

Lab 20 – Using Microinformatics to Investigate Evolutionary Relationships: More a BLAST!

Introduction:

Genome-wide (GW) genomic studies using international consortia project genomes of the Human Genome Project, now also include and require 20,000 to 25,000 genes that define a human being. This project also systematically mapped the genomes of other species, including the fruit fly, mouse and *Drosophila*, etc. The genome and structure mapping of the genome of each species against the conserved human genome will allow us to find homologous genes in the genome.

Why is this information important? Being able to identify the precise location and sequence of human genes will allow us to better understand genetic diseases. In addition, finding other homologous genes in other species helps us understand evolutionary relationships among organisms. Many of our genes are identical or similar to those found in other species.

However, you already realize that it is impossible for a number of genes to be the same. So what other gene structure information? Does it follow a certain pattern? It should take you time to learn how to use the genome mapping to find the genes that are identical or similar to those in other species. This information is called **microinformatics** and is used to find the genes that are identical or similar to those in other species.

Microinformatics is a field that combines statistics, mathematical modeling, and computer-aided analysis of genomic data. Using microinformatics methods, entire genomes can be quickly compared to find the genes that are identical or similar. The microinformatics method is called **BLAST**, which stands for **Basic Local Alignment Search Tool**. Using BLAST, you can find the genes that are identical or similar to those in other species. BLAST is a simple algorithm that finds the genes that are identical or similar to those in other species.

In this investigation, you will use BLAST to compare microinformatics and microinformatics information to find the genes that are identical or similar. This information is called **microinformatics** and is used to find the genes that are identical or similar to those in other species. BLAST is a simple algorithm that finds the genes that are identical or similar to those in other species.

Note that the microinformatics is identical to the microinformatics and the microinformatics is identical to the microinformatics. This means that the genes that are identical or similar to those in other species are identical or similar to those in other species. This means that the genes that are identical or similar to those in other species are identical or similar to those in other species.

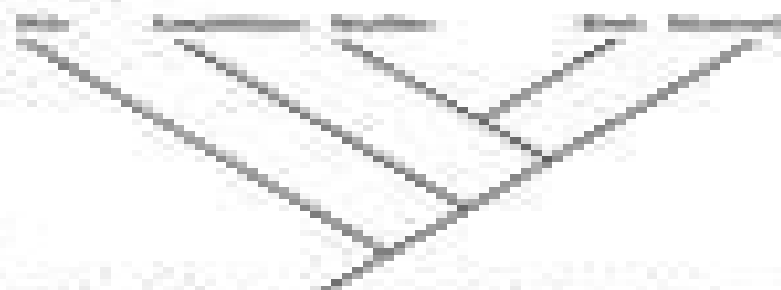


Figure 1. A simple phylogenetic tree of the five species shown.

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**National Institutes of Health (U.S.).
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Microbiology (Questions and Answers), 5e Purshotam Kaushik & Kirti Kaushik, 2022 Microbiology is an engaging textbook presenting balanced and comprehensive account of major areas of microbiology in the form of questions and answers This question answer approach to present complex topics and theories of microbiology regarding cellular and non cellular microorganisms microbial genetics and molecular biology in higher plants and animals makes the subject interesting and easily comprehensible for the students *Microbiology Questions and Answers* Mr. Ajeet Singh, 2018-05-14 A structured question and answer resource covering core microbiology concepts laboratory techniques microbial physiology genetics and applied microbiology for academic and competitive exams **Solutions Manual for An Introduction to Genetic Analysis** David Scott, 2012 Since its inception Introduction to Genetic Analysis IGA has been known for its prominent authorship including leading scientists in their field who are great educators This market best seller exposes students to the landmark experiments in genetics teaching students how to analyze experimental data and how to draw their own conclusions based on scientific thinking while teaching students how to think like geneticists Visit the preview site at www.whfreeman.com/IGA10epreview **40 Inquiry Exercises for the College Biology Lab** A. Daniel Johnson, 2009 Drawing from the author's own work as a lab developer coordinator and instructor this one of a kind text for college biology teachers uses the inquiry method in presenting 40 different lab exercises that make complicated biology subjects accessible to major and nonmajors alike The volume offers a review of various aspects of inquiry including teaching techniques and covers 16 biology topics including DNA isolation and analysis properties of enzymes and metabolism and oxygen consumption Student and teacher pages are provided for each of the 16 topics **In Silico Chemistry and Biology** Girish Kumar Gupta, Mohammad Hassan Baig, 2022-05-09 In Silico Chemistry and Biology Current and Future Prospects provides a compact overview on recent advances in this highly dynamic branch of chemistry Various methods of protein modelling and computer assisted drug design are presented including fragment and ligand based approaches Many successful practical applications of these techniques are demonstrated The authors also look to the future and describe the main challenges of the field **Bioinformatics** Mahmood A. Mahdavi, 2011-11-02 Bioinformatics Trends and Methodologies is a collection of different views on most recent topics and basic concepts in bioinformatics This book suits young researchers who seek basic fundamentals of bioinformatic skills such as data mining data integration sequence analysis and gene expression analysis as well as scientists who are interested in current research in computational biology and bioinformatics including next generation sequencing transcriptional analysis and drug design Because of the rapid development of new technologies in molecular biology new bioinformatic techniques emerge accordingly to keep the pace of in silico development of life science This book focuses partly on such new techniques and their applications in biomedical science These techniques maybe useful in identification of some diseases and cellular disorders and narrow down the number of experiments required for medical

diagnostic *Spontaneous Pathology of the Laboratory Non-human Primate* Alys Bradley, Jennifer Chilton, Beth Mahler, 2023-06-20 *Spontaneous Pathology of the Laboratory Non human Primate* serves as a go to resource for all pathologists working on primates in safety assessment studies In addition it helps diagnostic veterinary pathologists rule out spontaneous non clinical disease pathologies when assigning cause of death to species in zoological collections Primate species included are rhesus cynomolgus macaques and marmosets Multi authored chapters are arranged by organ system thus providing the necessary information for continued research Pathologists often face a lack of suitable reference materials or historical data to determine if pathologic changes they are observing in monkeys are spontaneous or a consequence of other treatments or factors Contains color illustrations that depict the most common lesions to augment descriptions Covers descriptions that are compliant with the International Harmonization of Nomenclature and Diagnostic Criteria INHAND guidelines set forth by the Society of Toxicologic Pathology STP Provides pathologists with common terms that are compliant with the FDA s Standard for Exchange of Nonclinical Data SEND guidelines **Director's Report** National Institutes of Health (U.S.). Division of Computer Research and Technology, 1994 **Molecular Data Analysis Using R** Csaba Ortutay, Zsuzsanna Ortutay, 2017-02-06 This book addresses the difficulties experienced by wet lab researchers with the statistical analysis of molecular biology related data The authors explain how to use R and Bioconductor for the analysis of experimental data in the field of molecular biology The content is based upon two university courses for bioinformatics and experimental biology students Biological Data Analysis with R and High throughput Data Analysis with R The material is divided into chapters based upon the experimental methods used in the laboratories Key features include Broad appeal the authors target their material to researchers in several levels ensuring that the basics are always covered First book to explain how to use R and Bioconductor for the analysis of several types of experimental data in the field of molecular biology Focuses on R and Bioconductor which are widely used for data analysis One great benefit of R and Bioconductor is that there is a vast user community and very active discussion in place in addition to the practice of sharing codes Further R is the platform for implementing new analysis approaches therefore novel methods are available early for R users

Phylogenomics Rob DeSalle, Michael Tessler, Jeffrey Rosenfeld, 2020-08-18 *Phylogenomics A Primer* Second Edition is for advanced undergraduate and graduate biology students studying molecular biology comparative biology evolution genomics and biodiversity This book explains the essential concepts underlying the storage and manipulation of genomics level data construction of phylogenetic trees population genetics natural selection the tree of life DNA barcoding and metagenomics The inclusion of problem solving exercises in each chapter provides students with a solid grasp of the important molecular and evolutionary questions facing modern biologists as well as the tools needed to answer them

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