

APPLICATION OF COMPLETE BIPARTITE GRAPH IN GENETIC FIELDS TO COMPUTE PHENOTYPE RATIO AND GENOTYPE RATIO

A. Pradeepa¹ and Dr.O.V.Shanmuga Sundaram²

1. Research Scholar, Dept. of . Mathematics, Sree Saraswathi Thyagaraja college, Pollachi.

Email:pradeepavennila17@gmail.com

2. Associate Professor, Dept. of . Mathematics, Sree Saraswathi Thyagaraja college, Pollachi.

Email:ovs3662@gmail.com

Abstract:

One of the important areas in graph theory is complete bipartite graph. It is a convenient tool to understand gene, and crossing one pair that differ in alleles. Adjacency matrix obtained from complete bipartite graph. Input an Adjacency matrix solution in Python. Genotype ratio and Phenotype ratio analysis of Trihybrid crosses using a Python program, combined imaging tool.

MSC Classification: 05C05,05C22,05C90,92D15,97P50.

Key words: bipartite graph, bi adjacency matrix, Gene, phenotype ratio, genotype ratio.

1. Introduction:

Euler was the father of graph theory (1707-1782). Euler's work on the Konigsberg bridges problem begun in 1735[2]. Euler states that, seven crossing the bridge and returning to the starting point, could not come without swimming in the river [1][5]. Mendel is known as the 'father of genetics'. Gregor Johann Mendel was interested in learning the method to offspring. He started experiments on a pea plant [6][7]. Connectivity can be represented by a graph. Many real life problems can be clearly defined in graph theory. Graph theory applied to Internet, electric networks, bio-chemistry, medical field, computer science, communication network, genetics [1] [15] [13]. A complete bipartite graph whose vertices can be partitioned into two subsets M and F [16]. Complete bipartite graph is a convenient tool to understand gene. Crossing single pair that differ in hair. A weighted bipartite graph has a join for both M and F gametes [3] [6] [14]. Obtain the Bi adjacency matrix from a complete bipartite graph. A bi adjacency matrix is used to find Trihybrid M₂ generation [3] [12]. Python Program is applied to combined imaging tool. Python combine image tool use to genotype ratio and phenotype ratio of trihybrid cross [4] [9] [10].

2. Basic definitions of graph theory:

2.1 Graph:

A graph contains of points and lines. Points on a graph are labelled vertices. Lines on a graph are labelled edges. Every edge connects the points to another points.

2.2 Tree:

A tree has vertices and edges and has no rotation.

2.3 Bipartite graph:

Bipartite graph is said to be complete if all the vertices in set-1 are connected to vertices of set-2.

2.4 Complete Bipartite graph:

Complete bipartite graph is said to be complete if all the vertices in set-1 are connected to every vertex of set-2.

So, if set-1 has Male Gametes (M) and set-2 has Female gametes(F) then the total number of edges will be $M \times F$.

2.5 Weighted Bipartite graph:

A graph is a Weighted Bipartite graph, then the elements are taken to be the weight of the edge respectively.

2.6 Bi adjacency Matrix:

Let $G(M, F, E)$ be a bipartite graph with parts $M = \{m_{\{1\}}, \dots, m_{\{r\}}\}$, $F = \{f_{\{1\}}, \dots, f_{\{s\}}\}$ and edges E . the bi adjacency Matrix is the $M \times F$.

If G is a Weighted Bipartite graph, then the elements b_{mf} are taken to be the weight of the edge $\{m_{\{1\}} f_{\{1\}}, \dots, m_{\{r\}} f_{\{s\}}\}$ respectively.

3. Basics of Genetics:

3.1 Heredity

Transmission of genetic characters from parent to offspring.

3.2 Variation

Individuals have some differences these are called variation.

3.3 Gene

One of a group of units that line up on chromosomes and are thought to influence the visual characteristics of offspring.

3.4 Locus:

The place on a chromosome, where an allele can be established.

3.5 Allele:

A pair of genes controlling the same character and located at the same locus in the homologous chromosome.

3.6 Trait:

It is a unique genetic trait of a structure.

3.7 Genome [11]

The entire set of genes in an organism.

- The gene that carry all traits.
- Two different forms of the same Gene Alleles.
- Ex: Gene: Hair

Alleles: Kinky, Pure.

3.8 Dominant Allele:

Expressed even when the dominant allele is combined with the recessive allele [11].

3.9 Recessive Allele:

When two recessive alleles are combined, the recessive allele is visible. [11].

3.10 Homozygous Allele:

Two alleles identical for a trait are homozygous alleles. [8].

3.11 Heterozygous Alleles:

Two alleles different for a trait are heterozygous alleles. [8].

3.12 Genotype:

The genetic structure of each individual organism is known as genotype.

3.13 Phenotype:

Phenotype is the physical looks of a particular trait.

3.14 Genotype Ratio:

Genotype Ratio is the communicate of genes in the generation gained after a gene.

3.15 Phenotype Ratio:

Phenotype Ratio is the communicate of physical features in the generation gained after a gene.

3.16 Gametes:

Gametes are the reproductive cells of an organism. Female gametes are ova and Male gametes are sperm.

3.17 Monohybrid cross:

Monohybrid cross is a cross between single pair that differ in single traits.

3.18 Dihybrid cross:

Dihybrid cross is a cross between single pair that differ in three traits.

3.19 Trihybrid cross:

Trihybrid cross is a cross between single pair that differ in three traits.

4. Main results

4.1 Trihybrid Cross:

A Trihybrid cross is a combination of three separate Monohybrid cross.

We have taken a single pair that differ by three traits. The selected three traits Hair style, Skin colour, Nose shape. Here, the example

Human hair type [kinky hair- ϕ , pure hair- δ], Human skin colour [dark skin - μ , bright skin - β], Human Nose type [fleshy nose - α , Sharp nose - γ].

4.2 Problem 1

4.2.1 M_1 [Maternity] Generation:

The M_1 generation is the first son or daughter generation of a Trihybrid cross. A genetic cross of that concentrate on the inheritance of two separate traits.

4.2.2 Parents of M_1 Generation:

A generation that normally homozygous store for one or more traits. Parents were selected to be applied in the M_1 generation cross of a genetic testing. The M_1 Generation are two persons that are same hybrid for two traits. One parent is homozygous dominant another parent is homozygous recessive. M_1 Generation shows the homozygous dominant allele. The Fig.1 expos that Trihybrid cross M_1 generation.

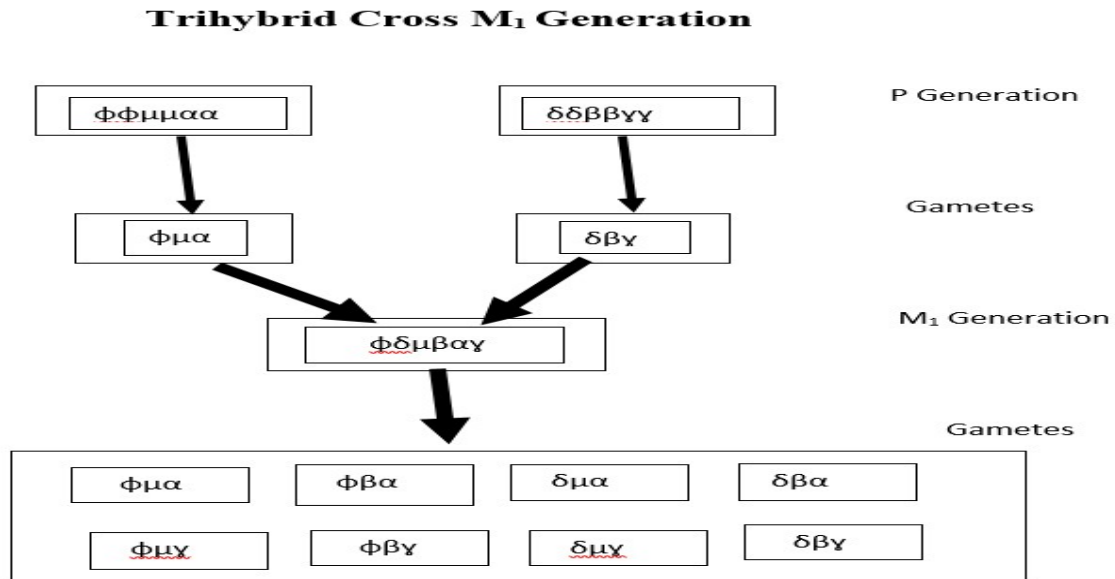


Fig.1. Trihybrid cross in M₁ Gametes

4.2.3 Result 1:

Genotype ratio:

The M₁ generation exposes an Eight gametes that is Heterozygous for pair of features.

4.2.4 Result -2

Phenotype ratio:

M₁ generation exposes a three phenotype that is dominant heterozygous for pair of features. So, first generation exhibits a kinky hair, Dark skin, Fleshy nose.

5 Problem 2.

5.1 M₂ Generation:

The M₂ Generation is the second maternity generation of the Trihybrid cross. A genetic cross that focuses on the inheritance of two separate M₁ Generation.

5.2 Parents of M₂ Generation:

The M₂ generation are heterozygous for pair of features. Male gametes have heterozygous alleles. Female gametes have heterozygous alleles.

5.3 Complete bipartite graph:

A complete bipartite graph is used to M₂ generation. The M₂ generation are heterozygous for pair of features. Crossing single pair that differ in Hair type, Skin colour, Nose shape.

Kinky hair denoted by ϕ and Pure hair by δ .

Dark skin colour denoted by μ and bright skin colour by β .

Fleshy nose shape denoted by α and sharp nose shape by γ .

A graph Whose vertices can be partitioned in to two subsets M and F.

Every vertex of set M is joined to every vertex of set F. Set M has Male gametes for kinky hair, pure hair, Dark skin, bright skin, Fleshy nose, and sharp nose. Set F has Female gametes for kinky hair, pure hair, kinky hair, pure hair, Dark skin, bright skin, Fleshy nose, and sharp nose.

We calculate the total number of edges will be multiplied by number of male gametes and number of female gametes.

A weighted of bipartite graph has a join for both Male gametes and Female gametes. The Fig.2 expos that Trihybrid cross of M_2 generation.

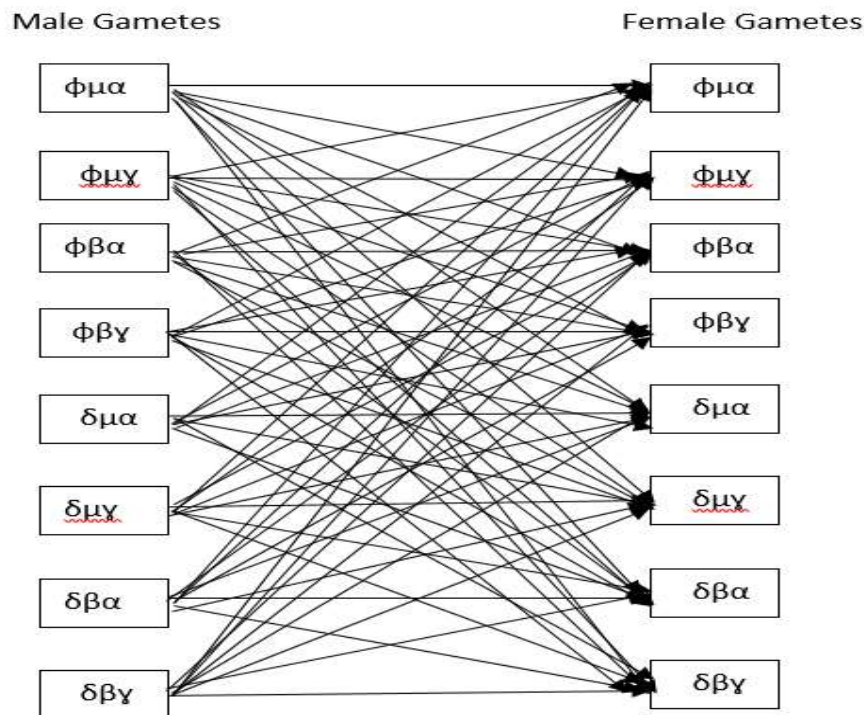


Fig 2. Trihybrid cross in M_2 generation

5.4 Bi adjacency matrix:

A bi adjacency matrix is used to find Trihybrid M_2 generation. Adjacency matrix expos a square matrix. Let's construct the adjacency Matrix through a complete bipartite graph[fig.2]. The factor of the matrix specified if both of vertices are adjacent in the graph.

5.5 Result -1

5.5.1 Genotype:

Parent's differ by a Three traits

Crossing single pair that differ in style, colour, shape.

$\{\phi\mu\alpha, \phi\mu\gamma, \phi\beta\alpha, \phi\beta\gamma, \delta\mu\alpha, \delta\mu\gamma, \delta\beta\alpha, \delta\beta\gamma\}$ this type of Male Gametes married with $\{\phi\mu\alpha, \phi\mu\gamma, \phi\beta\alpha, \phi\beta\gamma, \delta\mu\alpha, \delta\mu\gamma, \delta\beta\alpha, \delta\beta\gamma\}$ type of Female Gametes. We can see what kind of child it is in the adjacency matrix. The Fig.3 expos that Genotype Adjacency Matrix.

+	FM	φμα	<u>φμγ</u>	φβα	φβγ	δμα	<u>δμγ</u>	δβα	δβγ
M									
	φμα	<u>φφμμαα</u>	<u>φφμμαγ</u>	<u>φφμβαα</u>	<u>φφμβαγ</u>	<u>φδμμαα</u>	<u>φδμμαγ</u>	<u>φδμβαα</u>	<u>φδμβαγ</u>
	<u>φμγ</u>	<u>φφμμγα</u>	<u>φφμμγγ</u>	<u>φφμβγα</u>	<u>φφμβγγ</u>	<u>φδμμγα</u>	<u>φδμμγγ</u>	<u>φδμβγα</u>	<u>φδμβγγ</u>
	φβα	<u>φφβμαα</u>	<u>φφβμαγ</u>	<u>φφββαα</u>	<u>φφββαγ</u>	<u>φδβμαα</u>	<u>φδβμαγ</u>	<u>φδββαα</u>	<u>φδββαγ</u>
	φβγ	<u>φφβμγα</u>	<u>φφβμγγ</u>	<u>φφββγα</u>	<u>φφββγγ</u>	<u>φδβμγα</u>	<u>φδβμγγ</u>	<u>φδββγα</u>	<u>φδββγγ</u>
	δμα	<u>φδμμαα</u>	<u>φδμμαγ</u>	<u>φδμβαα</u>	<u>φδμβαγ</u>	<u>δδμμαα</u>	<u>δδμμαγ</u>	<u>δδμβαα</u>	<u>δδμβαγ</u>
	<u>δμγ</u>	<u>φδμμγα</u>	<u>φδμμγγ</u>	<u>φδμβγα</u>	<u>φδμβγγ</u>	<u>δδμμγα</u>	<u>δδμμγγ</u>	<u>δδμβγα</u>	<u>δδμβγγ</u>
	δβα	<u>φδμβαα</u>	<u>φδμβαγ</u>	<u>φδββαα</u>	<u>φδββαγ</u>	<u>δδμβαα</u>	<u>δδμβαγ</u>	<u>δδββαα</u>	<u>δδββαγ</u>
	δβγ	<u>φδμβαγ</u>	<u>φδμβγγ</u>	<u>φδββγα</u>	<u>φδββγγ</u>	<u>δδμβαγ</u>	<u>δδμβγγ</u>	<u>δδβαγβ</u>	<u>δδββγγ</u>

Fig 3. Genotype Adjacency Matrix.

Solution :

M₂ generation genotype in 27 different types are obtained:

Genotype ratio for 1 :2 :1: 2: 4 : 2 : 1 : 2 : 1 : 2 : 4: 2 :4: 8:4:2:4:2:1:2:1:2:4:2:1:2:1

- 1: φφμμαα-kinky hair, dark skin, fleshy nose child
- 2: φφμμαγ- kinky hair, dark skin, medium nose child
- 1: φφμμγγ- kinky hair, dark skin, sharp nose child
- 2: φφμβαα- kinky hair, light skin, fleshy nose child
- 4: φφμβαγ- kinky hair, light skin, medium nose child
- 2: φφμβγγ- kinky hair, light skin, sharp nose child
- 1: φφββαα- kinky hair, bright skin, fleshy nose child
- 2: φφββαγ- kinky hair, bright skin, medium nose child
- 1: φφββγγ- kinky hair, bright skin, sharp nose child
- 2: φδμμαα-Wavy hair,dark skin, fleshy nose child
- 4: φδμμαγ- Wavy hair, dark skin, medium nose child
- 2: φδμμγγ- Wavy hair, dark skin, sharp nose child
- 4: φδμβαα- Wavy hair, light skin, fleshy nose child
- 8: φδμβαγ- Wavy hair, light skin, medium nose child
- 4: φδμβγγ- Wavy hair, light skin, sharp nose child
- 2: φδββαα- Wavy hair, bright skin, fleshy nose child
- 4: φδββαγ- Wavy hair, bright skin, medium nose child
- 2: φδββγγ- Wavy hair, bright skin, sharp nose child
- 1: δδμμαα- pure hair, dark skin, fleshy nose child
- 2: δδμμαγ- pure hair, dark skin, medium nose child
- 1: δδμμγγ- pure hair, dark skin, sharp nose child
- 2: δδμβαα- pure hair, light skin, fleshy nose child
- 4: δδμβαγ- pure hair, light skin, medium nose child

- 2: δδμβγγ- pure hair, light skin, sharp nose child
- 1: δδββαα - pure hair, bright skin, fleshy nose child
- 2: δδββαγ - pure hair, bright skin, medium nose child
- 1: δδββγγ - pure hair, bright skin, sharp nose child.

5.5.2. Python combined image tool:

Python combined image tool is applied to get the child image. Input a Bi- adjacency matrix solution in Python program. Python combined image tool used to genotype ratio of Trihybrid cross. Finally, output for Trihybrid genotype ratio.

5.6 Result -2

5.6.1 Bi adjacency matrix:

Phenotype:

Parent’s differ by a Three traits

Crossing single pair that differ in style, colour, shape.

{φμα, φμγ, φβα, φβγ, δμα, δμγ, δβα, δβγ} this type of Male Gametes married with {φμα, φμγ, φβα, φβγ, δμα, δμγ, δβα, δβγ} type of Female Gametes. We can see what kind of child it is in the adjacency matrix. The Fig.4 expos that Phenotype Adjacency Matrix.

+	FM	φμα	φμγ	φβα	φβγ	δμα	δμγ	δβα	δβγ
M									
	φμα	φμα	φμα	φμα	φμα	φμα	φμα	φμα	φμα
	φμγ	φμα	φμγ	φμα	φμγ	φμα	φμγ	φμα	φμγ
	φβα	φμα	φμα	φβα	φβα	φμα	φμα	φβα	φββγ
	φβγ	φμα	φμγ	φβα	φβγ	φμα	φμα	φβα	φμγ
	δμα	φμα	φμα	φμα	φμα	δμα	δμα	δμα	δμα
	δμγ	φμα	φμγ	φμα	φμγ	δμα	δμγ	δμα	δμγ
	δβα	φμα	φμα	φβα	φβα	δμα	δμα	δβα	δβα
	δβγ	φμα	φμγ	φβα	φβγ	δμα	δμγ	δβγ	δβγ

Fig 4 Phenotype Adjacency Matrix.

Solution:

Phenotype Ratio:

M₂ generation phenotype 8 different types are obtained:

Phenotype ratio for 27: 9: 9: 9: 3: 3: 3: 1

- 27: φμα→ kinky hair, dark skin, fleshy nose child
- 9: φμγ→ kinky hair, dark skin, sharp nose child
- 9: φβα→ kinky hair, bright skin, fleshy nose child
- 9: φβγ→ kinky hair, bright skin, sharp nose child
- 3: δμα→ pure hair, dark skin, fleshy nose child
- 3: δμγ→ pure hair, dark skin, sharp nose child

3: $\delta\beta\alpha \rightarrow$ pure hair, bright skin, fleshy nose child

1: $\delta\beta\gamma \rightarrow$ pure hair, bright skin, sharp nose child

5.6.2 Python program to count occurrences of in list using count:

Python combined image tool is applied to get the child image. Input a Bi- adjacency matrix solution in Python program. Python combined image tool used to phenotype ratio of Trihybrid cross. Finally, output for Trihybrid phenotype ratio.

Conclusion

In this paper we have discussed about trihybrid cross in Genotype ratio and phenotype ratio. Crossing single pair that differ in Hair type, Skin colour, and Nose shape. A bi-adjacency matrix can be constructed from a complete bipartite graph. The adjacency matrix Solution is used as Python input to find the Genotype ratio and phenotype ratio in the three types of traits. Finally, Genotype ratio and Phenotype ratio method determine the characteristics of the offspring based on the characteristics of the parents.

References:

- [1] Bondy J.A. and Murty U.S.R , Graph Theory with applications, Newyork Mac mill Ltd. Press(1976)
- [2] R.balakrishnan, K.Ranganathan , A Text book of Graphtheory , Springer –verlag, ISSN 0172-5939 Universitextseries.
- [3] R.B.Bapat, Graphs and Matrices.ISBN 978-1-84882-980-0.e-ISBN 978-1-84882-981-7.DOI 10.1007/978-1-84882-981-7.Springer London Dordrecht Heidelberg Newyork.
- [4] Eric Matthes , Python crash course: A hands –on, Project- based Introduction to programming .
- [5] Frank Harary, graph theory, Narosa Publishing House Pvt.ltd.ISBN:978-81-85015-55-2.
- [6] Gregor Johann Mendel By “Experiments on plant Hybridization”. ISSN:978-1-60520-257-0.
- [7] <http://en.wikipedia.org/wiki/Graph> % 28 abstract data type %2a.
- [8] <https://www.healthline.com/health/homozygous#risk-factors>.
- [9] <http://www.geeksforgeeks.org/graph-and-its-representations/>.
- [10] http://www.tutorialspoint.com/python_pillow/python_pillow_tutorial.pdf.
- [11] <http://www.yourgenome.org/facts/what-are-dominant-and-recessive-alleles/>
- [12] Klug,Cummings, spencer palladino, Killian, Concepts of Genetics, 12th edition. ISBN-13.978-0134604718, ISBN:-10:0134604717.
- [13] Leland.H.Hartwell, Michel.L.Goldberg,Janicea.fischer,Leroy.hood,'Genetics from Genes to Genomes' 5th edition. Mc Graw Hill Education.
- [14] Lewis.R, Human Genetics : Concepts and Applications.12th Edition .
- [15] Nara Singh Deo, Graph theory with Applications to Engineering & Computer Science.
- [16] Weisstein,EricW.”BipartiteGraph”.From MathWorld –Awolframweb Resource. <https://mathworld.wolfram.com/BipartiteGraph.html>.