

Theory and Unresolved Issues in Discrete Time-Tree Combinatorics

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Abstract

A time-tree is a rooted phylogenetic tree with all internal and leaf nodes equipped with absolute divergence and sampling dates, respectively. Although these time-trees have emerged as a major focus of phylogenetics research, little is known about their parameter space. From a graph-theoretic and algorithmic point of view, we present and investigate a hierarchy of discrete time-tree space approximations in this article. The NNI graph, one of the most fundamental and widely used phylogenetic graphs, is our hierarchy's lowest level and roughest approximation. The sampling dates and relative timing of evolutionary divergence are discretized by more refined approximations.

Keywords: Systems biology • Algebraic model reduction • Combinatorics

Introduction

Combinatorics is a branch of mathematics that deals with counting, arrangements and selection of elements from finite sets. It has applications in computer science, physics, statistics and many other fields. Combinatorics is a fascinating subject that involves the study of discrete structures such as graphs, networks and permutations. In this essay, we will explore the basic concepts of combinatorics, including counting principles, permutations, combinations and generating functions.

Literature Review

Counting principles are fundamental to combinatorics and they are used to solve many problems in the field. The three basic counting principles are the product rule, the sum rule and the inclusion-exclusion principle. The product rule states that if there are m ways to do one thing and n ways to do another, then there are mn ways to do both things together. For example, if we have 3 shirts and 4 pants, then there are $3 \times 4 = 12$ outfits we can make. The sum rule states that if there are m ways to do one thing and n ways to do another and there is no overlap between the two sets of ways, then there are $m + n$ ways to do one or the other. For example, if we have 5 red balls and 6 blue balls, then there are $5 + 6 = 11$ balls in total. The inclusion-exclusion principle is used when we have sets that overlap. If we have two sets A and B , then the number of elements in either A or B is the sum of the number of elements in A and the number of elements in B minus the number of elements in both A and B . Mathematically, this can be written as $|A \cup B| = |A| + |B| - |A \cap B|$. For example, if we have a class of 30 students and 15 students play basketball and 12 students play soccer and 6 students play both sports, then the number of students who play at least one sport is $15 + 12 - 6 = 21$ [1].

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Received: 28 September, 2022, Manuscript No. glta-23-90832; **Editor Assigned:** 30 September, 2022, PreQC No. P-90832; **Reviewed:** 14 October, 2022, QC No. Q-90832; **Revised:** 20 October, 2022, Manuscript No. R-90832; **Published:** 28 October, 2022, DOI: 10.37421/1736-4337.2022.16.354

Discussion

A permutation is an arrangement of objects in a specific order. In combinatorics, we are often interested in finding the number of permutations of a set of objects. The number of permutations of n objects is denoted by $n!$. For example, if we have 4 books, the number of ways to arrange them on a bookshelf is $4! = 24$. When we have a set of n objects and we want to choose r of them and arrange them in a specific order, we use the permutation formula:

$$nPr = \frac{n!}{(n-r)!}$$

For example, if we have 7 books and we want to choose 3 of them and arrange them on a bookshelf, the number of ways to do this is:

$$7P3 = \frac{7!}{(7-3)!} = \frac{7!}{4!} = 7 \times 6 \times 5 = 210$$

The problem of finding the shortest paths and the size of neighborhoods are among the fundamental graph-theoretic concerns we investigate for these graphs. By applying Sleator, Tarjan and Thurston's idea of graph grammars to our graphs, we answer many of these questions. We show that 1-neighborhood sizes remain linear, allowing for efficient local exploration and construction of these graphs despite the significant increase in the number of possible trees caused by time values. These graphs' r -neighborhood sizes are also given upper bounds by us, including a lower bound than was previously known for NNI. Theoretical research into the graph-theoretic and algorithmic properties of time-tree graphs is now possible thanks to our findings, which provide a number of new avenues for exploration. We provide a list of prominent unsolved phylogenetic applications-related open problems and discuss the most important directions. In particular, we speculate that the split theorem is applicable to time-tree graph shortest paths, a property that is not shared by the general NNI case [2,3].

A combination is a selection of objects from a set without regard to the order in which they are selected. In combinatorics, we are often interested in finding the number of combinations of a set of objects. The number of combinations of n objects taken r at a time is denoted by nCr . The formula for nCr is [4]

$$nCr = \frac{n!}{(n-r)! r!}$$

For example, if we have 7 books and we want to choose 3 of them to take on a trip, the number of ways to do this is:

$$7C3 = \frac{7!}{(7-3)! 3!} = \frac{7!}{(4! 3!)} = 35$$

Generating functions are a powerful tool in combinatorics

Canonical α -structures, also known as partial matchings composed of irreducible motifs of the genus without isolated arcs or 1-arcs, are the focus

of our research in this paper. Irreducible shadows are the name given to these designs. First, we establish a functional connection between the irreducible shadows' generating function and that of γ -matchings. We find a polynomial $P(u, X)$ whose unique solution equals the generating function of γ -matchings by using this relation. The Harer-Zagier recurrence is then used to obtain a recurrence of the generating function of irreducible shadows. After that, a Puiseux-series is used to expand the unique generating function of γ -matchings at its dominant singularity. By means of transfer theorems, this calls for straightforward asymptotic formulas for the number of γ -matches [5].

Conclusion

The solution to Problem 1 for a fixed tree is a linear algebra problem. However, Rzhetsky and Nei demonstrated that elegant and effective combinatorial formulas could be used to calculate the OLS edge lengths. Vach made the observation that OLS edge lengths adhere to the desirable independence of irrelevant pairs (IIP) property, which was the foundation for their conclusion. A linear edge length estimator for e is a linear function from dissimilarity maps to real numbers, $\hat{e}_{ij} = \sum_{k \in T} D_{ij}^k$, where T is a phylogenetic X -tree and e is an edge in T . When the path from i to j in T (referred to as i, j) does not contain either of e 's endpoints, we say that such an estimator satisfies the IIP property if $\hat{e}_{ij} = 0$.

Acknowledgement

None.

Conflict of Interest

None.

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How to cite this article: Yang, Zhen. "Theory and Unresolved Issues in Discrete Time-Tree Combinatorics." *J Nucl Med Radiat Ther* 16 (2022): 354.