

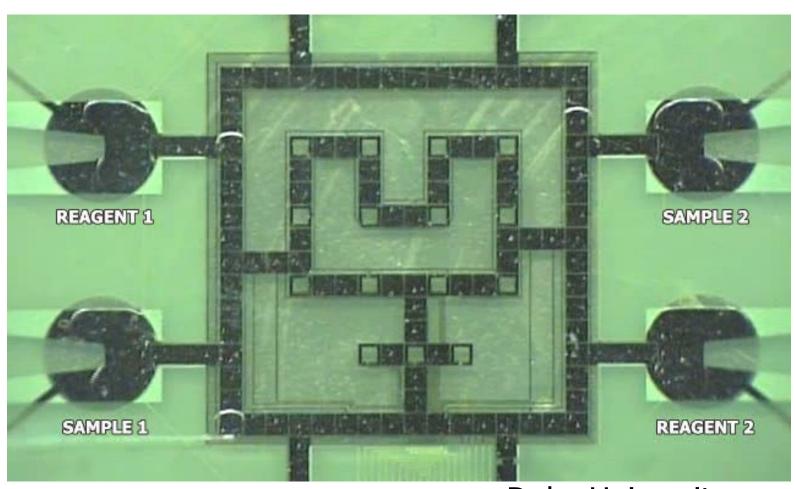
Synthesis of Digital Microfluidic Biochips with Reconfigurable Operation Execution

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DTU Informatics





Digital Microfluidic Biochip



Duke University



Applications

- Sampling and real time testing of air/water for biochemical toxins
- Food testing
- DNA analysis and sequencing
- Clinical diagnosis
- Point of care devices
- Drug development















Advantages & Challenges

• Advantages:

- High throughput (reduced sample / reagent consumption)
- Space (miniaturization)
- Time (parallelism)
- Automation (minimal human intervention)

Challenges:

- Design complexity
- Radically different design and test methods required
- Integration with microelectronic components in future SoCs



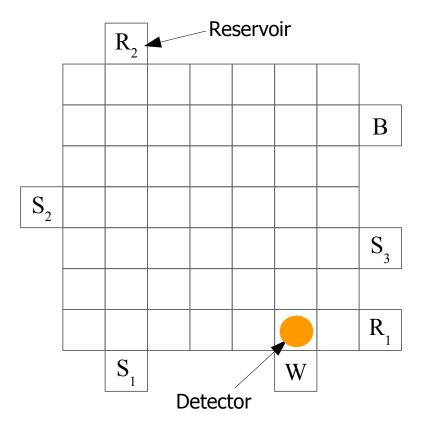
Outline

- Motivation
- Architecture
- Operation Execution
- Contribution I
 - Module-Based Synthesis with Dynamic Virtual Devices
- Contribution II
 - Routing-Based Synthesis
- Contribution III
 - Droplet-Aware Module-Based Synthesis
- Conclusions & Future Directions

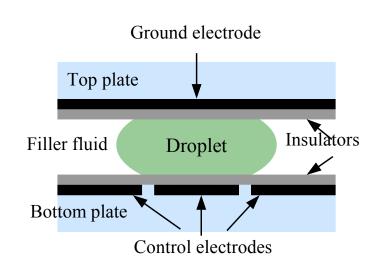


Architecture and Working Principles

Biochip architecture



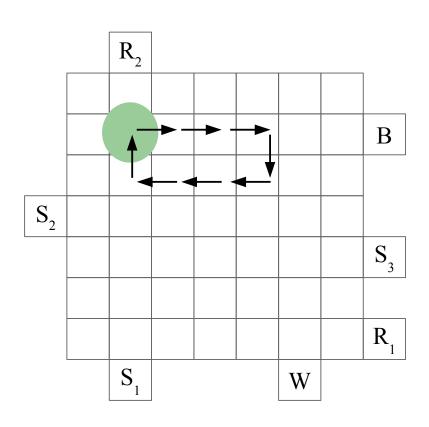
Cell architecture



Electrowetting-on-dielectric



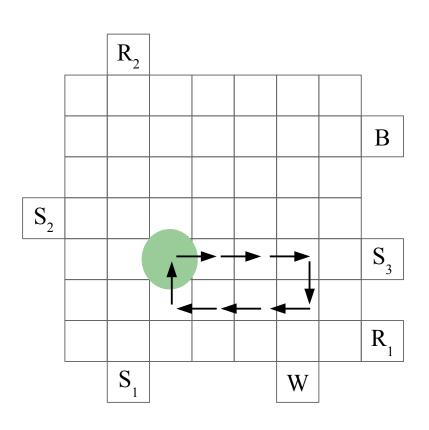
Microfluidic Operations



- Dispensing
- Detection
- Splitting/Merging
- Storage
- Mixing/Dilution



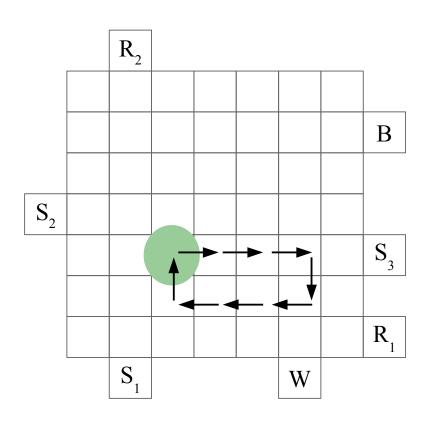
Reconfigurability



- Dispensing
- Detection
- Splitting/Merging
- Storage
- Mixing/Dilution



Reconfigurability

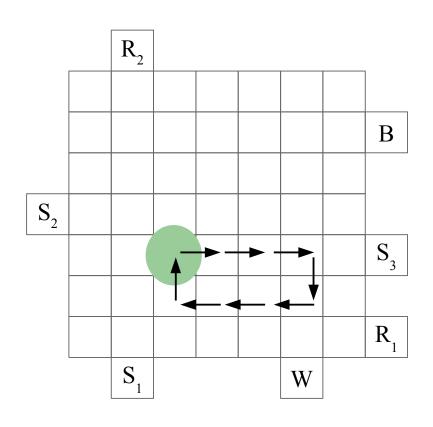


Non-reconfigurable

- Dispensing
- Detection
- Splitting/Merging
- Storage
- Mixing/Dilution



Reconfigurability



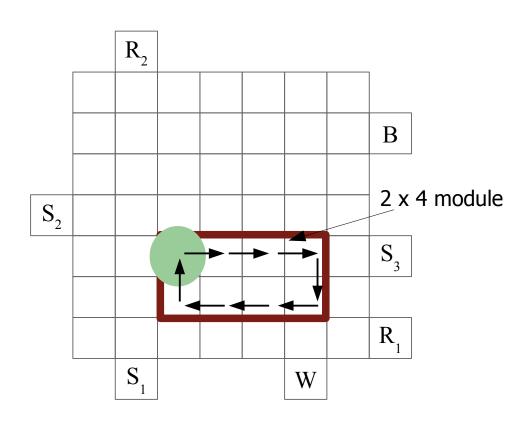
Non-reconfigurable

- Dispensing
- Detection

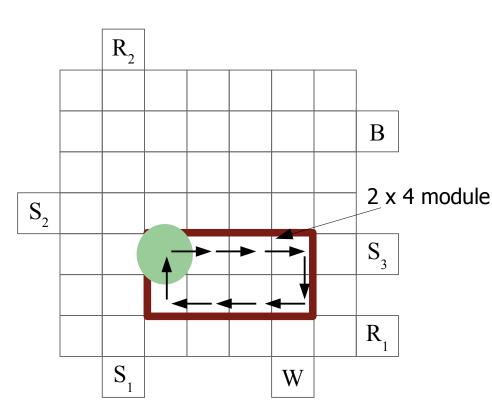
Reconfigurable

- Splitting/Merging
- Storage
- Mixing/Dilution





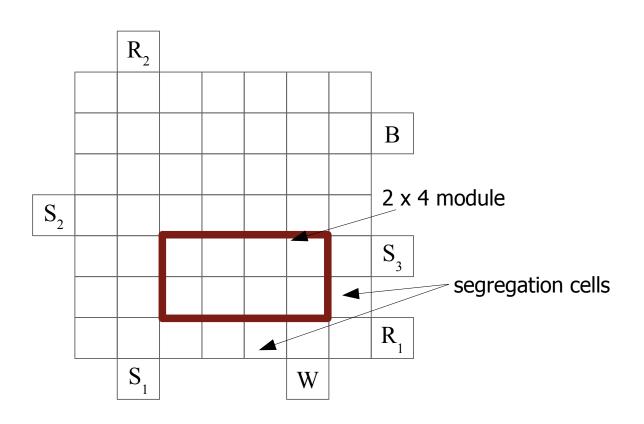




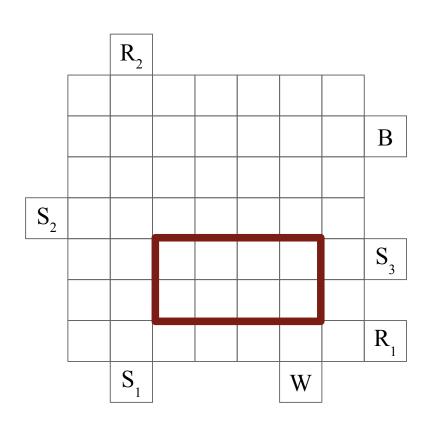
Operation	Area (cells)	Time (s)
Mix	2 x 4	3
Mix	2 x 2	4
Dilution	2 x 4	4
Dilution	2 x 2	5

Module library



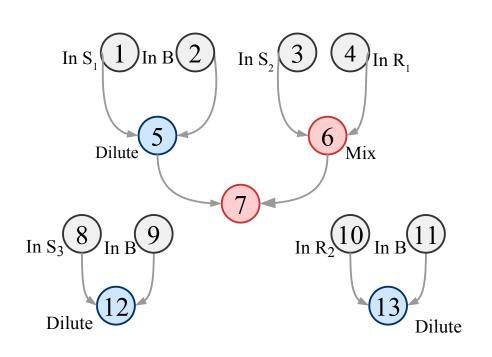




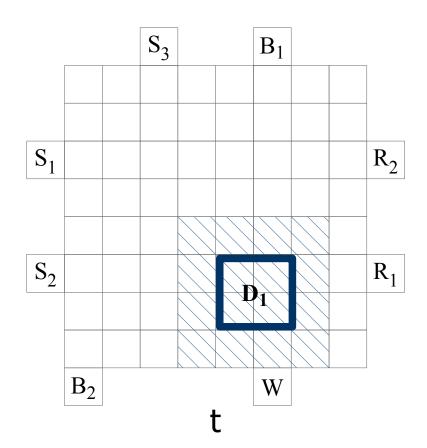


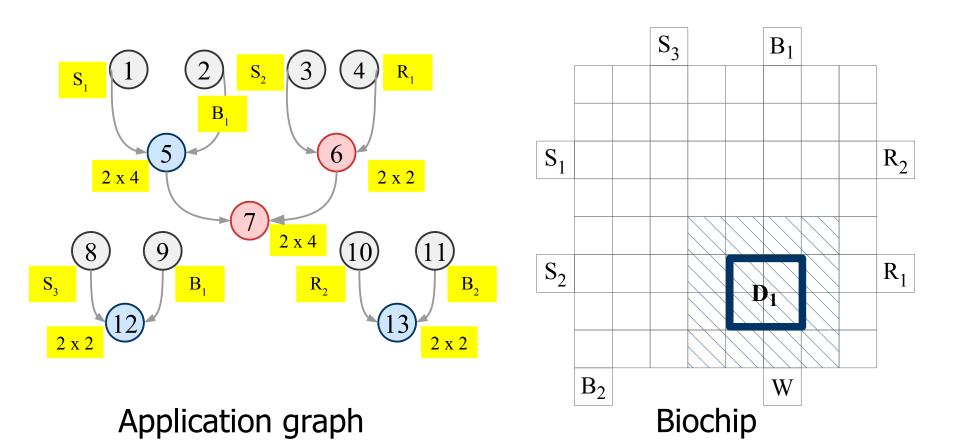
- Operations confined to rectangular, fixed modules
- Positions of droplets inside modules ignored
- Segregation cells

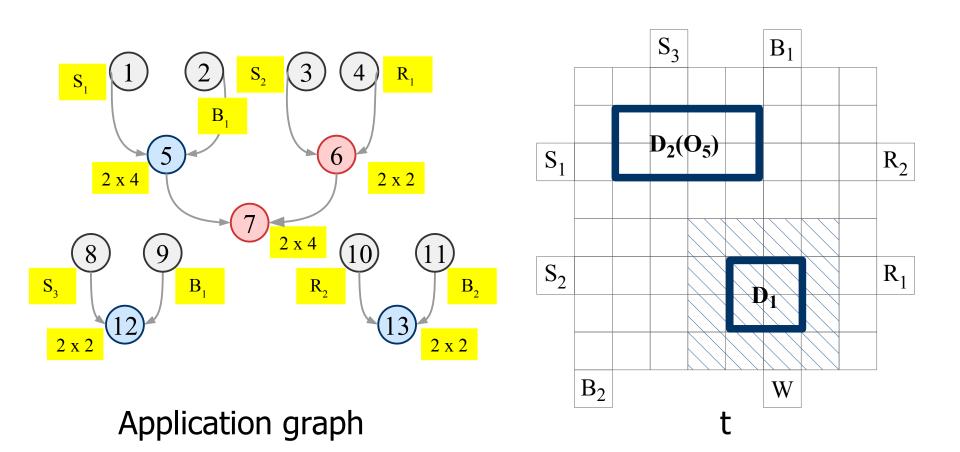
Module-Based Synthesis with Dynamic Virtual Modules

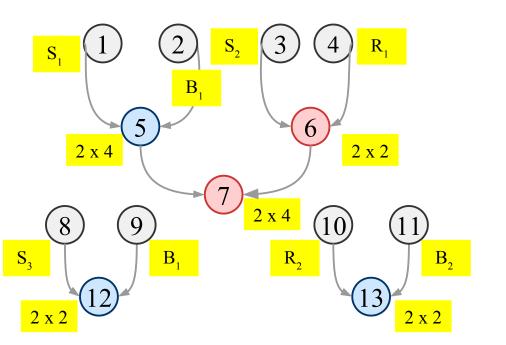


Application graph

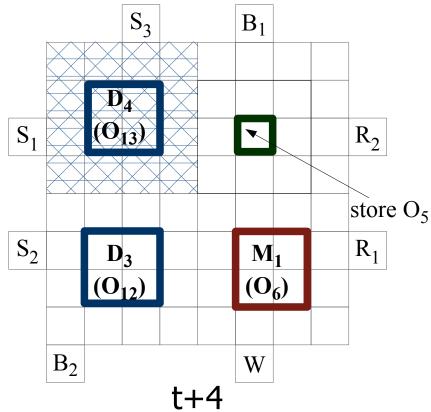


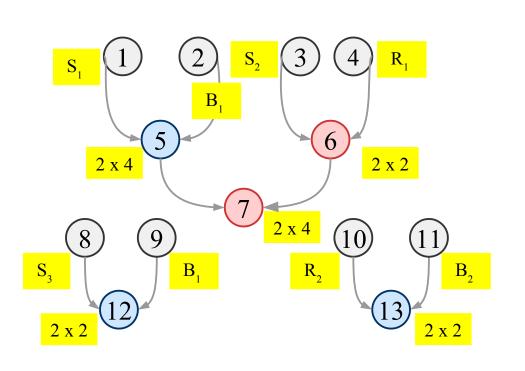




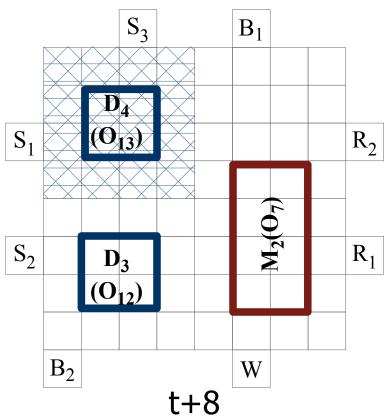


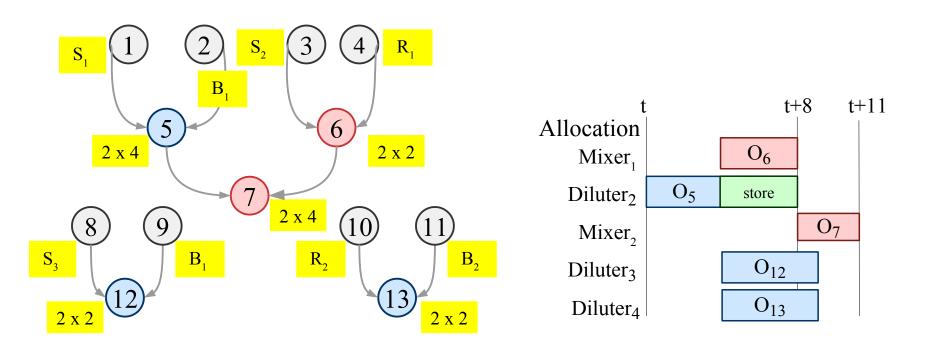






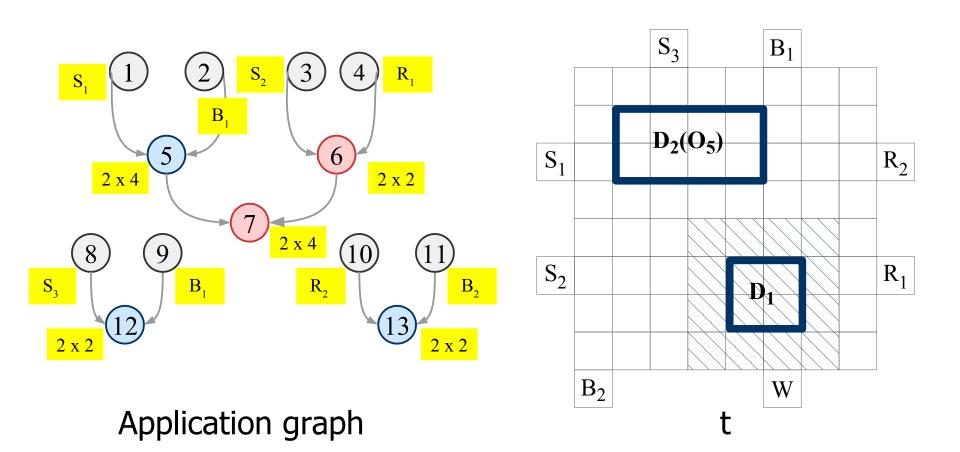


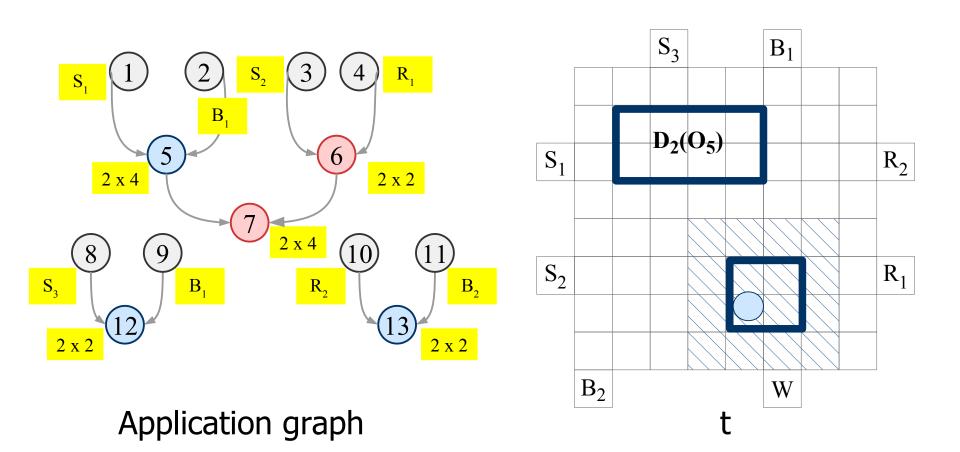


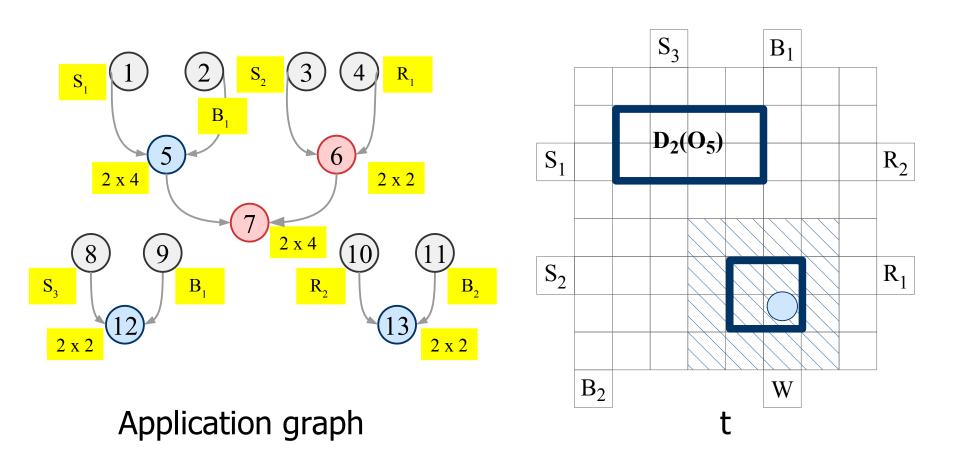


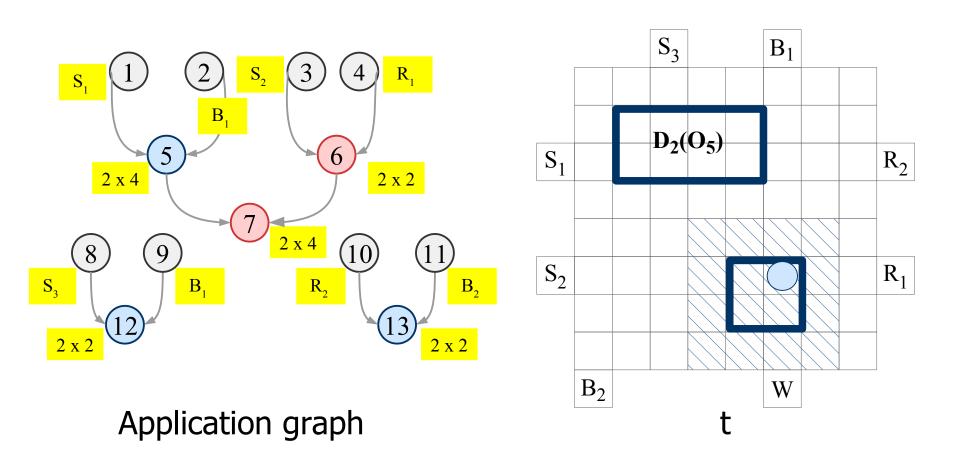
Application graph

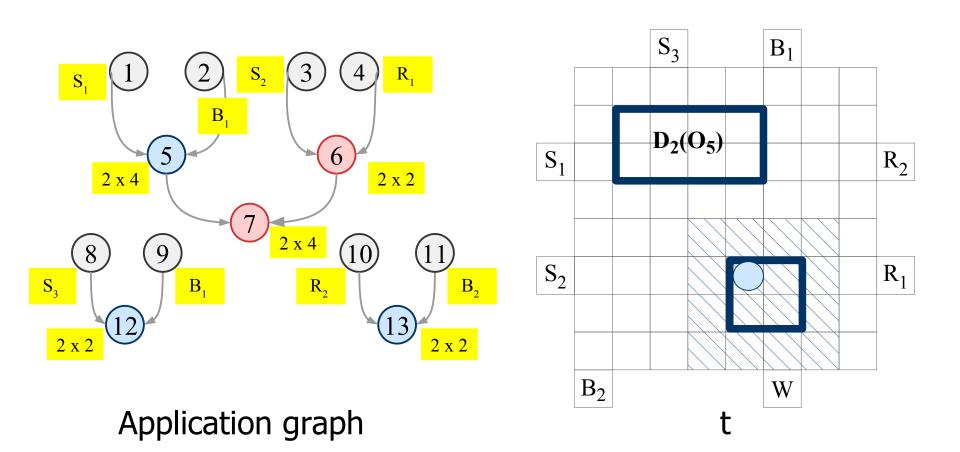
Schedule

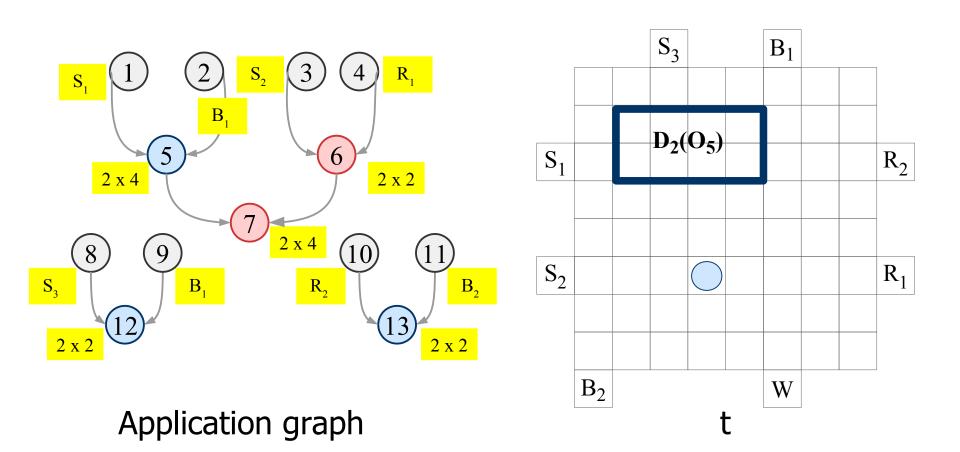


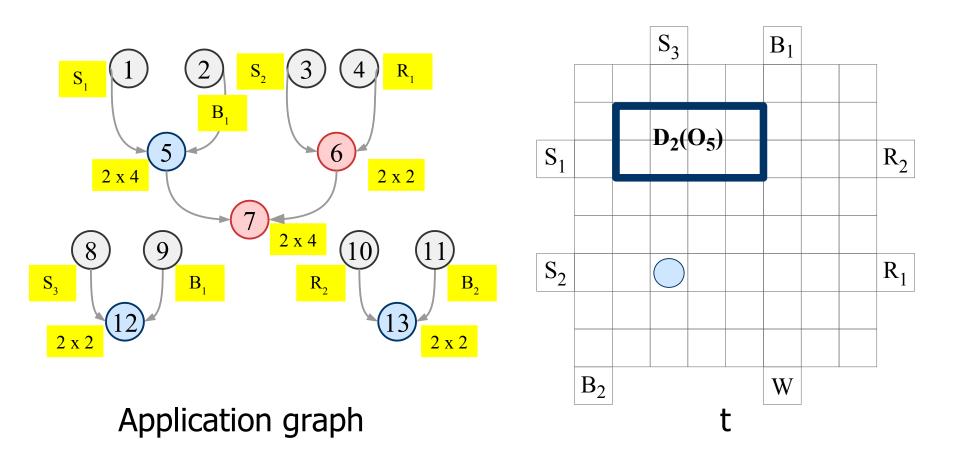


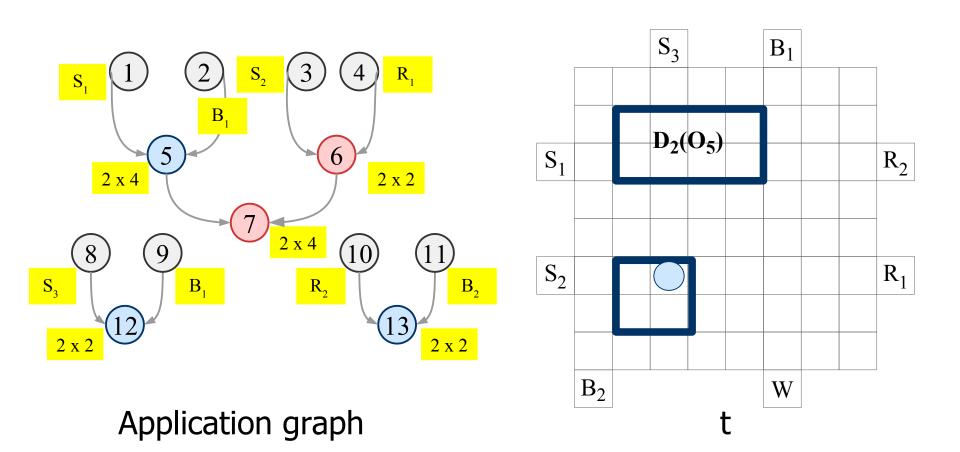


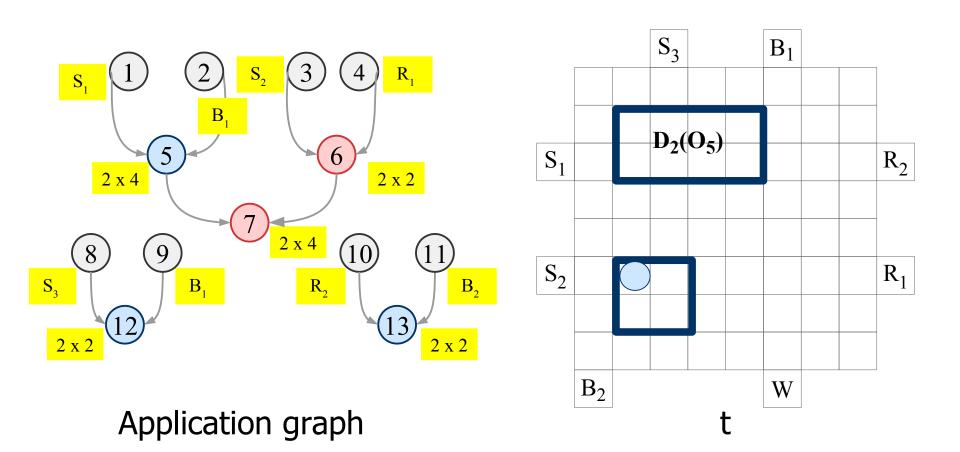


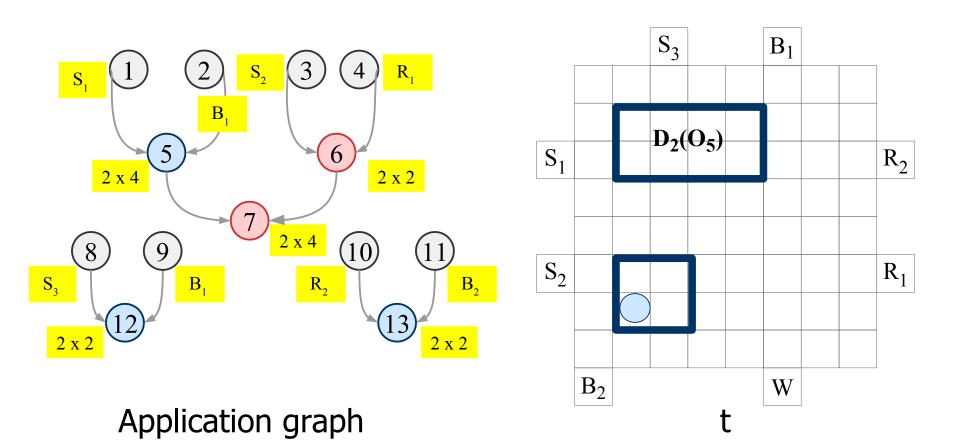


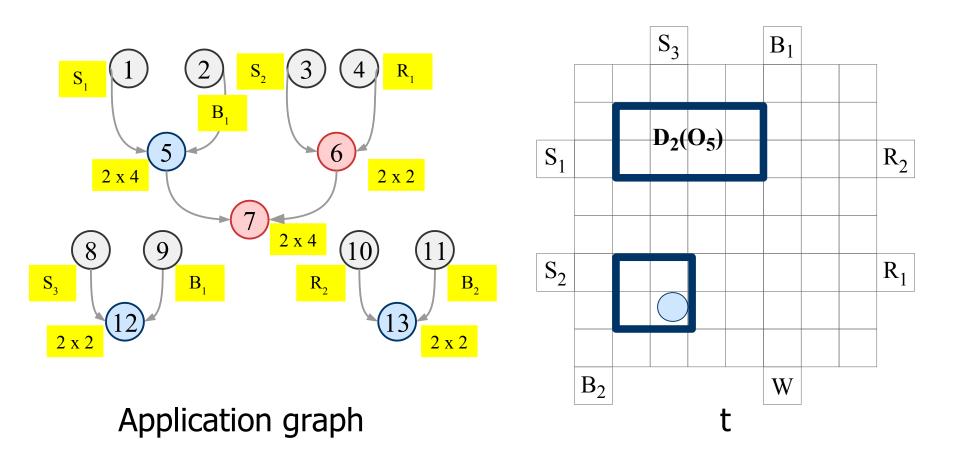


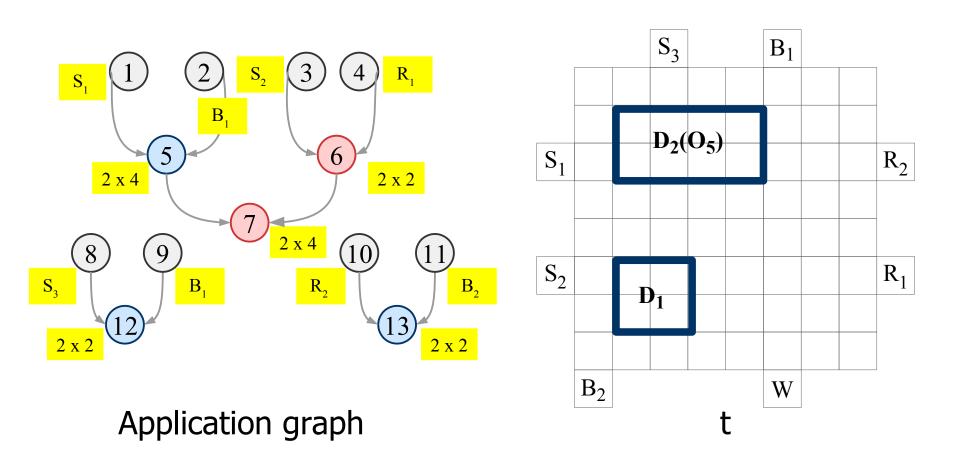


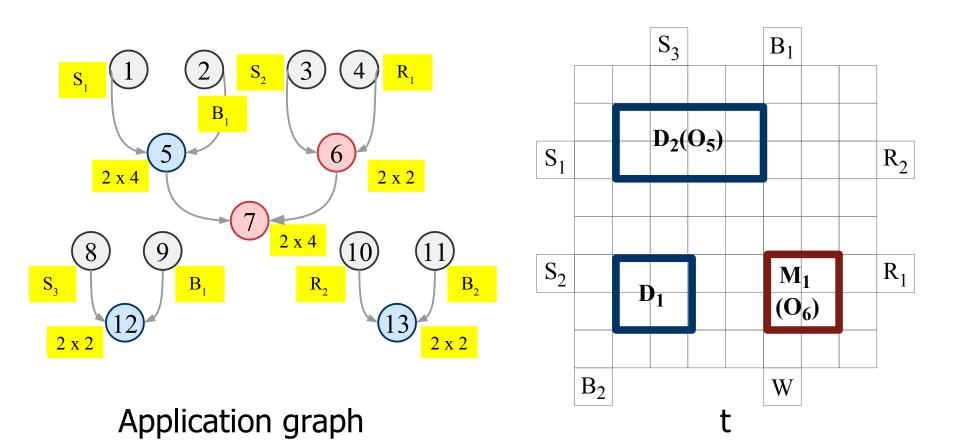


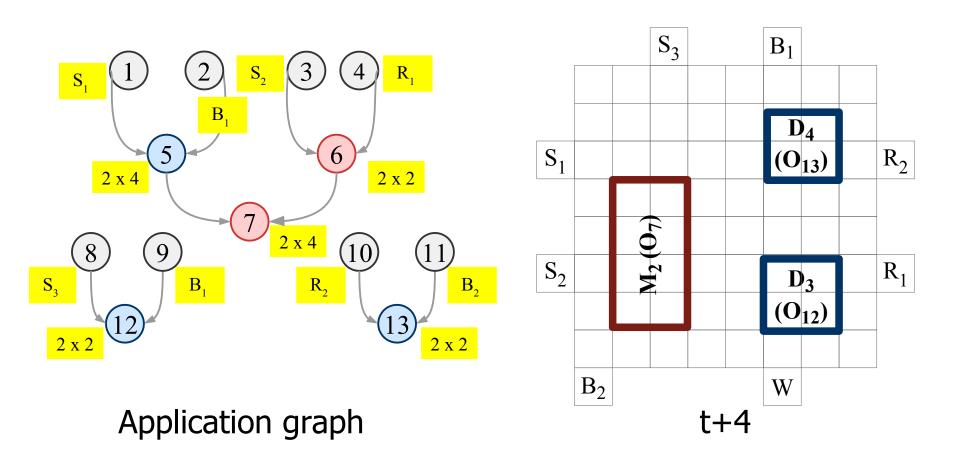


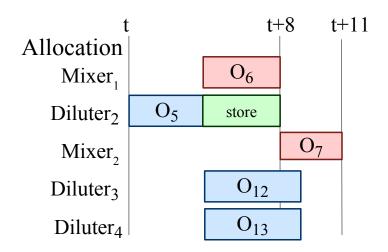


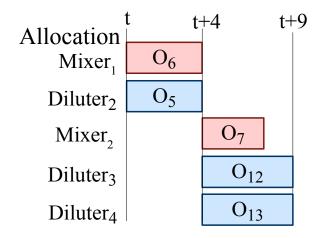












Schedule – operation execution with fixed virtual modules

Schedule – operation execution with dynamic virtual modules

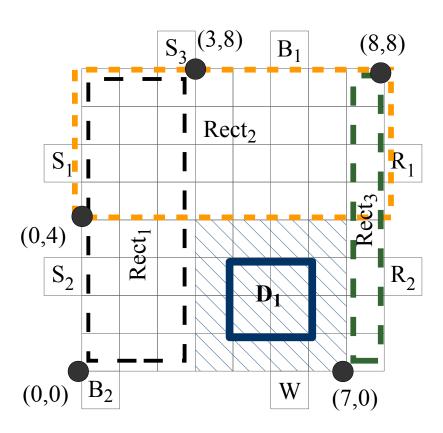
Binding of modules to operations

Tabu Search

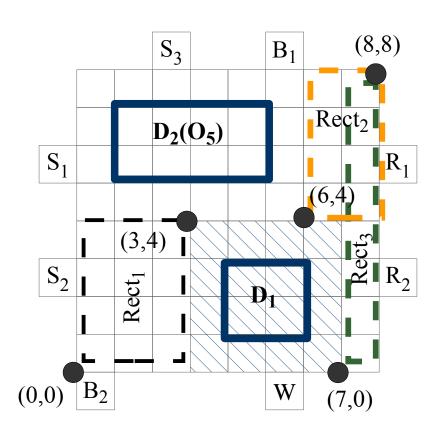
Schedule of the operations

- **List Scheduling**
- Placement of modules performed inside scheduling
- Placement of the modules
 Maximal Empty Rectangles
 - Free space manager based on [Bazargan et al. 2000] that divides free space on the chip into overlapping rectangles

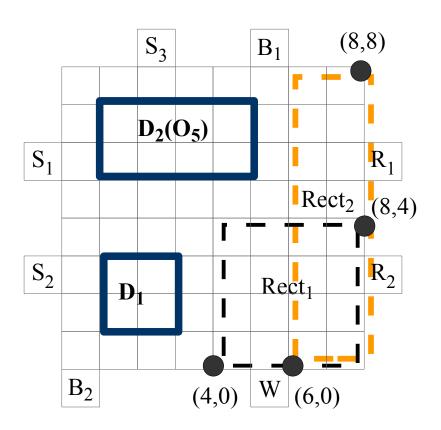
Dynamic Placement Algorithm



Dynamic Placement Algorithm



Dynamic Placement Algorithm



- Tabu Search-based algorithm implemented in Java
- Benchmarks
 - Real-life applications
 - Colorimetric protein assay
 - In-vitro diagnosis
 - Polymerase chain reaction mixing stage
 - Synthetic benchmarks
 - 10 TGFF-generated benchmarks with 10 to 100 operations
- Comparison between:
 - Module-based synthesis with fixed modules (MBS)
 - T-Tree [Yuh et al. 2007]
 - Module-based synthesis with dynamic modules (DMBS)

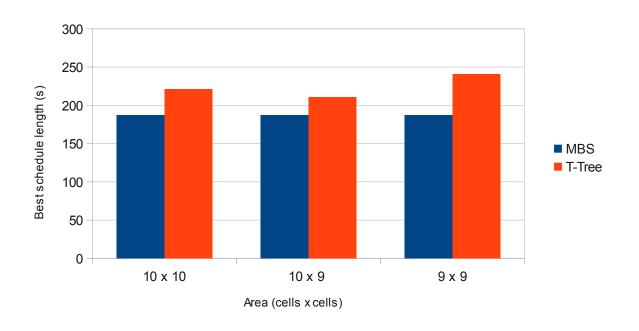
Best-, average schedule length and standard deviation out of 50 runs for MBS

Colorimetric protein assay

Area	Time limit (min)	Best (s)	Average (s)	Standard dev. (%)
13 x 13	60	182	189.99	2.90
	10	182	192.00	3.64
	1	191	199.20	4.70
12 x 12	60	182	190.86	3.20
	10	185	197.73	6.50
	1	193	212.62	10.97
11 x 12	60	184	192.50	3.78
	10	194	211.72	14.37
	1	226	252.19	15.76

Best schedule length out of 50 runs for MBS vs. T-Tree

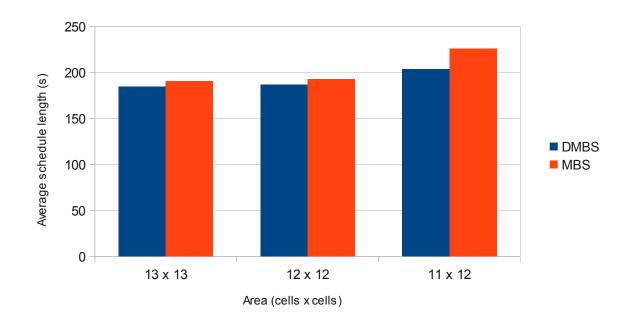
Colorimetric protein assay



22.91 % improvement for 9 x 9

Average schedule length out of 50 runs for DMBS vs. MBS

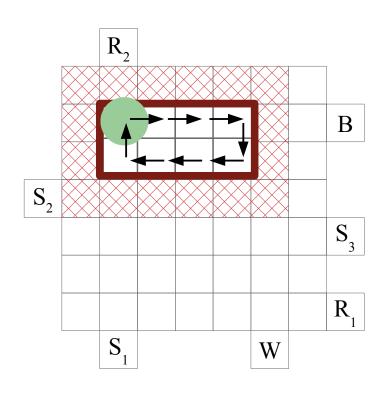
Colorimetric protein assay

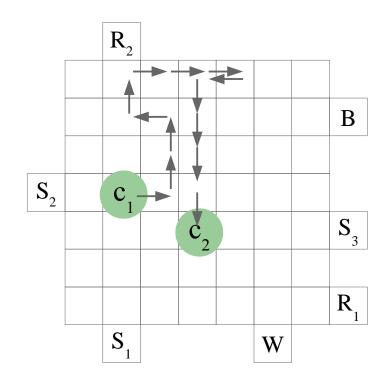


7.68 % improvement for 11 x 12

Routing-Based Operation Execution

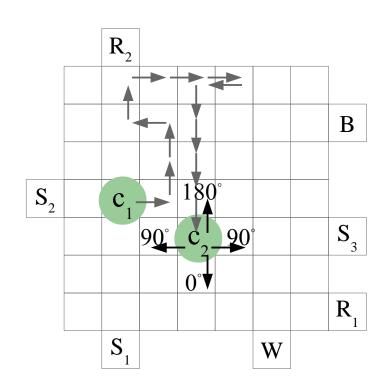
Module-Based vs. Routing-Based Operation Execution



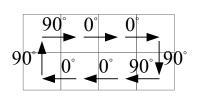


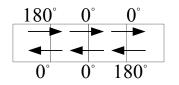
Operation Execution Characterization

 p^{90} , p^{180} , p^{0} ?

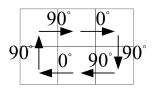


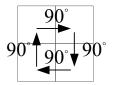
Operation Execution Characterization





p⁹⁰, p¹⁸⁰, p⁰





Туре	Area (cells)	Time (s)
Mix/Dlt	2 x 4	2.9
Mix/Dlt	1 x 4	4.6
Mix/Dlt	2 x 3	6.1
Mix/Dlt	2 x 2	9.9
Input	-	2
Detect	1 x 1	30

Electrode pitch size = 1.5 mm, gap spacing = 0.3 mm, average velocity rate = 20 cm/s.

Operation Execution Characterization

$$p^{90} = 0.1 \%$$

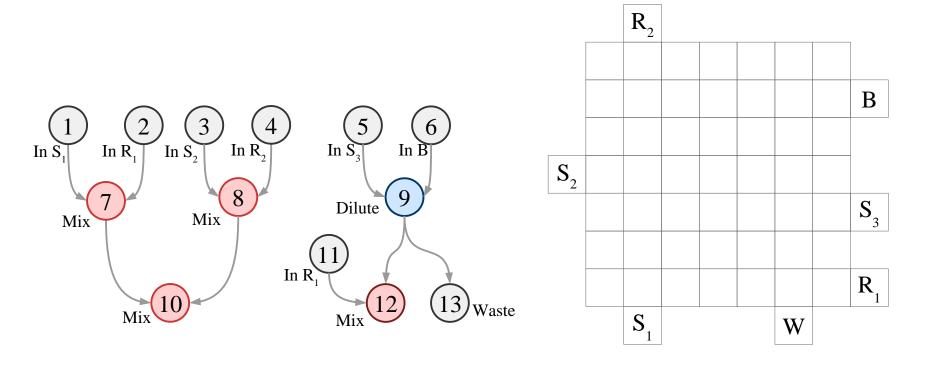
$$p^{180} = -0.5 \%$$

$$p_1^0 = 0.29 \%$$

$$p_{2}^{0} = 0.58 \%$$

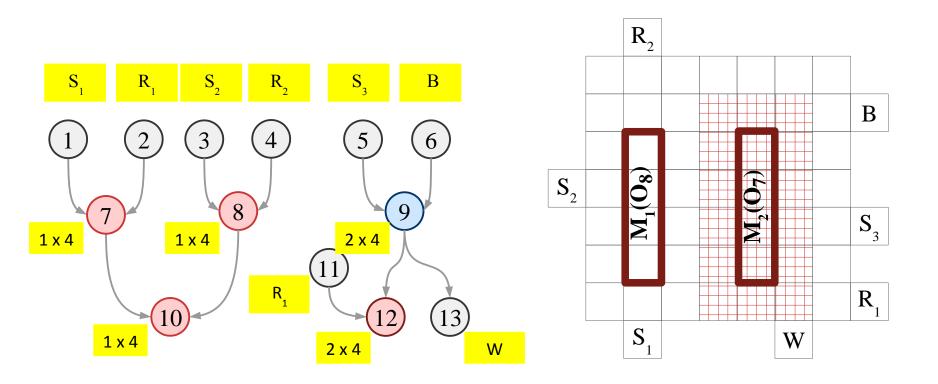
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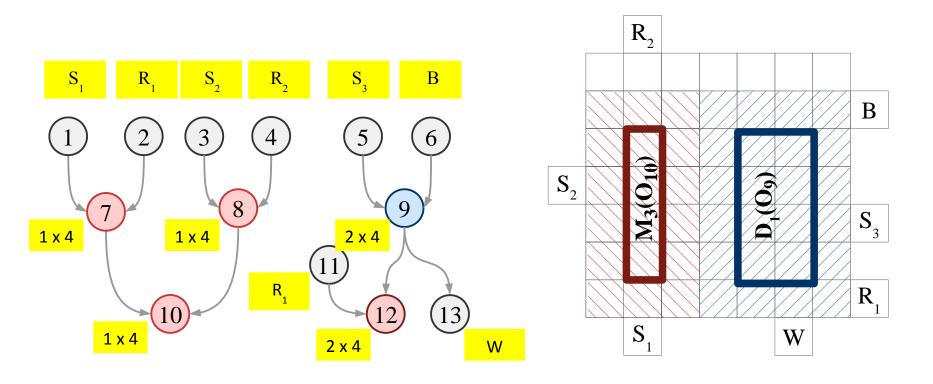


Application graph

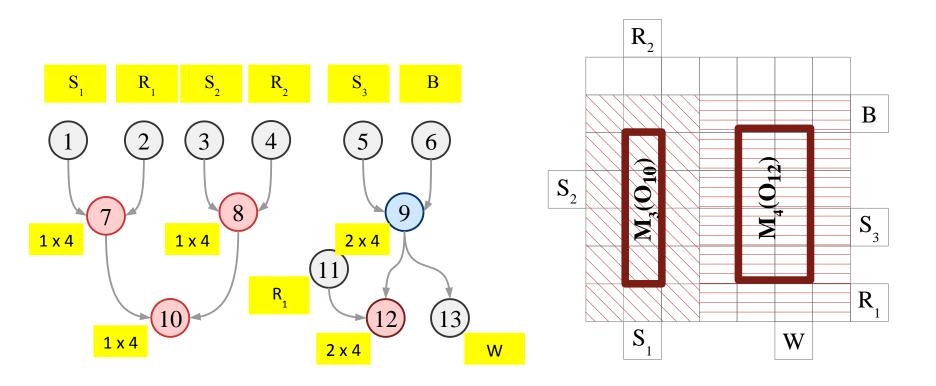
Biochip



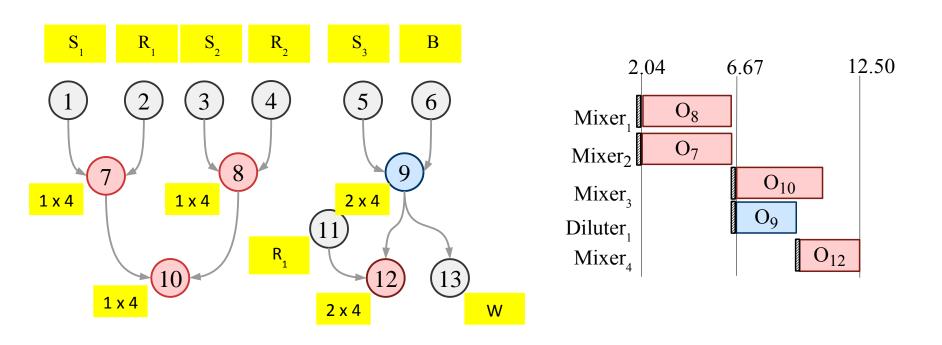
t = 2.04 s



t = 6.67 s

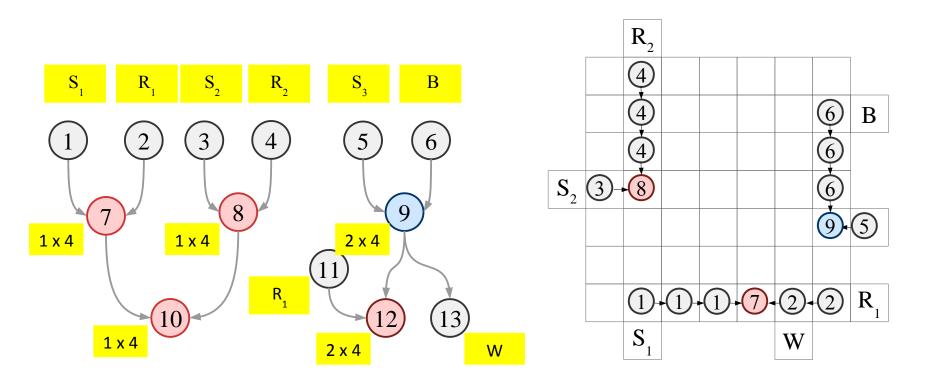


t = 9.5 s

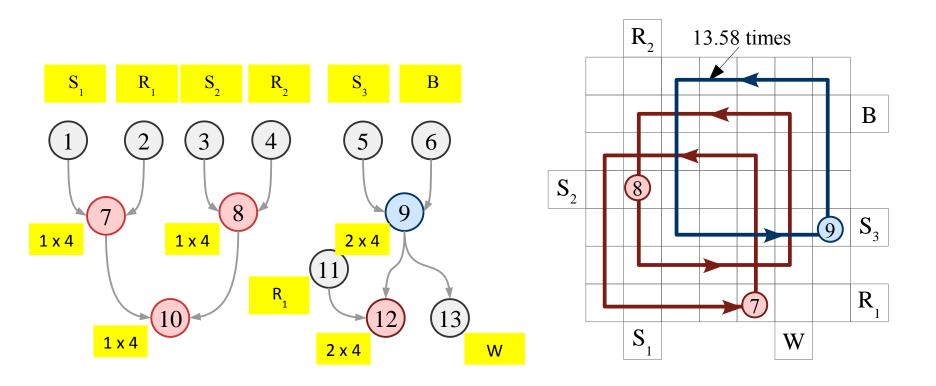


Application graph

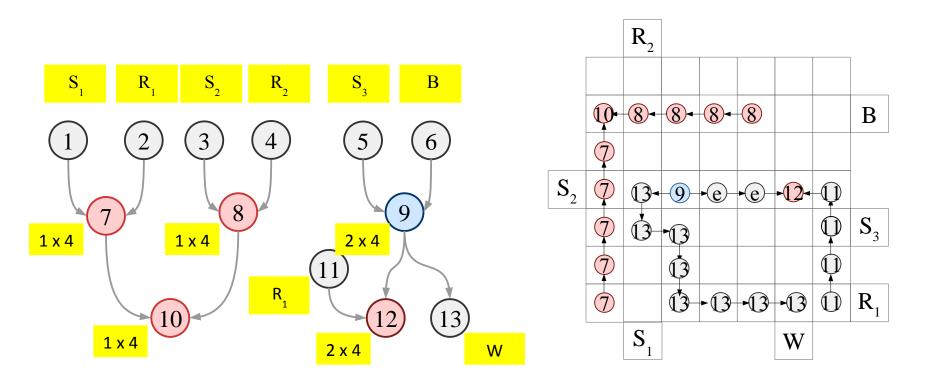
Schedule



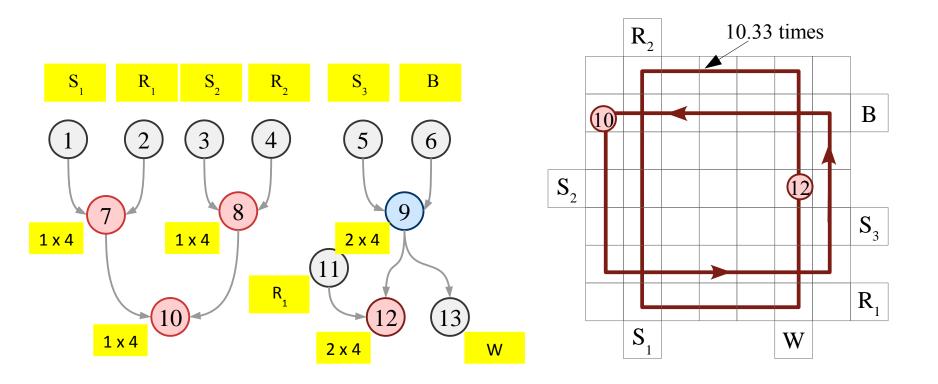
t = 2.03 s



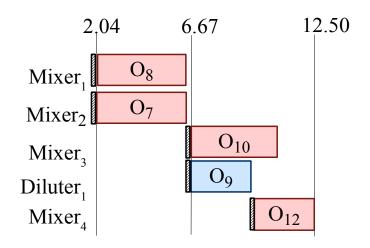
t = 4.20 s

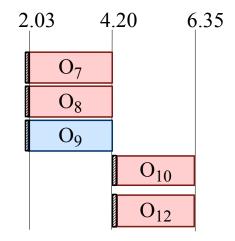


t = 4.28 s



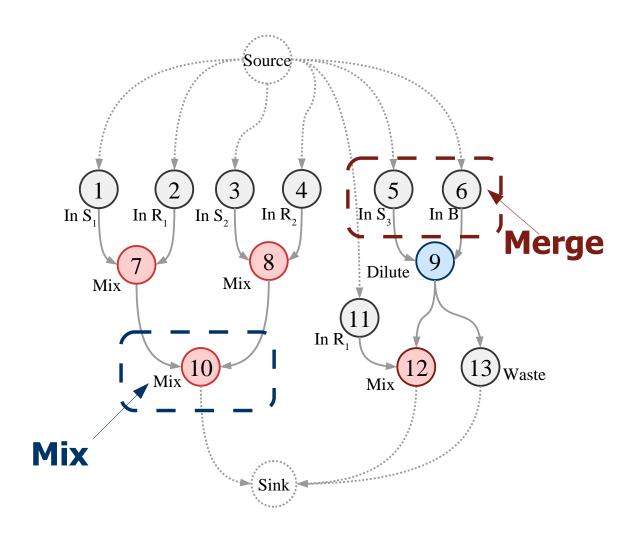
t = 6.34 s

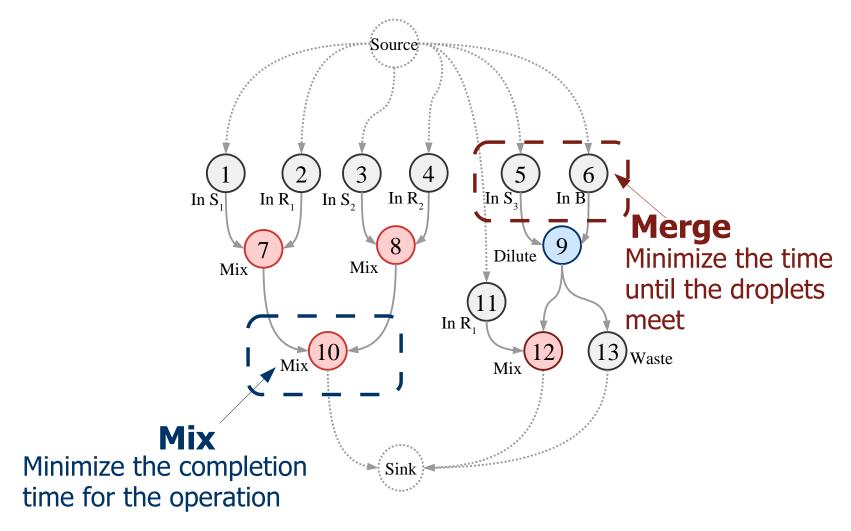


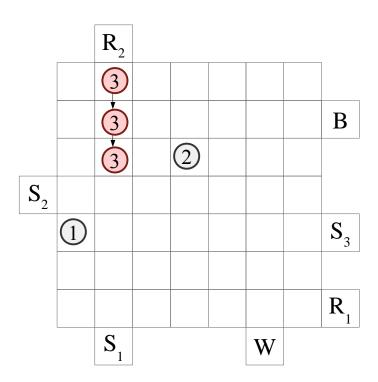


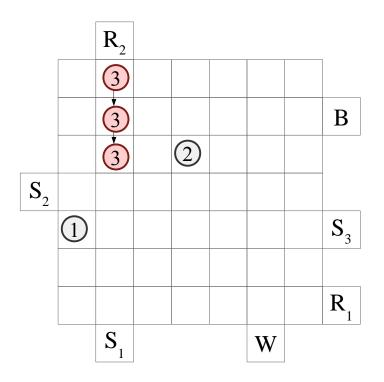
Schedule – module-based operation execution

Schedule – routing-based operation execution

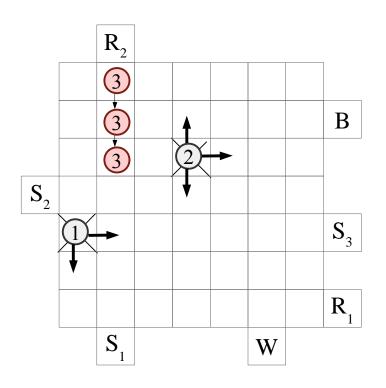




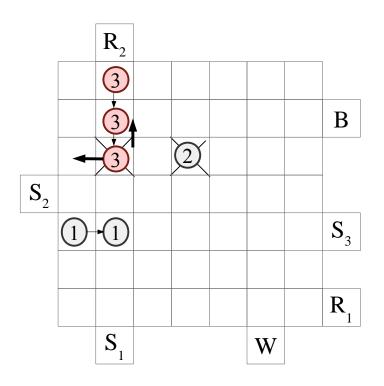




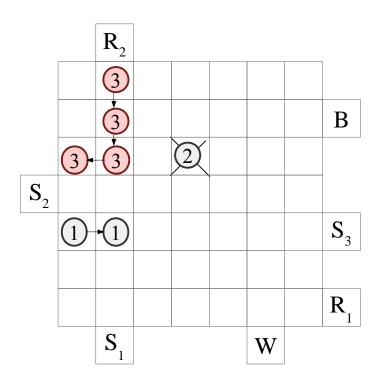
- For each droplet:
 - Determine possible moves
 - Evaluate each move
 - Merge: minimize Manhattan distance
 - Mix: maximize operation execution
 - Make a list of the best N moves
 - Perform a random move from N



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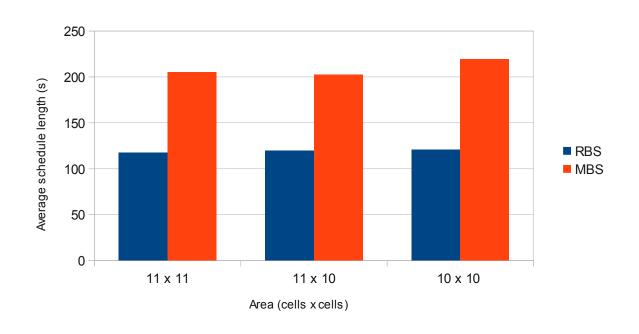


- For each droplet:
 - Determine possible moves
 - Evaluate each move
 - Merge: minimize Manhattan distance
 - Mix: maximize operation execution
 - Make a list of the best N moves
 - Perform a random move from N

- GRASP-based algorithm implemented in Java
- Benchmarks
 - Real-life applications
 - Colorimetric protein assay
 - Synthetic benchmarks
 - 10 TGFF-generated benchmarks with 10 to 100 operations
- Comparison between:
 - Routing-based synthesis (RBS)
 - Module-based synthesis with fixed modules (MBS)

Average schedule length out of 50 runs for RBS vs. MBS

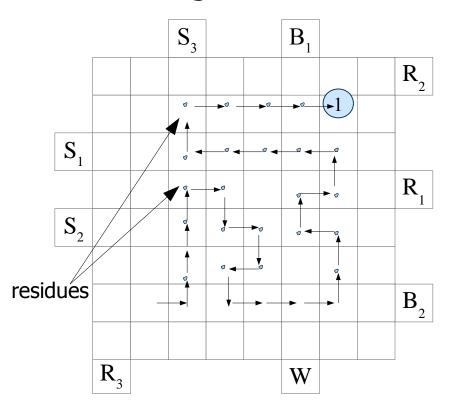
Colorimetric protein assay



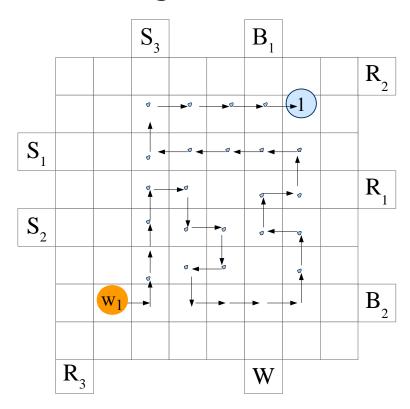
44.95 % improvement for 10 x 10

- Improved completion time compared to module-based synthesis
- Challenge: contamination

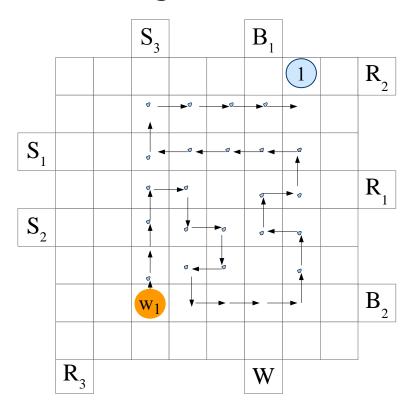
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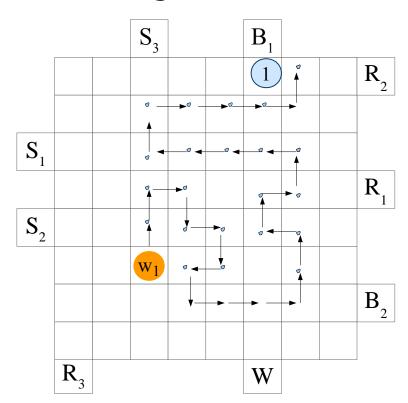
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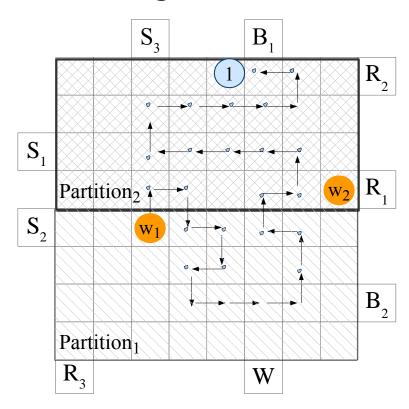
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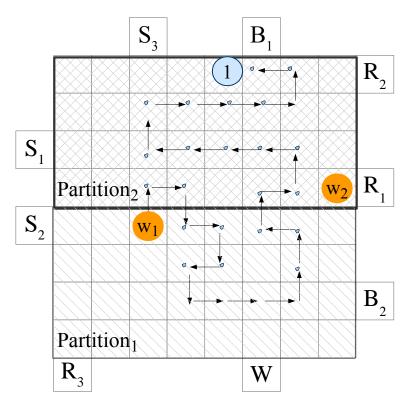
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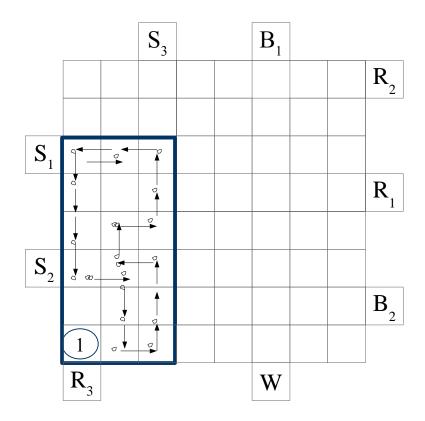


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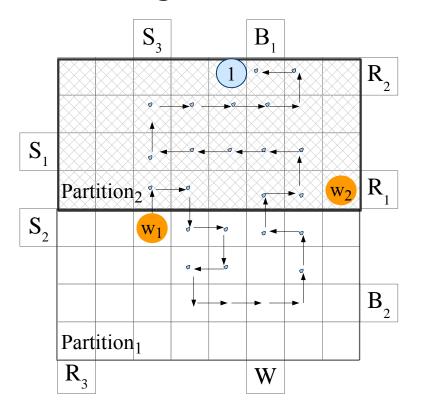


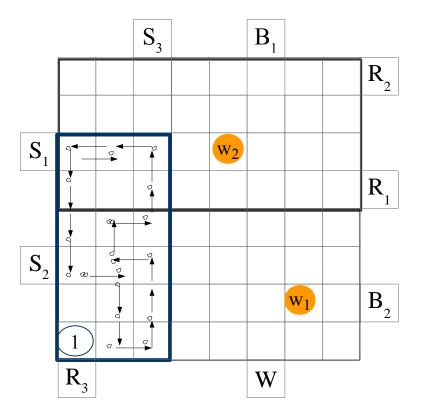
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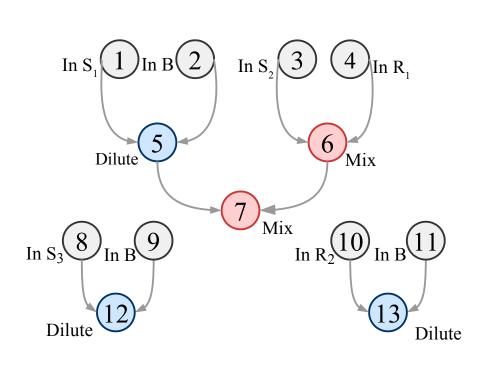


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- Challenge: contamination

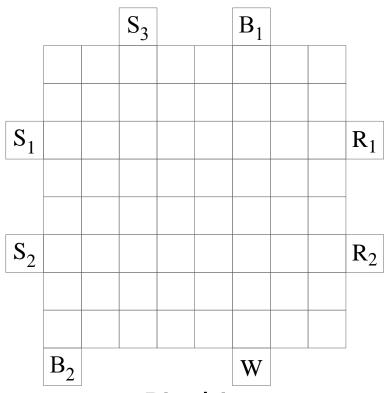




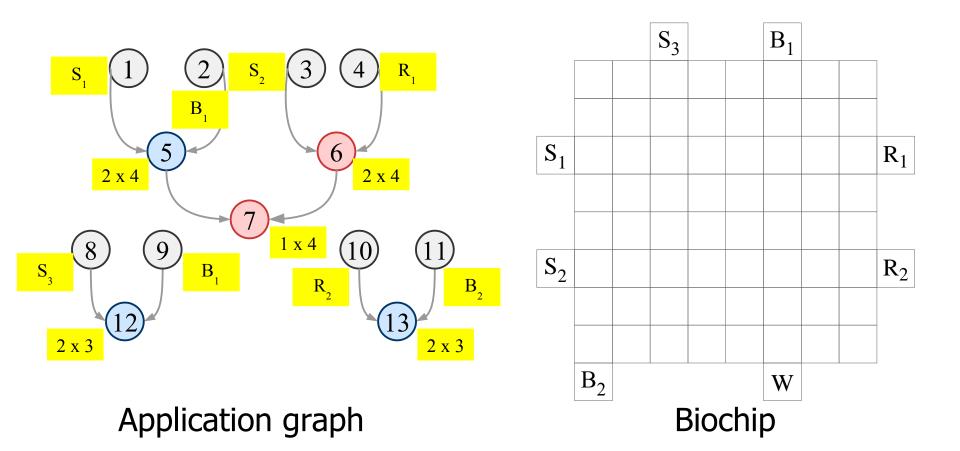
Droplet-Aware Operation Execution without Contamination

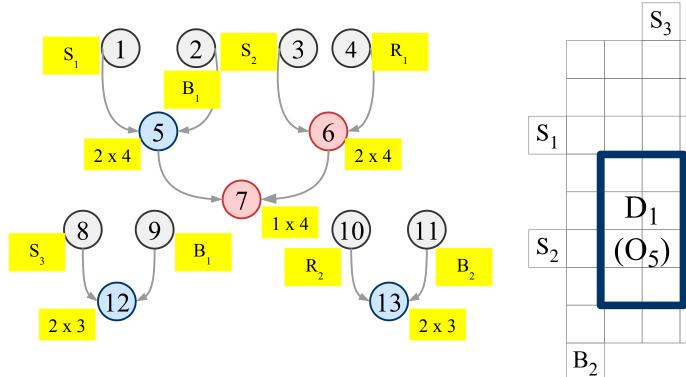


Application graph

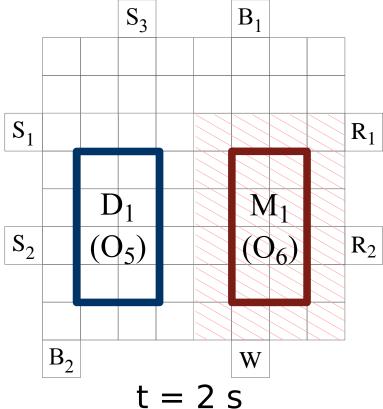


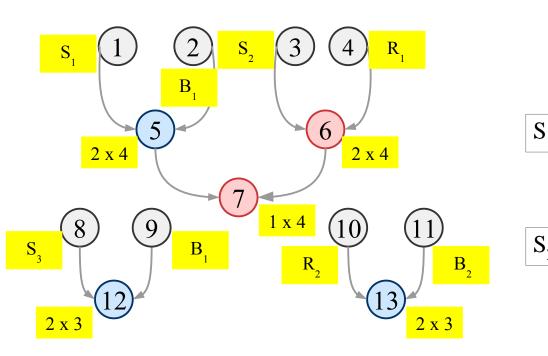
Biochip



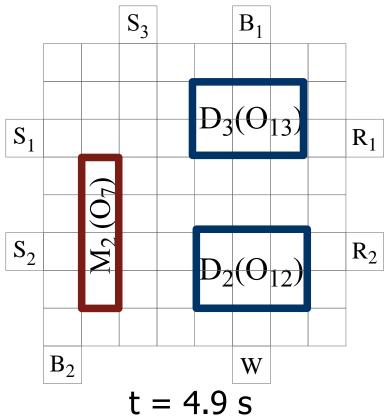


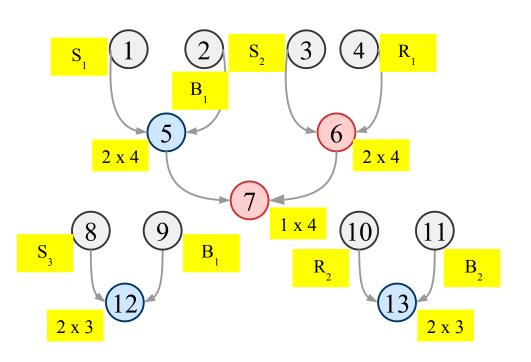
Application graph





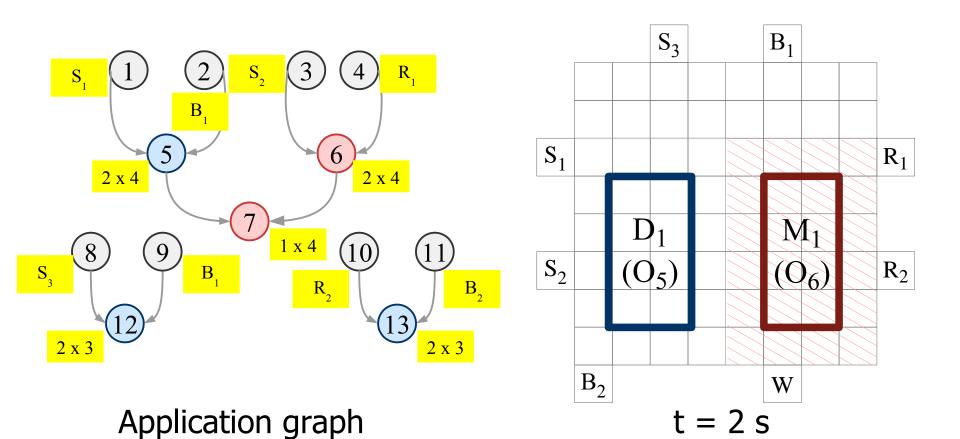
Application graph

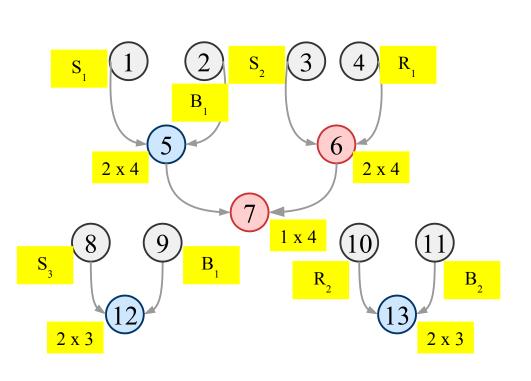




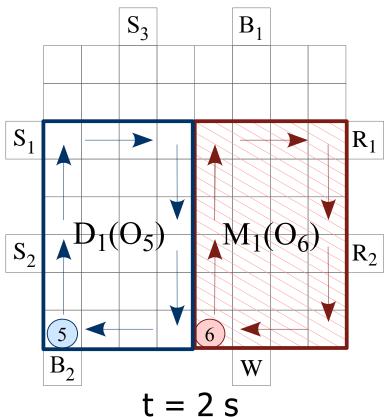
Application graph

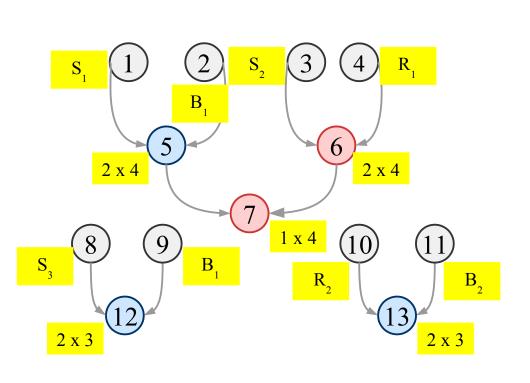
Schedule



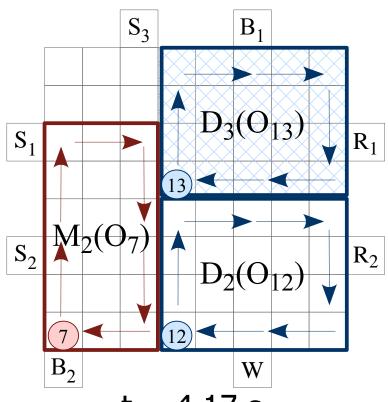


Application graph

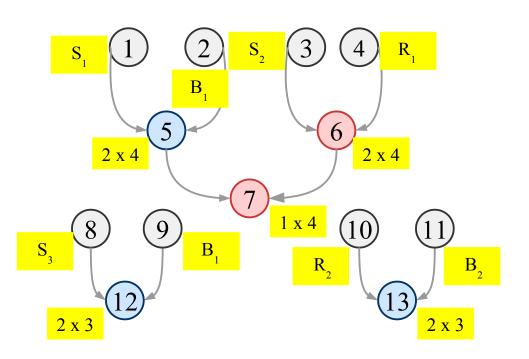




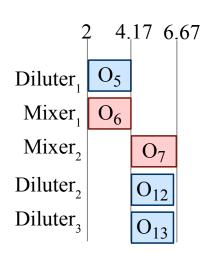
Application graph



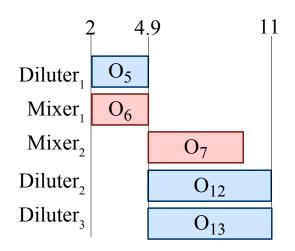
t = 4.17 s



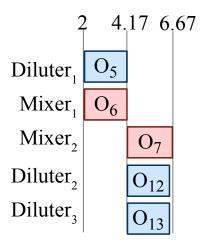
Application graph



Schedule



Schedule – module-based operation execution

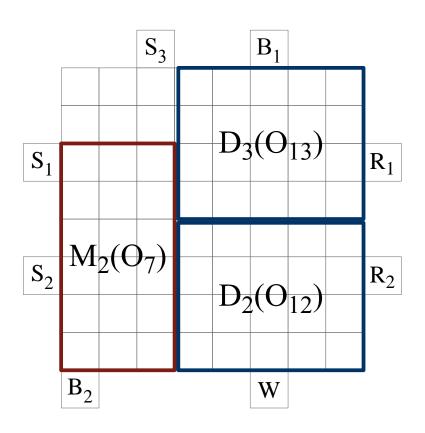


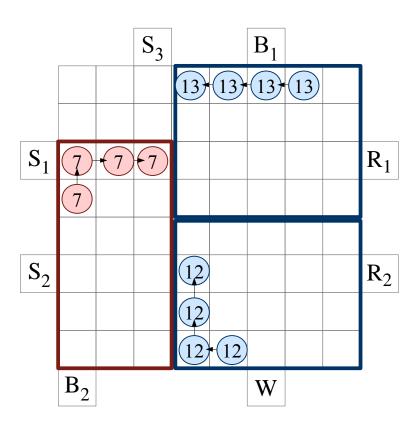
Schedule – droplet-aware operation execution

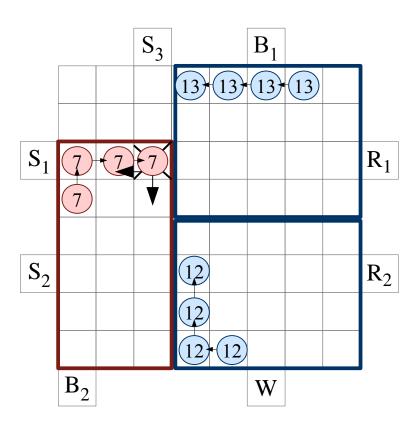


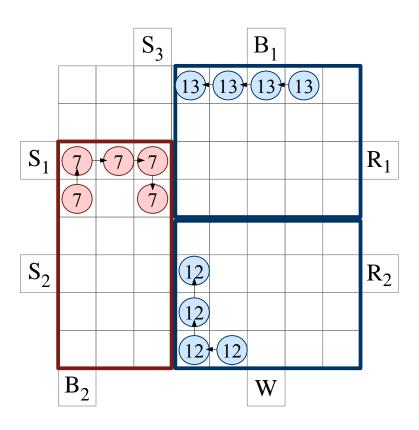
Solution

- Location of modules determined using Tabu Search
- Greedy movement of droplets inside modules
- Routing of droplets between modules and between modules and I/O ports determined using GRASP





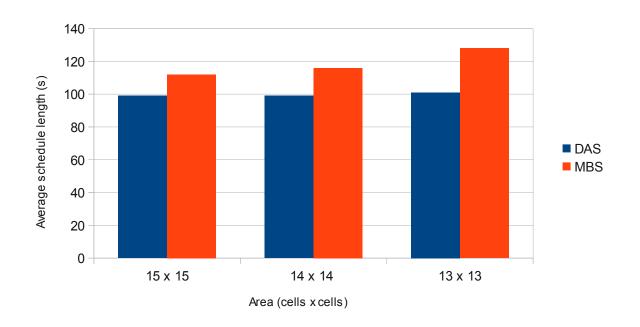




- Algorithm implemented in Java
- Benchmarks
 - Real-life applications
 - In-vitro diagnosis
 - Colorimetric protein assay
 - Synthetic benchmarks
 - 3 TGFF-generated benchmarks with 20, 40, 60 operations
- Comparison between:
 - Droplet-aware module-based synthesis (DAS)
 - Module-based synthesis (MBS)

Average schedule length out of 50 runs for DAS vs. MBS

Colorimetric protein assay

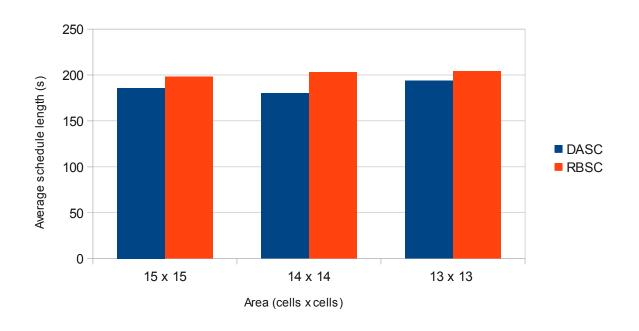


21.55 % improvement for 13 x 13

- Algorithm implemented in Java
- Benchmarks
 - Real-life applications
 - Colorimetric protein assay
 - Synthetic benchmarks
 - 3 TGFF-generated benchmarks with 20, 40, 60 operations
- Comparison between:
 - Droplet-aware module-based synthesis (DASC)
 - Routing-based synthesis (RBSC)
 - with contamination avoidance

Average schedule length out of 50 runs for DASC vs. RBSC

Colorimetric protein assay



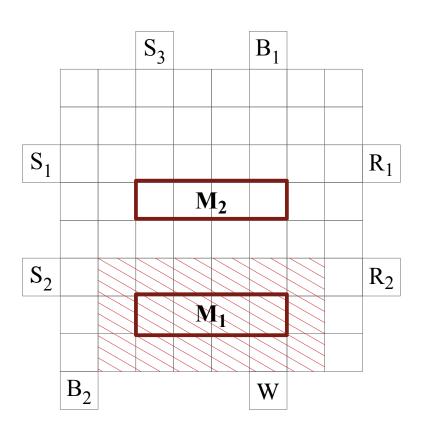
11.19 % improvement for 14 x 14

Contributions

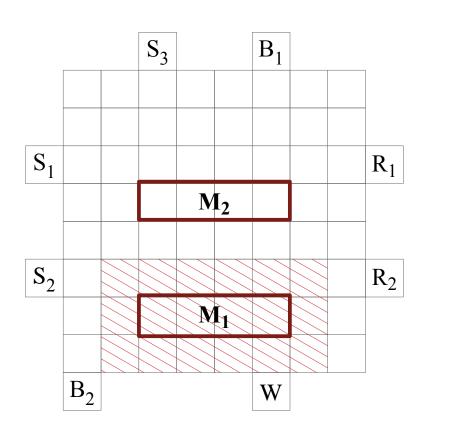
- Tabu Search-based algorithm for the module-based synthesis with fixed devices [CASES09]
- Module-based synthesis with virtual devices [CASES09]
- Module-based synthesis with non-rectangular virtual devices [DAEM10]
- Analytical method for operation execution characterization [CASES10]
- Routing-based synthesis [CASES10] + contamination [DAEM, submitted]
- Droplet-aware module based synthesis [JETC, submitted]
- ILP formulation for the synthesis of digital biochips [VLSI-SoC08]

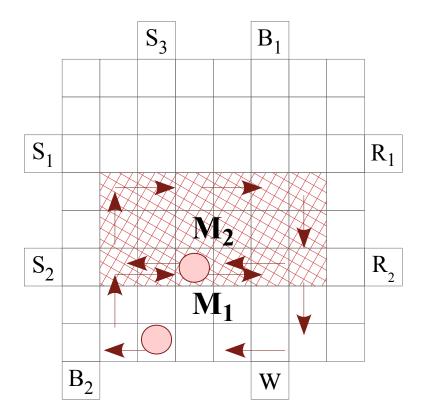
Conclusions

- Proposed several synthesis techniques for DMBs
- Considered the reconfigurability characteristic of DMBs
- Shown that by considering reconfigurability during operation execution improvements in the completion time of applications can be obtained

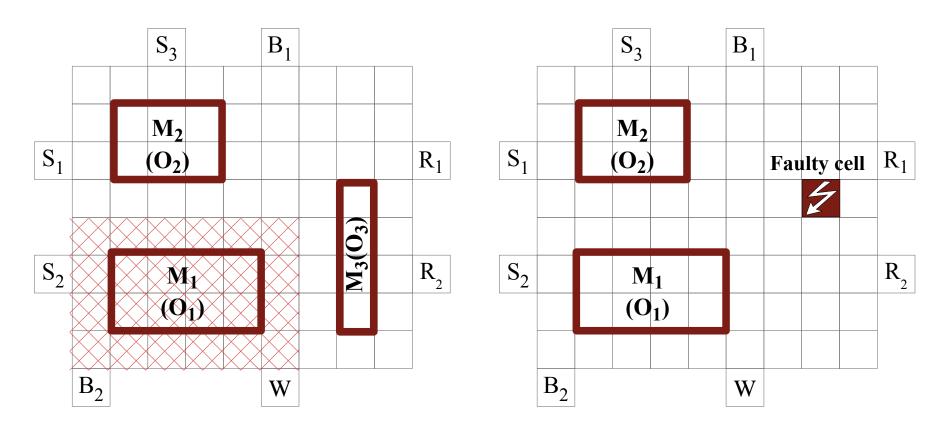


Module-Based Synthesis with Overlapping Devices

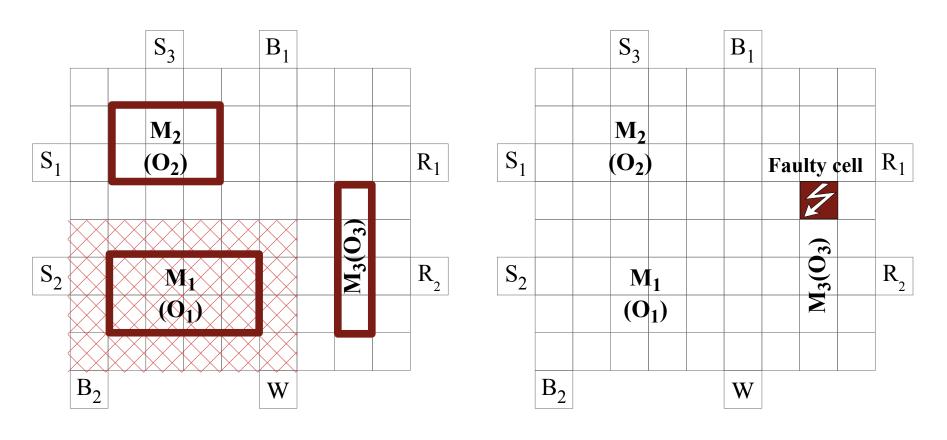




Fault-Tolerant Module-Based Synthesis



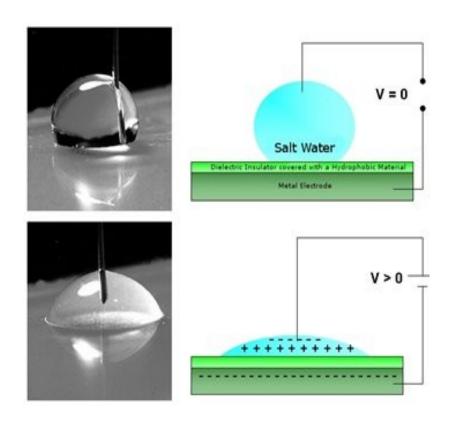
Fault-Tolerant Module-Based Synthesis



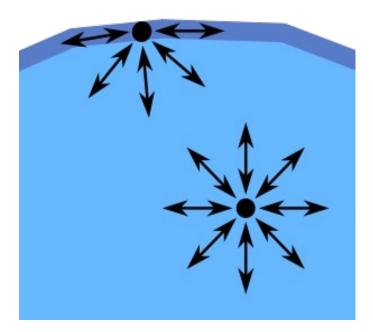


Back-up slides

Electrowetting

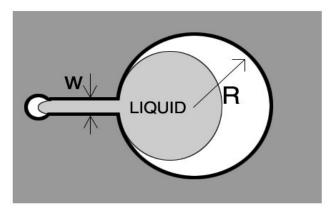


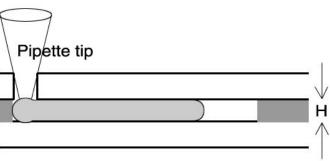
Surface Tension



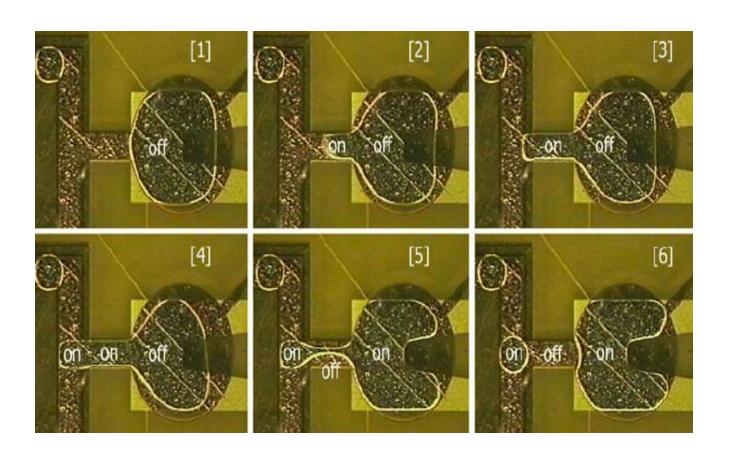
Imbalance of forces between molecules at an interface (gas/liquid, liquid/liquid, gas/solid, liquid/solid)

Dispensing

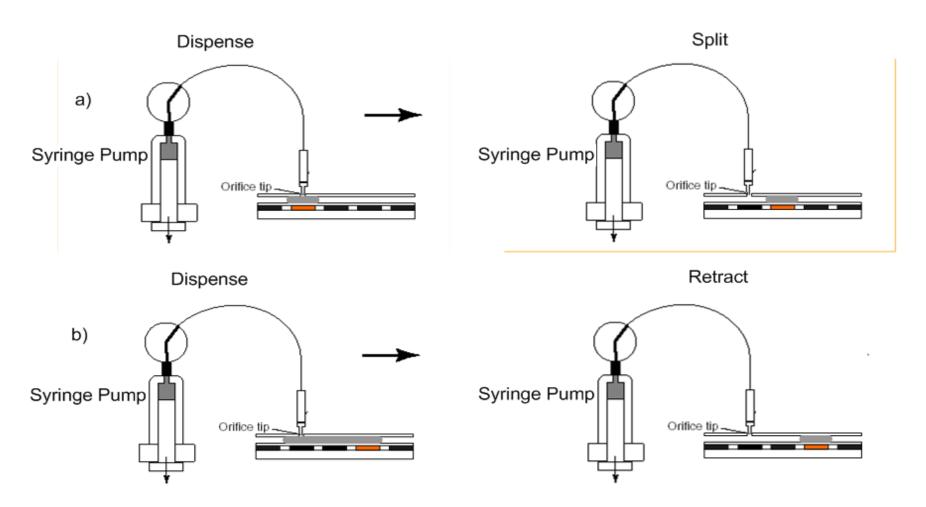




Dispensing



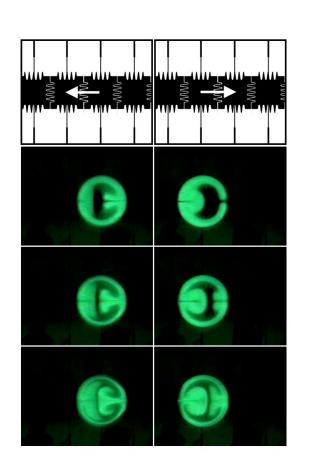
Dispensing

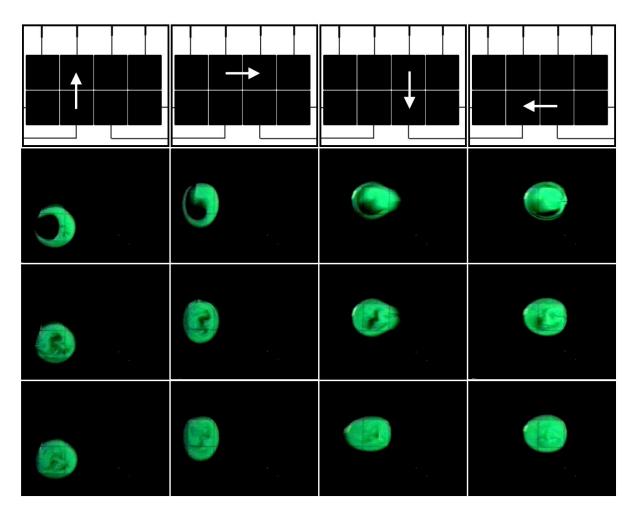


Splitting

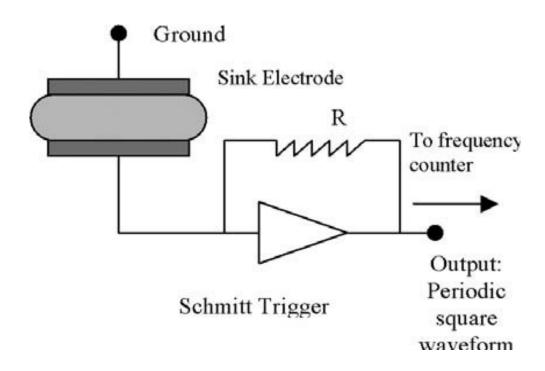


Mixing

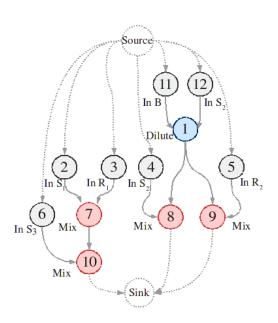




Capacitive sensor



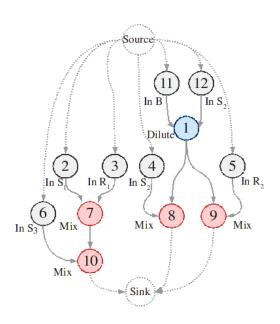


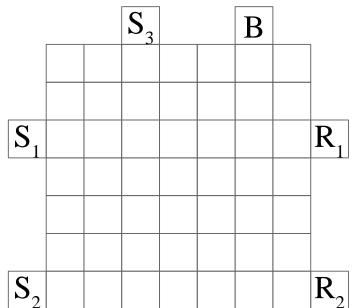


Design Tasks

Operation	Area(cells)	Time(s)
Mix	2 x 2	10
Mix	1 x 3	5
Dilute	1 x 3	8
Dilute	2 x 5	3







Design Tasks

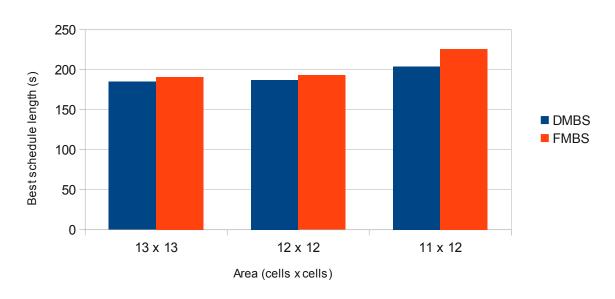
Operation	Area(cells)	Time(s)
Mix	2 x 2	10
Mix	1 x 3	5
Dilute	1 x 3	8
Dilute	2 x 5	3

Experimental Evaluation

Quality of the solution compared to classical operation execution Best out of 50

Colorimetric protein assay

DMBS vs. FMBS



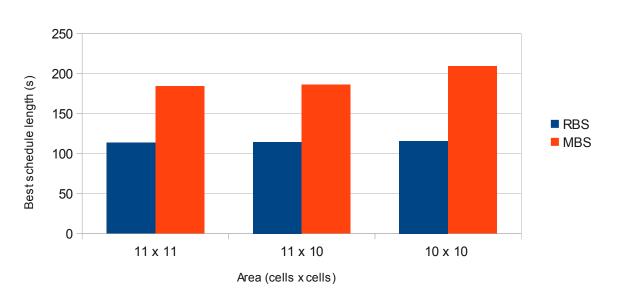
9.73% improvement for 11 x 12

Experimental Evaluation

Quality of the solution compared to classical operation execution Best out of 50

Colorimetric protein assay

RBS vs. MBS



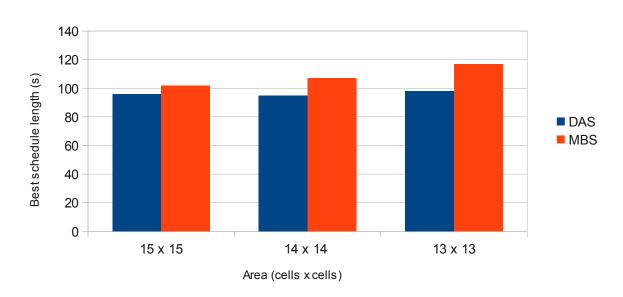
44.63% improvement for 10 x 10

Experimental Evaluation

Quality of the solution compared to classical operation execution Best out of 50

Colorimetric protein assay

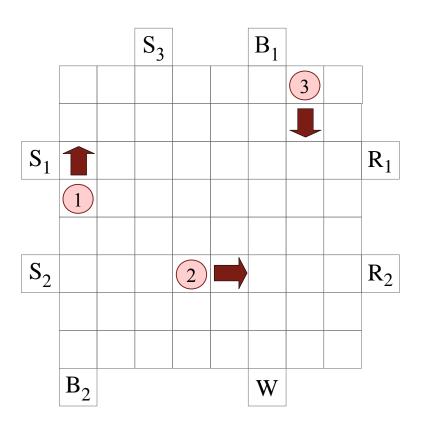
DAS vs. MBS



15.76% improvement for 13 x 13

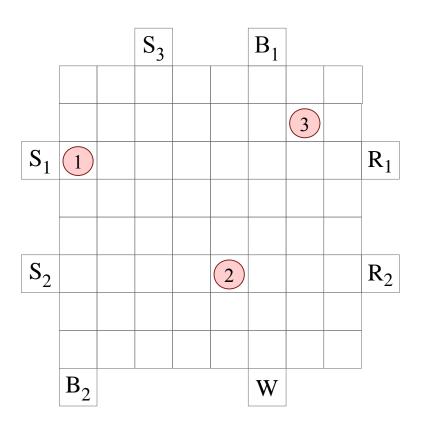
Future Directions

Pin-Constrained Routing-Based Synthesis



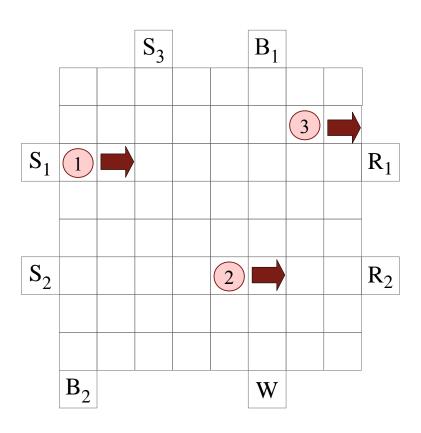
Future Directions

Pin-Constrained Routing-Based Synthesis

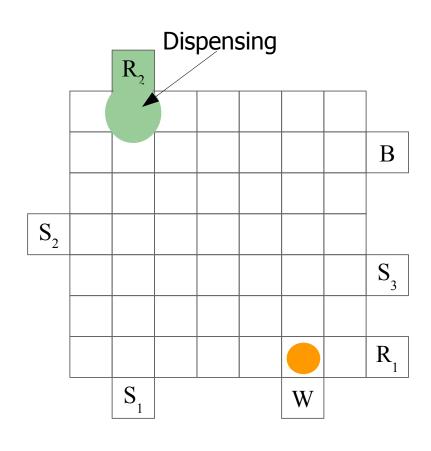


Future Directions

Pin-Constrained Routing-Based Synthesis

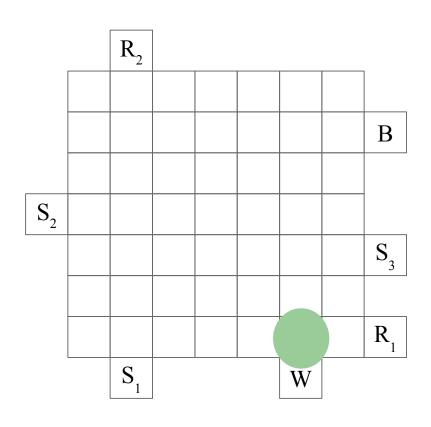






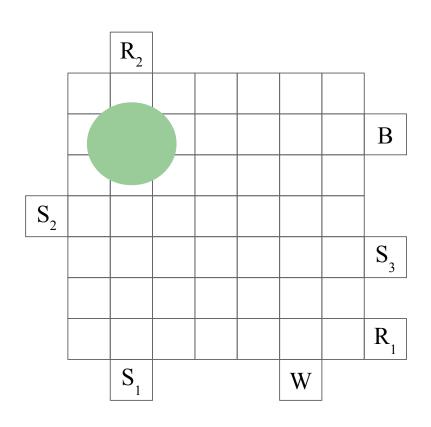
Dispensing





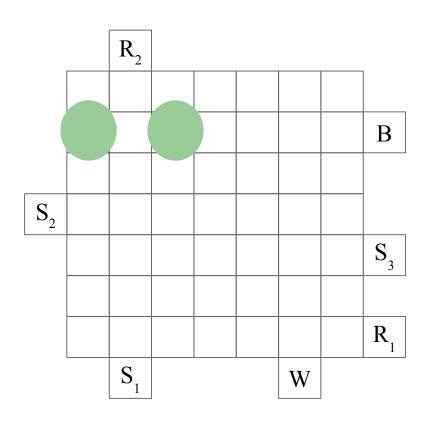
- Dispensing
- Detection





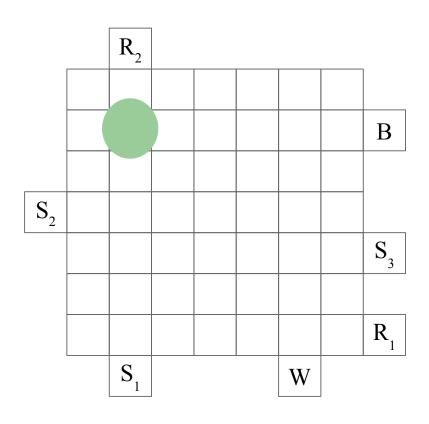
- Dispensing
- Detection
- Splitting/Merging





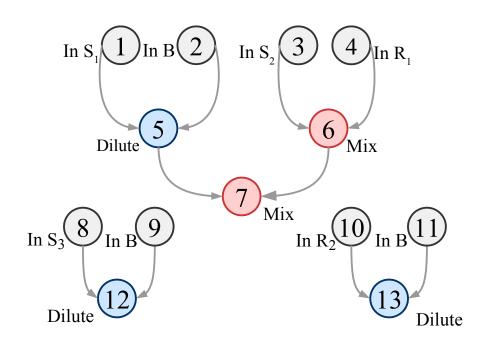
- Dispensing
- Detection
- Splitting/Merging





- Dispensing
- Detection
- Splitting/Merging
- Storage

Motivational Example (for the first contrib)

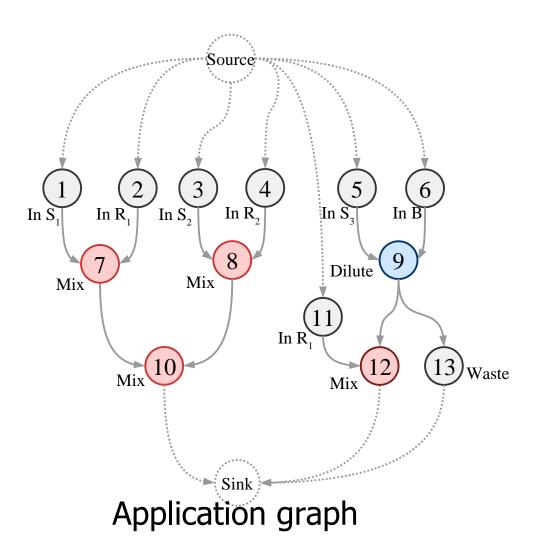


Operation	Area(cells)	Time(s)
Mix	2 x 4	3
Mix	2 x 2	4
Dilution	2 x 4	4
Dilution	2 x 2	5
Dispense	-	2

Application graph

Module library

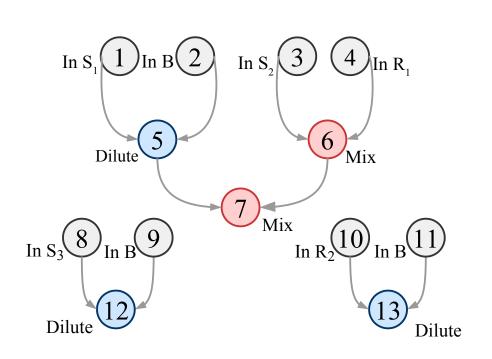
Motivational Example(for the 2nd contrib)



Туре	Area (cells)	Time (s)
Mix/DIt	2 x 4	2.9
Mix/DIt	1 x 4	4.6
Mix/DIt	2 x 3	6.1
Mix/DIt	2 x 2	9.9
Input	-	2
Detect	1 x 1	30

Module library

Example(for the 3rd contrib)



Туре	Area (cells)	Time (s)
Mix/DIt	2 x 4	2.9
Mix/DIt	1 x 4	4.6
Mix/DIt	2 x 3	6.1
Mix/DIt	2 x 2	9.9
Input	-	2
Detect	1 x 1	30

Application graph

Module library