Dept. of Computer Science
School of Mathematics
Tel Aviv University
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Algorithmic Problems in the Human Genome Project - Seminar Syllabus

Instructor: Prof. Ron Shamir

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The seminar will concentrate on some central algorithmic and mathematical problems arising in DNA chips and microarray technology.

Key references: [PL94] is a very good introduction to the mathematics of Sequencing by Hybridization. [MH98] is a more recent overview of chip technology with an emphasis on the companies and products. http://www.math.tau.ac.il/~shamir/algmb/algmb98.html contains my lecture notes and in particular basic references on computational biology.

Date	Paper	Speaker	Topic and comments
DNA chips (Format II)			
April 18	[Pev89]	Omer Berkman	SBH: Eulerian formulation
April 25	[PLK+91]	Ronny Machluf	SBH: gapped probes
April 25	[PFU99]	Iddo Lev	SBH: improved gapped probes
May 2	[DFS94]	Dror Irony	SBH: probabilistic analysis. (Mention also [AMRW97])
May 9	[HFL+96]	Ori Shalev	Positional SBH
May 9	[BDPSS99]	Yoel Shkolnisky	Positional SBH
May 16	[BFK+99]	Rinat Kol	errors in SBH
May 26	[SS95]	Dina Dohovny	variants of SBH
June 2	[Hub99]	Omri Weissman	Multiplex SBH
June 9	[BHKdW99]	Haim Linhart	DNA graphs
DNA microarrays (Format I)			
June 16	[HSL+99] [HS99]	Oren Boyman	cDNA clustering (mention also [Mil95])
June 22	[MS99]	Niv Efron	physical mapping

NOTE: **Dates are tentative and can change with short notice**. Updates will be announced in class.

References

[AMRW97] R. Arratia, D. Martin, G. Reinert, and M. S. Waterman. Poisson process approximation for sequence repeats, and sequencing by hybridization. *Journal of Computational Biology*, 3(3):425–463, 1997.

[BDPSS99] A. Ben-Dor, I. Pe'er, R. Shamir, and R. Sharan. On the complexity of positional sequencing by hybridization. In *Proceedings of the Tenth International Conference on Combinatorial Pattern Matching (CPM'99)*, pages 88–100, New York, 1999. ACM Press.

[BFK+99] J. Blazewicz, P. Formanowicz, K. Kasprzak, W. T. Markeiwicz, and J. Weglarz. DNA sequencing with positive and negative errors. *Journal of Computational Biology*, 6(1):113–123, 1999.

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[HS99] E. Hartuv and R. Shamir. A clustering algorithm based on graph connectivity. Technical report, Tel Aviv University, Dept. of Computer Science, March 1999.

[HSL+99] E. Hartuv, A. Schmitt, J. Lange, S. Meier-Ewert, H. Lehrach, and R. Shamir. An algorithm for clustering cDNAs for gene expression analysis using short oligonucleotide fingerprints. In *Proceedings Third International Symposium on Computational Molecular Biology (RECOMB 99)*, pages 188–197, April 1999.

[Hub99] E. Hubbell. Multiplex sequencing by hybridization. Technical report, University of Southern California, Department of Mathematics, 1999.

[MH98] A. Marshall and J. Hodgson. DNA chips: an array of possibilities. *Nat Biotechnol*, 16:27–31, 1998.

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[Pev89] P. A. Pevzner. l-tuple DNA sequencing: computer analysis. *J. Biomol. Struct. Dyn.*, 7:63–73, 1989.

[PFU99] F. Preparata, A. Frieze, and E. Upfal. Optimal reconstruction of a sequence from its probes. *Journal of Computational Biology*, 6(3-4):361–368, 1999.

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[SS95] S. S. Skiena and G. Sundaram. Reconstructing strings from substrings. *J. Comput. Biol.*, 2:333–353, 1995.