

Windows:

- Microsoft Windows operating system within a MacOS emulator is required.

MacClade 4 is a complex program that allows users to construct phylogenetic trees. This program is a welcome addition to the growing field of cladistics (considered the best method for establishing phylogenetic analysis). The range of information that can be possibly obtained through a cladogram is enormous. There are some fundamental concepts that need to be properly understood before engaging in cladistic methods:

- **Taxa** refer to the units (e.g., species) being studied. For teaching purposes, using few taxa makes phylogeny construction easier.
- **Characters** refer to observable features of the organism. In cladistic analyses, characters are the data being used to perform an analysis.
- **Outgroup and ingroup** are designations given to the taxa being studied. The outgroup includes taxa that are not in our study group. The ingroup includes the species for which we want to know the evolutionary relationships. The outgroup serves as a reference point to determine the direction of character evolution.
- **Parsimony** refers to the simplest explanation. In cladistics, parsimony is used to find the cladogram that minimizes the number of character variations within a data matrix. When striving for parsimony, one must select phylogeny that involves the fewest number of hypotheses of convergence. This is purely a technical choice and by no means implies simplicity of the evolution process itself.
- **Character state designations** are terms (*homology* and *analo-*

gy) that describe the evolutionary origin of the characters. In general, cladograms allow us to address questions regarding these designations.

- **Cladogram** is a hierarchical branching that displays the relationships in a group of taxa. It may be represented in a tree form, and illustrates closeness in evolutionary relationships.

The program consists of 26 chapters aimed at accomplishing various strategies in phylogenetic analysis. For those unfamiliar with the software and/or cladistics, Chapter 2 (*A Tutorial Overview of MacClade*) is essential. This tutorial will guide the user step by step through data files, and all the basic functions of **MacClade 4**. Chapters 3-4 deal with phylogenetic theory and should be “must read” material for any undergraduate evolution course. Chapter 4 (*Reconstructing Character Evolution Using Parsimony*) describes all the assumptions and methods behind cladistic analysis. Chapters 5-25 deal with specific aspects of phylogenetic analysis, importing and exporting files, sharing data files, creating and manipulating taxa, and many other methodological issues of cladistic analysis.

MacClade 4 is not trivial software. It may be appropriate for advanced undergraduates, beginning graduate students, and those wishing to become immersed in a dynamic and fascinating (sometimes limited) field that incorporates genetics, evolution, taxonomy, and a fundamental sense of logic that aims at hypothesizing relationships among organisms.

I wish to thank Professor Ross Nehm of City College of New York for sharing extremely useful teaching materials using cladistics that helped me prepare this review.

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VISUALIZING THE CENTRAL DOGMA

Visualizing the Central Dogma. (2004). Animation created by David Spector, Cold Spring Harbor Laboratory. Available online at www.cshl.edu/public/releases/dogma.html.

For over fifty years the term “central dogma of biology” has propelled a stampede of research to find the details of the processes that lead to DNA → RNA → proteins. Although the general pathway has been modified since the discovery of the enzyme Reverse Transcriptase, the notion of the central dogma continues to be addressed in textbooks, research papers, and many other venues. However, at the classroom level, much of the discussion about the flow of genetic information ends without a clear visualization of the holistic process, due to its inherent complexity. Consequently, biology instructors and students end up approaching the central dogma from a reductionist perspective.

Researchers at Cold Spring Harbor Laboratory, led by Dr. David Spector, have put together a short but incredibly illuminating 30-second movie that illustrates the central dogma (flow of genetic information) in a single-step animation. This short clip captures the process that in 2004 still fascinates scientists conducting basic and applied research. It shows time-lapse images of an inducible gene being transcribed, spliced, and translated. Although viewers may need to replay it several times, the power of this animation is undeniable. Skeptical students can visualize the process in unison, and hopefully get a better appreciation of one of the most fascinating concepts in molecular biology.

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