

Chapter 1 : Phylogenetic Trees Made Easy | University of Minnesota Duluth

Phylogenetic Trees Made Easy A How-To MAnuAl Fourth Edition Barry G. Hall University of Rochester, Emeritus and Bellingham Research Institute Sinauer Associates, Inc. Publishers.

Sinauer Associates, Sunderland, Massachusetts. Perhaps no other aspect of evolutionary biology is used more and understood less than phylogenetics. For most biologists, the estimation of evolutionary relationships from genetic data takes on a mystical quality. Much like polling data used to predict election results, a single set of DNA sequences can go through one of several seemingly related analyses and yield different answers. Furthermore, a single task, such as making a presentable phylogenetic tree, can require the use of several quirky programs with different formats and inadequate manuals. While this book is unlikely to close significantly the gap between the use and deep understanding of phylogenetic methods, it ought to help eradicate proxies for evolutionary relationships such as percent similarity tables and gently introduce a new generation of users to practical and theoretical phylogenetics. PTME is an immensely useful tool for newcomers to phylogenetic tree construction, particularly those who cross over from molecular biology and bioinformatics, and it will serve intermediate users as a handy reference. Reviews of the first edition of PTME often described it as a cookbook-like guide. This quality is intact in the second edition, which contains some important organizational changes, content additions, and updates, as is expected for a book whose content is attached to ever-changing computer software. In addition, PTME is accompanied by a useful website [http:](http://) Hall divides the second edition into four chapters. Hall simply shows how someone desperate to make a quick tree might use little more than PubMed tools, ClustalX, and TreeView to make a neighbor-joining tree. The second chapter is a concise guide to phylogenetic tree reconstruction and covers the implementation of the major methods for creating trees. Example files provided with this chapter seem particularly useful to novice users. The third chapter briefly covers how one might get involved in the two emerging cottage industries, recovery of ancestral sequences and detection of positive selection. *Phylogenetic Trees Made Easy* is well written. Major points are lucid and jargon is avoided when appropriate. Although cookbook-like and not an appropriate source for those interested in learning phylogenetic theory, PTME contains a trail of references that allow a novice user to gain a deeper understanding of the material covered in the book. On complex issues, Hall often defers to more specialized sources, such as *Molecular Systematics* Hillis et al. It is likely that future editions will heavily reference *Inferring Phylogenies* Felsenstein. One could take issue with many small omissions in PTME, but I have found only one necessary improvement that could easily be addressed. Hall fails to point out the value that extra time and care taken in phylogenetic analyses could potentially add to the results. Most researchers spend many months applying for funding, conducting experiments, and obtaining the related data, including gene sequences. They then balk at a day-long computer run that could potentially improve the quality of their phylogenetic analyses. In a brief discussion of trade-offs among different methods in phylogenetic analysis, Hall leaves it to the discretion of an inexperienced user to determine the appropriate run length, although he puts in a good word for overnight runs. He missed an opportunity to emphasize that the relevance of the results, not impatience, should govern the appropriate amount of effort. Of course, this is true for all steps covered in the book—alignment, tree construction, analysis, and presentation. Still, the shortcomings of PTME are few, and the strengths are many. Some critics are sure to complain that only a few of many available programs are covered in the book. They should remember that the first edition of PTME was well received in part because it was kept slim. It is a simple guide describing the essentials. *Phylogenetic Trees Made Easy* should be included with a lab bench for young graduate students in many evolution-related fields and could be essential for more senior biologists expecting to dabble in phylogenetic reconstruction. It is also a useful teaching tool for advanced undergraduate courses. To the delight of laypeople, and perhaps to the dismay of some phylogeneticists, PTME allows relative novices to follow a crisply written recipe and construct a phylogenetic tree. Hopefully it will not give them the impression that they are liberated from thoughtful consideration of the methods that they are employing.

Chapter 2 : Interactive Tree Of Life v2: online annotation and display of phylogenetic trees made easy.

Phylogenetic Trees Made Easy A How-To Manual. Fifth Edition. Barry G. Hall. Sinauer Associates is an imprint of Oxford University Press "Learn More" boxes present background on the various concepts and methods.

How to Make Phylogenetic Trees By Allia Nelson; Updated April 24, A phylogenetic tree is a graphic representation of evolutionary relationships that demonstrates how organisms could possibly have diverged from a common ancestor. Previously, this was done through comparison of anatomy and physiology of living organisms and fossils, but now genetic information taken from DNA nucleotide sequences is commonly used. A phylogenetic tree is a method for understanding species and evolutionary changes in organisms. This can be done with a species, breed or nucleotide sequence that represents an organism. An example organism could be a cow. The rest of the tree would demonstrate how closely related a cow is to other organisms based on genetic traits. An outgroup is a less closely related organism or vastly different nucleotide sequence. If the model organism is a cow, then a possible outgroup would be a fish. The more different two organisms are, the farther down on the phylogenetic tree will be their diverging branch point. Time is represented with the oldest date at the bottom of the chart and present day being at the top of the chart. The placement of the branches shows approximately when in the past an evolutionary trait possibly changed an ancestral organism into different species. Examples include "has four legs," "chews cud," "gives live birth" or "grows hair. When one organism does not contain the desired trait, a branch is made in the phylogenetic tree. Paste the picture or sequence of a cow in the upper corner of the poster board and the fish in the opposite corner and draw two lines from them to the base of the paper in an intersecting V shape. Place the image of the sheep near the picture of the fish and draw a line that connects in a V shape down to the branch of the cow. Paste the picture of the deer between the cow and sheep and draw another line into a V shape that intersects above the fish and sheep lines. When each species has a single branch, the phylogenetic tree has been completed. Tip Choose a finite set of organisms or sequences. Pick characteristics or sequences that divide the organisms into separate groups. Have multiple characteristic supports to demonstrate organism relationships. Warning Phylogenetic placement can be debated based on many characteristics, and much support is required for placement choices. Mathematical equations may be necessary to demonstrate the statistical likelihood of evolutionary changes. Probability of divergence on the genetic level leaves room for possible inaccuracies in phylogenetic trees. Things Needed Data set i.

Chapter 3 : Simple Phylogenetic Tree < Phylogeny < EMBL-EBI

Phylogenetic Trees Made Easy, Fifth Edition helps the reader get started in creating phylogenetic trees from protein or nucleic acid sequence data. Although aimed at molecular and cell biologists, who may not be familiar with phylogenetic or evolutionary theory, it also serves students who have a theoretical understanding of phylogenetics but need guidance in transitioning to a practical.

These programs can help in phylogenetic tree construction. You can ask questions like what is the evolutionary relationship between a set of sequences from different species? Or how have certain microbial strains arisen? This nifty yet powerful resource matches your sequence to the millions of sequences stored in genomic and nucleotide databases. The tool comes up with the sequences most similar to yours. It also gives insights as to the possible identity of those sequences. The results include homologues across species and in similar tissues. Blast is important as it helps to confirm that sequences are homologues and not just lucky alignments. The basics of using BLAST for nucleotide sequence searches has already been covered in this wonderful article. This is a great way to find out the possible products and functions of your sequence! Compares your sequence against other nucleotide sequences, optimal for finding very similar sequences of putatively related species. It casts a tighter net. As such it is a one stop source for phylogenetic tree construction. This is located on the launch bar of the main MEGA window. This lets you add one by one the sequences for your alignment into the visual explorer. After adding all the sequences, you the option to align them using one to two different programs that are commonly used. The two alignment programs differ in their operation. ClustalW uses a progressive algorithm for alignment. It aligns two sequences at each step, then aligns the alignment with another sequence, and so on. It achieves better results than ClustalW across key parameters. These parameters include alignment accuracy as well as lower time and space complexity using progressive, rather than an iterative, alignment. Go to Alignment, and choose Align by Muscle. As a beginning user, the presets are fine to use, as they serve the purpose of most people. Your output should look something like that shown below. Save your alignment as a. This way, you can use it later without having to spend time adding and aligning sequences again. These are various approaches to tree construction, each with their own pros and cons, and suitability for your particular purpose. For a given method chosen, Mega will help you find the best model for your DNA or protein sequence substitution rates. You can always go back and redraw the tree using other methods! After choosing and clicking Compute, you get a Tree that looks something like this: To make that a little easier to read shown below , click on the button above Display Only Topology. Tree Explorer This tree gives us a lot of information about the sequence! This is a surprising fact, considering their geographical locations in Africa. Guinea is in north Africa and Gabon lies across the Gulf of Guinea. This suggest that bats may be an important transmitter of the ebolavirus between these locations. This has been a very brief introduction to the power of MEGA. Note, the reliability of the tree can be estimated using the bootstrap method.

Phylogenetic Trees Made Easy helps beginners get started in creating phylogenetic trees from protein or nucleic acid sequence data.

It comes as no surprise, then, that the two previous editions of this book, received reviews that varied from enthusiastic Van de Peer, ; Nepokroeff, ; Fitch, ; Smith, to noncommittal Meyer, ; Elgar, ; Smith, to disappointed Wright, ; Kumar, ; Ronquist, ; Igic, to downright critical Macey, ; Grant et al. A look at the third edition of this book is thus a worthwhile exercise, to see whether anything has changed with the various revisions. Sadly, this review is not going to be, in essence, any different to those of the latter two groups. It is a pity to criticize a book like this, because what it tries to do it does rather well. It covers many relevant topics in a readable manner, the ideas are accessible, and the instructions are easy to follow. Ultimately, however, the book is far too uneven for me to claim that it is a particularly good one. It targets a specific group of researchers, and that target audience may see some value in it. Readers of this journal are not likely to be members of that audience. I venture to suggest that there are three basic attitudes to phylogenetic analysis, which I will label as bioinformatic, protocol, and phylogenetic. The bioinformatic approach sees the analysis as an investigation of multivariate patterns in a data set, producing a tree as one means of representing those patterns. The protocol approach sees the analysis as a component of a larger project, with the tree as simply one tool of many for investigating evolutionary patterns often focusing on gene trees. The spotlight is on having an adequate protocol for the data analysis, analogous to the protocol used for laboratory work. The focus is on getting the best tree possible of the species not the genes, with full understanding of the value that almost always comes from taking extra time and care. The distinction between these three attitudes is not trivial. For example, I have recently conducted a review of sequence-alignment practices in 26 journals covering the areas of phylogenetics, systematics, evolutionary biology, molecular biology, and microbiology. I found major differences in the practices between these areas, in spite of the fact that the boundaries between the areas are very hazy. In particular, the first two areas fit neatly into the phylogenetics category, whereas the latter three fit firmly into the protocol category. There is not enough computational information to interest the bioinformatics group and not enough consideration given to the uniqueness of each data set to satisfy the phylogenetics group. Most of the many books aimed at the bioinformatics group either treat phylogenetic analysis as one possibly minor aspect of a much broader class of analyses for molecular data. There are not many books aimed at the phylogenetics group. For the protocol group, a phylogenetic analysis is usually part of a pipeline, with the sequence data going in at one end and a publishable analysis coming out at the other end. Ideally, this pipeline would be automated and fast. However, it is difficult to control the quality of the output if there is no manual quality control of the processing. High-quality phylogenetic analyses are not easy, because each data set has its own array of characteristics, and these characteristics must not be allowed to cause problems in the final output. Phylogenetic analysis requires careful thought and a great deal of understanding, if it is going to be effective. This is hard to reconcile with a fast, automated pipeline for analysis. Barry Hall clearly cares about quality, but he does not make it the focus of his book, the focus instead being on speed and ease of use. The motivation is to get the reader started on phylogenetic analysis of a gene, not to produce analyses that will stand the test of time. The majority of the space in the book is devoted to screenshots from the computer programs, illustrating the recipes used in the tutorials, with little consideration of how to decide which recipe might be the one needed. If readers follow the recipes in the book and can adapt those recipes to their own data, then it is clear that they will get a tree based on each of the methods discussed. Introductory books are hard to write precisely because the answers to the key philosophical questions are never obvious. How much of a protocol is someone supposed to truly understand before they can be expected to use the protocol competently; and when in the process are they expected to acquire that understanding? Barry Hall has chosen his answers and, after three editions of his book, they are presumably carefully chosen answers. Unfortunately, reviewers of the previous editions have not always been impressed with those answers. Hall communicates the bare minimum of information possible for

constructing a tree. When dealing with data analyses, biologists sometimes produce a rather time-worn analogy with driving a car rather than with cooking: Unfortunately, this analogy has one fatal flaw: In contrast, data analyses can produce complete nonsense without the user realizing it at all, if the analyses are not performed in an appropriate manner; and computerized analyses can produce such nonsense at a very fast rate indeed. It is a pity that so many biologists seem to put a lot of time and effort into collecting high-quality data because they understand their laboratory protocol and then analyze it in an unsuitable manner because they do not understand their data analysis protocol. Data analysis is an iterative process of calculation and thought, not a pipeline. So, a book based on protocols has an inbuilt limitation. This book will get you started on phylogenetic analysis, but it does not tell you how much more there is to do. This is both its greatest strength and its greatest weakness. Ultimately, this duality results in the situation where each important topic is introduced but not enough understanding is provided to create competent program users. This is what generates the obvious unevenness in the book. Recipes are very useful if you simply want to repeat an analysis of your own, but they are not a good way to teach data analysis—recipes best document what you did, rather than what someone else should do. One simple example will suffice to illustrate the unevenness. It is good for the book to have an appendix about data formats for different computer programs, because this is often the biggest frustration for both beginners and experts. Problems can arise in programs from: Thus, the important issue of data formats is introduced but is not covered in an effective manner. The rest of the book suffers the same type of problem—the choice of topics to be discussed and their depth seem somewhat arbitrary. So, as far as the underlying philosophy is concerned, there is little difference between this edition and its predecessors Zwickl. Indeed, very few of the criticisms of the previous editions seem to have been addressed in this edition. On the other hand, the most obvious difference between the three editions is the computer programs that are used to implement the protocols. The first edition focused on Apple Macintosh computers, whereas the second edition broadened the scope to include Windows and Unix PCs. This new edition focuses on Windows PCs, with the expectation that the other two user groups will adapt to this situation such as by using the Wine API, which is a long way short of usable on a Macintosh. So, the MEGA program is used for most of the analyses, along with PhyML for maximum likelihood and MrBayes for bayesian analysis the latter being the only hangover from the first two editions. Other programs are briefly mentioned in an appendix, but with the usual unevenness regarding the amount of information given and its correctness. Ease of use can be a very good thing in computing, but it should not come at the expense of thinking, which is what inevitably happens unless the user is guided through a thorough exploration of their data before they do the analysis. The closest competitor for this book is probably the one edited by Salemi and Vandamme. The latter deals with many more computer programs, covers the theory in more depth, and includes a wider range of topics. It is not, however, a how-to tutorial, and thus cannot stand on its own as a practical guide to phylogenetic trees Morrison,

Chapter 5 : Phylogenetic Trees Made Easy - Barry G. Hall - Oxford University Press

Phylogenetic Trees Made Easy should be included with a lab bench for young graduate students in many evolution-related fields and could be essential for more senior biologists expecting to dabble in phylogenetic reconstruction. It is also a useful teaching tool for advanced undergraduate courses.

Chapter 6 : Phylogenetic Tree Construction Made Easy with Blast & Mega - Bitesize Bio

Download Packages. The packages specific to each platform include the files and templates indicated by the Download icon in the text of Phylogenetic Trees Made Easy, Fourth Edition and include the Utility programs that are discussed in Chapter

Chapter 7 : How to Make Phylogenetic Trees | Sciencing

Phylogenetic Tree Construction with MEGA Version 6 Now comes the fun part! MEGA has a variety of options for phylogenetic tree construction, including UPGMA tree, Maximum Parsimony, Neighbor-Joining, and Maximum Likelihood.

Chapter 8 : Phylogenetic Trees Made Easy: A How-To Manual

Phylogenetic Trees Made Easy, Fourth Edition, helps students get started in creating phylogenetic trees from protein or nucleic acid sequence data. Although aimed at molecular and cell biologists, who may not be familiar with phylogenetic or evolutionary theory, it also serves those who have a theoretical understanding of phylogenetics but need.

Chapter 9 : ARC Resources for Phylogenetic Trees Made Easy, Fifth Edition

Phylogenetic Trees Made Easy, Fifth Edition leads the reader, step by step, through identifying and acquiring the sequences to be included in a tree, aligning the sequences, estimating the tree by one of several methods, and drawing the tree for presentation to an intended audience.