–7]. The COVID-19 pandemic has shocked the world for the first time in decades, resulting in an extraordinary impact on human life [8]. The number of patients worldwide increases consistently, and the number of patients closely infected follows an exponential trend [9]. Researchers from different countries have recently contributed to the application of different technologies that can help medical and healthcare providers stop this pandemic, such as the transfusion framework of convalescent plasma (CP) [10]. CP transfusion to COVID-19 patients, which is considered as one of the most successful protocols, is used in hospitals to treat this disease [11, 12]. Moreover, integration amongst hospitals in terms of the intelligent transfusion of CP across centralised/decentralised telemedicine architecture is necessary to help doctors in the rapid delivery of COVID-19 treatment [10]. For a clear view on how to support the hospital community in managing a CP-transfusion-rescue intelligent framework across the centralised/decentralised telemedicine architecture for the COVID-19 pandemic, five sequential questions are raised and answered as follows.

> First question: '*What is the importance of CP transfusion to COVID-19 patients*'?

People who have recently recovered from the threat of deteriorating COVID-19 have antibodies to the coronavirus circulating in their blood [10]. Studies have reported that the virus can be eliminated by managing the healthcare quality of patients and providing them with protective antibodies from the blood of recovered patients via strong practice [13–15]. Thus, the transfusion of these antibodies to deteriorating patients can theoretically boost their immune system. Convalescent blood products (CBPs) are obtained by collecting plasma from a patient who has recovered from a viral or bacterial infection and has developed immunity against the pathogen causing the disease [16]. When transfused, CBPs can neutralise viruses and bacteria, thereby suppressing them in the blood [17]. Furthermore, the transfusion of CBPs from patients who recovered from COVID-19 can be the primary approach for preventing rapid virus spread and treating the disease [18]. For plasma=protein therapies, general safety measures have been established regarding plasma collection from donors. Patients treated with CP (donors) demonstrate shorter hospital stay and lower mortality than those not treated with CP; work is ongoing to test this theory on patients with COVID-19 [19]. Thus, the evaluation of suitability and efficacy of CP towards transfusion is important at this stage. Biologically, convalescent subjects must meet the donor-selection plasma criteria and must comply with the national health requirements and known standard routine procedures [10].

> Second question: '*How can suitability and efficacy of CP towards transfusion be evaluated and what is the key direction*'?

Pooled plasma from recovered COVID-19 donors for anti-COVID-19 antibody therapy may undergo several general tests in two stages [10]. The first stage involves general plasma requirements. The second stage is considered as an evaluation of plasma suitability/efficacy by using protein biomarkers that indicate plasma safety/suitability. These biomarkers include PAO2/FIO2, C-reactive protein (CRP; mg/L), IL-6 (pg/mL; cytokines), albumin (g/L), and IgM (enzyme-linked immunosorbent assay [ELISA] titre). In these contexts, the mentioned biomarkers are the suitable CP criteria that can be utilised for transfusion from infected patients to recovered ones (donors). The procedure can ideally help strengthen the immunity of infected patients [20].

The key direction of the above-mentioned points is to select the best CP for the most critical patients with COVID-19 whilst considering the blood types. This process is considered as a problem of multicriteria decision-making (MCDM) and as an intelligent computing concern, which complies with the national health requirements and known standard routine procedures. Thus, an automated intelligent computing framework for selecting the suitable CP for the most critical patients with COVID-19 is proposed [10]. However, at present, many points have not been achieved yet.

> Third question: '*What is the criticism and gap analysis for academic literature that attempt to provide an automated intelligent computing solution to select the best CP for the most critical patients with COVID-19*'?

Based on literature, one study has attempted to provide an automated intelligent computing solution as a rescue intelligent framework to select the best CP for the most critical patients with COVID-19 on the basis of the biological requirements using MCDM methods [10]. Two challenge aspects are considered. The first is related to distributed hospital-management issues, and the second is related to technical issues.

Regarding the first challenge aspect related to distributed hospital-management issues, hospitals' capability may lack an accurate plan for transfusion management care particularly when this pandemic has affected a large scale of patients in different countries [21]. Moreover, major challenges face the health sector when hospitals lack CPs for critical patients, thereby increasing the complexity related to the entire transfusion process in the hospital's community [22, 23]. Meanwhile, identifying an adequate number of blood donors for COVID-19 patients is difficult particularly because some blood types are almost rare [24]. The health providers during this pandemic still face serious aspects regarding distributed hospital management; for example, patients may be increased in a particular hospital but not in others [25]. This scenario is becoming common for hospital workflow when the demand for CPs increases as in COVID-19. Furthermore, the dataset for COVID-19 in literature either presents with limited number of patients/donors or lacks the use of sufficient biomarker criteria that affect the prioritisation process [26, 27]. COVID-19 samples are difficult to collect because of protection of patient privacy. Finally, the issue of fair management and efficient distribution of CPs amongst patients and donors regarding distributed hospitals simultaneously has not been considered [10]. Accordingly, the full picture of intelligent managing patients/donors with COVID-19 in terms of prioritisation with regard to connected hospitals simultaneously is not presented yet, and this aspect is considered as the primary distributed hospital-management issue.

In the shade of the second challenge linked with technical issues, two decision matrices (DMs) are proposed for the prioritisation of patients or donors based on five serological/protein biomarker criteria in a unique hospital. No results are produced because existing published works are insufficient to produce a satisfied patient/donor dataset considering the serological/protein biomarker criteria for dealing with this subject [28]. This aspect is considered as the first technical issue. Accordingly, the validation phase of the prioritisation results are not discussed in the presented methodology. Similar to the above-mentioned unavailability datasets, an intelligent matching process amongst critical patients has not presented suitable donors, and this aspect is considered as the second technical issue. Thus, providing a full solution to address the two above-mentioned challenge aspects and their issues is necessary.

> Fourth question '*What are the recommended solution for such challenge aspects and their issues*'*?*

According to the first challenge of the distributed hospital-management issues, the use of telemedicine architecture is proposed to provide integration within hospitals to fight the COVID-19 pandemic. It is incorporated to optimise care whilst minimising exposures and viral transmission. The architecture of telemedicine is categorised into three tiers: Tier 1, Tier 2, and Tier 3 [29]. Tiers 1 and 2 are responsible for clients' side. This architecture is a medical centre connected to distributed hospital servers. This architecture is also called centralised connected hospitals and is considered as the first recommended direction when no shared medical data resources are found amongst the countries [30–32], which can benefit countries during the COVID-19 pandemic by establishing a medical centre. For example, the ministry of health, which controls all hospitals either private or public, can customise the proposed framework [10] and share hospital-data resources to COVID-19 patients and donors. However, the second recommended direction is to determine whether shared medical-data resources can be found amongst the countries. This process can benefit countries through the blockchain technology. This proposed technology can eliminate the third party of centralised phenomena with regard to authentication and adapt to the telemedicine architecture, namely, decentralised connected hospitals [33]. Blockchain technology maintains a continuous update of all transactions occurring across distributed hospital networks in COVID-19 patients and donors.

Based on the above-mentioned discussion contexts on centralised or decentralised telemedicine, a new intelligent healthcare framework must be connected with several hospitals to boost the availability of service, share medical resources, and evade acute shortage of CPs between patients and donors to help doctors hasten COVID-19 treatment. Therefore, the distributed hospital-management issues can be addressed. The current scenario of the hospital interoperability for both architectures with regard to the status of the current pandemic is presented in Fig. 1.

As shown in Fig. 1, the management system within each hospital admits patients with COVID-19 whose health severity differs amongst one another. Three levels are considered for the infected patients: mild, severe, and critical [34]. Moreover, the donors are admitted to the hospitals for the donation process where convalescent subjects must meet donor selection plasma criteria and comply with the national health requirements and known standard routine procedures. Thus, the transfusion of the best CP to the most critical patients with COVID-19 based on serological/protein biomarker measures for all blood types is required, considering that this scenario must be accomplished amongst the connected hospitals to avoid acute plasma shortages or an increase in the number of patients in a particular hospital.

Regarding the second challenge aspect that inlinks with technical issues, a simulation data of 80 patients and 80 donors based on the five biomarker criteria with four blood types (i.e., A, B, AB and O) are produced for the first time for COVID-19 case study. The new dataset is generated on the basis of reliable reference ranges and expert-validated occurrence records in the respiratory field with more than 10 years of experience to include different health conditions. Based on these new datasets,

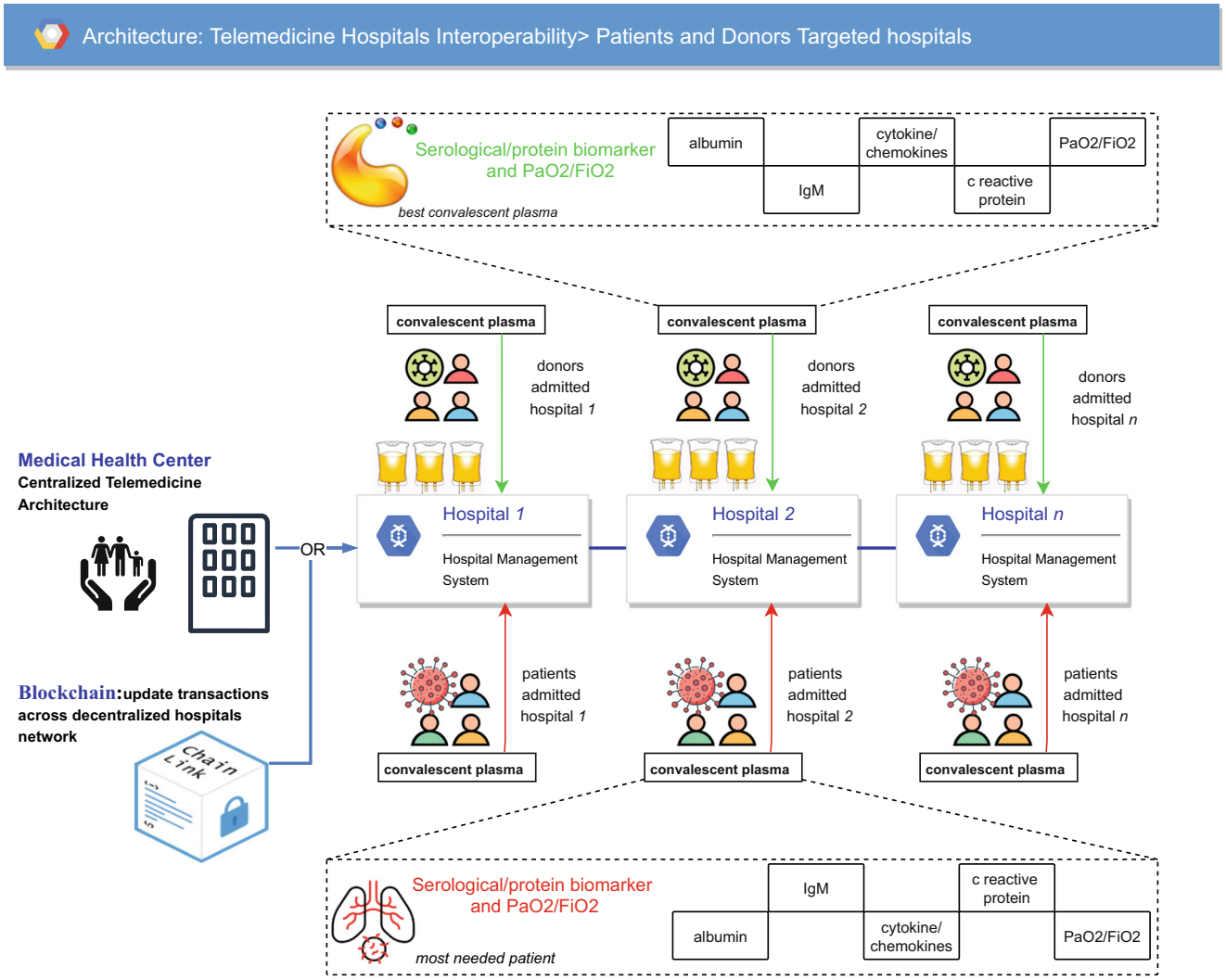

Fig. 1 Conceptual diagram for hospital interoperability in centralised/decentralised telemedicine

the outcome of prioritisation configuration results is used in the transfusion of CPs through a new matching component guideline between patients and donors' CPs considering the four blood types. Thus, the technical issues can be addressed.

From the above-mentioned points, the development of a rescue interoperability intelligent framework across telemedicine architecture in centralised or decentralised hospital connections for prioritisation of patients and donors based on the generation datasets can provide a complete solution. A scalable management framework can withstand the CP load amongst connected hospitals, and the proper donor can be matched with compatible patients to improve balance control between patients and donors. In these contexts, balancing a huge number of patients/donors to avoid an acute shortage of CPs can be accomplished. If this framework is appropriately developed, then it would exhibit the potential to save more lives. One way of achieving this aim is to develop a rescue framework that achieves the transfusion approach of CPs. Moreover, the matching process must be considered to enable balance across distributed hospitals. Thus, a prioritisation methodology is often conducted to ensure that CP is given in an appropriate and timely manner [35]. Therefore, for a sustainable health system and best care, improvements must be made to satisfy current requirements, particularly the need to present an interoperability rescue intelligent framework to manage the transfusion of best CPs between patients and donors with COVID-19 across centralised and decentralised connected hospitals. This intelligent framework must be able to integrate the work process of the prioritisation of patients and donors amongst these hospitals simultaneously.

Fifth question: '*What is the contribution, novelty, and implication of the present study*'?

This study has proposed a novel CP-transfusion-rescue intelligent framework across centralised/decentralised

telemedicine hospitals on the basis of the matching component process to provide an efficient CP from eligible donors to the most critical patients by using the integrated AHP-TOPSIS methods. A dataset of COVID-19 patients/donors that met the important criteria in the virology field must be augmented to improve the developed intelligent framework. The proposed intelligent framework can improve balancing and scalability across telemedicine hospitals between patients and donors simultaneously.

2 Methodology

The development methodology of the proposed CP-transfusion-rescue intelligent framework is divided into four sequence phases (i.e., data augmentation [DA] for patients/donors; identification of patients/donors distribution within telemedicine hospitals; development and presentation of CP-transfusion-rescue intelligent framework for COVID-19, including three stages; and objective validation of the constructed results). Figure 2 shows the structure of the research-methodology phases.

2.1 Phase 1: DA

The augmentation of COVID-19 patient/donor datasets based on serological/protein biomarkers is accomplished in this section. Experts are needed to generate reliable clinical datasets to annotate labels. Given the complexity of the biomarker medical data, a COVID-19 medical dataset, whose labels are completely reliable, is unavailable [36]. For these challenges, DA can be used to generate dummy data to help prioritise patients/donors with COVID-19. An expert in the virology field with more than 10 years of experience provides a subjective judgment and generates an augmented dataset on the basis of medical-reference ranges (Tables 10 and 11 in the Appendix) to reduce this gap. These tables also present the reference ranges that serve as an indicator to identify the emergency health levels for the patients. A sample of first patient and donor based on each blood type from the augmented

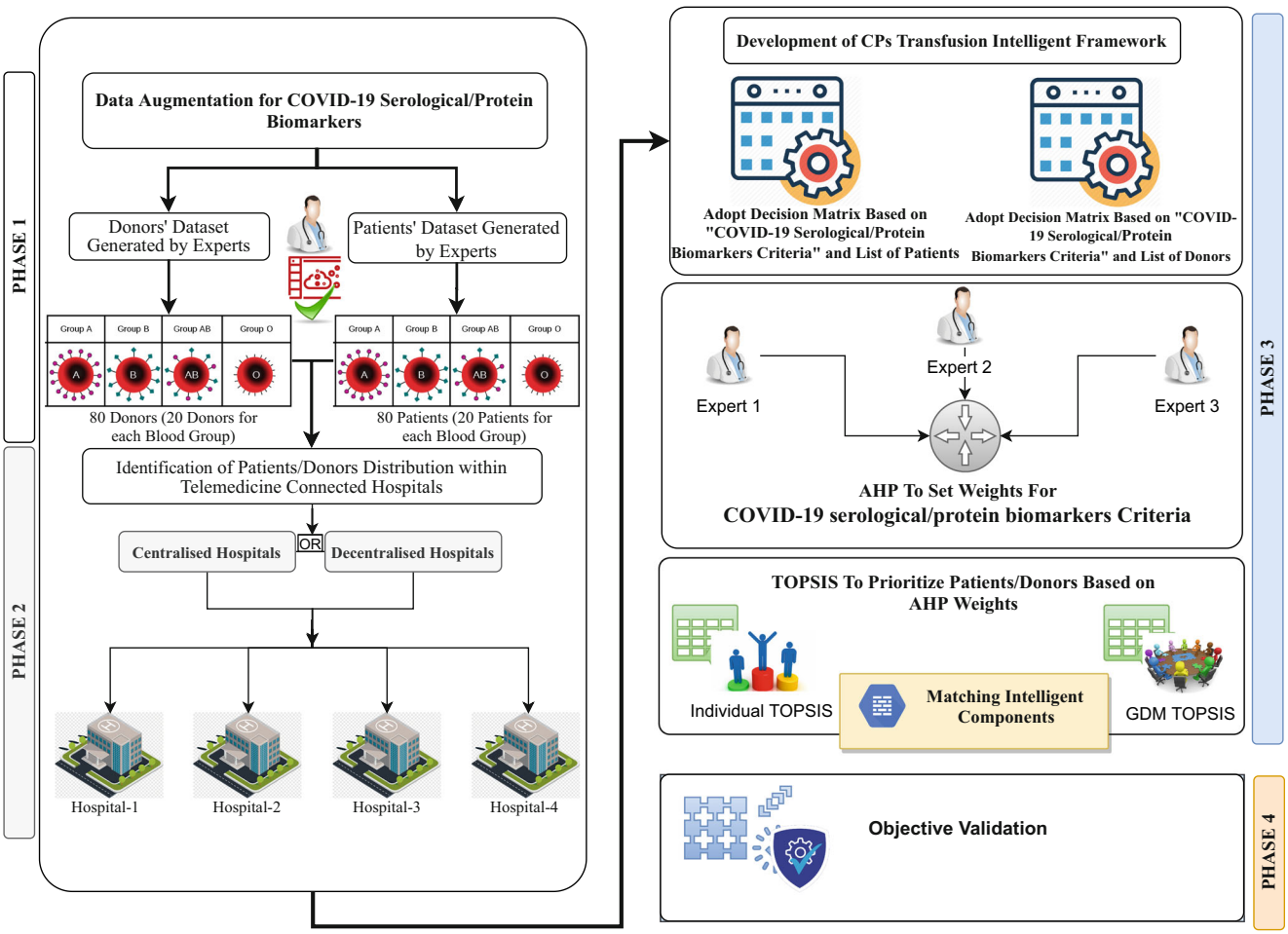

Fig. 2 Methodology phases for the CP-transfusion-rescue intelligent framework

dataset is presented in Table 1. The specifications of the dataset are as follows.

- The dataset includes 80 patients and 80 donors, as well as four blood types (i.e., A, B, AB, and O).
- Patient/donor clinical data measurements are generated according to five biomarker measurements (i.e., PAO2/FIO2, CRP (mg/L), IL-6 (pg/mL; cytokines), albumin (g/L), and IgM (ELISA titre).
- Biomarker measurements for the generated data are varied with regard to the health emergency level (mild, moderate, or severe) based on medical perspective and depend on reliable biomarker-reference ranges.

A brief description for each biomarker is illustrated as follows.

1. PAO2/FIO2 ratio is defined as the ratio of the partial pressure of arterial oxygen to the percentage of inspired oxygen [35], and its reference range must be between 100 and 300.
2. CRP is a serum amyloid P component belonging to the pentraxin family of calcium-dependent ligand-binding proteins. It serves as a marker of inflammation and ranges between 8 and 250. SARS-CoV-2 seems to increase the CRP levels significantly because of inflammatory reaction, and related tissue destruction was also observed in 2002 in the SARS epidemic. High concentrations indicate a severe disease linked to lung damage and poor prognosis [37].
3. IL-6 (pg/mL; cytokines) is released by T cells and activated macrophages during the acute-phase response following injury or trauma and may lead to inflammation or infection; it should be between 6 and 300. IL-6 has pro- and anti-inflammatory properties [38].
4. Albumin is an essential binding and transport protein for various substances in plasma and maintains the osmotic pressure of blood [39]. The reference range is between 5 and 55.
5. ELISA is used to detect immunoglobulin M (IgM) and IgG antibodies against capsular and O antigens of *Haemophilus influenzae*. It ranges between 100 and 800.

For further discussion on the augmented data, the P1_A (for example) indicates that this patient is the first augmented one and his blood type is A. Furthermore, the measurements of his biomarker criteria are explained. A total of 20 patients and 20 donors are identified for each blood type.

2.2 Phase 2: Identification of patient/donor distribution within telemedicine hospitals

This study adopts four hospitals as 'a proof of concept' to represent the managing of patients and donors. Our identification phase proposes that the first hospital has admitted a large scale of patients (40 patients) and a small number of donors (only eight donors) to test the proposed CP-transfusion-rescue intelligent framework. The second hospital has admitted 20 patients, and the number of available donors is 12. The third hospital has admitted 12 patients, and the number of available donors is 20. Finally, the fourth hospital has admitted eight patients and a large number of available donors (40). The scenario of identification of all patients and donors within the four hospitals are shown in Table 2.

As shown in Table 2, the number of patients and donors varies across hospitals. This variety is important to test the proposed CP-transfusion-rescue intelligent framework when the hospital has an inverse relationship with regard to distribution between patients and donors either in centralised or decentralised telemedicine connections. In these contexts, any hospital that lacks donors and admits a large number of patients can be tested and vice versa. Thus, the development

Table 1 Patient and donor samples from the augmented datasets

	PAO2/FIO2 >300	C-reactive protein, mg/L (<8)	IL-6, pg/mL (cytokines) (normal range, 0–7)	Albumin (40–55) g/L	IgM ELISA titre (<200) titres (<200)
Patients	Serological/Protein Biomarker Measurements				
P1_A	128	93	244	21	94.09
P1_B	136	83.64	168	24	154
P1_AB	167	69.36	216	29	199
P1_O	182	141.78	78	31	263
Donors	Serological/Protein Biomarker Measurements				
D1_A	453	1.3	1.4	41.6	64.99
D1_B	425	3.96	1.98	44.44	32.01
D1_AB	449	2.97	4.95	47.47	37.83
D1_O	445	5.94	3.96	55.55	35.89

Table 2 Identification scenario of patient/donor distribution within the four hospitals

	Hospital-1 Distribution		Hospital-2 Distribution		Hospital-3 Distribution		Hospital-4 Distribution	
Blood Type	Admitted Patients	Available Donors	Admitted Patients	Available Donors	Admitted Patients	Available Donors	Admitted Patients	Available Donors
Blood group A	P1_A	D1_A	P11_A	D3_A	P16_A	D6_A	P19_A	D11_A
	P2_A	D2_A	P12_A	D4_A	P17_A	D7_A	P20_A	D12_A
	P3_A		P13_A	D5_A	P18_A	D8_A		D13_A
	P4_A		P14_A			D9_A		D14_A
	P5_A		P15_A			D10_A		D15_A
	P6_A							D16_A
	P7_A							D17_A
	P8_A							D18_A
	P9_A							D19_A
	P10_A							D20_A
Blood group B	P1_B	D1_B	P11_B	D3_B	P16_B	D6_B	P19_B	D11_B
	P2_B	D2_B	P12_B	D4_B	P17_B	D7_B	P20_B	D12_B
	P3_B		P13_B	D5_B	P18_B	D8_B		D13_B
	P4_B		P14_B			D9_B		D14_B
	P5_B		P15_B			D10_B		D15_B
	P6_B							D16_B
	P7_B							D17_B
	P8_B							D18_B
	P9_B							D19_B
	P10_B							D20_B
Blood group AB	P1_AB	D1_AB	P11_AB	D3_AB	P16_AB	D6_AB	P19_AB	D11_AB
	P2_AB	D2_AB	P12_AB	D4_AB	P17_AB	D7_AB	P20_AB	D12_AB
	P3_AB		P13_AB	D5_AB	P18_AB	D8_AB		D13_AB
	P4_AB		P14_AB			D9_AB		D14_AB
	P5_AB		P15_AB			D10_AB		D15_AB
	P6_AB							D16_AB
	P7_AB							D17_AB
	P8_AB							D18_AB
	P9_AB							D19_AB
	P10_AB							D20_AB
Blood group O	P1_O	D1_O	P11_O	D3_O	P16_O	D6_O	P19_O	D11_O
	P2_O	D2_O	P12_O	D4_O	P17_O	D7_O	P20_O	D12_O
	P3_O		P13_O	D5_O	P18_O	D8_O		D13_O
	P4_O		P14_O			D9_O		D14_O
	P5_O		P15_O			D10_O		D15_O
	P6_O							D16_O
	P7_O							D17_O
	P8_O							D18_O
	P9_O							D19_O
	P10_O							D20_O

of the CP-transfusion intelligent framework is needed as presented in the next phase.

2.3 Phase 3: Development of the CP-transfusion intelligent framework

This phase includes a three-stage development process as illustrated in Fig. 3. The process can be achieved in either centralised or decentralised telemedicine workflow architecture in the same processes.

1. Two DMs for the prioritisation of patients and donors are adopted from a previous work [10]. The first DM is for the prioritisation of admitted patients across the four identified hospitals simultaneously in either centralised or decentralised telemedicine workflow architecture. Therefore, any patient in any hospital must be compared and evaluated with all other patients admitted in other hospitals. The second DM can prioritise all donors in the same context.
2. The best MCDM techniques for the adopted DMs are analysed and selected for handling the prioritisation configurations. In this stage, the evaluation and prioritisation of patients and donors based on the five biomarker criteria are achieved.
3. The findings of the prioritisation results from the previous stages are operated with the matching component stage. The developed stage has identified four

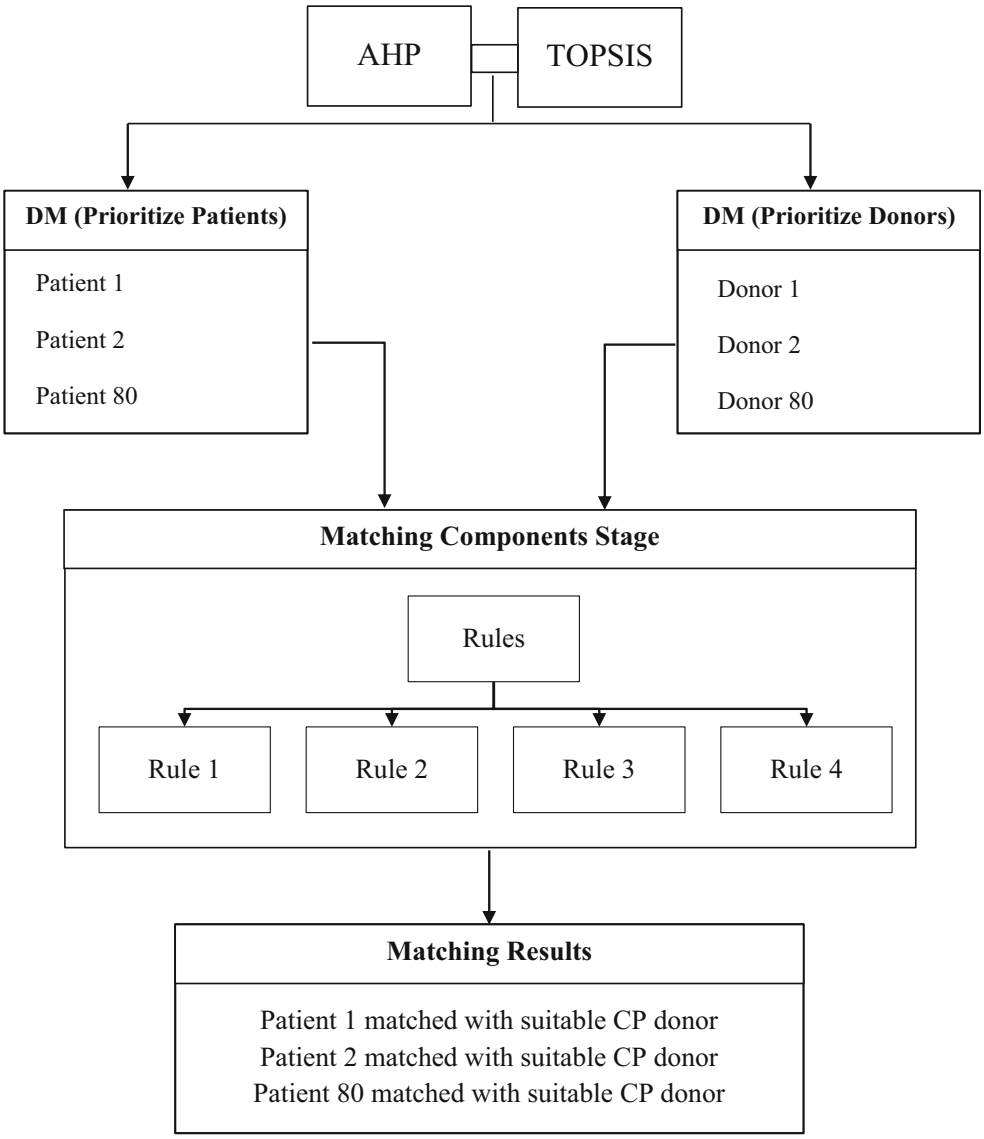

Fig. 3 CP-transfusion framework stages

rules to complete the intelligent-transfusion process between patients and donors.

2.3.1 Adopted DMs for the prioritisation of patients/donors

Both DMs are demonstrated in Table 3.

The adopted DM for patients is constructed on the basis of the intersection between 'serological/protein biomarker criteria' and 'COVID-19 infected patient list'. Furthermore, the DM for donors is constructed on the basis of the intersection between 'serological/protein biomarker criteria' and 'COVID-19 donor list'. However, according to the specific problems of the management of COVID-19 patients/donors, prioritisation is achieved through the integration of decision-making methods to considerably reducing the problem complexity.

2.3.2 Adopted MCDM techniques

The recommended solution for our study is to use MCDM that deals with decision problems with regard to the decision criteria. MCDM has the potential to contribute to a fair, transparent, and rational priority-setting process [40–50]. Prioritisation is considered challenging for different kinds of medical perspectives [51–61]. With regard to the adopted DMs, a previous work [10] has suggested the use of the SODOSM method in handling prioritisation. However, the SODOSM method is conducted with regard to the idle solution amongst each criterion within the CP DM. The ideal solution is an alternative for specific criteria [62], and this concept cannot be applied to the COVID-19 case study. The problem in identifying the ideal solution with regard to the reference range for the COVID-19 serological/protein biomarkers has not been detected and recognised [34]. Thus,

Table 3 Prioritisation DM for patients and donors

Serological/Protein Biomarker Criteria Patient Identification Information		C1	C2	C3	C4	C5
Patients	Hospital Number					
Patient1	H1 or H2 or H3 or H4	C1-P1	C2- P1	C3-P1	C4-P1	C5-P1
Patient2	H1 or H2 or H3 or H4	C1-P2	C2-P2	C3-P2	C4-P2	C5-P2
Patient3	H1 or H2 or H3 or H4	C1-P3	C2-P3	C3-P3	C4-P3	C5-P3
Patient n	H1 or H2 or H3 or H4	C1-P80	C2-P80	C3-P80	C4-P80	C5-P80
Serological/Protein Biomarker Criteria Donor Identification Information		C 1	C 2	C 3	C 4	C 5
Donors	Hospital Number					
Donor1	H1 or H2 or H3 or H4	C1-D1	C2- D1	C3-D1	C4-D1	C5-D1
Donor2	H1 or H2 or H3 or H4	C1-D2	C2-D2	C3-D2	C4-D2	C5-D2
Donor3	H1 or H2 or H3 or H4	C1-D3	C2-D3	C3-D3	C4-D3	C5-D3
Donor n	H1 or H2 or H3 or H4	C1-D80	C2-D80	C3-D80	C4-D80	C5-D80

C 1= PAO2/FIO2 >300, C 2= C-reactive protein, mg/L (<8), C 3 = IL-6, pg/mL (Cytokines; normal range, 0–7), C4 = Albumin (40–55) g/L, C5 = IgM ELISA titre (<200), P = Patient, D= Donor, H= Hospital

the use of existing MCDM methods is recommended in the present study.

The newest trend regarding the use of MCDM methods is to combine two or more methods to recoup the weaknesses of a single method [63–73]. AHP and TOPSIS have become a commonly integrated MCDM method [74–76]. One MCDM methodology to address the above-mentioned issues is to apply and require high-level stages of patients' data.

Integrated AHP-TOPSOS This subsection describes the integration of both methods. Several steps are implemented to assign proper weights to the serological/protein biomarker criteria by using the AHP method together with the TOPSIS method for the prioritisation of patients/donors. The integrated AHP and TOPSIS steps are shown in Fig. 4.

AHP for setting weights for COVID-19 serological/protein biomarker criteria This section describes in detail the weighting attributes and proposes a precise approach for setting subjective weights to the COVID-19 serological/protein biomarker criteria for patients and donors on the basis of the AHP method. This section also aims to investigate the effective criteria for such investigation for patients and donors. The procedure of the AHP method is represented by the following steps [77–81].

A. Decomposition of a Decision Problem into a Decision Hierarchy

Problem modelling as a hierarchy consists of the decision goal that must be designed for the criteria in AHP. Figure 5 illustrates the hierarchy of the criteria used in the AHP pairwise comparison for serological/protein biomarkers to obtain criterion weights. The top of the hierarchy represents the goal, which is achieved by the eight criteria. Pairwise comparison must be performed amongst all criteria.

B. Construction of Pairwise Comparison Matrix

AHP can build a pairwise comparison matrix to establish a decision:

$$A = \begin{pmatrix} x_{11} & x_{12} & \cdots & \cdots & x_{1n} \\ x_{21} & x_{22} & \cdots & \cdots & x_{2n} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ x_{n1} & x_{n2} & \cdots & \cdots & x_{nn} \end{pmatrix} \text{ where, } \begin{cases} x_{ii} = 1 \\ x_{ji} = \dfrac{1}{x_{ij}} \end{cases} \quad (1)$$

Elements *Xij* are obtained from Fig. 5. The comparisons (relative importance) of each criterion are measured according to a numerical scale from 1 to 9 [82, 83]. Table 4 illustrates the relative scales (1–9) used to show each expert's judgments for each comparison. Experts must critically set these judgments on the basis of their experience and knowledge.

C. Obtaining Priority-Judgment Ranking Scores

A pairwise comparison questionnaire was designed and distributed to a geographically diverse convenience sample of experts with expertise in respiratory diseases. The experts were asked to show their judgments and the relative importance for all criteria by using the nine scales for comparison. Figure 6 presents a sample of the criteria for pairwise comparisons in the evaluation form distributed amongst the experts.

The number of required pairwise comparisons is $n \times (n-1)/2$, where n is the number of criteria used during evaluation.

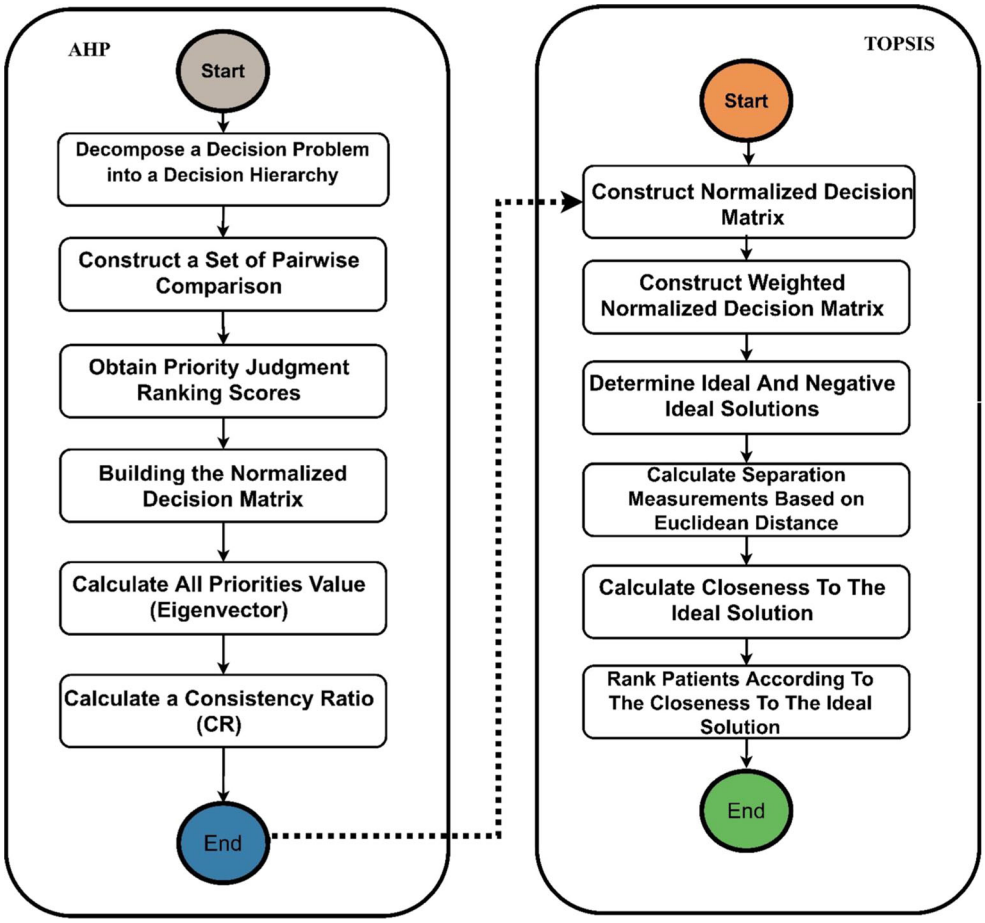

Fig. 4 Integrated AHP-TOPSIS model for prioritisation using multicriteria decision-making

At this stage, AHP extracts the weight of importance of all serological/protein biomarker COVID-19 criteria from the pairwise comparison by user preferences and judgments from the decision-making team. 'AHP is technically valid and does not require a large sample size' [84]. Hence, in this research, three experts with more than 10 years of experience are selected to show their preferences and judgments. Three copies of the evaluation forms are revised by the experts, achieving a total of 10 comparisons by each expert. All comparisons for all criteria are made at this point.

D. Construction of Normalised DM

Every element of matrix A is normalised by dividing each element in a column by the sum of the elements in the same column to create a normalised pairwise comparison matrix *Anorm*. *Anorm* is the normalised matrix of *A*(*1*), where *A*(*xij*) is given by Eq. (2). *Anorm (aij)* is expressed as follows:

$$a_{ij} = \frac{x_{ij}}{\sum_{i=1}^{n} xij} \tag{2}$$

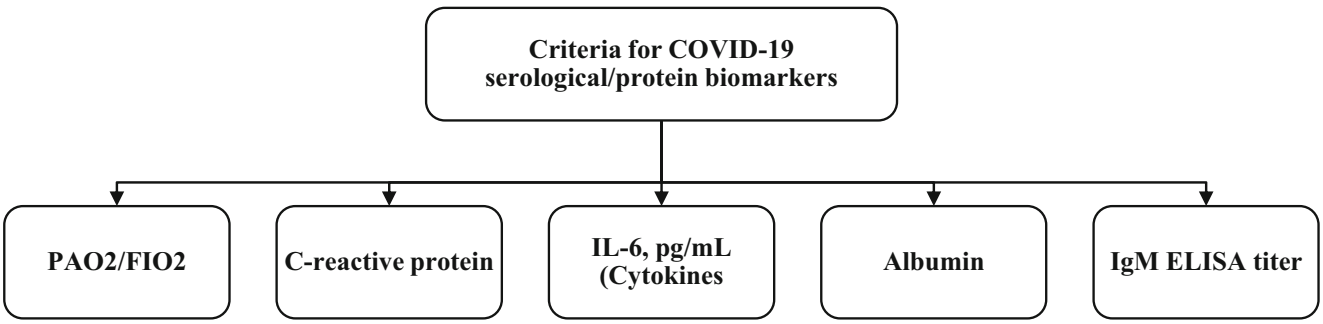

Fig. 5 Hierarchy of AHP for the serological/protein biomarker COVID-19 criteria

Table 4 Nine scales of pairwise comparisons

Intensity of Importance	Definition	Explanation
1	Equal importance	Two activities contribute equally to the objective
3	Weak importance of one over another	Experience and judgment slightly favour one activity over another
5	Essential or strong importance	Experience and judgment strongly favour one activity over another
7	Demonstrated importance	Activity is strongly favoured and its dominance is demonstrated in practice
9	Absolute importance	The evidence favouring one activity over another is of the highest possible order of affirmation
2,4,6,8	Intermediate values between the two adjacent judgments	When compromise is needed

$$A_{\text{norm}} = \begin{pmatrix} a_{11} & a_{12} & \cdots & \cdots & a_{1n} \\ a_{21} & a_{22} & \cdots & \cdots & a_{2n} \\ \vdots & \vdots & \vdots & \ddots & \vdots \\ a_{n1} & a_{n2} & \cdots & \cdots & a_{nn} \end{pmatrix} \quad (3)$$

E. Calculation of all Priority Values (Eigenvector)

AHP pairwise comparison uses mathematical calculations to convert judgments to provide weights for all criteria. After obtaining the responses on the pairwise comparisons, a reciprocal matrix is created from the pairwise comparisons. The weights of decision factor i can be calculated as Eq. (4):

$$w_i = \frac{\sum_{j=1}^{n} a_{ij}}{n} \; and \; \sum_{j=1}^{n} w_i = 1 \quad (4)$$

where n is the number of the compared elements. The AHP measurement steps must be designed to obtain the weights based on the evaluator's preference.

F. Calculation of Consistency Ratio (CR)

CR, which expresses the internal consistency of judgments, is calculated. The following terms are defined to develop a quantitative measure of the degree of inconsistency within a pairwise comparison matrix [85]. The consistency index (CI) is calculated with Eq. (5):

$$\text{CI} = \frac{\lambda \, \text{max} - \text{n}}{\text{n} - 1} \quad (5)$$

The random index (RI) is calculated with Eq. (6):

$$RI = \frac{1.98\ (n-1)}{n}.CI \quad (6)$$

CI measures the degree of inconsistency. RI is the corresponding measure of the degree of inconsistency of a pairwise comparison matrix. CR is defined in Eq. (7):

$$CR = \frac{CI}{RI} \quad (7)$$

CR is the ratio of CI to RI. CR has been previously proposed [86]; it is a quantitative measure of the degree of

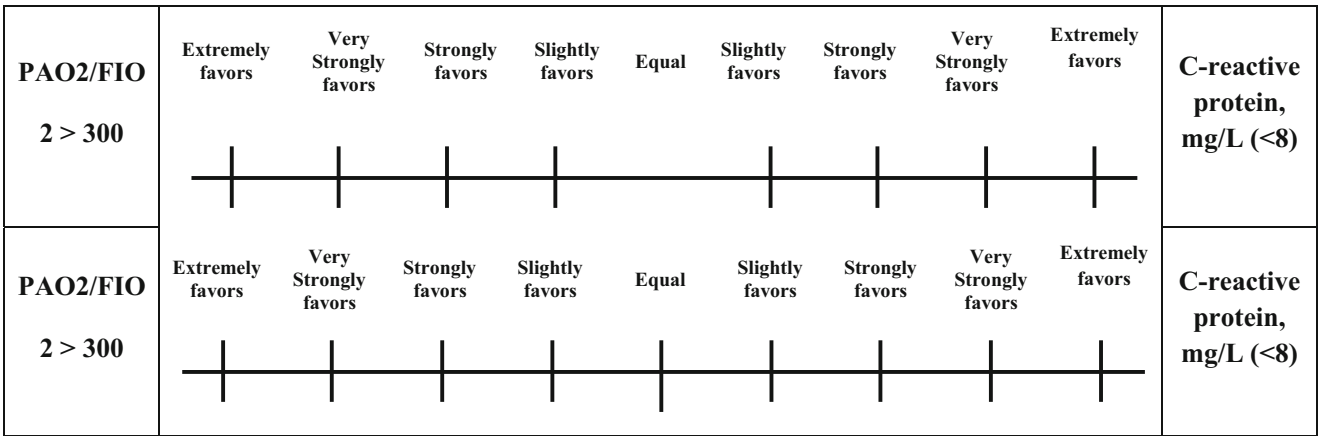

Fig. 6 Sample evaluation form

inconsistency of a pairwise comparison matrix. A pairwise comparison matrix with a corresponding CR must not exceed 10% or 0.1. In this case, the obtained weights are acceptable [87]; otherwise, the obtained weights must be ignored, and decision makers must be asked to answer the designed questionnaires again to reach the acceptable CR ratio.

TOPSIS for the prioritisation of COVID-19 patients/donors In this stage, TOPSIS is used to prioritise COVID-19 patients/donors based on the weighted criteria from the AHP method to tackle the major weakness of TOPSIS, which is the lack of provision weight for the evaluation criteria [88–91]. In general, the evaluation criteria can be classified into two types: benefit and cost [92, 93]. Benefit criterion indicates that a larger value is more valuable, whereas cost criteria are the opposite. From a medical point of view, all criteria of the serological/protein biomarkers are considered important except for C2 = 'C-reactive protein' and C3 = 'IL-6 (pg/mL, cytokines)', which are considered as cost criteria. Thus, transferring physicians' preferences and experiences to an expert system can be proven effective. TOPSIS allocates the scores to each alternative on the basis of their geometric distance from positive and negative ideal solutions. The best alternative is selected, which according to this technique obtains the shortest geometric distance to the positive ideal solution and longest geometric distance to the negative ideal solution. The results of patients' prioritisation are ranked in descending order, indicating that the patient in order 1 has the poorest critical health condition, and the patient in order 80 has the least critical health condition. In the same context, the results of donors' prioritisation are also ranked in a descending order, indicating that the donor in order 1 is the least efficient donor, and the donor in order 80 is the most efficient donor. The steps of the TOPSIS method [35] are described as follows.

A. Construction of the Normalised Decision Matrix

This process may transform the various attribute dimensions into non-dimensional attributes. This process enables comparison across the attributes. The matrix $(x_{ij})_{m*n}$ is then normalised from $(x_{ij})_{m*n}$ to the matrix, $R = (r_{ij})_{m*n}$ by using the normalisation method shown in Eq. (8):

$$r_{ij} = x_{ij} / \sqrt{\sum_{i=1}^{m} x_{ij}^2} \tag{8}$$

This process results in a new matrix R, where R is shown as follows:

$$R = \begin{bmatrix} r_{11} & r_{12} & \dots & r_{1n} \\ r_{21} & r_{22} & \dots & r_{2n} \\ \vdots & \vdots & \vdots & \vdots \\ r_{m1} & r_{m2} & \dots & r_{mn} \end{bmatrix} \tag{9}$$

B. Construction of the Weighted Normalised Decision Matrix

In this process, a set of weights, $w = w_1, w_2, w_3, \dots, w_j, \dots, w_n$, from the decision maker is accommodated to the normalised DM. The resulting matrix can be calculated by multiplying each column from the normalised DM (R) with its associated weight w_j. Notably, the set of weights is equal to 1, as illustrated in Eq. (10).

$$\sum_{j=1}^{m} w_j = 1 \tag{10}$$

This process results in a new matrix V, where V is shown as follows:

$$V = \begin{bmatrix} v_{11} & v_{12} & \dots & v_{1n} \\ v_{21} & v_{22} & \dots & v_{2n} \\ \vdots & \vdots & \vdots & \vdots \\ v_{m1} & v_{m2} & \dots & v_{mn} \end{bmatrix} = \begin{bmatrix} w_1 r_{11} & w_2 r_{12} & \dots & w_n r_{1n} \\ w_1 r_{21} & w_2 r_{22} & \dots & w_n r_{2n} \\ \vdots & \vdots & \vdots & \vdots \\ w_1 r_{m1} & w_2 r_{m2} & \dots & w_n r_{mn} \end{bmatrix} \tag{11}$$

C. Determining the Ideal and Negative Ideal Solutions

In this process, two artificial alternatives, A^* (the ideal alternative) and A^- (the negative ideal alternative), are defined by Eqs. (12) and (13), respectively:

$$A^* = \left\{ \left(\left(\max_i v_{ij} | j \in J \right), \left(\min v_u | j \in J^- \right) | i = 1, 2, \dots, m \right) \right\} = \left\{ v_1^*, v_2^*, \dots, v_j^*, \cdots v_n^* \right\} \tag{12}$$

$$A^- = \left\{ \left(\left(\min_i v_{ij} | j \in J \right), \left(\max_i v_{ij} | j \in J^- \right) | i = 1, 2, \dots, m \right) \right\} = \left\{ v_1^-, v_2^-, \dots, v_j^-, \cdots v_n^- \right\} \tag{13}$$

where J is the subset of $\{i = 1, 2, \dots, m\}$, which presents the benefit attribute (i.e., offering an increasing utility with high values), and J^- is the complement set of J. The opposite can be added for the cost-type attribute denoted by J^c.

D. Separation-Measurement Calculation Based on Euclidean Distance

In this process, separation measurement is performed by calculating the distance between each alternative in V and the ideal vector A^* by using the Euclidean distance, which is given by Eq. (14):

$$S_{i^*} = \sqrt{\sum_{j=1}^{n} \left(v_{ij} - v_j^* \right)^2}, i = (1, 2, \cdots m) \tag{14}$$

Similarly, the separation measurement for each alternative in 'V from the negative ideal A^-' is given by Eq. (15):

$$S_{i^-} = \sqrt{\sum_{j=1}^{n} \left(v_{ij} - v_j^-\right)^2}, i = (1, 2, \cdots m) \quad (15)$$

At the end of step 4, two values, namely, S^*_i and S^-_i, for each alternative have been counted, and these two values represent the distance between each alternative and the ideal and negative ideal.

E. Closeness to the Ideal-Solution Calculation

In this process, the closeness of Ai to the ideal solution A^* is defined, as shown in Eq. (16):

$$C^*_i = S_i/(S_i + S_i), 0 < C^*_i < 1, i = (1, 2, \cdots m) \quad (16)$$

$C^*_i = 1$ if and only if $Ai = A^-$; similarly, $C^*_i = 0$ if and only if $A_i = A^-$.

F. Ranking the Alternative According to Closeness to the Ideal Solution

The set of the alternative Ai can be ranked according to the descending order of C^*_i, indicating that a higher value corresponds with better performance.

G. Group Decision-Making (GDM) Context

GDM is a situation faced when the decision required more than one decision-maker to select the best alternative. GDM methods systematically collect and combine the knowledge and judgment of experts in respiratory diseases. In the group context, each expert gives his/her judgment to the serological/protein biomarker COVID-19 criteria that require subjective judgment. The idea of GDM is to aggregate the result of multiple decisions from the three experts into one unique decision using the arithmetic mean. The academic literature in the area of GDM configurations is applied for several medical domains [94, 95]. In this study, GDM is used to combine the ranking results extracted from each expert preference, and then these ranks are aggregated into one final prioritisation of patients and donors. The use of aggregation can eliminate the variation amongst the obtained results from experts and unify a unique rank.

2.3.3 Matching components

This stage develops a new process for intelligent matching between prioritised patients and prioritised donors across identified hospitals. The rules that enable patient matching with the suitable donors are presented as follows.

Rule1: IF PATIENT GROUP ∈ (A), THEN COMPATIBLE PLASMA DONOR is (A) or (O)

Rule2: IF PATIENT GROUP ∈ (B), THEN COMPATIBLE PLASMA DONOR is (B) or (O)

Rule3: IF PATIENT GROUP ∈ (AB), THEN COMPATIBLE PLASMA DONOR is (AB) or (A) or (B) or (O)

Rule4: IF PATIENT GROUP ∈ (O), THEN COMPATIBLE PLASMA DONOR is (O)

At the end of this step, the transfusion of sufficient CPs from suitable donors to the proper patients can be demonstrated. This transfusion-rescue intelligent process can yield a balancing solution in either centralised or decentralised telemedicine connections and can thus address the lack of CPs.

2.4 Phase 4: Objective validation

The results are validated by utilising the objective validation in accordance with previously described methods [66]. The following steps are conducted for each ranking result (patients/donors) to ensure that the results are statistically ranked.

1. The final prioritisation results are categorised into four equal groups, with each group comprising 20 patients/donors. However, the number of groups or the alternative number within each group does not affect the validation result [80].
2. The mean ± standard deviation (M ± SD) of each group is obtained on the basis of the normalisation of patient/donor datasets. The first group is statistically proven to be the highest amongst all other groups. The second group must be lower than or equal to those of the first group. The third group must be lower than those of the first and second groups or equal to those of the second group. The fourth group must be lower than those of the first, second, and third groups or equal to those of the third group [96].

Equation (17) indicates the mean ($\overline{x}$) that represents the average of the sum of all the observed results from the sample divided by the total number (n):

$$\overline{x} = \frac{1}{n} \sum_{i=1}^{n} x_i, \quad (17)$$

Equation (18) presents the measurement of the standard deviation to quantify the variation amount or dispersion of a set of data values.

$$s = \sqrt{\frac{1}{N-1} \sum_{i=1}^{N} \left(x_i - \overline{x}\right)^2} \quad (18)$$

3 Results and discussion

This section presents the results of the prioritisation CP-transfusion-rescue intelligent framework. The results of weights of the serological/protein biomarker criteria based on the AHP method for the three experts are presented. Afterwards, individual TOPSIS configurations are applied to provide the ranks of the three experts considering the obtained weights of serological/protein biomarkers. Additionally, the GDM TOPSIS context is applied to eliminate the variation amongst the obtained results from the experts and unify a unique rank. Finally, the results of the intelligent matching component and objective validation are operated in different sections. The sequences of results are illustrated as follows.

3.1 AHP weighting results

The AHP results are presented and explained after applying all previously illustrated steps. The results of the weights for the serological/protein biomarker criteria present the importance of each attribute based on the three experts. The weighting results of the three experts are shown in Table 5.

Table 5 shows that the first expert has given 'C3=IL-6 (pg/mL; cytokines)' the highest importance (0.407), whereas 'C2=C-reactive protein, mg/L' has received the lowest importance (0.067). The second expert has given 'C5=IgM ELISA titre' the highest importance (0.491), whereas 'C1=PAO2/FIO2' and 'C4=albumin (g/L)' have received the lowest importance (0.054). The third expert has given 'C1=PAO2/FIO2' the highest importance (0.427), whereas 'C4=albumin (g/L)' has received the lowest importance (0.061). The overall CR for the first, second, and third expert is 0.07, 0.09, and 0.06, respectively, which are considered as Additionally, Therefore, the obtained weights from the three experts are acceptable. At this step, the criteria assess the importance of patients and donors according to the best and poorest CP according to the experts through the AHP method.

3.2 TOPSIS prioritisation results

In this stage, TOPSIS is used in the prioritisation of COVID-19 patients and donors and can rapidly identify the most suitable option. Furthermore, the AHP method can derive the overall weights. Sample results of individual AHP-TOPSIS for the prioritisation of patients and donors of the three experts are shown in Tables 6 and 7 (the samples include the first 10 orders for each result). Meanwhile, the overall prioritisation results of patients and donors of the three experts based on individual TOPSIS are shown in Tables 12 and 13 (Appendix). The presented results consider the following points.

- The set of patients and donors are ranked according to the descending order of *C_ (i*)*, and high values indicate optimal performance for both.
- A patient who is near the high record and far from the poorest record (i.e., the patient that gain order 1) is an optimal health condition case and must be given the lowest priority level. Conversely, the patient who is far the high record and near from the poorest record (i.e., the patient who gains order 80) is in the poorest health condition and must be given the highest priority level.
- A donor who is near the high record and far from the poorest record (i.e., the donor that gain order 1) is the most highly efficient donor and must be matched with the patients in the poorest health condition.

No unique prioritisation results based on the weights obtained from the three experts are found when the TOPSIS method is applied. Results show variances amongst the ranks obtained from the three experts. Considering the GDM TOPSIS context to provide final and unique prioritisation concerning all decision makers is important to address this challenge. Thus, Table 8 shows the sample ranking results for the first 10 patients and donors based on GDM TOPSIS, whereas the overall prioritisation results are shown in Table 14 (Appendix).

For all ranks, the prioritisation of the 80 patients and 80 donors is stated. The set of patients is ranked in descending order starting from the critical health condition to the mild one. Moreover, donor prioritisation is ranked in descending order from the least efficient donor to the most highly efficient one.

3.3 Intelligent matching component results

The result of this section follows the significance of the four rules presented previously to match a proper donor with the

Table 5 Weights of the serological/protein biomarker criteria for the three experts based on AHP

Serological/Protein Biomarker Criteria	C1	C2	C3	C4	C5
First Expert Weights	0.343	0.067	0.407	0.086	0.098
Second Expert Weights	0.054	0.118	0.283	0.054	0.491
Third Expert Weights	0.427	0.199	0.199	0.061	0.113

Table 6 Samples of the first 10 ranks of patient prioritisation based on individual AHP-TOPSIS

Patient Rank	First Expert Results			Second Expert Results			Third Expert Results		
	Patient Identification Information		C_(i*) Final Score	Patients Identification Information		C_(i*) Final Score	Patient Identification Information		C_(i*) Final Score
	Patients	Hospital		Patients	Hospital		Patients	Hospital	
1	P3_AB	H1	0.886284	P16_A	H3	0.808919	P19_AB	H4	0.784513
2	P19_AB	H4	0.810943	P4_O	H1	0.795971	P3_AB	H1	0.762962
3	P14_O	H2	0.750282	P1_O	H1	0.781401	P7_O	H1	0.726115
4	P7_O	H1	0.747701	P14_O	H2	0.731976	P15_O	H2	0.689345
5	P20_AB	H4	0.739635	P9_B	H1	0.677319	P14_O	H2	0.682247
6	P8_AB	H1	0.739048	P14_AB	H2	0.667573	P4_O	H1	0.665293
7	P4_O	H1	0.72548	P13_AB	H2	0.656204	P20_AB	H4	0.658588
8	P1_O	H1	0.698919	P17_O	H3	0.655859	P17_O	H3	0.643114
9	P8_O	H1	0.695913	P3_B	H1	0.650131	P6_AB	H1	0.634803
10	P12_A	H2	0.683078	P17_AB	H3	0.630744	P16_A	H3	0.627233

suitable patient after achieving prioritisation. A sample of 10 results of the matching component stage is shown in Table 9, whereas the overall results are described in Table 15 (Appendix).

As shown in the above-mentioned results, each patient is matched with a suitable CP donor on the basis of prioritisation results. Additionally, the matching between patients and donors is operated across four connected hospitals. For example, patient (P1_A) admitted to hospital 1 obtains the suitable CP from donor (D8_A), who is admitted to hospital 2. In these contexts, balancing across hospitals is achieved for all patients/donors and proven within the four hospitals. Moreover, matching amongst patients and donors could be achieved by the inverse relationship between them. For example, the patient (P3_AB) who gains order 1 with score = 0.74719 is considered the most critical condition amongst all patients, and the suitable donor for this patient is the last donor (D12_B) who gains order 80 with a score of 0.09808 according to Rule 3. Therefore, the intelligent matching process of CP transfusion between patients and donors is tested and verified towards the balancing approach across either centralised or decentralised telemedicine hospitals simultaneously.

Table 7 Samples of the first 10 ranks of donor prioritisation based on individual AHP-TOPSIS

Donor Rank	First Expert Results			Second Expert Results			Third Expert Results		
	Donor Identification Information		C_(i*) Final Score	Donor Identification Information		C_(i*) Final Score	Donor Identification Information		C_(i*) Final Score
	Donors	Hospital		Donors	Hospital		Donors	Hospital	
1	D17_A	H4	0.766737	D20_AB	H4	0.737167	D20_AB	H4	0.584245
2	D8_A	H3	0.755732	D6_A	H3	0.690513	D7_A	H3	0.548145
3	D20_AB	H4	0.718893	D1_A	H1	0.673066	D8_A	H3	0.526714
4	D14_A	H4	0.663588	D17_AB	H4	0.574109	D1_A	H1	0.521456
5	D18_B	H4	0.662994	D8_A	H3	0.551806	D17_A	H4	0.507695
6	D6_O	H3	0.651069	D15_O	H4	0.547102	D2_A	H1	0.498713
7	D11_A	H4	0.640164	D5_B	H2	0.546464	D3_AB	H2	0.483957
8	D6_A	H3	0.540643	D6_O	H3	0.539688	D15_O	H4	0.427792
9	D1_A	H1	0.534718	D16_O	H4	0.532662	D3_A	H2	0.425142
10	D2_A	H1	0.413798	D9_O	H3	0.532389	D8_O	H3	0.422213

Table 8 Samples of the first 10 ranks of patients and donors based on the TOPSIS GDM contexts

Patient/Donor Rank	Patient Ranking Results			Donor Ranking Results		
	Patient Identification Information		C_(i*) Final Score	Donor Identification Information		C_(i*) Final Score
	Patients	Hospital		Donors	Hospital	
1	P3_AB	H1	0.74719	D20_AB	H4	0.68010
2	P4_O	H1	0.72891	D8_A	H2	0.61142
3	P14_O	H2	0.72150	D17_A	H4	0.58684
4	P7_O	H1	0.68548	D1_A	H1	0.57641
5	P19_AB	H4	0.68329	D6_O	H3	0.53056
6	P16_A	H3	0.68104	D6_A	H3	0.52952
7	P20_AB	H4	0.67497	D14_A	H4	0.50619
8	P1_O	H1	0.66003	D18_B	H4	0.49735
9	P8_AB	H1	0.64651	D11_A	H4	0.48283
10	P17_O	H3	0.59967	D7_A	H3	0.47616

3.4 Validation results

In this section, as explained in phase 6, objective validation can be achieved by dividing the prioritisation results for patients and donors into four equal groups. Each group comprises 20 patients. The mean ± SD is calculated for each group on the basis of normalisation scores generated by TOPSIS to ensure that the prioritised patients/donors undergo systematic ranking. The prioritisation results presented in Table 8 are visualised in graphical formats (Fig. 7 for patients and Fig. 8 for donors) after categorising them into four groups based on descending patients' scores for comparison.

The initial observation of the ranking results of the four patients and donors groups show that the groups are systematically distributed as the ranking results of the second group starting from the end of the ranking results of the first group and so on for other groups. Statistical analysis is performed amongst the patient groups, and Eqs. (15) and (16) are applied to obtain the M ± SD. In the first group, the value is M = 0.14538 ± 0.08301. The first group obtains the highest score amongst the four groups. The second group has a value of M = 0.11977 ± 0.07101 and a lower score than the first group but higher scores than the third and fourth groups. The third group has a value of M = 0.10887 ± 0.05795 and a lower score than the first, second, and third groups but a higher score than the fourth groups. The fourth group has a value of M = 0.09705 ± 0.04771 and has the lowest scores amongst the four groups. Furthermore, statistical analysis is performed amongst the donor groups, and Eqs. (15) and (16) are applied to obtain the M ± SD. In the first group, the value is M = 0.12993 ± 0.08581. The first group obtains the highest score amongst the four groups. The second group has a value of M = 0.10759 ± 0.07600 and has a lower score than the first group but higher scores than the third and fourth groups. The third group has a value of M = 0.10041 ± 0.07080 and has a lower score than the first, second, and third groups but higher scores than the

Table 9 Matching results between patients and donors

Patient Rank	Patients/admitted hospital	Suitable CP donors/admitted hospital
1	P3_AB/H1	D13_AB/H4
2	P4_O/H1	D14_O/H4
3	P14_O/H2	D5_O/H2
4	P7_O/H1	D19_O/H4
5	P19_AB/H4	D8_AB/H3
6	P16_A/H3	D19_A/H3
7	P20_AB/H4	D5_AB/H2
8	P1_O/H1	D13_O/H4
9	P8_AB/H1	D4_AB/H2
10	P17_O/H3	D12_O/H4

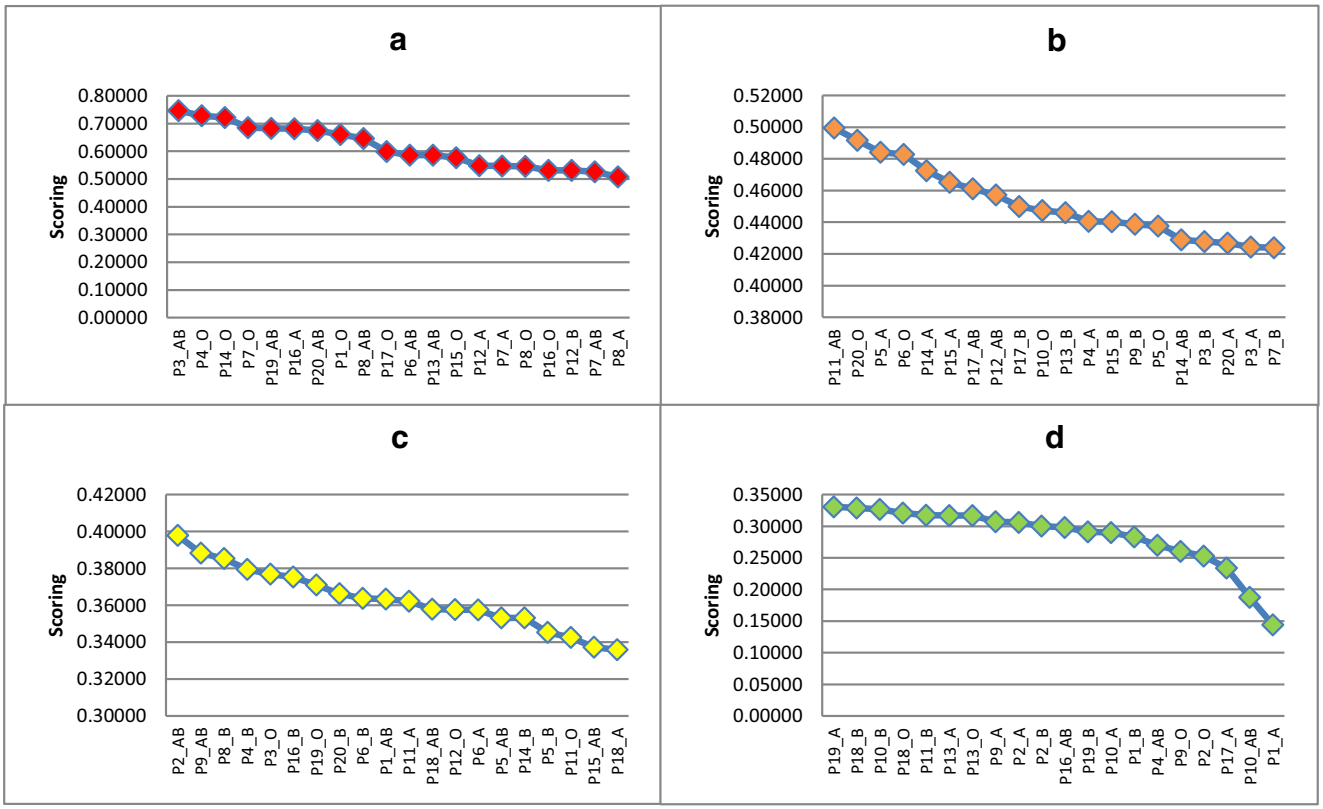

Fig. 7 Results of the four groups of patients. **a** First group. **b** Second group. **c** Third group. **d** Fourth group

fourth groups. The fourth group has a value of M = 0.08921 ± 0.06532 and the lowest scores amongst the four groups. The statistical results for patients and donors indicate that the results have undergone systematic ranking and are valid.

4 Claim points

The claim points of this study can be summarised as follows.

- *Serological/Protein Biomarkers and Strength Weights*: Even within the area of infectious-disease research, various disciplines in clinical research such as molecular biology, microbiology, mycology, and epidemiology are involved. Despite this multidisciplinary mix, some efforts have been made to prioritise patients based on the criteria that are applicable and defined. According to the scope of the presented study which is COVID-19, the indication of the safety and suitability of CP for patients and donors is demarcated through the constructed weights of biomarker criteria for the first time based on three experts.
- *New COVID-19 Datasets and Evaluation:* The augmented dataset is generated by a specialised expert based on standard medical-reference ranges that are applicable to patients and donors. Thus, we describe new measurement data about COVID-19-related CPs for patients/donors and release such data for public use. In this context, the transparency of the developed intelligent framework and associated processes is confirmed.
- *Intelligent Matching Component Execution:* We We demonstrate the enhanced mechanical priority of two-dimensional patients/donors by using the new components of the four rules. Thus, the prioritisation results make the scoring more transparent for matching each of the critical patients with suitable donors according to their severity and blood types explicitly. The transfusion and balancing approach across the distributed telemedicine hospitals are involved in improving hospital management. In the case of a new patient or donor admitted to any hospital, the DM can repeat the rank across the distributed hospitals in real time.
- *Scalable Transfusion of CP within Centralised/Decentralised Connected Hospitals*: Identifying and selecting eligible donors with a sufficient amount of plasma for efficient utilisation can be challenging within distributed hospitals. The selection of the best CP for critical COVID-19 patients is also challenging because this process is considered as a problem of MCDM, which complies with the national health requirements and known standard routine procedures [97]. The present study addresses these issues and indicates valid results on the basis of a fully automated intelligent computing framework.

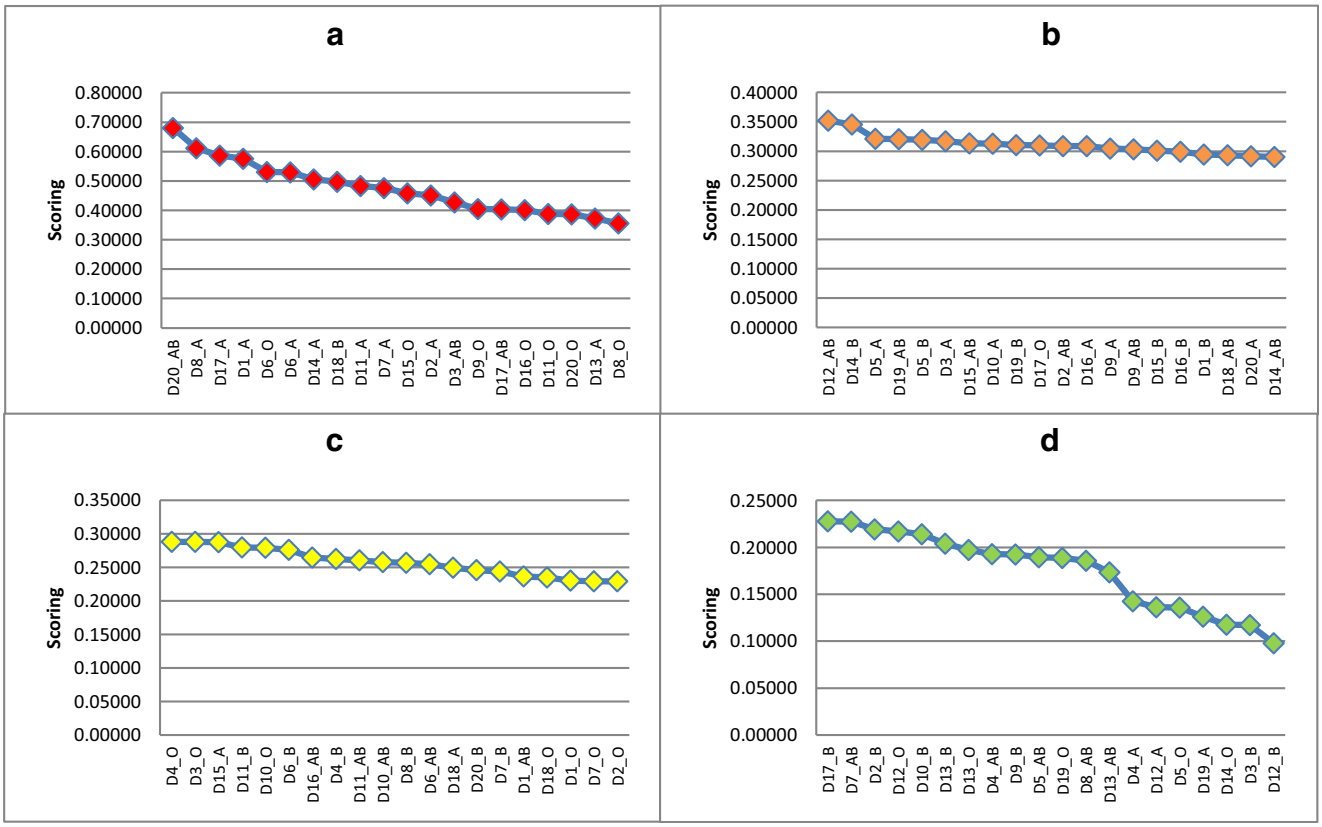

Fig. 8 Results of the four groups of donors. **a** First group. **b** Second group. **c** Third group. **d** Fourth group

Thus, the transfusion of the CPs amongst patients and donors in either centralised or decentralised connected hospitals is accomplished, and the shortages of acute plasma in any hospital can be avoided.

5 Conclusion

The COVID-19 pandemic is critical; it requires rapid scalable load balancing, collaborative management, and decision making. This paper develops a novel interoperability CP-transfusion-rescue intelligent framework across centralised/decentralised telemedicine hospitals on the basis of the matching component process to provide an efficient CP from eligible donors to the most critical patients using the MCDM methods. A dataset, including COVID-19 patients/donors that have met the important criteria in the virology field, is augmented to improve the developed framework and achieve multiface requirements that can address multidimensional problems in the risk management of the COVID-19 pandemic. One main characteristic of the methodology described in this study is that it addresses the prioritisation task on the basis of the same DM for patients and donors. However, the field of COVID-19 infectious diseases has numerous aspects that need to be addressed comprehensively and continuously because this pandemic has shocked clinical organisations for the first time in decades. Therefore, various questions have emerged, and they should be assessed carefully before establishing the prioritisation characteristic intelligent framework. Do the five criteria cover all clinical characteristic aspects for the prioritisation configurations of patients and donors? If other criteria are missing, then how could the newly defined clinical criteria be added to the proposed DMs to be sufficient for the prioritisation process? How large should the group of participating clinical experts be and how should it be composed? If the methodology of prioritisation follows this COVID-19 clinical characteristic approach, then the original purpose for the transfusion of CP would be severely constrained and would result in desirable scalable load balancing amongst patients and donors within telemedicine hospitals. However, this new type of disease often requires more methodological approaches. Therefore, a patient/donor priority list may still be beneficial if decision makers keep in mind how to identify the importance of COVID-19 criteria from clinical prospective studies after collecting baseline information.

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Appendix 1

Table 10 Augmented dataset for patients

Patients	Serological/Protein Biomarkers Measurements				
	PAO2/FIO2 >300	C-reactive protein, mg/L (<8)	IL-6, pg/mL (Cytokines) (normal range, 0-7)	Albumin (40–55) g/l	IgM ELISA titer (<200)titers (<200)
Blood group A					
P1_A	128	93	244	21	94.09
P2_A	128	88	294	26	237.65
P3_A	146	59	197	25	265.78
P4_A	143	124	99	11	181.39
P5_A	201	56	277	19	298.76
P6_A	267	84	291	19	90.21
P7_A	214	110	125	34	227.95
P8_A	262	80	344	24	260.93
P9_A	183	115	318	11	188.18
P10_A	131	138	285	17	246.38
P11_A	233	117	292	19	159.08
P12_A	189	99	79	18	139.68
P13_A	134	135	264	23	257.05
P14_A	106	127	78	13	173.63
P15_A	215	60	358	22	265.78
P16_A	203	55	104	27	297.79
P17_A	108	95	332	26	198.85
P18_A	121	100.98	115	13	142.59
P19_A	200	111.18	170	16	127.07
P20_A	211	154.02	280	19	258.02
Blood group B					
P1_B	136	83.64	168	24	154
P2_B	113	68.34	162	22	165
P3_B	103	63.24	151	28	264
P4_B	258	133.62	270	27	141
P5_B	131	55.08	142	29	136
P6_B	115	125.46	135	26	212
P7_B	148	117.3	139	13	247
P8_B	159	99.96	292	28	288
P9_B	111	120.36	123	12	270
P10_B	147	125.46	231	17	241
P11_B	174	105.06	141	14	111
P12_B	263	84.66	197	13	236
P13_B	276	160.14	211	10	174
P14_B	118	136.68	155	13	240
P15_B	201	104.04	180	25	222
P16_B	211	56.1	242	19	148
P17_B	284	102	299	10	183
P18_B	118	162.18	286	29	288
P19_B	139	61.2	188	10	153
P20_B	159	143.82	260	26	270

Table 10 (continued)

Patients	Serological/Protein Biomarkers Measurements				
	PAO2/FIO2 >300	C-reactive protein, mg/L (<8)	IL-6, pg/mL (Cytokines) (normal range, 0-7)	Albumin (40–55) g/l	IgM ELISA titer (<200)titers (<200)
Blood group AB					
P1_AB	167	69.36	216	29	199
P2_AB	183	100.98	267	12	262
P3_AB	288	98.94	72	27	186
P4_AB	129	63.24	186	28	133
P5_AB	112	124.44	173	31	248
P6_AB	280	116.28	167	17	268
P7_AB	266	122.4	158	20	207
P8_AB	208	112.2	79	27	206
P9_AB	212	74.46	166	28	129
P10_AB	138	102	274	18	145
P11_AB	234	88.74	191	10	240
P12_AB	259	130.56	168	24	163
P13_AB	225	98.94	128	29	255
P14_AB	109	129.54	129	25	269
P15_AB	183	123.42	190	21	174
P16_AB	141	66.3	269	12	199
P17_AB	143	67.32	134	16	246
P18_AB	280	124.44	258	16	90
P19_AB	261	61.2	81	26	137
P20_AB	207	55.08	77	15	198
Blood group O					
P1_O	182	141.78	78	31	263
P2_O	158	54.06	282	21	94
P3_O	206	55.08	233	22	150
P4_O	232	88.74	90	23	271
P5_O	188	78.54	267	17	285
P6_O	260	158.1	214	21	220
P7_O	272	94.86	93	25	202
P8_O	196	82.62	77	16	100
P9_O	159	142.8	245	16	176
P10_O	218	79.56	191	22	201
P11_O	158	55.08	258	26	188
P12_O	192	144.84	194	19	185
P13_O	105	92.82	124	22	149
P14_O	282	145.86	90	11	259
P15_O	285	82.62	151	27	208
P16_O	261	80.58	298	26	285
P17_O	250	79.56	149	19	268
P18_O	171	169.32	243	13	211
P19_O	171	57.12	294	28	208
P20_O	268	132.6	232	11	228

Table 11 Augmented dataset for donors

Donors	Serological/Protein Biomarkers Measurements				
	PAO2/FIO2 >300	C-reactive protein, mg/L (<8)	IL-6, pg/mL (Cytokines) (normal range, 0-7)	Albumin (40–55) g/l	IgM ELISA titer (<200)
Blood group A					
D1_A	453	1.3	1.4	41.6	64.99
D2_A	524	2	2.1	50.8	51.41
D3_A	301	0.54	4.1	43.8	44.62
D4_A	331	5.4	5.5	38.9	43.65
D5_A	450	4.41	2	54.7	34.92
D6_A	347	3.3	1.22	50	66.93
D7_A	541	1.2	2.5	47.5	56.26
D8_A	380	1.3	0.8	43.9	39.77
D9_A	471	4.7	3.6	45.7	44.62
D10_A	318	1.8	2.22	45.45	52.38
D11_A	304	5.88	0.9	40.4	32.98
D12_A	341	2.94	3.5	49.49	33.95
D13_A	462	2.94	3.5	42.42	59.17
D14_A	326	1.96	0.9	50.5	32.01
D15_A	369	5.88	2.6	48.48	51.41
D16_A	495	6.86	3.5	51.51	41.71
D17_A	456	3.92	0.9	53.53	37.83
D18_A	342	6.86	4.4	54.54	57.23
D19_A	307	6.86	4.4	49.49	40.74
D20_A	335	0.98	5.2	55.55	55.29
Blood group B					
D1_B	425	3.96	1.98	44.44	32.01
D2_B	301	3.96	5.94	44.44	57.23
D3_B	347	6.93	3.96	45.45	33.95
D4_B	420	1.98	2.97	53.53	38.8
D5_B	318	2.97	2.97	44.44	66.93
D6_B	399	3.96	4.95	49.49	54.32
D7_B	340	1.98	4.95	40.4	55.29
D8_B	358	2.97	1.98	53.53	33.95
D9_B	307	6.93	2.97	43.43	44.62
D10_B	394	5.94	5.94	54.54	44.62
D11_B	326	0.99	6.93	46.46	56.26
D12_B	334	3.96	3.96	43.43	32.01
D13_B	423	3.96	5.94	49.49	37.83
D14_B	485	5.94	2.97	51.51	47.53
D15_B	352	0.99	4.95	43.43	56.26
D16_B	304	0.99	4.95	40.4	60.14
D17_B	396	3.96	6.93	45.45	47.53
D18_B	387	3.96	0.99	54.54	32.98
D19_B	403	6.93	4.95	50.5	62.08
D20_B	358	0.99	4.95	40.4	44.62
Blood group AB					
D1_AB	449	2.97	4.95	47.47	37.83
D2_AB	462	5.94	4.95	44.44	50.44
D3_AB	478	0.99	3.96	49.49	62.08

Table 11 (continued)

Donors	Serological/Protein Biomarkers Measurements				
	PAO2/FIO2 >300	C-reactive protein, mg/L (<8)	IL-6, pg/mL (Cytokines) (normal range, 0-7)	Albumin (40–55) g/l	IgM ELISA titer (<200)
D4_AB	375	3.96	6.93	50.5	44.62
D5_AB	418	5.94	3.96	42.42	33.95
D6_AB	403	6.93	5.94	43.43	51.41
D7_AB	457	5.94	4.95	49.49	35.89
D8_AB	325	0.99	3.96	48.48	32.01
D9_AB	486	5.94	3.96	41.41	43.65
D10_AB	391	5.94	6.93	50.5	54.32
D11_AB	314	2.97	2.97	48.48	54.32
D12_AB	458	6.93	1.98	44.44	41.71
D13_AB	366	2.97	6.93	45.45	42.68
D14_AB	346	2.97	6.93	50.5	67.9
D15_AB	368	4.95	3.96	54.54	65.96
D16_AB	318	0.99	5.94	53.53	52.38
D17_AB	382	5.94	1.98	51.51	64.99
D18_AB	407	2.97	6.93	41.41	58.2
D19_AB	370	6.93	2.97	49.49	62.08
D20_AB	417	0.99	0.99	50.5	58.2
Blood group O					
D1_O	445	5.94	3.96	55.55	35.89
D2_O	419	6.93	4.95	47.47	42.68
D3_O	417	1.98	2.97	40.4	44.62
D4_O	460	1.98	6.93	45.45	45.59
D5_O	330	2.97	6.93	48.48	41.71
D6_O	358	2.97	0.99	54.54	45.59
D7_O	458	2.97	6.93	55.55	35.89
D8_O	483	1.98	2.97	54.54	46.56
D9_O	449	1.98	2.97	47.47	64.02
D10_O	457	5.94	3.96	40.4	43.65
D11_O	486	4.95	5.94	55.55	66.93
D12_O	434	1.98	6.93	41.41	36.86
D13_O	399	6.93	4.95	44.44	40.74
D14_O	382	4.95	6.93	52.52	29.1
D15_O	478	3.96	1.98	45.45	61.11
D16_O	444	1.98	2.97	52.52	64.02
D17_O	398	2.97	6.93	43.43	64.02
D18_O	329	4.95	6.93	46.46	59.17
D19_O	437	4.95	5.94	49.49	32.98
D20_O	471	2.97	4.95	42.42	66.93

Table 12 Overall ranks of 80 patients prioritization based on individual AHP-TOPSIS for three experts

1st Expert Results			2nd Expert Results			3rd Expert Results		
Patients Identification Information		C_(i*) Final Score	Patients Identification Information		C_(i*) Final Score	Patients Identification Information		C_(i*) Final Score
Patients	Hospital		Patients	Hospital		Patients	Hospital	
P3_AB	H1	0.886284	P16_A	H3	0.808919	P19_AB	H4	0.784513
P19_AB	H4	0.810943	P4_O	H1	0.795971	P3_AB	H1	0.762962
P14_O	H2	0.750282	P1_O	H1	0.781401	P7_O	H1	0.726115
P7_O	H1	0.747701	P14_O	H2	0.731976	P15_O	H2	0.689345
P20_AB	H4	0.739635	P9_B	H1	0.677319	P14_O	H2	0.682247
P8_AB	H1	0.739048	P14_AB	H2	0.667573	P4_O	H1	0.665293
P4_O	H1	0.72548	P13_AB	H2	0.656204	P20_AB	H4	0.658588
P1_O	H1	0.698919	P17_O	H3	0.655859	P17_O	H3	0.643114
P8_O	H1	0.695913	P3_B	H1	0.650131	P6_AB	H1	0.634803
P12_A	H2	0.683078	P17_AB	H3	0.630744	P16_A	H3	0.627233
P16_A	H3	0.606973	P20_AB	H4	0.626686	P12_B	H2	0.618863
P14_A	H2	0.560024	P8_AB	H1	0.625991	P7_AB	H1	0.606251
P15_O	H2	0.536998	P5_A	H1	0.624698	P16_O	H3	0.602225
P13_AB	H2	0.527616	P6_AB	H1	0.623437	P17_B	H3	0.593097
P7_A	H1	0.521426	P3_A	H1	0.613166	P8_A	H1	0.592788
P4_A	H1	0.501926	P7_B	H1	0.605747	P12_AB	H2	0.575087
P6_AB	H1	0.500115	P5_O	H1	0.602552	P8_AB	H1	0.57448
P17_O	H3	0.500046	P16_O	H3	0.596653	P13_AB	H2	0.574055
P7_AB	H1	0.493374	P8_B	H1	0.595689	P6_A	H1	0.573011
P12_AB	H2	0.465017	P3_AB	H1	0.592334	P20_O	H4	0.570277
P12_B	H2	0.438512	P7_A	H1	0.58831	P13_B	H2	0.568594
P13_B	H2	0.433319	P18_B	H3	0.58774	P18_AB	H3	0.567191
P6_O	H1	0.41936	P7_O	H1	0.582611	P6_O	H1	0.553197
P20_O	H4	0.414859	P5_AB	H1	0.573807	P11_AB	H2	0.551208
P18_AB	H3	0.41028	P20_B	H4	0.570063	P8_O	H1	0.549262
P17_B	H3	0.406853	P14_B	H2	0.564311	P4_B	H1	0.535843
P18_A	H3	0.400997	P15_A	H2	0.559983	P7_A	H1	0.530552
P9_AB	H1	0.399452	P2_AB	H1	0.557422	P15_A	H2	0.523621
P11_AB	H2	0.398956	P11_AB	H2	0.54805	P16_B	H3	0.520682
P16_O	H3	0.396287	P8_A	H1	0.547855	P10_O	H1	0.520308
P6_A	H1	0.384405	P13_A	H2	0.544517	P5_A	H1	0.515585
P4_B	H1	0.383991	P20_A	H4	0.540935	P3_O	H1	0.515107
P8_A	H1	0.383015	P12_B	H2	0.537488	P12_A	H2	0.514782
P17_AB	H3	0.377267	P14_A	H2	0.525715	P9_AB	H1	0.512719
P9_B	H1	0.37621	P10_B	H1	0.521287	P1_O	H1	0.499758
P10_O	H1	0.375685	P6_B	H1	0.516879	P11_A	H2	0.484766
P11_B	H2	0.373836	P10_A	H1	0.51471	P15_B	H2	0.449937
P14_AB	H2	0.363693	P15_B	H2	0.5078	P20_A	H4	0.431079
P15_B	H2	0.363396	P2_A	H1	0.503824	P5_O	H1	0.42917
P7_B	H1	0.359767	P15_O	H2	0.502961	P19_O	H4	0.422135
P13_O	H2	0.359723	P20_O	H4	0.489727	P19_A	H4	0.420023
P19_A	H4	0.355443	P4_A	H1	0.487784	P11_O	H2	0.399588
P5_B	H1	0.341733	P7_AB	H1	0.479225	P3_A	H1	0.387438
P6_B	H1	0.34124	P6_O	H1	0.475615	P1_AB	H1	0.385577
P11_A	H2	0.33166	P19_AB	H4	0.454427	P2_O	H1	0.383869

Table 12 (continued)

1st Expert Results			2nd Expert Results			3rd Expert Results		
Patients Identification Information		C_(i*) Final Score	Patients Identification Information		C_(i*) Final Score	Patients Identification Information		C_(i*) Final Score
Patients	Hospital		Patients	Hospital		Patients	Hospital	
P16_B	H3	0.319742	P12_A	H2	0.44901	P12_O	H2	0.379677
P3_O	H1	0.319142	P10_O	H1	0.446525	P2_AB	H1	0.376916
P12_O	H2	0.31455	P19_O	H4	0.445208	P17_AB	H3	0.375411
P5_A	H1	0.312335	P18_O	H3	0.434178	P5_B	H1	0.374349
P15_A	H2	0.311932	P1_AB	H1	0.433836	P15_AB	H2	0.359753
P3_B	H1	0.3108	P16_AB	H3	0.413322	P11_B	H2	0.356557
P20_A	H4	0.308699	P11_O	H2	0.398876	P9_A	H1	0.33866
P15_AB	H2	0.303549	P17_A	H3	0.392736	P19_B	H4	0.333125
P14_B	H2	0.281547	P8_O	H1	0.391768	P4_A	H1	0.332214
P5_O	H1	0.281045	P12_O	H2	0.378872	P14_A	H2	0.331591
P3_A	H1	0.27223	P2_B	H1	0.358304	P8_B	H1	0.324628
P1_AB	H1	0.270697	P9_A	H1	0.356457	P3_B	H1	0.32238
P1_B	H1	0.269371	P17_B	H3	0.349989	P4_AB	H1	0.31215
P5_AB	H1	0.265328	P15_AB	H2	0.348087	P16_AB	H3	0.310323
P2_B	H1	0.263247	P13_O	H2	0.347496	P7_B	H1	0.306191
P2_AB	H1	0.259332	P18_A	H3	0.344381	P18_O	H3	0.297537
P19_O	H4	0.245389	P13_B	H2	0.336169	P20_B	H4	0.294602
P4_AB	H1	0.240941	P12_AB	H2	0.33184	P2_B	H1	0.279074
P8_B	H1	0.235501	P9_O	H1	0.328232	P1_B	H1	0.27047
P20_B	H4	0.234221	P5_B	H1	0.319709	P9_B	H1	0.262294
P19_B	H4	0.231782	P1_B	H1	0.309748	P18_A	H3	0.26198
P18_O	H3	0.231169	P19_B	H4	0.307888	P14_AB	H2	0.255414
P11_O	H2	0.229241	P3_O	H1	0.296477	P9_O	H1	0.25272
P9_A	H1	0.226233	P16_B	H3	0.285519	P10_B	H1	0.251555
P10_B	H1	0.207789	P11_A	H2	0.270201	P2_A	H1	0.243476
P2_O	H1	0.200036	P4_AB	H1	0.256901	P13_O	H2	0.243129
P9_O	H1	0.199245	P9_AB	H1	0.252691	P6_B	H1	0.232698
P18_B	H3	0.187665	P10_AB	H1	0.223641	P13_A	H2	0.221635
P13_A	H2	0.184238	P11_B	H2	0.22145	P5_AB	H1	0.220233
P2_A	H1	0.170126	P4_B	H1	0.218409	P14_B	H2	0.213446
P16_AB	H3	0.169731	P19_A	H4	0.216628	P18_B	H3	0.21112
P10_A	H1	0.156469	P2_O	H1	0.175417	P10_AB	H1	0.199954
P1_A	H1	0.141967	P6_A	H1	0.114848	P10_A	H1	0.199111
P10_AB	H1	0.138655	P1_A	H1	0.102404	P1_A	H1	0.188651
P17_A	H3	0.12837	P18_AB	H3	0.095855	P17_A	H3	0.180453

Table 13 Overall ranks of 80 donors prioritization based on individual AHP-TOPSIS for three experts

1st Expert Results			2nd Expert Results			3rd Expert Results		
Patients Identification Information		C_(i*) Final Score	Patients Identification Information		C_(i*) Final Score	Patients Identification Information		C_(i*) Final Score
Donors	Hospital		Donors	Hospital		Donors	Hospital	
D17_A	H4	0.766737	D20_AB	H4	0.737167	D20_AB	H4	0.584245
D8_A	H3	0.755732	D6_A	H3	0.690513	D7_A	H3	0.548145
D20_AB	H4	0.718893	D1_A	H1	0.673066	D8_A	H3	0.526714
D14_A	H4	0.663588	D17_AB	H4	0.574109	D1_A	H1	0.521456
D18_B	H4	0.662994	D8_A	H3	0.551806	D17_A	H4	0.507695
D6_O	H3	0.651069	D15_O	H4	0.547102	D2_A	H1	0.498713
D11_A	H4	0.640164	D5_B	H2	0.546464	D3_AB	H2	0.483957
D6_A	H3	0.540643	D6_O	H3	0.539688	D15_O	H4	0.427792
D1_A	H1	0.534718	D16_O	H4	0.532662	D3_A	H2	0.425142
D2_A	H1	0.413798	D9_O	H3	0.532389	D8_O	H3	0.422213
D15_O	H4	0.400626	D15_AB	H4	0.516875	D18_B	H4	0.411704
D7_A	H3	0.391255	D20_O	H4	0.516373	D14_A	H4	0.409338
D12_AB	H4	0.374731	D3_AB	H2	0.510694	D6_O	H3	0.400915
D5_A	H2	0.366625	D14_AB	H4	0.510371	D9_O	H3	0.391128
D1_B	H1	0.347927	D11_O	H4	0.506859	D11_O	H4	0.390001
D17_AB	H4	0.341155	D19_AB	H4	0.504252	D16_A	H4	0.389733
D8_B	H3	0.310224	D7_A	H3	0.489081	D14_B	H4	0.389617
D8_O	H3	0.30895	D17_A	H4	0.486081	D16_O	H4	0.385066
D14_B	H4	0.307588	D17_O	H4	0.482839	D20_O	H4	0.384847
D16_A	H4	0.292773	D16_B	H4	0.479175	D13_A	H4	0.375746
D9_O	H3	0.289059	D19_B	H4	0.474147	D9_AB	H3	0.375283
D16_O	H4	0.28668	D13_A	H4	0.471106	D12_AB	H4	0.373154
D3_AB	H2	0.285781	D14_A	H4	0.44564	D5_A	H2	0.365358
D13_A	H4	0.271212	D10_A	H3	0.444453	D11_A	H4	0.364972
D9_AB	H3	0.270683	D11_A	H4	0.443351	D9_A	H3	0.362415
D11_O	H4	0.269023	D2_A	H1	0.441505	D4_O	H2	0.359316
D9_A	H3	0.266369	D15_B	H4	0.441453	D6_A	H3	0.357396
D10_A	H3	0.26265	D18_O	H4	0.43704	D2_AB	H1	0.341342
D20_O	H4	0.259857	D18_A	H4	0.432796	D7_O	H3	0.334193
D4_B	H2	0.246033	D18_AB	H4	0.431051	D10_O	H3	0.333499
D3_O	H2	0.24153	D20_A	H4	0.43014	D1_B	H1	0.326476
D10_O	H3	0.240912	D11_B	H4	0.429708	D1_AB	H1	0.325502
D15_A	H4	0.237096	D11_AB	H4	0.429375	D7_AB	H3	0.323743
D2_AB	H1	0.235943	D2_B	H1	0.42278	D4_B	H2	0.319451
D1_O	H1	0.230526	D18_B	H4	0.417339	D3_O	H2	0.316964
D7_AB	H3	0.224468	D7_B	H3	0.414701	D15_B	H4	0.314912
D4_O	H4	0.221377	D15_A	H4	0.401604	D1_O	H1	0.312265
D19_AB	H4	0.220892	D6_B	H3	0.398269	D12_O	H4	0.311765
D7_O	H3	0.21809	D16_AB	H4	0.391845	D20_B	H4	0.306247
D1_AB	H1	0.216447	D10_AB	H3	0.386365	D20_A	H4	0.302403
D5_B	H2	0.201861	D3_A	H2	0.35722	D17_AB	H4	0.297005
D19_O	H2	0.193937	D6_AB	H3	0.354627	D19_O	H4	0.289054
D5_AB	H2	0.193746	D2_AB	H1	0.349268	D11_B	H4	0.287616
D19_B	H4	0.190788	D14_B	H4	0.339489	D16_B	H4	0.285548
D15_AB	H4	0.187655	D8_O	H3	0.3356	D16_AB	H4	0.280959

Table 13 (continued)

1st Expert Results			2nd Expert Results			3rd Expert Results		
Patients Identification Information		C_(i*) Final Score	Patients Identification Information		C_(i*) Final Score	Patients Identification Information		C_(i*) Final Score
Donors	Hospital		Donors	Hospital		Donors	Hospital	
D12_O	H4	0.187542	D12_AB	H4	0.308846	D8_AB	H3	0.274243
D2_O	H1	0.184113	D3_O	H2	0.304589	D18_AB	H4	0.27346
D11_AB	H4	0.182128	D17_B	H4	0.302468	D13_B	H4	0.271593
D13_B	H4	0.179719	D20_B	H4	0.297695	D17_O	H4	0.270768
D17_O	H4	0.175689	D9_B	H3	0.293812	D19_B	H4	0.267146
D6_B	H3	0.175511	D9_A	H3	0.283956	D2_O	H1	0.26436
D18_AB	H4	0.175187	D4_O	H2	0.283001	D5_AB	H2	0.262083
D3_A	H2	0.167935	D10_B	H3	0.264197	D6_B	H3	0.253384
D6_AB	H3	0.164975	D9_AB	H3	0.263613	D6_AB	H3	0.243856
D9_B	H3	0.164596	D10_O	H3	0.262724	D19_AB	H4	0.237116
D13_O	H4	0.157727	D4_AB	H2	0.26172	D15_AB	H4	0.236321
D10_AB	H3	0.156258	D4_A	H2	0.248961	D8_B	H3	0.234667
D10_B	H3	0.154847	D16_A	H4	0.243037	D17_B	H4	0.231083
D17_B	H4	0.150147	D2_O	H1	0.238695	D10_A	H3	0.230732
D15_B	H4	0.147314	D13_AB	H4	0.233873	D10_AB	H3	0.230139
D14_AB	H4	0.145891	D5_A	H2	0.231365	D13_O	H4	0.225875
D18_A	H4	0.142861	D8_B	H3	0.225048	D10_B	H3	0.223239
D20_A	H4	0.142591	D4_B	H2	0.221769	D15_A	H4	0.223182
D12_A	H4	0.138953	D5_O	H2	0.219149	D14_AB	H4	0.214246
D16_B	H4	0.13349	D19_A	H4	0.211467	D5_B	H2	0.209854
D20_B	H4	0.133264	D1_B	H1	0.208165	D7_B	H3	0.196095
D14_O	H4	0.126624	D13_O	H4	0.207723	D4_AB	H2	0.190488
D8_AB	H3	0.126349	D1_AB	H1	0.167554	D14_O	H4	0.187058
D4_AB	H2	0.126309	D13_B	H4	0.160432	D13_AB	H4	0.17699
D11_B	H4	0.122043	D8_AB	H3	0.15659	D18_A	H4	0.172942
D16_AB	H4	0.121491	D12_O	H4	0.151545	D11_AB	H4	0.169562
D7_B	H3	0.120812	D1_O	H1	0.147353	D18_O	H4	0.15621
D3_B	H2	0.117283	D7_O	H3	0.134908	D12_A	H4	0.14229
D18_O	H4	0.110488	D7_AB	H3	0.134244	D2_B	H1	0.136447
D13_AB	H4	0.109836	D12_A	H4	0.127914	D3_B	H2	0.124586
D12_B	H4	0.104592	D5_AB	H2	0.112471	D9_B	H3	0.119028
D2_B	H1	0.09837	D3_B	H2	0.110035	D5_O	H2	0.116156
D19_A	H4	0.088171	D12_B	H4	0.085178	D12_B	H4	0.104485
D4_A	H2	0.075218	D19_O	H4	0.083312	D4_A	H2	0.103468
D5_O	H2	0.072702	D14_O	H4	0.038946	D19_A	H4	0.079094

Table 14 Overall ranks of 80 patients and 80 donors prioritization based on external TOPSIS GDM contexts for three experts

Patients/Donors Rank	Patients Ranking Results			Donors Ranking Results		
	Patients Identification Information		C_(i*) Final Score	Donors Identification Information		C_(i*) Final Score
	Patients	Hospital		Donors	Hospital	
1	P3_AB	H1	0.74719	D20_AB	H4	0.68010
2	P4_O	H1	0.72891	D8_A	H2	0.61142
3	P14_O	H2	0.72150	D17_A	H4	0.58684
4	P7_O	H1	0.68548	D1_A	H1	0.57641
5	P19_AB	H4	0.68329	D6_O	H3	0.53056
6	P16_A	H3	0.68104	D6_A	H3	0.52952
7	P20_AB	H4	0.67497	D14_A	H4	0.50619
8	P1_O	H1	0.66003	D18_B	H4	0.49735
9	P8_AB	H1	0.64651	D11_A	H4	0.48283
10	P17_O	H3	0.59967	D7_A	H3	0.47616
11	P6_AB	H1	0.58612	D15_O	H4	0.45851
12	P13_AB	H2	0.58596	D2_A	H1	0.45134
13	P15_O	H2	0.57643	D3_AB	H2	0.42681
14	P12_A	H2	0.54896	D9_O	H3	0.40419
15	P7_A	H1	0.54676	D17_AB	H4	0.40409
16	P8_O	H1	0.54565	D16_O	H4	0.40147
17	P16_O	H3	0.53172	D11_O	H4	0.38863
18	P12_B	H2	0.53162	D20_O	H4	0.38703
19	P7_AB	H1	0.52628	D13_A	H4	0.37269
20	P8_A	H1	0.50789	D8_O	H3	0.35559
21	P11_AB	H2	0.49940	D12_AB	H4	0.35224
22	P20_O	H4	0.49162	D14_B	H4	0.34556
23	P5_A	H1	0.48421	D5_A	H3	0.32112
24	P6_O	H1	0.48272	D19_AB	H4	0.32075
25	P14_A	H2	0.47244	D5_B	H2	0.31939
26	P15_A	H2	0.46518	D3_A	H2	0.31677
27	P17_AB	H3	0.46114	D15_AB	H4	0.31362
28	P12_AB	H2	0.45731	D10_A	H3	0.31261
29	P17_B	H3	0.44998	D19_B	H4	0.31069
30	P10_O	H1	0.44751	D17_O	H4	0.30977
31	P13_B	H2	0.44603	D2_AB	H1	0.30885
32	P4_A	H1	0.44064	D16_A	H4	0.30851
33	P15_B	H2	0.44038	D9_A	H3	0.30425
34	P9_B	H1	0.43861	D9_AB	H3	0.30319
35	P5_O	H1	0.43759	D15_B	H4	0.30123
36	P14_AB	H2	0.42889	D16_B	H4	0.29940
37	P3_B	H1	0.42777	D1_B	H1	0.29419
38	P20_A	H4	0.42690	D18_AB	H4	0.29323
39	P3_A	H1	0.42428	D20_A	H4	0.29171
40	P7_B	H1	0.42390	D14_AB	H4	0.29017
41	P2_AB	H1	0.39789	D4_O	H2	0.28790
42	P9_AB	H1	0.38829	D3_O	H2	0.28769
43	P8_B	H1	0.38527	D15_A	H4	0.28729
44	P4_B	H1	0.37941	D11_B	H4	0.27979
45	P3_O	H1	0.37691	D10_O	H3	0.27905

Table 14 (continued)

Patients/Donors Rank	Patients Ranking Results			Donors Ranking Results		
	Patients Identification Information		C_(i*) Final Score	Donors Identification Information		C_(i*) Final Score
	Patients	Hospital		Donors	Hospital	
46	P16_B	H3	0.37531	D6_B	H3	0.27572
47	P19_O	H4	0.37091	D16_AB	H4	0.26477
48	P20_B	H4	0.36630	D4_B	H2	0.26242
49	P6_B	H1	0.36361	D11_AB	H4	0.26036
50	P1_AB	H1	0.36337	D10_AB	H3	0.25759
51	P11_A	H2	0.36221	D8_B	H3	0.25665
52	P18_AB	H3	0.35778	D6_AB	H3	0.25449
53	P12_O	H2	0.35770	D18_A	H4	0.24953
54	P6_A	H1	0.35742	D20_B	H4	0.24574
55	P5_AB	H1	0.35312	D7_B	H3	0.24387
56	P14_B	H2	0.35310	D1_AB	H1	0.23650
57	P5_B	H1	0.34526	D18_O	H4	0.23458
58	P11_O	H2	0.34257	D1_O	H1	0.23005
59	P15_AB	H2	0.33713	D7_O	H3	0.22906
60	P18_A	H3	0.33579	D2_O	H1	0.22906
61	P19_A	H4	0.33070	D17_B	H4	0.22790
62	P18_B	H3	0.32884	D7_AB	H3	0.22748
63	P10_B	H1	0.32688	D2_B	H1	0.21920
64	P18_O	H3	0.32096	D12_O	H4	0.21695
65	P11_B	H2	0.31728	D10_B	H3	0.21409
66	P13_A	H2	0.31680	D13_B	H4	0.20391
67	P13_O	H2	0.31678	D13_O	H4	0.19711
68	P9_A	H1	0.30712	D4_AB	H2	0.19284
69	P2_A	H1	0.30581	D9_B	H3	0.19248
70	P2_B	H1	0.30021	D5_AB	H2	0.18943
71	P16_AB	H3	0.29779	D19_O	H4	0.18877
72	P19_B	H4	0.29093	D8_AB	H3	0.18573
73	P10_A	H1	0.29010	D13_AB	H4	0.17357
74	P1_B	H1	0.28320	D4_A	H2	0.14255
75	P4_AB	H1	0.27000	D12_A	H4	0.13639
76	P9_O	H1	0.26007	D5_O	H2	0.13600
77	P2_O	H1	0.25311	D19_A	H4	0.12624
78	P17_A	H3	0.23385	D14_O	H4	0.11754
79	P10_AB	H1	0.18742	D3_B	H2	0.11730
80	P1_A	H1	0.14434	D12_B	H4	0.09808

Table 15 Overall matching results between patients and donors

Patients Rank	Patients/admitted Hospital	Suitable CP donors/ admitted Hospital
1	P3_AB/ H1	D13_AB/ H4
2	P4_O/ H1	D14_O/ H4
3	P14_O/ H2	D5_O/ H2
4	P7_O/ H1	D19_O/ H4
5	P19_AB/ H4	D8_AB/ H3
6	P16_A/ H3	D19_A/ H3
7	P20_AB/ H4	D5_AB/ H2
8	P1_O/ H1	D13_O/ H4
9	P8_AB/H1	D4_AB/ H2
10	P17_O/ H3	D12_O/ H4
11	P6_AB/ H1	D7_AB/ H3
12	P13_AB/ H2	D1_AB/ H1
13	P15_O/ H2	D2_O/ H1
14	P12_A/ H2	D12_A/ H4
15	P7_A/ H1	D4_A/ H2
16	P8_O/ H1	D7_O/ H3
17	P16_O/ H3	D1_O/ H1
18	P12_B/ H2	D12_B/ H4
19	P7_AB/ H1	D6_AB/ H3
20	P8_A/ H1	D18_A/ H4
21	P11_AB/ H2	D10_AB/ H3
22	P20_O/ H4	D18_O/ H4
23	P5_A/ H1	D15_A/ H4
24	P6_O/ H1	D10_O/ H3
25	P14_A/ H2	D20_A/ H4
26	P15_A/ H2	D9_A/ H3
27	P17_AB/ H3	D11_AB/ H4
28	P12_AB/ H2	D16_AB/H4
29	P17_B/ H3	D3_B/ H2
30	P10_O/ H1	D3_O/ H2
31	P13_B/ H2	D9_B/ H3
32	P4_A/ H1	D16_A/ H4
33	P15_B/ H2	D13_B/ H4
34	P9_B/ H1	D10_B/ H3
35	P5_O/ H1	D4_O/ H2
36	P14_AB/ H2	D14_AB/H4
37	P3_B/ H1	D2_B/ H1
38	P20_A/H4	D10_A/ H3
39	P3_A/ H1	D3_A/ H2
40	P7_B/ H1	D17_B/ H4
41	P2_AB/ H1	D18_AB/ H4
42	P9_AB/ H1	D9_AB/ H3
43	P8_B/ H1	D7_B/ H3
44	P4_B/ H1	D20_B/ H4
45	P3_O/ H1	D17_O/ H4
46	P16_B/ H3	D8_B/ H3
47	P19_O/ H4	D8_O/ H3
48	P20_B/ H4	D4_B/ H2
49	P6_B/ H1	D6_B/ H3
50	P1_AB/ H1	D2_AB/ H1
51	P11_A/ H2	D5_A/ H3
52	P18_AB/ H3	D15_AB/ H4
53	P12_O/ H2	D20_O/ H4
54	P6_A/ H1	D13_A/ H4
55	P5_AB/ H1	D19_AB/ H4
56	P14_B/ H2	D11_B/ H4
57	P5_B/ H1	D1_B/ H1
58	P11_O/ H2	D11_O/ H4
59	P15_AB/H2	D12_AB/ H4
60	P18_A/H3	D2_A/ H1
61	P19_A/ H4	D7_A/ H3
62	P18_B/ H3	D16_B/ H4
63	P10_B/ H1	D15_B/ H4
64	P18_O/ H3	D16_O/ H4
65	P11_B/ H2	D19_B/ H4
66	P13_A/ H2	D11_A/ H4
67	P13_O/ H2	D9_O/ H3
68	P9_A/ H1	D14_A/ H4
69	P2_A/ H1	D6_A/ H3
70	P2_B/ H1	D5_B/ H2
71	P16_AB/ H3	D17_AB/ H4
72	P19_B/ H4	D14_B/ H4
73	P10_A/ H1	D1_A/ H1
74	P1_B/ H1	D18_B/ H4
75	P4_AB/ H1	D3_AB/ H2
76	P9_O/ H1	D15_O/ H4
77	P2_O/ H1	D6_O/ H3
78	P17_A/ H3	D17_A/ H4
79	P10_AB/ H1	D20_AB/ H4
80	P1_A/ H1	D8_A/ H2

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