A Two-Stage ILP-Based Droplet Routing Algorithm for Pin-Constrained Digital Microfluidic Biochips

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***Abstract*—With the increasing design complexities, the design of pin-constrained digital microfluidic biochips (PDMFBs) is of practical importance for the emerging marketplace. However, the solution of current pin-count aware technique is inevitably limited by simply adopting it after the droplet routing stage. In this paper, we propose the *first* droplet routing algorithm for PDMFBs that can integrate pin-count technique with droplet routing stage. Furthermore, our algorithm is capable of *simultaneously* minimizing the number of control pins, the number of used cells, and the latest arrival time. We first present a basic integer linear programming (ILP) formulation to optimally solve the droplet routing problem for PDMFBs with simultaneous multi-objective optimization. Due to the complexity of this ILP formulation, we also propose a two-stage technique of global routing followed by *incremental* ILP-based routing to reduce the solution space. To further reduce the runtime, we present a *deterministic* ILP formulation that casts the original routing optimization problem into a decision problem, and solve it by a binary solution search method that searches in logarithmic time. Extensive experiments demonstrate that in terms of the number of the control pins, the number of the used cells, and the latest arrival time, we acquire much better achievement than all the state-of-the-art algorithms in any aspect.**

***Index Terms*—Broadcast-addressing biochips, routing, integer linear programming**

I. Introduction

As the microfluidics technology advances, digital microfluidic biochips (DMFBs) have attracted much attention recently. Compared with the conventional laboratory experiment procedures, which are usually cumbersome and expensive, these miniaturized and automated DMFBs show numerous advantages such as high portability, high throughput, high sensitivity, minimal human intervention, and low sample/reagent volume consumption.

Nonetheless, while more bioassays are executed concurrently on the digital microfluidic platforms, the complexity of the system and the number of the electrodes are bound to increase steadily [8]. Recently, a DMFB that embeds more than 600,000 20 μm by 20 μm electrodes has been demonstrated [2]. Thus, the design of droplet control scheme with pin minimization is of great practical importance for the pin-constrained DMFBs (PDMFBs).

In the most common droplet control scheme, each electrode is directly addressed and controlled by a dedicated control pin, which allows each electrode to be individually activated. In this paper, we refer to these types of DMFBs as *direct-addressing* DMFBs. The previous droplet routing algorithms mainly focus on direct-addressing DMFBs [3], [4], [6], [7], [9], [11]. This scheme maximizes the freedom of the droplet manipulation, but it suffers from the major deficiency that the number of control pins rapidly increases as the system complexity increases. Moreover, a large number of control pins necessitate multiple PCB layers, which potentially raise the price of production cost. Pin-constrained design for direct-addressing DMFBs was addressed in [8]. However, this method is for the exclusive use of some target biofluidic applications, which is not applicable to large-scale PDMFBs.

Recently, a novel *broadcast-addressing* design scheme for PDMFBs has been proposed to overcome the drawbacks of the previous two schemes [10]. This scheme provides high throughput for bioassays and reduces the number of control pins by identifying and connecting them with "compatible" activation sequences. Another advantage of the broadcast-addressing scheme is that it provides the maximum freedom of droplet movement as the direct-addressing scheme. The compatible activation sequences can be derived by applying minimal clique partitioning to electrodes. However, the minimal clique partitioning problem is known to be NP-hard. Furthermore, the solution is inevitably limited by simply using the direct-addressing-based routing result as the input to apply the broadcast-addressing scheme. Therefore, the traditional broadcast-addressing scheme may result in suboptimal solutions.

A. Our Contribution

In this paper, we propose the *first* droplet routing algorithm for PDMFBs that *simultaneously* minimizes the number of control pins, the number of used cells, and the latest arrival time. We first present a basic integer linear programming (ILP) formulation to optimally solve the droplet routing problem for PDMFBs. Due to its complexity, we also propose a two-stage technique of global routing followed by incremental ILP-based routing to reduce the solution space effectively. Our algorithm divide the original routing problem to global routing paths spatially to reduce the solution space of ILP formulations. In this way, the original problem is reduced to a manageable size, then we can practically apply an incremental ILP-based method to finding a high-quality solution within reasonable CPU time. To achieve further efficiency, we propose a *deterministic* ILP formulation that casts the original optimization into a decision problem and solve it by a logarithmic search technique. The major contributions of this paper include the followings:

- We propose the *first* droplet routing algorithm that considers the droplet routing and the broadcast-addressing scheme *simultaneously* for PDMFBs. In contrast with the previous works that start with an initial direct-addressing-based routing result, our algorithm has higher flexibility to solve the droplet routing problem on PDMFBs globally.
- Unlike the previous works that only minimize the number of control pins, our algorithm can *simultaneously* minimize not only the number of the control pins but also the number of used cells and the latest arrival time, which is attributed to the well-founded formulation of the constraints into our ILP formulations.
- To tackle the complexity of the basic ILP formulations, we propose a two-stage routing scheme of global routing followed by incremental ILP-based routing. For the basic ILP, the problem instance is the whole 2D plane and it handles all droplets simultaneously. For our two-stage ILP, the problem instance is reduced to global routing paths and the droplets are routed in incremental manner that reduce the solution space significantly. Therefore, our algorithm can obtain a high-quality solution within reasonable CPU time.
- To further reduce the runtime, we present a *deterministic* ILP formulation that casts the original routing optimization problem into a decision problem, and then solves it by a binary solution search method that searches in logarithmic time.

Compared with the direct-addressing and the broadcast-addressing schemes, the extensive experiments demonstrate that in terms of the number of the control pins, the number of the used cells and the latest arrival time, we acquire much better achievement than all the current state-of-the-art algorithms in any aspect.

II. Problem Formulation

A. Problem Formulation

In addition to minimizing the number of control pins in PDMFBs, it is desirable to minimize the number of unit cells that are used during routing. Furthermore, it is desirable to minimize the latest arrival time among all droplets to achieve fast bioassay execution and better reliability [5], [11]. Besides the objectives, there are two routing constraints in droplet routing:

the fluidic constraint and the timing constraint. The fluidic constraint is used to avoid the unexpected mixtures between two droplets of different nets during their transportation and it can further be divided into the static and dynamic fluidic constraints [7]. Besides the fluidic constraint, there exists the timing constraint. The timing constraint specifies the maximum arrival time of a droplet from its source to sink. The droplet routing problem for the PDMFBs can be formulated as follows:

Input: A netlist of n droplets $D = \{d_1, d_2, \ldots, d_n\}$, the locations of blockages, and the timing constraint T_{max}.

Constraint: Both fluidic and timing constraints are satisfied.

Objective: Route all droplets from their source cells to their sink cells while minimizing (1) the number of pins, (2) the number of used cells, and (3) the latest arrival time among all droplets.

III. ILP Formulation for Droplet Routing

In this section, we propose the *first* basic ILP formulation that considers the droplet routing and the broadcast-addressing scheme *simultaneously* for PDMFBs. We show the objectives of the ILP formulation and the associated constraints. For the sake of brevity and generality, we focus on 2-pin net routing.

A. Objective

Our goal is to minimize the number of control pins, the number of used cells, and the latest arrival time.

B. Constraints

There are total ten constraints in our basic ILP formulations.

1) *Source requirement:* All droplets are at their source location at time zero.
2) *Sink requirements:* All droplets must reach their sinks within timing constraint. Once a droplet reaches its sink, it remains there.
3) *Exclusivity constraint:* Each droplet has only one location at each time step.
4) *Droplet movement constraint:* A droplet can have only five possible movements; stall or move to four adjacent cells from t to $t+1$.
5) *Fluidic constraints:* There are two fluidic constraints: static and dynamic fluidic constraints. Static fluidic constraint states the minimum spacing between two droplets must be one cell. In other words, there are no other droplets in the 3×3 region centered by a droplet. To prevent unexpected mixing during droplet movement, dynamic fluidic constraint requires that at time $t+1$, d_i cannot move to the cell (x, y), which is the neighboring cells of d_j's location at time t.
6) *Electrode constraints:* The electrode constraints can be detailed as the following two rules.
   - **EC-Rule I:** If a droplet d_i stalls at time t, the exact number of must-be-deactivated cells is 8; otherwise, if d_i moves to the four adjacent cells at time t, the exact number of must-be-deactivated cells is 11.
   - **EC-Rule II:** The cells that have no impact on droplets transportation are don't care terms.
7) *Broadcast constraints:* The broadcast constraints contains three major rules and can be represented as follows [10].
   - **BC-Rule I:** Two activation sequences are compatible if and only if the corresponding binary values are the same.
   - **BC-Rule II:** If the activation sequences of two cells are incompatible, we cannot broadcast the two cells with the same control pin.
   - **BC-Rule III:** If the activation sequences of two cells are compatible, we can broadcast the two cells with the same control pin *or not*.

IV. Two-Stage ILP-Based Algorithm

Although the basic ILP formulations can optimally solve the droplet routing problem for PDMFBs, it is still limited in handling the dramatically growing complexity in practical bioassays. In this section, we propose a two-stage ILP-based droplet routing algorithm of global routing followed by incremental ILP-based routing for PDMFBs. In the first stage, we perform the global routing to find the initial routing paths for droplets such that the solution space can be reduced from the entire 2D plane to these paths. Then, we propose a heuristic to determine the routing order and introduce an incremental-ILP-based method to solve the droplet routing problem.

TABLE I: NOTATIONS USED IN OUR TWO-STAGE ILP FORMULATION.

G_i	set of used cells in global routing path for droplet d_i
G'_i	set of used cells by the previous routed droplet d_i
N	netlist among all subproblems
T^i_{max}	maximum available completion time that can be used for routing droplet d_i
P^i_{max}	maximum available number of control pins that can be used for routing droplet d_i
M_i	routing resources for droplet d_i to route with the previous routed droplets
IS	increasing scalar of routing resources
BB_i	set of available cells in bounding box of droplet d_i
E_b	set of blockage cells
E_{s_i}	set of available cells in the 3×3 area center by source s_i
E_{t_i}	set of available cells in the 5×5 area center by target t_i

A. Global Routing

The goal of global routing is to schedule the initial droplet routing paths to reduce the complexity of the solution space in the ILP formulations from the whole 2D plane to global routing paths. With the increased design complexities, any naïve routing path may violate the timing and fluidic constraints easily. Furthermore, if droplets route disorderly, a large number of cells and independent control pins will be used. Hence, the reliability and fault tolerance for bioassays will be significantly degraded. To overcome these drawbacks, we construct the global routing tracks with the preferred moving direction to derive an initial routing path on these tracks for each droplet. Due to the fluidic constraints, it is desirable to maintain a minimum space when droplets move on the microfluidic array. Therefore, the initial global routing tracks are constructed on non-adjacent rows and columns. Then we determine the preferred moving direction of these tracks by analyzing the preferred moving direction of each net. We define $pmdl_i(x, y)$, $pmdr_i(x, y)$, $pmdu_i(x, y)$, and $pmdd_i(x, y)$ to represent the cell (x, y) with the left, right, up, and down preferred moving directions, respectively, within the bounding box of net n_i. Therefore, the preferred moving direction of global routing tracks can be defined as follows:

- For tracks on rows (tr_j):
  If
  $$\sum_{(x,y)\in tr_j} \sum_{n_i \in N} pmdr_i(x, y) \geq \sum_{(x,y)\in tr_j} \sum_{n_i \in N} pmdl_i(x, y)$$
  , the preferred moving direction is right; otherwise it is left.
- For tracks on columns (tc_j):
  If
  $$\sum_{(x,y)\in tc_j} \sum_{n_i \in N} pmdu_i(x, y) \geq \sum_{(x,y)\in tc_j} \sum_{n_i \in N} pmdd_i(x, y)$$
  , the preferred moving direction is up; otherwise it is down.

After that, we model the routing path of droplet d_i as $P_{d_i} = \{v_1, v_2, \ldots, v_n\}$ where each node v_i represents the cell used in microfluidic array, then apply A* maze searching to find a min-cost routing path for each droplet. Note that v_1 is the location of source and v_n is the location of sink. If droplet moves along the preferred moving direction from v_i to v_{i+1}, we assign the routing cost c_1; otherwise, we assign a higher routing cost c_2 for penalty. In this paper, we set c_1 and c_2 to be 1 and 3, respectively.

B. Net Criticality Calculation

A key issue in the droplet routing problem is the determination of the droplet routing order. A droplet d_i is said to be critical if d_i has fewer possible solutions (routing paths and schedules) due to the severe interferences with other droplets or blockage cells. We use $crit(d_i)$ to denote the criticality of droplet d_i and $crit(d_i)$ is defined as follows:

$$crit(d_i) = \frac{(|E^i_b| + |E^i_s|) - |E^i_t|}{|BB_i|} \quad (1)$$

where

$$
\begin{aligned}
E_b^i &= \{c | c \in E_b \cap BB_i\} \\
E_s^i &= \{c | c \in E_{s_j} \cap BB_i, \forall d_j \in D/d_i\} \\
E_t^i &= \{c | c \in E_{t_j} \cap BB_i, \forall d_j \in D/d_i\}
\end{aligned}
$$

The intuition behind the net criticality can be described as follows. Due to the blockage constraints and fluidic property, the cell of blockages and source cells inside BB_i will have detrimental effects on the routability of droplet d_i. On the contrary, since the target cells will become blockages after they are routed, a droplet with many target cells inside its bounding box has more routing solutions before these target cells are routed. In this paper, we first route a droplet with the highest criticality.

C. Incremental ILP-Based Routing

After the global routing stage, the solution space is reduced significantly from the whole 2D plane to global routing paths. To further reduce the solution space that directly considers all droplets at the same time, the incremental ILP-based routing routes an un-routed droplet with the previous routed droplets incrementally. Thus, for an un-routed droplet d_i and a previous routed droplet d_j, we reformulate the ILP constraints by replacing the whole 2D available cell set C with the cell set G_i which is used in its global routing path and the cell set G'_j which is used by the previous routed paths, respectively.

To further reduce the runtime, we cast the original optimization problem into a decision problem by solving the DILP formulations. In each iteration, we select an un-routed droplet with the highest criticality, then route it with the previous routed droplets by solving the DILP formulations incrementally. To search a feasible solution within minimal routing resources efficiently, we perform a binary solution search method that searches the feasibility in logarithmic time.

Although the above proposed method can solve the droplet routing problem in a reasonable runtime by global routing followed by incremental routing. However, as the increased design complexity of DMFBs, if the routing paths are restricted to the global routing paths, the freedom of droplets is also restricted, which may cause routability problem. Therefore, if we cannot route an un-routed droplet d_i with the previous routed droplets in the cell set G_i of global routing path, we increase the cell set G_i by one bounding box and reroute it. Finally, iteration terminates until all droplets are routed.

1) DILP Formulation: By global routing and incremental routing scheme, the solution space is reduced significantly. However, the ILP formulation is still limited in handling the dramatically growing complexity in current and future PDMFBs. To further reduce the runtime, we propose a DILP formulation that casts the original routing optimization problem into a decision problem. Thus, we redefine the objective function as follows:

$$Minimize : 1 \tag{2}$$

Instead of directly searching the original objective function within the fixed maximum available set T_{max} and P_{max}, the DILP determines a feasible solution only within the minimal routing resources. Therefore, for an un-routed droplet d_i with the previous routed droplets, the routing resources in our DILP formulation are T^i_{max} and P^i_{max}. In the constraints formulation, we replace the ILP sets of maximum completion time T_{max} with T^i_{max}, and the maximum available control pins P_{max} with P^i_{max}, respectively. Thus, the DILP try to minimize these two routing resources and determine if there exists a feasible routing solution within them.

2) Solution Search of DILP: The key issue in the DILP formulations is to minimize the routing resources that we can successfully route an un-routed droplet d_i with the previous routed droplets. A naïve approach is to exhaustively search all the permutation of routing resources among the range of [0, T_{max}] and [0, P_{max}]. This method is time-consuming due to the time complexity is $O(T_{max} \times P_{max})$. Furthermore, it is hard to directly handle the two objective functions T^i_{max} and P^i_{max} efficiently. To remedy these deficiencies, we use a linear combination of these two objective functions to be one single objective function M_i and define the increasing scalar to characterize the growth rate of routing resources. Thus, the routing resources M_i can be defined as follows:

$$M_i = (T^i_l + \sigma_1 \cdot IS) + (P^i_l + \sigma_2 \cdot IS) \tag{3}$$

where IS is the growth rate of routing resources M_i and both σ_1 and σ_2 are user specified constants. As the experimental setting, we set σ_1 and σ_2 to be 1 and 0.5, respectively. Based on the definition, we have the following lemma.

Lemma 1: Given two increasing scalars IS_1 and IS_2 where $IS_1 < IS_2$. If droplet d_i can be routed with IS_1, then droplet d_i can be also routed with IS_2.

This lemma follows true since the increasing scalar IS of routing resources increases monotonically. If we have found a feasible routing resources that can route an un-routed droplet d_i, increasing the routing resources only increases the solution space of our DILP formulations. The lemma shows the *continuous* relationship of increasing scalar and feasibility of DILP formulations. This feature of increasing scalar shows the capability of solving in logarithmic time by performing a binary search method. Therefore, to avoid the runtime overhead caused by the exhaustive permutations, we propose a binary solution search method to optimally search the minimum increasing scalar, denoted by IS^*, for routing resources to route the un-routed droplet d_i successfully. By the binary solution searching algorithm, the complexity of iterations is reduced to $O(log(IS_u - IS_l))$. Compared with the exhaustively searching, the proposed algorithm reduces the runtime significantly.

V. Experimental Results

Our two-stage ILP-based droplet routing algorithm was implemented in the C++ language and ran on a 2GHz 64-bit Linux machine with 8GB memory, and GLPK [1] was used as our ILP solver. We evaluated all routing algorithms on the two practical bioassays used in the previous work [11]: the in-vitro diagnostics and the colorimetric protein assay. Table II shows the statistics of each benchmark. To show the effectiveness and the robustness of our algorithm, we conducted three experiments for the number of control pins, the number of used cells, and the latest arrival time among the direct-addressing ([11], [4]), the broadcast-addressing scheme([11] + [10] and [4] + [10]), and ours ([11] + IILP, [4] + IILP, and two-stage ILP) in Table III. For fair comparison, we compare the maximum and average values among all subproblems. We also conduct an experiment on integrating our IILP routing approach with those direct-addressing-based droplet routing algorithms to demonstrate the effectiveness and efficiency of our IILP formulations in Table IV.

For the first experiment, we compared the number of control pins among different schemes. Compared with the direct-addressing scheme ([11], [4]), the respective maximum and average number of control pins among all subproblems are (4.53×, 3.82×) and (4.44×, 4.03×) of our algorithm. Compared with the broadcast-addressing scheme ([11] + [10], [4] + [10]), the respective maximum and average number of control pins among all subproblems are (1.74×, 1.90×) and (1.78×, 2.06×) of our algorithm. To demonstrate the effectiveness of our IILP formulations, compared with the integrated scheme ([11] + IILP, [4] + IILP), the respective maximum and average number of control pins among all subproblems are (1.32×, 1.73×) and (1.54×, 1.83×) of our algorithm.

In the second experiment, we compared the number of used cells among different schemes. For the direct-addressing scheme ([11], [4]), the number of used cells among all subproblems are (1.02×, 1.07×) of our algorithm. Since the broadcast-addressing scheme is directly applied to the direct-addressing-based routing result, the number of used cells are the same with the direct-addressing scheme. Compared with the integrated scheme ([11] + IILP, [4] + IILP), the number of used cells among all subproblems are (1.00×, 1.02×) of our algorithm.

In the third experiment, we compared the latest arrival time among different schemes. Compared with the direct-addressing scheme ([11], [4]), the respective maximum and average latest arrival time among all subproblems are (1.01×, 1.05×) and (1.04×, 1.14×) of our algorithm. Since the broadcast-addressing scheme is directly applied to the direct-addressing-based routing result, the statistics of the latest arrival time are the same with the direct-addressing scheme. To demonstrate the effectiveness of our IILP formulations, compared with the integrated scheme ([11] + IILP, [4] + IILP), the average latest arrival time among all subproblems are (1.03×, 1.08×) of our algorithm.

Table IV shows the runtime comparison among the basic ILP, direct-addressing + IILP, and our two-stage ILP algorithm. For the basic ILP, the problem instance is the whole 2D plane and it solves all the droplets simultaneously. For our two-stage ILP, the problem instance is reduced to global routing paths and the droplets are routed in incremental manner that reduce the solution space significantly. The results show that the basic ILP

TABLE III: COMPARISONS FOR NUMBER OF PINS, NUMBER OF USED CELLS,AND LATEST ARRIVAL TIME AMONG THE DIRECT-ADDRESSING, BROADCAST-ADDRESSING, AND OURS

Benchmark	Direct Addressing				Broadcast Addressing				Two-Stage ILP					
	[11]		[4]		[11]+[10]		[4]+[10]		[11]+IILP		[4]+IILP		Ours	
	P_{max}	P_{avg}	P_{max}	P_{avg}	P_{max}	P_{avg}	P_{max}	P_{avg}	P_{max}	P_{avg}	P_{max}	P_{avg}	P_{max}	P_{avg}
vitro_1	45	21.55	50	23.45	21	9.48	22	10.11	15	9.11	18	9.49	13	4.51
vitro_2	50	15.73	42	16.40	21	8.95	24	10.64	17	8.03	17	9.21	12	5.01
protein_1	67	25.28	75	26.38	18	9.52	18	10.55	14	8.54	15	9.25	12	5.43
protein_2	54	12.03	46	12.35	23	8.73	21	8.55	17	7.72	23	7.38	11	4.43
	4.53	3.82	4.44	4.03	1.74	1.90	1.78	2.06	1.32	1.73	1.54	1.83	1	1

Benchmark	Direct Addressing		Broadcast Addressing		Two-Stage ILP		
	[11]	[4]	[11]+[10]	[4]+[10]	[11]+IILP	[4]+IILP	Ours
	U.C.	U.C.	U.C.	U.C.	U.C.	U.C.	U.C.
vitro_1	237	258	237	258	231	243	231
vitro_2	236	246	236	246	231	229	229
protein_1	1618	1688	1618	1688	1597	1627	1582
protein_2	939	963	939	963	927	943	930
	1.02	1.07	1.02	1.07	1.00	1.02	1

Benchmark	Direct Addressing				Broadcast Addressing				Two-Stage ILP					
	[11]		[4]		[11]+[10]		[4]+[10]		[11]+IILP		[4]+IILP		Ours	
	Max. T_i	Avg. T_i	Max. T_i	Avg. T_i	Max. T_i	Avg. T_i	Max. T_i	Avg. T_i	Max. T_i	Avg. T_i	Max. T_i	Avg. T_i	Max. T_i	Avg. T_i
vitro_1	20	13.00	19	14.30	20	13.00	19	14.30	19	12.47	19	13.55	18	12.41
vitro_2	17	11.33	20	12.00	17	11.33	20	12.00	17	11.01	17	11.48	18	10.46
protein_1	20	16.31	20	16.55	20	16.31	20	16.55	20	16.08	20	15.44	20	15.42
protein_2	20	10.51	20	12.19	20	10.51	20	12.19	20	10.33	20	11.52	20	10.22
	1.01	1.05	1.04	1.14	1.01	1.05	1.04	1.14	1.00	1.03	1.00	1.08	1	1

■ P_{max}: maximum number of control pins among all subproblems. ■ **Avg. T_i**: average latest arrival time among all subproblems.
■ **U.C.**: total number of unit cells used for routing. ■ **Max. T_i**: maximum latest arrival time among all subproblems.
■ P_{avg}: average number of control pins among all subproblems.

needs at least five days to solve all 2D planes of one benchmark, which is not feasible for this problem; in contrast, our two-stage ILP algorithm needs at most 30.13 second due to the significantly smaller solution space. To demonstrate the effectiveness of our IILP formulations, compared with the integrated scheme ([11] + IILP, [4] + IILP), our algorithm reduced the runtime by about (34%, 55%).

Based on the evaluation of four experiments, our two-stage ILP-based droplet routing algorithm achieves the best result of the number of control pins, the number of used cells, and the latest arrival time over the existing algorithms within reasonable CPU times. The experimental results demonstrate that our algorithm is very effective for droplet routing on PDMFBs.

TABLE II: STATISTICS OF THE ROUTING BENCHMARKS

Benchmark	Size	#Sub	T_{max}	#Nets	$\#D_{max}$
vitro_1	16 X 16	11	20	28	5
vitro_2	14 X 14	15	20	35	6
protein_1	21 X 21	64	20	181	6
protein_2	13 X 13	78	20	178	6

■ Size: size of microfluidic array. ■ #Sub: number of subproblems. ■ T_{max}: timing constraint.
■ #Nets: total number of nets. ■ $\#D_{max}$: maximum number of droplets among subproblems.

TABLE IV: COMPARISONS FOR RUNTIME AMONG BASIC ILP, DIRECT-ADDRESSING + IILP, AND OURS

Benchmark	Basic ILP	[11]+IILP	[4]+IILP	Ours
	CPU (min)	CPU (sec)	CPU (sec)	CPU (sec)
vitro_1	> 7200	14.33	15.31	10.11
vitro_2	> 7200	16.49	18.38	8.32
protein_1	> 7200	28.43	34.51	30.13
protein_2	> 7200	22.16	28.33	21.38
	N.C.	1.34	1.55	1

■ N.C.: Non comparable

VI. Conclusion

In this paper, we proposed the *first* droplet routing algorithm that considers the droplet routing and the broadcast-addressing scheme *simultaneously* for PDMFBs. We first presented a basic integer linear programming (ILP) formulation to optimally solve the droplet routing problem with simultaneously minimizing the number of control pins, the number of used cells, and the latest arrival time. Due to its complexity, we also proposed a two-stage technique of global routing followed by incremental ILP-based routing. To further reduce the runtime, we presented a *deterministic* ILP formulation that casts the original routing optimization problem into a decision problem, and then solves it by a binary solution search method that searches in logarithmic time. Extensive experiments demonstrate that in terms of the number of the control pins, the number of the used cells and the latest arrival time, we acquire much better achievement than all the state-of-the-art algorithms in any aspect.

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