Mathematical Applications in Zoology a Concept of Zoo-Mathematics

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Abstract- *Zoology, often referred to as animal science, involves the study of animals and their life processes. While statistical methods find application in zoological research, the incorporation of mathematics extends beyond statistics. Within various zoological branches such as Ecology, Animal Physiology, Genetics, and Evolution, mathematical formulas play a critical role. While other branches might also leverage mathematics, this paper emphasizes the significance of its application in the aforementioned areas.*

In Ecology, mathematical formulas underpin investigations into community dynamics, population ecology, ecosystem functioning, and birth and death rates. Animal Physiology delves into chapters on Biochemical Reactions, Diffusion, Osmosis, and Excitability, where mathematical relationships are evident. The paper underscores the profound role of Mathematics and Statistics in elucidating genetics and evolution concepts.

Keyword: Zoology, Mathematics, Statistics, Interdisciplinary, Ecology, Animal Physiology, Genetics, Evolution, Bio-Mathematics, Bio-Physics, Bio-Chemistry, Bio-Geography, Bio-Geology, Zoological Branches, Mathematical Applications.

Introduction

Zoology's role as the study of animals' life and function, alongside Botany and Microbiology for plants and microorganisms. Zoology and Botany seek precise and quantitative principles for living system organization. While biology draws from Physics and Chemistry, its unique life processes require distinct explanations. Mathematical expressions capture numerous biological phenomena, while the essence of Mathematics as the logic of shape, quantity, and arrangement influences every facet of life.

Mathematics' close ties with Physics, Chemistry, Commerce, Economics, and other disciplines foster interdisciplinary links. It transcends Science to encompass Arts, Commerce, Management, and Economics. Statistics, a sibling to Mathematics, also finds its place in biological research.

Bio Physics, Bio Chemistry, Bio Geography, Bio Geology, and Bio Statistics exemplify interdisciplinary bridges in Biology. Similarly, the amalgamation of Biology and Mathematics births the discipline of Bio-Mathematics. As Zoology is a branch of Biology, Zoo-Physics, Zoo-

Chemistry, Zoo-Geography, Zoo-Geology, Zoo-Statistics, and Zoo-Mathematics stand as conceivable extensions.

Objective

The primary objective of this paper is to illuminate the pivotal role of mathematics in shaping and enhancing the field of Zoology. By examining diverse branches within Zoology, such as Ecology, Animal Physiology, Genetics, and Evolution, the paper seeks to elucidate how mathematical principles and formulas underpin critical aspects of these disciplines. Through a comprehensive exploration of real-world applications, case studies, and theoretical frameworks, the paper aims to demonstrate how the integration of mathematics empowers researchers and scientists to formulate precise models, make informed predictions, and drive impactful advancements in understanding and addressing complex zoological phenomena. Ultimately, the paper aims to foster a deeper appreciation for the interdisciplinary synergy between mathematics and Zoology, shedding light on the concept of "Zoo-Mathematics" as a distinctive and valuable domain within the broader scientific landscape.

Methods and Procedure

Collection of study materials from different reference materials related with all key words.

Ecological Mathematics

Related keyword is Eco-mathematics. Ecology is the study of concentrations in nature; it is the study of how organisms interact with one another and with their environment. It is a biological science that studies the relationship between living organisms and their environment.

Population ecology is important in conservation biology, especially in the development of population viability analysis (PVA) which makes it possible to predict the long-term probability of a species persisting in a given habitat pate.

In a closed system where immigration and emigration does not take place, the rate of change in the number of individuals in a population can be described as:

$$\frac{dN}{dt} = B - D = bN - dN = (b - d)N = rN$$

N=Total number of individuals in a population

B=Raw number of births

D=Raw number of death

b=Per capita rates of birth

d=Per capita rates of death

The Biotic Potential

Rate of reproduction directly affects the size of population, therefore an estimate of the individual organism's own population reproductive rate or biotic potential.

$Pz^n(R^{n-1})$ = Biotic Potential

P	=	Number of female started with
n	=	Number of generation in a given unit of time
R	=	Proportion of females in each generation (=0.5 when sexes are Equal; when all females parthenogenesis)
z	=	Number of young produces by each females.

Population Density

It is a measurement of population per unit area. The population density refers to the number of people living in an area per kilometer square.

Basal Area

The Basal area of individuals of a particular species as a proportion of the total basal area of ll species.

b.a. = Area occupied at breast height.

Relative Density

Number of individuals of a particular species as a proportion of the total number of individuals of all species.

Relative dominance

The combined basal area of a single species as a population of the total basal area of all species.

$$\text{Relative Dominance} = \frac{\text{Combined b.a. of a single species}}{\text{Total b.a. of all species}} \times 100$$

Relative Frequency

The frequency of a given species as a proportion of the sum of frequencies for all species.

Relative diversity

Number of species is one family as a proportion of the total number of species.

$$\text{Relative Diversity} = \frac{\text{Number of species in one family}}{\text{Total No. of species}} \times 100$$

Mortality Rate

Mortality or death rate is a measure of the number of death in a particular population is called to the size of population.

Death rate = d/p x 1000

d = death occurring within a time period.

p = size of population

Natality Rate

Notality or birth rate is a measure of the number of birth in a particular populations called to the size of population.

Mathematics in Animal Physiology

Related keyword is physiol Mathematic. Animal physiology is a discipline of biological science (zoology) that focuses on the function of tissue, organs and organisms, in light of natural selection. The organisms' body is formed by solids and fluids. The fluid part is more than 2/3 of the whole body. Water forms most of the fluid part of the body.

Measurement of Volume of Body Fluids

(By Indicator Dilution Method)

$$V = M/C$$

V= The volume of fluid in the compartment

M = Mass of total quantity of marker substance injected.

C = Concentration of the marker substance in the sample of fluid.

Mathematics in Genetics

Characters that pass from the parents to the offspring are called hereditary characters and the study of such characters and the way they are handed over to the offspring generation after generation is known as Genetics.

Crossing Over and Linkage Maps

1. **Recombination frequencies from a test-cross (A three-point testcross)**

Since recombination frequencies are directly proportional to distances between genes in question, these values can be used in preparation of linkage maps. A three-point testcross (involving three genes) to be discussed in this section not only gives us information regarding relative distances between these genes, but also tells us the linear order in which these genes should be present on the chromosome. The underlying basic principle involved in preparation of linkage maps can be explained by using a hypothetical example.

Let us presume that there are three genes *A*, *B* and *C* present on the same chromosome (i.e. these are linked). There could be three possible linear orders in which these genes may be present on a chromosome. These are *A-B-C, A-C-B* or *B-A-C.* As is obvious, that in one case *B* is present in the middle while in the other two cases *C* and *A* respectively are present at the middle position. Therefore, in finding out the linear order, one has to really find out the gene which is present in the centre. For this purpose, a three-point test-cross is made, which involves crossing of a trihybrid *ABC/abc* (obtained from a cross *ABC/ABC* x *abc/abc)* with triple homozygous recessive *abc/abc*. The progeny obtained will represent the gametes formed by the hybrid presuming *A-B-C* as the order of genes.

If crossing over, i.e. recombination value (per cent) between A and B is called X, that between B and C is called Y and that between A and C is called Z, then

(a) Crossing over *(A-B)* (where *A* and *B* separated)

$$= \mathrm{x} = \frac{\mathrm{c}+\mathrm{d}+\mathrm{g}+\mathrm{h}}{\mathrm{T}} \times 100$$

(b) Crossing over *(B-C)* (where *B* and *C* separated)

$$= \mathrm{x} = \frac{\mathrm{e}+\mathrm{f}+\mathrm{g}+\mathrm{h}}{\mathrm{T}} \times 100$$

(c) Crossing over *(A-C)* (where *A* and C separated)

$$= \mathrm{x} = \frac{\mathrm{c}+\mathrm{d}+\mathrm{e}+\mathrm{f}}{\mathrm{T}} \times 100$$

From the above values of X, Y and Z, order of genes can be worked and the linkage map can be prepared using the following criteria: if Z l X + Y, order of genes is *A-B-C*; if Z = X - Y, order of genes is A-C and if Z = Y - X, order of genes is B-A-C

Preparation of a linkage map can be further illustrated by using an example from maize involving three endosperm characters. These three characters are *coloured aleurone* (C) versus *colourless aleurone* (c), *full endosperm* (*Sh*) versus *shrunken endosperm (sh*) and *non-waxy endosperm (Wx)* versus waxy *endosperm (wx).* As shown previous hypothetical example, three recombination values i.e. *C-Sh*, *Sh-Wx*and *C-Wx* would be worked out in order to find out the linear order of *the*three genes *C*, *Sh* and *Wx.*

$$\text{Therefore, recombination } C - \text{sh} = \frac{229+6}{6708} \times 100 = 3.5\%$$

$$\text{recombination } sh - Wx \ = \ \frac{1227+6}{6708} \times 100 = 18.4\%$$

$$\text{recombination C} - Wx \ = \ \frac{229+1227}{6708} \times 100 = 21.7\%$$

In this case, recombination value *C-Wx* (21.7%) is close to *(C-sh)+(sh-Wx)* = 3.5 + 18.4 = 21.9%. Therefore, *sh* should be located between C and *Wx.* The slight difference between the total of two individual values and the third value is due to the fact that in the third value (C-Wx) double-cross-over's are not included. However, if *(C-Wx)* were close to (C-sh) - *(sh-Wx)*, then *Wx* would be between *C* and *sh.* where 1 map .... (m.u.) is considered equal to *1%* recombination. A map unit is sometime referred to as centiMorgan (cM) in honour of Thomas Hunt Morgan (for low distances on a map the linear relationship between cM units recombination frequency does not hold good; see later for details):

2. **Recombination frequencies from F_2 data**

Test cross data like the above obtained in a three point test-cross are M always available and cannot be easily obtained. In such cases, if two linked genes exhibit complete dominance, recombination frequencies can be calculated from F_2 data. These data can be obtained easily and routinely from F_1 x F_1 crosses or by selfing F_1 individuals (in plants). As a first step the data will be subjected to chi-square (χ^2) test for independence (see later in this chapter). If the test indicates significant deviation from expected results linkage can be detected and recombination frequencies can be calculated.

If we assume a recombination frequency of P between two genes A *B*, then in gametes derived from *AaBb*, the frequencies of recombinant gametes will be P/2 each and the parental types will be (1 - P)/2 each. From these gametic frequencies, expected zygotic frequencies can be calculated using a checkerboard. Utilizing information given in this table, one of the following two methods can be used for calculating recombination frequencies from F_2 data.

Theoretical series in F_2 from *AaBb* in repulsion *(Ab/aB)*, assuming a recombination frequency of P between *A* and *B*.

	F_1 gametes or F_2 phenotypes				Total
	AB	Ab	Ab	ab	
1. Frequencies of different gamete types	P/2	1-P/2	1-P/2	P/2	1
2. Observed F_2 frequencies	a	b	C	d	n
3. Expected F_2 frequencies	$2+P^2/4$	$1-P^2/4$	$l-P^2/4$	$P^2/4$	1
Product PCI ratio = z = $\frac{ad}{bc} = \frac{P^2\ (2 + P^2)}{(1-P^*)^2}$					

Product ratio method

The F_2 data is derived from a heterozygote as *AaBb*, which in its turn may be derived from parents either in sampling phase *(AABB***x** *aabb)* or in repulsion phase *(AAbb* x *aaBB).* In both uses, if independent assortment holds good, then *9AB* : 3*Ab* : 3*aB* : *lab* ratio should hold good. If chi-square test gives lack of independence between *A* and Brecombination frequencies can be calculated from the product ratio (z) derived as follows, where *AB* = a, *Ab* = b, *aB* = c and *ab* = d

Coupling phase *(AABB* x *aabb*–z ss (b x c)/(a x d)

Repulsion phase *(AAbb* x *aaBB*z.ss (a x d)/(b x c) gp.

The recombination frequency **P** (as per cent) can be obtained for calculated value of *z*,for which Tables are available in advanced books i||nn3ult author's another text book '*Genetics*'.

Maximum likelihood method: This method is based on the principle Hit a recombination value **(P),** whose variance is minimum, will be the best estimate of recombination frequency. Therefore, **P** value is calculated using differential calculus, so that the probability of getting the observed results is Maximum. Without giving the mathematics involved in the derivation of the formula used for such computation, we like to give here the final formula used for computation of recombination value **(P).**

$$\boldsymbol{P^2 = \frac{-S \pm \sqrt{S^2 - 4nt}}{2n}}$$

Where, S= (-a-2b-2c-d)
t =(-2d)
n= (a+b+c+d)

As an illustration, suppose in a cross, following F_2 data (n = 1415) are obtained: a = 753, b = 292, c = 351 and d = 19. The values can be substituted in the above formula as follows

$$P^2 = \frac{-552 \pm \sqrt{(552)^2 - 4(1415)(-38)}}{2(1415)}$$

$$= .05970334$$

or $\mathbf{P} = \sqrt{\mathbf{.05970334}}$ = 0.24434 or 24.43%

Mathematics in Evolution

Evolution is change in the heritable characteristics of biological populations over successive generation. These characteristics are the expression of genes that are passed on from parent to offspring during reproduction. Evolutionary biologists have continued to study various aspects of evolution by forming and testing hypothesis as well as constructing theories based on evidence from the field or laboratory an on data generated by the methods mathematical and theoretical biology.

Hardy Weinberg Law - the Law of Genetic Equilibrium or Stability

After the revival of Mendel's laws of heredity, a hard fact remained unexplained. It was this: *why not the dominant characteristics continue to increase in a given population, and eventually replace the recessive ones*? This problem was independently solved around 1908 by the mathematician **G.H. Hardy** in England and the geneticist **W.Weinberg** in Germany. Both came to identical conclusion that **the proportion of dominant and recessive characters in a sexually reproducing population remains almost constant provided that** (i) mating is random in the large population, *(ii)* mutations do not occur, and *(iii)* the large population is not reduced to a small population by natural or unnatural causes.

Random mating

Mating in large populations is quite random because mates do not select partners with the intention of improving some dominant characteristic or eliminating some recessive one.

But the fact is otherwise. All genotypes (individuals with different genetic make-ups) do not contribute equally to gene pool of the species for the next generation, because some genotypes may be more fertile some may be sterile and some may not reach the reproductive age. Thus mating will be practically non-random, there will be survival of the fittest and consequently natural selection leading gen® frequencies and evolutionary change. **Mutations** cannot be ruled out in sexually reproducing large populations. They may favour some characteristics or disfavour others. This will again bring-in change in the gene frequencies or ratios of the dominant and recessive genes in the populations, eventually leading to evolutionary change. Large population, may be reduced to small populations due to mutations, environment and unnatural circumstances, **A reduced 'gene pool' will lead to genetic drift** resulting in significant variation in a limited number of dominant and recessive gene characteristics. Such variations will be contrary to Hardy-Weinberg law, and will account for evolutionary change.

Taking for granted that the three conditions laid down for the validity of Hardy-Weinberg Law are fulfilled, the gene frequencies of the genetic constitution of a sexually reproducing population in equilibrium, can be formulated by a mathematical equation put forth by the makers of this law.

Suppose that by sampling a given population of animals or plants we find that proportions of three possible genotypes with regard to the dominant gene B and recessive allele b are like this:

BB	bb	Bb
25% (or 0.25)	25% (or 0.25)	50% (or 0.5)

The frequencies of genes B and b and will be the same as the possible frequencies of gametes carrying each gene. If we presume that all individuals of the population produce roughly the same quantity of gametes, then BB genotypes (individuals) representing 25% of total population will produce 25% of the total gametes produced, each containing B gene. Similar proportionate figures will work out for the genotype bb. But the individuals Bb sharing 50% of the total population will be producing two kinds of gametes, 25% of B gene and 25% of b gene. Thus the proportion of gamete's with respect to genes B and b and therefore of the frequencies of these genes in the population, adds up to 50% (or 0.5) for B and 50% (or 0.5) for b as shown below:

I Population:
25% BB 25%bb 50%Bb

II Gametes
25% B 25% b >25% B, and 25% b

III Overall gamete proportions 50% B, 50% b and therefore gene frequencies

IV Result genetic stability.

As a consequence of random mating in the given population, the l! proportions or frequencies of genotypes in the next generation will be the same as in the last generation as illustrated below:

Female gametes ⟶

Male gametes ⟶

	0.5B	0.5 b
0.5B	0.25 BB	0.25 Bb
0.5 b	0.25 Bb	0.25 bb

0.25BBdominant homozygous
0.50 Bb heterozygous
0.25 bb recessive homozygous

Such frequencies of genes as illustrated above were formulated by Hardy- Weinberg in terms of an equation

$$p^2 + 2pq + q^2 = 1 = 100\%$$

where p represents the frequency of the dominant, q the gene frequency of its recessive allele, and 2pq of the hybrids in a large population.

Results and Discussion

The discipline of mathematics may also take a good stand in the study of life science especially animal science. It may create a new branch of interdisciplinary science, which is known as mathematical biology or biomathematics. It aims at the mathematical representation and modeling of biological processes, using techniques and tools of applied mathematics and it can be useful in both theoretical and practical research and study in animal science.

Conclusion and Implications

After completion this study, it may be concluded that biomathematic is also an important inter disciplinary branch of biology and under study of zoology it may be known as zoo mathematics. The discipline of zoomathematics makes also zoology in new form. Students can explain various concepts of zoology in mathematical forms. This concept of zoomathematics can increase the mathematical abilities and skills of students of biological science.

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