

# Robotic Validation of AFM, Scale-freeness, Local Communication etc.

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May 2010

## Outline

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### Introduction

- The Model and the Problem
- The Integrated Approach

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### Bad News: Hardness Results

- Hardness of PP-Partitioning of Haplotype Matrices
- Hardness of PP-Partitioning of Genotype Matrices

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### 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.