

Improving the Layout of Oligonucleotide Microarrays: Pivot Partitioning

Sérgio A. de Carvalho Jr.^{1,2,3} Sven Rahmann^{1,2}

¹Algorithms and Statistics for Systems Biology, Genome Informatics,
Technische Fakultät, Universität Bielefeld, Germany

²International NRW Graduate School in Bioinformatics and Genome Research

³Graduiertenkolleg Bioinformatik

6th Workshop on Algorithms in Bioinformatics
Zürich, Sep 2006

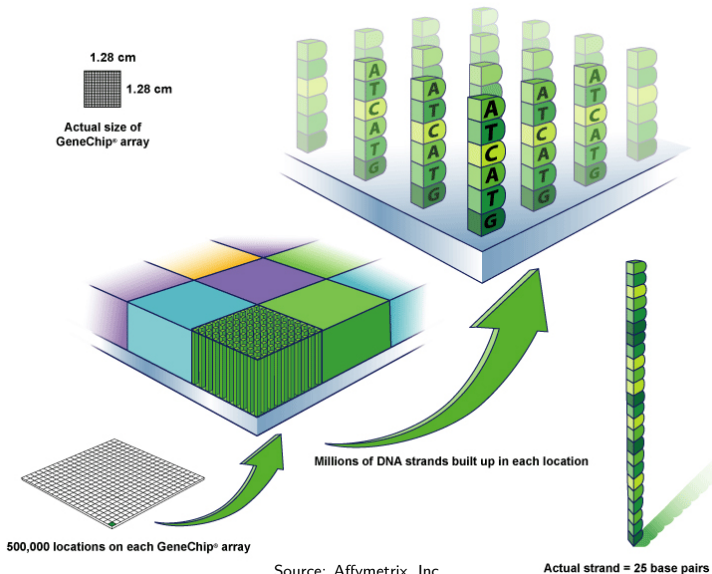
Outline

- 1 Introduction: Microarray Layout
- 2 Conflict Index Evaluation Model
- 3 Pivot Partitioning Algorithm

Outline

- 1 Introduction: Microarray Layout
- 2 Conflict Index Evaluation Model
- 3 Pivot Partitioning Algorithm

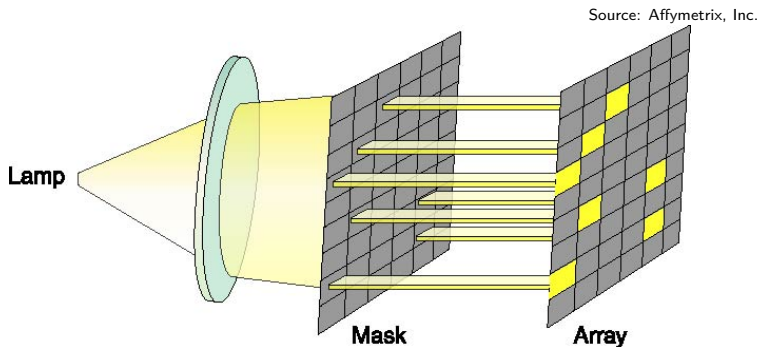
High-Density Oligonucleotide Microarrays



Source: Affymetrix, Inc.

Actual strand = 25 base pairs

Probe Synthesis: Photolithographic Masks



- Probes are synthesized on the chip in a series of **steps**
- Each step appends a particular nucleotide to **selected regions**
- Selection occurs by exposure to light

Deposition Sequence and Probe Embeddings

Show animation with masks

Problem: Unintended Illumination

Border Length Minimization Problem

Outline

- 1 Introduction: Microarray Layout
- 2 Conflict Index Evaluation Model
- 3 Pivot Partitioning Algorithm

Motivation

Outline

- 1 Introduction: Microarray Layout
- 2 Conflict Index Evaluation Model
- 3 Pivot Partitioning Algorithm

Previous work

Summary

Thanks!



- Prof. Dr. Jens Stoye
- Prof. Dr. Robert Giegerich
- AG Genominformatik
- Graduiertenkolleg Bioinformatik
- Graduate School in Bioinformatics and Genome Research

Thank you for your attention!