

Soft Computing Techniques for Fuzzy Digraph Analysis

Tharani S¹, Kavitha T¹, Deepa R¹ and Sarala N²

¹Department of Mathematics, E.G.S. Pillay Engineering College, Nagapattinam, Tamil Nadu, India

²Department of Mathematics, A.D.M. College for Women (Affiliated to Bharathidasan University),
Nagapattinam, Tamil Nadu, India

Keywords: Fuzzy Soft Bipartite Digraph, Punnette Square, Genetic Skin Colour.

Abstract: This study explores the use of bipartite fuzzy soft digraphs as an innovative approach for the comprehensive modeling of inherited skin tone determination. Skin tone is a multidimensional trait influenced by combined environmental and hereditary factors. It is important in dermatology, genetics, and customized medicine. Due to their inherent complexity and ambiguity, traditional modeling tools occasionally fail to capture the complex relationships between various components. In order to create a reliable model of genetic skin tone determination, we suggest combining fuzzy logic and soft computing techniques with bipartite fuzzy soft digraphs. This approach takes into consideration the inherent ambiguity in the relationships between genes and environmental influences by defining vertices for genes, external variables, and phenotypic outcomes, and edges for the connections between them. We go over how we created this model and its implications for comprehending the basic processes underlying skin pigmentation.

1 INTRODUCTION

Molodtsov introduced the concept of "soft sets," which address uncertainty. Building on this foundation, Rosenfeld expanded the notion of fuzzy graphs by examining fuzzy interactions within the fuzzy sets initially proposed by Zadeh in 1965. Mordeson and C.S. Peng explored various operations related to fuzzy graphs. Following this, Ali and his team examined fuzzy soft sets that emerge from soft sets within the framework of set theory. In 2015, M. Akram and S. Nawaz presented the concept of fuzzy soft graphs for the first time. Concurrently, T. K. Samanta and Sumitmohinta also introduced fuzzy soft graphs independently.

The basic structural and operational unit of heredity is the gene. Genes are constructed from DNA. Sometimes, genes act as the building blocks for the production of proteins. In contrast, a significant portion of genes do not need to code for proteins. The majority of human genes are made up of only a few hundred more than 2 million DNA nucleotides. According to the Genome Project, a multinational initiative to elucidate the human genome's structure and catalog its genes, humans are believed to have between 20,000 and 25,000 genes.

Each individual carries two copies of every gene, inherited from their parents. Although less than 1 percent of genes show small variations among individuals, most genomes remain similar throughout the population. Alleles are the variations in these genes, marked by slight differences in their sequences of base pairs. These small variations play a role in shaping the unique physical traits of every individual.

The suggested approach creates opportunities for further study in the creation of sophisticated computational models for comprehending and forecasting complicated genetic features, leading to a better knowledge of the complex interactions between genetic variables and their phenotypic manifestations. This article illustrates how fuzzy soft bipartite digraphs can be applied to the analysis of the most prevalent human skin tones.

2 GENETIC SKIN COLOUR

The concept of "polygenic inheritance" pertains to the transmission of traits that are shaped by multiple genes. When these polygenes are expressed together, they give rise to specific traits. This differs from Mendelian inheritance, where traits are dictated by a single gene. In polygenic inheritance, the interactions

among various alleles can lead to a diverse range of phenotypes (observable characteristics). Human traits such as skin color, eye color, hair color, body shape, height, and weight exemplify those inherited through polygenic inheritance. For instance, skin color is regulated by at least three genes, with the possibility of additional genes also influencing this trait. The level of melanin, a dark pigment in the skin, plays a crucial role in determining skin tone. Each gene responsible for skin color has two alleles, which are located on different chromosomes. Only the three genes known to affect skin tone need be taken into account; each gene has two alleles, one for dark and one for light skin tones. Dark skin colour (D) allele is more prevalent than light skin colour (L) allele (d). How many dark alleles a person possesses determines their skin tone. If a person inherits only dark alleles, their skin colour will be very dark, whereas if they inherit no dark alleles, their skin colour will be very light. The phenotypes of different skin tones will be present in people who inherit various combinations of the light and dark alleles. A medium skin tone occurs when there is a balanced presence of both dark and light alleles. Conversely, a darker skin tone is the result of inheriting a greater number of dark alleles. The melanocortin 1 receptor (MC1R) gene is the main gene linked to skin color. This gene codes for the production of a protein that is essential in identifying the kind of melanin that melanocytes make. In addition, other genes that are implicated in the process include TYR, OCA2, SLC24A5, and SLC45A2. Diversities in these genes are responsible for the great diversity of skin tones found in human

communities. For instance, darker skin is a result of some genetic differences linked to greater melanin synthesis, whereas lighter skin is a result of genetic variations linked to decreased melanin production. Table 1 shows the Various Shades of Human Skin Colour.

Table 1: Various Shades of Human Skin Colour.

Phenotypes	Genotypes	Units of pigment
Extremely dark	AABBCC	6
Very dark	AaBBCC	5
Dark	AaBbCC	4
Intermediate	AaBbCc	3
Light	aaBbCc	2
Very light	aabbCc	1
Extremely light	aabbcc	0

The Punnett square is a tabular summary of possible combinations of maternal alleles with paternal alleles. These tables can be used to examine the genotypic outcome probabilities of the offspring of a single trait (allele) or when crossing multiple traits from the parents. Phenotypes may be predicted with at least better-than-chance accuracy using a Punnett square, but the phenotype that may appear in the presence of a given genotype can in some instances be influenced by many other factors, as when polygenic inheritance and/or epigenetic are at work.

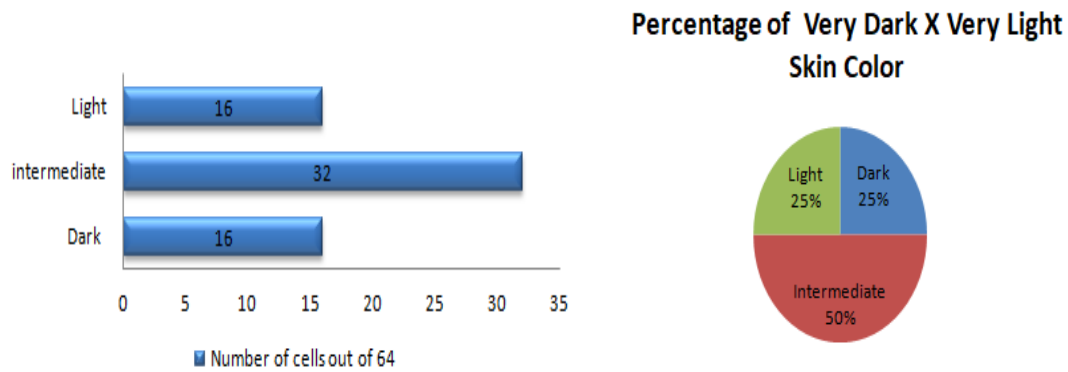
Example Crosses: Shown on a Punnett Square

Example 2.1

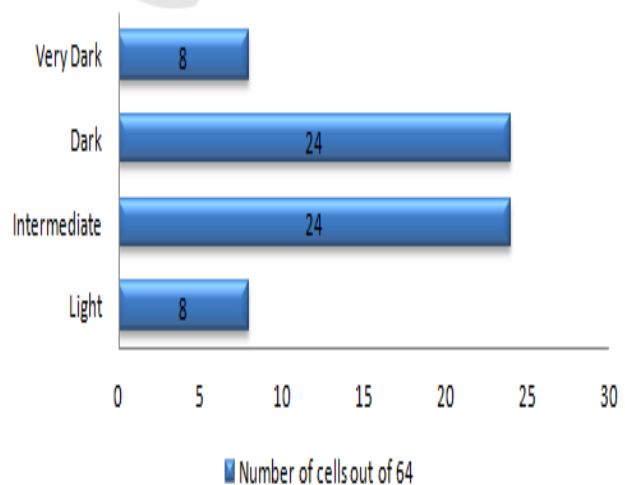
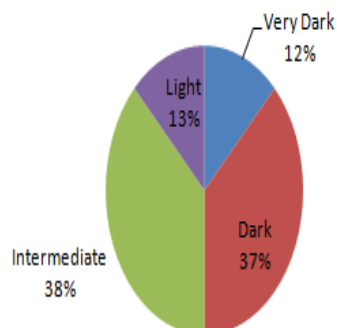
Parent 1: Very Dark Skin Colour, Genotype: AaBBCC

Parent 2: Very Light Skin Colour, Genotype: aabbCc

Pt-1:	ABC	ABC	ABC	ABC	aBC	aBC	aBC	aBC
Pt-2:	abC	AaBbCC	AaBbCC	AaBbCC	AaBbCC	aaBbCC	aaBbCC	aaBbCC
	4	4	4	4	3	3	3	3
abc	AaBbCc	AaBbCc	AaBbCc	AaBbCc	aaBbCc	aaBbCc	aaBbCc	aaBbCc
	3	3	3	3	2	2	2	2
abC	AaBbCC	AaBbCC	AaBbCC	AaBbCC	aaBbCC	aaBbCC	aaBbCC	aaBbCC
	4	4	4	4	3	3	3	3
abc	AaBbCc	AaBbCc	AaBbCc	AaBbCc	aaBbCc	aaBbCc	aaBbCc	aaBbCc
	3	3	3	3	2	2	2	2
abC	AaBbCC	AaBbCC	AaBbCC	AaBbCC	aaBbCC	aaBbCC	aaBbCC	aaBbCC
	4	4	4	4	3	3	3	3
abc	AaBbCc	AaBbCc	AaBbCc	AaBbCc	aaBbCc	aaBbCc	aaBbCc	aaBbCc
	3	3	3	3	2	2	2	2

**Example 2.2****Parent 1: Very Dark Skin Colour, Genotype: AaBBCC****Parent 2: Light Skin Colour, Genotype: aaBbCc**

Pt-1:	ABC	ABC	ABC	ABC	aBC	aBC	aBC	aBC
Pt-2:	aBC	AaBBCC	AaBBCC	AaBBCC	AaBBCC	aaBBCC	aaBBCC	aaBBCC
	5	5	5	5	4	4	4	4
	aBc	AaBBCc	AaBBCc	AaBBCc	AaBBCc	aaBBCc	aaBBCc	aaBBCc
	4	4	4	4	3	3	3	3
	abC	AaBbCC	AaBbCC	AaBbCC	AaBbCC	aaBbCC	aaBbCC	aaBbCC
	4	4	4	4	3	3	3	3
	abc	AaBbCc	AaBbCc	AaBbCc	AaBbCc	aaBbCc	aaBbCc	aaBbCc
	3	3	3	3	2	2	2	2
	aBC	AaBBCC	AaBBCC	AaBBCC	AaBBCC	aaBBCC	aaBBCC	aaBBCC
	5	5	5	5	4	4	4	4
	aBc	AaBBCc	AaBBCc	AaBBCc	AaBBCc	aaBBCc	aaBBCc	aaBBCc
	4	4	4	4	3	3	3	3
	abC	AaBbCC	AaBbCC	AaBbCC	AaBbCC	aaBbCC	aaBbCC	aaBbCC
	4	4	4	4	3	3	3	3
	abc	AaBbCc	AaBbCc	AaBbCc	AaBbCc	aaBbCc	aaBbCc	aaBbCc
	3	3	3	3	2	2	2	2

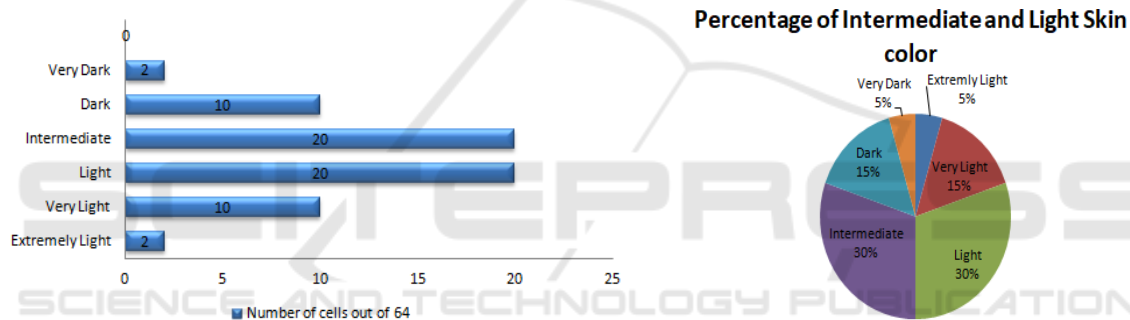
percentage of Very Dark X Light Skin Color

Example 2.3

Parent 1: Intermediate Skin Colour, Genotype: AaBbCc

Parent 2: Light Skin Colour, Genotype: aaBbCc

Pt-1:	ABC	ABc	AbC	Abc	aBC	aBc	abC	abc
Pt-2:	aBC	AaBBCC	AaBBCc	AaBbCC	AaBbCc	aaBBCC	aaBBCc	aaBbCC
	5	4	4	3	4	3	3	2
aBc	AaBBCC	AaBBcc	AaBbCc	AaBbcc	aaBBCC	aaBBcc	aaBbCc	aaBbcc
	4	3	3	2	3	2	2	1
abC	AaBbCC	AaBbCc	AabbCC	AabbCc	aaBbCC	aaBbCc	aabbCC	aabbCc
	4	3	3	2	3	2	2	1
abc	AaBbCc	AaBbcc	AabbCc	Aabbcc	aaBbCc	aaBbcc	aabbCc	aabbcc
	3	2	2	1	2	1	1	0
aBC	AaBBCC	AaBBCc	AaBbCC	AaBbCc	aaBBCC	aaBBCc	aaBbCC	aaBbCc
	5	4	4	3	4	3	3	2
aBc	AaBBCC	AaBBcc	AaBbCc	AaBbcc	aaBBCC	aaBBcc	aaBbCc	aaBbcc
	4	3	3	2	3	2	2	1
abC	AaBbCC	AaBbCc	AabbCC	AabbCc	aaBbCC	aaBbCc	aabbCC	aabbCc
	4	3	3	2	3	2	2	1
abc	AaBbCc	AaBbcc	AabbCc	Aabbcc	aaBbCc	aaBbcc	aabbCc	aabbcc
	3	2	2	1	2	1	1	0

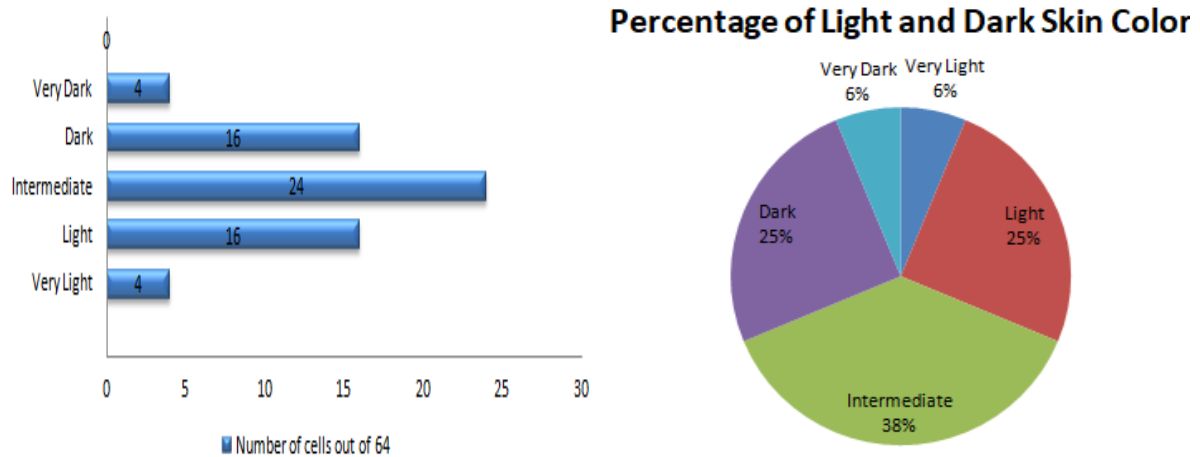


Example 2.4

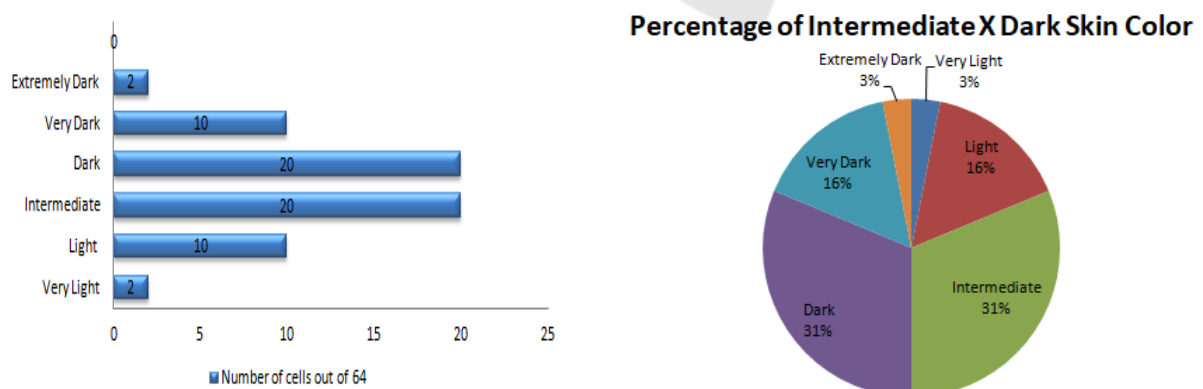
Parent 1: Light Skin Colour, Genotype: aaBbCc

Parent 2: Dark Skin Colour, Genotype: AaBbCC

Pt-1:	aBC	aBc	abC	abc	aBC	aBc	abC	abc
Pt-2:	ABC	AaBBCC	AaBBCc	AaBbCC	AaBbCc	AaBBCC	AaBBCc	AaBbCC
	5	4	4	3	5	4	4	3
ABC	AaBBCC	AaBBCc	AaBbCC	AaBbCc	AaBBCC	AaBBCc	AaBbCC	AaBbCc
	5	4	4	3	5	4	4	3
AbC	AaBbCC	AaBbCc	AabbCC	AabbCc	AaBbCC	AaBbCc	AabbCC	AabbCc
	4	3	3	2	4	3	3	2
AbC	AaBbCC	AaBbCc	AabbCC	AabbCc	AaBbCC	AaBbCc	AabbCC	AabbCc
	4	3	3	2	4	3	3	2
aBC	aaBBCC	aaBBCc	aaBbCC	aaBbCc	aaBBCC	aaBBCc	aaBbCC	aaBbCc
	4	3	3	2	4	3	3	2
aBC	aaBBCC	aaBBCc	aaBbCC	aaBbCc	aaBBCC	aaBBCc	aaBbCC	aaBbCc
	4	3	3	2	4	3	3	2
abC	aaBbCC	aaBbCc	aabbCC	aabbCc	aaBbCC	aaBbCc	aabbCC	aabbCc
	3	2	2	1	3	2	2	1
abC	aaBbCC	aaBbCc	aabbCC	aabbCc	aaBbCC	aaBbCc	aabbCC	aabbCc
	3	2	2	1	3	2	2	1

**Example 2.5****Parent 1: Intermediate Skin Colour, Genotype: AaBbCc****Parent 2: Dark Skin Colour, Genotype: AaBbCC**

Pt-1: Pt-2:	ABC	ABc	AbC	Abc	aBC	aBc	abC	abc
ABC	AABBCC	AABBCc	AABbCC	AABbCc	AaBBCC	AaBBCc	AaBbCC	AaBbCc
	6	5	5	4	5	4	4	3
ABc	AABBCC	AABBCc	AABbCC	AABbCc	AaBBCC	AaBBCc	AaBbCC	AaBbCc
	6	5	5	4	5	4	4	3
AbC	AABbCC	AABbCc	AAbbCC	AAbbCc	AaBbCC	AaBbCc	AabbCC	AabbCc
	5	4	4	3	4	3	3	2
Abc	AABbCC	AABbCc	AAbbCC	AAbbCc	AaBbCC	AaBbCc	AabbCC	AabbCc
	5	4	4	3	4	3	3	2
aBC	AaBBCC	AaBBCc	AaBbCC	AaBbCc	aaBBCC	aaBBCc	aaBbCC	aaBbCc
	5	4	4	3	4	3	3	2
aBc	AaBBCC	AaBBCc	AaBbCC	AaBbCc	aaBBCC	aaBBCc	aaBbCC	aaBbCc
	5	4	4	3	4	3	3	2
abC	AaBbCC	AaBbCc	AabbCC	AabbCc	aaBbCC	aaBbCc	aabbCC	aabbCc
	4	3	3	2	3	2	2	1
abc	AaBbCC	AaBbCc	AabbCC	AabbCc	aaBbCC	aaBbCc	aabbCC	aabbCc
	4	3	3	2	3	2	2	1



3 THE UTILIZATION OF FUZZY SOFT BIPARTITE DIGRAPHS IN EXAMINING THE PREDOMINANT HUMAN SKIN TONES

The explanation of discussions involving Punnett Squares can be enhanced through the use of fuzzy soft bipartite digraphs. The following pattern explains the chances of the young acquiring the colour of their skin

Vertex Set 1: { p_1 stands for Parent 1 ; p_2 stands for Parent 2 } ;

Vertex Set 2: { c_1 stands for child with Very Dark Skin ;

c_2 stands for child with Dark Skin ;

c_3 stands for child with Intermediate Skin ;

c_4 stands for child with Light Skin,

c_5 stands for child with Very Light Skin ;

c_6 stands for child with Extremely Light Skin ;

c_7 stands for child with Extremely Dark Skin. }

We can fix the parameters for argument

e_1 represents the colour of the skin of parents: p_1 : Very Dark Skin & p_2 : Very Light Skin.

e_2 represents the colour of the skin of parents: p_1 : Very Dark Skin & p_2 : Light Skin.

e_3 represents the colour of the skin of parents: p_1 : Intermediate Skin & p_2 : Light Skin.

e_4 represents the colour of the skin of parents: p_1 : Light Skin & p_2 : Dark Skin.

e_5 represents the colour of the skin of parents: p_1 : Intermediate Skin & p_2 : Dark Skin.

e_6 represents the colour of the skin of parents: p_1 : Extremely Dark Skin & p_2 : Light Skin.

e_7 represents the colour of the skin of parents: p_1 : Extremely Light Skin & p_2 : Dark Skin.

Example: 3.1

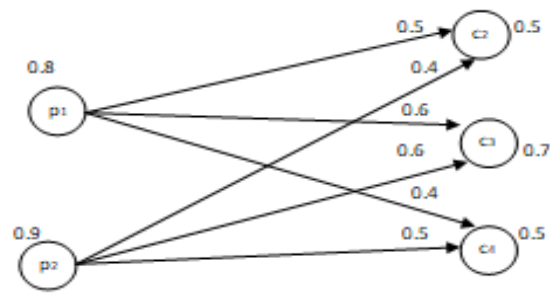
Consider $V_1 = \{ p_1, p_2 \}$; $V_2 = \{ c_1, c_2, c_3, c_4, c_5 \}$ and $E = \{ e_1, e_2, e_3, e_4, e_5, e_6, e_7 \}$.

Let $A = \{ e_1, e_2, e_3, e_4, e_5 \}$. $D_{A,V}$ is characterized by a table and

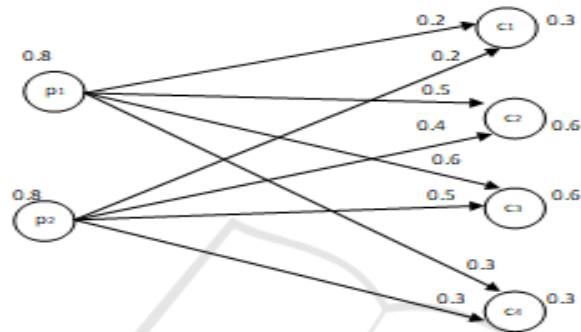
$\mu_e(x_i, x_j) = 0 \quad \forall (x_i, x_j) \in V_1 \times V_2 \setminus ((p_1, c_1), (p_1, c_2), (p_1, c_3), (p_1, c_4), (p_1, c_5), (p_2, c_1), (p_2, c_2), (p_2, c_3), (p_2, c_4), (p_2, c_5))$ and $e \in A$.

Table 2.

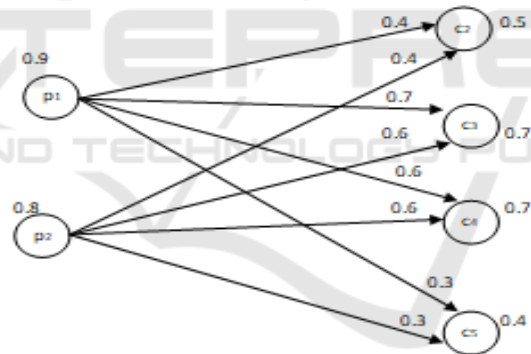
μ_D	Parent 1 (p_1)	Parent 2 (p_2)	Very Dark Skin Child (c_1)	Dark Skin Child (c_2)	Intermediate skin Child (c_3)	Light Skin Child (c_4)	Very Light Skin Child (c_5)
e_1 VDS x VLS	0.8	0.9	0	0.5	0.7	0.5	0
e_2 VDS x LS	0.8	0.8	0.3	0.6	0.6	0.3	0
e_3 IM x LS	0.9	0.8	0	0.5	0.7	0.7	0.4
e_4 LS x DS	0.7	0.8	0	0.6	0.7	0.5	0
e_5 IM x DS	0.9	0.8	0.5	0.7	0.8	0.4	0
μ_D	Parent 1 – Very Dark Skin Child (p_1, c_1)	Parent 1 – Dark Skin Child (p_1, c_2)	Parent 1 – Intermediate skin Child (p_1, c_3)	Parent 1 – Light Skin Child (p_1, c_4)	Parent 1 – Very Light Skin Child (p_1, c_5)		
e_1 VDS x VLS	0	0.5	0.6	0.4	0		
e_2 VDS x LS	0.2	0.5	0.6	0.3	0		
e_3 IM x LS	0	0.4	0.7	0.6	0.3		
e_4 LS x DS	0	0.5	0.6	0.4	0		
e_5 IM x DS	0.4	0.7	0.7	0.3	0		
μ_D	Parent 2 – Very Dark Skin Child (p_2, c_1)	Parent 2 – Dark Skin Child (p_2, c_2)	Parent 2 – Intermediate skin Child (p_2, c_3)	Parent 2 – Light Skin Child (p_2, c_4)	Parent 2 – Very Light Skin Child (p_2, c_5)		
e_1 VDS x VLS	0	0.4	0.6	0.5	0		
e_2 VDS x LS	0.2	0.4	0.5	0.3	0		
e_3 IM x LS	0	0.4	0.6	0.6	0.3		
e_4 LS x DS	0	0.5	0.6	0.5	0		
e_5 IM x DS	0.3	0.6	0.7	0.3	0		



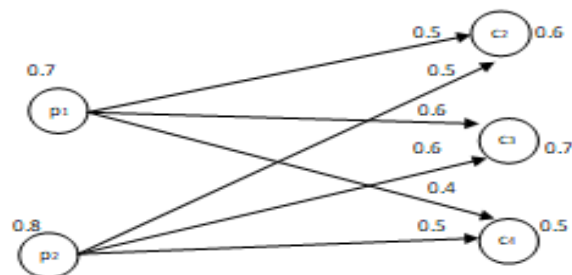
Corresponding to the parameter $e_1, H(e_1)$



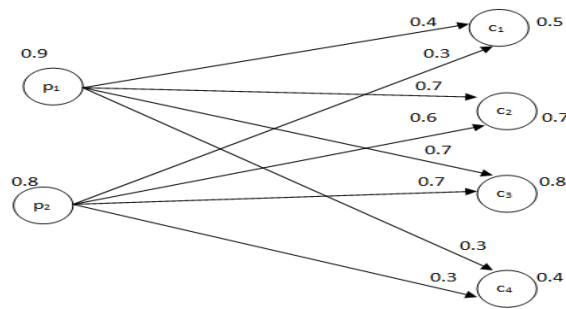
Corresponding to the parameter $e_2, H(e_2)$



Corresponding to the parameter $e_3, H(e_3)$



Corresponding to the parameter $e_4, H(e_4)$



Corresponding to the parameter $e_5, H(e_5)$

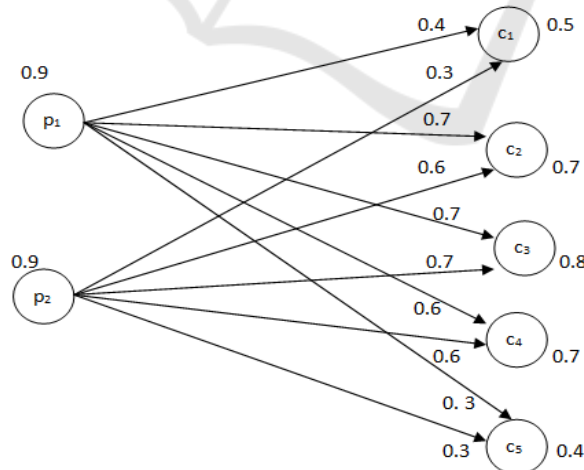
Fig.3.1 Fuzzy Soft Bipartite Digraph $D_{A,V} = \{H(e_1), H(e_2), H(e_3), H(e_4), H(e_5)\}$

By taking the Union of fuzzy digraphs $\tilde{H}(e_1), \tilde{H}(e_2), \tilde{H}(e_3), \tilde{H}(e_4)$ and $\tilde{H}(e_5)$, we derive a resultant fuzzy digraph. $\tilde{H}(t), t = e_1 \cup e_2 \cup e_3 \cup e_4 \cup e_5$

Table 3.2

ρ_D	Parent 1 (p_1)	Parent 2 (p_2)	Very Dark Skin Child (c_1)	Dark Skin Child (c_2)	Intermediate skin Child (c_3)	Light Skin Child (c_4)	Very Light Skin Child (c_5)
t $= \{e_1 \cup e_2$ $\cup e_3 \cup e_4$ $\cup e_5\}$	0.9	0.9	0.5	0.7	0.8	0.7	0.4

μ_D	Parent 1 – Very Dark Skin Child (p_1, c_1)	Parent 1 – Dark Skin Child (p_1, c_2)	Parent 1 – Intermediate skin Child (p_1, c_3)	Parent 1 – Light Skin Child (p_1, c_4)	Parent 1 – Very Light Skin Child (p_1, c_5)
t	0.4	0.7	0.7	0.6	0.3
μ_D	Parent 2 – Very Dark Skin Child (p_2, c_1)	Parent 2 – Dark Skin Child (p_2, c_2)	Parent 2 – Intermediate skin Child (p_2, c_3)	Parent 2 – Light Skin Child (p_2, c_4)	Parent 2 – Very Light Skin Child (p_2, c_5)
t	0.3	0.6	0.7	0.6	0.3



Corresponding to the parameter $t, H(t = \{e_1 \cup e_2 \cup e_3 \cup e_4 \cup e_5\})$

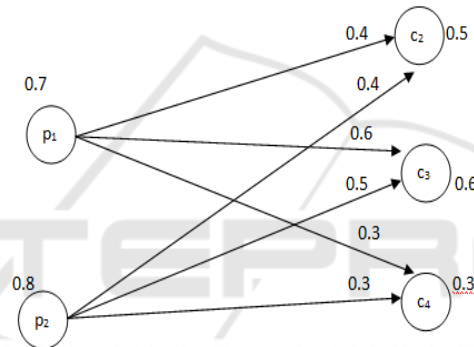
Fig.3.2 Union of Fuzzy Bipartite Digraph $H(t) = \{H(e_1) \cup H(e_2) \cup H(e_3) \cup H(e_4) \cup H(e_5)\}$

By taking the Intersection of fuzzy digraphs $\tilde{H}(e_1), \tilde{H}(e_2), \tilde{H}(e_3), \tilde{H}(e_4)$ and $\tilde{H}(e_5)$, we derive a resultant fuzzy digraph. $\tilde{H}(d), d = d_1 \cap d_2 \cap d_3 \cap d_4 \cap d_5$

Table 3.

ρ_D	Parent 1 (p_1)	Parent 2 (p_2)	Very Dark Skin Child (c_1)	Dark Skin Child (c_2)	Intermediate skin Child (c_3)	Light Skin Child (c_4)	Very Light Skin Child (c_5)
d $= \{e_1 \cap e_2$ $\cap e_3 \cap e_4$ $\cap e_5\}$	0.7	0.8	0	0.5	0.6	0.3	0

μ_D	Parent 1 – Very Dark Skin Child (p_1, c_1)	Parent 1 – Dark Skin Child (p_1, c_2)	Parent 1 – Intermediate skin Child (p_1, c_3)	Parent 1 – Light Skin Child (p_1, c_4)	Parent 1 – Very Light Skin Child (p_1, c_5)
d	0	0.4	0.6	0.3	0
μ_D	Parent 2 – Very Dark Skin Child (p_2, c_1)	Parent 2 – Dark Skin Child (p_2, c_2)	Parent 2 – Intermediate skin Child (p_2, c_3)	Parent 2 – Light Skin Child (p_2, c_4)	Parent 2 – Very Light Skin Child (p_2, c_5)
d	0	0.4	0.5	0.3	0



Corresponding to the parameter $d, H(d) = \{e_1 \cap e_2 \cap e_3 \cap e_4 \cap e_5\}$

Fig.3.3 Intersection of Fuzzy Bipartite Digraph $H(d) = \{H(e_1) \cap H(e_2) \cap H(e_3) \cap H(e_4) \cap H(e_5)\}$

Table 4.

D_{AV}	Deg (c_1) child with Very Dark Skin	Deg (c_2) child with Dark Skin	Deg (c_3) Intermediate Skin	Deg (c_4) Light Skin	Deg (c_5) child with Very Light Skin
$H(t)$	0.5	0.7	0.8	0.7	0.4
$H(d)$	0	0.5	0.6	0.3	0
Deg	0.5	1.2	1.4	1.0	0.4

The vertex C_3 has a greater degree than the other skin color. As a result, the most prevalent skin tone is only intermediate.

4 CONCLUSIONS

In summary, the range of skin tones observed in human populations can be attributed to the interplay of multiple genes, particularly those involved in the

synthesis and control of melanin. The enormous variety of skin tones that may be found all across the world is influenced by both genetic variations inherited from our ancestors and environmental factors. Finally, we are able to agree that skin tones that are genetically intermediate will predominate

over other tones. Applying mathematical values to genetic phenomena has proven this. This kind of research can be used in a variety of fields, such as diseases and transportation scenarios that call for complex judgments to be made.

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