NAPX: A Polynomial Time Approximation Scheme for the Noah’s Ark Problem

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Abstract. The Noah’s Ark Problem (NAP) is an NP-Hard optimization problem with relevance to ecological conservation management. It asks to maximize the phylogenetic diversity (PD) of a set of taxa given a fixed budget, where each taxon is associated with a cost of conservation and a probability of extinction. NAP has received renewed interest with the rise in availability of genetic sequence data, allowing PD to be used as a practical measure of biodiversity. However, only simplified instances of the problem, where one or more parameters are fixed as constants, have as of yet been addressed in the literature. We present NAPX, the first algorithm for the general version of NAP that returns a $1 - \epsilon$ approximation of the optimal solution. It runs in $O\left(\frac{nB^2h^2}{\log^2(1-\epsilon)}(\log n + \log \frac{1}{\epsilon})^2\right)$ time where $n$ is the number of species, and $B$ is the total budget and $h$ is the height of the input tree. We also provide improved bounds for its expected running time.

Key words: Noah’s Ark Problem, phylogenetic diversity, approximation algorithm

1 Introduction

1.1 Motivation

Measures of biodiversity are commonly used as indicators of environmental health. Biodiversity is presently being lost at an alarming rate, due largely to human activity. It is speculated that this loss can lead to disastrous consequences if left unchecked \cite{9}. Consequently, the discipline of conservation biology has arisen and a considerable amount of resources are being allocated to research and implement conservation projects around the world.

A conservation strategy will necessarily depend on the measure of biodiversity used. Traditionally, indices based on species richness and abundance have been used to quantify the biodiversity of an ecosystem \cite{8}. These indices are based on counting and do not account for genetic variance. Phylogenetic diversity (PD) \cite{3} addresses this issue by taking into account evolutionary relationships derived from DNA or protein samples. The use of PD in biological conservation
has become increasingly widespread as more phylogenetic information becomes available [7]. It is also used to determine diverse sequence samples in comparative genomics [10].

The Noah’s Ark Problem (NAP) [13] is an abstraction of the fundamental problem of many conservation projects: how best to allocate a limited amount of resources to maximally conserve phylogenetic diversity. This is in turn a generalization of the Knapsack Problem [4] and is therefore NP-Hard. Several algorithms have been proposed to solve special cases of the problem but, as yet, no non-heuristic solutions have been proposed to solve general instances of NAP. Given that NAP itself is an abstraction of realistic scenarios, it is important to have a general solution in order to be able to extend this framework to useful applications. For this reason, we present an algorithm that can be used to compute an approximate solution for NAP in polynomial time, so long as the approximation factor is held constant, and total budget is polynomial in the input size.

1.2 Definitions

Throughout this paper, we use the following definition of a phylogenetic tree $T$, with notation consistent with that of [6]. $T$ has a root of degree 2, interior vertices of degree 3, and $n$ leaves, each associated with a species from set $X$.

If an edge $e$ of $T$ is incident to a leaf, it is called a pendant edge. Otherwise $e$ has exactly two adjacent edges, $l$ and $r$, below it (not on the path from $e$ to the root) and these are referred to as $e$’s children. $\lambda$ is a function that assigns a non-negative branch length to each edge in $T$. The phylogenetic diversity of $T$, $PD(T)$ is defined as

$$\sum_{e} \lambda(e), \quad (1)$$

where the summation is over each edge $e$ of the tree. Intuitively, this measure corresponds to the amount of evolutionary history represented by $T$.

The Noah’s Ark Problem has the objective of maximizing the expected $PD$, $\mathbb{E}(PD)$, under the following constraints. Each taxon $i \in X$ is associated with an initial survival probability $a_i$, which can be increased to $b_i$ at some integer cost $c_i$; and the total expenditure cannot exceed the budget $B$. Since $B$ is a factor in the running time, we assume that the budget and each cost have been divided by the greatest common divisor of all the costs. In the original formulation of NAP, each species was also associated with a utility value. However, in [6] it was shown that these values are redundant as they can be incorporated into the branch lengths without altering the problem. To avoid accounting for degenerately small probability values, we make the assumption that the conserved survival probabilities are not exponentially small in $n$. In other words, there exists a constant $k$ such that $b_i \geq n^{-k}$ for each $i \in X$. We feel this assumption is reasonable as it is unrealistic that money would be allocated to obtain such a negligible probability of survival.

If a species survives, the information represented by its path to the root is conserved. Consequently, the probability that an edge survives is equivalent to
the probability that at least one leaf below it in $T$ survives. Let $C_e$ be the set of leaves below $e$ in the tree and $S$ be the set of species selected for protection. $\mathbb{E}(PD|S)$, can be derived from (1) as follows:

$$\mathbb{E}(PD|S) = \sum_e \lambda(e) \left( 1 - \prod_{i \in C_e \cap S} (1 - b_i) \prod_{j \in C_e - S} (1 - a_j) \right),$$

(2)

where the summation is over all edges. NAP asks to maximize $\mathbb{E}(PD|S)$ subject to

$$\sum_{s \in S} c_s \leq B.$$

Our algorithm is based on decomposing $T$ into clades which are associated with the edges of the tree. A clade corresponding to edge $e$, denoted $K_e$, is the minimal subtree of $T$ containing $e$ and $C_e$, the set of leaves below it. The $\mathbb{E}(PD)$ of $K_e$ can be computed as in (2) but summing only over edges in the clade. The entire tree can be considered a clade by attaching an edge of length 0 to its root. If $e$ has two descendant edges $l$ and $r$, then we say $K_e$ has two child clades $K_l$ and $K_r$.

1.3 Related Work

Let $a_i \xrightarrow{c_i} b_i$ NAP refer to the problem as described above, where the survival probabilities and cost of each taxon are input variables. Fixing one or more of these variables as constants produces a hierarchy of increasingly simpler sub-problems [11]. The simplest, $0 \xrightarrow{1} 1$ NAP, is equivalent to finding the set of $B$ leaves whose induced subtree (including the root) has maximum PD and can be solved by a greedy algorithm [12] [10]. $0 \xrightarrow{c_i} 1$ NAP on ultrametric (all leaves equidistant from the root) trees and $(1 - x_i) \xrightarrow{1} (1 - \kappa x_i)$ for general trees where $x_i$ is a variable probability and $\kappa$ is a constant factor such that $0 \leq \kappa \leq 1$ can likewise be solved in polynomial time by greedy algorithms [6]. Given that $0 \xrightarrow{c_i} 1$ NAP is itself a generalization of the Knapsack problem which is NP-Hard, it is extremely unlikely that an exact, polynomial-time solution for this kind of NAP or any generalizations will ever be found. Pardi and Goldman [11] did find a pseudopolynomial-time dynamic programming algorithm for the $0 \xrightarrow{c_i} 1$ NAP on general (non-ultrametric) trees that makes the realistic assumption that $B$ is polynomial in $n$. They also show that any instance of $a_i \xrightarrow{c_i} 1$ NAP can be transformed to an instance of $0 \xrightarrow{c_i} 1$ NAP, allowing their algorithm to solve such instances as well.

This algorithm relies upon the observation that the solution to $0 \xrightarrow{c_i} 1$ NAP for any clade can be obtained from the solutions to its two child clades [11]. Which solutions to use depends on how the budget is allocated to the two sub-problems. If the budget at $K_e$ is $b$, then there are $b + 1$ ways to split it across $K_l$ and $K_r$. By solving these $b + 1$ pairs of subproblems, the optimal solution can be found in the pair with maximum total $\mathbb{E}(PD)$ (plus the expected contribution
of \( e \)). Recursively proceeding in this fashion from the root down would not yield an efficient algorithm as the number of possible budget divisions increases exponentially with each level of the tree. Instead, the clades are processed bottom-up from the leaves. All \( b + 1 \) scores are computed and stored in a dynamic programming table for each clade. Each score can be determined by taking the maximum of \( b + 1 \) possible scores of its child clades, which are already computed or computed directly from (2) if the clade contains a single leaf. Each table entry can therefore be computed in \( O(B) \) time. There are \( O(B) \) entries per clade and \( O(n) \) clades in the tree giving a total running time of \( O(nB^2) \).

This procedure does not work for \( a_i \xrightarrow{c_i} b_i \) NAP because this version of the problem does not display the same optimal substructure \([11]\). In \( 0 \xrightarrow{c_i} 1 \), the dynamic programming algorithm implicitly maximizes the survival probability of the clade in addition to its \( E(PD) \) value. The total score of the tree is a function of both of these values which is why the algorithm works for this case. In \( a_i \xrightarrow{c_i} b_i \) NAP, a budget assignment that maximizes survival probability of the clade does not guarantee that it will have maximal \( E(PD) \) and vice versa. The correct allocation cannot be made without knowledge of the entire tree; hence, the optimal substructure exploited by \([11]\) for \( 0 \xrightarrow{c_i} 1 \) NAP is not present. As an example, consider the instance of NAP in Figure 1 with \( B = 3 \). The optimal solution is to conserve \( w \) and \( y \) for \( E(PD) = 225 \). However, locally computing the best allocation of budget 1 for the clade containing \( y \) and \( z \) will select \( z \) for conservation, and any chance of obtaining the optimal solution will be lost. In this case, it is more important to maximize the survival probability of the clade rather than \( E(PD) \), but there is no way for an algorithm to be aware of this without globally solving the entire tree.

![Fig. 1. An example why the dynamic programming algorithm of [11] does not work for general instances of NAP. The optimal allocation for the clade containing \( y \) and \( z \) is not part of a globally optimal solution.](image-url)
2 NAPX Algorithm

2.1 Description

In this section we present NAPX, an $O\left(\frac{nB^2h^2(\log n+\log \frac{1}{\epsilon})^2}{\log(1-\epsilon)}\right)$ dynamic programming algorithm for $a_i \xrightarrow{b_i} \text{b}_i$ NAP that produces a $(1-\epsilon)$-approximation of the optimal solution, where $h$ denotes the height of $T$. As that in [11], our algorithm is only polynomial if $B$ is polynomial in $n$. This assumption is justifiable if, for example, $B$ is expressed in millions of dollars and its value will be a reasonably small integer. Without loss of generality, we also assume that no single cost exceeds the budget.

NAPX essentially generalizes the dynamic programming table of [11] by computing for each clade, each desired survival probability of the clade, and any budget between 1 and $B$, the maximum $\mathbb{E}(PD)$ score achievable while guaranteeing this survival probability. This way, we need not make the choice between maximizing $\mathbb{E}(PD)$ or probability as the tables are constructed. From the definition of $\mathbb{E}(PD)$ in (2), the probability of survival of an edge can be written as a function of its two children. Let $P_e$ denote the survival probability of edge $e$, and $l$ and $r$ be $e$’s children. Then

$$P_e = P_l + P_r - P_l P_r.$$  \hspace{1cm} (3)

In the optimal solution for NAP on $T$, assume $b$ dollars are assigned to clade $K_e$ and $e$ survives with probability $p$. It follows that $i$ and $b-i$ dollars are assigned to $K_l$ and $K_r$ respectively where $0 \leq i \leq b$. These subclades must survive with probabilities $j$ and $\frac{p-j}{1-j}$ (or 0 when $p = j = 1$), for some $0 \leq j \leq p$, in order to satisfy (3). Because the probability is continuous, we discretize it into intervals by rounding it down to the nearest multiple of a chosen constant $\alpha$. Probabilities less than a chosen cutoff value $p_{\text{min}}$ are rounded to zero.

$$p \in \left\{0, \alpha^{\lfloor \log \alpha p_{\text{min}} \rfloor}, \ldots, \alpha^2, \alpha, 1\right\}$$

If two non-zero probabilities lie in the same interval, their ratio is at most $\alpha$. If they are in consecutive intervals, their ratio is likewise bounded by $\alpha^2$. For notational convenience, we define a mapping $\pi(\cdot)$ that rounds a probability to the lower bound of its corresponding interval.

$$\pi(p) = \begin{cases} 0 & \text{if } p < p_{\text{min}} \\ \alpha^{\lfloor \log \alpha p_{\text{min}} \rfloor} & \text{otherwise.} \end{cases}$$

We now formally describe our algorithm. For each edge $e$, we construct a two-dimensional table $T_e$ where $T_e(b, p)$ stores the optimal expected diversity of $K_e$ given that $b$ dollars are assigned to it and it survives with a probability that lies no less than $p$. The table is constructed in the following manner if $e$ is a pendant
edge incident to the leaf for species $s$.

$$T_e(b, p) = \begin{cases} 
    a_s \lambda(e) & \text{if } b < c_s \text{ and } p = \pi(a_s), \\
    b_s \lambda(e) & \text{if } b \geq c_s \text{ and } p = \pi(b_s), \text{ or} \\
    -\infty & \text{otherwise.}
\end{cases} \quad (4)$$

Otherwise, $T_e$ is computed from the tables of its two children, $T_l$ and $T_r$.

$$T_e(b, p) = p\lambda(e) + \max_{i,j,k} \{T_l(i, j) + T_r(b - i, k)\} \quad (5)$$

subject to

$$i \in \{0, 1, 2, ..., b\},$$

$$j, k \in \{0, \alpha^{\lceil \log_\alpha p_{\min} \rceil}, ..., \alpha^2, \alpha, 1\},$$

$$\pi(j + k - jk) = p$$

The $E(PD)$ score for the entire tree can be obtained by attaching an edge $e_r$ of length 0 to the root and finding $\max_j \{T_e(B, j)\}$. The tables are computed from the bottom up, and each time an entry is filled, pointers are kept to the two entries in the child tables from which it was computed. This way the optimal budget allocation can be obtained by following the pointers down from the entry for the optimal score for $e_r$.

### 2.2 Approximation Ratio

In this section, we express the worst-case approximation ratio as a function of the constants $p_{\min}$ and $\alpha$ introduced above, beginning with $p_{\min}$. Note that since any species $s$ with $c_s > B$ can be transformed into a new species $s'$ with $c_{s'} = 0, b_{s'} = a_s$ and $a_{s'} = a_s$ without affecting the outcome, we can safely assume that $c_s \leq B$ for all $s \in X$.

**Lemma 1.** Let $I$ be an instance of NAP for which there exists a constant $k$ such that $b_i \geq n^{-k} \geq p_{\min}$ for all $i \in S$. Consider a transformed instance $I'$ where all $a_i$ values in the range $(0, p_{\min})$ are rounded to 0. Let $OPT(I)$ and $OPT(I')$ be the expected PD scores of the optimal solutions to $I$ and $I'$ respectively. Then the ratio of these scores is bounded as follows:

$$OPT(I') \geq (1 - n^{k+1}p_{\min})OPT(I)$$

**Proof.** Let $\text{path}(s)$ be the set of edges comprising the path from leaf $s$ to the root. We define $w(s)$ as the expected diversity of the path from $s$ to the root if $s$ is conserved:

$$w(s) = b_s \sum_{e \in \text{path}(s)} \lambda(e).$$

Let $w_{\max} = \max_{s \in X} \{w(s)\}$. This value allows us to place a trivial lower bound on the optimal solution (recalling that we can assume that $c_s \leq B$).

$$w_{\max} \leq OPT(I). \quad (6)$$
We also observe that if any species \( s \) survives with a non-zero probability smaller than \( p_{\text{min}} \) in the optimal solution, its contribution to \( \text{OPT}(I) \) will be bounded by \( \frac{p_{\text{min}}w(s)}{b_s} \). It follows that

\[
\text{OPT}(I') \geq \text{OPT}(I) - \sum_{s \in X} \frac{p_{\text{min}}w(s)}{b_s}.
\]

Since \( b_s \geq n^{-k} \) and \( w(s) \leq w_{\text{max}} \), we can express the bound as

\[
\text{OPT}(I') \geq \text{OPT}(I) - n p_{\text{min}} w_{\text{max}} n^{-k}.
\]

Dividing by \( \text{OPT}(I) \) yields

\[
\frac{\text{OPT}(I')}{\text{OPT}(I)} \geq 1 - n^{k+1} p_{\text{min}}.
\]

From (6) we obtain

\[
\frac{\text{OPT}(I')}{\text{OPT}(I)} \geq 1 - n^{k+1} p_{\text{min}},
\]

which completes the proof. \( \square \)

The size of the probability intervals in the tables, determined by \( \alpha \), also affects the approximation ratio. This relationship is detailed in the following lemma.

**Lemma 2.** Let \( \text{OPT}_e(b, p) \) denote the optimal expected PD score for clade \( K_e \) if \( e \) survives with probability exactly \( p \) and \( b \) dollars are allocated to it. Now consider an instance of NAP such that all \( a_s \) and \( b_s \) are either 0 or at least \( p_{\text{min}} \). For any \( \text{OPT}_e(b, p) \) where \( e \) is at height \( h \) in the tree, there exists a table entry \( T_e(b, p') \) constructed by NAPX such that the following conditions hold:

\( i) \) \( T_e(b, p') \geq \alpha^h \text{OPT}_e(b, p) \)

\( ii) \) \( p' \geq \alpha^h p \)

**Proof.** If \( p = 0 \), then \( \text{OPT}_e(b, p) = 0 \) and the lemma holds. For the remainder of the proof, we assume \( p \geq p_{\text{min}} \). The proof will proceed by induction on \( h \), the height of \( e \) in the tree, beginning with the base case where \( h = 1 \) and \( e \) is a pendant connected to leaf \( s \). We need only consider the cases where the optimal solution is defined. So without loss of generality, assume we have \( \text{OPT}_e(b, a_s) = \lambda(e)a_s \). From (4), we know there is an entry \( T_e(b, \pi(a_s)) = a_s \lambda(e) \) and therefore both \( i) \) and \( ii) \) hold.

We now assume that the lemma holds for \( h \leq x \) and consider some edge \( e \) at height \( x + 1 \). By definition, \( \text{OPT}_e(b, p) \) can be expressed in terms of its children \( l \) and \( r \).

\[
\text{OPT}_e(b, p) = p\lambda(e) + \text{OPT}(i, j) + \text{OPT}_r(b - i, k)
\]
where \( j + k - jk = p \). From the induction hypothesis, there exist

\[
T_l(i, j') \geq \alpha^x OPT_l(i, j) \quad \text{and} \quad T_r(b - i, k') \geq \alpha^x OPT_r(b - i, k)
\]

where \( j' \geq \alpha^x j \) and \( k' \geq \alpha^x k \). Let \( q = j' + k' - j'k' \). It follows that

\[
q \geq \alpha^x j + \alpha^x k - \alpha^2 x jk \geq \alpha^x p.
\] (7)

The left inequality in (7) holds because \( j' + k' - j'k' \) increases as \( j' \) or \( k' \) increase, so long as their values do not exceed 1. This can be checked by observing that the partial derivatives with respect to \( j' \) and \( k' \) are \( 1 - k' \) and \( 1 - j' \), respectively.

\( T_l(i, j') \) and \( T_r(b - i, k') \) will be considered when computing the entry \( T_e(b, p') \) where \( p' = \pi(q) \). Since \( q \geq p_{\text{min}} \), we have \( \pi(q) \geq \alpha q \) because it simply rounds \( q \) to the nearest multiple of \( \alpha \). Therefore, \( p' \geq \alpha^{x+1} p \) and \( T_e(b, p') \) can be expressed as follows.

\[
T_e(b, p') \geq p' \lambda(e) + T_l(i, j') + T_r(b - i, k') \\
\geq \alpha^{x+1} p \lambda(e) + \alpha^x OPT_l(i, j) + \alpha^x OPT_r(b - i, k) \\
\geq \alpha^{x+1} (p \lambda(e) + OPT_l(i, j) + OPT_r(b - i, k)) \\
\geq \alpha^{x+1} OPT_e(b, p)
\]

\( \Box \)

Combining Lemmas 1 and 2 allows us to state that \text{NAPX} returns a solution that is at least a factor of \( (1 - n^{k+1} p_{\text{min}}) \alpha^h \) of the optimal solution. In this section we show that these results also imply that a \( (1 - \epsilon) \) approximation can be obtained in polynomial time for an arbitrary constant \( \epsilon \).

**Lemma 3.** \( O \left( \frac{h(\log n + \log \frac{1}{\epsilon})}{|\log(1 - \epsilon)|} \right) \) probability intervals are required in the table in order to obtain a \( 1 - \epsilon \) approximation.

*Proof.* The number of probability intervals, \( t \), required for the table is bounded by the number of times 1 must be multiplied by \( \alpha \) to reach \( p_{\text{min}} \). Hence \( \alpha^t \leq p_{\text{min}} \) and

\[
t = \left\lceil \frac{\log p_{\text{min}}}{\log \alpha} \right\rceil.
\] (8)

From Lemmas 1 and 2 we can obtain the desired approximation ratio by selecting \( \alpha = \sqrt{(1 - \epsilon)^2} \) and \( p_{\text{min}} = \frac{1 - \sqrt{1 - \epsilon}}{\pi} \). Plugging these values into (8) gives

\[
t = \left\lceil \frac{\log \left( \frac{1 - \sqrt{1 - \epsilon}}{\pi} \right)}{\log \sqrt{(1 - \epsilon)^2}} \right\rceil = \left\lceil 2h \log \left( 1 - \sqrt{1 - \epsilon} - (k + 1) \log n \right) \right\rceil.
\]
It can be shown that $\log(1 - \sqrt{1 - \epsilon})$ is $O(\log \epsilon)$, so multiplying by $\frac{1}{\epsilon}$ we can express $t$ asymptotically as

$$t \in O\left(\frac{h (\log n - \log \epsilon)}{-\log(1 - \epsilon)}\right) = O\left(\frac{h (\log n + \log \frac{1}{\epsilon})}{\log(1 - \epsilon)}\right).$$

\[\square\]

**Theorem 1.** NAPX is a $(1 - \epsilon)$-approximation with time complexity

$$O\left(\frac{nB^2h^2 (\log n + \log \frac{1}{\epsilon})^2}{\log^2 (1 - \epsilon)}\right).$$

**Proof.** For each table entry $T(b, p)$, we must find the maximum of all possible combinations of entries in the left and right child tables that satisfy $b$ and $p$. These combinations correspond to the possible $\{i, j, k\}$ triples from (5). There are $O(Bt^2)$ such combinations as $i$ corresponds to the budget and $j$ and $k$ correspond to probability intervals. Furthermore, for fixed values of $p$ and $j$, there are potentially $O(t)$ different values of $k$ that could satisfy $\pi(j + k - jk)$ due to rounding. It follows that a naive algorithm would have to compare all $O(Bt^2)$ combinations when computing the maximum in (5) for each table entry.

Fortunately, because $\pi(j + k - jk)$ is monotonically nondecreasing with respect to either $j$ or $k$, we can directly compute for any fixed $p$ and $j$ the interval of $k$ entries that satisfy $\pi(j + k - jk) = p$:

$$\left[\left\lfloor \log_{\alpha} \left( \frac{\alpha p - j}{1 - j} \right) \right\rfloor, \left\lceil \log_{\alpha} \left( \frac{p - j}{1 - j} \right) \right\rceil \right].$$

Finding the value of $k$ in the interval such that $T(b - i, k)$ is maximized is effectively a range maxima query (RMQ) on an array. Regardless of the size of the interval, such a query can be performed in constant time if instead of an array, the values are stored in a RMQ structure as described in [1]. Such structures are linear both in space and the time they take to create, meaning that we can use them to store each column in the table (corresponding to budget value $i$) without adversely affecting the complexity. Now, when given a pair $\{i, j\}$, the optimal value of $k$ can be computed in constant time, bringing the complexity of filling a single table entry to $O(Bt)$, the number of combinations of the pair $\{i, j\}$.

There are $O(Bt)$ entries in each table, and a table for each of the $O(n)$ edges in the tree. The space complexity is therefore $O(nBt)$ and the time complexity is $O(nB^2t^2)$. Substituting $t$ for the value that yields a $(1 - \epsilon)$ approximation ratio shown in Lemma 3 gives $O\left(\frac{nB^2h^2 (\log n + \log \frac{1}{\epsilon})^2}{\log^2 (1 - \epsilon)}\right)$.

### 2.3 Expected Running Time

Since in general the height of a phylogenetic tree with $n$ leaves is $O(n)$, the running time derived above is technically cubic in $n$. Fortunately, for most inputs
we can expect the height to be much smaller. In this section, we will provide improved running times for trees generated by the two principal random models. Additionally we will show that caterpillar trees, which should be the pathological worst-case topology according to the above analysis, actually have a much lower complexity.

The Yule-Harding model \cite{14,5}, also known as the equal-rates-Markov model, assumes that trees are formed by a succession of random speciation events. The expected height of trees formed in this way, regardless of the speciation rate, is $O(\log n)$ \cite{2} giving a time complexity of $O\left(\frac{nB^2 \log^2 n(\log n + \log \frac{1}{\epsilon})^2}{\log^2(1-\epsilon)} \right)$.

A caterpillar tree is a tree where all internal nodes are on a path beginning at the root, and therefore has height $n$. This implies that every internal edge has at least one child edge that is incident to a leaf. Suppose edge $e$ has child $l$ that is incident to the leaf for species $s$. This table only contains two meaningful values: $T_l(0, a_s)$ and $T_l(c_s, b_s)$. Therefore to compute entry $T_e(b, p)$, only $O(1)$ combinations of child table entries need to be compared and the time complexity is improved to $O\left(\frac{n^2 B(\log n + \log \frac{1}{\epsilon})}{\log(1-\epsilon)} \right)$.

3 Conclusion

NAPX is, to our best knowledge, the first polynomial-time algorithm for $\text{NAP} \xrightarrow{\epsilon} b$ NAP that places guarantees on the approximation ratio. While there are still some limitations, especially for large budgets or tree heights, our algorithm still significantly increases the number of instances of NAP that can be solved. Moreover, our expected running time analysis shows that the algorithm will usually be much more efficient than its worst-case complexity suggests. This work towards a more general solution is important if the Noah’s Ark Problem framework is to be used for real conservation projects. Some interesting questions do remain, however. Does NAP remain NP-Hard when the budget is constrained to be polynomial in $n$? We conjecture that it is, but the usual reduction from Knapsack is clearly no longer valid. We would also like to find an efficient algorithm whose complexity is independent of $h$ and/or $B$.

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