



## Graphing and Analyzing Scientific Data

Graphing is an important procedure used by scientist to display the data that is collected during a controlled experiment. There are three main types of graphs:

Pie/circle graphs: Used to show parts of a whole.

Bar graphs: Used to compare amounts.

Line graphs: Use to show the change of one piece of information as it relates to another change.



Both bar and line graphs have an "X" axis (horizontal) and a "Y" axis (vertical).

### Parts of a Graph:

Title: Summarizes information being represented in ANY graph.

Independent Variable: The variable that is controlled by the experimenter, such as, time, dates, depth, and temperature. This is placed on the X axis.

Dependent Variable: The variable that is directly affected by the I.V. It is the result of what happens as time, dates, depth and temperature are changed. This is placed on the Y axis.

Scales for each Variable: In constructing a graph, one needs to know where to plot the points representing the data. In order to do this a scale must be employed to include all the data points.

A. Graph the following information in a **BAR** graph. Label and number the x and y-axis appropriately.

| Month | # of deer |
|-------|-----------|
| Sept  | 38        |
| Oct   | 32        |
| Nov   | 26        |
| Dec   | 20        |
| Jan   | 15        |
| Feb   | 12        |



1. What is the independent variable? \_\_\_\_\_
2. What is the dependent variable? \_\_\_\_\_
3. What is an appropriate title? \_\_\_\_\_

# Analyzing Genetic Data Answers

**Sean McClure**

A red circular graphic with a gradient, appearing as a partial circle or a thick arc, located to the right of the author's name.

## Analyzing Genetic Data Answers:

*Handbook on Analyzing Human Genetic Data* Shili Lin, Hongyu Zhao, 2009-10-13 The discipline of statistical genetics is highly computational. Both exact computational methods and simulation-based or hybrid of the two computational packages are indispensable tools and constant companions of researchers in the field. This handbook is intended to provide human geneticists and other biomedical researchers with guidance on selections of appropriate computational methods and software packages for their specific genetic problems. It may also be used by students and other learners as a reference in conjunction with a more theoretical and/or methodologically oriented textbook. This book tries to strike a balance between methodological expositions and practical guidelines for software selections. Wherever possible, comparisons among the competing methods and software are made to highlight the relative advantages and disadvantages of the approaches so that the reader can make informed choices to best match their specific needs. Human genetics has been undergoing an evolution in the past several years as new knowledge and technologies are transforming the field, leading to numerous new discoveries of genes associated with complex traits such as cancer, obesity, and diabetes. Many recent genome-wide association studies employ the case-control design where the study subjects consist of unrelated affected individuals and normal controls. For each individual, a large number of genetic markers are queried.

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*Mathematical and Statistical Methods for Genetic Analysis* Kenneth Lange,2012-12-06 During the past decade geneticists have cloned scores of Mendelian disease genes and constructed a rough draft of the entire human genome The unprecedented insights into human disease and evolution offered by mapping cloning and sequencing will transform medicine and agriculture This revolution depends vitally on the contributions of applied mathematicians statisticians and computer scientists *Mathematical and Statistical Methods for Genetic Analysis* is written to equip students in the mathematical sciences to understand and model the epidemiological and experimental data encountered in genetics research Mathematical statistical and computational principles relevant to this task are developed hand in hand with applications to population genetics gene mapping risk prediction testing of epidemiological hypotheses molecular evolution and DNA sequence analysis Many specialized topics are covered that are currently accessible only in journal articles This second edition expands the original edition by over 100 pages and includes new material on DNA sequence analysis diffusion processes binding domain identification Bayesian estimation of haplotype frequencies case control association studies the gamete competition model QTL mapping and factor analysis the Lander Green Kruglyak algorithm of pedigree analysis and codon and rate variation models in molecular phylogeny Sprinkled throughout the chapters are many new problems

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real world scenarios ensuring that you not only learn how to answer questions but also understand the context in which these concepts are applied in professional settings

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**Statistics and Data Analysis for Microarrays Using R and Bioconductor** Sorin Draghici, 2016-04-19 Richly illustrated in color Statistics and Data Analysis for Microarrays Using R and Bioconductor Second Edition provides a clear and rigorous description of powerful analysis techniques and algorithms for mining and interpreting biological information Omitting tedious details heavy formalisms and cryptic notations the text takes a hands on example based approach that teaches students the basics of R and microarray technology as well as how to choose and apply the proper data analysis tool to specific problems New to the Second Edition Completely updated and double the size of its predecessor this timely second edition replaces the commercial software with the open source R and Bioconductor environments Fourteen new chapters cover such topics as the basic mechanisms of the cell reliability and reproducibility issues in DNA microarrays basic statistics and linear models in R experiment design multiple comparisons quality control data pre processing and normalization Gene Ontology analysis pathway analysis and machine learning techniques Methods are illustrated with toy examples and real data and the R code for all routines is available on an accompanying downloadable resource With all the necessary prerequisites included this best selling book guides students from very basic notions to advanced analysis techniques in R and Bioconductor The first half of the text presents an overview of microarrays and the statistical elements that form the building blocks of any data analysis The second half introduces the techniques most commonly used in the analysis of microarray data

**Exploring Bioinformatics** Caroline St. Clair, Jonathan Visick, 2010 Exploring Bioinformatics A Project Based Approach Is Intended For An Introductory Course In Bioinformatics At The Undergraduate Level Through Hands On Projects Students Are Introduced To Current Biological Problems And Then Explore And Develop Bioinformatic Solutions To These Issues Each Chapter Presents A Key Problem Provides Basic Biological Concepts Introduces Computational Techniques To Address The Problem And Guides Students Through The Use Of Existing

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**Discovered, Not Designed: Building Things in the Age of Complexity** Sean McClure, 2024-06-25 To build is to be human Creating things is part of our nature and our principal mode of survival The things we have built throughout history have always relied on design to turn discoveries into workable tools But the underlying premise of design is that we can reason about the pieces and connections that make a thing work From the stone axe to the rocket engine design is predicated on our ability to see causal connections between the parts of a system But what happens when such causality is no longer apparent When the things we must build to solve our challenges have inner workings that cannot be discerned The answer lies in nature Nature fashions truly complex objects that solve categorically hard problems Complex things produce their most important outputs via emergence whereby a system s structures and behaviors arise in ways that cannot be designed This book argues that we are entering an age where humanity must build truly complex things to continue our progress This means learning to build as nature builds and as it turns out forces us to redefine knowledge and skill and more broadly our scientific and engineering paradigm

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