

GENETICS AND EVOLUTION

ATUL SINGH ARORA



Biology Lab III

Dr. N. G. Prasad and Dr. Rajesh Ramachandran
Indian Institute of Science Education and Research, Mohali

August-December, 2012

*Every honest researcher I know admits he's just a professional amateur.
He's doing whatever he's doing for the first time. That makes him an
amateur. He has sense enough to know that he's going to have a lot of
trouble, so that makes him a professional.*

— Charles F. Kettering (1876-1958) (Holder of 186 patents)

ACKNOWLEDGEMENTS

I express my sincere gratitude to our instructors, Dr. N. G. Prasad and Dr. Rajesh Ramachandran, for not only describing the experiments and their science in depth, but also for teaching us the art of observing, that of performing experiments, so we can appreciate the intellect behind the procedures, rather than mindlessly following them.

I also thank Vivek Sagar (MS11017) for his contribution to this report as my lab-partner, who made the task of performing experiments immensely comfortable and productive at the same time.

CONTENTS

I	EXPERIMENTS	1	
1	INTRODUCTORY SESSION	3	
1.1	Objective	3	
1.2	Theory	3	
1.2.1	Morphology	3	
1.2.2	Life Cycle	3	
1.2.3	Difference between Males and Females	4	
1.3	Experiment	5	
1.4	Observations	6	
1.4.1	Coarse Focus	6	
1.4.2	Fine Focus	6	
1.4.3	High Power Microscope	7	
1.4.4	Mutants	7	
1.5	Acknowledgements	7	
2	UNDERSTANDING GENETICS USING DROSOPHILA MELANOGASTER	9	
2.1	Objective	9	
2.2	Material Required	9	
2.3	Idea	9	
2.4	Procedure Essentials	10	
2.5	Observations and Analysis	11	
2.6	Discussion	12	
2.7	Reference	14	
2.8	Acknowledgement	14	
3	THE TASTE EXPERIMENT	15	
3.1	Objective	15	
3.2	Requirements	15	
3.3	Background Theory	15	
3.4	Statistical Analysis	16	
3.5	Procedure	16	
3.6	Observations and Results	17	
3.7	Acknowledgement	17	
3.8	References	17	
4	SELECTION AND GENETIC DRIFT	21	
4.1	Objective	21	
4.2	Requirements	21	
4.3	Theory: Basics	21	
4.4	Procedure	22	
4.5	Theory: Calculations	23	
4.5.1	Computing Allele Frequencies	23	
4.5.2	Male Mating Success	24	
4.5.3	Egg to Adult Survivorship	24	

4.6	Results	25
4.7	Acknowledgement	25
4.8	References	26
5	PHYLOGENETIC TREE	27
5.1	Objective	27
5.2	Requirements	27
5.3	Brief Theory	27
5.4	Procedure	28
5.5	Acknowledgement	29
6	ARE HUMANS EVOLVING	31
6.1	Objective	31
6.2	Requirements	31
6.3	Procedure	31
6.4	Observations and Results	31
6.5	Acknowledgement	32
II	THE SHOWCASE	35
	BIBLIOGRAPHY	37

LIST OF FIGURES

Figure 1	Drosophila Life Cycle	3
Figure 2	Male and Female Drosophila	4
Figure 3	Drosophila eye colour	14
Figure 4	Observations and Calculations	18
Figure 5	The T-Table	19
Figure 6	ClustalX	29
Figure 7	Treeview and Phylip	30
Figure 8	Offspring Height vs Mid-Parent Height	32
Figure 9	Number of Offspring vs Father's Height	33
Figure 10	Number of Offspring vs Mother's Height	33
Figure 11	Frequency vs Month of Birth of the first off- spring	34

LIST OF TABLES

Table 1	F1 Crosses	10
Table 2	Cross 1: F1 Crosses (Scarlet Male with Red Fe- male)	12
Table 3	Cross 1: F2 Crosses (Red (F1) Male with Red (F1) Female)	12
Table 4	Cross 2: F1 Crosses (Red Male with Scarlet Fe- male)	13
Table 5	Cross 2: F2 Crosses (Red (F1) Male with Red (F1) Female)	13
Table 6	C: F1 Crosses (White Male with Red Female)	13
Table 7	C: F2 Crosses (Red (F1) Male with Red (F1) Fe- male)	13
Table 8	Cross 4: F1 Crosses (Red Male with White Fe- male)	13

Table 9	Cross 4: F2 Crosses (Red (F1) Male with Red (F1) Female)	14
---------	--	----

LISTINGS

Listing 1	Format of the source file	29
-----------	---------------------------	----

ACRONYMS

Part I

EXPERIMENTS

INTRODUCTORY SESSION

1.1 OBJECTIVE

To learn the art of observation and thereby analyse the morphological features of the wild type and mutant *Drosophila melanogaster*.

1.2 THEORY

1.2.1 Morphology

Morphology is the study of form and structure of organisms.

Drosophila melanogaster is a small fly. It has two red coloured compound eyes, made up of 700-800 hexagonal units. It has two translucent wings, and a pair of halteres. It has a hairy body. It also has a pair of antennae. The abdomen is striped with visible differences between males and females.

1.2.2 Life Cycle

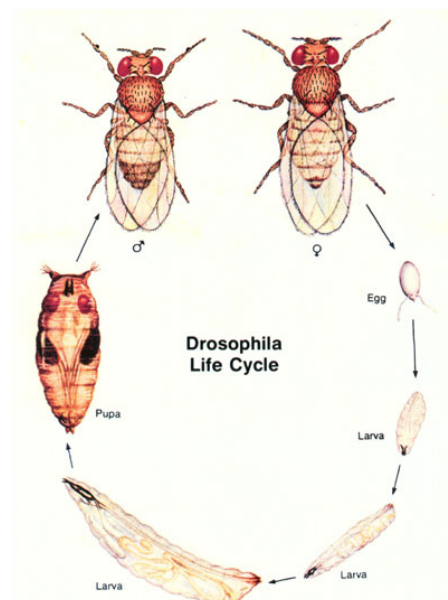


Figure 1: *Drosophila* Life Cycle [?]

1. Embryo: The first stage is from the fertilization of the egg, till the embryo hatches (under ideal conditions (at 25 °C), takes 12-

16 hours), inside the mother. The insect starts as a single cell, and then develops into the larval form before it hatches.

2. Larva: The second stage is from birth until the larva pupates. This stage is generally worm-like. It grows for about 4 days while *molting* twice (into 2nd- and 3rd-instar larvae), at about 24 and 48 h after hatching. They feed on the micro-organisms that decompose the fruit, as well as on the sugar of the fruit itself, during this period.
3. Pupa: this is the third stage, from pupation till eclosion. This stage is marked by reduced movement and often sealed with a cocoon. The metamorphosis takes about 4 days.
4. Imago: In this stage, the holometabolous insects are adults and usually have wings and functioning reproductive organs.



Holometabolism:
This term is used to describe the specific kind of insect development which includes all four life stages.

Holometabolic development gives the offspring a very unique advantage of not being forced to compete with the adults since they inhabit different ecological niches due to the morphological differences in the different stages of their life cycle.

1.2.3 Difference between Males and Females

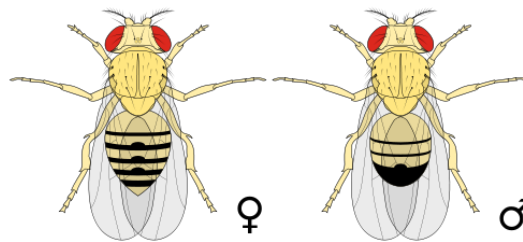


Figure 2: Male and Female *Drosophila*

1. Females have a shorter life compared to males.
2. On an average, females are larger than males (although not necessarily individually true)
3. Males have a larger portion of their back black compared to females. However, this distinction is not very clear until they're mature.
4. Males have sex-comb which is the most reliable distinguishing feature amongst males and females. It is present in the first leg.

1.3 EXPERIMENT

We were divided into groups of three and each group was given a vial containing over 30 *Drosophila melanogaster*. Our objective was to analyse them under a stereo microscope and study their morphology within 45 minutes.

My team consisted of Vivek Sagar (MS11017), Biplob Nandy (MS11004) and I (MS11003). The issue at hand was to focus a moving organism with the microscope. We came up with the following solution.

- A. Locate a cylindrical object with a small diameter.
- B. Use the object to push the cotton away from the walls of the container, while gradually moving into the container.
- C. Continue the process till a fly gets into the gap between cotton and the vial wall, upon occurrence of which, release the cotton to firmly hold the fly.
- D. This ensures that the fly has very restricted movements and is still alive.

This was followed by a discussion about the observations, after which we were told how to put the flies to “sleep”, or more precisely, anaesthetising them. The method was straight forward. It involved the use of ether, which inhibits neurological pathways in *drosophila*. The protocol followed was:

- A. Locate a funnel. At the terminal part of its conical region, attach a cotton ring.
- B. Add a few drops of the anaesthesia to the cotton.
- C. Now take an empty vial and place the funnel on its mouth, covering it completely.
- D. Locate the vial which contains the *drosophila* desired to be anaesthetised.
- E. Remove the cotton plug and instantly place the mouth of the vial on the funnel
- F. The *drosophila* will fall through the funnel into the empty vial, unconscious.
- G. Remove the funnel after a suitable duration.

One such unconscious fly's front leg was taken and focussed under a high power microscope and observed.

And lastly, Mutants were setup for viewing under stereo microscopes and we were asked to observe them.



After the flies recover their consciousness, their behaviour ceases to be normal.

1.4 OBSERVATIONS

1.4.1 *Coarse Focus*

1. Flies were of different size.
2. There were 3 pairs of legs.
3. All of them had Red coloured eyes.
4. All had their abdomen striped with Yellow Brown and Black
5. In most, there were 5 stripes.

1.4.2 *Fine Focus*

Observations of a particular fly

1. 2 hair like protrusions from the head were observed. Most likely they were antennae.
2. There were only 2 pairs of wings.
3. Back colour was Yellowish Brown
4. The body was shiny and globular.

Observations of a different fly

1. Hair like projections were visible on all three legs.
2. Abdomen was white in colour.
3. Halteres were observed.

Observations of yet another fly

1. Most of the body had black coloured hair, including the face.
2. Legs had a hook like structure
3. It seemed to be releasing a black shiny liquid
4. Lines in the wings were distinctly visible (later told to be veins)
5. Hexagonal eyes were visible. Could see the hexagonal elements.
6. Could see a slightly darker circle in the eye (later told to be sensory nerves)

Non-microscopic Observations

1. The flies try to run *away* from gravity.
2. The flies run *towards* light.

1.4.3 *High Power Microscope*

The sex comb was explicitly visible in the front leg.

1.4.4 *Mutants*

1. Barred eyes
2. Eye Colour
 - a) White
 - b) Orange
 - c) Brown
3. Curly Wings
4. Gray and Yellow Body

1.5 ACKNOWLEDGEMENTS

I thank both my team members, Biplob Nandy (MS11004) and Vivek Sagar (MS11017) for their contribution to the performance of the experiment.

UNDERSTANDING GENETICS USING DROSOPHILA MELANOGASTER

2.1 OBJECTIVE

To understand how the genes for eye colour are inherited in *Drosophila*, by setting up various crosses of the pure breeds which have only.

2.2 MATERIAL REQUIRED

1. Virgin *Drosophila* (Wild type, Scarlet and Red eyed)
2. Wild type
3. Scarlet
4. White
5. Vials containing food
6. Empty Vials
7. Cotton plugs
8. Ice box and Ice pack
9. Paint Brush
10. Binocular Microscope
11. Needles
12. Tissue Paper
13. Yeast as extra food
14. Ether as anaesthesia
15. Funnel

2.3 IDEA

The wild type (the “normal”) of *drosophila* has Red eye colour. We also have a bunch of mutants. In this experiment we’ll use White and Scarlet eye coloured mutants. We take their pure breeds and do the crosses as listed in [Table 1](#). For the actual experiment, we use 2 females and 2 males for each type. Also, we do the same cross thrice to be moderately rigorous.



*Pure Breed:
When bread
amongst themselves,
they yield the same
phenotype*

Red (wild type) Male	White Female
Red (wild type) Female	White Male
Red (wild type) Male	Scarlet Female
Red (wild type) Female	Scarlet Male


Table 1: F1 Crosses

We then observe their phenotype (eye colour) in the generation obtained, let's call them F₁. We then note that in F₁, for a given sex, there's only one phenotype. We count them. Then we self them and again observe their phenotype. (although this time it's more painful, since we've to observe males females and their phenotypes, so no running away from the microscope for amateurs like us!)


The objective is to investigate the mechanism by which genes are passed from one generation to another and since this experiment got Morgan the Nobel, therefore it's rather obvious that there's more to it than the typical mono-hybrid cross.

2.4 PROCEDURE ESSENTIALS


There is not much significance of re-writing the detailed sequential procedure. The repetitive modules, interesting, unexpected steps have been listed here.



We dry them cause else the moisture condenses and that's not good for the flies



The air bubbles will be at a higher temperature!



To prevent the unconscious flies from getting stuck on the vials

1. When labels were put on the vials that were intended to be kept in the freezer, they were taped. Sounds trivial but was very essential.
2. The method of setting up a cross:
 - a) Took the vials, dried them and cooled them using ice.
 - b) Then transferred the flies into these vials, put the cotton plug swiftly and put it back for cooling (for retaining the low temperature)
 - c) When the flies become inactive, put them on an icepack with a tissue paper on top, which doesn't have air bubbles.
 - d) Then selected the required males and females with the desired phenotypes, by observing them under a microscope if the need be, and transferred them into a new food vial, and plugged the cotton.
 - e) Kept the food vial horizontal until the flies start moving and then restored the vials to a vertical position.
 - f) Labelled the vial accordingly and stored it at 25°C, in an incubator and waited for about 36 hours.

- g) Checked if there were enough flies. If not, waited for another 12 hours. Then the parent flies were discarded in a soap solution.
 - h) Periodically, the new flies were transferred into new vials.
3. We used an improvised method for keeping the flies anaesthetized as listed below:
- a) Took a petridish and filled it with crushed ice to the brim, without closing the lid.
 - b) Using an aluminium foil, covered the surface of the petridish.
 - c) Put a tissue paper on it



To prevent overcrowding of eggs.



How does overcrowding make a difference here

2.5 OBSERVATIONS AND ANALYSIS

Observations in this experiment are restricted to the number of flies of specific eye colour and sex, in a given generation. As described earlier, F₁ is the first generation and F₂ is the second generation. For various crosses, the observations have been summarized as below:

- 1. Cross 1: Scarlet Male with Red Female
 - a) F₁: [Table 2](#)
 - b) F₂: [Table 3](#)
- 2. Cross 2: Scarlet Male with Red Female
 - a) F₁: [Table 4](#)
 - b) F₂: [Table 5](#)
- 3. Cross 3: White Male with Red Female
 - a) F₁: [Table 6](#)
 - b) F₂: [Table 7](#)¹
- 4. Cross 4: Red Male with White Female
 - a) F₁: [Table 8](#)
 - b) F₂: [Table 9](#)

For analysing the data, we used what's known as a χ^2 test. The mathematical analysis has been appended, in accordance to which, our experiment confirmed the expected hypothesis². For Cross 1 and 2, with parents as Scarlet and Red, the hypothesis that Scarlet Eye colour is a typical single locus, recessive trait was verified. Quantitatively, Cross 1 was found to have $\chi^2 = 0.0$, which was rather co-incidental, and for Cross 2, χ^2 was found to be 0.31 which is less than 3.148, the value



Don't think we performed the experiment really well!

¹ total's excluding Vial 1

² However, we did reject data collected from one vial in Cross 3, as it had been contaminated

F1	RED MALE	RED FEMALE
VIAL 1	57	63
VIAL 2	32	27
VIAL 3	28	40
TOTAL	117	130

Table 2: Cross 1: F1 Crosses (Scarlet Male with Red Female)

F2	RED MALE	RED FEMALE	SCARLET MALE	SCARLET FEMALE
VIAL 1	41	55	18	12
VIAL 2	45	58	21	14
VIAL 3	42	59	9	26
TOTAL	Red	300	Scarlet	100

Table 3: Cross 1: F2 Crosses (Red (F1) Male with Red (F1) Female)


corresponding to 5% and single degree of freedom.

Now for the more interesting ones, Cross 3 and Cross 4, were subjected to two tests. First we assumed a null hypothesis similar to that of the first case, viz. White Eye colour is a typical single locus, recessive trait. For this, Cross 3 yielded $\chi^2 > 12.9$. Cross 4 produced results distinctly in contrast with the null hypothesis:

1. A significant number of White Female flies were observed which according to the hypothesis should *not* be observed at all
2. No Red Females were observed, which according to the hypothesis should constitute *half* the progeny.

This confirmed that the inheritance of White Eye colour can't be explained by the hypothesis.

The other null hypothesis was that the White Eye colour trait is recessive and sits on the X chromosome. According to this hypothesis, χ^2 was found to be 0.601 and 1.91 for Cross 3 and 4 respectively. Since both these numbers were found to be less than 3.841, the value corresponding to, again 5% and single degree of freedom, the null hypothesis satisfactorily explains inheritance of the White Eye colour.

 Degree of
freedom in this case
was
 $(n-1)(n-1) = 1,$
for $n = 2$

2.6 DISCUSSION

So far so good, but here's the catch; if there's a locus for eye colour on the autosome, *and* there's a locus for eye colour on the X chromosome, what happens when you attempt to cross a Scarlet with a White?

We could perform a experiments and find out. Others who've already performed and analysed them, explain the phenomenon as the

F1	RED MALE	RED FEMALE
VIAL 1	47	47
VIAL 2	45	56
VIAL 3	68	73
TOTAL	160	176

Table 4: Cross 2: F1 Crosses (Red Male with Scarlet Female)

F2	RED MALE	RED FEMALE	SCARLET MALE	SCARLET FEMALE
VIAL 1	23	50	13	14
VIAL 2	42	36	19	13
VIAL 3	24	27	5	9
TOTAL	Red	202	Scarlet	73

Table 5: Cross 2: F2 Crosses (Red (F1) Male with Red (F1) Female)

F1	RED MALE	RED FEMALE
VIAL 1	96	74
VIAL 2	76	102
VIAL 3	98	72
TOTAL	117	130

Table 6: C: F1 Crosses (White Male with Red Female)

F2	WHITE MALE	WHITE FEMALE	RED MALE	RED FEMALE
VIAL 1	11	16	7	16
VIAL 2	28	60	18	0
VIAL 3	11	34	22	0
TOTAL	39	94	40	0

Table 7: C: F2 Crosses (Red (F1) Male with Red (F1) Female)

F1	WHITE MALE	RED FEMALE
VIAL 1	85	70
VIAL 2	62	68
VIAL 3	54	75
TOTAL	201	213

Table 8: Cross 4: F1 Crosses (Red Male with White Female)

F ₂	RED MALE	RED FEMALE	WHITE MALE	WHITE FEMALE
VIAL 1	15	22	11	21
VIAL 2	17	14	12	12
VIAL 3	24	34	39	37
TOTAL	Red	300	White	100

Table 9: Cross 4: F₂ Crosses (Red (F₁) Male with Red (F₁) Female)

following: the eye colour, is controlled by a two pathways. When both pathways are functional, the wild type, Red eye colour is obtained. When both are non-functional, then White eye colour is obtained. The other two cases result in Brown and Scarlet, as is given in Figure 3.

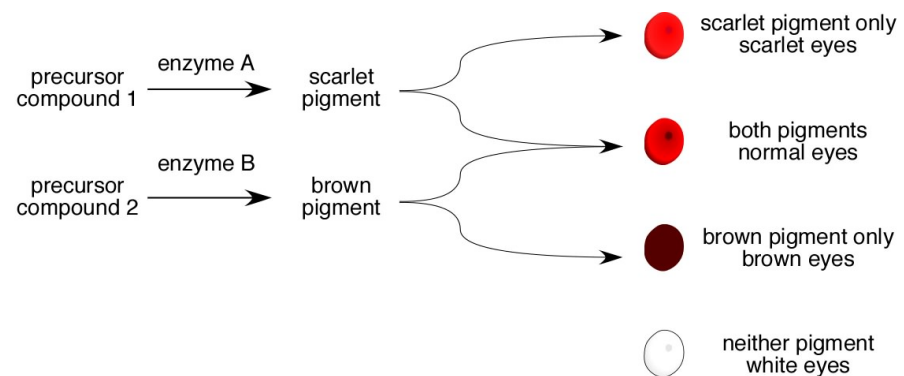


Figure 3: Drosophila eye colour

2.7 REFERENCE

http://www.indiana.edu/~oso/lessons/Genetics/bw_st.html

2.8 ACKNOWLEDGEMENT

I would like to sincerely thank Mr. Biplob Nandy, who helped us perform the experiment as a team member. I also acknowledge Vivek Sagar for his contribution to the project, as a team member. I thank our instructor, Dr. N. G. Prasad for his expert guidance and novel teaching methods.

THE TASTE EXPERIMENT

3.1 OBJECTIVE

To find out if there exists a relation between the number of papillae and a specific compound tasting ability of humans from varied geographical locations, using a small sample size.

3.2 REQUIREMENTS

1. Blue Food Colouring
2. Tooth picks
3. PROP Test Paper (6-n-propylthiouracil)
4. White Paper
5. A pair of Scissors, pencil and a ruler

3.3 BACKGROUND THEORY

Certain compounds are bitter to some humans and completely tasteless to others. The bitterness has two levels, which we call super tasters and tasters. The compound used initially for this analysis was PCT and it was hypothesized that there're two alleles that control this, like a typical mendelian system, with the dominant homozygote as super taster, heterozygote as taster and the recessive homozygote as non-taster.

Eventually when the PTC gene was located, it was found that it encodes for one of the 25 bitter taste receptor proteins present in the taste buds of human tongue. There are 3 different kinds of Single Nucleotide Polymorphisms which result in 5 haplotypes. The two most common are *PAV*, a major taster haplotype and *AVI*, a major non-taster haplotype. When both are *PAV*, the individual is very likely a super taster and when both are *AVI*, the individual's very likely to be a non-taster.

Here, we try to see if there's a relation between the number of receptors and the tasting ability. According to prior research, density usually helps tasting. The method to identify the density, harnesses the fact that the filiform papillae stain dark blue (filiform are those that do NOT contain any taste buds) and the fungiform papillae (fungiform papillae contain taste buds) stain lighter and can be easily distinguished under sufficient light.

3.4 STATISTICAL ANALYSIS

We make a very simple assumption here. We assume that for the total population, the number of papillae is independent of individuals being tasters or non-tasters and that the distribution is normal. This is our Null hypothesis. If there is a relation between the papillae count and the tasting ability, then the Null hypothesis must get rejected after the analysis. Now, assuming the Null hypothesis to be true, what we have is two means and two variances, one for the tasters and other for the non-tasters. In accordance with the hypothesis, these are simply two samples taken from the aforesaid population. If we now take the difference of these means, then it's likely to be close to zero, if the hypothesis is true that is. We now just need a method to quantify how close, rather how far must these means be so that we can reject the Null hypothesis. Since the sample size is extremely small we use student's T distribution which depends on only the the degrees of freedom of the system being analysed. If we can relate our means and variances with this distribution, it becomes simply a matter of looking up values to find the probability of their occurrence, assuming the Null hypothesis to be true. We now define a less than 5% probability of occurrence to mean that the *means* are too different to belong to the aforesaid population, and thus the null hypothesis must be rejected.

That might sound a wee-bit complicated, but practically here's what needs to be done. We've found experimentally, m_1 , m_2 , s_1 , s_2 , n_1 and n_2 , which are means, variances and degrees of freedom respectively. We find the t value using the following equation

$$t = \frac{m_1 - m_2}{\sqrt{\frac{s_1^2}{N_1} + \frac{s_2^2}{N_2}}} \quad (1)$$

Also, we find the degrees of freedom, given by

$$df = (N_1 - 1) + (N_2 - 1) = (N_1 + N_2 - 2) \quad (2)$$

Now all we have to do is look up the value in a t-table corresponding to 0.025 and df as calculated. If $t_{\text{calculated}} > t_{\text{table}}$, then the Null hypothesis is rejected. Else, the null hypothesis can not be rejected.

We used 0.025 for the t-table instead of 0.5 simply because we're assuming our distribution to be symmetric and thus 0.025 on both sides adds up to a 5% probability, consistent with our previous benchmark. What we've performed is a two tailed test (name should now be obvious).

3.5 PROCEDURE

1. Took a PROP taste paper and placed it on the tongue to identify each individual as a super taster, taster or non-taster.

2. Dabbed some food colour on a toothpick and swabbed the tongue with it, till an appropriately distinguishable set of spots were visible.
3. Placed a paper with 1 cm^2 area on the tongue. The tongue was held static (teeth were used) while a person counted the fungi-form papillae on the tongue.
4. This was repeated for another position on the tongue.
5. Both these counts were recorded.
6. Both numbers were recorded and means and variances calculated as described earlier.

3.6 OBSERVATIONS AND RESULTS

Observations and calculations are given in [Figure 4](#). The t value was found to be 0.1044 which is much smaller than $t_{df=15, \alpha=0.025} = 2.080$ as given in [Figure 5](#), thus the Null hypothesis can NOT be rejected.

3.7 ACKNOWLEDGEMENT

I thank Mr. Vivek Sagar for helping me count the papillae on my tongue. I acknowledge the contribution of everyone in our section for performing the experiment.

I am grateful to our Instructor, Prof. N. G. Prasad for the rest (which is statistically the most significant part anyway).

3.8 REFERENCES

1. McMohan, K.A. 2008. Supertasters-Updating the taste test for the A and P laboratory. Pages 398-405, in Tasted Studies for Laboratory Teaching, Volume 29 (K.L. Clase, Editor)
2. statstutorstl.blogspot.com for the t -table.

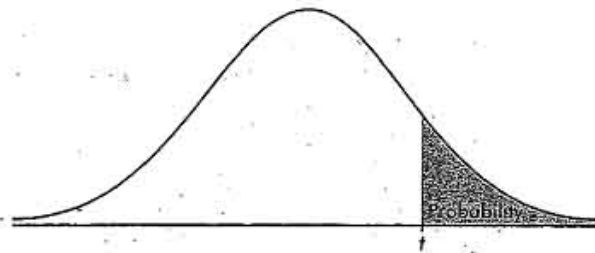
Name	Count A	Count B	Mean	Type
Neha	19	27	23	Non Taster
Abhinav	22	37	29.5	Non Taster
Vivek Sagar	33	27	30	Non Taster
Diksha	48	18	33	Non Taster
Prashansa	21	54	37.5	Non Taster
Atul	45	41	43	Non Taster
Shiven	105	112	108.5	Non Taster
Akshay	72	78	75	Non Taster
Joydeep	32	36	34	Non Taster
Deepanshu	32	32	32	Non Taster
Kishor	43		43	Non Taster
Biplob	49	65	57	SuperTaster
Srijit	113		113	SuperTaster
Love	33	37	35	SuperTaster
Abhishek	22	44	33	Taster
Jopaul	37	31	34	Taster
Akhil Francis	40	44	42	Taster
Saumya	61	32	46.5	Taster
Garima	44	54	49	Taster
Athira John	36	38	37	Taster
Athira Niar	31	33	32	Taster
Akhil Rag	35		35	Taster
Ritu	32	32	32	Taster

#	Variance	Standard Deviation	Mean	
11	637.59091	25.250563	44.40909	Non Taster
12	514.52083	22.683052	45.45833	Tasters

Mean Sample
44.95652

t value	0.1044866
---------	-----------

Figure 4: Observations and Calculations

TABLE B: *t*-DISTRIBUTION CRITICAL VALUES

df	Tail probability <i>p</i>											
	.25	.20	.15	.10	.05	.025	.02	.01	.005	.0025	.001	.0005
1	1.000	1.376	1.963	3.078	6.314	12.71	15.89	31.82	63.66	127.3	318.3	636.6
2	.816	1.061	1.386	1.886	2.920	4.303	4.849	6.965	9.925	14.09	22.33	31.60
3	.765	.978	1.250	1.638	2.353	3.182	3.482	4.541	5.841	7.453	10.21	12.92
4	.741	.941	1.190	1.533	2.132	2.776	2.999	3.747	4.604	5.598	7.173	8.610
5	.727	.920	1.156	1.476	2.015	2.571	2.757	3.365	4.032	4.773	5.893	6.869
6	.718	.906	1.134	1.440	1.943	2.447	2.612	3.143	3.707	4.317	5.208	5.959
7	.711	.896	1.119	1.415	1.895	2.365	2.517	2.998	3.499	4.029	4.785	5.408
8	.706	.889	1.108	1.397	1.860	2.306	2.449	2.896	3.355	3.833	4.501	5.041
9	.703	.883	1.100	1.383	1.833	2.262	2.398	2.821	3.250	3.690	4.297	4.781
10	.700	.879	1.093	1.372	1.812	2.228	2.359	2.764	3.169	3.581	4.144	4.587
11	.697	.876	1.088	1.363	1.796	2.201	2.328	2.718	3.106	3.497	4.025	4.437
12	.695	.873	1.083	1.356	1.782	2.179	2.303	2.681	3.055	3.428	3.930	4.318
13	.694	.870	1.079	1.350	1.771	2.160	2.282	2.650	3.012	3.372	3.852	4.221
14	.692	.868	1.076	1.345	1.761	2.145	2.264	2.624	2.977	3.326	3.787	4.140
15	.691	.866	1.074	1.341	1.753	2.131	2.249	2.602	2.947	3.286	3.733	4.073
16	.690	.865	1.071	1.337	1.746	2.120	2.235	2.583	2.921	3.252	3.686	4.015
17	.689	.863	1.069	1.333	1.740	2.110	2.224	2.567	2.898	3.222	3.646	3.965
18	.688	.862	1.067	1.330	1.734	2.101	2.214	2.552	2.878	3.197	3.611	3.922
19	.688	.861	1.066	1.328	1.729	2.093	2.205	2.539	2.861	3.174	3.579	3.883
20	.687	.860	1.064	1.325	1.725	2.086	2.197	2.528	2.845	3.153	3.552	3.850
21	.686	.859	1.063	1.323	1.721	2.080	2.189	2.518	2.831	3.135	3.527	3.819
22	.686	.858	1.061	1.321	1.717	2.074	2.183	2.508	2.819	3.119	3.505	3.792
23	.685	.858	1.060	1.319	1.714	2.069	2.177	2.500	2.807	3.104	3.485	3.768
24	.685	.857	1.059	1.318	1.711	2.064	2.172	2.492	2.797	3.091	3.467	3.745
25	.684	.856	1.058	1.316	1.708	2.060	2.167	2.485	2.787	3.078	3.450	3.725
26	.684	.856	1.058	1.315	1.706	2.056	2.162	2.479	2.779	3.067	3.435	3.707
27	.684	.855	1.057	1.314	1.703	2.052	2.158	2.473	2.771	3.057	3.421	3.690
28	.683	.855	1.056	1.313	1.701	2.048	2.154	2.467	2.763	3.047	3.408	3.674
29	.683	.854	1.055	1.311	1.699	2.045	2.150	2.462	2.756	3.038	3.396	3.659
30	.683	.854	1.055	1.310	1.697	2.042	2.147	2.457	2.750	3.030	3.385	3.646
40	.681	.851	1.050	1.303	1.684	2.021	2.123	2.423	2.704	2.971	3.307	3.551
50	.679	.849	1.047	1.299	1.676	2.009	2.109	2.403	2.678	2.937	3.261	3.496
60	.679	.848	1.045	1.296	1.671	2.000	2.099	2.390	2.660	2.915	3.232	3.460
80	.678	.846	1.043	1.292	1.664	1.990	2.088	2.374	2.639	2.887	3.195	3.416
100	.677	.845	1.042	1.290	1.660	1.984	2.081	2.364	2.626	2.871	3.174	3.390
1000	.675	.842	1.037	1.282	1.646	1.962	2.056	2.330	2.581	2.813	3.098	3.300
∞	.674	.841	1.036	1.282	1.645	1.960	2.054	2.326	2.576	2.807	3.091	3.291
	50%	60%	70%	80%	90%	95%	96%	98%	99%	99.5%	99.8%	99.9%
	Confidence level <i>C</i>											

Figure 5: The T-Table

SELECTION AND GENETIC DRIFT

4.1 OBJECTIVE

To study selection and Genetic Drift using 10 small drosophila populations.

4.2 REQUIREMENTS

1. Vials with 15 flies each:
 - a) 2 Vials of White Males
 - b) 2 Vials of Red Males
 - c) 4 Vials of +/-w Red Females
2. 10 Food Vials each week (3 weeks)
3. Black Chart Paper

Rest of the apparatus is same as in [Chapter 2](#),

4.3 THEORY: BASICS

Let us start with discussing a few terms.

1. Evolution: Change in allelic frequencies over generations, within a Population and Species is called Evolution.
It's driven by four major forces: Mutation, Selection, Gene Flow and Random Genetic Drift
2. Mutation: This brings new variation into the population. Generally the rates of mutation are extremely small, and they're usually deleterious.
3. Recombination: This is responsible for creating new variation over short periods of time, using existing genetic material.
4. Selection: Differential survival of different individuals in a populations, such that the variation is heritable.
Consequently, the frequency of certain alleles increases over time at the expense of others. *Natural Selection* refers to survival differences owing to the environment. *Sexual Selection* is caused by difference in fertility (or mating success) of one sex, affected by the other.

5. Gene Flow: Individuals from one population migrate to another population and interbreed to create a flow gene.

In our experiment, we don't have any Gene Flow (unless the experiment's performed in a novel faulty manner!)

6. Genetic Drift: Random variation in allelic frequencies caused by sampling error.

Smaller populations are more adversely affected by genetic drift as sampling variation is higher in such cases.

For this experiment, we have no gene flow, and mutations are ignored (which is justified, as the rates are much smaller compared to the population size and number of generations this experiment deals with). For a locus, the change in allelic frequency will depend on the following factors:

1. Selection (strength of selection, for or against an allele)
2. Population Size (smaller the size, larger the drift, as explained earlier)

An important thing to know here, apart from the learning based on the previous experiments, is that the white eyed individuals can't see (this is what we'll use for selection). Also, the white mutation has pleiotropic effects.

4.4 PROCEDURE

Complete details of the experiment have been omitted since they're very similar to those in [Chapter 2](#). The essential steps have been listed below.

1. Week 1

- a) Transferred 6 +/-w Red Females into each of the 10 food vials.
- b) Transferred 3 Red and 3 White Males, into each of the 10 vials.
- c) Randomly selected 5 vials and covered them with black chart paper.
- d) Labelled all the vials uniquely
- e) Adults were discarded after 24 hours.

Vials were tested every 2-3 days and instructor informed once the progeny started eclosing.

2. Week 2

- a) Anaesthetised an old vial and transferred at random, six females to a corresponding food vial with yeast granules and noted their phenotypes.
- b) The vial was labelled and covered with black paper, in accordance with the source vial.
- c) The rest of the flies were counted, noting their sex and eye colour, and details noted.
- d) Repeated the previous steps for all vials, maintaining proper labels and ensuring none of them get mixed.
- e) After a day (when the flies have laid enough eggs), discarded the females.

3. Week 3

Flies from the last generation were counted.

4.5 THEORY: CALCULATIONS

4.5.1 *Computing Allele Frequencies*

Let the frequency of Red eye Allele (wild type) = p

Let the frequency of the White eye Allele = q

Let the phenotypic frequency of Red = P

and that of White = Q

Further, let p_m represent these values for males and p_f represent the same for females.

4.5.1.1 *Male Allele Frequencies*

Since the eye colour allele is X chromosome linked, we have

$$p_m = P_m \quad (3)$$

$$q_m = (1 - p_m) = Q_m = (1 - P_m) \quad (4)$$

4.5.1.2 *Female Allele Frequency*

Since Red is dominant, heterozygotes and homozygotes can't be distinguished. However, a white female must carry two copies of the white eye allele. Thus we have $Q_f = q_f^2$. Consequently we have,

$$q_f = \sqrt{Q_f} \quad (5)$$

$$p_f = (1 - q_f) \quad (6)$$

4.5.1.3 *Population Allele Frequency*

Females carry two copies of the Eye colour alleles. Males carry only one. Thus we have a weighted average as

$$p_{\text{pop}} = \frac{2p_f + 1p_m}{3} \quad (7)$$

$$q_{\text{pop}} = 1 - p_{\text{pop}} \quad (8)$$

4.5.2 *Male Mating Success*

Recall the fact that in the parent generation, all females were taken to be of $+/w$ type. Amongst the males, half were $_/w$ type and the other half were $_/+$ type.

Now sons are quite useless for this purpose because think about it, they get their X chromosome from their mothers, and there's a 50% expectancy for both Red and White eye colour. The Y chromosome which is inherited from the father, doesn't play any role here. Which essentially means, the eye colour of the sons is independent of which type of male their mother mated with.

We thus use the daughters to estimate the male mating success. We consider two cases:

1. If a female $(+/w)$ mates with $(_/w)$ male:
 - a) 50% daughters $(+/w)$ Red eyed.
 - b) 50% daughters (w/w) White eyed.
2. If a female $(+/w)$ mates with $(_/+)$ male:
 - a) 50% daughters $(+/+)$ Red eyed.
 - b) 50% daughters $(w/+)$ Red eyed.

Assuming equal mating success of red and white eyed males, we conclude that the expected frequency of white eyed daughters is 0.25

Thus, $Q_f = q_f^2 = 0.25$ which evaluates to, Expected $q_f = 0.5$

$$\text{Mating Success of White} = \frac{\text{Observed frequency of white allele}(q_f)}{\text{Expected frequency of white allele}(0.5)} \quad (9)$$

4.5.3 *Egg to Adult Survivorship*

Now we bring back the sons of the first generation. In the parent generation, the females are expected to produce an equal number of red eyed and white eyed males. Thus, if survivorship of the two types

were equal, we would expect half the males in the first generation to be red and half to be white. Thus for each vial we have

$$\text{Relative Survivorship (red)} = \frac{\text{Observed frequency of Red Males } (P_m)}{\text{Expected frequency of Red males}(0.5)} \quad (10)$$

and similarly,

$$\text{Relative Survivorship (white)} = \frac{\text{Observed frequency of White Males } (Q_m)}{\text{Expected frequency of White males}(0.5)} \quad (11)$$

Note however, that the final value must be an average across the ten vials, which is essentially the same as taking the average P_m and Q_m values for calculation.

4.6 RESULTS

The results obtained are as follows:

LIGHT

Mating Success of White Males 0.601840564

Egg to Adult Survivorship (Red) 1.075768196

Egg to Adult Survivorship (White) 0.924231804

DARK

Mating Success of White Males 0.47819326

Egg to Adult Survivorship (Red) 1.27307654

Egg to Adult Survivorship (White) 0.72692346

It was expected that the White Males will have a higher mating success in the Dark compared to in the Light, but that doesn't seem to have happened. Also what is strange is the fact that the Egg to Adult Survivorship is almost the same for both Eye colours in the Light Vials whereas in the Dark vials, the result is just the opposite.

Further, there was no monotonic trend in the frequency of the white allele over generations, in neither the Dark nor the Light vials.

4.7 ACKNOWLEDGEMENT

I would like to sincerely thank Mr. Biplob Nandy, who helped us perform the experiment as a team member. I also acknowledge Vivek Sagar for his contribution to the project, as a team member. I thank our instructor, Dr. N. G. Prasad for his invaluable teaching and guidance all along.

4.8 REFERENCES

1. Prof. N.G. Prasad's Notes

PHYLOGENETIC TREE

5.1 OBJECTIVE

Use genetic information to find the phylogenetic tree of given species.

5.2 REQUIREMENTS

1. Computer with Mac/Windows/Linux
2. Internet Access
3. Phylip from <http://evolution.gs.washington.edu/phylip/getme.html>
4. Treeview from <http://taxonomy.zoology.gla.ac.uk/rod/treeview.html>
5. Clustal from <http://www.clustal.org/download/current/> (for windows use `clustalx-2.1-win.msi`)
6. mRNA data from <http://www.ncbi.nlm.nih.gov/> of the coding region only (this is specified on the page) for the following
 - a) rohu
 - b) gonius
 - c) kontius
 - d) fimbriatus
 - e) bata

5.3 BRIEF THEORY

The basic essence of this experiment hinges on the fact that there are coding and non coding regions in the DNA. The non-coding region can accumulate mutations over time without affecting the individual too much. However, the non-coding region can't tolerate high levels of divergence since that's closely related to the Darwinian fitness of the organism. It is for this reason, that we, to compare relatedness of species, use the coding region, which is easiest to obtain from the mRNA data. We look at a specific protein's, viz. the Growth Hormone's m-RNA data in various species and compare them.

The non-coding region helps us establish, given two sets of species with equal relatedness, which had a common ancestor closer in the past.

5.4 PROCEDURE

1. The data downloaded in accordance with [item 6](#) and put in the format given in [Listing 1](#) using any text editor (I used Sublime Text) and saved it, as say, 'input.txt'.
2. ClustalX
 - a) Now opened this file in ClustalX (the instructions may be biased towards windows henceforth for unavoidable reasons)
 - b) Selected Alignment -> Output Format, and in the dialogue box checked PHYLIP format.
 - c) Then, selected Alignment -> Do Complete Alignment, selected the right location and hit okay.
 - d) Copied the PHYLIP file, wherever it was chosen to be created in the previous step, to the exe folder of phylip-3.69, renamed to infile, without any extension.

A screenshot's given in [Figure 6](#)

3. Phylip

This is a collection of executable files, which expect a file named input and create a file named output, on the basis of the parameters specified by the user, when the program is executed. ¹ We will use the outputted files as inputs from one program to the next. Below is an ordered list of programs and the parameters to be specified, to be used sequentially (redundancy is used for emphasis).

- a) seqboot
- b) dnapsars
 - i. M (Analyse multiple data set)
 - ii. D (Multiple Data sets, not multiple weights)
 - iii. 30 (Number of Data Sets)
 - iv. 1/3/7 (Enter Seed, input any odd number)
 - v. 500 (Number of times to Juggle)

You could also modify the number of trees to save.

- c) consensus

¹ The last program produces a file named outtree

Listing 1: Format of the source file

```

>rohu
atggctagagcattagtgctgttgctcggtggtgctggtagttt....
>gonius
atggctagagcattagtgctgttgctcggtggtgctggtagtct....
>kontius
atggctagagcattagtgctgttgctcggtggtgctggtagttt....
>fimbriatus
atggctagagcattagtgctgttgctcggtggtgctggtagttt....
>bata
atggctagagcattagtgctgttgctcggtggtgctggtagttt....

```

4. Treeview

Use the outtree file created in the previous step and obtain the required tree. A screenshot's given in [Figure 7](#)

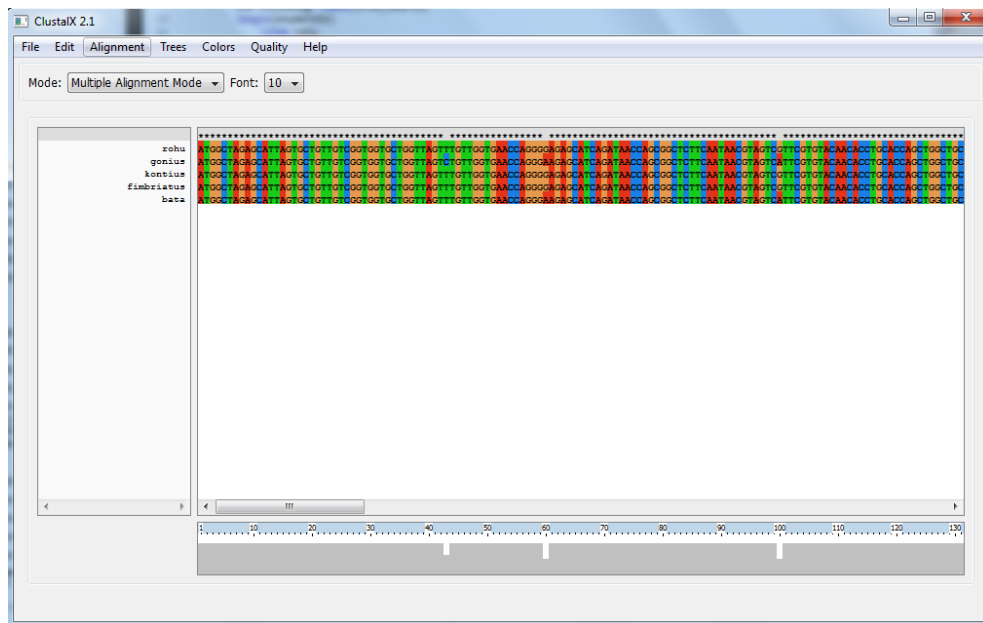


Figure 6: ClustalX

5.5 ACKNOWLEDGEMENT

I am thankful to my friend, Mr. Vivek Sagar, for taking notes while the experiment was being performed. I sincerely express my gratitude for Dr. Sanjay Mandal, who introduced us to this aspect of Biological analysis.

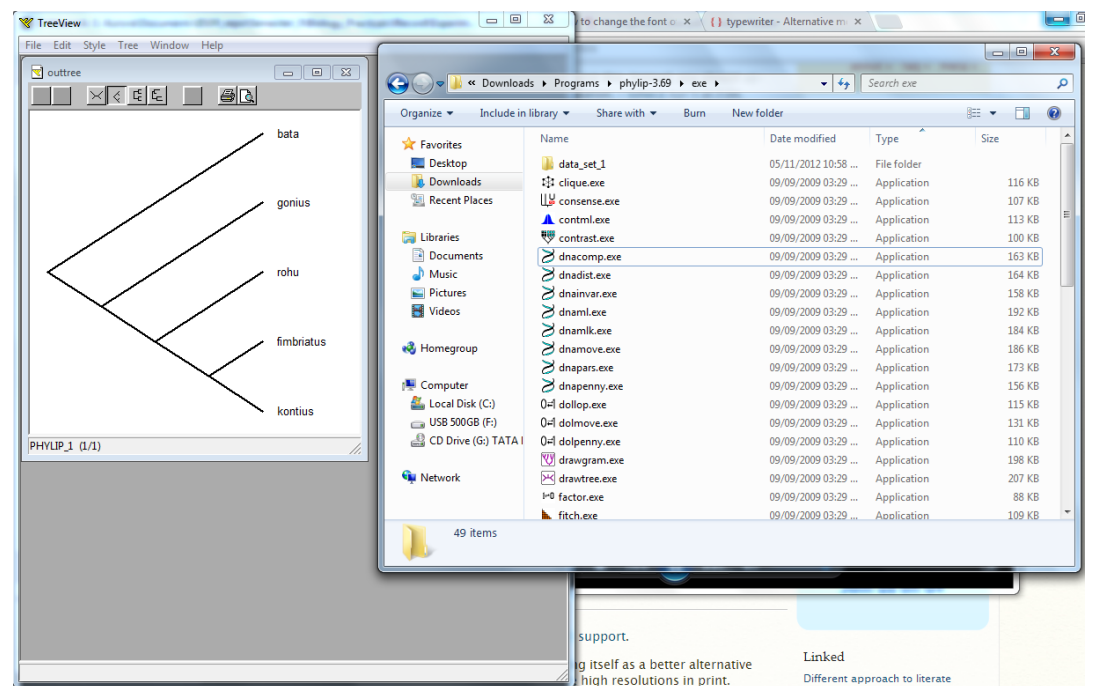


Figure 7: Treeview and Phylip

ARE HUMANS EVOLVING

6.1 OBJECTIVE

To study the

1. heritability of height in humans
2. effect of height on Darwinian fitness

6.2 REQUIREMENTS

1. A measuring tape
2. Weighing balance
3. Set of humans from various parts of the country interested in performing the experiment

6.3 PROCEDURE

1. The set of humans was asked to collect pedigree data for their families, where data means height of the individual (if age > 18 years), date of birth, date of marriage, weight and region.
2. The data was then collected into a single file to preserve privacy of the people involved.

6.4 OBSERVATIONS AND RESULTS

1. Heritability of Height:

Offspring height, when plotted against the mid-parent height yields heritability. This measures the proportion of observable difference in a trait between individuals within a population that is due to genetic differences. Heritability is essentially a genetic component of variation, in the total phenotypic variation. The graph obtained is given in [Figure 8](#). The heritability was found to be 0.554 which manifests that height is heritable.

NOTE: The points seems very scattered as the graph doesn't start from zero.

2. Effect of Height on number of offspring

I did not get a chance to react to the idea of this analysis, since Vivek had already described to me how this appeared to be

rather pointless on the basis of cause, as family planning and other aspects dominate such issues and yet a co-relation exists as is manifested in Figure 9 and in Figure 10.

The data seems to suggest that Darwinian fitness of females are high if they're taller than average or shorter than average. However, their fitness is lower if their height is close to the average.

For Males, the data suggests that taller males are better in terms of Darwinian fitness.

3. Distribution of month of birth of the first child

A graph of frequency of children vs month of their birth was plotted and to it, a 2nd degree polynomial fitted. The result obtained is shown in Figure 11. Although the graph does seem to have a curve, suggesting a 'preferred' set of months, however, on performing a chi-square test for an equal probability (linear fit), it was found that the Null hypothesis can't be rejected.

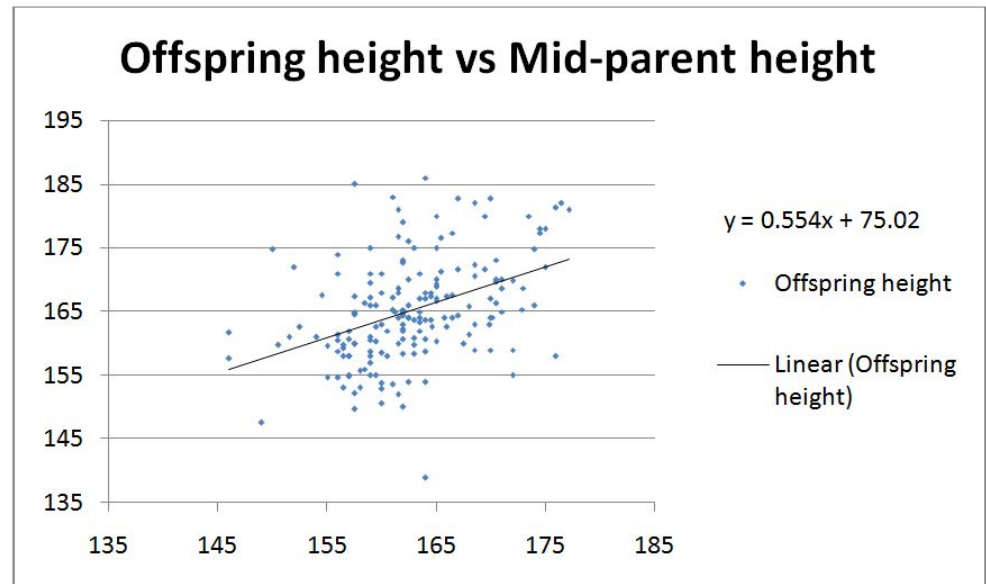


Figure 8: Offspring Height vs Mid-Parent Height

6.5 ACKNOWLEDGEMENT

I sincerely thank Mr. Vivek Sagar for helping me analyse this experiment since I'd missed out on the session when this was discussed.

I am grateful to our Instructor, Prof. N. G. Prasad.

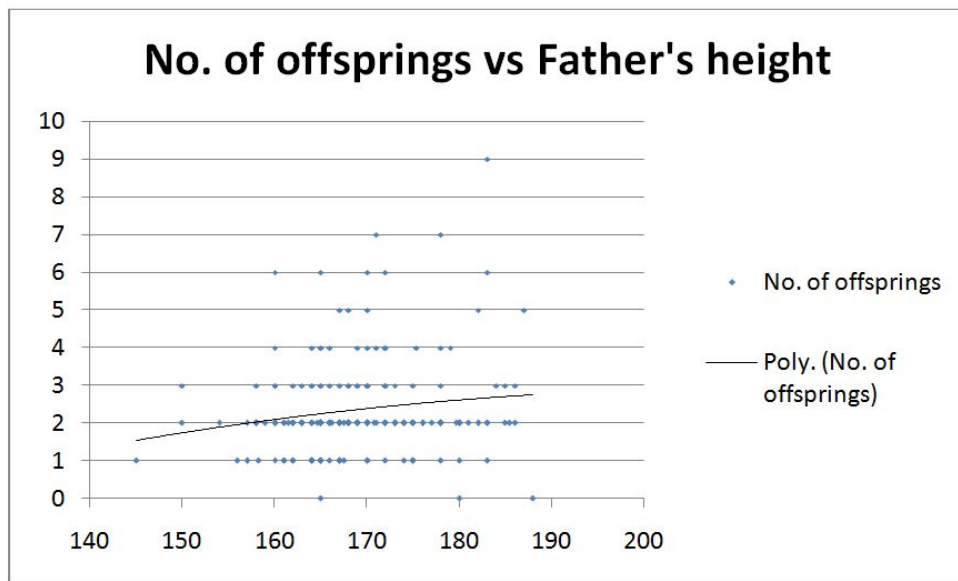


Figure 9: Number of Offspring vs Father's Height

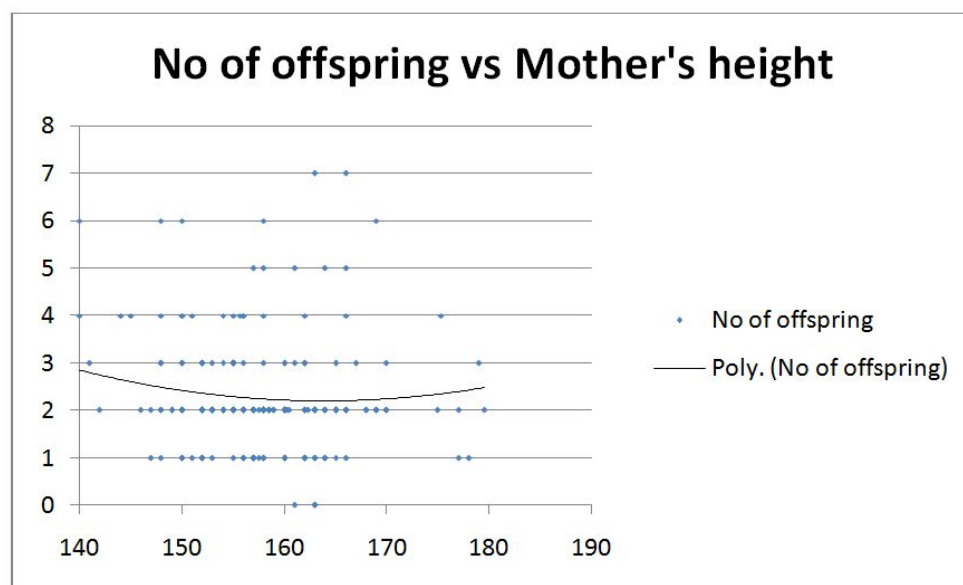


Figure 10: Number of Offspring vs Mother's Height

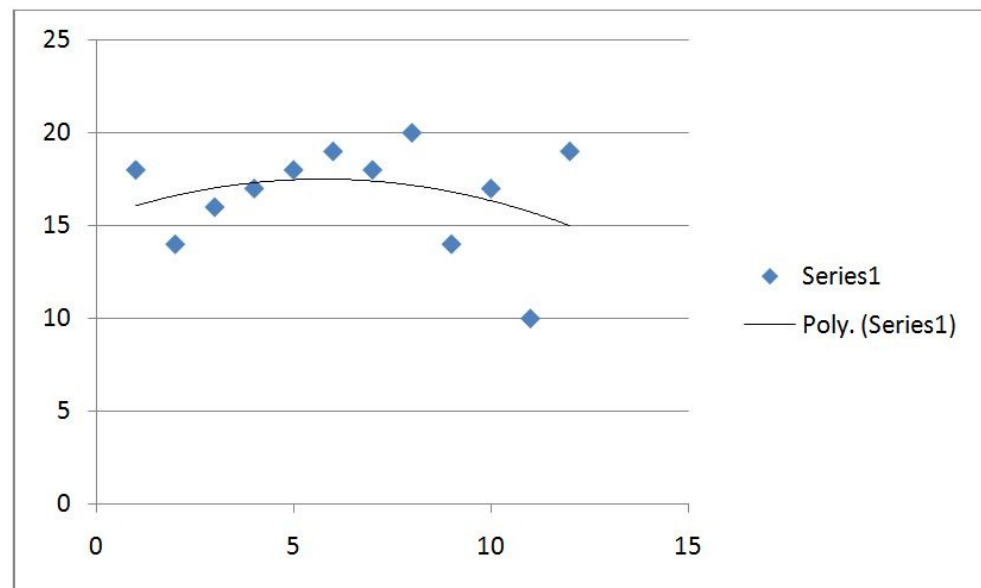


Figure 11: Frequency vs Month of Birth of the first offspring

Part II

THE SHOWCASE

You can put some informational part preamble text here. Illo principalmente su nos. Non message *occidental* anglo-romanian da. Debitas effortio simplicate sia se, auxiliar summarios da que, se avantiate publicationes via. Pan in terra summarios, capital interlingua se que. Al via multo esser specimen, campo responder que da. Le usate medical addresses pro, europa origine sanctificate nos se.

COLOPHON

This document was typeset using the typographical look-and-feel `classicthesis` developed by André Miede, for \LaTeX .
The style was inspired by Robert Bringhurst's seminal book on typography "*The Elements of Typographic Style*".

The latest version of this document is available online at:

https://github.com/toAtulArora/IISER_repo