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A Mathematical Modeling to Determine the Evolutionary Relationships Between Bat and Human Corona Virus

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ABSTRACT: In this article, we present novel correlation coefficients for measuring the relationship between two fuzzy sets. Here we put forward mathematical models to determine the evolutionary relationships between SARS-CoV & SARS-CoV-2 and five other commonly known corona viruses in human which includes MERS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63 and HCoV-HKU1 and two bat corona viruses (RsSHC014 and RaTG13) with special emphasis on their correlation. The work can be considered as a pioneer in the field of application of fuzzy set theory in the study of this zoonsis.

Key Words: Correlation Coefficient, epidemic model, SARS-CoV-2.

Contents

1. Introduction

The pandemic by the name COVID-19 that the world saw recently needs no introduction as it significantly impacted the whole world, most fearful part of it being very fast human to human transmission [30]. It was on 30 January 2020, this severe outbreak of the corona virus was declared as a public health emergency of international concern by the World Health Organization. On March 11, 2020 it was declared as the global pandemic. The 2019 novel corona virus also known by the name SARS-CoV-2 is the causative organism of COVID-19. This virus comes from the family coronaviradae. This family also has an epidemic causing legacy of two other viruses previously namely SARS-CoV and MERS-CoV [10]. The SARS-CoV & SARS-CoV-2 are speculated to be having their root of origin from bat. Investigation of genome of SARS- CoV-2 viruses shows its close relationship with that of structure of RNA of corona virus found in the bats [29].

The SARS-CoV-2 full length genome sequences showed a comparatively low similarity of about 79.6 percent to that of SARS-CoV that is roughly less than 80 percent and at the same time, it is also very precisely similar with bat corona virus [29] having the whole length genome sequence identical upto 96 percent. RaTG13 is the nearest to SARS-CoV-2 [29]. This similarity being the prime reason for believing the fact that the corona virus has its origins lying in bat. For the purpose of infection in the host, the fusion of the cell membrane of both host and the virus is very essential. This is regulated by the surface glycoprotein named spike's S2 subunits of the COVID-19 virus. This production of spike protein is very crucial to determine the binding specificity and also the infection level of host. The different facets of relation specially the phylogentic relationship of SARS-CoV-2 with its further contemporary corona viruses is one of the dynamically expanding field of research now a days. The frequently used methods of

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investigation of phylogenetic status of various corona viruses and their origin includes genome sequencing, sequence alignment and the similarity analysis. Regarding the origin of SARS-CoV-2 various hypothesis have surfaced, while some advocate for bats origin [17], for others pangolin is the probable origin [16]. Of many corona viruses seven are quiet popularly known to human which includes SARS-CoV, SARS-CoV-2, MERS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63 and HCoV-HKU1 and some of which are known to be transferred from bats [1]. Other than these, two corona viruses RsSHC014 and RaTG13 of bat origin have also been closely examined here as they are thought to be the ancestors of SARS-CoV and SARS-CoV-2.

This study aims to investigate and analyse the phylogenetic relationship of SARS-CoV & SARS-CoV-2 using the very essential protein spike and comparing it with other closely related corona viruses considered for study using non conserved region. When it comes to deal with the data and their interrelationships correlation is the most trusted way. It can be further ascertained by the fact that the correlation coefficient or the Pearsons coefficient is the mostly broadly applied indices in statistics [20]. Correlation reflects the degree of closeness in terms of linear relationship of two variables. It has a wide range of application in various fields like medical, economic, legal, educational to just name a few.

Zadeh [27] gave a powerful modelling tool by the name Fuzzy set theory which is widely used for imprecise and vague situations when the exact application becomes either very tough or impossible. The interdependence of the two variables and their joint relationship can be scrutinized using correlation analysis. Many authors applied and analysed the concept of correlation in fuzzy set theory. Chiang and Lin [9] studied the correlation of fuzzy sets, Chaudhuri and Bhattacharya [8] studied the correlation between two fuzzy sets on the same universal support, Murthy et al. [18] on the other hand studied the correlation between two fuzzy membership functions, Yu [26] investigated correlation coefficient of fuzzy numbers. Numerous mathematical models came into existence to understand in depth the phylogeny of COVID-19. Bora et al. [5] 2022 in there study utilised a unique graph theory approach to understand phylogenetic relationships of SARS-CoV-2, using spike simultaneously comparing the closely related contemporary viruses taking into account the non conserved region. They came to the conclusion that the applied method is capable enough to be pipeline to perform phylogenetic analysis on protein sequences having a common physio-chemical feature in adjacent amino acid residues. Their main focus was on non conserved sequences which was earlier more or less neglected in the previous studies and they also took into account both direct and corelated values. They studied the relationship between the two corona viruses of bat believed to be the relatives of SARS-CoV-2 and SARS-CoV and the other contemporary human corona viruses consider here. They used maximum likelihood (ML) method for the purpose of constructing the phylogenetic tree of seven corona viruses (SARS-CoV, SARS-CoV-2, MERS-CoV, HCoV-NL63, HCoV-OC43, HCoV-229E, HCoV-HKU1) and other two coronaviruses (RsSHC014 and RaTG13)of bat origin. They used Network Merge application embedded in for merging the whole module graph and further validated their outcomes of phylogenetic tree utilizing the centrality measures with their correlation.

In our works, data set of degree distribution of nine sequence graphs has been considered from Bora et al. [5] and finally we determined the evolutionary relationships between Bat corona viruses and SARS-CoV & SARS-CoV-2 and other mentioned human corona viruses with respect to fuzzy sets.

We structured this article in the followig way: Some preliminary findings are given in the Section “Preliminary results”. The definition of correlation between the fuzzy sets is discussed in the Section “Correlation between fuzzy sets”. In the Section “mathematical modeling to determine the evolutionary relationships between Bat corona virus and SARS-CoV & SARS-CoV-2”, we place an application and then a further elaborate discussion on fuzzy sets pertinent to coronaviruses.

2. Model Configuration Results

In this part of the article, we review several fundamental ideas and terms related to fuzzy sets and correlation coefficients:

Definition 2.1 *[27]* Consider the universe of discourse Z. A fuzzy set is therefore described as follows:

$$\Gamma = \{(l, \varrho_A(l)) : l \in Z\},$$

that define the membership criterion ϱ_Γ maps from Z to $[0, 1]$; here the term $\varrho_\Gamma(l)$ represents the degree of membership of the element.

Example 2.1 *Let* $\Gamma = \{(\varrho_1, 0.3), (\varrho_2, 0.2), (\varrho_3, 0.8)\}$, $\Lambda = \{(\varrho_1, 0.2), (\varrho_2, 0.4), (\varrho_3, 0.6)\}$ $\Pi = \{(\varrho_1, 0.8), (\varrho_2, 0.2), (\varrho_3, 0.7)\}$ *be three fuzzy sets. In tabular form of* Γ, Λ *and* Π.

Table 1: Tabular Form of Γ, Λ *and* Π

	Γ	Λ	Π
ϱ_1	0.3	0.2	0.8
ϱ_2	0.2	0.4	0.2
ϱ_3	0.8	0.6	0.7

Definition 2.2 *[9]* Suppose a random sample $l_1, l_2, l_3, ..., l_n \in L$ with a sequence of paired data

$$(\varrho_A(l_1), \varrho_B(l_1)), (\varrho_A(l_2), \varrho_B(l_2)), \ldots, (\varrho_A(l_n), \varrho_B(l_n))$$

that correspond to the membership values of fuzzy sets A and B defined on Z, then the correlation coefficient $r_f(A, B)$ is given as:

$$r_f(A, B) = \frac{\sum_{i=1}^{n} (\varrho_A(l_i) - \bar{\varrho_A})(\varrho_B(l_i) - \bar{\varrho_B})}{\left(\sum_{i=1}^{n} (\varrho_A(l_i) - \bar{\varrho_A})^2\right)^{\frac{1}{2}} \left(\sum_{i=1}^{n} (\varrho_B(l_i) - \bar{\varrho_B})^2\right)^{\frac{1}{2}}},$$

where $\bar{\varrho_A} = \frac{1}{n}\sum_{i=1}^{n} \varrho_A(l_i), \bar{\varrho_B} = \frac{1}{n}\sum_{i=1}^{n} \varrho_B(l_i)$.

3. Correlation Between Fuzzy Sets

The seven known corona viruses and bat virus in the protein sequence alignment were studied and based on their similarities and differences between the 20 known amino acids sequences a formula was derived for their correlation using the mathematical tool fuzzy set.

Definition 3.1 Suppose that there are two fuzzy sets concerning (Z, E), are Λ and Γ. Next, $\tilde{r_Z}(\Gamma, \Lambda)$, the correlation among them in the meantime, is outlined as follows:

$$\tilde{r_Z}(\Gamma, \Lambda) = \frac{\sum_{t=1}^{20} \left\{ \left(\mu_\Gamma(h_t) - \frac{1}{20} \sum_{t=1}^{20} \{\varrho_\Gamma(h_t)\} \right) \left(\varrho_\Lambda(h_t) - \frac{1}{20} \sum_{t=1}^{20} \{\varrho_\Lambda(h_t)\} \right) \right\}}{\left\{ \sum_{t=1}^{20} \left(\varrho_\Gamma)(h_t) - \frac{1}{20} \sum_{t=1}^{20} \{\varrho_\Gamma(h_t)\} \right)^2 \right\}^{\frac{1}{2}} \left\{ \sum_{t=1}^{20} \left(\varrho_\Lambda)(h_t) - \frac{1}{20} \sum_{t=1}^{20} \{\varrho_\Lambda(h_t)\} \right)^2 \right\}^{\frac{1}{2}}},$$

and $i = 1, 2, \ldots, 20;\ j = 1, 2, \ldots, 20$.

Example 3.1 *Let* $\Gamma = \{(\varrho_1, 0.65), (\varrho_2, 0.2), (\varrho_3, 0.45), (\varrho_4, 0.25), (\varrho_5, 0.7), (\varrho_6, 0.6), (\varrho_7, 0.55), (\varrho_8, 0.7), (\varrho_9, 0.35), (\varrho_{10}, 0.4), (\varrho_{11}, 0.55), (\varrho_{12}, 0.55), (\varrho_{13}, 0.45), (\varrho_{14}, 0.05), (\varrho_{15}, 0.5), (\varrho_{16}, 0.65), (\varrho_{17}, 0.35), (\varrho_{18}, 0.4), (\varrho_{19}, 0.15), (\varrho_{20}, 0.1)\}$,
$\Lambda = \{(\varrho_1, 0.65), (\varrho_2, 0.4), (\varrho_3, 0.6), (\varrho_4, 0.5), (\varrho_5, 0.7), (\varrho_6, 0.75), (\varrho_7, 0.55), (\varrho_8, 0.65), (\varrho_9, 0.5), (\varrho_{10}, 0.55), (\varrho_{11}, 0.65), (\varrho_{12}, 0.5), (\varrho_{13}, 0.5), (\varrho_{14}, 0.55), (\varrho_{15}, 0.7), (\varrho_{16}, 0.45), (\varrho_{17}, 0.2), (\varrho_{18}, 0.4), (\varrho_{19}, 0.1), (\varrho_{20}, 0.1)\}$.

Table 2: Tabular Form of Γ *and* Λ

	Γ	Λ
ϱ_1	0.65	0.65
ϱ_2	0.2	0.4
ϱ_3	0.45	0.6
ϱ_4	0.25	0.5
ϱ_5	0.7	0.7
ϱ_6	0.6	0.75
ϱ_7	0.55	0.55
ϱ_8	0.7	0.65
ϱ_9	0.35	0.5
ϱ_{10}	0.4	0.55
ϱ_{11}	0.55	0.65
ϱ_{12}	0.55	0.5
ϱ_{13}	0.45	0.5
ϱ_{14}	0.05	0.55
ϱ_{15}	0.5	0.7
ϱ_{16}	0.65	0.45
ϱ_{17}	0.35	0.2
ϱ_{18}	0.4	0.4
ϱ_{19}	0.15	0.1
ϱ_{20}	0.1	0.1

Therefore $\tilde{r_Z}(\Gamma, \Lambda) = 0.65984$

Proposition 3.1 Assume that (Z, E) contains two fuzzy sets, Λ and Γ. Then

(i) $\tilde{r_Z}(\Gamma, \Lambda) = \tilde{r_Z}(\Lambda, \Gamma)$.

(ii) If $\Gamma = \Lambda$ then $\tilde{r_Z}(\Gamma, \Lambda) = 1$.

(iii) $\tilde{r_Z}(\Gamma, \Lambda) \leq 1$.

Proof: The proof is skipped since (i), (ii), and (iii) are clear.

4. Mathematical Modeling to Determine the Evolutionary Relationships Between Bat Corona Virus and SARS-CoV & SARS-CoV-2

In our works, data set of degree distribution of nine sequence graphs has been considering from Bora et al. [5]. Finally determine the evolutionary relationships between Bat corona virues and SARS-CoV & SARS-CoV-2 at along with the other five contemporary human corona viruses with respect to fuzzy sets. We cosider the symbols of human and bat corona viruses as following form:

Table 3: Symbols of Human and Bat corona viruses

Corona Virus	Correlation Coefficient
RaTG13	β_1
RsSHC014	β_2
SARS-CoV	ψ_1
SARS-CoV-2	ψ_2
HCoV-229E	ψ_3
HCoV-NL63	ψ_4
HCoV-HKU1	ψ_5
MERS-CoV	ψ_6
HCoV-OC43	ψ_7

The aforementioned algorithms were employed.

Enhanced Algorithms:

Step (i) To collect degree distribution of sequence graphs from Bora et al. [5] in tabular form.
Step (ii) To convert Step (i) data to tabular form of mentioned human and bat coronaviruses with respect to SARS-CoV and SARS-CoV-2 respectively.
Step (iii) Find the correlation between fuzzy sets of first column and another seven columns of first table.
Step (iv) Arranged Step(iii) data in tabular form.
Step (v) Applying Step(iii) and Step (iv) in second table.

Table 4: Tabular form of human and bat corona viruses about SARS-CoV(ψ_1) & SARS-CoV-2(ψ_2)

$AminoAcid$	ψ_1	ψ_2	β_1	β_2	ψ_3	ψ_4	ψ_5	ψ_6	ψ_7
$Valine(V)$	$\frac{13}{20}$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{13}{20}$	$\frac{4}{5}$	$\frac{3}{10}$	$\frac{13}{20}$	$\frac{7}{20}$
$Arginine(R)$	$\frac{2}{5}$	$\frac{2}{5}$	$\frac{3}{10}$	$\frac{2}{5}$	$\frac{1}{5}$	$\frac{3}{10}$	$\frac{3}{10}$	$\frac{1}{4}$	$\frac{1}{4}$
$Proline(P)$	$\frac{7}{10}$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{9}{20}$	$\frac{7}{20}$	$\frac{9}{20}$	$\frac{3}{5}$	$\frac{9}{20}$
$Glutamicacid(E)$	$\frac{7}{20}$	$\frac{1}{2}$	$\frac{11}{20}$	$\frac{7}{20}$	$\frac{1}{4}$	$\frac{1}{4}$	$\frac{7}{20}$	$\frac{11}{20}$	$\frac{3}{10}$
$Glycine(G)$	$\frac{13}{20}$	$\frac{7}{10}$	$\frac{7}{10}$	$\frac{3}{4}$	$\frac{7}{10}$	$\frac{1}{2}$	$\frac{1}{2}$	$\frac{3}{5}$	$\frac{3}{5}$
$Leucine(L)$	$\frac{7}{10}$	$\frac{3}{4}$	$\frac{7}{10}$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{17}{20}$	$\frac{13}{20}$
$Asparagine(N)$	$\frac{7}{10}$	$\frac{11}{20}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{11}{20}$	$\frac{11}{20}$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{11}{20}$
$Phenylalanine(F)$	$\frac{7}{10}$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{7}{10}$	$\frac{3}{5}$	$\frac{1}{2}$	$\frac{3}{5}$
$Asparticacid(D)$	$\frac{1}{2}$	$\frac{1}{2}$	$\frac{3}{5}$	$\frac{9}{20}$	$\frac{7}{20}$	$\frac{3}{10}$	$\frac{11}{20}$	$\frac{1}{2}$	$\frac{3}{5}$
$Lysine(K)$	$\frac{3}{5}$	$\frac{11}{20}$	$\frac{13}{20}$	$\frac{11}{20}$	$\frac{2}{5}$	$\frac{9}{20}$	$\frac{7}{20}$	$\frac{7}{20}$	$\frac{1}{2}$
$Threonine(T)$	$\frac{11}{20}$	$\frac{13}{20}$	$\frac{3}{4}$	$\frac{9}{20}$	$\frac{11}{20}$	$\frac{13}{20}$	$\frac{11}{20}$	$\frac{7}{10}$	$\frac{13}{20}$
$Alanine(A)$	$\frac{11}{20}$	$\frac{1}{2}$	$\frac{3}{5}$	$\frac{1}{2}$	$\frac{11}{20}$	$\frac{7}{20}$	$\frac{3}{10}$	$\frac{11}{20}$	$\frac{1}{2}$
$Isoleucine(I)$	$\frac{1}{2}$	$\frac{1}{2}$	$\frac{3}{5}$	$\frac{9}{20}$	$\frac{9}{20}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{9}{20}$	$\frac{11}{20}$
$Glutamine(Q)$	$\frac{2}{5}$	$\frac{11}{20}$	$\frac{9}{20}$	$\frac{9}{20}$	$\frac{1}{20}$	$\frac{3}{10}$	$\frac{1}{4}$	$\frac{1}{2}$	$\frac{9}{20}$
$Serine(S)$	$\frac{13}{20}$	$\frac{7}{10}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{1}{2}$	$\frac{7}{10}$	$\frac{7}{10}$	$\frac{17}{20}$	$\frac{13}{20}$
$Tyrosine(Y)$	$\frac{3}{5}$	$\frac{9}{20}$	$\frac{1}{2}$	$\frac{9}{20}$	$\frac{13}{20}$	$\frac{3}{4}$	$\frac{1}{2}$	$\frac{13}{20}$	$\frac{11}{20}$
$Histidine(H)$	$\frac{1}{10}$	$\frac{1}{5}$	$\frac{1}{4}$	$\frac{1}{5}$	$\frac{7}{20}$	$\frac{2}{5}$	$\frac{1}{10}$	$\frac{1}{4}$	$\frac{1}{5}$
$Cysteine(C)$	$\frac{2}{5}$	$\frac{2}{5}$	$\frac{2}{5}$	$\frac{3}{10}$	$\frac{2}{5}$	$\frac{7}{20}$	$\frac{9}{20}$	$\frac{9}{20}$	$\frac{1}{2}$
$Tryptophan(W)$	$\frac{1}{5}$	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{3}{20}$	$\frac{3}{20}$	$\frac{1}{4}$	$\frac{1}{5}$	$\frac{1}{5}$
$Methionine(M)$	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{1}{10}$	0	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{3}{10}$	$\frac{1}{5}$

The displayed figure (FIGURE 1) hereunder summarizes the information from Table 4.

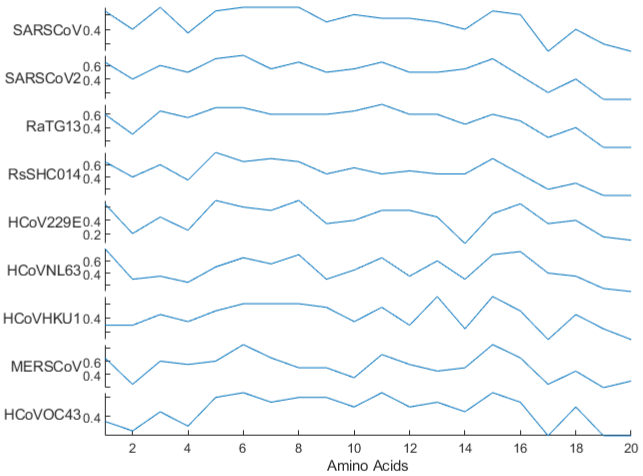

Figure 1:

Table 5: Tabular form of human and bat corona viruses about SARS-CoV(ψ_1)

$AminoAcid$	ψ_1	β_1	β_2	ψ_3	ψ_4	ψ_5	ψ_6	ψ_7
$Valine(V)$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{13}{20}$	$\frac{4}{5}$	$\frac{3}{10}$	$\frac{13}{20}$	$\frac{7}{20}$
$Arginine(R)$	$\frac{2}{5}$	$\frac{3}{10}$	$\frac{2}{5}$	$\frac{1}{5}$	$\frac{3}{10}$	$\frac{3}{10}$	$\frac{1}{4}$	$\frac{1}{4}$
$Proline(P)$	$\frac{7}{10}$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{9}{20}$	$\frac{7}{20}$	$\frac{9}{20}$	$\frac{3}{5}$	$\frac{9}{20}$
$Glutamicacid(E)$	$\frac{7}{20}$	$\frac{11}{20}$	$\frac{7}{20}$	$\frac{1}{4}$	$\frac{1}{4}$	$\frac{7}{20}$	$\frac{11}{20}$	$\frac{3}{10}$
$Glycine(G)$	$\frac{13}{20}$	$\frac{7}{10}$	$\frac{3}{4}$	$\frac{7}{10}$	$\frac{1}{2}$	$\frac{1}{2}$	$\frac{3}{5}$	$\frac{3}{5}$
$Leucine(L)$	$\frac{7}{10}$	$\frac{7}{10}$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{17}{20}$	$\frac{13}{20}$
$Asparagine(N)$	$\frac{7}{10}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{11}{20}$	$\frac{11}{20}$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{11}{20}$
$Phenylalanine(F)$	$\frac{7}{10}$	$\frac{3}{5}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{7}{10}$	$\frac{3}{5}$	$\frac{1}{2}$	$\frac{3}{5}$
$Asparticacid(D)$	$\frac{1}{2}$	$\frac{3}{5}$	$\frac{9}{20}$	$\frac{7}{20}$	$\frac{3}{10}$	$\frac{11}{20}$	$\frac{1}{2}$	$\frac{3}{5}$
$Lysine(K)$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{11}{20}$	$\frac{2}{5}$	$\frac{9}{20}$	$\frac{7}{20}$	$\frac{7}{20}$	$\frac{1}{2}$
$Threonine(T)$	$\frac{11}{20}$	$\frac{3}{4}$	$\frac{9}{20}$	$\frac{11}{20}$	$\frac{13}{20}$	$\frac{11}{20}$	$\frac{7}{10}$	$\frac{13}{20}$
$Alanine(A)$	$\frac{11}{20}$	$\frac{3}{5}$	$\frac{1}{2}$	$\frac{11}{20}$	$\frac{7}{20}$	$\frac{3}{10}$	$\frac{11}{20}$	$\frac{1}{2}$
$Isoleucine(I)$	$\frac{1}{2}$	$\frac{3}{5}$	$\frac{9}{20}$	$\frac{9}{20}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{9}{20}$	$\frac{11}{20}$
$Glutamine(Q)$	$\frac{2}{5}$	$\frac{9}{20}$	$\frac{9}{20}$	$\frac{1}{20}$	$\frac{3}{10}$	$\frac{1}{4}$	$\frac{1}{2}$	$\frac{9}{20}$
$Serine(S)$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{1}{2}$	$\frac{7}{10}$	$\frac{7}{10}$	$\frac{17}{20}$	$\frac{13}{20}$
$Tyrosine(Y)$	$\frac{3}{5}$	$\frac{1}{2}$	$\frac{9}{20}$	$\frac{13}{20}$	$\frac{3}{4}$	$\frac{1}{2}$	$\frac{13}{20}$	$\frac{11}{20}$
$Histidine(H)$	$\frac{1}{10}$	$\frac{1}{4}$	$\frac{1}{5}$	$\frac{7}{20}$	$\frac{2}{5}$	$\frac{1}{10}$	$\frac{1}{4}$	$\frac{1}{5}$
$Cysteine(C)$	$\frac{2}{5}$	$\frac{2}{5}$	$\frac{3}{10}$	$\frac{2}{5}$	$\frac{7}{20}$	$\frac{9}{20}$	$\frac{9}{20}$	$\frac{1}{2}$
$Tryptophan(W)$	$\frac{1}{5}$	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{3}{20}$	$\frac{3}{20}$	$\frac{1}{4}$	$\frac{1}{5}$	$\frac{1}{5}$
$Methionine(M)$	$\frac{1}{10}$	$\frac{1}{10}$	0	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{3}{10}$	$\frac{1}{5}$

The displayed figure (FIGURE 2) hereunder summarizes the information from Table 5.

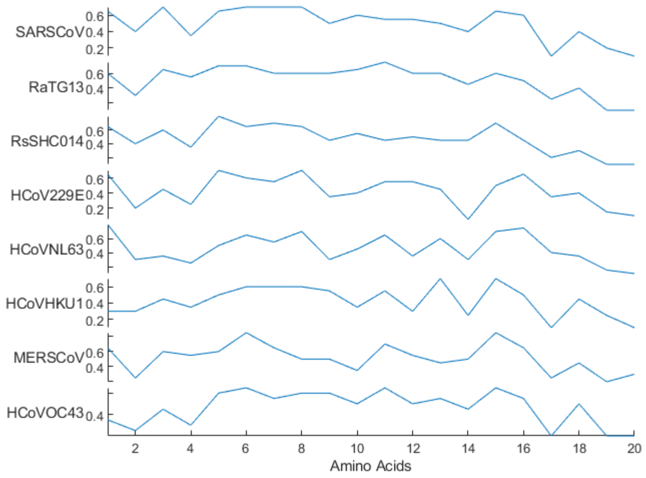

Figure 2:

Table 6: Tabular form of human and bat corona viruses about SARS-CoV-2(ψ_2)

$AminoAcid$	ψ_2	β_1	β_2	ψ_3	ψ_4	ψ_5	ψ_6	ψ_7
$Valine(V)$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{13}{20}$	$\frac{4}{5}$	$\frac{3}{10}$	$\frac{13}{20}$	$\frac{7}{20}$
$Arginine(R)$	$\frac{2}{5}$	$\frac{3}{10}$	$\frac{2}{5}$	$\frac{1}{5}$	$\frac{3}{10}$	$\frac{3}{10}$	$\frac{1}{4}$	$\frac{1}{4}$
$Proline(P)$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{9}{20}$	$\frac{7}{20}$	$\frac{9}{20}$	$\frac{3}{5}$	$\frac{9}{20}$
$Glutamicacid(E)$	$\frac{1}{2}$	$\frac{11}{20}$	$\frac{7}{20}$	$\frac{1}{4}$	$\frac{1}{4}$	$\frac{7}{20}$	$\frac{11}{20}$	$\frac{3}{10}$
$Glycine(G)$	$\frac{7}{10}$	$\frac{7}{10}$	$\frac{3}{4}$	$\frac{7}{10}$	$\frac{1}{2}$	$\frac{1}{2}$	$\frac{3}{5}$	$\frac{3}{5}$
$Leucine(L)$	$\frac{3}{4}$	$\frac{7}{10}$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{17}{20}$	$\frac{13}{20}$
$Asparagine(N)$	$\frac{11}{20}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{11}{20}$	$\frac{11}{20}$	$\frac{3}{5}$	$\frac{13}{20}$	$\frac{11}{20}$
$Phenylalanine(F)$	$\frac{13}{20}$	$\frac{3}{5}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{7}{10}$	$\frac{3}{5}$	$\frac{1}{2}$	$\frac{3}{5}$
$Asparticacid(D)$	$\frac{1}{2}$	$\frac{3}{5}$	$\frac{9}{20}$	$\frac{7}{20}$	$\frac{3}{10}$	$\frac{11}{20}$	$\frac{1}{2}$	$\frac{3}{5}$
$Lysine(K)$	$\frac{11}{20}$	$\frac{13}{20}$	$\frac{11}{20}$	$\frac{2}{5}$	$\frac{9}{20}$	$\frac{7}{20}$	$\frac{7}{20}$	$\frac{1}{2}$
$Threonine(T)$	$\frac{13}{20}$	$\frac{3}{4}$	$\frac{9}{20}$	$\frac{11}{20}$	$\frac{13}{20}$	$\frac{11}{20}$	$\frac{7}{10}$	$\frac{13}{20}$
$Alanine(A)$	$\frac{1}{2}$	$\frac{3}{5}$	$\frac{1}{2}$	$\frac{11}{20}$	$\frac{7}{20}$	$\frac{3}{10}$	$\frac{11}{20}$	$\frac{1}{2}$
$Isoleucine(I)$	$\frac{1}{2}$	$\frac{3}{5}$	$\frac{9}{20}$	$\frac{9}{20}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{9}{20}$	$\frac{11}{20}$
$Glutamine(Q)$	$\frac{11}{20}$	$\frac{9}{20}$	$\frac{9}{20}$	$\frac{1}{20}$	$\frac{3}{10}$	$\frac{1}{4}$	$\frac{1}{2}$	$\frac{9}{20}$
$Serine(S)$	$\frac{7}{10}$	$\frac{3}{5}$	$\frac{7}{10}$	$\frac{1}{2}$	$\frac{7}{10}$	$\frac{7}{10}$	$\frac{17}{20}$	$\frac{13}{20}$
$Tyrosine(Y)$	$\frac{9}{20}$	$\frac{1}{2}$	$\frac{9}{20}$	$\frac{13}{20}$	$\frac{3}{4}$	$\frac{1}{2}$	$\frac{13}{20}$	$\frac{11}{20}$
$Histidine(H)$	$\frac{1}{5}$	$\frac{1}{4}$	$\frac{1}{5}$	$\frac{7}{20}$	$\frac{2}{5}$	$\frac{1}{10}$	$\frac{1}{4}$	$\frac{1}{5}$
$Cysteine(C)$	$\frac{2}{5}$	$\frac{2}{5}$	$\frac{3}{10}$	$\frac{2}{5}$	$\frac{7}{20}$	$\frac{9}{20}$	$\frac{9}{20}$	$\frac{1}{2}$
$Tryptophan(W)$	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{3}{20}$	$\frac{3}{20}$	$\frac{1}{4}$	$\frac{1}{5}$	$\frac{1}{5}$
$Methionine(M)$	$\frac{1}{10}$	$\frac{1}{10}$	0	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{1}{10}$	$\frac{3}{10}$	$\frac{1}{5}$

The displayed figure (FIGURE 3) hereunder summarizes the information from Table 6.

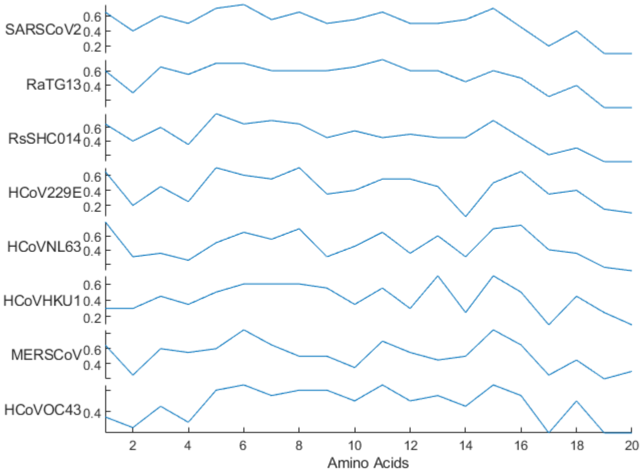

Figure 3:

Table 7: Correlation of Human and Bat corona viruses in tabular form about SARS-CoV (ψ_1)

Corona Virus	Correlation Coefficient
RaTG13(β_1)	0.868154
RsSHC014(β_2)	0.929265
HCoV-229E(ψ_3)	0.718481
HCoV-NL63(ψ_4)	0.710465
HCoV-HKU1 (ψ_5)	0.744961
MERS-CoV (ψ_6)	0.754277
HCoV-OC43 (ψ_7)	0.797594

Table 8: Correlation of human and bat corona viruses in tabular form about SARS-CoV-2(ψ_2)

Corona Virus	Correlation Coefficient
RaTG13 (β_1)	0.929533
RsSHC014 (β_2)	0.906864
HCoV-229E(ψ_3)	0.65984
HCoV-NL63(ψ_4)	0.704429
HCoV-HKU1 (ψ_5)	0.693143
MERS-CoV (ψ_6)	0.819376
HCoV-OC43(ψ_7)	0.799087

5. Results and Discussion

Here, the two corona viruses SARS-CoV-2 & SARS-CoV and the seven other contemporary corona viruses including two from bats (RsSHC014 and RaTG13) have been examined for their correlation. We have taken the data table from Bora et al. [5] and expressed in fuzzy form in Table 4. A brief representation of the information gathered from Table 4 can be found in FIGURE 1. After that we have expressed SARS-CoV and other corona viruses data in Table 5 and represented by FIGURE 2. Similarly SARS-CoV-2 and other corona viruses data are expressed in Table 6 and represented by FIGURE 3. It was found that in case of SARS-CoV and the seven comtemporaries all the other viruses showed a good correlation with all of them being atleast 70 percent correlated.Table 7 and 8 gives the correlation analysis result.The results indicates that the maximum correlation was seen in between SARS CoV and RsSHC014 where their correlation value was 0.929265 ie nearly 93 percent suggesting their very strong phylogenetic relation. Whereas in case of SARS-CoV-2 all its contemporaries showed a good correlation where all were atleast 65 percent correlated. SARS-CoV-2 showed the highest correlation value 0.929533 which is nearlty about 93 percent with RaTG13. This indicates a close phylogenetic relationship between SARS- CoV-2 and RaTG13. The seven corona viruses are quiet popularly known to human which includes SARS-CoV, SARS-CoV-2, MERS-CoV, HCoV-OC43, HCoV-229E, HCoV-NL63 and HCoV-HKU1 and some of which are known to be transferred from bats [1]. Other than these two coronaviruses RsSHC014 and RaTG13.

6. Concluding Summary

In this paper we used the mathematical tool fuzzy set theory and with the help of mathematical modelling, determined the evolutionary relationships of SARS-CoV & SARS-CoV-2 and their few contemporary known human and bat corona viruses using the correlation between them. We reached the conclusion that SARS-CoV is closely associated with RsSHC014 of bat origin whereas SARS-CoV-2 is closely associated to RaTG13. Presently there is no available literature of mathematical modelling which used the fuzzy set theory taking into account the correlation between the corona viruses and comparing it with those of biological determined phylogenetic tree. Therefore our work is the stepping stone in this direction and has future scopes for further development.

These type of mathematical modelings can be very crucial in predicting and preventing such future pandemics. A rough estimation and assessment of the advent of the disease based on the phylogenetic relationships can be a determinant in preventing the disease in the near future. It can be useful for research and development, predicting evolutionary trends and many more. Such kind of data's can also prove to be very important for the future policy development in this regards.

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