0368-4159: First Course in Derandomization 15/10/2018 – Lecture 1

The Perfect Match (PM) Problem

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Given a bipartite graph $G = (V, W, E)$ s.t. $|V| = |W| = n$, the **Perfect Match (PM)** problem is a decision problem L s.t. a bipartite graph $G \in L \iff G$ has a perfect matching; i.e. a subset $E' \subseteq E$ s.t. every $x \in V$ touches exactly one edge $e \in E'$.

We present the notions of parallel and concurrent computation, and construct a randomized algorithm with poly-logarithmic runtime for both the decision problem (does G have a perfect matching?) and the construction problem (construct a perfect matching or return *null* if no match exists).

1 The $CREW$ Model

Definition 1 *Given a language L (some decision problem) and some input $x \in \{0,1\}^n$, the **PRAM** model assumes we have a polynomial $p(n)$ number of CPUs and a polynomial $q(n)$ sized shared memory. In every 'clock cycle', each CPU may (in parallel):*

1. *Read a cell of the shared memory*
2. *Perform some (short, constant time) local computation*
3. *Write to a cell in the shared memory*

Definition 2 *The **CREW** model stands for **C**oncurrent **R**eads **E**xclusive **W**rites, which simplifies the **PRAM** model somewhat by exempting us from discussing race conditions.*

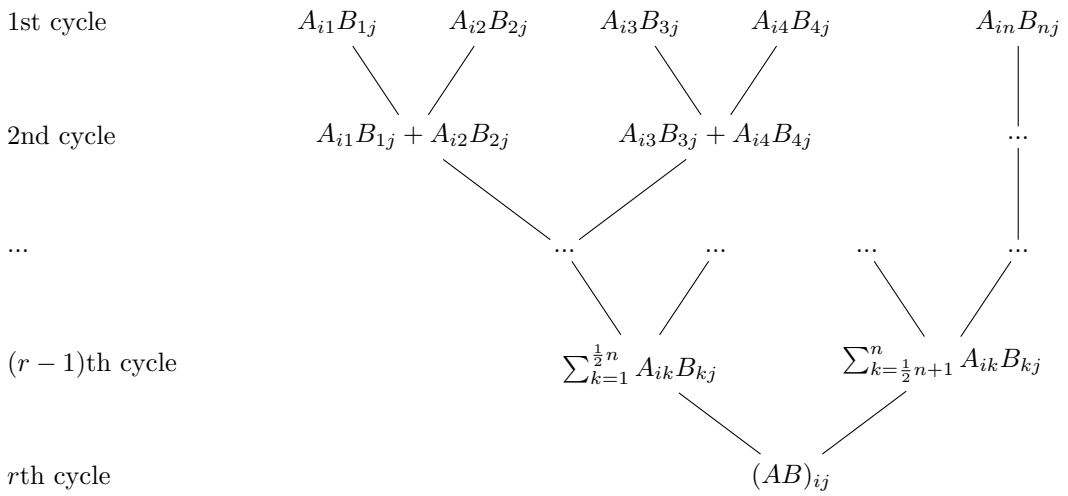
Example 3 *Matrix product.*

For some $A, B \in \mathbb{R}^{n \times n}$ we can take n^2 CPU cores; core (i, j) will compute:

$$(AB)_{ij} = \sum_{k=1}^{n} A_{ik} B_{kj}$$

As these all run in parallel and each core computes n sums and products, with n^2 cores we get a parallel runtime of $O(n)$. This is still polynomial runtime; a naive non-parallel approach also runs in polynomial ($O(n^3)$) time. Can we do better?

Fix some i, j. Core (i, j) must compute $\sum_k A_{ik} B_{kj}$; if we use n cores to compute the n products in parallel and then perform the addition in a tree-like way, we can improve the runtime to $O(\log(n))$. To illustrate, assume $n = 2^r$ for some $r \in \mathbb{N}$:



The depth of the above computation is $r = O(\log(n))$. By adding n cores per previous core, we now have a parallel logarithmic-time algorithm utilizing $O(n^3)$ cores; much better than linear time.

1.1 Remarks:

- The above product/sum tree can be described as a circuit; the complete circuit that computes the matrix product is of size $O(n^3)$ and depth $O(\log(n))$

2 Decision problem

Tne next algorithm is from [2].

2.1 Algorithm

PM is the decision problem that given $G = (V, E)$ accepts $\iff$ G has a perfect matching. We will discuss only those cases where G is a bipartite graph; we shall henceforth denote $G = (V, W, E)$ where $|V| = |W| = n$ are the two sides (node sets) of the graph.

Remark 4 *The problem of counting how many such perfect matchings exist is #P-complete!*

Our algorithm begins with the definition of the following matrix of variables:

$$M_{ij} = \begin{cases} 0 & (i,j) \notin E \\ x_{ij} & (i,j) \in E \end{cases}$$

where x_{ij} denote n^2 distinct variables. The algorithm does as follows:

1. For every i, j fix some random $a_{ij} \in \{1, 2, 3, ..., 2n\}$
2. Substitute every x_{ij} in M as a_{ij} (zero entries remain zero) to create the matrix A:

$$A_{ij} = \begin{cases} 0 & (i,j) \notin E \\ a_{ij} & (i,j) \in E \end{cases}$$

3. Compute $\det(A)$

4. Accept $\iff \det(A) \neq 0$

Definition 5 *Given a matrix $A \in \mathbb{R}^{n\times n}$, the determinant $\det(A)$ is defined:*

$$\det(A) = \sum_{\pi \in S_n} sign(\pi) \prod_{i=1}^{n} A_{i,\pi(i)}$$

where S_n denotes the set of all permutations on the set $\{1, ..., n\}$.

Proposition 6 *If there is no perfect matching, the above algorithm always rejects.*

Proof: Assume there is no perfect matching and let $\pi \in S_n$. If, for every i, we have $(i, \pi(i)) \in E$, then the set $\{(i, \pi(i)) : 1 \leqslant i \leqslant n\}$ is a perfect matching; hence there must exist some i s.t. $(i, \pi(i)) \notin E$ and therefore $M_{i,\pi(i)} = 0$ by definition. As such, for any $\vec{a} = (a_{11}, ..., a_{nn}) \in \{1, 2, ..., 2n\}^{n^2}$ chosen at step 1 of the algorithm:

$$\prod_{j=1}^{n} A_{j,\pi(j)} = 0 \cdot \prod_{j\neq i} A_{j,\pi(j)} = 0$$

This is true for any $\pi \in S_n$, so for any $\vec{a}$ chosen:

$$\det(A) = \sum_{\pi \in S_n} sign(\pi) \prod_{i=1}^{n} A_{i,\pi(i)} = \sum_{\pi \in S_n} sign(\pi) \cdot 0 = 0$$

and the algorithm will reject. ■

Proposition 7 *If a perfect matching exists, the algorithm accepts with probability $\frac{1}{2}$ or better.*

To prove this proposition we recall the following lemma:

Lemma 8 (Schwartz-Zippel lemma) *Given a field F, a subset $A \subseteq F$ and a polynomial $0 \not\equiv p \in F[x_1, ..., x_m]$:*

$$Pr_{(a_1,...,a_m)\in A^m}(p(a_1, ..., a_m) = 0) \leqslant \frac{\deg(p)}{|A|}$$

Note that it is important that $p \not\equiv 0$!

Proof (Prop. 7): If a perfect matching $\{(i_k, j_k) : 1 \leqslant k \leqslant n\}$ exists, it can be defined by some permutation $\pi(i_k) = j_k$. Fix such a permutation π.

Observe $\det(M)$. As M is a matrix of variables, $\det(M)$ is a polynomial in n^2 variables:

$$\det(M) = p(x_{11}, ..., x_{nn})$$

By the definition of the determinant as stated above, one of the summed elements is:

$$sign(\pi) \prod_{i=1}^{n} x_{i,\pi(i)}$$

This term is not zero (as π defines a perfect matching) and cannot be canceled out by any other term of p (because different permutations define different variables appearing in the term), so we know $p \not\equiv 0$. We also know that each non-zero term is a product of n variables, so $\deg(p) = n$. By applying SZ-lemma:

$$Pr_{(a_{11},...,a_{nn})\in\{1,2,...,2n\}^{n^2}}(p(a_{11}, ..., a_{nn}) = 0) \leqslant \frac{\deg(p)}{|\{1, 2, ..., 2n\}|} = \frac{n}{2n} = \frac{1}{2}$$

This is precisely the probability of rejecting! Step 1 of the algorithm randomly chooses a vector $\vec{a} \in \{1, ..., 2n\}^{n^2}$ and rejects $\iff \det(A) = p(\vec{a}) = 0$. ■

It remains to be shown that we may compute $\det(A)$ efficiently. Note that up to this point we did not introduce parallelism (maybe only to generate the $O(n^2)$ random values of A in logarithmic time); parallelism will be employed heavily to compute the determinant.

Although we will not prove this method formally, a general outline and ideas employed will be presented.

2.2 Computing $det(A)$ in parallel

We give highlights of Csanky's algorith [1]. Denote $\lambda_1, ..., \lambda_n$ as the eigenvalues of A. We know $\det(A) = \prod_i \lambda_i$, so $\det(A)$ is symmetric in $\lambda_1, ..., \lambda_n$.

The space of symmetric functions on λ_i can be expressed using the following basis of symmetric functions:

$$\sum_{i=1}^{n} \lambda_i$$
$$\sum_{i<j} \lambda_i \lambda_j$$
$$\sum_{i<j<k} \lambda_i \lambda_j \lambda_k$$
$$\vdots$$
$$\prod_{i=1}^{n} \lambda_i$$

However, there exists another basis for all symmetric functions:

$$\sum_{i=1}^{n} \lambda_i = Tr(A)$$
$$\sum_{i=1}^{n} \lambda_i^2 = Tr(A^2)$$
$$\sum_{i=1}^{n} \lambda_i^3 = Tr(A^3)$$
$$\vdots$$
$$\sum_{i=1}^{n} \lambda_i^n = Tr(A^n)$$

This can be parallelized easily by computing the matrices A^i and their trace values (poly-logarithmic time, using the example above with matrix products); using this basis to compute $\prod \lambda_i = \det(A)$ can also be parallelized and $\det(A)$ can be computed in parallel, logarithmic time.

Remarks:

- It is yet unknown if there exists a *deterministic*, parallel polylog-time algorithm for the PM problem
- Why do we not simply compute $p(\vec{x}) = \det(M)$ and test if $p \equiv 0$?

  p has $n!$ terms; testing if $p \equiv 0$ implies we know all $n!$ terms are zero. Merely describing such a polynomial in memory would require $\Omega(n!)$ memory!

Also, if we could describe p fully, we could count the number of non-zero terms and the result would be the number of perfect matchings on the graph - computation of which is a $\#P$-complete problem as remarked in the previous section.

3 Construction problem

Given a bipartite graph $G = (V, W, E)$, we would like to construct a perfect matching (if such a matching exists). The following sequential approach could be applied:

1. Set $X \leftarrow \phi$
2. Check if G has a perfect matching. If not, return "no PM"
3. Choose some $e \in E$ and define $G' = (V, W, E \setminus \{e\})$.
4. Check if G' has a perfect matching:
   - If so, set $G \leftarrow G'$ and return to step 3.
   - Otherwise:
     (a) Set $X \leftarrow X \cup \{e\}$
     (b) Remove e and both the vertices it touches from G
     (c) Return to step 3

This works, but requires polynomial runtime and is sequential in execution (no obvious way to parallelize).

However, if we know that there is precisely one perfect matching X, we *can* improve on this algorithm by testing all edges $e \in E$ in parallel: if there is no perfect match without e then it must be $e \in X$, and if there is a perfect match without e then by uniqueness of X it follows that $e \notin X$.

Applying the efficient parallel algorithm for the decision problem in $|E|$ separate instances, we can efficiently construct a perfect matching.

We must now reduce the problem to the case where there is at most one perfect matching.

3.1 The Isolation Lemma

Tne Isolation Lemma is from [2].

Lemma 9 (The Isolation Lemma) *Let X be some set of n elements and fix some $\Omega \subseteq 2^X$ (where $2^X = \{S : S \subseteq X\}$). Let $m \in \mathbb{N}$. For a given **weight function** $w : X \to [m]$ (where $[m] = \{1, 2, ..., m\}$) define the natural extension $w : 2^X \to \{1, ..., m\}$ as $w(S) = \sum_{x \in S} w(x)$. We say the minimal set in Ω is **uniquely defined** if there exists a unique set $S \in \Omega$ s.t. $w(S) = \min\{w(S') : \emptyset \neq S' \in \Omega\}$.*

When w is sampled uniformly over all possible weight functions:

$$Pr_{w:X\to[m]}(\text{the minimal set in } \Omega \text{ is uniquely defined}) \geqslant (1 - \frac{1}{m})^n$$

Example 10 $\Omega = 2^X$.

In this case there are $2^n - 1$ sets to consider (disregarding the empty set, the definition of uniquely defined minimum does not consider the empty set) but values of any w range in $0 < w(S) \leqslant n \cdot m$; many more sets than possible weight values. However, as $w(x) \geqslant 1$ for any $x \in X$, if $S_1 \subsetneq S_2$ then $w(S_1) < w(S_2)$. When $\Omega = 2^X$ this means we should only consider singletons (sets of cardinality 1) and the isolation lemma becomes intuitive (and easy to prove).

Example 11 $\Omega = \{S \subseteq X : |S| = \frac{1}{2}n\}$ *(n even).*

We get $|\Omega| = \binom{n}{\frac{1}{2}n} \approx \frac{2^n}{\sqrt{n}}$, which is still a very large number of sets;. Intiuitively, we might expect that each possible value is obtained many times. To see why we should be more cautious, consider what happens if we toss 2^n independent coins, each taking a random value in $\{1, \ldots, m\}$. Then, we expect the result to be heavily centered around the mean $\frac{1}{2}m$. The questions whether we get a *unique* minimal (or maximal) values is then delicate. However, in our case the 2^n values are dependent (only the wights to the base elements are independent). The isolation lemma tells us we get a unique minimum/maximum with a good probability.

Example 12 *Given a bipartite graph $G = (V, W, E)$ where $|V| = |W| = n$, denote $X = E$ and set:*

$$\Omega = \{\tilde{E} \subseteq E : \tilde{E} \textit{ is a perfect matching}\}$$

By definition, every $S \in \Omega$ satisfies $|S| = n$. By applying the isolation lemma, if we randomly set values $w(e) \in [2n]$ for every $e \in E$, with *constant probability* there exists a perfect matching in Ω that is *minimal* and *unique*.

Proof (The Isolation Lemma): Denote $W = \{w : X \to [m]\}$ (the set of all weight functions) and define a 'good' subset of W:

$$Good = \{w \in W : \text{the minimal set is uniquely obtained}\}$$

We call a weight function w **non-borderline** if $w(x) \geqslant 2$ for every $x \in X$ and denote by C the set of all non-borderline weight functions.

It's easy to see that $|C| = (m-1)^n$, and the density of C in W (which we denote $\rho_W(C)$) is:

$$\rho_W(C) = \frac{|C|}{|W|} = \frac{(m-1)^n}{m^n} = (1 - \frac{1}{m})^n$$

We shall now prove $|Good| \geqslant |C|$ by defining a 1-1 mapping $\phi : C \to Good$. Given some $w \in C$ set some $S \in argmin_{S' \in \Omega}(w(S'))$ (S is not necessarily unique), define:

$$\tilde{w}(x) = \begin{cases} w(x) - 1 & x \in S \\ w(x) & x \notin S \end{cases}$$

Note that $\tilde{w} : X \to [m]$ is well defined because $w \in C$ and therefore $w(x) \geqslant 2$. It's easy to see that S is unique and minimal in Ω relative to $\tilde{w}$: S is the only set that has had $|S|$ subtracted from it's previous value respective to w, other than strict supersets of S which must have strictly larger weights. By choosing a minimal set S for every $w \in C$, the mapping $\phi(w) = \tilde{w}$ is a well defined mapping $\phi : C \to Good$.

Given some $\tilde{w} \in Good$, the minimal set $S \in \Omega$ is unique respective to $\tilde{w}$; by defining:

$$w(x) = \begin{cases} \tilde{w}(x) + 1 & x \in S \\ \tilde{w}(x) & x \notin S \end{cases}$$

we get a uniquely defined source w s.t. $\phi(w) = \tilde{w}$, proving ϕ is 1-1 and therefore $|Good| \geqslant |C|$. Finally:

$$Pr_{w \in W}(Minimal\ S \in \Omega\ is\ unique) = \rho_W(Good) = \frac{|Good|}{|W|} \geqslant \frac{|C|}{|W|} = (1 - \frac{1}{m})^n$$

■

3.2 Algorithm

How do we find a perfect matching?

Given the matrix of variables M from section 2.1, replace each x_{ij} by $2^{w_{ij}}$ after randomly sampling n^2 values $w_{ij} \in [2n]$. We'll get:

$$\det(M) = \sum_{\pi \in S_n} sign(\pi) \prod_{i=1}^{n} M_{i,\pi(i)}$$

Recall that if $\pi \notin PM$ (the permutation π doesn't define a perfect matching $(i, \pi(i))$) then $\prod M_{i,\pi(i)} = 0$; otherwise we get $\prod M_{i,\pi(i)} = \prod x_{i,\pi(i)}$:

$$\begin{aligned} &= \sum_{\pi \in PM} sign(\pi) \prod_{i=1}^{n} x_{i,\pi(i)} \\ &= \sum_{\pi \in PM} sign(\pi) \prod_{i=1}^{n} 2^{w_{i,\pi(i)}} \\ &= \sum_{\pi \in PM} sign(\pi) 2^{w(\pi)} \end{aligned}$$

where $w(\pi)$ is the weight of the perfect matching defined by π. The isolation lemma tells us that with a good probability the minimal weight matching is unique.

Also note that if we observe the binary representation of $\det(M)$, assuming there is a minimal unique perfect matching π then $2^{w(\pi)}$ is the smallest value in the sum and it appears exactly once, so $w(\pi)$ is the index of the least significant *set* bit in the binary representation of $\det(M)$.

We arrive at the following algorithm:

1. Set $S \leftarrow \phi$
2. Choose (in parallel) random values $w_{ij} \in [2n]$
3. Replace $x_{ij} \leftarrow 2^{w_{ij}}$ in M and calculate $\det(M)$
4. Check the least significant set bit i in the binary representation of $\det(M)$
5. In parallel, for each $e \in E$ remove e from the graph, construct the new M' and repeat steps 3 and 4 (do *not* change w) to get i':
   - If $i' \neq i$, add e to S
6. Output S

As mentioned before the algorithm, at step 4 we know i is equal to the weight of the unique minimal perfect matching (assuming it's unique).

If we remove some $e \in \pi$ (where π is the minimal perfect matching) from G, the new minimal value must be greater than i because π was *unique* in reaching i; so if $i' \neq i$ then this implies $e \in \pi$. This proves $S \subseteq \pi$.

If we remove some $e \notin \pi$ from G, then $i' = i$ because no new matchings were created so $\pi \subseteq S$, and the returned set S is a perfect matching!

If the minimal set is not unique, the resulting S may not be a perfect matching (this can be tested during runtime in parallel $O(1)$ time). However, as the probability of sampling a weight function that induces a unique minimal set is constant, by running the entire algorithm in a polynomial number of separate instances and simply choosing any PM one of them outputs, we can greatly reduce the probability of outputting "no

PM" when a PM exists (reduce probability of false negatives to almost zero).

Steps 1-4 can be done in parallel, logarithmic time, as shown previously. Step 5 is one more parallel iteration of steps 3-4, yielding a logarithmic runtime for construction of a perfect matching!

Remarks:

- Step 5 of this algorithm improves upon the sequential approach presented in section 1.3 by parallelizing all checks for each $e \in E$. This became possible once identified a unique solution to search for - the original problem has no 'minimality' requirement.

References

[1] Laszlo Csanky. Fast parallel matrix inversion algorithms. In *Foundations of Computer Science, 1975., 16th Annual Symposium on*, pages 11–12. IEEE, 1975.

[2] Ketan Mulmuley, Umesh V Vazirani, and Vijay V Vazirani. Matching is as easy as matrix inversion. In *Proceedings of the nineteenth annual ACM symposium on Theory of computing*, pages 345–354. ACM, 1987.