Theoretical Computer Science 454 (2012) 51–63

Contents lists available at SciVerse ScienceDirect

Theoretical Computer Science

journal homepage: www.elsevier.com/locate/tcs

The binary perfect phylogeny with persistent characters

Paola Bonizzoni[a,*], Chiara Braghin[b], Riccardo Dondi[c], Gabriella Trucco[b]

[a] *Dipartimento di Informatica Sistemistica e Comunicazione, Univ. degli Studi di Milano - Bicocca, Viale Sarca 336, 20126 Milano, Italy*

[b] *Dipartimento di Tecnologie dell'Informazione Univ. degli Studi di Milano, Crema, Italy*

[c] *Dipartimento di Scienze dei Linguaggi, della Comunicazione e degli Studi Culturali, Univ. degli Studi di Bergamo, Bergamo, Italy*

A B S T R A C T

The binary perfect phylogeny model is too restrictive to model biological events such as back mutations. In this paper, we consider a natural generalization of the model that allows a special type of back mutation. We investigate the problem of reconstructing a near perfect phylogeny over a binary set of characters where characters are *persistent*: characters can be gained and lost at most once. Based on this notion, we define the problem of the Persistent Perfect Phylogeny (referred as P-PP). We restate the P-PP problem as a special case of the Incomplete Directed Perfect Phylogeny, called Incomplete Perfect Phylogeny with Persistent Completion, (refereed as IP-PP), where the instance is an incomplete binary matrix M having some missing entries, denoted by symbol ?, that must be determined (or completed) as 0 or 1 so that M admits a binary perfect phylogeny. We show that the IP-PP problem can be reduced to a problem over an edge colored graph since the completion of each column of the input matrix can be represented by a graph operation. Based on this graph formulation, we develop an exact algorithm for solving the P-PP problem that is exponential in the number of characters and polynomial in the number of species.

1. Introduction

The perfect phylogeny is one of the most investigated models in different areas of computational biology. This model derives from a restriction of the parsimony methods used to reconstruct the evolution of species (taxa). Such methods assume that each taxon is characterized by a set of attributes, called characters. In this paper, we focus on the binary perfect phylogeny model; characters can take only the values (or states) zero or one, usually interpreted as the presence or absence of the attribute in the taxa. Restrictions on the type of changes from zero to one and vice versa lead to a variety of specific models (Felsenstein, [6]). In the Dollo parsimony, a character may change state from zero to one only once, but from one to zero multiple times [13]. In the variant of Camin–Sokal parsimony [2], characters are *directed*, only changes from zero to one are admissible on any path from the root to a leaf. This fact means that the root is assumed to be labeled by the ancestral state with all zero values for each character, and no character change back to 0 is allowed. This last variant is known as the binary directed perfect phylogeny, and it has a linear time solution [8].

Such a model has been successfully applied in the context of haplotype inference, starting from the seminal work by Gusfield on the Perfect Phylogeny Haplotyping Problem [9]. This last problem has been widely investigated, and very efficient polynomial time solutions have been proposed, including linear-time algorithms [4,16,1]. However, the real data usually do not fit the simple model of the binary perfect phylogeny and thus in the past years generalizations of the model have been proposed. Some models are surveyed in [7].

* Corresponding author.

E-mail addresses: bonizzoni@disco.unimib.it (P. Bonizzoni), chiara.braghin@unimi.it (C. Braghin), gabriella.trucco@unimi.it (R. Dondi), riccardo.dondi@unibg.it (G. Trucco).

0304-3975/$ – see front matter © 2012 Elsevier B.V. All rights reserved.
doi:10.1016/j.tcs.2012.05.035

A central goal in this investigation of the binary perfect phylogeny model is to extend its applicability by taking into account the biological complexity of data, while retaining the computational efficiency where possible. More precisely, the binary perfect phylogeny model though allowing a very efficient reconstruction is quite restrictive to explain the evolution of data where homoplasy events such as back mutations, also called reversals, are present. In order to include such events, the problem of reconstructing the near-perfect phylogeny has been formalized and investigated. Some work has been done to produce algorithmic solutions to the problem, mainly fixed-parameter algorithms have been provided [15,18]. However, the near-perfect phylogeny model appears to be too general for some biological applications. The model does not distinguish the main two types of homoplasy occurring in a phylogenetic tree: recurrent mutation and back mutations. Back mutations are changes in the state of the character that only occur along the same path from the root of the tree. On the contrary, recurrent mutations are changes in the state of the character that occur along different paths of the tree, since the character is allowed to label multiple edges of the tree. In this paper we address the problem of constructing a perfect-phylogeny under the assumption that only a special type of back mutation may occur in the tree. A character may change state only twice in the tree, precisely from 0 to 1 and from 1 to 0, and the changes occur along the same path from the root of the tree T. These characters have already been considered in the literature and called *persistent* by Przytycka [14] in a general framework of tree inference. More precisely, in [14], the change of a character from state 0 to 1 models the gain of the character, while the change from 1 to 0 models the loss of the character. The use of the notion of persistent character is quite relevant when reconstructing phylogenies that describe the gain and loss of genomic characters [19]. An example of a promising class of genomic characters (also called rare genomic changes—RGC) is given by insertion and deletion of introns in protein-coding genes during the evolution of eukaryotes. In this framework, persistent characters allow to infer phylogenies by using the gain and loss of introns [19].

We define a generalization of the (rooted) binary directed perfect phylogeny where each character may be persistent. Clearly our model is a restriction of the Dollo parsimony, where characters can be lost several times, i.e. a character can be lost along different paths from a root to a leaf. Acquisition or loss of characters (i.e. attributes) when unrestricted could make the reconstruction of an evolutionary tree difficult, if not possible.

Assume that $S = \{s_1, \ldots, s_n\}$ is a set of *species* and $C = \{c_1, \ldots, c_m\}$ is a set of *characters*. In the paper we consider binary matrices representing species and characters. More precisely, a binary matrix M of size $n \times m$ has columns associated with the set C of characters, i.e. column j represents character $c_j \in C$, while rows of M are associated with the set S of species, i.e. row i represents species s_i. Then $M[i, j] = 1$ if and only if species s_i has character c_j, otherwise $M[i, j] = 0$.

In the rest of the paper, to simplify the notation, we identify rows with species and columns with characters.

The gain of a character in a phylogenetic tree is usually represented by an edge labeled by the character. In order to model the presence of persistent characters, the loss of a character c in the tree is represented by an edge that is labeled by the negation of c, or negated character, denoted by $\bar{c}$. Clearly, an edge labeled by a negated character follows an edge labeled by the character along a path from the root to a leaf. The following definition is based on the general coalescent model given in [5] to represent the evolution of haplotype sequences and assume that nodes are labeled by vector states of characters.

Formally, we have:

Persistent Perfect Phylogeny: let M be a binary matrix of size $n \times m$. Then a *persistent perfect phylogeny*, in short *p-pp tree* for M, is a rooted tree T that satisfies the following properties:

1. each node x of T is labeled by a vector l_x of length m;
2. the root of T is label by a vector of all zeros, while for each node x of T the value $l_x[j] = 0, 1$ represents the state, 0 or 1 respectively, of character c_j in tree T;
3. for each character c_j there are at most two edges $e = (x, y)$ and $e' = (u, v)$ such that $l_x[j] \neq l_y[j]$ and $l_u[j] \neq l_v[j]$ (representing a change in the state of c_j) such that e, e' occur along the same path from the root of T to a leaf of T; if e is closer to the root than e', then the edge e where c_j changes from 0 to 1 is labeled c_j, while edge e' is labeled $\bar{c}_j$,
4. each row of M labels exactly one leaf of T.

In the classical definition of a Perfect Phylogeny Tree, in short *pp* tree, no negated characters are allowed in the tree (see [17]) (see definition in Section 2). Observe that by the above definition of p-pp tree, for each leaf s of tree T, the positive characters that label edges that are along the unique path from the root to s and do not occur as negated along the same path, specify exactly the characters that have value 1 in the row s of M.

Thus, let us state the main problem investigated in the paper.

The **Persistent Perfect Phylogeny problem (P-PP):** given a binary matrix M, returns a p-pp tree for M if such a tree exists.

In the paper we investigate the solution of the P-PP problem. Our main contribution is a graph-based restatement of the problem that allows us to provide an exact algorithm for the problem having a worst time complexity that is polynomial in the number n of rows of the matrix and exponential in the number m of characters. Since in real data the number of characters is usually small, while the number of species may be very large, the algorithm could be efficient even on large instances as shown by an experimental analysis illustrated in Section 6.

The graph-based solution of the P-PP problem is obtained by restating the problem as a variant of the Incomplete Directed Perfect Phylogeny [12], called Incomplete Perfect Phylogeny with Persistent Completion (IP-PP), where the input data of this last problem is a specific incomplete matrix M over values 0, 1, ? and the goal is to complete values ? into 0 or 1 so that M admits a classical perfect phylogenetic tree. Then we show that the IP-PP problem reduces to the problem of reducing a

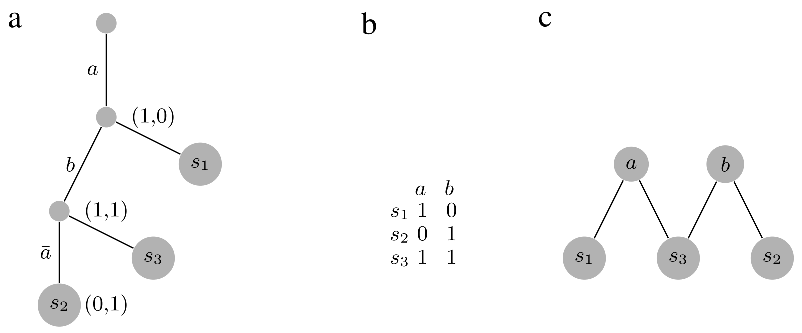


Fig. 1. (a) illustrates the perfect persistent phylogeny for the forbidden matrix reported in (b) and the Σ-graph for the forbidden matrix in (c).

colored graph by a graph operation that represents a completion of a column of the input matrix. Based on these ideas we discuss our exact algorithm for the P-PP problem.

We believe that the graph-based formulation of the problem could help in investigating polynomial time solutions to the problem.

2. The Perfect Phylogeny model: preliminaries

Let us give the definition of a perfect phylogeny for a binary matrix and some relevant basic results that will be used in the paper.

Perfect Phylogeny

Let M be a binary matrix of size $n \times m$. Then a *directed perfect phylogeny*, in short *pp tree* for M, is a rooted tree T that satisfies the following properties:

1. each node x of T is labeled by a vector l_x of length m;
2. the root is labeled by a vector of zeros, while for each node x, the value $l_x[j] = 0, 1$ represents the state, 0 or 1 respectively, of character c_j in tree T;
3. for each character c_j there is at most one edge $e = (u, v)$, labeled c_j, such that $l_u[j] \neq l_v[j]$ (notice that $l_u[j] = 0$, while $l_v[j] = 1$); edge e represents a changing of state of c_j;
4. each row of matrix M labels exactly one leaf of T.

The algorithmic solution of the Perfect Phylogeny model has been investigated in [8], where a linear time algorithm is provided. In particular, the paper [8] provides a well known characterization of matrices admitting a perfect phylogeny. A binary matrix M admits a perfect phylogeny if and only if it does not contain a pair of columns and three rows inducing the configurations (0, 1), (1, 0) and (1, 1), also known as *forbidden matrix* (see Fig. 1(b)). We will use this characterization in the paper.

In particular, the forbidden matrix has a representation by means of a graph consisting of a path of length four containing three species and two characters; this graph is called Σ-graph. Such a graph is obtained by drawing an edge between every pair of species and characters having value 1 in the matrix (see Fig. 1(c)).

Notice that the forbidden matrix is the smallest matrix that does not admit a pp tree. However, by allowing a character to be persistent, the matrix admits a persistent perfect phylogeny, as shown in Fig. 1(a).

A well known concept that has been used several times in the framework of the perfect phylogeny is a graph representation of the four configurations (0, 1), (1, 1), (1, 0) and (0, 0) (called four gametes): the *conflict graph*. We say that two positive characters c, c' of matrix M are in *conflict* in matrix M, if and only if the pair of columns u, v of M induces the four gametes.

Definition 1 (*Conflict Graph*)**.** Let M be a binary matrix. The *conflict graph* associated with matrix M is the undirected graph $G_c = (C, E \subseteq C \times C)$ where a pair $(u, v) \in E$ if and only if u, v are in conflict in matrix M.

Notice that when M has a conflict graph with no edges, M does not necessarily admit a rooted perfect phylogeny, since M could contain an occurrence of the forbidden matrix. For example, the forbidden matrix has a conflict-graph with no edges.

In this paper we define a variant of the Incomplete Directed Perfect Phylogeny (in short IDP) [12]. The input data of the IPP problem is a matrix over symbols 0, 1, ? where symbol ? is used to denote an entry of the matrix that is not determined. Then the IPP problem is finding a completion of the matrix, i.e. assigning values 0, 1 to ? symbols so that the matrix admits a perfect phylogeny.

For basic notions of graph theory used in the paper see [3].

a
$$\begin{array}{ccccc}
a & b & c & d & e \\
0 & 0 & 1 & 1 & 0 \\
0 & 1 & 0 & 0 & 0 \\
1 & 0 & 0 & 0 & 0 \\
1 & 0 & 0 & 0 & 1 \\
1 & 1 & 1 & 0 & 0
\end{array}$$

b
$$\begin{array}{cccccccccc}
a & \bar{a} & b & \bar{b} & c & \bar{c} & d & \bar{d} & e & \bar{e} \\
? & ? & ? & ? & 1 & 0 & 1 & 0 & ? & ? \\
? & ? & 1 & 0 & ? & ? & ? & ? & ? & ? \\
1 & 0 & ? & ? & ? & ? & ? & ? & ? & ? \\
1 & 0 & ? & ? & ? & ? & ? & ? & 1 & 0 \\
1 & 0 & 1 & 0 & 1 & 0 & ? & ? & ? & ?
\end{array}$$

c
$$\begin{array}{cccccccccc}
a & \bar{a} & b & \bar{b} & c & \bar{c} & d & \bar{d} & e & \bar{e} \\
1 & 1 & 1 & 1 & 1 & 0 & 1 & 0 & 0 & 0 \\
0 & 0 & 1 & 0 & 0 & 0 & 0 & 0 & 0 & 0 \\
1 & 0 & 1 & 1 & 1 & 1 & 0 & 0 & 0 & 0 \\
1 & 0 & 1 & 1 & 1 & 1 & 0 & 0 & 1 & 0 \\
1 & 0 & 1 & 0 & 1 & 0 & 0 & 0 & 0 & 0
\end{array}$$

Fig. 2. The figure illustrates a binary matrix M(a) and its extended matrix M_e (b) and a completion of M_e (c).

3. The incomplete Perfect Phylogeny with persistent completion

Let M be a binary $n \times m$ matrix which is an instance of the P-PP problem. The *extended matrix* associated with M is a matrix M_e of size $n \times 2m$ over alphabet $\{0, 1, ?\}$ which is obtained by replacing each column c of M by a pair of columns $(c, \bar{c})$, where c is the positive character, while $\bar{c}$ is the negated character, moreover for each row s of M, it holds:

1. if $M[s, c] = 1$, then $M_e[s, c] = 1$ and $M_e[s, \bar{c}] = 0$,
2. if $M[s, c] = 0$, then $M_e[s, c] =?$ and $M_e[s, \bar{c}] =?$.

Informally, the assignment of the pair $(?, ?)$ in a species row s for the pair of entries in columns c and $\bar{c}$ means that character c could be persistent in species s, i.e. it is gained and then lost. On the contrary, by definition of a persistent perfect phylogeny, the pair $(1, 0)$ assigned in a species row s for the pair of entries in columns c and $\bar{c}$, means that character c is only gained by the species s.

In the paper, we will use the term extended matrix to denote an extended matrix associated with a binary matrix and defined as above. A *completion of a character* c of matrix M_e is obtained by solving the pair $(?, ?)$ given in the pair of columns $c, \bar{c}$ by the value $(0, 0)$ or $(1, 1)$. If a character c is completed, then it is called *active*.

A *completion of matrix* M_e is a completion of all characters of M_e, while a *partial completion of* M_e is a completion of zero or more characters of M_e.

Fig. 2(a) shows an example of input matrix M for the P-PP problem. Then Fig. 2(b) shows the incomplete matrix M_e associated with M. A possible completion of M_e is given in Fig. 2(c).

We introduce below a problem to which we reduce P-PP, as shown in Theorem 1.

Incomplete Perfect Phylogeny with Persistent Completion Problem (IP-PP)

Instance: An extended matrix M_e over $\{0, 1, ?\}$.

Question: give a completion M' of the extended matrix M_e such that M' admits a perfect phylogeny, if it exists.

Thus we state the first result of the paper. In order to prove the result we assume that the input matrix M does not have columns consisting of zeros, that is for each character c, there must exist a species having the character. As a consequence of this assumption, given the extended matrix M_e of M, it must be that for each positive character c there is a species having the positive character c and not the negated character $\bar{c}$.

Theorem 1. *Let M be a binary matrix and M_e the extended matrix associated with M. Then M admits a p-pp tree if and only if there exists a completion of M_e admitting a pp tree.*

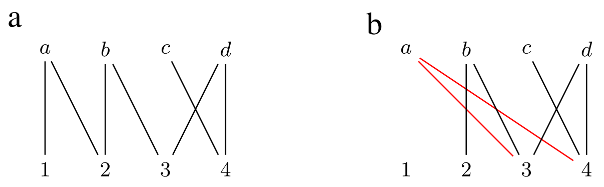
Proof. (*If*) Let M' be a completion of matrix M_e such that M' admits a perfect phylogeny T.

In the following we show that apart from the labeling of internal nodes of tree T, the tree T is a p-pp tree for matrix M. More precisely, we obtain a p-pp tree T' for matrix M by changing the labeling of tree T as follows. In order to distinguish the labeling of node x in tree T from the new labeling of the same node x in tree T', we denote the new labeling of x in T' by the vector l'_x. Given a node x of tree T labeled by a $2m$ vector l_x, then the label l'_x of node x in tree T' is defined as follows:

for each j, with $1 \leq j \leq m$, $l'_x[j] = 1$ if and only if $l_x[2j-1] = 1$ and $l_x[2j] = 0$, otherwise $l'_x[j] = 0$. Informally, a character c_j has value 1 in vector l'_x if and only if c_j occurs as 1 in vector l_x and it is does not occur as negated in l_x, that is character $\bar{c}_j$ has value 0 in l_x.

We first show that property (4) of the definition of a persistent perfect phylogeny holds for tree T' for matrix M, i.e. each row s of M labels a leaf in tree T'. Now, row s of the completion M' labels a leaf l_s of tree T. We can easily show that l'_s is equal to row s in matrix M. This fact follows from the observation that characters that have value 1 in row s of M still have value 1 in row s of the completion M'. By definition of a completion, only a character having value 0 in M may be persistent along a path of tree T, i.e. it labels an edge of the path and its negated character labels another edge of the same path. Consequently, the characters associated with the edges along the unique path of T from the root to s and which are not negated are exactly those having value 1 in row s of M, that is l'_s is equal to row s of M, as required.

Now, properties (1)–(3) given by definition of a persistent perfect phylogeny T' for matrix M follow from the fact that T is a perfect phylogeny for matrix M', and thus each character is associated with exactly one edge of the tree, which implies the same property for each negated character $\bar{c}$. Observe that by definition of extended matrix a negated character occurs in a row if and only if its positive character occurs in the same row. Moreover, since we assume that for each character c matrix M must have a species that contains the positive character c, but not the negated character $\bar{c}$, it is immediate to verify that every negated character $\bar{c}$ follows character c along a path from the root to a leaf, thus proving that change of state of $\bar{c}$ from 0 to 1 (that is from 1 to 0 in tree T') occurs after the change of state from 0 to 1 of character c. In fact, by definition of



c

$$\begin{array}{cccccccc} a & \bar{a} & b & \bar{b} & c & \bar{c} & d & \bar{d} \\ 1 & 0 & ? & ? & ? & ? & ? & ? \\ 1 & 0 & 1 & 0 & ? & ? & ? & ? \\ \mathbf{1} & \mathbf{1} & 1 & 0 & ? & ? & 1 & 0 \\ \mathbf{1} & \mathbf{1} & ? & ? & 1 & 0 & 1 & 0 \end{array}$$

Fig. 3. (a) illustrates the graph G_{RB} of the extended matrix associated with the matrix of Example 1. Then (b) illustrates the graph G_{RB} after the realization of character a. Then (c) illustrates M_e after the completion of a. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

a completion the set of species having character c includes the set of species having character $\bar{c}$, since columns c and $\bar{c}$ both have values 1 or c has value 1 and $\bar{c}$ has value 0.

(*Only if*) Vice versa, let us now show that if there exists a persistent perfect phylogeny T for matrix M, then there exists a completion M' of M_e such that M' admits a perfect phylogeny. We can associate to tree T a matrix M_T of size $n \times 2m$ as follows. For each character c of M add a new column $\bar{c}$. Then consider each row s of matrix M_T such that a negated character $\bar{c}$ occurs along the path from the root to s. Then set value 1 for row s in columns c and $\bar{c}$ of matrix M_T. Notice that M_T is a completion of M_e and clearly T is a perfect phylogeny for M_T. $\square$

4. The red–black graph

In this section we give a graph representation of an extended matrix, and we define a graph operation that represents a special type of completion of the pair of columns of the matrix associated with a character.

Let M_e be an extended matrix M_e, then the *red–black* graph G_{RB} for matrix M_e consists of the edge colored graph (V, E) where $V = C \cup S$, given $C = \{c_1, \ldots, c_m\}$ and $S = \{s_1, \ldots, s_n\}$ the set of positive characters and species of matrix M_e, while E is defined as follows: $(s, c) \in E$ is a black edge if and only if $M_e[s, c] = 1$ and $M_e[s, \bar{c}] = 0$.

Then we define a graph operation on nodes (characters) of the graph G_{RB} that represents a *canonical* completion of characters and consists of adding red edges, removing black or red edges. This graph operation over characters (nodes) of the red–black graph may be iterated till the graph has only *active* characters, as defined below.

Realization of a character c and its canonical completion

Let $\mathcal{C}(c)$ be the connected component of graph G_{RB} containing node c. The *realization of character c* in graph G_{RB} consists of:

- (a) adding red edges connecting character c to all species nodes s that are in $\mathcal{C}(c)$ and such that (c, s) is not an edge of G_{RB},
- (b) removing all black edges (c, s) in graph G_{RB}, Then c is labeled *active*.
- (c) if a character c' is connected by red edges to all species of $\mathcal{C}(c)$, then c' is called *free*. Then its outgoing edges are deleted from the graph.

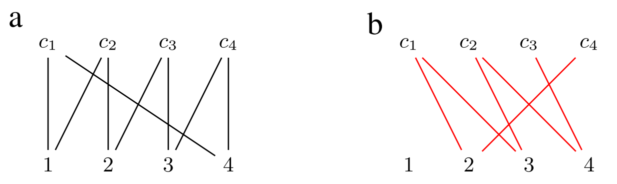
The realization of a character c is associated with a special completion in matrix M_e of the given character, called canonical. The *canonical* completion of character c in matrix M_e is defined by completing each pair (?, ?) occurring in the pair of columns c and $\bar{c}$ as follows: the pair (?, ?) is completed by (1, 1) in every species s that is in the component $\mathcal{C}(c)$ of graph G_{RB}, while value (0, 0) is assigned in the remaining rows.

Example 1. Fig. 3(a) illustrates the red–black graph of the extended matrix associated with matrix M consisting of rows 1000, 1100, 0101, 0011, numbered 1, 2, 3 and 4, respectively. Characters of M are denoted by letters a, b, c and d. Then Fig. 3(b) illustrates the red–black graph obtained after the realization of character a, while Fig. 3(c) reports the corresponding canonical completion in M_e of character a.

Informally, the red edges of graph G_{RB} incident to a character c that has been realized represent the pairs (?, ?) in columns $(c, \bar{c})$ that are completed as (1, 1) in matrix M_e.

In the following we call *e-empty* a red–black graph without edges.

Remark 1. Let r be a sequence of all characters of a red–black graph for an extended matrix M_e, and let G_r be the graph produced after the realization of the characters in r one after another. Clearly, the realization of characters in r produces a completion of the matrix M_e. Then, either G_r is e-empty or G_r contains two nodes inducing a Σ-graph. Observe that if G_r is not e-empty, it must have only red edges that are incident to at least two characters of the graph. In fact, assume on the contrary that G_r has a single character c that is incident to red edges. Then c must be connected to all species nodes in the same connected component of the graph. But, this fact leads to a contradiction since c is free and all red edges incident to c are deleted from the graph. By inspection of the possible cases, it is easy to verify that the minimum size connected component of G_r induces a Σ-graph consisting of two characters and three species. Such a graph represents the presence of a forbidden matrix in the completion M' of matrix M_e, and hence M' does not admit a perfect phylogeny (see Section 2).



c

$$\begin{array}{cccccccc}
c_1 & \bar{c}_1 & c_2 & \bar{c}_2 & c_3 & \bar{c}_3 & c_4 & \bar{c}_4 \\
1 & 0 & 1 & 0 & 0 & 0 & 0 & 0 \\
1 & 1 & 1 & 0 & 1 & 0 & 1 & 1 \\
1 & 1 & 1 & 1 & 1 & 0 & 1 & 0 \\
1 & 0 & 1 & 1 & 1 & 1 & 1 & 0
\end{array}$$

Fig. 4. (a) illustrates the red–black graph of the Example 2 . Then (b) illustrates graph G_R of the example, while (c) illustrates the completion of M_e induced by the realization of sequence r. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

The following example illustrates an application of the previous Remark 1.

Example 2. Let M be a matrix having the four characters c_1, c_2, c_3 and c_4 and rows $(1, 1, 0, 0)$, $(0, 1, 1, 0)$, $(0, 0, 1, 1)$ and $(1, 0, 0, 1)$, numbered 1, 2, 3 and 4, respectively. Let G_R be the graph obtained after the realization of the sequence $r = \langle c_1, c_2, c_3, c_4\rangle$ of characters. Then G_R consists of the path $\langle c_4, 2, c_1, 3, c_2, 4, c_3\rangle$ with red edges. Then graph G_R induces the Σ-graph consisting of path $\langle 2, c_1, 3, c_2, 4\rangle$. Observe that the completion M' of the extended matrix M_e of M consists of rows $(1, 0, 1, 0, 0, 0, 0, 0)$, $(1, 1, 1, 0, 1, 0, 1, 1)$, $(1, 1, 1, 1, 1, 0, 1, 0)$ and $(1, 0, 1, 1, 1, 1, 1, 0)$ and such a matrix does not admit a perfect phylogeny as characters c_1 and c_2 and species 2, 3, 4 induce the forbidden matrix in the completion M'. Fig. 4 illustrates the example.

Since we are interested in computing canonical completions of the matrix that admit a pp tree by the previous Remark 1 only canonical completions that are obtained by the realization of special sequences of characters of the red–black graph are considered, as defined below.

Definition 2. Given a graph G_{RB} for an extended matrix M_e, a *successful reduction* of G_{RB} is an ordering $r = \langle c_{i_1}, \dots, c_{i_m}\rangle$ of the set of positive characters $\{c_1, \dots, c_m\}$ of the matrix such that the consecutive realization of each character in r (which removes black edges from graph G_{RB}) leaves an e-empty red–black graph.

In Section 4.1, we show that finding a solution to an instance of the IP-PP problem is equivalent to computing the existence of a successful reduction for the red–black graph for the input matrix. More precisely, let M_e be an instance of the IP-PP problem. In the following Theorem 2, we prove that if M_e admits a pp tree T, then there exists a successful reduction of graph G_{RB}. Vice versa, we show that a successful reduction of the red–black graph for M_e provides a completion M' of the matrix M_e that admits a pp tree, thus giving a solution to the IP-PP instance.

Theorem 2. *Let M_e be an extended matrix. Then M_e admits a perfect phylogeny, if and only if there exists a successful reduction of the graph G_{RB} for M_e.*

4.1. Building a successful reduction from a pp tree

This section is devoted to the proof of one direction of Theorem 2, that is showing how to get a successful reduction from a pp tree. We will use the following remark that holds for extended matrices.

In this section, given a node v of tree T, by $T(v)$ we denote the subtree of T having root v. Moreover, we assume that edges of a tree T are oriented. The orientation of edges is from the root to a leaf node.

Remark 2. Let T be a pp tree for a completion of an extended matrix M_e. Then by definition of a perfect phylogeny is immediate to verify that the root of tree T is a 0^{2m} binary vector of size $2m$, moreover each internal node x is labeled by a $2m$-vector l_x defined as follows: each entry i has value 1 if and only if the corresponding ith character (positive or negated) occurs along the path from the root of the tree T to node x.

Example 3. Fig. 5(a) illustrates the pp tree for matrix M' of Fig. 2 (c). Notice that rows of matrix M' are numbers 1, 2, 3, 4, 5, while the positive characters are a, b, c, d, e. Then Fig. 5(b) illustrates the vectors labeling each internal node of tree T.

Then we need to state some technical lemmas and introduce a normal form for a pp tree, called *standard*. A tree T is in *standard form* when it is in *simple form* as defined below and satisfies the properties stated in Definition 3.

A pp tree T is in *simple form* if and only if each edge of the tree is exactly labeled by one character and T does not contain two edges e, e' incident to the same node, one labeled by character c and the other labeled by $\bar{c}$, respectively.

Given T a pp tree for a completion M, we can show that tree T can be reduced to one in simple form. This fact implies that we can obtain from M a completion M' that admits a tree in simple form. Then the completion M' is called *simple completion*.

Lemma 1. *If M_e has a completion that admits a pp tree, then there exists a simple completion M' of M_e.*

Proof. Let T be the pp tree for a completion of M_e and assume that T is not in simple form. We first transform the tree T into a tree T' such that each edge has only one label. Tree T' is obtained by replacing each edge with $k > 1$ labels with a path of k edges each one labeled with a distinct label of the replaced edge e. On the contrary, an edge without labels is contracted, in the sense that the two end nodes of the edge are collapsed to a unique node. Clearly, the above two operations do not change the completion M.

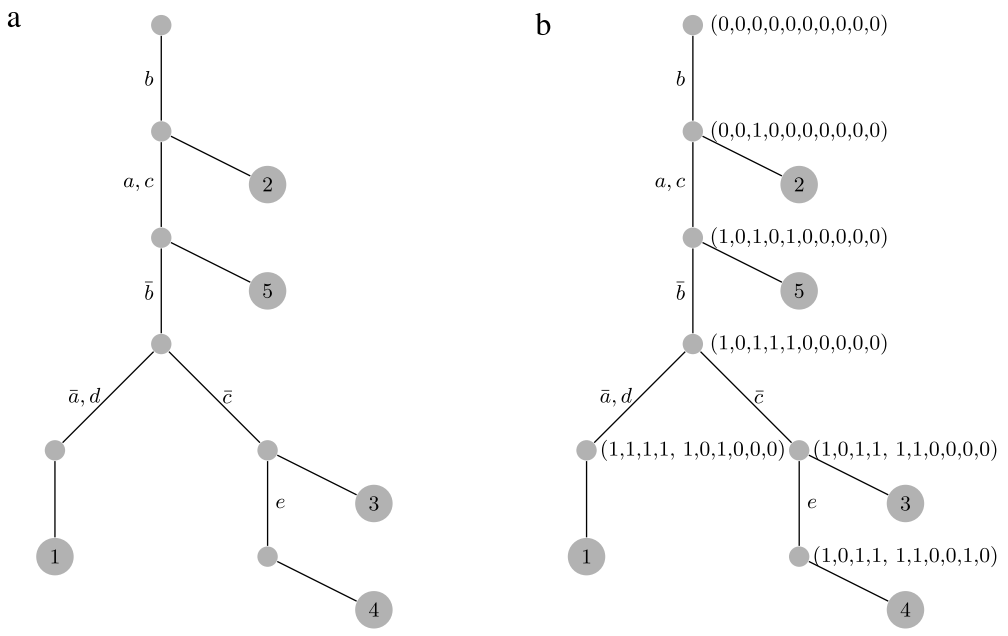


Fig. 5. (a) illustrates a perfect persistent phylogeny T for the matrix of Example 3. (b) reports the vector l_x for each node x of the tree T.

Assume now that there exists two edges e, e' in tree T' that are incident to the same node and are labeled by characters c and $\bar{c}$, respectively. Assume that $e = (x, v)$ and $e' = (v, u)$.

Then we can move tree $T(u)$ as a subtree of node x by removing edge (v, u) and making the root u adjacent with node x. Then change the completion M by replacing all pairs $(1, 1)$ induced by the columns c and $\bar{c}$ and species row in subtree $T(u)$, by the pair $(0, 0)$, obtaining the completion M'. It is easy to verify that T' is the tree representation of the completion M'. We can iterate the above operation and obtain a tree in standard form, as required by the lemma. □

Let G_{RB} be the red–black graph for an extended matrix M_e and let T be the pp tree of a completion of M_e.

We require that a tree T that is in simple form satisfies an additional property that relates the tree T to the red–black graph G_{RB}. Observe that we associate to each node u of T the red–black graph that is obtained by the realization of the positive characters that have value 1 in vector l_u where if a negated character c is free, then its incident red edges are removed from the graph if and only if c has value 1 in vector l_u. We define such a graph, denoted as G_u, the *red–black graph for node u* of T.

Definition 3 (*Standard Property*). Let T be a pp tree in simple form for a completion M_e. Then T is in standard form if and only if the following property holds: for each node u of T such that (u, x) is an edge of the tree T labeled c or $\bar{c}$, all species of tree $T(x)$ are the same species that are in the connected component of graph G_u containing node c.

Lemma 2. *Let M_e be an extended matrix admitting a pp tree. Then, matrix M_e admits a completion that is represented by a tree T in standard form.*

Proof. By Lemma 1 we can assume that the matrix M_e has a simple completion M_c that is represented by a tree T in simple form. To prove the existence of a tree in standard form, we iterate the application of the following procedure to T till it is in standard form. Each iteration of the procedure corresponds to changes to the completion M_c, such that the final computed completion M' is represented by the new tree in standard form. Let u be the node that is closest to the root r of T, such that u does not satisfy the property stated in Definition 3. Eventually, u may be the root of T. Let $\mathcal{C}(c)$ be the connected component of the red–black graph G_u having node c. Since property of Definition 3 is violated then the following two cases are possible. Case 1: there exists a species s' in component $\mathcal{C}(c)$ and s' is not in subtree $T(x)$. Case 2: there exists a set S' of species in the subtree $T(x)$ that are not in $\mathcal{C}(c)$.

In the following we show that Case 1 leads to a contradiction, while in Case 2 we built from tree T a new pp tree T' for a completion of matrix M_e where node u does not verify Case 2 and thus u must satisfy Definition 3.

Case 1.

Assume that there exists a species in component $\mathcal{C}(c)$ that is not in subtree $T(x)$. In the following we show that we obtain a contradiction. If Case 1 holds, then there must exist a species s' that is not in tree $T(x)$ and is connected in component $\mathcal{C}(c)$ (by red or black edges) to a species s of tree $T(x)$ by means of character c_1. More precisely, in component $\mathcal{C}(c)$ s is connected to characters c and c_1, while s' is connected to character c_1. Since s' is not in tree $T(x)$, species s and s' must have a common ancestor that is a node v along the path π_{ru} from the root r to node u. Then character c_1 labels an edge that occur on path π_{ru} and thus v occurs before node u. Consequently, c_1 is realized in graph G_u, thus implying that c_1 is connected only by red edges to species s and s'. This fact implies that both s, s' do not have character c_1 and thus it holds that $\bar{c}_1$ labels an edge that occurs along the path from the root of T to the common ancestor node v of s and s'. Since Definition 3 holds for each node that precedes u, it follows that all species in $T(u)$ are in a connected component $\mathcal{C}(c')$ that contains c_1, where c_1 is connected to all species in $T(u)$ by red edges. Consequently, c_1 is free in G_u and thus all red edges connecting s to s' are removed from the red–black graph G_u, by definition of red–black graph associated to a node, a contradiction with the previous assumption. It follows that species s' cannot be in component $\mathcal{C}(c)$, thus implying that no other species different from the ones in $T(x)$ can be in component $\mathcal{C}(c)$.

Case 2.

Assume that S' is the largest set of species that are in $T(x)$ and are not in the component $\mathcal{C}(c)$. By definition of pp tree, it must be that the set of species S' is in the subtree $T(v)$ for a node v of degree at least 2 that is along the path from node x to a leaf and is the end node of the edge (z, v) labeled $\bar{c}$. In fact, since S' contains species that are not in $\mathcal{C}(c)$, by definition of graph G_{RB} it means that such species do not have character c and consequently they must occur in the subtree induced by the end node of the edge labeled $\bar{c}$.

Now, consider the path π_{xv} from node x to the node v. Let y be the node on path π_{xv} such that given the unique path π_{yv} from node y to v, it consists of only degree 2 nodes. If such y does not exist, then pose $y = z$.

Let T_y be the subtree of T consisting of path π_{yv} and subtree $T(v)$. Clearly, all species s' of T_y are the ones of subtree $T(v)$, by construction of T_y.

Consider subtree T'_y which is obtained from subtree T_y after removing the edge labeled $\bar{c}$ (see Fig. 6). In the following we show that subtree T'_y can be moved as a subtree of node u thus obtaining a new tree T' such that is a pp tree for a completion of matrix M_e. By construction, in tree T' subtree $T(x)$ does not contain the set S' of species that are not in component $\mathcal{C}(c)$ and thus Case 2 does not hold for node u in tree T'. Moreover, by application of the constructive procedure given in the proof of Lemma 1, tree T' can be reduced to a simple form, thus proving what required.

Assume to the contrary that tree T'_y cannot be moved as subtree of node u to obtain a pp tree for a completion of matrix M_e. Observe that a species s in subtree T_y of T has all positive characters of the path from the root r to node x that are not negated along the path π_{xy}. Moreover s has positive characters that occur in π_{xy}. Thus, tree T'_y cannot be moved as subtree of node u in T', if two cases hold: (i) tree T'_y has a species s containing a positive character e that belongs to path π_{xy} or (ii) s does not have a character e that occurs as negated in path π_{xy} and occurs as positive in the path from the root r to node x. Let us consider case (i). Thus assume first that tree T_y has a species s having character e that is on the path π_{xy}. Since y has degree bigger than 2, there exists a species s' such that e is a character of s' and s' occurs at the end of a path leaving node y that is distinct from the path π_{yv} from node y to node v. Moreover, c must be a character in s', since the character $\bar{c}$ occurs after node y along path π_{yv}. Consequently, in the red–black graph G_{RB} species s' is connected to characters c and e, where e is connected to character s. It follows that s is connected to c by means of character e. This situation of the red–black graph G_{RB} is also present in the graph G_u, as both e, c are not realized in graph G_u, being c, e labels of edges that occur after node u. Consequently, s is in the connected component $\mathcal{C}(c)$, thus obtaining a contradiction with the fact that $s \in S'$. Let us consider case (ii). Thus assume now that tree T_y has a species s that does not have character e, where e occurs as positive on the path from the root r to node x, while character $\bar{e}$ occurs on the path π_{xy}. Similarly as above, since y has degree bigger than 2, there exists a species s' occurring at the end of a path leaving node y that is distinct from path π_{yv} and s' contains characters $\bar{e}$ and character c. Clearly, e labels an edge (l_1, v) that occurs before node u and since the standard property holds for each node above u, it follows that s' and s are in the same connected component of graph G_{l_1} having character e and character c. Thus, when character e is realized in graph G_{l_1}, both species s, s' are connected to e by red-edges, thus implying that s is in the same connected component of node c. Observe that this property holds also for graph G_u. In fact, $\bar{e}$ occurs after node u, and thus red-edges incident to node e cannot be removed from graph G_u. Consequently, s is in the connected component $\mathcal{C}(c)$, thus contradicting the assumption that $s \in S'$. Since case (i) and (ii) are not possible, it follows that all species in subtree T'_y do not have (positive or negated) characters of path π_{xy} in the completion of matrix M_e. It follows that tree T'_y can be moved as a subtree of node u to obtain tree T' where T' is a pp tree for the completion M' of matrix M_e obtained by replacing in all rows S' of the completion M_c the entry $(1, 1)$ in columns c and $\bar{c}$ by the pair $(0, 0)$. In fact, species in S' will not have the character c and its negated character in the new tree T' and thus T' is the pp tree for the new completion M'. This observation completes the proof of Case 2. $\square$

We show the first preliminary lemma that allows us to prove the main Theorem of the paper.

Lemma 3. *Let T be a tree in standard form representing the completion M' of an extended matrix M_e. Let G_x be the red–black graph for a node x of T. Then, given C' the set of positive characters having value 1 in vector l_x, the completion of C' in M' is canonical, i.e. it is given by the realization of characters C' in graph G_{RB}. Moreover, a negated character c changes value from 0 to 1 in l_x if and only if it is free in graph G_x. Then edges incident to c are removed from G_x.*

Proof. Let G_{RB} the red–black graph for the extended matrix M_e. We show the lemma by induction on the number k of ones occurring in a node l_x of tree T. Assume first that $k = 1$ and c is the character that has value 1 in vector l_x. Clearly, c is the label of the edge (r, x) where r is the root of tree T and c is a positive character. Observe that the completion of columns c and $\bar{c}$ in M' is a canonical completion, i.e. it is obtained by the realization of node c in graph G_{RB}. In fact, since by Definition 3 of a standard tree the species of tree $T(x)$ are the same ones of the connected component of graph G_{RB} having character c, it holds that they must have value $(1, 1)$ or $(1, 0)$ in the pair of columns $(c, \bar{c})$ of matrix M'.

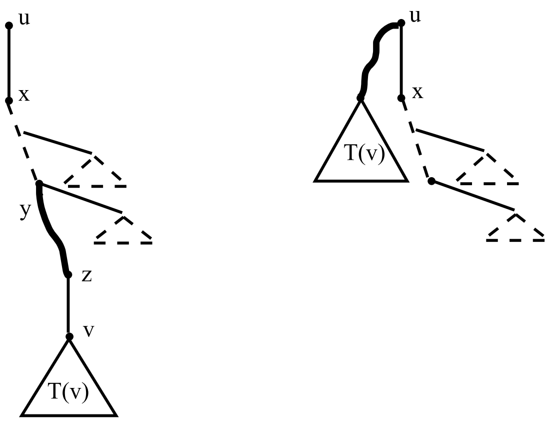


Fig. 6. The figure illustrates Case 2 of Lemma 2, more precisely it represents the operation of moving tree T'_y as subtree of node u. Observe that tree T'_y consists of subtree $T(v)$ and the path π_{yv} where edge (z, v) labeled $\bar{c}$ has been removed.

Now, assume that the number of entries with value 1 in vector l_x is $k > 1$ and the edge (u, x) is incident to node x (assuming that edges are oriented following every path from the root r). Given vector l_u, since the number of entries that are 1 in l_u is less than the number of entries that are 1 in l_x, by induction, the completion of all characters C' that are in l_u is given by the realization of the set C' in graph G_{RB}, thus obtaining the red–black graph G_u for node u. Since T is in a standard form, two cases are possible: (1) edge (u, x) is labeled by a positive character c or (2) a negated character $\bar{c}$.

Let us consider case (1) first. Clearly, character c is non-active in G_u as it has 0 value in vector l_u. By Definition 3 of a standard tree all species in $T(x)$ are the same ones that are in the connected component of graph G_u having character c. Notice that species in $T(x)$ specify the rows where column c and $\bar{c}$ must have the value (1, 1) or (1, 0) in the completion M'. Consequently, the completion of c in matrix M' corresponds to the realization of c in the red–black graph G_u. Thus the completion in matrix M' of the set $C' \cup \{c\}$ of characters in l_x is given by the realization of such characters in graph G_{RB}, thus proving that the lemma holds in this case.

Let us consider case (2). Assume that edge (u, x) is labeled by the negated character $\bar{c}$. Then by induction the completion of all columns for positive characters in l_u is given by their realization in graph G_{RB}. Since edge (u, x) is labeled by a negated character, it follows that the red–black graph G_x is obtained by the realization of positive characters in l_u. Consequently, G_u and G_x are the same graph, thus showing that the completion of positive characters in l_x is given by the realization of positive characters in G_x. Since $\bar{c}$ has value 1 in node l_x and value 0 in node u, we must show that c is free in graph G_u. In fact, all species in $T(x)$ do not have character c, and by Lemma 2 these species are exactly the species that are in the connected component of node c in graph G_u. This fact implies that character c is free in graph G_u.

Now, let us show that character c cannot be free in graph G_v, for v a node that is an ancestor of u. In fact, since tree T is in standard form, it must be that all species in subtree $T(v)$ are in the same connected component of a character c_1 where c_1 labels an edge (v, z). But, since $\bar{c}$ occurs after node z, it follows that there exists a species s in subtree $T(v)$ that has the positive character c and therefore no red edge incident to s a node c is given in graph G_v. This fact implies that c is not free in graph G_v.

This fact completes the proof of the lemma. □

By Lemma 3, the completion of characters in an extended matrix M_e that admits a tree in standard form is a canonical one.

Corollary 1. *Let T be a tree in standard form representing the completion M' of an extended matrix M_e. Then M' is a canonical completion.*

Proof. The result is a direct consequence of the previous Lemma 3. In fact, given a node x of tree T, by induction on the number of 0 that are in vector l_x, it is easy to show by direct application of Lemma 3 that the completion of all characters in tree $T(x)$ is given by their realization in the red–black graph G_x for node x. This fact implies that the completion of all characters in tree T is canonical. □

In the following we can show that a pp tree T represents a successful reduction of the red–black graph.

Lemma 4. *Let G_{RB} be the red–black graph for an extended matrix M_e. If M_e admits a pp tree, then there exists a successful reduction of graph G_{RB}.*

Proof. By Lemma 2, there is a completion M for M_e that admits a tree T in standard form. Let G_x be the red–black graph for node x of T. Then we prove that there exists a successful reduction of G_x, by induction on the number $k \geq 0$ of 0 entries that are left in the root vector of tree $T(x)$. Assume first that $k = 0$, i.e. all entries of the root have value 1. This fact implies that all characters have been realized in the red–black graph. By construction, the red–black graph can only have red edges. By Remark 1, if it is not e-empty it means that it has a Σ-graph. But, this fact implies a contradiction with the existence of the tree T. In fact, the Σ-graph represents the existence in M of the induced forbidden matrix. Assume that a and b are the two characters of the forbidden matrix. Since by Corollary 1, the completion of columns for a and b in M is canonical, i.e. is associated with the realization of a and b in graph G_{RB}, we obtain a contradiction. Thus G_x must reduce to the e-empty graph, i.e. a successful reduction of G_x must exist.

Assume now that the number of entries 0 in vector l_x is equal to k, with $k = m$ and $m > 0$. Then the root x of tree $T(x)$ has an outgoing edge (x, u) that is labeled by a character c which means that the entry of c in vector l_u is 1, while it is 0 in l_x. Two distinct cases must be considered (1) either c is positive or (2) c is negated.

Case 1. Assume c is positive. Since vector l_u has one zero less than the root of tree T, that is $k = m - 1$. By induction it holds that the red–black graph G_u reduces to the e-empty graph. Since graph G_x differs from graph G_u by the realization of c, it follows that G_x reduces to the e-empty graph by the realization of c and non-active characters in G_u.

Case 2. If c is negated, by Lemma 3 the red–black graph G_x for node x is equal to the red–black graph G_u and c is free in G_u. Since vector l_u has a 0 entry less than the number of 0 entries in l_x, by induction G_u reduces to the e-empty graph and consequently also G_x reduces to the e-empty graph. Thus, both cases prove that there exists a successful reduction of graph G_x. □

The previous Lemma 4 provides the proof of the *Only if* direction of Theorem 2.

4.2. Building a pp tree from a successful reduction

In this section we complete the proof of Theorem 2 by showing that a successful reduction provides a completion for a matrix Me admitting a pp tree.

Theorem 3. *Let M_e an extended matrix. If there exists a successful reduction of the graph G_{RB}, then M_e admits a perfect phylogeny.*

Proof. Let M be the completion of matrix M_e obtained from a successful reduction of the red–black graph for M_e. In the following we show that M has no forbidden matrix. This fact will prove that M admits a pp tree. Let G_R be the red–black obtained after the realization of the characters of the successful reduction. Assume to the contrary that M has two characters c, c_1 that induce a forbidden matrix F, and let s_1, s_2, s_3 be the species of M having the configuration (1, 1), (1, 0) and (0, 1) in F, respectively.

We must consider the following cases.

Case 1. Assume that the forbidden matrix is induced by two negated characters. This fact implies that G_R will have an induced Σ-graph, thus contradicting the fact that G_R is e-empty.

Case 2. Assume that the forbidden matrix is induced by two positive characters.

Then c, c_1 must be in the same connected component of the red–black graph before their realization, as species s_1 is connected to both characters (we do not know if s_1 is connected by a black or red edge). Now, the realization of c produces the red edge (c, s_3), since $M_e[s_3, c] =?$. Then $M[s_3, c] = 1$ in the completion M, a contradiction with the assumption.

Case 3. Assume that the forbidden matrix is induced by a positive and negated character.

Assume that c is the negated character. Since c and c_1 share a species in the forbidden matrix F, it means that c and c_1 are in the same connected component of the red–black graph when c_1 and c are realized in the graph. Since (0, 1) is given in the matrix F in row s_2, by definition of realization of c_1, it must be that $M[s_2, c_1] = 1$ and $M[s_2, \bar{c_1}] = 1$ as $M_e[s_2, c_1] = 0$. But this is a contradiction. □

Example 4. Let us consider the 5×5 input matrix M_e shown in Fig. 2(b). In the following we detail the realization of characters of a successful reduction $r = \langle b, a, c, d, e\rangle$ of graph G_{RB}. First of all, observe that Fig. 7(a) illustrates the initial red–black graph G_{RB}. In the following we say that a species is realized when it is a singleton in the red–black graph.

First character b is realized (Fig. 7(b)) and then the species 2 is realized. Then character a is realized (Fig. 7(c)). Note that we do not add any edge incident to species 2, since it has been already realized. Then character c is realized (Fig. 7(d)). and species 5 is realized. Moreover, character b is free since it is connected by red edges to all species of the same connected component of b (Fig. 7(e)). Since character a is connected to all species of its connected component with red edges, a is free. The same fact holds for character c. At this point, species 3 is a singleton, so it is realized (Fig. 7(f)). Then character d is realized (Fig. 7(g)) and species 1 is realized. Finally, character e is realized and so species 4 is realized. At this point (Fig. 7(h)), G_{RB} does not contain any edge.

Notice that the successful reduction provides the completion that is given in Fig. 2(c).

Observe that a successful reduction of the red–black graph provides the main steps of the process of building a pp tree. More precisely, the realization of a single character leads to an operation in the pp tree, which is either adding an edge labeled by a character or adding a leaf node corresponding to a species node.

5. An exact algorithm for the P-PP problem

In this section we propose an algorithm for the P-PP problem that is based on Theorems 1 and 2. The algorithm reduces an instance M of P-PP to an instance M_e of the IP-PP problem. By the proof of Theorem 1 M_e admits a pp tree T if and only if T is a solution of matrix M. Then by the characterization given by Theorem 2, M_e admits a pp tree T if and only if there exists

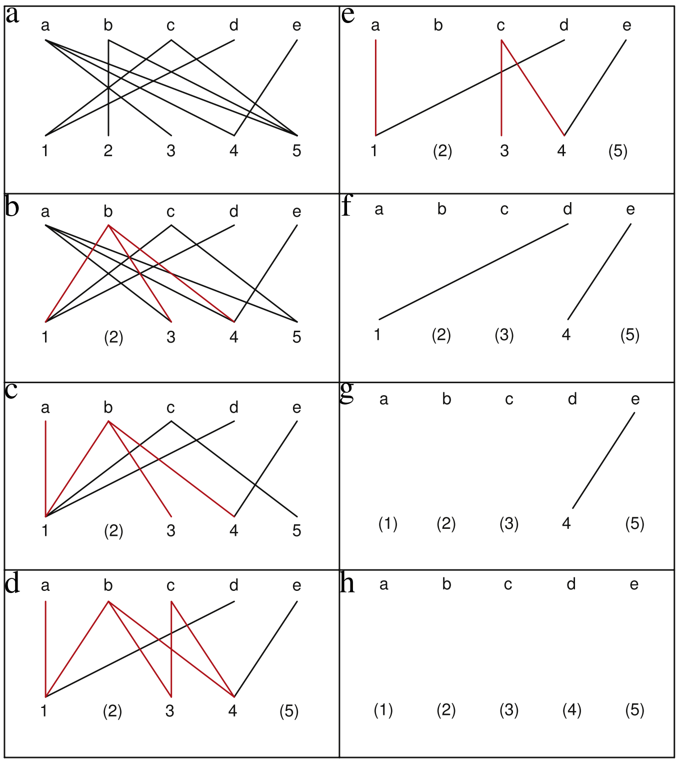


Fig. 7. The main steps of the successful realization of graph G_{RB} described in Example 4. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

a successful reduction of the red–black graph for M_e. We design an algorithm, called **Decide-pp** that builds a decision tree that explores all permutations of the set C of characters of M_e in order to find one that is a successful reduction, if it exists. More precisely, each edge of the decision tree represents a character and each path of the tree from the root to a leaf is a distinct permutation of the set C. The algorithm works in a branch and bound like manner, in the sense that if a branch of the decision tree ending in node x does not lead to a solution, then the decision tree below x is discarded. More precisely, each branch ending in node x gives a partial permutation π that consists of all characters labeling the path from root r to node x. A partial completion M_π is computed by realizing characters provided by the partial permutation π. Whenever M_π contains the forbidden matrix, then the branch ending in x does not lead to a solution, and x is labeled as a *fail* node.

Below we give a general procedure for the realization of a single character in the red–black graph built during the realization of characters.

Procedure Realize(c, M',G_{RB} **)**

Input: a character c, a partial completion M' and a red–black graph G_{RB}

Output: character c is realized in graph G_{RB} and c is completed in M'

– Step 1. Mark character c as *active*.
– Step 2. Compute the connected component $\mathcal{C}$ of graph G_{RB} containing character c
– Step 3. Realize character c:
  - add red edges connecting character c to all species nodes s' in $\mathcal{C}$ such that c is not connected to s',
  - remove all black edges (c, s) in $\mathcal{C}$,
  - update the graph G_{RB} by removing all red-edges outgoing from a character c' of G_{RB} that is *free*.
– Step 4. Complete the columns of characters c and $\bar{c}$ in M' as follows: in every row s such that (c, s) is a red edge in G_{RB}, , replace the pairs $(?, ?)$ by $(1, 1)$, otherwise by $(0, 0)$.

Let us now describe the main algorithm that consists of **Decide-pp(**M_e, r, $\{r\}$**)** call, where r is the root of the decision tree, and initially the visited tree consists of set $\{r\}$.

Algorithm Decide-pp(M', x, T**)**

Input: a partial depth-first visit tree T of the decision tree $\mathcal{T}$ and a leaf node x of $\mathcal{T}$, a partial completion M' obtained by the realization of the characters labeling a path π from r to node x

Output: the tree T extended with the depth-first visit of $\mathcal{T}$ from node x. The procedure eventually outputs a successful reduction or a complete visit of $\mathcal{T}$ that fails to find such a successful reduction.

Table 1
Summary table.

n × m	Total time (s)	Average time (s)	No p-pp	Total conflicts	Average conflicts
50 × 15	32.323	0.646	6	236	4.72
100 × 15	194.625	3.893	4	175	3.5
200 × 15	43.212	0.864	3	147	2.94
500 × 15	889.433	17.789	7	219	4.38

Table 2
Average execution time in seconds to solve 10 matrices with a single conflict.

50 × 15	100 × 15	200 × 15	500 × 15
0.015	0.031	0.047	0.093

– Step 1. if the edge incident to node x is labeled c, then **Realize(**c, M', G_{RB} **)**.
If the matrix M' has a forbidden matrix, then label x as a *fail* node. Otherwise, if x is a leaf node, then mark x as a successful node and output the permutation labeling the path from the root r of tree T and leaf node x.
– Step 2. For each node x_i that is a child of node x in tree $\mathcal{T}$ and is labeled by a non-active character, apply **Decide-pp**(M', x_i, $T \cup \{x_i\}$).

5.1. *Complexity*

The worst case time of the algorithm is achieved when the whole permutation tree $\mathcal{T}$ is visited. Generating all permutations requires $m!$ time. Each time a character c is realized all species of the matrix are examined in the worst scenario. Moreover, the connected components of the red–black graph must be updated each time. Thus, the realization of m characters has a time complexity that is $O(n \cdot m) \times O(g(n, m))$, where $g(n, m)$ is the cost of maintaining connected components of a graph whose size is $O(n^2 \times m)$. Since red edges are added to the graph, in the worst scenario each species will have $O(n)$ incident red-edges.

A trivial implementation of the connected component update would require $\alpha(n^2 \cdot m)$ each time a character is realized, α being the inverse of the Ackerman function. More efficient implementations can be obtained by using dynamic algorithms [10]. Thus totally, the time is $O(m! \cdot n \cdot m \cdot \alpha(n^2 \cdot m))$. This time improves over the complexity of a trivial algorithm that tries all possible substitutions for the pairs (?, ?), and would require a worst time that is exponential in both the number of species and columns of the input matrix.

6. An experimental analysis

In this section we discuss an implementation of the **Decide-pp** algorithm. In order to optimize the time complexity, an ad hoc iterative version of the algorithm has been implemented.

We have implemented and tested the **Decide-pp** algorithm over simulated data produced by the tool *ms* by Hudson [11]. The test set consisted in a random data set of matrices generated with a recombination rate of 1 over 15. The main goal of the experimental analysis has been to test the applicability of the algorithm to matrices with different complexities in terms of size and number of conflicts (i.e. edges) in the conflict graph.

We have implemented the algorithm in C++ and the experiments have been run on a standard windows workstation with 4 GB of main memory.

A preliminary experiment has been done to evaluate the performance of the algorithm with respect to specific parameters related to the complexity of the input matrix under mutation events. Table 1 reports the time computation to solve sets of 50 matrices for each dimension (50, 15), (100, 15), (200, 15), and (500, 15) with a recombination rate 1 over 15. The table has additional entries to specify the average time to solve a single matrix (calculated as the ratio between the total time and the number of considered matrices), the number of matrices that do not admit a p-pp tree, the total number of conflicts in the conflict graphs of the matrices of each set, and the average number of conflicts for each matrix of the set. Notice that conflicts are measured as the number of edges in graph G_c. Each considered matrix has a conflict graph G_c that consists of a single non-trivial component. The sets contain only matrices that are solved within 5 min. Clearly, the number of unsolved matrices increases with the size of the input matrices.

Observe that in general the average running time of the algorithm increases with the size of the input matrix but also with the number of conflicts that are present in the conflict graph. This last behavior is suggested by the results reported in Table 2 .

Another experiment has been done with 10 matrices of the same size 50 × 15 and different number of edges in the conflict graph. The average time was 0.015, 0.031 and 0.051, respectively for the case of 1, 5 and 10 conflicts.

In order to test the performance of the algorithm for large matrices in terms of number of species we have processed a matrix of size 1000 × 15 with a conflict graph having 9 conflicts (edges). It took 35.5 s to find the solution to the matrix.

7. Conclusions

In this paper, we formalize the problem of reconstructing a Persistent Perfect Phylogeny over binary values (P-PP problem); the problem generalizes the classical directed perfect phylogeny by allowing each character to change from 1 to 0 at most once in the tree. Then, we show that solving the problem P-PP reduces to a graph-reduction problem. Based on this combinatorial interpretation of the problem of the persistent perfect phylogeny problem, we give an exact algorithm for the P-PP problem that has a worst time complexity that is exponential in the number of characters, but polynomial in the number of species. An experimental analysis of the implemented algorithm for the P-PP problem shows the applicability of the model to incorporate biological complexity due to back mutation events in the data.

Acknowledgments

The first author, PB would like to thank Russel Schwartz for indicating applications of the model. Moreover, the authors would like to thank Gianluca Della Vedova for comments on a preliminary version of the paper and Francesca Scoglio for technical support in the experimental analysis. All authors are grateful to the anonymous referees for helpful suggestions on the presentation of the paper.

References

[1] P. Bonizzoni, A linear time algorithm for the Perfect Phylogeny Haplotype problem, Algorithmica 48 (3) (2007) 267–285.
[2] J. Camin, R. Sokal, A method for deducting branching sequences in phylogeny, Evolution 19 (1965) 311–326.
[3] T.H. Cormen, C. Stein, R.L. Rivest, C.E. Leiserson, Introduction to Algorithms, McGraw-Hill Higher Education, 2001.
[4] Z. Ding, V. Filkov, D. Gusfield, A linear time algorithm for Perfect Phylogeny Haplotyping (pph) problem, Journal of Computational Biology 13 (2) (2006) 522–553.
[5] E. Eskin, E. Halperin, R. Karp, Efficient reconstruction of haplotype structure via perfect phylogeny, Journal of Bioinformatics and Computational Biology 1 (2003) 1–20.
[6] J. Felsenstein, Inferring Phylogenies, Sinauer Associates, 2004.
[7] D. Fernandez-Baca, in: D.Z. Du, X. Cheng (Eds.), The Perfect Phylogeny Problem, Kluwer Academic Publishers, 2000, Steiner Trees in Industries.
[8] D. Gusfield, Efficient algorithms for inferring evolutionary trees, Networks (1991) 19–28.
[9] D. Gusfield, Haplotyping as perfect phylogeny: conceptual framework and efficient solutions, in: Proc. 6th Annual Conference on Research in Computational Molecular Biology, RECOMB 2002, 2002, pp. 166–175.
[10] J. Holm, K. de Lichtenberg, M. Thorup, Poly-logarithmic deterministic fully-dynamic algorithms for connectivity, minimum spanning tree, 2-edge, and biconnectivity, J. ACM 48 (4) (2001) 723–760.
[11] R.R. Hudson, Generating samples under a wright-fisher neutral model of 31 genetic variation, Bioinformatics 18 (2) (2002) 337–338.
[12] I. Peer, T. Pupko, R. Shamir, R. Sharan, Incomplete directed perfect phylogeny, Siam Journal on Computing 33 (3) (2004) 590–607.
[13] T. Przytycka, G. Davis, N. Song, D. Durand, Graph theoretical insights into dollo parsimony and evolution of multidomain proteins, Journal of Computational Biology 13 (2) (2006) 351–363.
[14] T.M. Przytycka, An important connection between network motifs and parsimony models, in: Proc. 10th Annual Conference on Research in Computational Molecular Biology, RECOMB 2006, 2006, pp. 321–335.
[15] R. Satya, A. Murkherjee, G. Alexe, L. Parida, G. Bhanot, Constructing near-perfect phylogenies with multiple homoplasy events, Bioinformatics 22 (14) (2006) 514–522.
[16] V. Satya, A. Mukherjee, An optimal algorithms for perfect phylogeny haplotyping, Journal of Computational Biology 13 (4) (2006) 897–928.
[17] J.C. Setubal, J. Meidanis, Introduction to Computational Molecular Biology, PWS Publishing Company, 1997.
[18] S. Sridhar, k. Dhamdhere, G.E. Blelloch, E. Halperin, R. Ravi, R. Schwartz, Algorithms for efficient near-perfect phylogenetic tree reconstruction in theory and practice, IEEE/ACM Transections on Computational Biology and Bioinformatics 4 (2007) 561–571.
[19] J. Zheng, I.B. Rogozin, E.V. Koonin, T.M. Przytycka, Support for the coelomata clade of animals from a rigorous analysis of the pattern of intron conservation, Mol. Biol. Evol. 24 (11) (2007) 2583–2592.