On the Complexity of SNP Block Partitioning Under the Perfect Phylogeny Model

Jens Gramm[1] Tzvika Hartman[2] Till Nierhoff[3]
Roded Sharan[4] Till Tantau[5]

[1]Universität Tübingen, Germany
[2]Bar-Ilan University, Ramat-Gan, Israel
[3]International Computer Science Institute, Berkeley, USA
[4]Tel-Aviv University, Israel
[5]Universität zu Lübeck, Germany

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Outline

1. **Introduction**
   - The Model and the Problem
   - The Integrated Approach
2. **Bad News: Hardness Results**
   - Hardness of PP-Partitioning of Haplotype Matrices
   - Hardness of PP-Partitioning of Genotype Matrices
3. **Good News: Tractability Results**
   - Perfect Path Phylogenies
   - Tractability of PPP-Partitioning of Genotype Matrices

What is haplotyping and why is it important?

You hopefully know this after the previous three talks. . .

General formalization of haplotyping.

Inputs

- A genotype matrix G.
- The rows of the matrix are taxa / individuals.
- The columns of the matrix are SNP sites / characters.

Outputs

- A haplotype matrix H.
- Pairs of rows in H explain the rows of G.
- The haplotypes in H are biologically plausible.

Our formalization of haplotyping.

Inputs

- A genotype matrix G.
- The rows of the matrix are individuals / taxa.
- The columns of the matrix are SNP sites / characters.
- The problem is directed: one haplotype is known.
- The input is biallelic: there are only two homozygous states (0 and 1) and one heterozygous state (2).

Outputs

- A haplotype matrix H.
- Pairs of rows in H explain the rows of G.
- The haplotypes in H form a perfect phylogeny.

We can do perfect phylogeny haplotyping efficiently, but . . .

1. Data may be missing.
   - This makes the problem NP-complete . . .
   - . . . even for very restricted cases.

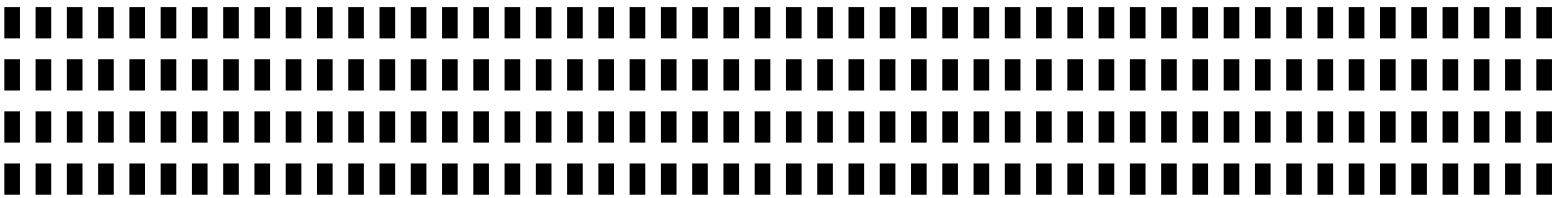
   Solutions:
   - Additional assumption like the rich data hypothesis.
2. No perfect phylogeny is possible.
   - This can be caused by chromosomal crossing-over effects.
   - This can be caused by incorrect data.
   - This can be caused by multiple mutations at the same sites.

   Solutions:
   - Look for phylogenetic networks.
   - Correct data.
   - Find blocks where a perfect phylogeny is possible.

How blocks help in perfect phylogeny haplotyping.

1. Partition the site set into overlapping contiguous blocks.
2. Compute a perfect phylogeny for each block and combine them.
3. Use dynamic programming for finding the partition.

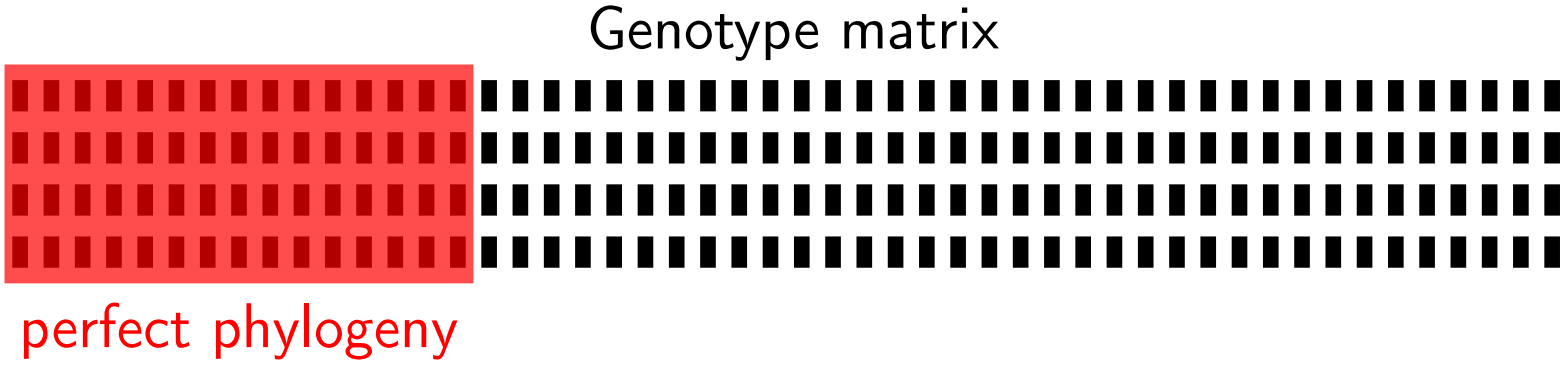
Genotype matrix



no perfect phylogeny

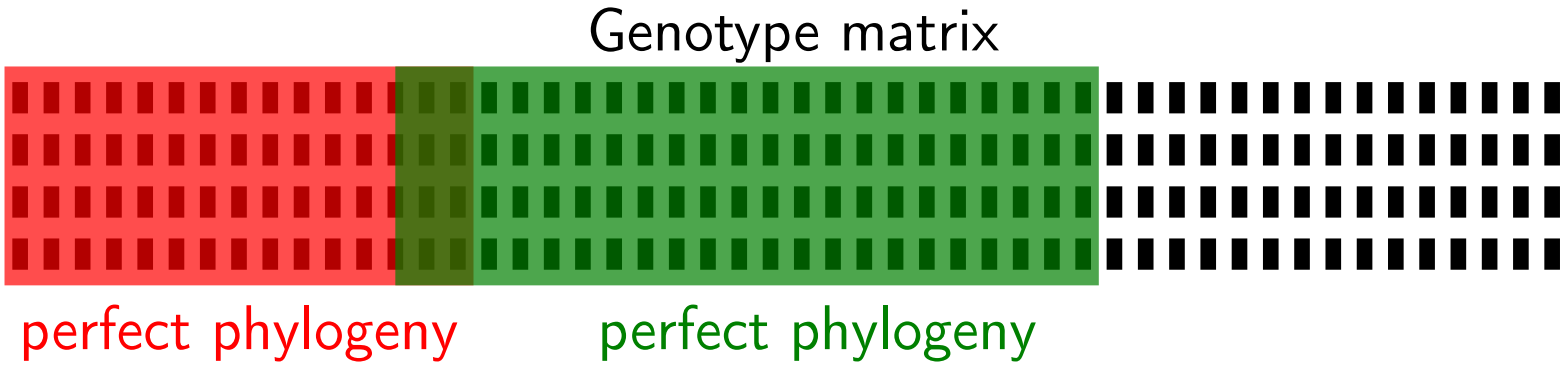
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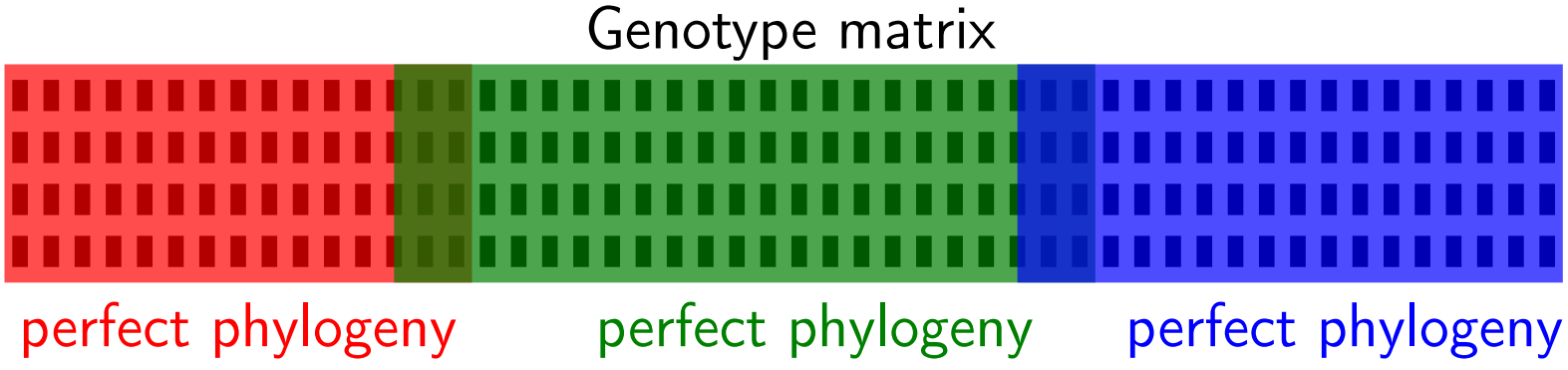
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How blocks help in perfect phylogeny haplotyping.

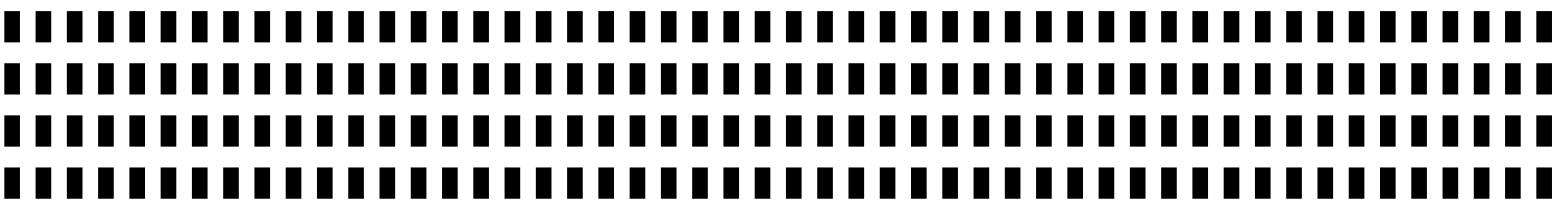
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3. Use dynamic programming for finding the partition.



Objective of the integrated approach.

1. Partition the site set into noncontiguous blocks.
2. Compute a perfect phylogeny for each block and combine them.
3. Compute partition while computing perfect phylogenies.

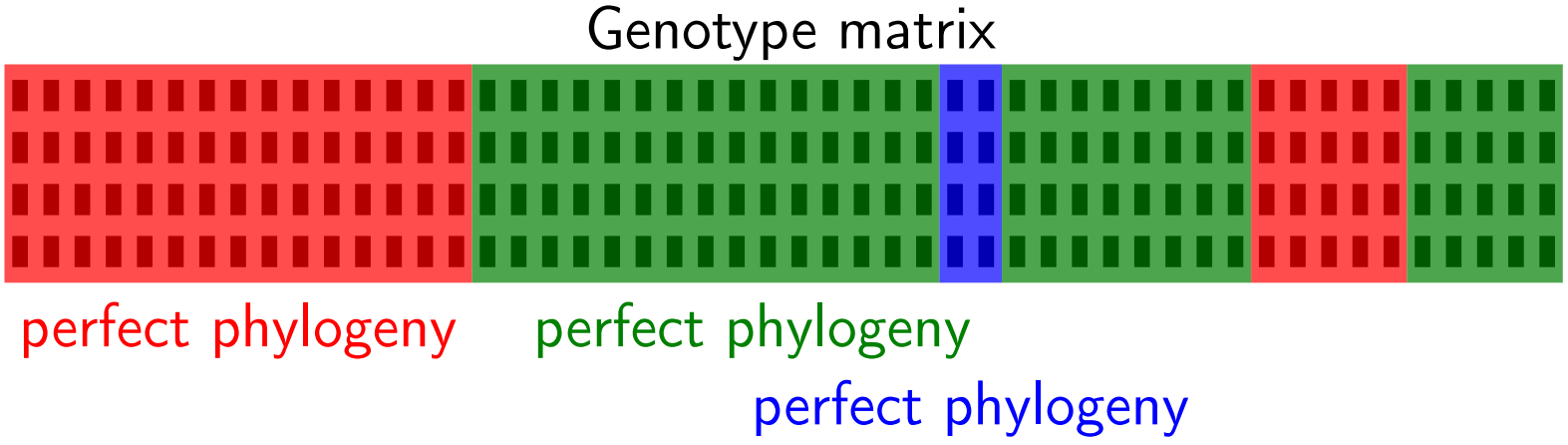
Genotype matrix



no perfect phylogeny

Objective of the integrated approach.

1. Partition the site set into noncontiguous blocks.
2. Compute a perfect phylogeny for each block and combine them.
3. Compute partition while computing perfect phylogenies.



The formal computational problem.

We are interested in the computational complexity of the function χ_{PP}:

- It gets genotype matrices as input.
- It maps them to a number k.
- This number is minimal such that the sites can be covered by k sets, each admitting a perfect phylogeny.
  (We call this a pp-partition.)

Finding pp-partitions of haplotype matrices.

We start with a special case:

- The inputs M are already haplotype matrices.
- The inputs M do not allow a perfect phylogeny.
- What is $\chi_{\mathrm{PP}}(M)$?

Example

$$M: \quad \begin{matrix} 0 & 0 & 0 & 1 \\ 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 \\ 1 & 0 & 0 & 0 \\ 0 & 1 & 0 & 1 \\ 1 & 1 & 0 & 0 \\ 0 & 0 & 1 & 0 \\ 1 & 0 & 1 & 0 \end{matrix}$$

No perfect phylogeny is possible.

Finding pp-partitions of haplotype matrices.

We start with a special case:

- The inputs M are already haplotype matrices.
- The inputs M do not allow a perfect phylogeny.
- What is $\chi_{\text{PP}}(M)$?

Example

M:

0	0	0	1
0	1	0	0
1	0	0	0
0	1	0	0
1	0	0	0
0	1	0	1
1	1	0	0
0	0	1	0
1	0	1	0

Perfect phylogeny
Perfect phylogeny
$\chi_{\text{PP}}(M) = 2$.

Bad news about pp-partitions of haplotype matrices.

Theorem

Finding optimal pp-partition of haplotype matrices is equivalent to finding optimal graph colorings.

Proof sketch for first direction.

1. Let G be a graph.
2. Build a matrix with a column for each vertex of G.
3. For each edge of G add four rows inducing the submatrix $\begin{pmatrix} 0 & 0 \\ 0 & 1 \\ 1 & 0 \\ 1 & 1 \end{pmatrix}$.
4. The submatrix enforces that the columns lie in different perfect phylogenies. □

Implications for pp-partitions of haplotype matrices.

Corollary

If $\chi_{\mathsf{PP}}(M) = 2$ for a haplotype matrix M, we can find an optimal pp-partition in polynomial time.

Corollary

Computing χ_{PP} for haplotype matrices is

- NP-*hard*,
- *not fixed-parameter tractable, unless* $\mathsf{P} = \mathsf{NP}$,
- *very hard to approximate.*

Finding pp-partitions of genotype matrices.

Now comes the general case:

- The inputs M are genotype matrices.
- The inputs M do not allow a perfect phylogeny.
- What is $\chi_{\text{PP}}(M)$?

Example

$$M: \begin{matrix} 2 & 2 & 2 & 2 \\ 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 \\ 0 & 0 & 1 & 0 \\ 0 & 2 & 2 & 0 \\ 1 & 1 & 0 & 0 \end{matrix}$$

No perfect phylogeny is possible.

Finding pp-partitions of genotype matrices.

Now comes the general case:

- The inputs M are genotype matrices.
- The inputs M do not allow a perfect phylogeny.
- What is $\chi_{\mathrm{PP}}(M)$?

Example

M:

2	2	2	2
1	0	0	0
0	0	0	1
0	0	1	0
0	2	2	0
1	1	0	0

Perfect phylogeny

Perfect phylogeny

$\chi_{\mathrm{PP}}(M) = 2.$

Bad news about pp-partitions of haplotype matrices.

Theorem

Finding optimal pp-partition of genotype matrices is at least as hard as finding optimal colorings of 3-uniform hypergraphs.

Proof sketch.

1. Let G be a 3-uniform hypergraph.
2. Build a matrix with a column for each vertex of G.
3. For each hyperedge of G add four rows inducing the submatrix $\begin{pmatrix} 2 & 2 & 2 \\ 1 & 0 & 0 \\ 0 & 1 & 0 \\ 0 & 0 & 1 \end{pmatrix}$.
4. The submatrix enforces that the three columns do not all lie in the same perfect phylogeny. □

Implications for pp-partitions of genotype matrices.

Corollary

Even if we know $\chi_{\mathsf{PP}}(M) = 2$ *for a genotype matrix* M*, finding a pp-partition of any fixed size is still*

- NP-*hard*,
- *not fixed-parameter tractable, unless* $\mathsf{P} = \mathsf{NP}$,
- *very hard to approximate.*

Automatic optimal pp-partitioning is hopeless, but...

- The hardness results are worst-case results for highly artificial inputs.
- Real biological data might have special properties that make the problem tractable.
- One such property is that perfect phylogenies are often perfect path phylogenies:
  In HapMap data, in 70% of the blocks where a perfect phylogeny is possible a perfect path phylogeny is also possible.

Example of a perfect path phylogeny.

Genotype matrix

G:

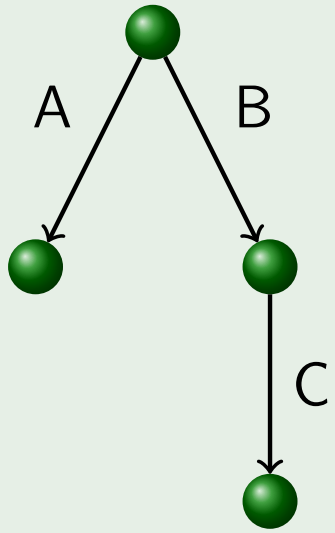
A	B	C
2	2	2
0	2	0
2	0	0
0	2	2

Haplotype matrix

H:

A	B	C
1	0	0
0	1	1
0	0	0
0	1	0
0	0	0
1	0	0
0	0	0
0	1	1

Perfect path phylogeny



The modified formal computational problem.

We are interested in the computational complexity of the function χ_{PPP}:

- It gets genotype matrices as input.
- It maps them to a number k.
- This number is minimal such that the sites can be covered by k sets, each admitting a perfect path phylogeny. (We call this a ppp-partition.)

Good news about ppp-partitions of genotype matrices.

Theorem

Optimal ppp-partitions of genotype matrices can be computed in polynomial time.

Algorithm

1. Build the following partial order:
   - Can one column be above the other in a phylogeny?
   - Can the columns be the two children of the root of a perfect path phylogeny?
2. Cover the partial order with as few compatible chain pairs as possible.
   For this, a maximal matching in a special graph needs to be computed.

▸ The algorithm in action

Summary

- Finding optimal pp-partitions is intractable.
- It is even intractable to find a pp-partition when just two noncontiguous blocks are known to suffice.
- For perfect path phylogenies, optimal partitions can be computed in polynomial time.

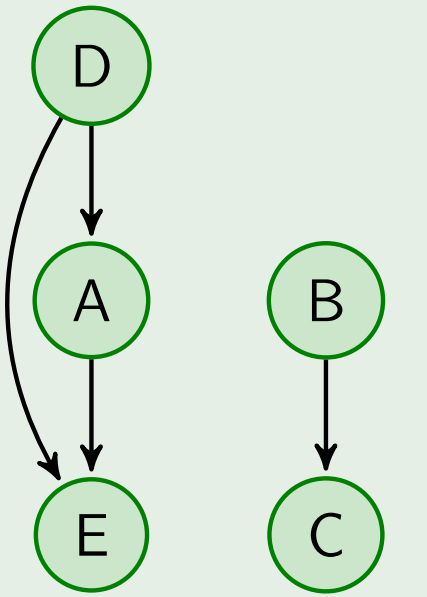
The algorithm in action.

Computation of the partial order.

Genotype matrix

	A	B	C	D	E
	2	2	2	2	2
G:	0	1	2	1	0
	1	0	0	1	2
	0	2	2	0	0

Partial order



Partial order: $\longrightarrow$

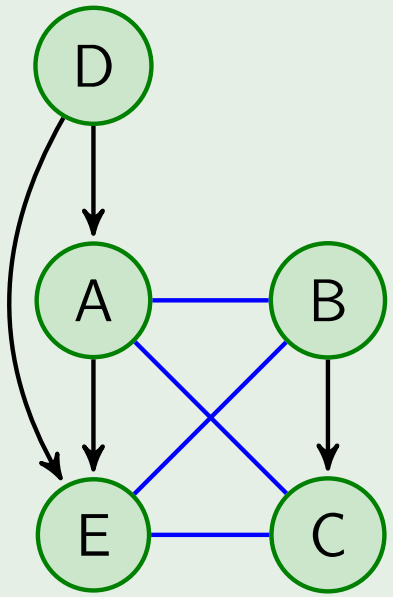
The algorithm in action.

Computation of the partial order.

Genotype matrix

	A	B	C	D	E
	2	2	2	2	2
G:	0	1	2	1	0
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Partial order



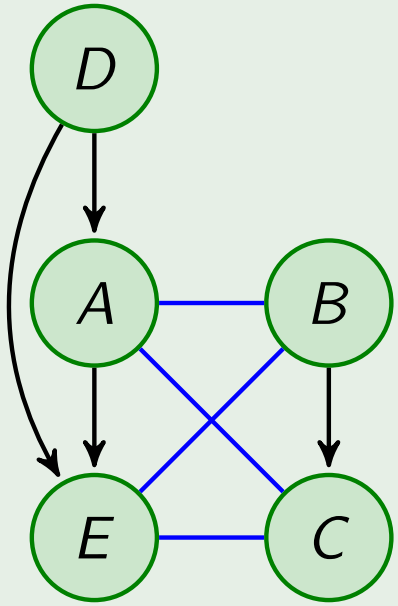
Partial order: $\longrightarrow$

Compatible as children of root: ——

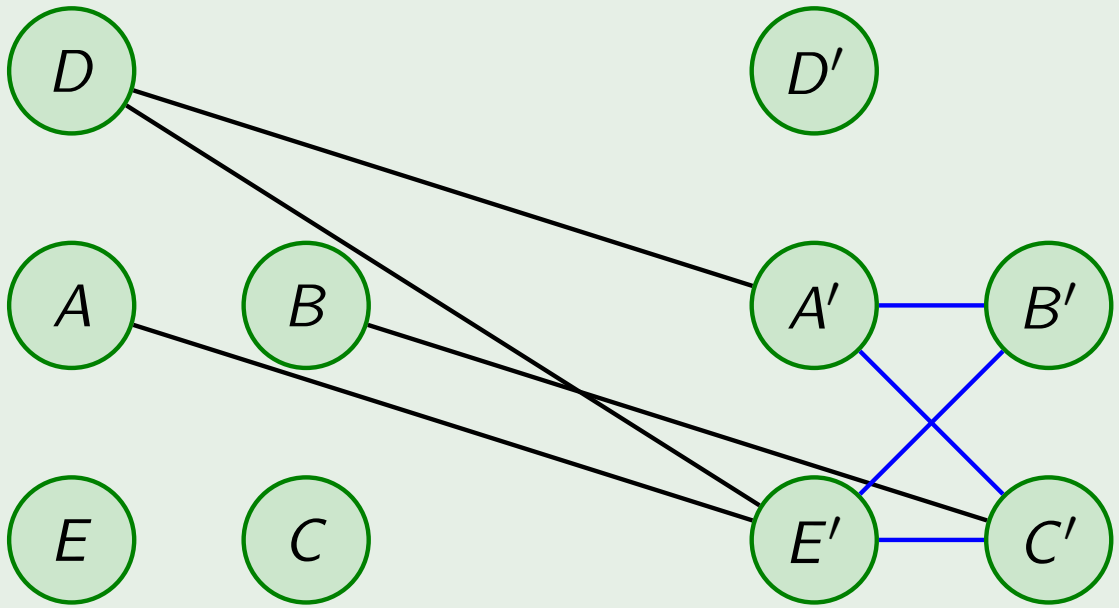
The algorithm in action.

The matching in the special graph.

Partial order



Matching graph

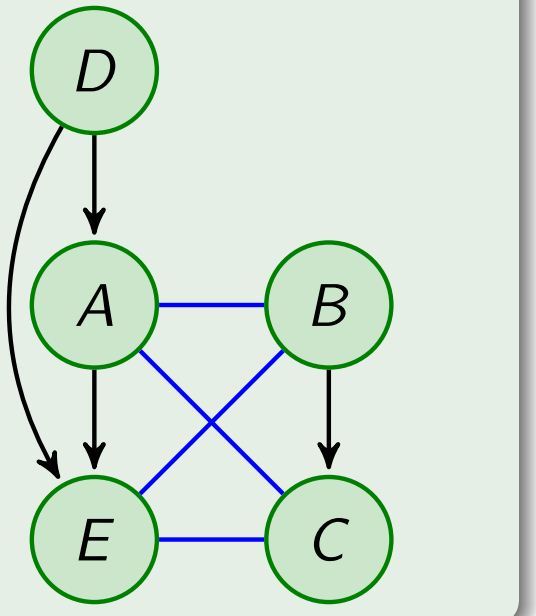


Return

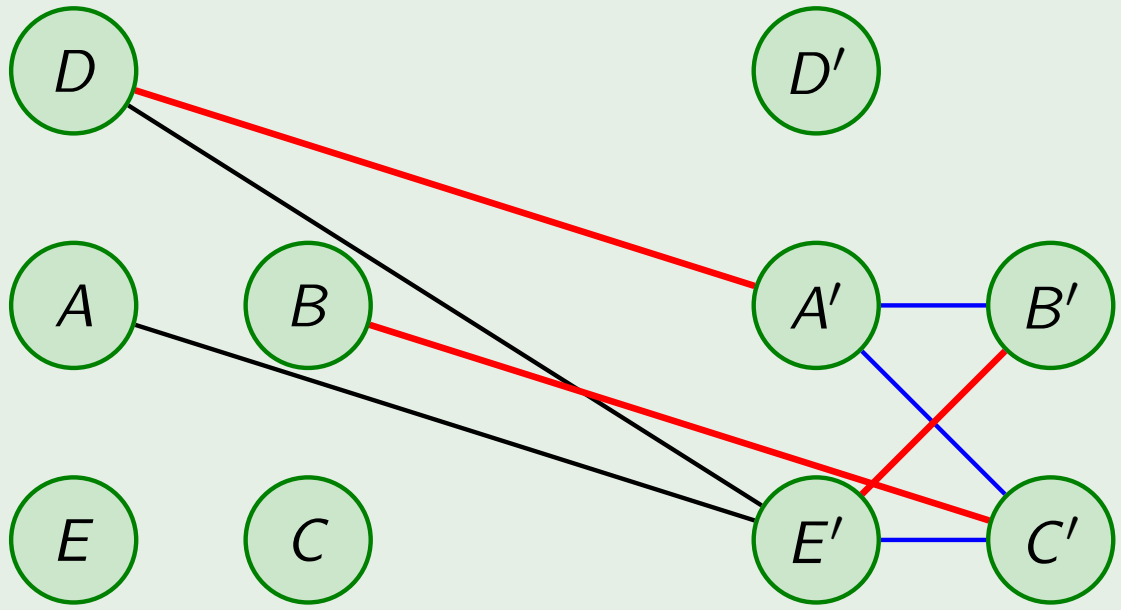
The algorithm in action.

The matching in the special graph.

Partial order



Matching graph



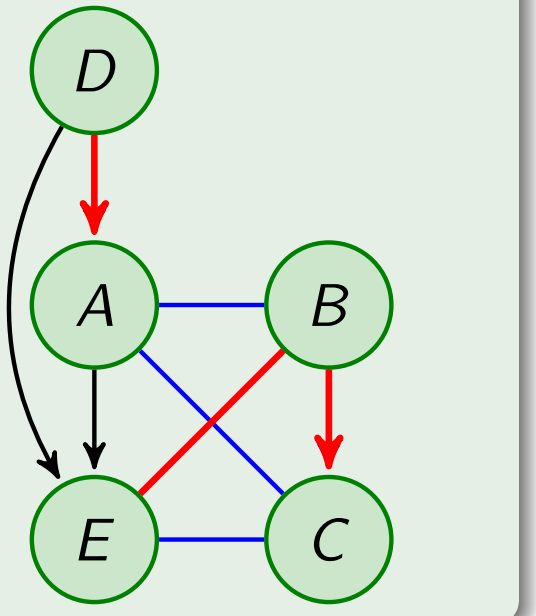
A maximal matching in the matching graph

Return

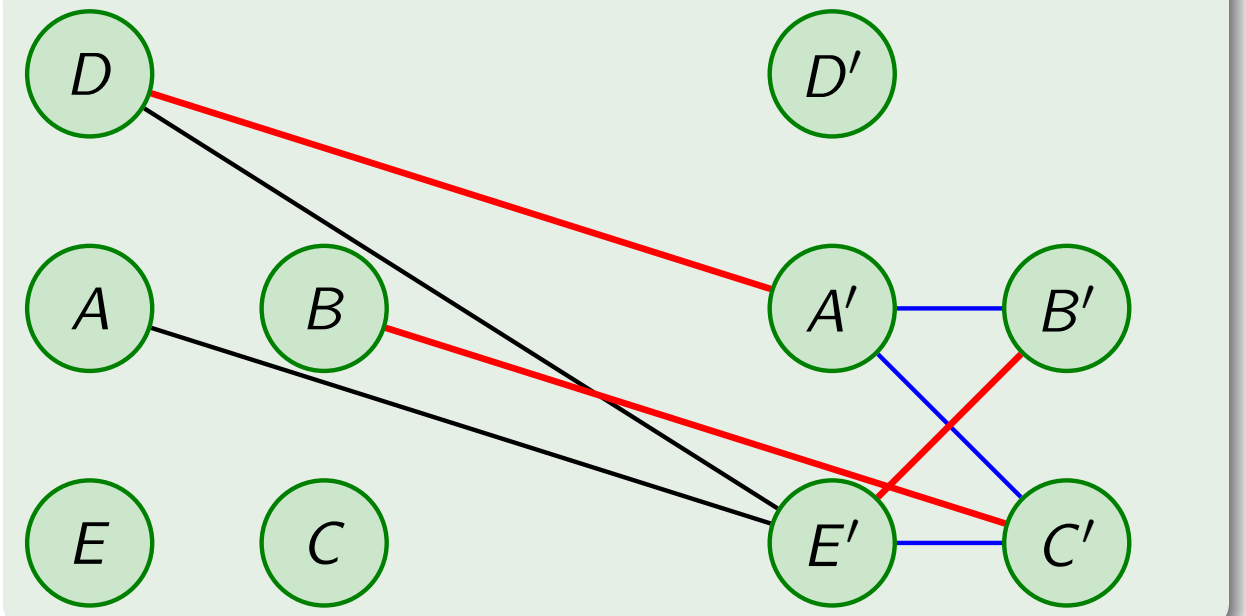
The algorithm in action.

The matching in the special graph.

Partial order



Matching graph



A maximal matching in the matching graph induces perfect path phylogenies.

◂ Return