

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

Jens Gramm¹ Tzvika Hartman² Till Nierhoff³
Roded Sharan⁴ **Till Tantau⁵**

¹Universitt Tbingen, Germany

²Bar-Ilan University, Ramat-Gan, Israel

³International Computer Science Institute, Berkeley, USA

⁴Tel-Aviv University, Israel

⁵Universitt zu Lbeck, Germany

Workshop on Algorithms in Bioinformatics, 2006

Outline

- 1 **Introduction**
 - The Model and the Problem

What is haplotyping and why is it important?

basjhf kjsdh lkjdfs

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

General formalization of haplotyping.

scottishwoman.wav

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**.