what is a phylogenetic tree

what is a phylogenetic tree is a fundamental question in the fields of evolutionary biology and bioinformatics. A phylogenetic tree is a diagrammatic representation that illustrates the evolutionary relationships among various biological species or entities based upon similarities and differences in their physical or genetic characteristics. These trees help scientists understand the common ancestry and divergence of species over time, shedding light on the history of life on Earth. In this article, the concept of phylogenetic trees will be explored in depth, including their structure, types, construction methods, and applications in modern science. Additionally, the significance of phylogenetic trees in taxonomy, genetics, and ecology will be discussed to provide a comprehensive understanding of their role. By the end, readers will gain clarity on what a phylogenetic tree is and its crucial importance in biological research and classification.

Definition and Purpose of Phylogenetic Trees

A phylogenetic tree is essentially a branching diagram that represents the inferred evolutionary relationships among various organisms based on genetic, morphological, or molecular data. It is a graphical hypothesis about the historical lineage and diversification of species or genes. The primary purpose of a phylogenetic tree is to illustrate how species or groups have evolved from common ancestors over time, revealing patterns of descent and divergence. This visualization aids researchers in identifying evolutionary pathways, understanding the genetic connections between organisms, and reconstructing the evolutionary history of life.

Evolutionary Relationships and Common Ancestry

Phylogenetic trees depict evolutionary relationships by grouping organisms according to shared traits inherited from a common ancestor. These relationships are hierarchical; species closer together on the tree are more closely related, while those farther apart have a more distant common

ancestor. This concept is fundamental in evolutionary biology, allowing scientists to trace lineage splits and the emergence of new species.

Significance in Biological Classification

Traditional biological classification systems are enhanced by phylogenetic trees, which provide a framework based on evolutionary history rather than solely on morphological similarities. This phylogenetic approach leads to more accurate and meaningful classifications, reflecting true evolutionary relationships and helping to resolve ambiguities in taxonomy.

Structure and Components of a Phylogenetic Tree

Understanding what a phylogenetic tree is requires familiarity with its basic structure and components. A phylogenetic tree consists of nodes, branches, and sometimes labels that together depict the evolutionary pathways from ancestral forms to current species.

Nodes

Nodes represent points of divergence where a common ancestor splits into two or more descendant lineages. Internal nodes correspond to hypothetical ancestors, whereas terminal nodes (also called leaves or tips) represent extant or extinct species.

Branches

Branches connect nodes and represent evolutionary lineages. The length of branches can sometimes indicate the amount of genetic change or evolutionary time, depending on the type of tree and data used.

Root

The root of a phylogenetic tree is the most ancestral node, representing the common origin of all entities depicted. Rooting the tree provides directionality to evolution, illustrating the sequence of divergence events.

Additional Elements

Some phylogenetic trees include scale bars, bootstrap values, or support values at nodes to indicate the confidence or amount of evolutionary change, enhancing the tree’s interpretive value.

Types of Phylogenetic Trees

There are several types of phylogenetic trees, each serving specific analytical purposes and constructed based on different assumptions and data types. The main types include cladograms, phylograms, and ultrametric trees.

Cladograms

Cladograms depict relationships among species based solely on the order of branching without representing the amount of evolutionary change or time. Branch lengths in cladograms are typically arbitrary, focusing on relative relatedness.

Phylograms

Phylograms include branch lengths proportional to the amount of evolutionary change or genetic divergence. These trees provide more detailed information about the extent of differences between species or lineages.

Ultrametric Trees

Ultrametric trees are scaled to represent time, where all terminal nodes are equidistant from the root. These trees are useful for studying evolutionary timelines and estimating divergence dates.

Methods of Constructing Phylogenetic Trees

Constructing a phylogenetic tree involves analyzing data sets such as DNA sequences, protein sequences, or morphological characteristics to infer evolutionary relationships. Various computational and statistical methods are used to create accurate and reliable trees.

Distance-Based Methods

Distance methods calculate evolutionary distances between pairs of taxa and use these distances to build trees. Common methods include Neighbor-Joining and UPGMA (Unweighted Pair Group Method with Arithmetic Mean). These approaches are relatively fast and efficient for large data sets.

Character-Based Methods

Character-based methods analyze discrete characters, such as nucleotide or amino acid positions, to find the tree that best explains the observed data.

Maximum Parsimony and Maximum Likelihood are popular character-based approaches that consider different evolutionary models.

Bayesian Inference

Bayesian methods use probability to estimate the likelihood of trees based on prior knowledge and observed data. This statistical approach provides posterior probabilities for tree topologies, offering a robust framework for phylogenetic inference.

Data Sources

- Genomic sequences (DNA, RNA)
- Protein sequences
- Morphological traits
- Behavioral characteristics

Applications of Phylogenetic Trees in Science

Phylogenetic trees are invaluable tools across multiple scientific disciplines. They enable researchers to explore evolutionary biology, genetics, ecology, and even medical sciences.

Taxonomy and Systematics

In taxonomy, phylogenetic trees assist in classifying organisms based on evolutionary relationships rather than superficial similarities. This leads to more scientifically sound groupings that reflect shared ancestry and divergence.

Evolutionary Studies

Phylogenetic trees allow scientists to investigate the origins of species, evolutionary innovations, and the timing of divergence events. They help elucidate patterns of speciation and adaptive radiation.

Comparative Genomics

By comparing phylogenetic trees derived from genomic data, researchers can identify conserved genes, functional elements, and evolutionary pressures acting on genomes across species.

Ecology and Conservation Biology

Phylogenetic information informs conservation priorities by identifying evolutionarily distinct lineages and assessing biodiversity. It aids in understanding ecosystem dynamics and species interactions over evolutionary time.

Medical and Epidemiological Research

In medicine, phylogenetic trees track the evolution of pathogens, such as viruses and bacteria. They are essential for understanding disease outbreaks, transmission pathways, and the development of drug resistance.

Frequently Asked Questions

What is a phylogenetic tree?

A phylogenetic tree is a diagram that represents the evolutionary relationships among various biological species or entities based on their genetic or physical characteristics.

Why are phylogenetic trees important in biology?

Phylogenetic trees help scientists understand the evolutionary history of species, track the origin of traits, and study how different organisms are related to each other.

What types of data are used to construct a phylogenetic tree?

Phylogenetic trees can be constructed using data from DNA sequences, protein sequences, morphological traits, and sometimes behavioral characteristics.

How do scientists interpret the branches of a phylogenetic tree?

Each branch point, or node, represents a common ancestor, and the length of branches can indicate the amount of genetic change or evolutionary time

between species.

What is the difference between a cladogram and a phylogenetic tree?

A cladogram shows the relationships among species based on shared characteristics without indicating evolutionary time or genetic distance, while a phylogenetic tree often includes this additional information.

Can phylogenetic trees be used to study viral evolution?

Yes, phylogenetic trees are widely used to track the evolution and spread of viruses by comparing genetic sequences, which is crucial for understanding outbreaks and developing treatments.

What software tools are commonly used to create phylogenetic trees?

Common tools for constructing phylogenetic trees include MEGA, PhyML, RAxML, and BEAST, which analyze genetic data and generate evolutionary trees.

Additional Resources

1. *Phylogenetic Trees Made Easy: A How-To Manual*
This book offers a clear and accessible introduction to the construction and interpretation of phylogenetic trees. It guides readers through the fundamental concepts using practical examples and user-friendly software tools. Ideal for students and researchers new to evolutionary biology, the manual demystifies complex topics with straightforward explanations.

2. *Inferring Phylogenies*
Written by a leading expert, this comprehensive text delves into the theory and methods behind phylogenetic tree inference. It covers various algorithms, models of evolution, and statistical approaches used in constructing trees from molecular and morphological data. The book balances mathematical rigor with biological relevance, making it suitable for advanced students and professionals.

3. *Phylogenetics: Theory and Practice of Phylogenetic Systematics*
This book provides an in-depth overview of phylogenetic systematics and its theoretical foundations. It discusses the principles of cladistics, tree-building techniques, and the interpretation of evolutionary relationships. The text is enriched with case studies that illustrate how phylogenetic trees inform taxonomy and evolutionary biology.

4. *Molecular Evolution and Phylogenetics*

Focusing on molecular data, this book explores how DNA, RNA, and protein sequences are used to reconstruct phylogenetic trees. It explains molecular evolutionary processes and the statistical methods applied to analyze sequence data. The work is a valuable resource for those interested in the intersection of molecular biology and evolutionary theory.

5. *Evolutionary Analysis*
This textbook integrates phylogenetics within a broader context of evolutionary biology. It introduces the construction and interpretation of phylogenetic trees alongside natural selection, population genetics, and comparative methods. With detailed examples and illustrations, it helps readers understand how phylogenies contribute to evolutionary research.

6. *The Phylogenetic Handbook: A Practical Approach to Phylogenetic Analysis and Hypothesis Testing*
A practical guide designed for researchers, this handbook covers various methods of phylogenetic analysis, including maximum likelihood and Bayesian inference. It offers step-by-step instructions and software recommendations for hypothesis testing using phylogenetic trees. The book is particularly useful for applied evolutionary studies.

7. *Understanding Molecular Phylogenetics*
This book simplifies the complex subject of molecular phylogenetics, emphasizing concepts behind tree construction and evolutionary inference. It explains sequence alignment, model selection, and tree validation in an approachable manner. Suitable for beginners, the text aims to build foundational knowledge for further study.

8. *The Tree of Life: A Phylogenetic Classification*
Presenting a comprehensive view of the diversity of life, this book arranges organisms according to their evolutionary relationships depicted in a phylogenetic tree. It discusses the history of life on Earth and the classification systems derived from phylogenetic insights. The book combines scientific detail with engaging visuals to illustrate life's interconnectedness.

9. *Phylogenetic Trees and the Evolution of Species*
This book focuses on how phylogenetic trees reveal the patterns and processes of species evolution. It addresses speciation, adaptive radiation, and the role of phylogenies in conservation biology. Through rich examples, it demonstrates the practical applications of phylogenetic trees in understanding biodiversity.

What Is A Phylogenetic Tree

what is a phylogenetic tree: Phylogenetic Trees Made Easy Barry G. Hall, 2008 Barry G. Hall helps beginners get started in creating phylogenetic trees from protein or nucleic acid sequence data.

what is a phylogenetic tree: Phylogeny Mike Steel, 2016-09-29 Phylogenetics is a topical and growing area of research. Phylogenies (phylogenetic trees and networks) allow biologists to study and graph evolutionary relationships between different species. These are also used to investigate 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.?

what is a phylogenetic tree: Lizards in an Evolutionary Tree Jonathan B. Losos, 2011-02-09 In a book both beautifully illustrated and deeply informative, Jonathan Losos, a leader in evolutionary ecology, celebrates and analyzes the diversity of the natural world that the fascinating anoline lizards epitomize. Readers who are drawn to nature by its beauty or its intellectual challenges—or both—will find his book rewarding.—Douglas J. Futuyma, State University of New York, Stony Brook This book is destined to become a classic. It is scholarly, informative, stimulating, and highly readable, and will inspire a generation of students.—Peter R. Grant, author of How and Why Species Multiply: The Radiation of Darwin's Finches Anoline lizards experienced a spectacular adaptive radiation in the dynamic landscape of the Caribbean islands. The radiation has extended over a long period of time and has featured separate radiations on the larger islands. Losos, the leading active student of these lizards, presents an integrated and synthetic overview, summarizing the enormous and multidimensional research literature. This engaging book makes a wonderful example of an adaptive radiation accessible to all, and the lavish illustrations, especially the photographs, make the anoles come alive in one's mind.—David Wake, University of California, Berkeley This magnificent book is a celebration and synthesis of one of the most eventful adaptive radiations known. With disarming prose and personal narrative Jonathan Losos shows how an obsession, beginning at age ten, became a methodology and a research plan that, together with studies by colleagues and predecessors, culminated in many of the principles we now regard as true about the origins and maintenance of biodiversity. This work combines rigorous analysis and glorious natural history in a unique volume that stands with books by the Grants on Darwin's finches among the most informed and engaging accounts ever written on the evolution of a group of organisms in nature.—Dolph Schluter, author of The Ecology of Adaptive Radiation

what is a phylogenetic tree: The Phylogenetic Handbook Marco Salemi, Anne-Mieke Vandamme, 2003-08-27 Sample Text

what is a phylogenetic tree: *Mathematics of Evolution and Phylogeny* Olivier Gascuel, 2005-02-24 This book considers evolution at different scales: sequences, genes, gene families, organelles, genomes and species. The focus is on the mathematical and computational tools and concepts, which form an essential basis of evolutionary studies, indicate their limitations, and give them orientation. Recent years have witnessed rapid progress in the mathematics of evolution and phylogeny, with models and methods becoming more realistic, powerful, and complex. Aimed at graduates and researchers in phylogenetics, mathematicians, computer scientists and biologists, and including chapters by leading scientists: A. Bergeron, D. Bertrand, D. Bryant, R. Desper, O. Elemento, N. El-Mabrouk, N. Galtier, O. Gascuel, M. Hendy, S. Holmes, K. Huber, A. Meade, J. Mixtacki, B. Moret, E. Mossel, V. Moulton, M. Pagel, M.-A. Poursat, D. Sankoff, M. Steel, J. Stoye, J. Tang, L.-S. Wang, T. Warnow, Z. Yang, this book of contributed chapters explains the basis and

covers the recent results in this highly topical area.

what is a phylogenetic tree: Phylogenetics Charles Semple, Mike Steel, Both in the Department of Mathematics and Statistics Mike Steel, 2003 'Phylogenetics' is the reconstruction and analysis of phylogenetic (evolutionary) trees and networks based on inherited characteristics. It is a flourishing area of intereaction between mathematics, statistics, computer science and biology.The main role of phylogenetic techniques lies in evolutionary biology, where it is used to infer historical relationships between species. However, the methods are also relevant to a diverse range of fields including epidemiology, ecology, medicine, as well as linguistics and cognitive psychologyThis graduate-level book, based on the authors lectures at The University of Canterbury, New Zealand, focuses on the mathematical aspects of phylogenetics. It brings together the central results of the field (providing proofs of the main theorem), outlines their biological significance,and indicateshow algorithms may be derived. The presentation is self-contained and relies on discrete mathematics with some probability theory. A set of exercises and at least one specialist topic ends each chapter.This book is intended for biologists interested in the mathematical theory behind phylogenetic methods, and for mathematicians, statisticians, and computer scientists eager to learn about this emerging area of discrete mathematics.'Phylogenetics' in the 24th volume in the Oxford Lecture Series in Mathematics and its Applications. This series contains short books suitable for graduate students and researchers who want a well-written account of mathematics that is fundamental to current to research. The series emphasises futuredirections of research and focuses on genuine applications of mathematics to finance, engineering and the physical and biological sciences.

what is a phylogenetic tree: Botany For B.Sc. Students Semester V: Paper 2 | Molecular Biology & Bioinformatics | Experiments in Physiology, Biochemistry & Molecular Biology | NEP 2020 Uttar Pradesh Rashmi Upadhyay, This textbook has been designed to meet the needs of B.Sc. Fifth Semester students of Botany as per Common Minimum Syllabus prescribed for all Uttar Pradesh State Universities and Colleges under the recommended National Education Policy 2020. It comprehensively covers Paper 2, namely, Molecular Biology & Bioinformatics. The theory part of this book aptly discusses the understanding of nucleic acids, organization of DNA in prokaryotes and eukaryotes, DNA replication mechanism, genetic code and transcription process. Students would also learn about processing and modification of RNA and translation process, function and regulation of gene expression. This textbook further discusses the working knowledge of bioinformatics. Relevant experiments corresponding to the theoretical topics and examples have been presented systematically to help students achieve sound conceptual understanding and learn the experimental procedures.

what is a phylogenetic tree: Mammalian Evolutionary Morphology Eric J. Sargis, Marian Dagosto, 2008-05-21 This book celebrates the contributions of Dr. Frederick S. Szalay to the field of Mammalian Evolutionary Morphology. Professor Szalay is a strong advocate for biologically and evolutionarily meaningful character analysis. He has published about 200 articles, six monographs, and six books on this subject. This book features subjects such as the evolution and adaptation of mammals and provides up-to-date articles on the evolutionary morphology of a wide range of mammalian groups.

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what is a phylogenetic tree: Genomic Diversity in People of India Anthropological Survey Of India, 2021-07-02 This book is the output of Anthropological Survey of India's National Project DNA Polymorphism of Contemporary Indian Population conducted during 2000 to 2018. The book compiles the independent and collaborative work of 49 scientific personnel. Genomics facilitate the

study of genetic constitution and diversity at individual and population levels. Genomic diversity explains susceptibility, predisposition and prolongation of diseases; personalized medicine and longevity; prehistoric demographic events, such as population bottleneck, expansion, admixture and natural selection. This book highlights the heterogeneous, genetically diverse population of India. It shows how the central geographic location of India, played a crucial role in historic and pre-historic human migrations, and in peopling different continents of the world. The book describes the massive task undertaken by AnSI to unearth genomic diversity of India populations, with the use of Uni-parental DNA markers mtDNA (mitochondrial DNA) and Y –chromosome in 75 communities. The book talks about the 61 maternal and 35 paternal lineages identified through these studies. It brings forth interesting, hitherto unknown findings such as shared mutations between certain communities. This volume is a milestone in scientific research to understand biological diversity of Indian people at genomic level. It addresses the basic priority to identify different genes underlying various inborn genetic defects and diseases specific to Indian populations. This would be highly interesting to population geneticists, historians, as well as anthropologists.

what is a phylogenetic tree: *Intelligent Systems and Applications* Kohei Arai, 2021-08-02 This book presents Proceedings of the 2021 Intelligent Systems Conference which is a remarkable collection of chapters covering a wider range of topics in areas of intelligent systems and artificial intelligence and their applications to the real world. The conference attracted a total of 496 submissions from many academic pioneering researchers, scientists, industrial engineers, and students from all around the world. These submissions underwent a double-blind peer-review process. Of the total submissions, 180 submissions have been selected to be included in these proceedings. As we witness exponential growth of computational intelligence in several directions and use of intelligent systems in everyday applications, this book is an ideal resource for reporting latest innovations and future of AI. The chapters include theory and application on all aspects of artificial intelligence, from classical to intelligent scope. We hope that readers find the book interesting and valuable; it provides the state-of-the-art intelligent methods and techniques for solving real-world problems along with a vision of the future research.

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2021 in Hechi, China. The topics focus but are not limited to Internet of Things and Smart Systems, Artificial Intelligence and Applications, Communication System Detection, Analysis and Application, and Medical Engineering and Information Systems. Each part can be used as an excellent reference by industry practitioners, university faculties, research fellows and undergraduates as well as graduate students who need to build a knowledge base of the most current advances and state-of-practice in the topics covered by this conference proceedings. This will enable them to produce, maintain, and manage systems with high levels of trustworthiness and complexity.

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what is a phylogenetic tree: *Atlas of Protein Sequence and Structure* , 1969

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what is a phylogenetic tree: ,

what is a phylogenetic tree: Bioinformatics for Beginners Supratim Choudhuri, 2014-05-09 Bioinformatics for Beginners: Genes, Genomes, Molecular Evolution, Databases and Analytical Tools provides a coherent and friendly treatment of bioinformatics for any student or scientist within biology who has not routinely performed bioinformatic analysis. The book discusses the relevant principles needed to understand the theoretical underpinnings of bioinformatic analysis and demonstrates, with examples, targeted analysis using freely available web-based software and publicly available databases. Eschewing non-essential information, the work focuses on principles and hands-on analysis, also pointing to further study options. - Avoids non-essential coverage, yet fully describes the field for beginners - Explains the molecular basis of evolution to place bioinformatic analysis in biological context - Provides useful links to the vast resource of publicly available bioinformatic databases and analysis tools - Contains over 100 figures that aid in concept discovery and illustration

what is a phylogenetic tree: *Reconstructing Evolution* Olivier Gascuel, Mike Steel, 2007-06-28 Evolution is a complex process, acting at multiple scales, from DNA sequences and proteins to populations of species. Understanding and reconstructing evolution is of major importance in numerous subfields of biology. For example, phylogenetics and sequence evolution is central to comparative genomics, attempts to decipher genomes, and molecular epidemiology. Phylogenetics is also the focal point of large-scale international biodiversity assessment initiatives such as the 'Tree of Life' project, which aims to build the evolutionary tree for all extant species. Since the pioneering work in phylogenetics in the 1960s, models have become increasingly sophisticated to account for the inherent complexity of evolution. They rely heavily on mathematics and aim at modelling and analyzing biological phenomena such as horizontal gene transfer, heterogeneity of mutation, and speciation and extinction processes. This book presents these recent models, their biological relevance, their mathematical basis, their properties, and the algorithms to infer them from data. A number of subfields from mathematics and computer science are involved: combinatorics, graph

theory, stringology, probabilistic and Markov models, information theory, statistical inference, Monte Carlo methods, continuous and discrete algorithmics. This book arises from the Mathematics of Evolution & Phylogenetics meeting at the Mathematical Institute Henri Poincaré, Paris, in June 2005 and is based on the outstanding state-of-the-art reports presented by the conference speakers. Ten chapters - based around five themes - provide a detailed overview of key topics, from the underlying concepts to the latest results, some of which are at the forefront of current research.

what is a phylogenetic tree: Elements of dynamic and 2-SAT programming: paths, trees, and cuts Bentert, Matthias, 2021-11-18 In dieser Arbeit entwickeln wir schnellere exakte Algorithmen (schneller bezüglich der Worst-Case-Laufzeit) für Spezialfälle von Graphproblemen. Diese Algorithmen beruhen größtenteils auf dynamischem Programmieren und auf 2-SAT-Programmierung. Dynamisches Programmieren beschreibt den Vorgang, ein Problem rekursiv in Unterprobleme zu zerteilen, sodass diese Unterprobleme gemeinsame Unterunterprobleme haben. Wenn diese Unterprobleme optimal gelöst wurden, dann kombiniert das dynamische Programm diese Lösungen zu einer optimalen Lösung des Ursprungsproblems. 2-SAT-Programmierung bezeichnet den Prozess, ein Problem durch eine Menge von 2-SAT-Formeln (aussagenlogische Formeln in konjunktiver Normalform, wobei jede Klausel aus maximal zwei Literalen besteht) auszudrücken. Dabei müssen erfüllende Wahrheitswertbelegungen für eine Teilmenge der 2-SAT-Formeln zu einer Lösung des Ursprungsproblems korrespondieren. Wenn eine 2-SAT-Formel erfüllbar ist, dann kann eine erfüllende Wahrheitswertbelegung in Linearzeit in der Länge der Formel berechnet werden. Wenn entsprechende 2-SAT-Formeln also in polynomieller Zeit in der Eingabegröße des Ursprungsproblems erstellt werden können, dann kann das Ursprungsproblem in polynomieller Zeit gelöst werden. Im folgenden beschreiben wir die Hauptresultate der Arbeit. Bei dem Diameter-Problem wird die größte Distanz zwischen zwei beliebigen Knoten in einem gegebenen ungerichteten Graphen gesucht. Das Ergebnis (der Durchmesser des Eingabegraphen) gehört zu den wichtigsten Parametern der Graphanalyse. In dieser Arbeit erzielen wir sowohl positive als auch negative Ergebnisse für Diameter. Wir konzentrieren uns dabei auf parametrisierte Algorithmen für Parameterkombinationen, die in vielen praktischen Anwendungen klein sind, und auf Parameter, die eine Distanz zur Trivialität messen. Bei dem Problem Length-Bounded Cut geht es darum, ob es eine Kantenmenge begrenzter Größe in einem Eingabegraphen gibt, sodass das Entfernen dieser Kanten die Distanz zwischen zwei gegebenen Knoten auf ein gegebenes Minimum erhöht. Wir bestätigen in dieser Arbeit eine Vermutung aus der wissenschaftlichen Literatur, dass Length-Bounded Cut in polynomieller Zeit in der Eingabegröße auf Einheitsintervallgraphen (Intervallgraphen, in denen jedes Intervall die gleiche Länge hat) gelöst werden kann. Der Algorithmus basiert auf dynamischem Programmieren. k-Disjoint Shortest Paths beschreibt das Problem, knotendisjunkte Pfade zwischen k gegebenen Knotenpaaren zu suchen, sodass jeder der k Pfade ein kürzester Pfad zwischen den jeweiligen Endknoten ist. Wir beschreiben ein dynamisches Programm mit einer Laufzeit n^O((k+1)!) für dieses Problem, wobei n die Anzahl der Knoten im Eingabegraphen ist. Dies zeigt, dass k-Disjoint Shortest Paths in polynomieller Zeit für jedes konstante k gelöst werden kann, was für über 20 Jahre ein ungelöstes Problem der algorithmischen Graphentheorie war. Das Problem Tree Containment fragt, ob ein gegebener phylogenetischer Baum T in einem gegebenen phylogenetischen Netzwerk N enthalten ist. Ein phylogenetisches Netzwerk (bzw. ein phylogenetischer Baum) ist ein gerichteter azyklischer Graph (bzw. ein gerichteter Baum) mit genau einer Quelle, in dem jeder Knoten höchstens eine ausgehende oder höchstens eine eingehende Kante hat und jedes Blatt eine Beschriftung trägt. Das Problem stammt aus der Bioinformatik aus dem Bereich der Suche nach dem Baums des Lebens (der Geschichte der Artenbildung). Wir führen eine neue Variante des Problems ein, die wir Soft Tree Containment nennen und die bestimmte Unsicherheitsfaktoren berücksichtigt. Wir zeigen mit Hilfe von 2-SAT-Programmierung, dass Soft Tree Containment in polynomieller Zeit gelöst werden kann, wenn N ein phylogenetischer Baum ist, in dem jeweils maximal zwei Blätter die gleiche Beschriftung tragen. Wir ergänzen dieses Ergebnis mit dem Beweis, dass Soft Tree Containment NP-schwer ist, selbst wenn N auf phylogenetische Bäume beschränkt ist, in denen

jeweils maximal drei Blätter die gleiche Beschriftung tragen. Abschließend betrachten wir das Problem Reachable Object. Hierbei wird nach einer Sequenz von rationalen Tauschoperationen zwischen Agentinnen gesucht, sodass eine bestimmte Agentin ein bestimmtes Objekt erhält. Eine Tauschoperation ist rational, wenn beide an dem Tausch beteiligten Agentinnen ihr neues Objekt gegenüber dem jeweiligen alten Objekt bevorzugen. Reachable Object ist eine Verallgemeinerung des bekannten und viel untersuchten Problems Housing Market. Hierbei sind die Agentinnen in einem Graphen angeordnet und nur benachbarte Agentinnen können Objekte miteinander tauschen. Wir zeigen, dass Reachable Object NP-schwer ist, selbst wenn jede Agentin maximal drei Objekte gegenüber ihrem Startobjekt bevorzugt und dass Reachable Object polynomzeitlösbar ist, wenn jede Agentin maximal zwei Objekte gegenüber ihrem Startobjekt bevorzugt. Wir geben außerdem einen Polynomzeitalgorithmus für den Spezialfall an, in dem der Graph der Agentinnen ein Kreis ist. Dieser Polynomzeitalgorithmus basiert auf 2-SAT-Programmierung. This thesis presents faster (in terms of worst-case running times) exact algorithms for special cases of graph problems through dynamic programming and 2-SAT programming. Dynamic programming describes the procedure of breaking down a problem recursively into overlapping subproblems, that is, subproblems with common subsubproblems. Given optimal solutions to these subproblems, the dynamic program then combines them into an optimal solution for the original problem. 2-SAT programming refers to the procedure of reducing a problem to a set of 2-SAT formulas, that is, boolean formulas in conjunctive normal form in which each clause contains at most two literals. Computing whether such a formula is satisfiable (and computing a satisfying truth assignment, if one exists) takes linear time in the formula length. Hence, when satisfying truth assignments to some 2-SAT formulas correspond to a solution of the original problem and all formulas can be computed efficiently, that is, in polynomial time in the input size of the original problem, then the original problem can be solved in polynomial time. We next describe our main results. Diameter asks for the maximal distance between any two vertices in a given undirected graph. It is arguably among the most fundamental graph parameters. We provide both positive and negative parameterized results for distance-from-triviality-type parameters and parameter combinations that were observed to be small in real-world applications. In Length-Bounded Cut, we search for a bounded-size set of edges that intersects all paths between two given vertices of at most some given length. We confirm a conjecture from the literature by providing a polynomial-time algorithm for proper interval graphs which is based on dynamic programming. k-Disjoint Shortest Paths is the problem of finding (vertex-)disjoint paths between given vertex terminals such that each of these paths is a shortest path between the respective terminals. Its complexity for constant $k > 2$ has been an open problem for over 20 years. Using dynamic programming, we show that k-Disjoint Shortest Paths can be solved in polynomial time for each constant k. The problem Tree Containment asks whether a phylogenetic tree T is contained in a phylogenetic network N. A phylogenetic network (or tree) is a leaf-labeled single-source directed acyclic graph (or tree) in which each vertex has in-degree at most one or out-degree at most one. The problem stems from computational biology in the context of the tree of life (the history of speciation). We introduce a particular variant that resembles certain types of uncertainty in the input. We show that if each leaf label occurs at most twice in a phylogenetic tree N, then the problem can be solved in polynomial time and if labels can occur up to three times, then the problem becomes NP-hard. Lastly, Reachable Object is the problem of deciding whether there is a sequence of rational trades of objects among agents such that a given agent can obtain a certain object. A rational trade is a swap of objects between two agents where both agents profit from the swap, that is, they receive objects they prefer over the objects they trade away. This problem can be seen as a natural generalization of the well-known and well-studied Housing Market problem where the agents are arranged in a graph and only neighboring agents can trade objects. We prove a dichotomy result that states that the problem is polynomial-time solvable if each agent prefers at most two objects over its initially held object and it is NP-hard if each agent prefers at most three objects over its initially held object. We also provide a polynomial-time 2-SAT program for the case where the graph of agents is a cycle.

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