



Sequence-Pair-Based Placement and Routing for Flow-Based Microfluidic Biochips

Qin Wang¹, Yizhong Ru, Hailong Yao¹, Tsung-Yi Ho², Yici Cai¹

Tsinghua University
National Tsinghua University

- Background
- Problem Formulation
- Contributions
- Overall Design Flow
- Placement and Routing Method
- Routing Feedback and Placement Adjustment
- Experimental Results
- Summary

Flow-Based Microfluidic Biochips

- One of the many different types of biochips
- Based on multilayer soft lithography technology
- Functional units are fabricated by elastomer material (polydimethylsiloxane, PDMS)



http://groups.csail.mit.edu/cag/biostream/

Schematic of flow-based biochips



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Microvalve

- Used to control the movement of flow
- Located between control and flow channels at their intersection region
- 1. Load sample on top 2. Load sample on bottom 3. Rotary Mixing



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Design of Flow-Based Biochips



Flow-Layer Design



(1) Sequencing graph

A directed acyclic graph specifying the sequential order of operations

(2) Resource binding and scheduling Choosing the specific component for each operation Computing the starting and finishing time of each operation

(3) Component placement & channel routing

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Problem Formulation



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Contributions

- Integrated placement and routing method is proposed
- Sequence-pair-base placement with simulated annealing optimization
- Negotiation-based routing method is adopted for channel routing
- Placement adjustment method
- Routing feedback mechanism

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Overall Design Flow of Our Approach



Placement representation

Placement optimization

Single-layer routing with path intersections allowed

Congestion problem

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Sequence-pair (SP) representation

- SP enables a solution space polynomial-admissible
 - 1. The solution space is finite
 - 2. Every solution is feasible
 - 3. Realization of a code is possible in polynomial time
 - 4. There exists a code corresponds to one of the optimal solutions
- Set of components: M = {a, b, c, d, e, f}
- SP code: (s1, s2)
- Rule for explaining the SP code
 - A. If a is before b in both s1 and s2, then a is on the left side of b
 - B. If a is before b in s1, and after b in s2, then a is above b.

Sequence-pair (SP) representation

(s1, s2)=(ecadfb, fcbead)



Simulated annealing-based placement (1)

- Initial code SP = (s1, s2)
- Expanded spacing vector $EX = \{ex_i\}$ $EY = \{ey_i\}$ $e_{\min} \le ex_i$ $ey_i \le e_{\max}$
- Placement state ST = (s1, s2, EX, EY)
- Initial temperature T
- Energy function E(ST) for placement ST
- If E(ST') < E(ST) or p < p0, accept the new solution ST'

$$p_0 = e^{\frac{E(ST) - E(ST')}{T}} p \in [0, 1]$$

Simulated annealing-based placement (2)



Simulated annealing-based placement (3)

Energy function of placement state ST

$$\bigcup E(ST) = \alpha \cdot A + \beta \cdot C + \gamma \cdot L + \theta \cdot L_2$$

- A: area of the minimum bounding box of all placement components
- C: total number of crossings between line segments corresponding to the nets
- L: sum of Manhattan distances of the nets
- L2: sum of square of Manhattan distances corresponding to the nets

Negotiation-Based Routing

Cost function for history cost

$$C_h(g)^{r+1} = C_b + \lambda \cdot C_h(g)^r$$

- $C_h(g)^{r+1}$ is current history cost of routing grid g for iteration r+1
- C_b is the base history cost
- $C_h(g)^r$ is the history cost in iteration r
- λ is set to be 0.1

Negotiation-Based Routing



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Routing Feedback and Placement Adjustment



SP code keep the same

Corresponding components are pushed away

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With and without placement adjustment



1: PCR 2: ProteinSplit-1 3: ProteinSplit-2 4: InVitro-1 5: InVitro-2 6: InVitro-3

With and without placement adjustment



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Comparison with the other method



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Summary

- An effective integrated placement and routing flow
- Using sequence-pair-based iterative placement
- Routing feedback and placement adjustment
- Real-life biochemical applications validate the presented method effectiveness

