	Prologue
CZ.1.07/2.2.00/28.0041 Centrum interaktivních a multimediálních studijních opor pro inovaci výuky a efektivní učení sociální sociální fond v čr	You should spent most of your time thinking about what you should think about most of your time.
RANDOMIZED ALGORITHMS AND PROTOCOLS - 2020	WEB PAGE of the LECTURE

EXERCISES/TUTORIALS	CONTENTS - preliminary
EXERCISES/TUTORIALS: Thursdays 14.00-15.40, C525 TEACHER: RNDr. Matej Pivoluška PhD Language English NOTE: Exercises/tutorials are not obligatory	 Basic concepts and examples of randomized algorithms Types and basic design methods for randomized algorithms Basics of probability theory Simple methods for design of randomized algorithms Games theory and analysis of randomized algorithms Basic techniques I: moments and deviations Basic techniques II: tail probabilities inequalities Probabilistic method I: Markov chains - random walks Algebraic techniques - fingerprinting Fooling the adversary - examples Randomized proofs Probabilistic method II: Quantum algorithms
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 R. Motwami, P. Raghavan: Randomized algorithms, Cambridge University Press, UK, 1995 J. Gruska: Foundations of computing, International Thompson Computer Press, USA. 715 pages, 1997 J. Hromkovič: Design and analysis of randomized algorithms, Springer, 275 pages, 2005 N. Alon, J. H. Spencer: The probabilistic method, Willey-Interscience, 2008 	Part I Chapter 10. Fingerprinting - algebraic Techniques

Chapter 10. FINGERPRINTING - ALGEBRAIC TECHNIQUES	FINGERPRINTING METHOD - BASICS
Some of the most interesting results in the design of efficient computations were obtained using algebraic techniques combined with randomization.	
Fingerprinting technique Example: Decide equality of two elements x, y drawn from a large universe U . Complexity under any reasonable model is $\Omega(\lg U)$. Alternative approach: Pick a random mapping $f: U \longrightarrow V \qquad U >> V $. such that there is a good chance that f(x) = f(y) implies $x = yand declare that x = y (x \neq y) if f(x) = f(y) (f(x) \neq f(y).$	 The basic observation of this method is that in order to determine whether two given objects are equal (given their full representations), it is enough, with large probability successfully, to compare their fingerprints (their certain incomplete representations). First important requirement of this method is that fingerprints should always be chosen randomly from a large set of potential fingerprints. Second requirement is that fingerprints should preserve some essential differences between objects they represent. Third requirement is that fingerprints should be short, simple, and easy to obtain.
Complexity under any reasonable model is now $\Omega(\lg V)$ 1. Chapter 10. Fingerprinting - algebraic Techniques 9/26	IV054 1. Chapter 10. Fingerprinting - algebraic Techniques 10/26
BASIC TASK and SCHEME	FREIVALDS TECHNIQUE - I.
Given a set of objects \mathcal{O} , find a (much smaller) set \mathcal{F} of (so called) fingerprints and a set M of (simple enough) mappings $f: \mathcal{O} \leftrightarrow \mathcal{F}$ such that for any two different objects o_1 and o_2 from \mathcal{O} there is a lot of such mappings $f \in M$ that $f(o_1) \neq f(o_2)$. This allows to reduce the problem $o_1 = o_2$?, for any two $o_1, o_2 \in \mathcal{O}$ to a much simple problem $f(o_1) = f(o_2)$?. Fingerprint method can therefore be seen as a special case of the method of abundance of the witnesses discussed in the next chapter.	Matrix multiplication for matrices of degree n: classical (school/simple) algorithm has complexity — $O(n^3)$ best (sophisticated) algorithm has complexity— $O(n^{2.376})$ Problem: to check whether $AB = C$ for given n-dimensional matrices A, B and C.Method: choose a random column vector $r \in \{0,1\}^n$.Compute: $x = Br, y = Ax, z = Cr - {O(n^2) steps}$ declare $AB = C$ iff $y = z$.What is probability that such a conclusion is wrong? One can show that: probability is zero if $AB = C$ and less then $\frac{1}{2}$ if $AB \neq C$

FREIVALDS TECHNIQUE - II.

VERIFICATION of POLYNOMIAL IDENTITIES - I.

Theorem Let A, B, C be $n \times n$ matrices, such that $AB \neq C$. Then for randomly chosen $r \in \{0, 1\}^n$ it holds that $Pr[ABr = Cr] \leq \frac{1}{2}$. **Proof:** Denote $D = AB - C \neq 0$. We wish to upper-bound the probability that y = z ($\Leftrightarrow Dr = 0$)

Without loss of generality, we may assume that the first row in D has a non-zero element and that all its non-zero elements are first. Let d be the first row of D with the first k elements $\neq 0$. We now concentrate on the probability that $Dr \neq 0$. This will yield a lower bound on the probability that $y \neq z$.

$$Dr = 0$$
 iff $r_1 = \frac{-\sum_{i=2}^k d_i r_i}{d_1}$ (*).

Invoking the Principle of Deferred Decision we assume that r_2, \ldots, r_n are chosen (randomly) before r_1 . Since r_1 is also chosen randomly, the probability of $Dr \neq 0$ is $=\frac{1}{2}$.

Polynomial products verification problem

Given two polynomials of degree $n - P_1(x)$, $P_2(x)$ – and one of degree $2n - P_3(x)$ – verify whether $P_1(x) \cdot P_2(x) = P_3(x)$

polynomial evaluation complexity: O(n)multiplication complexity: $O(n \lg n)$

Randomized verification:Let *S* be a set of integers and $|S| \ge 2n + 1$.

Pick $r \in S$ uniformly and randomly and evaluate $P_1(r), P_2(r), P_3(r)$.

Declare the identity $P_1(x) \cdot P_2(x) = P_3(x)$ as correct unless $P_1(r) \cdot P_2(r) \neq P_3(r)$.

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VERIFICATION of POLYNOMIAL IDENTITIES - II.	SCHWARZ-ZIPPEL THEOREM - I
Analysis of the randomized method: Polynomial $Q(x) = P_1(x) \cdot P_2(x) - P_3(x)$ has degree $\leq 2n$, and has therefore at most $2n$ roots. Unless $Q(x) \equiv 0$, it holds $Q(r) = 0$ for at most $2n$ random choices of $r \in S$. The probability of error in the above verification is therefore at most $\frac{2n}{ S }$.	Theorem: Let $Q(x_1,, x_n)$ be a polynomial of a degree d . Fix any finite set S of reals, and let $r_1,, r_n$ be chosen independently and randomly from S . Then $Pr[Q(r_1,, r_n) = 0 Q(x_1, x_2,, x_n) \neq 0] \leq \frac{d}{ S }$ Proof: By induction on n .
The above verification procedure can be extended to verify any polynomial identity $P_1(x) = P_2(x)$, where P_1, P_2 are given implicitly. Example: Given a matrix	The case $n = 1$ was actually already discussed on the previous page. Induction step: Let $Q(x_1, x_2,, x_n) = \sum_{i=1}^k x_1^i Q_i(x_2,, x_n)$ where $Q_k \neq 0$. Since the total degree of Q_k is at most $d - k$, the induction hypothesis
$M = \begin{vmatrix} 1 & x_1 & x_1^2 & \dots & x_1^{n-1} \\ 1 & x_2 & x_2^2 & \dots & x_2^{n-1} \\ \vdots & & & \\ 1 & x_n & x_n^2 & \dots & x_n^{n-1} \end{vmatrix}$ Task: Verify that $Det(M) = \prod_{i < j} (x_j - x_i).$	shows, that the probability that $Q_k(r_2,, r_n) = 0$ is at most $d = k$, the induction hypothesis shows, that the probability that $Q_k(r_2,, r_n) = 0$ is at most $\frac{d-k}{ S }$. Suppose that $Q_k(r_2,, r_n) \neq 0$. Consider the following polynomial $q(x_1) = Q(x_1, r_2,, r_n) = \sum_{i=0}^k x_1^i Q_i(r_2,, r_n)$

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SCHWARZ-ZIPPEL THEOREM - II.

TESTING SIMILARITIES of MATRICES

Degree of q is k and $q(x_1) \neq 0$. The base case implies that the probability that
$q(r_1) = Q(r_1, \ldots, r_n) = 0 \text{ is at most } \frac{k}{ S }.$

Hence

$$Pr[Q_k(r_2, \dots, r_n) = 0] \le \frac{d-k}{|S|}$$

$$Pr[Q(r_1, r_2, \dots, r_n) = 0 \mid Q_k(r_2, \dots, r_n) \ne 0] \le \frac{k}{|S|}$$

$$\implies$$

$$Pr[Q(r_1, \dots, r_n) = 0] \le \frac{d}{|S|}$$

because for any two events \mathcal{E}_1 and \mathcal{E}_2 , it holds

$$\mathsf{Pr}(\mathcal{E}_1) \leq \mathsf{Pr}(\mathcal{E}_1|\bar{\mathcal{E}}_2) + \mathsf{Pr}(\mathcal{E}_2).$$

Definition Two $n \times n$ matrices A and B are called similar matrices if there exists a non-singular matrix T such that $TAT^{-1} = B$.

To decide whether two given matrices A and B are similar, one has to decide whether TA = BT for some matrix T such that det $(T) \neq 0$.

We can start by seeing entries of unknown T as variables and denote by \overline{t} the vector of such n^2 variables.

In such a case the equality TA = BT can be seen as a system of n^2 linear equations, with entries of \bar{t} as variables. These equations can be expressed as $C\bar{t} = 0$, where C is an $n^2 \times n^2$ matrix.

This way we get a homogeneous system of equations and it is possible to find, in polylog time on a parallel computer, a basis for the solution space.

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	PERFECT MATCHING in UNDIRECTED GRAPHS
Let $\{\overline{t}_1,\ldots,\overline{t}_k\}$ denote such a basis for the solution space of the equation $TA = BT$.	Let $G = (U, V, E)$ be a bipartite graph, $ U = V = n$. A matching of G is a collection of edges $M \subset E$ such that each node occurs at most once in an edge of M . A matching of size n is perfect. (A note: {Each perfect matching defines an inverse permutation π of the set $\{1, \ldots, n\}\}$).
In such a case any solution matrix has the form	Theorem Let A be an $n \times n$ matrix obtained from G as follows
$T = c_1 T_1 + c_2 T_2 + \ldots + c_k T_k,$ where the matrix T_i corresponds to the basis vector \overline{t}_i .	$egin{aligned} A_{ij} &= egin{cases} x_{ij} & ext{if} & (u_i, v_j) \in E \ 0 & ext{if} & (u_i, v_j) otin E \ \end{pmatrix} \end{aligned}$
We are interested now in a non-singular solution. Such a solution exists iff there is a c_1, \ldots, c_k vector for which $\det(T) \not\equiv 0$. That is if $\det(T)$, as a polynomial in the variables c_1, \ldots, c_k , is not identically zero. As we already know, we can checked efficiently whether $\det(T) \not\equiv 0$.	Then G has a perfect matching iff $det(A) \not\equiv 0$. Proof: If S_n is the set of all permutations of $\{1, 2,, n\}$, then $det(A) = \sum_{\pi \in S_n} sgn(\pi)A_{1\pi(1)} \cdots A_{n\pi(n)}$ Since each indeterminate x_{ij} occurs at most once in A there can be no cancellation of terms in the above sum.
	$\implies det(A) \neq 0 \text{ iff there exist a } \pi \in S_n \text{ such that } A_{1\pi(1)}, \dots, A_{n\pi(n)} \neq 0$ iff there is a perfect matching

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	VERIFICATION of EQUALITY of STRINGS - A REPETITION - I.
Implications: There is a simple randomized algorithm for testing the existence of a perfect matching in bipartite graphs	Problem story: Both Alice and Bob maintain a copy of database. Periodically they have to verify its consistency. How to do that efficiently? Alice's data: $a = (a_1,, a_n) \in \{0, 1\}^n$. Bob's data: $(b = b_1,, b_n) \in \{0, 1\}^n$. Solution: To use a fingerprinting mapping: Define first $num(a) = \sum_{i=1}^n a_i 2^{i-1}$, $num(b) = \sum_{i=1}^n b_i 2^{i-1}$ and then define the fingerprinting mapping: $F_p(x) = x \mod p$, where x is an integer and p is a prime. Aim: We would like that it holds: $a \neq b \Rightarrow F_p(num(a)) \neq F_p(num(b))$. At this technique the number of bits transmitted is $O(\lg p)$. This strategy can be easily fooled by an adversary. Way to get around: to choose p randomly.
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VERIFICATION of EQUALITY of STRINGS - A REPETITION - II.	PATTERN MATCHING
VERIFICATION of EQUALITY of STRINGS - A REPETITION - II. Lemma: The number of distinct prime divisors of any integer less than 2^n is at most n . The fingerprint comparison fails if p divides $ \operatorname{num}(a) - \operatorname{num}(b) $. Choose a threshold $\tau > n$, and choose $p < \tau$. Theorem $Pr[F_p(\operatorname{num}(a)) = F_p(\operatorname{num}(b)) \mid a \neq b] \leq \frac{n}{\pi(\tau)}$ and if $\tau = tn \ln tn$, then $Pr[F_p(\operatorname{num}(a)) = F_p(\operatorname{num}(b)) \mid a \neq b] \leq O(\frac{1}{t})$, where $\pi(x) = \frac{x}{\ln x}$ is the number of primes smaller than x .	

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Monte Carlo algorithm

Compare, for j = 1, ..., n - m, fingerprints of Y and X(j), and output the smallest j at which a match occurs.

Key fact for complexity analysis: The cost of computing $F_p(X(j+1))$ from $F_p(X(j))$ is only O(1) operations.

Indeed, for $1 \leq j \leq n - m + 1$,

$$\operatorname{num}(X(j+1)) = 2 \left[\operatorname{num}((X(j)) - 2^{m-1}x_j] + x_{j+m}\right]$$

 \implies

 $F_p(\operatorname{num}(X(j+1))) = (2[\operatorname{num}(F_p(X(j))) - 2^{m-1}x_j] + x_{j+m}) \mod p$

Conversion into a Las Vegas algorithm

Whenever a match occurs between the fingerprints of Y and X(j), we compare strings Y and X(j) in O(m) time. If this is a false match, we abandon the whole process in favor of using a brute-force (O(nm)) – algorithm.

Resulting algorithm does not make any error and has as the expected running time

$$O\left(m+(n)(1-\frac{1}{n})+nm(\frac{1}{n})\right)=O(n+m)$$

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