

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 sequenced the genomes of other species, including the fruit fly, mouse and *Drosophila*, etc. The sequence and structure comparison of the genomes of these different species are used to determine whether there are similarities and how different.

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, learning about the sequence of genes in other species helps us understand evolutionary relationships among organisms. Many of our human ailments can be traced to these found human genes.

However, you already realize that it is impossible for a computer, because its built into its own hard wired machine language. How is human evolution different? It should take you nearly 40 years to read through the entire human genome to try to locate the same amount of data as that in this file. This difficulty can be solved, via sophisticated technological methods as needed.

Microinformatics is a field that combines statistics, mathematical modeling, and computer assisted analysis biological data. Using microinformatics methods, entire genomes can be quickly compared to locate the shared genetic similarities and differences. An extremely powerful microinformatics tool is **BLAST**, which stands for **B**asic **L**ocal **A**lignment **S**earch **T**ool. Using **BLAST**, you can input a gene sequence or identify a particular gene sequence because the identity of similar sequences is a matter of seconds.

In this investigation, you will use **BLAST** to compare similarities and differences information as measured in **alignments**. An alignment (also called **homologous** gene) is an **evolutionary relationship** representation of species. **Figure 1** below depicts a typical alignment.

Note that this alignment is identical with **homologous** and **orthologous** relationships in specific species. The idea is that two species are found to have same, the **homologous** they share common ancestor.

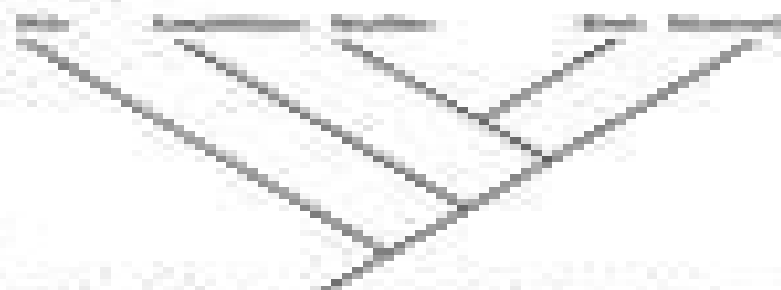


Figure 1. A simple diagram of the Phylogenetic Tree.

Bio Bioinformatics Lab Answers

Csaba Ortutay, Zsuzsanna Ortutay



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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

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