

practice phylogenetic trees

practice phylogenetic trees is an essential process for anyone interested in evolutionary biology, genetics, and bioinformatics. This article provides a comprehensive guide to understanding, constructing, and interpreting phylogenetic trees. Readers will discover the basic concepts of phylogenetics, explore the different types of phylogenetic trees, and learn valuable tips for practicing tree construction and analysis. The article also covers common mistakes, useful tools, and practical exercises for mastering phylogenetic trees. Whether you are a student, researcher, or enthusiast, this guide will help you develop the skills needed to interpret evolutionary relationships accurately. The content is optimized for search engines, ensuring that readers receive authoritative, up-to-date information about the practice of phylogenetic trees.

- Understanding Phylogenetic Trees
- Types of Phylogenetic Trees
- Steps for Constructing Phylogenetic Trees
- Tips for Practicing Phylogenetic Tree Interpretation
- Common Mistakes and How to Avoid Them
- Useful Tools for Practicing Phylogenetic Trees
- Practical Exercises for Mastering Phylogenetic Trees
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Understanding Phylogenetic Trees

Phylogenetic trees are graphical representations that illustrate the evolutionary relationships among various species or genes. They are widely used in evolutionary biology to depict how organisms are related through common ancestry. Practicing phylogenetic trees involves learning how to read, interpret, and construct these diagrams to understand the evolutionary paths and divergence events in the history of life. The ability to analyze phylogenetic trees is crucial for research in taxonomy, comparative genomics, and biodiversity studies. By mastering these skills, scientists and students can draw meaningful conclusions about the origins and connections among living organisms.

Key Concepts in Phylogenetics

To practice phylogenetic trees effectively, it is important to understand key concepts such as nodes, branches, clades, and outgroups. Nodes represent common ancestors, branches indicate the evolutionary path, clades are groups of organisms that share a common ancestor, and outgroups

help root the tree and provide context for evolutionary relationships. These elements form the foundation for constructing and interpreting phylogenetic trees accurately.

Applications of Phylogenetic Trees

Phylogenetic trees have diverse applications, including tracking the evolution of infectious diseases, classifying species, and studying gene families. Practicing the creation and interpretation of these trees enables researchers to make informed decisions in fields like conservation biology, medicine, and agriculture. By analyzing tree topology and branch lengths, scientists can infer evolutionary timelines and patterns.

Types of Phylogenetic Trees

There are several types of phylogenetic trees, each suited to specific research questions and data types. Practicing with different tree formats enhances understanding and helps in selecting the appropriate tree for analysis.

Rooted vs. Unrooted Trees

Rooted trees display a defined common ancestor, showing the direction of evolution from the root to the tips. Unrooted trees illustrate relationships without specifying an ancestral lineage, making them useful for examining genetic similarity without inferring evolutionary direction. Practicing with both rooted and unrooted trees is vital for comprehensive phylogenetic analysis.

Cladograms, Phylograms, and Dendrograms

- **Cladograms:** Show only the branching order, representing evolutionary relationships without considering branch lengths.
- **Phylograms:** Depict evolutionary relationships and branch lengths, which can suggest genetic distance or time since divergence.
- **Dendrograms:** Used in hierarchical clustering, these trees illustrate similarities among data points, often in genomics and bioinformatics.

Steps for Constructing Phylogenetic Trees

Practicing phylogenetic tree construction involves a series of methodical steps. Accurate tree

construction is essential for drawing valid evolutionary conclusions and for further analysis.

Data Collection and Preparation

Begin by selecting appropriate data, such as DNA sequences, protein sequences, or morphological traits. Sequence alignment is a critical step, ensuring that homologous positions across samples are compared accurately. Quality data preparation lays the foundation for reliable tree inference.

Choosing a Tree-Building Method

- **Distance-based methods:** Such as Neighbor-Joining, rely on genetic distance matrices to build trees.
- **Character-based methods:** Like Maximum Parsimony and Maximum Likelihood, use observed character states to infer evolutionary relationships.
- **Bayesian Inference:** Applies statistical models to estimate the probability of different tree topologies.

Practicing with multiple methods helps in understanding their strengths and limitations and in choosing the most suitable approach for specific datasets.

Tree Evaluation and Validation

Once a tree is constructed, it is essential to evaluate its quality using statistical support measures such as bootstrap values or posterior probabilities. Practicing with these techniques ensures confidence in the inferred evolutionary relationships and facilitates robust scientific conclusions.

Tips for Practicing Phylogenetic Tree Interpretation

Interpreting phylogenetic trees requires attention to detail and an understanding of evolutionary principles. Practice in tree reading and analysis sharpens skills and prevents misinterpretation.

Reading Branching Patterns

Examine where branches split to identify the most recent common ancestors and to group organisms into clades. Pay attention to branch lengths, which may indicate genetic distance or evolutionary time, depending on the tree type.

Using Outgroups Effectively

Including an outgroup helps root the tree and clarifies evolutionary direction. Practice selecting an appropriate outgroup that is closely related but outside the group of interest for accurate tree rooting.

Identifying Monophyletic, Paraphyletic, and Polyphyletic Groups

- **Monophyletic:** Includes a common ancestor and all its descendants.
- **Paraphyletic:** Includes a common ancestor and some, but not all, descendants.
- **Polyphyletic:** Includes organisms from different ancestors.

Practice distinguishing these groups to enhance understanding of evolutionary relationships.

Common Mistakes and How to Avoid Them

Mistakes in practicing phylogenetic trees can lead to incorrect interpretations and conclusions. Awareness of common errors is crucial for effective learning and analysis.

Misinterpreting Tree Topology

Confusing tree layout with evolutionary proximity is a frequent mistake. The arrangement of branches does not always reflect chronological order or relatedness. Practice focusing on branching patterns rather than tip proximity.

Ignoring Statistical Support

Failing to consider bootstrap values or posterior probabilities can result in overconfidence in weakly supported relationships. Practice evaluating statistical support before drawing conclusions.

Overlooking Data Quality

Poor sequence alignment or inaccurate data can distort tree inference. Practice careful data curation and validation to avoid misleading results.

Useful Tools for Practicing Phylogenetic Trees

Several computational tools and software packages facilitate the practice of phylogenetic tree construction and analysis. Experimenting with different tools enhances proficiency and broadens understanding.

Popular Phylogenetic Analysis Software

- MEGA (Molecular Evolutionary Genetics Analysis)
- PhyML (Phylogenetic Maximum Likelihood)
- MrBayes (Bayesian Inference of Phylogeny)
- RAxML (Randomized Axelerated Maximum Likelihood)
- Clustal Omega (Multiple sequence alignment)

These tools offer user-friendly interfaces and advanced algorithms for constructing, visualizing, and validating phylogenetic trees.

Online Resources and Databases

Practicing with curated datasets from public databases, such as GenBank, TreeBASE, and Ensembl, provides exposure to real-world data and broadens expertise in phylogenetic analysis.

Practical Exercises for Mastering Phylogenetic Trees

Hands-on practice is the most effective way to master phylogenetic tree construction and interpretation. Engaging in targeted exercises builds confidence and proficiency.

Sequence Alignment Practice

Begin by aligning DNA or protein sequences from multiple organisms. Use software like Clustal Omega or MUSCLE to practice generating alignments and evaluating their quality.

Constructing and Interpreting Trees

- Use a dataset of aligned sequences to build a tree using different methods (e.g., Neighbor-Joining, Maximum Likelihood).
- Practice interpreting branching patterns, root position, and support values.
- Compare trees generated by different methods to understand variability in results.

Evaluating Real-World Phylogenies

Analyze published phylogenetic trees from scientific literature. Practice identifying clades, outgroups, and evolutionary trends to reinforce theoretical knowledge with practical application.

Conclusion

Developing expertise in practice phylogenetic trees is fundamental for evolutionary biology, genetics, and related fields. With a solid grasp of key concepts, different tree types, construction methods, and interpretation techniques, practitioners can draw accurate evolutionary insights. By avoiding common mistakes and utilizing powerful analytical tools, individuals can enhance their skills and contribute meaningfully to scientific research. Consistent practice with real-world data and computational resources ensures mastery of phylogenetic analysis.

Q: What is the purpose of practicing phylogenetic trees?

A: Practicing phylogenetic trees helps individuals accurately interpret evolutionary relationships, understand the history of species divergence, and apply these insights to research in biology, genetics, and bioinformatics.

Q: Which data types are commonly used for constructing phylogenetic trees?

A: DNA sequences, protein sequences, and morphological traits are the primary data types used for constructing phylogenetic trees, each offering different insights into evolutionary relationships.

Q: What is the difference between rooted and unrooted phylogenetic trees?

A: Rooted trees show the direction of evolution from a common ancestor, while unrooted trees represent relationships among taxa without specifying an ancestral lineage.

Q: Why is sequence alignment important in the practice of phylogenetic trees?

A: Sequence alignment ensures homologous positions are compared across samples, providing the accurate data necessary for reliable tree inference and evolutionary analysis.

Q: How can statistical support values improve phylogenetic tree interpretation?

A: Statistical support measures, such as bootstrap values and posterior probabilities, indicate the reliability of branching patterns and help validate evolutionary relationships.

Q: What are monophyletic, paraphyletic, and polyphyletic groups?

A: Monophyletic groups include a common ancestor and all its descendants, paraphyletic groups include some descendants, and polyphyletic groups consist of organisms from different ancestors.

Q: Which software tools are recommended for practicing phylogenetic tree construction?

A: MEGA, PhyML, MrBayes, RAxML, and Clustal Omega are popular tools for phylogenetic tree construction, offering diverse methods and user-friendly interfaces.

Q: What common mistakes should be avoided when practicing phylogenetic trees?

A: Misinterpreting tree topology, ignoring statistical support, and overlooking data quality are frequent mistakes that can lead to incorrect evolutionary conclusions.

Q: How can outgroups be used effectively in phylogenetic tree analysis?

A: Outgroups help root the tree and clarify evolutionary direction; selecting an appropriate outgroup is essential for accurate tree interpretation.

Q: What practical exercises can help master phylogenetic tree skills?

A: Aligning sequences, constructing trees using various methods, interpreting real-world phylogenies, and evaluating published trees are effective exercises for mastering phylogenetic tree skills.

Practice Phylogenetic Trees

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Practice Phylogenetic Trees: Mastering the Art of Evolutionary Relationships

Are you struggling to grasp the complexities of phylogenetic trees? Do you find yourself staring blankly at branching diagrams, unsure of how to interpret the evolutionary relationships depicted? You're not alone! Phylogenetic trees, also known as cladograms or evolutionary trees, can seem daunting at first, but with consistent practice, they become accessible and even fascinating tools for understanding the history of life on Earth. This comprehensive guide will equip you with the knowledge and resources to confidently practice phylogenetic tree analysis, transforming you from a novice to a phylogenetic pro.

Understanding the Fundamentals: What are Phylogenetic Trees?

Before diving into practice exercises, let's briefly review the basics. A phylogenetic tree is a visual representation of the evolutionary relationships among different species or groups of organisms. Each branch point, or node, represents a common ancestor, while the tips of the branches represent extant (currently living) or extinct species. The length of branches often (but not always) reflects the amount of evolutionary change or time elapsed. Understanding these core principles is crucial for successful interpretation and construction.

Practice Phylogenetic Trees: Interactive Online Tools

The best way to learn is by doing! Several excellent online tools offer interactive practice with phylogenetic trees. These platforms allow you to build trees, analyze existing ones, and test your understanding through quizzes and challenges.

OneZoom: This visually stunning website provides a dynamic exploration of the Tree of Life, allowing users to zoom in and out, exploring relationships between various organisms. It's great for building intuition about the vast scope of evolutionary relationships.

Phylogram: While requiring some familiarity with phylogenetic terminology, Phylogram offers sophisticated tools for building and manipulating phylogenetic trees. It's a great resource for

intermediate to advanced learners.

iTOL (Interactive Tree Of Life): This is a powerful tool for visualizing and annotating phylogenetic trees. While not strictly a "practice" tool, its ability to manipulate and customize trees makes it invaluable for solidifying your understanding.

Practice Phylogenetic Trees: Interpreting Existing Trees

Beyond building trees, interpreting existing ones is essential. Practice analyzing published phylogenetic trees by focusing on these key aspects:

Root: Identify the root of the tree, which represents the most recent common ancestor of all the organisms in the tree.

Nodes: Understand that each node represents a speciation event (the splitting of one lineage into two).

Branches: Analyze the lengths of branches to infer evolutionary distances or time elapsed (if applicable). Note that branch lengths can be scaled to represent different things, so always check the legend.

Clades: Recognize clades (groups of organisms that share a common ancestor). This is crucial for understanding evolutionary relationships.

Practice Phylogenetic Trees: Building Your Own Trees

Constructing your own phylogenetic trees from data is a more advanced but highly rewarding skill. This typically involves using phylogenetic software and employing different methods (e.g., maximum parsimony, maximum likelihood, Bayesian inference). While mastering these techniques requires significant study, starting with simple character datasets and using user-friendly software can be a great starting point.

Simple Character Matrix Exercises:

A good starting point is creating trees from simple character matrices. These matrices list organisms and their characteristics (traits). You can use these matrices to deduce evolutionary relationships based on shared derived characteristics (synapomorphies). Numerous online resources and textbooks provide example datasets for practice.

Tips for Effective Practice

Start Simple: Begin with smaller, simpler trees before tackling complex ones.

Use Multiple Resources: Explore different online tools and textbooks to reinforce your understanding.

Focus on Concepts: Don't get bogged down in the technical details initially; prioritize grasping the core concepts.

Seek Feedback: If possible, share your analyses with others and seek feedback on your interpretations.

Be Patient: Mastering phylogenetic trees takes time and effort. Don't be discouraged by initial challenges.

Conclusion

Practicing phylogenetic trees is a journey, not a race. By utilizing the various online tools, focusing on fundamental concepts, and gradually tackling more complex analyses, you can build your confidence and expertise in this essential area of evolutionary biology. Remember to consistently review the core principles and use a variety of resources to enhance your understanding. With dedication, you'll soon be able to confidently interpret and even construct your own phylogenetic trees, unlocking a deeper appreciation for the intricate tapestry of life on Earth.

FAQs

1. What software is best for beginners practicing phylogenetic tree construction? For absolute beginners, tools emphasizing visual construction and requiring minimal coding are ideal. Many free online tools fit this description; research options like those mentioned above.
2. How do I interpret branch lengths in a phylogenetic tree? Branch lengths can represent different things depending on the analysis; check the legend! They might reflect evolutionary time, genetic distance, or the number of character changes.
3. What are the different methods used to construct phylogenetic trees? Common methods include parsimony, maximum likelihood, and Bayesian inference. Each method has its own strengths and weaknesses.
4. Where can I find datasets to practice with? Many textbooks, online databases (like NCBI), and dedicated phylogenetic websites offer example datasets for practicing tree construction.

5. Is it necessary to learn programming to work with phylogenetic trees? Not necessarily. While advanced phylogenetic analyses often involve scripting, many user-friendly software packages offer intuitive graphical interfaces for building and analyzing trees without requiring coding expertise.

practice phylogenetic trees: *Phylogenetics* E. O. Wiley, Bruce S. Lieberman, 2011-10-11 The long-awaited revision of the industry standard on phylogenetics Since the publication of the first edition of this landmark volume more than twenty-five years ago, phylogenetic systematics has taken its place as the dominant paradigm of systematic biology. It has profoundly influenced the way scientists study evolution, and has seen many theoretical and technical advances as the field has continued to grow. It goes almost without saying that the next twenty-five years of phylogenetic research will prove as fascinating as the first, with many exciting developments yet to come. This new edition of *Phylogenetics* captures the very essence of this rapidly evolving discipline. Written for the practicing systematist and phylogeneticist, it addresses both the philosophical and technical issues of the field, as well as surveys general practices in taxonomy. Major sections of the book deal with the nature of species and higher taxa, homology and characters, trees and tree graphs, and biogeography—the purpose being to develop biologically relevant species, character, tree, and biogeographic concepts that can be applied fruitfully to phylogenetics. The book then turns its focus to phylogenetic trees, including an in-depth guide to tree-building algorithms. Additional coverage includes: Parsimony and parsimony analysis Parametric phylogenetics including maximum likelihood and Bayesian approaches Phylogenetic classification Critiques of evolutionary taxonomy, phenetics, and transformed cladistics Specimen selection, field collecting, and curating Systematic publication and the rules of nomenclature Providing a thorough synthesis of the field, this important update to *Phylogenetics* is essential for students and researchers in the areas of evolutionary biology, molecular evolution, genetics and evolutionary genetics, paleontology, physical anthropology, and zoology.

practice phylogenetic trees: Modern Phylogenetic Comparative Methods and Their Application in Evolutionary Biology László Zsolt Garamszegi, 2014-07-29 Phylogenetic comparative approaches are powerful analytical tools for making evolutionary inferences from interspecific data and phylogenies. The phylogenetic toolkit available to evolutionary biologists is currently growing at an incredible speed, but most methodological papers are published in the specialized statistical literature and many are incomprehensible for the user community. This textbook provides an overview of several newly developed phylogenetic comparative methods that allow to investigate a broad array of questions on how phenotypic characters evolve along the branches of phylogeny and how such mechanisms shape complex animal communities and interspecific interactions. The individual chapters were written by the leading experts in the field and using a language that is accessible for practicing evolutionary biologists. The authors carefully explain the philosophy behind different methodologies and provide pointers – mostly using a dynamically developing online interface – on how these methods can be implemented in practice. These “conceptual” and “practical” materials are essential for expanding the qualification of both students and scientists, but also offer a valuable resource for educators. Another value of the book are the accompanying online resources (available at: <http://www.mpcm-evolution.com>), where the authors post and permanently update practical materials to help embed methods into practice.

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by each taxonomic school of each others' positions. This augurs a period in which the debates become more concrete and specific. Let us hope that they take place in a scientific atmosphere which has occasionally been lacking in the past. Since the order of presentation of papers in the meeting was affected by time constraints, I have taken the liberty of rearranging them into a more coherent subject ordering. The first group of papers, taken from the opening and closing days of the meeting, debate philosophies of classification. The next two sections have papers on congruence, clustering and ordination. A notable concern of these participants is the comparison and testing of classifications. This has been missing from many previous discussions of numerical classification.

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names of clades; species names will still be governed by traditional codes. The PhyloCode is designed so that it can be used concurrently with the rank-based codes. It is not meant to replace existing names but to provide an alternative system for governing the application of both existing and newly proposed names. Key Features Provides clear regulations for naming clades Based on expressly phylogenetic principles Complements existing codes of nomenclature Eliminates the reliance on taxonomic ranks in favor of phylogenetic relationships Related Titles: Rieppel, O. *Phylogenetic Systematics: Haeckel to Hennig* (ISBN 978-1-4987-5488-0) de Queiroz, K., Cantino, P. D. and Gauthier, J. A. *Phylonyms: A Companion to the PhyloCode* (ISBN 978-1-138-33293-5).

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detailed illustrations and phylogenetic trees, *The Invertebrate Tree of Life* is a must-have reference for biologists and anyone interested in invertebrates, and will be an ideal text for courses in invertebrate biology. A must-have and up-to-date book on invertebrate biology Ideal as both a textbook and reference Suitable for courses in invertebrate biology Richly illustrated with black-and-white and color images and abundant tree diagrams Written by authorities on invertebrate evolution and phylogeny Factors in the latest understanding of animal genomics and original fossil material

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practice phylogenetic trees: Molecular Evolution Ziheng Yang, 2014 Studies of evolution at the molecular level have experienced phenomenal growth in the last few decades, due to rapid accumulation of genetic sequence data, improved computer hardware and software, and the development of sophisticated analytical methods. The flood of genomic data has generated an acute need for powerful statistical methods and efficient computational algorithms to enable their effective analysis and interpretation. *Molecular Evolution: a statistical approach* presents and explains modern statistical methods and computational algorithms for the comparative analysis of genetic sequence data in the fields of molecular evolution, molecular phylogenetics, statistical phylogeography, and comparative genomics. Written by an expert in the field, the book emphasizes conceptual understanding rather than mathematical proofs. The text is enlivened with numerous examples of real data analysis and numerical calculations to illustrate the theory, in addition to the working problems at the end of each chapter. The coverage of maximum likelihood and Bayesian methods are in particular up-to-date, comprehensive, and authoritative. This advanced textbook is aimed at graduate level students and professional researchers (both empiricists and theoreticians) in the fields of bioinformatics and computational biology, statistical genomics, evolutionary biology, molecular systematics, and population genetics. It will also be of relevance and use to a wider audience of applied statisticians, mathematicians, and computer scientists working in computational biology.

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systematics textbook with a focus on parsimony-based approaches for students and biologists interested in systematics and comparative biology. Randall T. Schuh and Andrew V. Z. Brower cover: -the history and philosophy of systematics and nomenclature; -the mechanics and methods of analysis and evaluation of results; -the practical applications of results and wider relevance within biological classification, biogeography, adaptation and coevolution, biodiversity, and conservation; and -software applications. This new and thoroughly revised edition reflects the exponential growth in the use of DNA sequence data in systematics. New data techniques and a notable increase in the number of examples from molecular systematics will be of interest to students increasingly involved in molecular and genetic work.

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that are problematic or controversial. In the last part, novel topics in molecular evolution and systematics, like genomics, comparative methods in molecular evolution and the use of large data bases are described. The final chapter deals with problems in bacterial evolution, considering the increasing access to large numbers of complete genome sequences.

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among the earliest animal lineages. Within the last 20 years, the field of phylogenetics has grown rapidly, both in the quantity of data available for inference and in the number of methods available for phylogenetic estimation. The authors' first book, *Estimating Species Trees: Practical and Theoretical Aspects*, published in 2010, gave an overview of the state of phylogenetic practice for analyzing data at the time, but much has changed since then. The goal of this book is to serve as an updated reference on current methods within the field. The book is organized in three sections, the first of which provides an overview of the analytical and methodological developments of species tree inference. Section two focuses on empirical inference. Section three explores various applications of species trees in evolutionary biology. The combination of theoretical and empirical approaches is meant to provide readers with a level of knowledge of both the advances and limitations of species-tree inference that can help researchers in applying the methods, while also inspiring future advances among those researchers with an interest in methodological development--

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and Linux users, parallel instructions are provided in the margin and in an appendix. The book is designed to be used as a self-guided resource for researchers, a companion book in a course, or as a primary textbook. Practical Computing for Biologists will free you from the most frustrating and time-consuming aspects of data processing so you can focus on the pleasures of scientific inquiry.

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other evolutionary processes?for example, how languages developed or how different strains of a virus (such as HIV or influenza) are related to each other. This self-contained book addresses the underlying mathematical theory behind the reconstruction and analysis of phylogenies. The theory is grounded in classical concepts from discrete mathematics and probability theory as well as techniques from other branches of mathematics (algebra, topology, differential equations). The biological relevance of the results is highlighted throughout. The author supplies proofs of key classical theorems and includes results not covered in existing books, emphasizes relevant mathematical results derived over the past 20 years, and provides numerous exercises, examples, and figures.

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discussion in the media about creationism and 'Intelligent Design', virtually nothing has been said about the evidence in question - the evidence for evolution by natural selection. Yet, as this succinct and important book shows, that evidence is vast, varied, and magnificent, and drawn from many disparate fields of science. The very latest research is uncovering a stream of evidence revealing evolution in action - from the actual observation of a species splitting into two, to new fossil discoveries, to the deciphering of the evidence stored in our genome. Why Evolution is True weaves together the many threads of modern work in genetics, palaeontology, geology, molecular biology, anatomy, and development to demonstrate the 'indelible stamp' of the processes first proposed by Darwin. It is a crisp, lucid, and accessible statement that will leave no one with an open mind in any doubt about the truth of evolution.

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