Abstract:

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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.

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.