

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

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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.

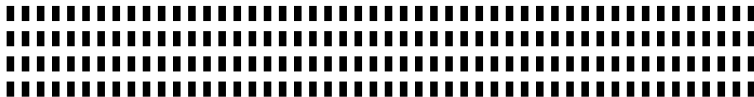
Solutions:

- 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.

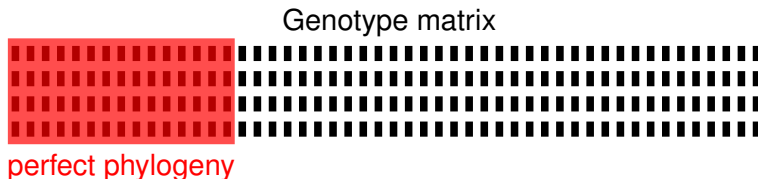
Genotype matrix



no perfect phylogeny

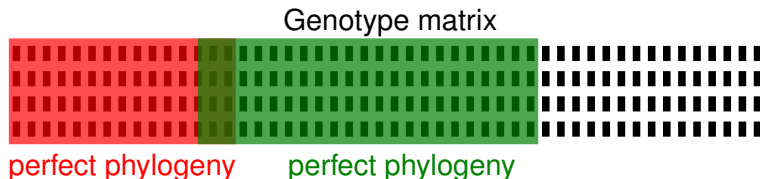
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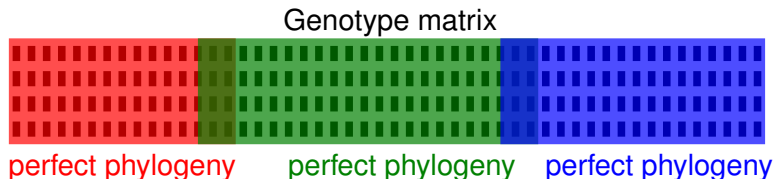
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How blocks help in perfect phylogeny haplotyping.

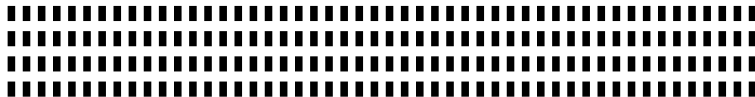
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- 3 Use dynamic programming for finding the partition.



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.**

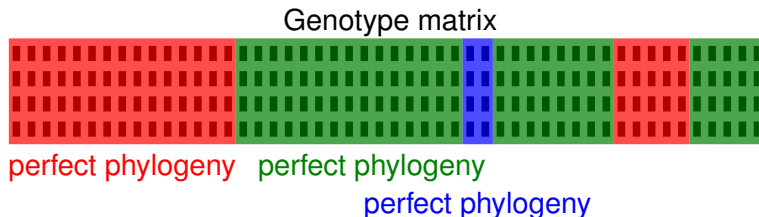
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Objective of the integrated approach.

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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 $\chi_{PP}(M)$?

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

No perfect phylogeny is possible.

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0	0	1	0
1	0	1	0

Perfect phylogeny

Perfect phylogeny

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

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 $\chi_{PP}(M) = 2$ 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 $P = NP$,*
- *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 $\chi_{PP}(M)$?

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

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 $\chi_{PP}(M)$?

Example

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

Perfect phylogeny

Perfect phylogeny

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

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 $\chi_{\text{PP}}(M) = 2$ for a genotype matrix M , finding a pp-partition of any fixed size is still

- *NP-hard,*
- *not fixed-parameter tractable, unless $P = NP$,*
- *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.

Perfect Path Phylogenies

Example of a perfect path phylogeny.

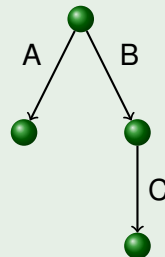
Genotype matrix

	A	B	C
	2	2	2
$G:$	0	2	0
	2	0	0
	0	2	2

Haplotype matrix

	A	B	C
	1	0	0
	0	1	1
	0	0	0
$H:$	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.

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**.

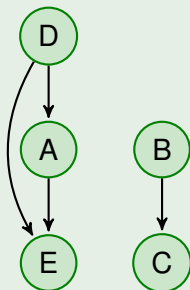
The algorithm in action.

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: →

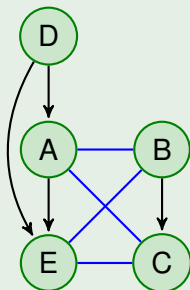
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Computation of the partial order.

Genotype matrix

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



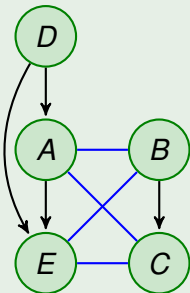
Partial order: →

Compatible as children of root: —

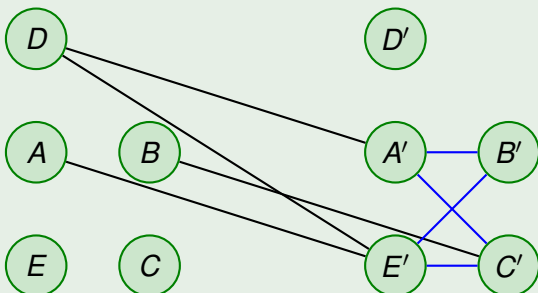
The algorithm in action.

The matching in the special graph.

Partial order



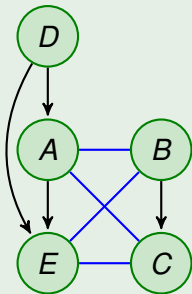
Matching graph



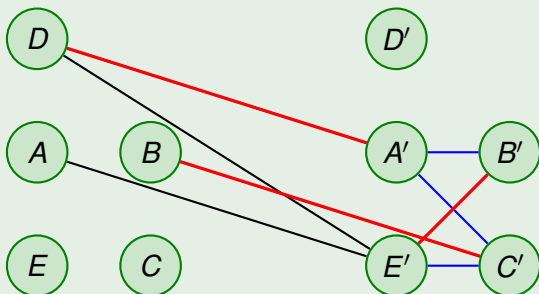
The algorithm in action.

The matching in the special graph.

Partial order



Matching graph

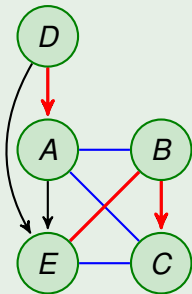


A **maximal matching** in the matching graph

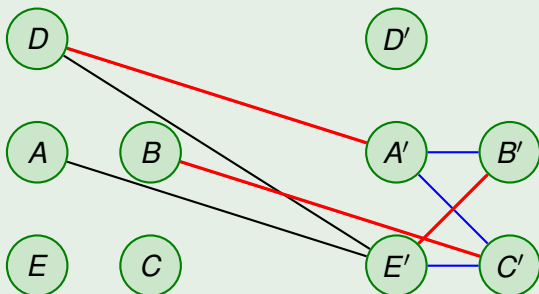
The algorithm in action.

The matching in the special graph.

Partial order



Matching graph



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