

Publications

A. Books and Edited Works

1. R. Shamir. "On the complexity of the Simplex method", Ph.D. dissertation, College of Engineering, University of California, Berkeley, 1984.
2. S. Istrail, P. Pevzner, R. Shamir, Editors. *Discrete Applied Mathematics*, Special volume on Computational Molecular Biology, Volume 71, issue 1-3, December 1996.
3. S. Istrail, P. Pevzner, R. Shamir, Editors. *Discrete Applied Mathematics*, Second Special volume on Computational Molecular Biology, Volume 88, issues 1-3, November 1998.
4. R. Shamir, S. Miyano, S. Istrail, P. Pevzner, M. Waterman, Editors. *RECOMB 2000: Proceedings of the Fourth Annual International Conference on Computational Molecular Biology*, April 8-11, 2000, Tokyo, Japan. ACM Press, 2000.
5. S. Miyano, R. Shamir, T. Takagi, Editors. *Currents in Computational Molecular Biology*, Frontiers of Science Series No. 30, Universal Academy Press, Tokyo, Japan 2000
6. S. Istrail, P. Pevzner, R. Shamir, Editors. *Discrete Applied Mathematics*, Third Special volume in the Computational Molecular Biology Series, Volume 104, issues 1-3, August 2000.
7. R. Shamir, Editor. Selected papers from RECOMB 2000. Special issue of *Journal of Computational Biology*, Vol 7 issues 3/4, 2000.
8. M. Li, P. Pevzner, R. Shamir, Guest editors. *Journal of Computer and System Sciences*, Special issue on Computational Biology, Volume 65, No. 3, November 2002.
9. S. Istrail, P. Pevzner, R. Shamir, Editors. *Discrete Applied Mathematics*, Fourth Special Issue in the Computational Molecular Biology Series, Volume 127, number 1, April 2003.
10. S. Istrail, P. Pevzner, R. Shamir, Editors. Computational Molecular Biology *Topics in Discrete Mathematics*, Volume 12, North-Holland, Amsterdam 2003. Reprinted from *Discrete Applied Mathematics*, Volume 127, number 1, April 2003.
11. P. Frasconi, R. Shamir, Editors. Artificial Intelligence and Heuristic Methods in Bioinformatics *NATO Science Series III: Computer and System Sciences*, Vol 183 IOS Press, Amsterdam, 2003.
12. R. M. Karp, M. Li, P. Pevzner, R. Shamir, Guest editors. *Journal of Computer and System Sciences*, 2nd special issue on Computational Biology, Volume 70, No. 3, May 2005.
13. S. Istrail, P. Pevzner, R. Shamir, Editors. *Discrete Applied Mathematics*, Fifth Special Issue in the Computational Molecular Biology Series, Volume 155, issues 6-7, April 2007.
14. R. M. Karp, M. Li, P. Pevzner, R. Shamir, Guest editors. *Journal of Computer and System Sciences*, 3rd special issue on Computational Biology, Volume 73, No. 7, November 2007.
15. S. Istrail, P. Pevzner, R. Shamir. F. Sun, Guest editors. *Communication in Information and Systems*, Special issues dedicated to Michael Waterman on the occasion of his 67th birthday. Vol 9 3-4 2009 and Vol 10 1-2 2010.
16. P. A. Pevzner, R. Shamir, Editors. Selected papers from the 2nd RECOMB satellite meeting on Bioinformatics Education (RECOMB-BE). *Journal of Computational Biology*, 18 (7), 2011.
17. P. A. Pevzner, R. Shamir, Editors. *Bioinformatics for Biologists*. Cambridge University Press, 2011.

B. Chapters in Books

18. R. Shamir. “Probabilistic analysis in linear programming”. Chapter 9 of *Probability and Algorithms*, pp 131–148, National Academy Press, Washington D.C. 1992.
19. I. Adler, R. Shamir. “Greedily solvable transportation networks and edge-guided vertex elimination”. *Network Optimization Problems: Algorithms, Complexity and Applications*, D.-Z. Du and P. M. Pardalos, Editors, pp. 1–22, World Scientific Press, Singapore, 1993.
20. I. Pe'er, R. Shamir. “Approximation Algorithms for the Median Problem in the Breakpoint Model” *Comparative Genomics: Empirical and Analytical Approaches to Gene Order Dynamics, Map Alignment and the Evolution of Gene Families*, D. Sankoff and J. H. Nadeau, Editors, pp. 225–241, Kluwer Academic Press (Dordrecht) 2000.
21. R. Shamir, R. Sharan. “Algorithmic approaches to clustering gene expression data”, in *Current Topics in Computational Molecular Biology*, T. Jiang, T. Smith, Y. Xu, M. Q. Zhang, Editors, pp. 269–300, MIT Press, 2002.
22. R. Sharan, R. Elkon, R. Shamir. “Cluster Analysis and its Applications to Gene Expression Data”, *Ernst Schering Research Foundation Workshop Volume 38: Bioinformatics and Genome Analysis*, H.-W. Mewes, H. Seidel, B. Weiss, Editors, pp. 83–108, Springer-Verlag, Berlin Heidelberg 2002.
23. A. Tanay, R. Sharan, R. Shamir. “Biclustering algorithms: A survey” *Handbook of Computational Molecular Biology*, S. Aluru, Editor, pp 26-1 – 26-17, Chapman and Hall/CRC Press, 2006.
24. R. Elkon, S. Rashi-Elkeles, R. Shamir, Y. Shiloh “Transcriptional responses to DNA damage: systems-level delineation by functional genomics”. *Microarrays and Transcription Networks*, M. Frances Shannon and S. Rao, Editors, Landes Biosciences, 2005.
25. C. Linhart and R. Shamir. “Degenerate Primer Design: Theoretical Analysis and the HYDEN program”. *PCR primer design*, A. Yuryev, Editor. Methods in Molecular Biology 402: 221–44 , Humana Press, 2007.
26. R. Zeira, R. Shamir. “Genome Rearrangement Problems with Single and Multiple Gene Copies: A Review”. *Bioinformatics and Phylogenetics: Seminal contributions of Bernard Moret*, T. Warnow, Editor, pp. 205–242, Springer Nature Switzerland AG 2019.

C. Journal Articles

27. I. Adler, R.M. Karp, R. Shamir, “A family of simplex variants solving an $m \times d$ linear program in expected number of pivots depending on d only”. *Mathematics of Operations Research*, 11, 4, 570–590 (1986).
28. I. Adler, R.M. Karp, R. Shamir, “A simplex variant solving an $m \times d$ linear program in $O(\min(m^2, d^2))$ expected number of pivot steps”. *Journal of Complexity*, Vol. 3, 372–387 (1987).
29. R. Shamir, “The efficiency of a simplex method: a survey”. *Management Science*, 33, 3, 301–334 (1987).
30. N. Alon, S. Cosares, D. Hochbaum, R. Shamir, “An algorithm for the detection and construction of Monge sequences”. *Linear Algebra and Its Applications*, Vol. 114/115, 669–680 (1989).
31. D. Hochbaum, R. Shamir, “An $O(n(\log n)^2)$ algorithm for the maximum weighted tardiness problem”. *Information Processing Letters*, Vol. 31, 215–219 (1989).
32. D. Hochbaum, R. Shamir, “Minimizing the number of tardy job units under release time constraints”. *Discrete Applied Mathematics*, Vol. 28, 45–57 (1990).
33. D. Hochbaum, R. Shamir, “Strongly polynomial algorithms for the high multiplicity scheduling problem”. *Operations Research*, Vol. 39 (4), 648–653 (1991).

34. D. Hochbaum, R. Shamir, G. Shanthikumar, “A polynomial algorithm for an integer quadratic nonseparable transportation problem”. *Mathematical Programming* 55, 359–371 (1992).
35. E. Boros, P. Hammer, R. Shamir, “A polynomial algorithm for balancing acyclic data flow graphs”. *IEEE Transactions on Computers*, Vol. 41 no. 11 1380–1385 (1992).
36. R. Shamir, “A fast algorithm for constructing Monge sequences in transportation problems with forbidden arcs”. *Discrete Mathematics*, Vol. 114, 435–444 (1993).
37. I. Adler, R. Shamir, “A randomized scheme for speeding-up algorithms for linear and convex programming problems with high constraints-to-variables ratio”. *Mathematical Programming*, Vol. 61, 39–52 (1993).
38. I. Adler, A. Hoffman, R. Shamir, “Monge and feasibility sequences in general flow problems”. *Discrete Applied Mathematics*, Vol 44, 21–38 (1993).
39. R. Shamir, “Probabilistic analysis in linear programming”. *Statistical Science*, Vol. 8 (1), 57–64 (1993).
40. M. C. Golumbic, R. Shamir, “Complexity and algorithms for reasoning about time: a graph-theoretic approach”. *JACM*, Vol. 40, 1108–1133 (1993).
41. Y. Pinto, R. Shamir, “Efficient algorithms for minimum cost flow problems with piecewise-linear convex costs”. *Algorithmica*, Vol. 11 256–277 (1994).
42. H. Kaplan and R. Shamir, “The domatic number problem on some perfect graph families”. *Information Processing Letters*, 49 51–56 (1994).
43. M. C. Golumbic, H. Kaplan and R. Shamir, “On the complexity of DNA Physical Mapping”. *Advances in Applied Mathematics* 15 251–261 (1994).
44. E. Boros, P. Hammer, M. E. Hartmann, R. Shamir, “Balancing problems in acyclic networks”. *Discrete Applied Mathematics*, Vol. 49 77–93 (1994).
45. P. W. Goldberg, M. C. Golumbic, H. Kaplan and R. Shamir, “Four Strikes Against Physical Mapping of DNA”. *Journal of Computational Biology*, 2(1) 139–152 (1995).
46. M. C. Golumbic, H. Kaplan and R. Shamir, “Graph Sandwich Problems”. *Journal of Algorithms* 19, 449–473 (1995).
47. H. Kaplan and R. Shamir, “Pathwidth, Bandwidth and Completion Problems to Proper Interval Graphs with Small Cliques”. *SIAM Journal on Computing*, 25(3) 540–561 (1996).
48. I. Pe'er, R. Shamir, “Satisfiability problems on intervals and unit intervals”. *Theoretical Computer Science*, 175 (2), 349–372 (1997).
49. I. Pe'er, R. Shamir, “Realizing interval graphs with size and distance constraints”. *SIAM Journal of Discrete Mathematics* 10 (4), 662–687 (1997).
50. H. Kaplan, R. Shamir, “Bounded Degree Interval Sandwich Problems”. *Algorithmica* 24 (2) 96–104, (1999).
51. H. Kaplan, R. Shamir, R. E. Tarjan “Tractability of parameterized completion problems on chordal, strongly chordal and proper interval graphs” *SIAM Journal of Computing*, 28 (5) 1906–1922 (1999).
52. H. Kaplan, R. Shamir, R. E. Tarjan, “Faster and Simpler Algorithm for Sorting Signed Permutations by Reversals”. *SIAM Journal of Computing*, 29 (3) 880–892 (1999).
53. G. Mayraz, R. Shamir, “Construction of Physical Maps From Oligonucleotide Fingerprints Data”. *Journal of Computational Biology*, 6 (2) 237–252 (1999).

54. R. M. Karp, R. Shamir, "Algorithms for Optical Mapping". *Journal of Computational Biology*, Vol 7 No. 1/2 pp. 303–316 (2000).
55. R. Shamir, D. Tsur, "Faster Subtree Isomorphism", *Journal of Algorithms*, 33, 267–280 (1999).
56. A. Ben-Dor, R. Shamir, Z. Yakhini, "Clustering gene expression patterns". *Journal of Computational Biology*, Vol 6 no. 3/4, 281–298 (1999).
57. T. Pupko, I. Pe'er, R. Shamir and D. Graur, "Fast Algorithm for Reconstruction of Ancestral Amino-Acid Sequences", *Molecular Biology and Evolution* , Vol 17 no. 6 pp. 890–896 (2000).
58. E. Hartuv, A. Schmitt, J. Lange, S. Meier-Ewert, H. Lehrach, R. Shamir, "An algorithm for clustering cDNA fingerprints". *Genomics*, Vol 66 no. 3, 249–256 (2000).
59. A. Natanzon, R. Shamir and R. Sharan, "A Polynomial Approximation Algorithm for the Minimum Fill-In Problem". *SIAM J. Computing*, Vol 30 no. 4, 1067–1079 (2000).
60. A. Natanzon, R. Shamir and R. Sharan, "Complexity classification of some edge modification problems". *Discrete Applied Mathematics*, Vol 113 no. 1, 109–128 (2001).
61. E. Hartuv, R. Shamir, "A clustering algorithm based on graph connectivity". *Information Processing Letters*, 76, 175–181 (2000).
62. R. M. Karp, I. Pe'er, R. Shamir, "An Algorithm Combining Discrete and Continuous Methods for Optical Mapping". *Journal of Computational Biology*, Vol 7 No. 5, 745–760 (2000).
63. P. Hell, R. Shamir, R. Sharan, "A Fully Dynamic Algorithm for Recognizing and Representing Proper Interval Graphs". *SIAM Journal on Computing*, Vol. 31 No. 1, 289–305 (2001).
64. A. Ben-Dor, I. Pe'er, R. Shamir, R. Sharan, "On the Complexity of Positional Sequencing by Hybridization". *Journal of Computational Biology*, Vol. 8 No. 4, 361–371 (2002). A full version in the *Electronic Colloquium of Computational Complexity* Report number TR01-054, (2001).
65. R. Shamir, D. Tsur, "Large scale sequencing by hybridization". *Journal of Computational Biology*, Vol. 9 No. 2, 413–428 (2002).
66. T. Fuchs, B. Malecova, C. Linhart, R. Sharan, M. Khen, R. Herwig, D. Shmulevich, R. Elkon, M. Steinfath, J. K. O'Brien, U.Radelof, H. Lehrach, D. Lancet, R. Shamir, " DEFOG: A practical scheme for deciphering families of genes". *Genomics* Vol. 80 No. 3 pp. 295–302 (2002).
67. I. Pe'er, N. Arbili, R. Shamir, "A computational method for resequencing long DNA targets by universal oligonucleotide arrays". *Proc. National Academy of Science USA* Vol. 99 pp 15497-15500 (2002)
68. R. Shamir, R. Sharan, "A fully dynamic algorithms for modular decomposition and representation of cographs". *Discrete Applied Mathematics* Volume 136, Issues 2-3, Pages 329-340 (2004)
69. A. Ben-Dor, R. M. Karp, B. Schwikowsky, R. Shamir, "The Restriction Scaffold Problem". *Journal of Computational Biology* Vol. 10 No. 3-4, pp. 385–398 (2003).
70. M. Ozery-Flato, R. Shamir, "Two notes on genome rearrangements". *Journal of Bioinformatics and Computational Biology* Vol. 1, No. 1 pp. 71–94 (2003).
71. R. Elkon, C. Linhart, R. Sharan, R. Shamir, Y. Shiloh, "Genome-wide In-silico Determination of Transcriptional Regulation Modules Controlling Cell Cycle in Human Cells". *Genome Research* Vol. 13(5) pages 773-780, (2003).
72. E. Halperin, S. Halperin, T. Hartman, R. Shamir, "Handling long targets and errors in Sequencing By Hybridization". *Journal of Computational Biology* Vol. 10 No. 3-4, pp. 483–498 (2003).

73. R. Sharan, A. Maron-Katz, R. Shamir, "CLICK and EXPANDER: A System for clustering and visualizing gene expression data". *Bioinformatics* Vol. 19 No. 14 pp. 1787–1799 (2003).
74. I. Gat-Viks, R. Sharan, R. Shamir, "Scoring clustering solutions by their biological relevance". *Bioinformatics* 19: 2381-2389 (2003).
75. T. Pupko, R. Sharan, M. Hasegawa, R. Shamir, D. Graur, "Detecting excess radical replacements in phylogenetic trees". *Gene* 319, 127–135 (2003).
76. T. Olander, T. Fuchs, C. Linhart, R. Shamir, M. Adams, F. Kalush, M. Khen, D. Lancet, "The canine olfactory subgenome". *Genomics* 83, 361–372 (2004).
77. I. Pe'er, N. Arbilli, Y. Liu, C. Enck, C. Gelfand, R. Shamir, "Advanced computational techniques for resequencing DNA with polymerase signaling assay arrays". *Nucleic Acids Research* 31(19):5667-75 (2003).
78. N. Orlev, R. Shamir, Y. Shiloh, "PIVOT: Protein interactions visualization tool". *Bioinformatics* 30 (3), 424–425 (2004).
79. R. B. Hayward, R. Shamir, "A note on tolerance graph recognition". *Discrete Applied Mathematics* Vol. 143 307–311 (2004).
80. A. Tanay, R. Shamir, "Multi-level modeling and inference of transcription regulation". *Journal of Computational Biology* Vol 11 No. 2-3, pp 357-376 (2004).
81. R. Sorek, R. Shamir, G. Ast, "How prevalent is functional alternative splicing in the human genome?". *Trends in Genetics* 20 (2), 68–71 (2004).
82. I. Pe'er, T. Pupko, R. Shamir, R. Sharan, "Incomplete directed perfect phylogeny". *SIAM Journal on Computing* Vol. 33 No. 3, 590–607 (2004).
83. A. Tanay, R. Sharan, M. Kupiec, R. Shamir, "Revealing modularity and organization in the yeast molecular network by integrated analysis of highly heterogeneous genomewide data". *Proc. National Academy of Science USA* 101 (9) 2981–2986 (2004).
84. G. Kimmel, R. Sharan, R. Shamir, "Computational problems in noisy SNP and haplotype analysis: Block scores, block identification and population stratification". *INFORMS Journal on Computing* Vol. 14 No. 4 pp. 360–370 (2004).
85. R. Shamir, R. Sharan, D. Tsur., "Cluster graph modification problems". *Discrete Applied Mathematics* 144: 173–182 (2004).
86. A. Tanay, I. Gat-Viks, R. Shamir, "A global view of the selection forces in the evolution of yeast cis-regulation". *Genome Research* 14: 829–834 (2004).
87. A. Akavia, H. Senderowitz, A. Lerner and R. Shamir, "Designing multi-route synthesis in combinatorial chemistry". *Journal of Combinatorial Chemistry* Vol. 6 No. 4 pp 540–548 (2004).
88. I. Gat-Viks, A. Tanay, R. Shamir, "Modeling and analysis of heterogeneous regulation in biological networks". *Journal of Computational Biology* Vol. 11 No. 6 pp 1034–1049 (2004).
89. R. Sorek, R. Shemesh, Y. Cohen, O. Basechess, G. Ast, R. Shamir, "A non-EST based method for exon-skipping prediction". *Genome Research* 14 pp 1314-1623 (2004).
90. R. Elkon, K. Zeller, C. Linhart, C. Dang, R. Shamir, Y. Shiloh, "In silico identification of transcriptional regulators associated with c-Myc". *Nucleic Acid Research* Vol. 32 No. 17, pp. 4955-4961 (2004).
91. G. Kimmel, R. Shamir, "The incomplete perfect phylogeny haplotype problem". *Journal of Bioinformatics and Computational Biology* Vol. 3 No. 2 1–25 (2005).

92. C. Linhart, R. Shamir, "The degenerate primer design problem: Theory and applications". *J. Computational Biology* 12 (4) 431–456 (2005).
93. G. Kimmel, R. Shamir, "GERBIL: Genotype resolution and block identification using likelihood". *Proc. National Academy of Science USA* 102: 158-162 (2005).
94. G. Dror, R. Sorek, R. Shamir, "Accurate identification of alternatively spliced exons using support vector machine". *Bioinformatics* 21: 897-901 (2005).
95. R. Sharan, T. Ideker, B. Kelley, R. Shamir, R. M. Karp, "Identification of protein complexes by comparative analysis of yeast and bacterial protein interaction data". *Journal of Computational Biology* Vol. 12 No. 6 pp. 835–846 (2005).
96. A. Tanay, A. Regev, R. Shamir, "Conservation and evolvability in regulatory networks: The evolution of ribosomal regulation in yeast". *Proc. National Academy of Science USA* Vol. 102 No. 20, 7203–7208 (2005).
97. R. Elkon, S. Rashi-Elkeles, Y. Lerenthal, C. Linhart, T. Tenne, N. Amariglio, G. Rechavi, R. Shamir, Y. Shiloh, "Dissection of a DNA damage-induced transcriptional network using a combination of microarrays, RNAi and computational promoter analysis". *Genome Biology* 6: R43 (2005).
98. A. Tanay, I. Steinfeld, M. Kupiec, R. Shamir, "Integrative analysis of genome-wide experiments in the context of a large high-throughput data compendium". *Molecular Systems Biology* doi: 10.1038/msb4100005 (2005).
99. A. M. Dudley, D. M. Janse, A. Tanay, R. Shamir, G. M. Church, "A global view of pleiotropy and phenotypically derived gene function in yeast". *Molecular Systems Biology* doi: 10.1038/msb4100004 (2005).
100. T. Barzuza, J. S. Beckmann, R. Shamir and I. Pe'er, "Typing without calling the allele: a strategy for inferring SNP haplotypes". *European Journal of Human Genetics* Vol 13, 898–901 (2005).
101. G. Kimmel and R. Shamir, "Improved disease association via a block-free hidden Markov model of genotypes". *Journal of Computational Biology* Vol. 12, No. 10: 1243-1260 (2005).
102. R. Shalgi, M. Lapidot, R. Shamir, Y. Pilpel, "A catalog of stability-associated sequence elements in 3' UTRs of yeast mRNAs". *Genome Biology* 6 (10): R86 (2005).
103. R. Shamir, A. Maron-Katz, A. Tanay, C. Linhart, I. Steinfeld, R. Sharan, Y. Shiloh, R. Elkon, "EXPANDER: an integrative suite for microarray data analysis". *BMC Bioinformatics* 6:232 (2005).
104. T. Hartman, R. Shamir, "A simpler and faster 1.5-approximation algorithm for sorting by transposition". *Information and Computation* 204(2), pp. 275–290 (2006).
105. C. Linhart, R. Elkon, Y. Shiloh, R. Shamir, "Deciphering transcriptional regulatory elements that encode specific cell-cycle phasing by comparative genomics analysis". *Cell Cycle* 4(12) pp. 1788–1797 (2005).
106. S. Rashi-Elkeles, R. Elkon, N. Weizman, C. Linhart, N. Amariglio, G. Sternberg, G. Rechavi, A. Barzilai, R. Shamir, Y. Shiloh, "Parallel induction of ATM-dependent pro- and anti-apoptotic signals in response to ionizing radiation in murine lymphoid tissue". *Oncogene* 25, 1584–1592 (2006).
107. I. Gat-Viks, R. Shamir, R. M. Karp, R. Sharan, "Reconstructing chain functions in genetic networks". *SIAM Journal on Discrete Mathematics* Vol 20 No. 3 pp. 727–740 (2007).
108. M. Koren, G. Kimmel, E. Ben-Asher, I. Gal, M. Z. Papa, J. S. Beckman, D. Lancet, R. Shamir, E. Friedman, "ATM haplotypes and breast cancer risk in Jewish high risk women". *British Journal of Cancer* 94 (10) pp. 1537-1543 (2006).
109. I. Gat-Viks, A. Tanay, D. Rajman, R. Shamir, "A probabilistic methodology for integrating knowledge and experiments on biological networks". *Journal of Computational Biology* Vol. 13, No. 2: 165-181 (2006).

110. R. Blum, I. Nakdimon, R. Elkon, R. Shamir, G. Rechavi, Y. Kloog, "E2F1 identified by promoter and biochemical analysis as a central target of glioblastoma cell-cycle arrest in response to RAS inhibition". *International Journal of Cancer* 119 (3) 527–538 (2006).
111. I. Gal, R. Gershoni-Baruch, G. Kimmel, M. Z. Papa, E. Dagan, R. Shamir, E. Friedman, "RAD51 haplotypes and breast cancer risk in Jewish non-Ashkenazi high risk women". *European Journal of Cancer*, 42(8) pp. 1129-34 (2006).
112. G. Kimmel, R. Shamir, "A fast method for computing high significance disease association in large population-based studies". *American Journal of Human Genetics*, Vol 79 pp. 481–492 (2006).
113. A. Belle, A. Tanay, L. Bitincka, R. Shamir, E. K. O'Shea, "Quantification of protein half-lives in the budding yeast proteome". *Proc. National Academy of Science USA* 103(35):13004-9 (2006).
114. R. Sorek, G. Dror, R. Shamir, "Assessing the number of ancestral alternatively spliced exons in the human genome". *BMC Genomics* 7:273 (2006).
115. R. Shamir, D. Tsur, "Improved algorithms for the random cluster graph model". *Random Structures and Algorithms* 31 (4), pp. 418–449 (2007).
116. T. Barzuza, J. Beckman, R. Shamir, I. Pe'er, "Computational problems in perfect phylogeny haplotyping: Typing without calling the allele". *IEEE/ACM Transactions on Bioinformatics and Computational Biology* 5(1), pp. 101–109 (2008).
117. I. Gat-Viks, R. Shamir, "Refinement and expansion of signaling pathways: the osmotic response network in yeast". *Genome Research* 17 (3) 358–367 (2007).
118. O. Davidovich, G. Kimmel, R. Shamir, "GEVALT: An integrated software tool for genotype analysis". *BMC Bioinformatics* 8:36 (2007).
119. I. Steinfeld, R. Shamir, M. Kupiec, "A genome-wide analysis in *Saccharomyces cerevisiae* demonstrates the influence of chromatin modifiers on transcription". *Nature Genetics* 39 (3) 303–309 (2007).
120. R. Sharan, I. Ulitsky, R. Shamir, "Network-based prediction of protein function". *Molecular Systems Biology* 3:88 (2007).
121. R. Blum, R. Elkon, S. Yaari, A. Zundelovich, J. Jacob-Hirsch, G. Rechavi, R. Shamir, Y. Kloog, "Gene expression signature of human cancer cell lines treated with the Ras inhibitor salirasib (S-Farnesylthiosalicylic acid)". *Cancer Research* 67, pp.3320-3328 (2007).
122. I. Ulitsky, R. Shamir, "Pathway redundancy and protein essentiality revealed in the *S. cerevisiae* interaction networks". *Molecular Systems Biology* 3:104 (2007).
123. I. Ulitsky, R. Shamir, "Identification of functional modules using network topology and high-throughput data". *BMC Systems Biology* 1:8 (2007).
124. A. Karban, I. Maza, O. Davidovich, E. Leshinsky-Silver, Gad Kimmel, H. Fidder, R. Shamir, M. Waterman, R. Eliakim, A. Levine, "Risk factors for Perianal Crohn's disease: The role of genotype, phenotype and ethnicity". *American Journal of Gastroenterology* 102 (8):1702–8 (2007).
125. M. Ozery-Flato, R. Shamir, "Sorting by reciprocal translocations via reversals theory". *Journal of Computational Biology* Vol. 14 No. 4, pp. 408–422 (2007).
126. E. Leshinsky-Silver, A. Karban, S. Cohen, M. Fridlander, O. Davidovich, G. Kimmel, R. Shamir and A. Levine, "Lack of association of the 3'-UTR polymorphism in the NFKBIA gene with Crohn's disease in an Israeli cohort". *International Journal of Colorectal Disease* Vol. 9 pp. 1021–1025 (2007).

127. A. Levine, S. Kugathasan, A. Vito, V. Biank, E. Leshinsky -Silver, O. Davidovich, G. Kimmel, R. Shamir, P. Orazio, U. Broeckel, S. Cucchiara, "Pediatric onset Crohn's disease is characterized by age and genotype-related colonic susceptibility". *Inflammatory Bowel Disease* Vol. 13 No. 12 1509-15 (2007).
128. G. Kimmel, M. Jordan, E. Halperin, R. Shamir, R. Karp, "A randomization test for controlling population stratification in whole-genome association studies". *American Journal of Human Genetics* Vol. 81 (5) pp. 895–905 (2007).
129. D. Rajzman, R. Shamir, A. Tanay, "Evolution and selection in yeast promoters: analyzing the combined effect of diverse transcription factor binding sites". *PLoS Computational Biology* Vol. 4, Issue 1, e7 (2008).
130. R. Elkon, C. Linhart, Y. Halperin, Y. Shiloh, R. Shamir, "Functional genomic delineation of TLRs-induced transcriptional networks". *BMC Genomics* Vol. 8 No. 394 (2007).
131. I. Ulitsky, I. Gat-Viks, R. Shamir, "MetaReg: A platform for modeling, analysis and visualization of biological systems using large-scale experimental data". *Genome Biology* Vol. 9 No. R1 (2008).
132. R. Elkon, R. Vesterman, N. Amit, J. Assa, I. Ulitsky, G. Steinfeld, R. Blechman, Y. Shiloh, R. Shamir, "SPIKE - A Database, Visualization and Analysis Tool for DNA Damage Response Signaling Pathways". *BMC Bioinformatics* 9:110 (2008).
133. L. C. Laurent, J. Chen, I. Ulitsky, F.-J. Mueller, C. Lu, R. Shamir, J-B. Fan, J. F. Loring, "Comprehensive microRNA profiling reveals a unique human embryonic stem cell signature dominated by a single seed sequence". *Stem Cells* 26 (6):1506-16 (2008).
134. C. Linhart, Y. Halperin, R. Shamir, "Transcription factor and microRNA motif discovery: The Amadeus platform and a compendium of metazoan target sets". *Genome Research* Vol 18 No. 7 pp. 1180–9 (2008).
135. F.-J. Mueller, R. Williams, D. Kostka, L. Laurent, I. Ulitsky, C. Lu, M. S. Rao, R. Shamir, P. H. Schwartz, N. O. Schmidt, J. F. Loring, "Regulatory networks define phenotypic classes of human stem cell lines". *Nature* Vol. 455 pp. 401–406 (2008).
136. M. Ozery-Flato, R. Shamir, "Sorting genomes with centromeres by translocations". *Journal of Computational Biology* Vol. 15 No. 7 pp 1–20 (2008).
137. I. Ulitsky, T. Shlomi, M. Kupiec, R. Shamir, "From E-MAPs to module maps: delineating genetic interactions using physical interactions". *Molecular Systems Biology* 4, 209 doi:10.1038/msb.2008.42 (2008).
138. C. Linhart, R. Shamir, "Faster pattern matching with character classes", *Journal of Computer and Systems Science* 75, 155–162 (2009).
139. G. Karlebach, R. Shamir, "Modeling and analysis of regulatory networks". *Nature Reviews Molecular Cell Biology*, 9, 771–780 doi:10.1038/nrm2503 (2008).
140. C. Linhart, R. Shamir, "Matching with don't-cares and a small number of mismatches". *Information Processing Letters* 109 (5) 273–277 (2009).
141. Y. Halperin, C. Linhart, I. Ulitsky, R. Shamir, "Allegro: Analyzing expression and sequence in concert to discover regulatory programs". *Nucleic Acids Research* 37:5, 1566-1579 (2009).
142. I. Ulitsky, R. Shamir, "Identifying functional modules using expression profiles and confidence-scored protein interactions". *Bioinformatics* 25 (9) 1158–1164 doi: 10.1093/bioinformatics/btp118 (2009).
143. M. Ozery-Flato, R. Shamir, "Sorting cancer karyotypes by elementary operations". *Journal of Computational Biology* 16 (10) 1445-1460 (2009).

144. O. Davidovich, G. Kimmel, E. Halperin, R. Shamir, "Increasing the Power of Association Studies by Imputation-based Sparse Tag SNP Selection" *Communications in Information and Systems* 9 (3) 269-282 (2009).
145. S. Bruckner, F. Hueffner, R. M. Karp, R. Shamir, R. Sharan. "TORQUE: topology querying of protein interaction networks". *Nucleic Acids Research* doi: 10.1093/nar/gkp474 (2009).
146. M. Gutkin, G. Dror, R. Shamir, "SlimPLS: a method for feature selection in gene expression-based disease classification". *PLoS One* Vol. 4 No. 7 e6416 (2009).
147. F. Swidan, R. Shamir, "Assessing the quality of whole genome alignments in bacteria". *Advances in Bioinformatics* Volume 2009, Article ID 749027, 8 pages doi:10.1155/2009/749027 (2009).
148. I. Ulitsky, A. Maron-Katz, S. Shavit, D. Sagir, C. Linhart, R. Elkon, A. Tanay, R. Sharan, Y. Shiloh, R. Shamir, "EXPANDER: From expression microarrays to networks and functions". *Nature Protocols* 5, 303–322 (2010).
149. P. Pevzner, R. Shamir, "Computing has changed biology - biology education must catch up". Education Forum, *Science* Vol. 325. no. 5940, pp. 541 - 542 (2009).
150. I. Ulitsky, N. Krogan, R. Shamir, "Towards accurate imputation of quantitative genetic interactions". *Genome Biology* 10:R140 (2009).
151. I. Gat-Viks, R. Meller, M. Kupiec, R. Shamir, "Understanding gene sequence variation in the context of transcription regulation in yeast". *PLoS Genetics* Vol. 6 No. 1 e1000800 (2010).
152. S. Bruckner, F. Hueffner, R. M. Karp, R. Shamir, R. Sharan, "Topology-free querying of protein interaction networks". *Journal of Computational Biology* 17(3) 237–252 (2010).
153. S. Yaari-Stark, M. Shaked, Y. Nevo-Caspi, J. Jacob-Hires, R. Shamir, G. Rechavi, Y. Kloog, "Ras inhibits ER stress in human cancer cells with amplified myc". *International Journal of Cancer* 126, 2268–2281 (2010).
154. G.-H. Romano, Y. Gurevich, O. Lavi, I. Ulitsky, R. Shamir, M. Kupiec. "Different sets of QTLs influence fitness variation in yeast". *Molecular Systems Biology* 6: 346 doi:10.1038/msb.2010.1 (2010).
155. G. Karlebach, R. Shamir, "Minimally perturbing a gene regulatory network to avoid a disease phenotype: the glioma network as a test case". *BMC Systems Biology* 4:15 (2010).
156. P. S. Aguilar, F. Froehlich, M. Rehman, M. Shales, N. Hubner, I. Ulitsky, A. Olivera-Couto, R. Shamir, P. Walter, M. Mann, C. Ejsing, N. J. Krogan, T. C. Walther, "A plasma membrane E-MAP reveals links between the eisosome, sphingolipid metabolism and endosomal trafficking". *Nature Structural and Molecular Biology* 17 (7) 901–908 (2010).
157. M. Ziv-Ukelson, I. Gat-Viks, Y. Wexler, R. Shamir, "A faster algorithm for simultaneous alignment and folding of RNA". *Journal of Computational Biology* 17(8):1051-65 (2010).
158. I. Ulitsky, L. Laurent, R. Shamir, "Towards computational prediction of microRNA function and activity". *Nucleic Acids Research* 1–13, doi:10.1093/nar/gkq570 (2010).
159. I. Ulitsky, A. Krishnamurthy, R. M. Karp, R. Shamir, "DEGAS: De novo discovery of dysregulated pathways in human diseases". *PLoS One* 5 (10) e13367 (2010).
160. M. Ozery-Flato and R. Shamir, "An $O(n^{3/2}\sqrt{\log(n)})$ algorithm for sorting by reciprocal translocations". *Journal of Discrete Algorithms* Vol 9, pp. 344-357 DOI 10.1016/j.jda.2011.04.003 (2011).
161. M. Bansal, R. Shamir, "A note on the fixed parameter tractability of the gene-duplication problem". *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 8 (3), art. no. 5557848, pp. 848-850 (2011).

162. A. Paz, Z. Brownstein, Y. Ber, S. Bialik, E. David, D. Sagir, I. Ulitsky, R. Elkon, A. Kimchi, K. B. Avraham, Y. Shiloh, R. Shamir, "Spike: A database of highly curated human signaling pathways". *Nucleic Acids Research* Vol. 39, Database issue D793–9 (2011).
163. L. C. Laurent, I. Ulitsky, I. Slavin, H. Tran, A. Schork, R. Morey, C. Lynch, J. V. Hamess, S. Lee, M. J. Barrero, S. Ku, M. Martynova, R. Semechkin, V. Galat, J. Gottesfeld, J. C. I. Belamonte, C. Murry, H. S. Kirstead, H-S. Park, U. Schmidt, A. L. Laslett, F-J. Muller, C. M. Nivergelt, R. Shamir, J. F. Loring, "Dynamic changes in the copy number of pluripotency and cell proliferation genes in human ESCs and iPSCs during reprogramming and time in culture". *Cell Stem Cell* 8 106–118 (2011).
164. M. Bansal, G. Banay, P. Gogarten, R. Shamir, "Detecting highways of horizontal gene transfer". *Journal of Computational Biology* 18 (9) 1087–1114 (2011).
165. H. Sharon, D. Amar, E. Levdansky, G. Mircus, Y. Shadkchan, R. Shamir, N. Osherov, "PrtT-regulated proteins secreted by Aspergillus fumigatus activate MAPK signaling in exposed A549 lung cells leading to necrotic cell death". *PLoS One* Vol. 6 No. 3, e17509 (2011).
166. T. Elkan-Miller, I. Ulitsky, R. Hertzano, A. Rudnicki, A. A. Dror, D. R. Lenz, R. Elkon, M. Irmler, J. Beckers, R. Shamir, K. B. Avraham, "Integration of transcriptomics, proteomics, and microRNA analyses reveals novel microRNA regulation of targets in the mammalian inner ear". *PLoS One* 6(4) e18195 (2011).
167. M. Ozery-Flato, C. Linhart, L. Trakhtenbrot, S. Izraeli, R. Shamir, "Large-scale analysis of chromosomal aberrations in cancer karyotypes reveals two distinct paths to aneuploidy". *Genome Biology* 12(6):R61 (2011).
168. S. Rashi-Elkeles, R. Elkon, S. Shavit, Y. Lerenthal, C. Linhart, A. Kupershtein, N. Amariglio, G. Rechavi, R. Shamir and Y. Shiloh, "Transcriptional modulation induced by ionizing radiation: p53 remains a central player". *Molecular Oncology* 5 336-348 (2011).
169. G. Karlebach, R. Shamir, 'Constructing logical models of gene regulatory networks by integrating transcription factor-DNA interactions with expression data: an entropy based approach'. *Journal of Computational Biology* 19(1): 30-41 (2012).
170. C. Linhart, Y. Halperin, A. Darom, S. Kidron, L. Broday, R. Shamir, "A novel candidate cis-regulatory motif pair in the promoters of germline and oogenesis genes in C. elegans". *Genome Research* 22 (1) 76-83 (2012).
171. L. Marom, I. Ulitsky, Y. Cabili, R. Shamir, O. Elroy-Stein, "A point mutation in translation initiation factor eIF2B leads to function- and time-specific changes in brain gene expression". *PLoS One* 6, 269920 (2011).
172. S. Hagag, P. Kubitschek-Barreira, G. W.P. Neves, D. Amar, W. Nierman, I. Shalit, R. Shamir, L. Lopes-Bezerra, N. Osherov, "Transcriptional and proteomic analysis of the Aspergillus fumigatus DeltaprtT protease-deficient mutant". *PLoS One* 7 (4), e33604 (2012).
173. O. Lavi, G. Dror, R. Shamir, "Network-induced classification kernels for gene expression profile analysis". *Journal of Computational Biology* 19 (6) 694–709 (2012).
174. R. Rozov, E. Halperin, R. Shamir, "MGMR: leveraging RNA-Seq population data to optimize expression estimation". Accepted to the second annual RECOMB satellite workshop on massively parallel sequencing (RECOMB-seq). *BMC Bioinformatics* 13 (Suppl 6):S2 (2012).
175. D. Marbach, J. C. Costello, R. Kueffner, N. Vega, R. J. Prill, D. M. Camacho, K. R. Allison, the DREAM5 Consortium (including G. Karlebach, R. Shamir) M. Kellis, J. J. Collins G. Stolovitzky, "Wisdom of crowds for robust gene network inference". *Nature Methods* 9 (8) 796–804 (2012).

176. Y. Orenstein, C. Linhart, R. Shamir, "Assessment of algorithms for motif finding based on protein binding microarray data". *PLoS One* 7(9): e46145. doi:10.1371/journal.pone.0046145 (2012).
177. O. Tzfadia, D. Amar, L. M. T. Bradbury, E. T. Wurtzel, R. Shamir, "The MORPH algorithm: ranking candidate genes for membership in *Arabidopsis thaliana* pathways". *Plant Cell* 24(11):4389-406, tpc.112.104513 (2012).
178. Y. Orenstein, E. Mick, R. Shamir, "RAP: Accurate and fast motif finding based on protein microarray data". *Journal of Computational Biology* 20(5): 375-382 (2013).
179. M. T. Weirauch, A. Cote, R. Norel, M. Annala, Y. Zhao, T. J. Riley, J. S. Rodriguez, T. Cokelaer, A. Vedenko, S. Talukder, DREAM5 consortium (including Y. Orenstein, C. Linhart, R. Shamir), H. J. Bussemaker, Q. D. Morris, M. L. Bulyk, G. Stolovitzky, T. R. Hughes, "Evaluation of methods for modeling transcription factor sequence specificity". *Nature Biotechnology* 31 (2) 126–134, doi:10.1038/nbt.2486 (2013).
180. M. S. Bansal, G. Banay, T. J. Harlow, J. P. Gogarten, R. Shamir, "Systematic inference of highways of horizontal gene transfer in prokaryotes". *Bioinformatics* 29 (5) pp. 571–579, (2013).
181. D. Amar, H. Safer, R. Shamir, "Dissection of regulatory networks that are altered in disease via differential co-expression". *PLoS Computational Biology* Vol. 9 (3) e1002955 (2013).
182. Y. Orenstein, R. Shamir, "Design of shortest double-stranded DNA sequences covering all k-mers with applications to protein-binding microarrays and synthetic enhancers". *Bioinformatics* Vol. 29 ISMB/ECCB 2013, pages i71–i79 (2013).
183. G. H. Romano, Y. Harari, T. Yehuda, A. Podhorzer, L. Rubinstein, R. Shamir, , A. Gottlieb, Y. Silberberg, D. Pe'er, E. Ruppin, R. Sharan, M. Kupiec, "Environmental stresses disrupt telomere length homeostasis". *PLoS Genetics* Sep 9(9):e1003721. doi: 10.1371/journal.pgen.1003721 (2013).
184. R. E Bell, M. Khaled, D. Netanely, S. Schubera, T. Golan, A. Buxbaum, M. M. Janas, B. Postolsky, R. Shamir, C. Levy, "Transcription factor/microRNA axis blocks melanoma invasion program by miR-211 targeting NUAK1". *Journal of Investigative Dermatology*. 134 (2) 441–51. doi: 10.1038/jid.2013.340 (2013).
185. D. Amar, R. Shamir, "Constructing module maps for integrated analysis of heterogeneous biological networks". *Nucleic Acids Research* doi: 10.1093/nar/gku102 (2014).
186. Y. Orenstein, R. Shamir, "A comparative analysis of transcription factor binding models learned from PBM, HT-SELEX and ChIP data". *Nucleic Acids Research* doi: 10.1093/nar/gku117 (2014).
187. S. Rashi-Elkeles, H-J. Warnatz, R. Elkon, A. Kupershtein, Y. Chobod, A. Paz, V. Amstislavskiy, M. Sultan, H. Safer, W. Neitfeld, Lehrach, R. Shamir, M-L. Yaspo, Y. Shiloh, "Parallel profiling of the transcriptome, cistrome, and epigenome in the cellular response to ionizing radiation". *Science Signaling* 7 (325) rs3 doi: 10.1126/scisignal.2005032 (2014).
188. A. Thevenin, L. Ein-Dor, M. Ozery-Flato, R. Shamir, "Functional gene groups are concentrated within chromosomes, among chromosomes and in the nuclear space of the human genome". *Nucleic Acids Research* doi: 10.1093/nar/gku667 (2014).
189. O. Sagy, R. Shamir, O. Rechavi, "Examination of exhaustive cloning attempts reveals that *C. elegans* piRNAs, transposons, and repeat sequences are efficiently cloned in yeast, but not in bacteria". *Frontiers in Genetics* 5: 275 doi: 10.3389/fgene.2014.00275 (2014).
190. A. Kedmi, Y. Zehavi, Y. Glick, Y. Orenstein, D. Ideses, C. Wachtel, T. Doniger, H. Waldman Ben-Asher, N. Muster, J. Thompson, S. Anderson, D. Avrahami, J. R. Yates 3rd, R. Shamir, D. Gerber, T. Juven-Gershon, "Drosophila TRF2 is a preferential core promoter regulator". *Genes and Development* 28 (19) pp. 2163 - 2174 (2014).

191. D. Amar, I. Frades, A. Danek, T. Goldberg, S. K. Sharma, P. Hedley, E. Proux-Wera, E. Andreasson, R. Shamir, O. Tzfadia, E. Alexandersson, “Evaluation and integration of functional annotation pipelines for non-model organisms: the potato genome as a test case”. *BMC Plant Biology* 14(1):329 (2014).
192. D. Amar, I. Frades, D. Chazanov, D. Zaltzman, N. Ghatan, P. Hedley, E. Alexandersson, O. Tzfadia, R. Shamir, “The MORPH-R web and software tool for predicting missing genes in biological pathways”. *Physiologia Plantarum* doi:10.1111/ppl.12326 (2015).
193. R. Ohana, B. Weiman-Kelman, A. Rinon, E. Tamm, A. Salomon, D. Netaneli, M. Pasmanik-Chor, R. Shamir, R. Ashery-Padan, “MicroRNAs of the RPE are essential for RPE differentiation and photoreceptor maturation”. *Development* pii: dev.121533. [Epub ahead of print] (2015).
194. A. Sloutskin, Y. M. Danino, Y. Zehavi, Y. Orenstein, T. Doniger, R. Shamir, T. Juven-Gershon, “ElemeNT: A computational tool for detecting core promoter elements”. *Transcription* 6:3, 41–50 (2015).
195. D. Amar, T. Hait, S. Israeli, R. Shamir. “Integrated analysis of numerous heterogeneous gene expression profiles for detecting robust disease-specific biomarkers and proposing drug targets”. *Nucleic Acids Research* doi: 10.1093/nar/gkv810 (2015).
196. Y. Orenstein, D. Avrahami, T. Zor, R. Shamir, D. Gerber, “Integrated microfluidic approach for quantitative high-throughput measurements of transcription factor binding affinities”. *Nucleic Acids Research* pii: gkv1327 (2015)
197. A. Maron-Katz, S. Vaisvaser, T. Lin, T. Hendl, R. Shamir, “A large-scale perspective on stress-induced alterations in resting-state networks”. *Scientific Reports* 6, 21503 doi:10.1038/srep21503 (2016)
198. R. E. Bell, T. Golan, A. Salamon, T. Liron, D. Sheinboim, S. Gelfman, Y. Gabet, R. Shamir, C. Levy. “Enhancer methylation dynamics contribute to cancer plasticity and patient mortality” *Genome Research* 26 (5) pp. 601 - 611 (2016).
199. A. Domingo, D. Amar, K. Grütz, L. Lee, R. Rosales, N. Brüggemann, R. D. Jamora, E. Cutiengco dela-Paz, K. Lohmann, R. Shamir, C. Klein, A. Westenberger. “Evidence of TAF1 dysfunction in peripheral models of X-linked dystonia-parkinsonism”. *Cellular and Molecular Life Sciences* DOI 10.1007/s00018-016-2159-4 (2015).
200. D. Netanely, A. Avraham, A. Ben-Baruch, E. Evron, R. Shamir. “Expression and methylation signatures partition Luminal-A breast tumors into distinct prognostic subgroups”. *Breast Cancer Research* 18:74 DOI 10.1186/s13058-016-0724-2 (2016).
201. A. Maron-Katz, D. Amar, E. Ben-Simon, T. Hendl, R. Shamir. “RichMind: a tool for improved inference from large-scale neuroimaging results”. *PLoS One* DOI:10.1371/journal.pone.0159643 (2016).
202. Y. Orenstein, R. Shamir. “Modeling protein-DNA binding via high throughput in vitro technologies”. *Briefings in Functional Genomics* doi: 10.1093/bfgp/elw030 (2016).
203. R. Golodnitsky, Y. Orenstein, D. Chen, C. Wachtel, D. Avrahami, R. Shamir, D. Gerber. “SELMAP - Selex Energy Landscape Mapping of transcription factor binding sites using integrated microfluidics”. *Scientific Reports* 6, Article number: 33351 doi:10.1038/srep33351 (2016)
204. R. Zeira, R. Shamir. “Sorting by cuts, joins and whole chromosome duplications”. *Journal of Computational Biology* Vol 24 no.2 127–137 (2017).
205. A. Nachshon, H. J. Abu-Toamih Atamni, R. Sheikh-Hamed, A. Dorman, R. Mott, J. C. Dohm, H. Lehrach, M. Sultan R. Shamir, S. Sauer, H. Himmelbauer, F. A. Iraqi, I. Gat-Viks. “Dissecting the effect of genetic variation on the hepatic expression of drug disposition genes across the collaborative cross mouse strains”. *Frontiers in Genetics* Vol 7, Article 172, doi: 10.3389/fgene.2016.00172 (2016).

206. R. Rozov, A. Kav Brown, D. Bogumil, E. Halperin, I. Mizrahi, R. Shamir. "Recycler: an algorithm for detecting plasmids from de novo assembly graphs" *Bioinformatics* 33(4):475-482 <https://doi.org/10.1093/bioinformatics/btw651> (2016).
207. D. Amar, S. Izraeli, R. Shamir. "Utilizing somatic mutation data from numerous studies for cancer research: proof of concept and applications". *Oncogene* doi: 10.1038/onc.2016.489 (2017).
208. L. Yang, Y. Orenstein, A. Jolma, J. Taipale, R. Shamir, R. Rohs. "Transcription factor family-specific DNA shape readout revealed by quantitative binding specificity models". *Molecular Systems Biology* 13, 910 DOI 10.15252/msb.20167238 (2017)
209. E. Ben-Simon, A. Maron-Katz, N. Lahav, R. Shamir, T. Hendl. "Tired and misconnected: A breakdown of brain modularity following sleep deprivation". *Human Brain Mapping* 38 (6) 3300–3314. doi: 10.1002/hbm.23596. (2017)
210. K. Perl, K. Ushakov, Y. Pozniak, O. Yizhar-Barnea, Y. Bhonker, S. Shavitzi, T. Geiger; K. B. Avraham, R. Shamir. "Reduced changes in protein compared to mRNA levels across non-proliferating tissues". *BMC Genomics* 18:305 DOI: 10.1186/s12864-017-3683-9 (2017).
211. M. El-Kebir, B. Raphael, R. Shamir, R. Sharan, S. Zaccaria, M. Zehavi, R. Zeira. "Copy number evolution problems: Complexity and algorithms". *Algorithms for Molecular Biology* 12:13 DOI: 10.1186/s13015-017-0103-2 (2017).
212. R. Shamir, M. Zehavi, R. Zeira. "A linear-time algorithm for the Copy Number Transformation problem". *Journal of Computational Biology* <https://doi.org/10.1089/cmb.2017.0060> (2017)
213. R. Shamir, C. Klein, D. Amar, E. J. Vollstedt, M. Bonin, M. Usenovic, Y. C. Wong, A. Maver, A. Troiano, S. Poths, H. Safer, J.-C. Corvol, S. Lesage, O. Lavi, G. Deuschl, G. Kuhlenbaeumer, H. Pawlack, I. Ulitsky, M. Kasten, O. Riess, A. Brice, B. Peterlin, D. Krainc. "Analysis of blood-based gene expression in idiopathic Parkinson disease". *Neurology* 89(16):1676-1683 (2017).
214. R. Rozov, G. Goldshlager, R. Shamir, E. Halperin. "Faucet: streaming de novo assembly graph construction". *Bioinformatics* 34 (1) 147–154, <https://doi.org/10.1093/bioinformatics/btx471> (2018).
215. D. Amar, R. Shamir, D. Yekutieli. "Extracting replicable associations across multiple studies: Empirical Bayes algorithms for controlling false discovery rate". *PLoS Computational Biology* 13(8): e1005700 (2017).
216. Y. Orenstein, D. Pellow, G. Marcais, R. Shamir, C. Kingsford. "Designing small universal k-mer hitting sets for improved analysis of high throughput sequencing". *PLoS Computational Biology* 13(10): e1005777 (2017).
217. R. Eitan, R. Shamir. "Reconstructing cancer karyotypes from short read data: the half full and half empty glass". *BMC Bioinformatics* 18:488 (2017). Also: bioRxiv 152447; doi: <https://doi.org/10.1101/152447>.
218. G. Gilam, A. Maron-Katz, E. Kliper, T. Lin, E. Fruchter, R. Shamir, T. Hendl. "Tracing the neural carryover effects of interpersonal anger on resting-state fMRI and their relation to traumatic stress symptoms in a subsample of soldiers". *Frontiers in Behavioral Neuroscience* <https://doi.org/10.3389/fnbeh.2017.00252> (2017).
219. D. Amar, A. Vizel, C. Levy, R. Shamir. "ADEPTUS: A discovery tool for disease prediction, enrichment and network analysis based on profiles from many diseases". *Bioinformatics* bty027, <https://doi.org/10.1093/bioinformatics/bty027> (2018).
220. A. Zwaenepoel, T. Diels, D. Amar, T. Van Parys, R. Shamir, Y. Van de Peer, O. Tzfadia. "MorphDB: Prioritizing genes for specialized metabolism pathways and gene ontology categories in plants". *Frontiers in Plant Science* <https://doi.org/10.3389/fpls.2018.00352> (2018).

221. T. Hait, D. Amar, R. Shamir, R. Elkon. “FOCS: a novel method for analyzing enhancer and gene activity patterns infers an extensive enhancer -- promoter map”. *Genome Biology* 19:56 <https://doi.org/10.1186/s13059-018-1432-2> (2018).
222. R. Zeira, R. Shamir. “Sorting cancer karyotypes using double-cut-and-joins, duplications and deletions”. *Bioinformatics* bty381, <https://doi.org/10.1093/bioinformatics/bty381> (2018).
223. K. Perl, R. Shamir, K. Avraham. “Computational analysis of mRNA expression profiling in the inner ear reveals candidate transcription factors associated with proliferation, differentiation, and deafness”. *Human Genomics* 12 (1) 30 <https://doi.org/10.1186/s40246-018-0161-7> (2018).
224. Z. Wang, H. Lou, R. Shamir, R. Jiang, T. Chen. “GePMI: A statistical model for personal intestinal microbiome identification”. *npj Biofilm and Microbiome* 4: 20 <https://doi.org/10.1038/s41522-018-0065-2> (2018).
225. I. Nurick, R. Shamir, R. Elkon. “Genomic meta-analysis of the interplay between 3D chromatin organization and gene expression programs under basal and stress conditions” BioRxiv doi: <https://doi.org/10.1101/337766>. *Epigenetics and Chromatin* 11 (1) 49 doi: [10.1186/s13072-018-0220-2](https://doi.org/10.1186/s13072-018-0220-2) (2018).
226. N. Rappoport, R. Shamir. “Multi-omic and multi-view clustering algorithms: review and cancer benchmark”. *Nucleic Acids Research* 46 (20) pp. 10546—10562, <https://doi.org/10.1093/nar/gky889> (2018).
227. N. Rappoport, R. Shamir. “NEMO: Cancer subtyping by integration of partial multi-omic data”. *Bioinformatics* btz058, <https://doi.org/10.1093/bioinformatics/btz058> (2019).
228. T. A. Hait, A. Maron-Katz., D. Sagir, D. Amar, I. Ulitsky, C. Linhart, A. Tanay, R. Sharan, Y. Shiloh, R. Elkon, R. Shamir. “The EXPANDER integrated platform for transcriptome analysis”. *Journal of Molecular Biology* <https://doi.org/10.1016/j.jmb.2019.05.013> (2019).
229. N. Rappoport, R. Shamir. “Inaccuracy of the logrank approximation in cancer data analysis”. *Molecular Systems Biology* 15:e8754 <https://doi.org/10.15252/msb.20188754> (2019).
230. G. Dinstag, D. Amar, E. Ingelsson, E. Ashley, R. Shamir. “Personalized prediction of adverse heart and kidney events using pre-enrollment and time course data from SPRINT and ACCORD trials”. *PLoS One* <https://doi.org/10.1371/journal.pone.0219728> (2019).
231. D. Netanely, N. Stern, I. Laufer, R. Shamir. “PROMO: An interactive tool for analyzing clinically-labeled multi-omic cancer datasets”. *BMC Bioinformatics* 20:732 <https://doi.org/10.1186/s12859-019-3142-5> (2019).
232. A. Kav Brown, R. Rozov, D. Bogmil, S. J. Sorensen, I. Benhar, E. Halperin, R. Shamir, I. Mizrahi. “Unraveling plasmidome distribution and interaction with its hosting microbiome” *Environmental Microbiology* <https://doi.org/10.1111/1462-2920.14813> (2019).
233. G. Dinstag, R. Shamir. “Prodigy: personalized prioritization of driver genes”. *Bioinformatics* btz815, <https://doi.org/10.1093/bioinformatics/btz815> (2019).
234. D. Coster, A. Wasserman, E. Fisher, O. Rogowski, D. Zeltser, I. Shapira, D. Bernstein, A. Meilik, E. Raykhshtat, S. Berliner, S. Shenhar-Tsarfaty, R. Shamir. “Using the kinetics of C-reactive protein response to improve the differential diagnosis between acute bacterial and viral infections”. *Infection* <https://doi.org/10.1007/s15010-019-01383-6> (2019).
235. N. S. Magal , L. Farhat-Younis , D. Rasoulouniriana , A. Glieberman , A. Gutwillig , L. Tal , D. Netanely, R. Shamir , R. Blau , H. Gutman , P. Rider, Y. Carmi. “Melanoma-secreted lysosomes trigger monocyte-derived dendritic cell apoptosis and limit cancer immunotherapy”. *Cancer Research* doi: [10.1158/0008-5472.CAN-19-2944](https://doi.org/10.1158/0008-5472.CAN-19-2944) (2020).

236. D. Pellow, I. Mizrahi, R. Shamir. "PlasClass improves plasmid sequence classification" *PLoS Computational Biology* 16(4): e1007781 (2020).
237. N. Rappoport, R. Safra, R. Shamir. "MONET: Multi-omic patient module detection by omic selection". *PLoS Computational Biology* 16 (9) e1008182 (2020).
238. H. Levi, R. Elkon, R. Shamir. "DOMINO - a novel network-based active module identification algorithm with reduced rate of false calls". *Molecular Systems Biology* 17:e9593 (2021).
239. D. Netanely, S. Leibou, R. Parikh, N. Stern, H. Vaknine, R. Brenner, S. Amar, R. Haiat Factor, T. Perluk, J. Frand, E Nizri, D. Hershkovitz, V. Zemser-Werner, C. Levy, R. Shamir. "Classification of node-positive melanomas into prognostic subgroups using keratin, immune and melanogenesis expression patterns". *Oncogene* <https://doi.org/10.1038/s41388-021-01665-0> (2021).
240. D. Pellow, M. Probst, O. Furman, A. Zorea, Arik Segal, I. Mizrahi, R. Shamir. "SCAPP: An algorithm for improved plasmid assembly in metagenomes". *Microbiome* 144 (2021)
241. T. Hait, R. Elkon, R. Shamir. "CT-FOCS: a novel method for inferring cell type-specific enhancer-promoter maps". *Nucleic Acids Research* gkac048, <https://doi.org/10.1093/nar/gkac048> (2022).
242. O. Noy*, D. Coster*, M. Metzger, I. Attar, S. Shenhari-Tsafraty, S. Berliner, G. Rahav, O. Rogowski, R. Shamir. "A machine learning model for predicting deterioration of COVID-19 inpatients". *Nature Scientific Reports* Article 2630 DOI 10.1038/s41598-022-05822-7 (2022).
243. H. Levi, N. Rahmanian, R. Elkon, R. Shamir. "The DOMINO web-server for active module identification analysis". *Bioinformatics*, btac067, <https://doi.org/10.1093/bioinformatics/btac067> (2022).
244. D. Flomin, D. Pellow, R. Shamir. "Dataset-adaptive minimizer order reduces memory usage in k-mer counting". *Journal of Computational Biology* <https://doi.org/10.1089/cmb.2021.0599> (2022).
245. A. Dutta*, D. Pellow*, R. Shamir. "Parameterized syncmer schemes improve long-read mapping". *PLoS Computational Biology* 28;18(10):e1010638. doi: 10.1371/journal.pcbi.1010638 (2022).
246. N. Rappaport, E. Chomsky, T. Nagano, C. Seibert, Y. Lubling, Y. Baran, A. Lifshitz, W. Leung, Z. Mukamel, R. Shamir, P. Fraser, A. Tanay. "Single cell Hi-C identifies plastic chromosome conformations underlying the gastrulation enhancer landscape". *Nature Communications* 14(1):3844. doi: 10.1038/s41467-023-39549-4 (2023)
247. D. Pellow, L. Pu, B. Ekim, L. Kotlar, B. Berger, R. Shamir, Y. Orenstein "Efficient minimizer orders for large values of k using minimum decycling sets". BioRxiv doi: <https://doi.org/10.1101/2022.10.18.512682> *Genome Research* DOI: 10.1101/gr.277644.123 (2023).
248. E. Shpigelman*, A. Hochstadt*, D. Coster, I. Merdler, E. Ghantous, Y. Szekely, Y. Lichter, P. Taieb, A. Banai, O. Sapir, Y. Granot, L. Lupu, A. Borohovitz, S. Sadon, S. Banai, R. Rubinshtein, Y. Topilsky, R. Shamir. "Clustering of clinical-echocardiographic phenotypes of covid-19 disease using machine-learning techniques" *Scientific Reports* 13:8832 doi: 10.1038/s41598-023-35449-1 (2023).
249. H. Levi, S. Carmi, S. Rosset, R. Yerushalmi, A. Zick, T. Yablonski-Peretz, (127 members of the BCAC Consortium)..., S. Ben-Shachar, N. Elefant*, R. Shamir* and R. Elkon*. "Evaluation of European-based polygenic risk score for breast cancer on Ashkenazi Jewish women". *Journal of Medical Genetics* doi:10.1136/jmg-2023-109185 (2023).
250. Y. Itai, N. Rappoport, R. Shamir. "Integration of gene expression and DNA methylation data across different experiments". *Nucleic Acids Research* gkad566, <https://doi.org/10.1093/nar/gkad566> (2023).

251. I. Shamir, Y. Assaf, R. Shamir. “Clustering the cortical laminae: in vivo parcellation”. *Brain Structure and Function* <https://doi.org/10.1007/s00429-023-02748-2> (2024).
252. H. Levi, R. Elkon*, R. Shamir*. “The predictive capacity of polygenic risk scores for disease risk is only moderately influenced by imputation panels tailored to the target population”. *Bioinformatics*, btae036, <https://doi.org/10.1093/bioinformatics/btae036> (2024).
253. A. Zorea, D. Pellow, L. Levin, S. Pilosof, J. Friedman, R. Shamir, I. Mizrahi. “Plasmids in the human gut reveal neutral dispersal and recombination that is overpowered by inflammatory diseases” *Nature Communications* 15, Article number: 3147 (2024)
254. A. Maier, M. Hartung, M. Abovsky, K. Adamowicz, G. D. Bader, S. Baier, D. B. Blumenthal, J. Chen, M. L. Elkjaer, C. Garcia-Hernandez, M. Hoffmann, I. Jurisica, M. Kotlyar, O. Lazareva, H. Levi, M. List, S. Lobentanzer, J. Loscalzo, N. Malod-Dognin, Q. Manz, J. Matschinske, M. Oubounyt, A. R. Pico, R. T. Pillich, J. M. Poschenrieder, D. Pratt, N. Pržulj, S. Sadegh, J. Saez-Rodriguez, S. Sakar, G. Shaked, R. Shamir, N. Trummer, U. Turhan, R. Wang, O/ Zolotareva, J. Baumbach. “Drugst.One – A plug-and-play solution for online systems medicine and network-based drug repurposing”. *Nucleic Acids Research* gkae388 (2024).
255. L. Pu, R. Shamir. “4CAC: 4-class classifier of metagenomic assemblies using machine learning and assembly graphs”. *Nucleic Acids Research* gkae799, <https://doi.org/10.1093/nar/gkae799> (2024).
256. E. Rannon, E. Goldschmidt, D. Bernstein, A. Wasserman, M. Roimi, A. Shrot, D. Coster, R. Shamir. “Predicting appropriateness of antibiotic treatment among ICU patients with hospital acquired infection”. *npj Digital Medicine* 8:87 (2025).

D. Refereed Conference Papers

257. R. Shamir, B. Dietrich, “Characterization and algorithms for greedily solvable transportation problems”. *Proceedings of the first ACM/SIAM Symposium on Discrete Algorithms*, 358–366 (1990).
258. M. C. Golumbic, R. Shamir, “Interval graphs, interval orders and the consistency of temporal events”. *Proceedings of the Israel Symposium on Theory of Computing and Systems (ISTCS-92), Lecture Notes In Computer Science*, vol. 601, D. Dolev, Z. Galil and M. Rodeh (eds.), Springer-Verlag, 32–42 (1992).
259. M. C. Golumbic, R. Shamir, “Algorithms and complexity for reasoning about time”. *Proceedings of the Tenth National Conference on Artificial Intelligence (AAAI-92)*, AAAI Press and MIT Press, Menlo Park, 741–747 (1992).
260. M. C. Golumbic, H. Kaplan and R. Shamir, “Algorithms and complexity of sandwich problems in graphs”. *Proceedings of the 19th International Workshop on Graph Theoretic Concepts in Computer Science (WG '93)*, J. van Leeuwen, ed. pp. 57–69, *Lecture Notes in Computer Science*, vol. 790, Springer, Berlin, 1994.
261. H. Kaplan, R. Shamir and R. E. Tarjan, “Tractability of parameterized completion problems on chordal and interval graphs: minimum fill-in and physical mapping”. *Proceedings of the 35th annual symposium on Foundations of Computer Science (FOCS)*, November 1994, IEEE Computer Science Press, 780–791.
262. I. Pe'er, R. Shamir, “Interval graphs with side (and size) constraints”. *Proceedings of the Third European Symposium on Algorithms (ESA 95)* Corfu, Greece, Springer, Berlin, 142–154.
263. H. Kaplan, R. Shamir, “Physical maps and interval sandwich problems: bounded degrees help”. *Proceedings of the Fourth Israel Symposium on Theory of Computing and Systems (ISTCS-96)*, Jerusalem, Israel, June 10–12, 1996, IEEE Computer Science Press 195–201 (1996).

264. H. Kaplan, R. Shamir, R. E. Tarjan, "Faster and simpler algorithm for sorting signed permutations by reversals". *Proc. Eighth Annual ACM-SIAM Symposium on Discrete Algorithms (SODA 97)*, New Orleans, Louisiana, January 5–7 1997, pages 344–351. Also: *Proc. First Annual International Conference of Computational Molecular Biology (RECOMB 97)*, page 163.
265. R. Shamir, D. Tsur, "Faster subtree isomorphism". *Proceedings of the Fourth Israel Symposium on Theory of Computing and Systems (ISTCS-97)*, pages 125–131.
266. R. Shamir, D. Tsur, "The maximum subforest problem: Approximation and exact algorithms". *Proc. Ninth Annual ACM-SIAM Symposium on Discrete Algorithms (SODA 98)*, San Francisco, California, January 25–27 1998, pages 394–399.
267. R. M. Karp, R. Shamir, "Algorithms for optical mapping". *Proceedings of the Second Annual International Conference on Computational Molecular Biology (RECOMB 98)*, ACM Press, pages 117–124, 1998.
268. A. Natanzon, R. Shamir, R. Sharan, "A polynomial approximation algorithm for the minimum fill-in problem". *Proc. Thirtieth Annual ACM Symposium on Theoretical Computer Science (STOC 98)*, Dallas, Texas, May 1998, ACM Press, 41–47 New York, 1998.
269. G. Mayraz, R. Shamir, "Construction of physical maps from oligonucleotide fingerprints data". *Proceedings of the Third Annual International Conference on Computational Molecular Biology (RECOMB 99)*, pp. 268–277, ACM Press, New York (1999).
270. E. Hartuv, A. Schmitt, J. Lange, S. Meier-Ewert, H. Lehrach, R. Shamir, "An algorithm for clustering cDNAs for gene expression analysis" *Proceedings of the Third Annual International Conference on Computational Molecular Biology (RECOMB 99)*, pp. 188–197, ACM Press, New York (1999).
271. R. M. Karp, I. Pe'er, R. Shamir. "An algorithm combining discrete and continuous methods for optical mapping". *Proc. Seventh International Conference on Intelligent Systems for Molecular Biology (ISMB '99)*, 159–168, AAAI Press, Menlo Park, CA (1999).
272. P. Hell, R. Shamir, R. Sharan, "A fully dynamic algorithm for recognizing and representing proper interval graphs". *Proc. 7th Annual European Symposium on Algorithms (ESA 99)*, pp. 527–539, LNCS 1643 (1999).
273. A. Ben-Dor, I. Pe'er, R. Shamir, R. Sharan, "On the complexity of positional sequencing by hybridization". *Proc. 10th Annual Symposium on Combinatorial Pattern Matching (CPM '99)*, M. Crochemore and M. Patterson (eds.), pages 88–100, Springer, Berlin, LNCS 1645 (1999).
274. A. Natanzon, R. Shamir and R. Sharan, "Complexity classification of some edge modification problems". *Proc. 25th International Workshop on Graph-Theoretic Concepts in Computer Science (WG 99)*, pp. 65–77, LNCS 1665 (1999).
275. I. Pe'er, R. Shamir, R. Sharan, "Incomplete directed perfect phylogeny". *Proc. 11th Combinatorial Pattern Matching (CPM 00)*, pp. 143–153 (1999).
276. R. Shamir, R. Sharan, "CLICK: A clustering algorithm with applications to gene expression analysis". *Proc. 8th International Conference on Intelligent Systems for Molecular Biology (ISMB '00)*, pp. 307–316 AAAI Press, Menlo Park, CA (2000).
277. I. Pe'er, R. Shamir, "Spectrum alignment: Efficient resequencing by hybridization". *Proc. 8th International Conference on Intelligent Systems for Molecular Biology (ISMB '00)*, pp. 260–268, AAAI Press, Menlo Park, CA (2000).
278. R. Shamir, D. Tsur, "Large scale sequencing by hybridization". *Proceedings of the Fifth Annual International Conference on Computational Molecular Biology (RECOMB 01)*, pp. 269–277, ACM Press, New York, NY (2001).

279. A. Tanay, R. Shamir, "Computational expansion of genetic networks". *Proceedings of the 9th International Conference on Intelligent Systems for Molecular Biology* (ISMB 01), Copenhagen, July 2001. *Bioinformatics* vol 17 Supplement 1 S270-S278 (2001).
280. T. Pupko, R. Sharan, D. Gordon, M. Gurevitz, R. Shamir, D. Graur, "A chemical-distance-based test for positive Darwinian selection", *Proceedings of the First Workshop on Algorithms in Bioinformatics* (WABI 01) pp. 142–155, Springer, LNCS 2149 (2001).
281. E. Halperin, S. Halperin, T. Hartman, R. Shamir "Handling long targets and errors in sequencing by hybridization". *Proceedings of the Sixth Annual International Conference on Computational Molecular Biology* (RECOMB 02) pp 176–185, ACM Press, New York, NY (2002).
282. A. Ben-Dor, R. M. Karp, B. Schwikowsky, R. Shamir "The restriction scaffold problem". *Proceedings of the Sixth Annual International Conference on Computational Molecular Biology* (RECOMB 02) pp 58–65, ACM Press, New York, NY (2002).
283. R. Shamir, R. Sharan, D. Tsur, "Cluster graph modification problems". Proceedings of the 28th International Workshop on Graph Theoretic Concepts in Computer Science (WG '02), L. Kucera (editor), LNCS 2573, pp. 379–390 (2002).
284. C. Linhart, R. Shamir, "The degenerate primer design problem". *Proceedings of the 10th International Conference on Intelligent Systems for Molecular Biology* (ISMB 02), Edmonton, August 2002. *Bioinformatics* Vol. 18 S172–S180 (2002).
285. A. Tanay, R. Sharan, R. Shamir, "Discovering statistically significant biclusters in gene expression data". *Proceedings of the 10th International Conference on Intelligent Systems for Molecular Biology* (ISMB 02), Edmonton, August 2002. *Bioinformatics* Vol. 18 S136–S144 (2002).
286. R. Shamir, D. Tsur, "Improved clustering algorithms for the random cluster graph model". *Proc. Eighth Scandinavian Workshop on Algorithm Theory* (SWAT 02), pp. 230–239 (2002).
287. I. Pe'er, R. Shamir, R. Sharan, "On the generality of phylogenies from incomplete directed characters". *Proceedings of the Eighth Scandinavian Workshop on Algorithm Theory* (SWAT 02), pp. 358–367 (2002).
288. A. Tanay, R. Shamir, "Modeling transcription programs: inferring binding site activity and dose - response model optimization" *Proceedings of the Seventh Annual International Conference on Computational Molecular Biology* (RECOMB 03), pp. 301–310, ACM Press (2003).
289. I. Gat-Viks, R. Shamir, "Chain functions and scoring functions in genetic networks". *Proceedings of the 11th International Conference on Intelligent Systems for Molecular Biology* (ISMB 03), Brisbane, Australia, July 2003. *Bioinformatics* Vol. 19 Supplement 1, pp. i108–i117 (2003).
290. G. Kimmel, R. Sharan, R. Shamir, "Identifying blocks and sub-populations in noisy SNP data". *Proceedings of the Workshop on Algorithms in Bioinformatics* (WABI 03), pp. 303–319 (2003).
291. I. Gat-Viks, R. Shamir, R. M. Karp, R. Sharan, "Reconstructing chain functions in genetic networks". *Proceedings of the Pacific Symposium on Biocomputing* (PSB 04) pp. 498–509 (2004).
292. G. Kimmel, R. Shamir, "Maximum likelihood resolution of multi-block genotypes". *Proceedings of the Eighth Annual International Conference on Computational Molecular Biology* (RECOMB 04), pp. 2–9 (2004).
293. R. Sharan, T. Ideker, B. Kelley, R. Shamir, R. M. Karp, "Identification of protein complexes by comparative analysis of yeast and bacterial protein interaction data". *Proceedings of the Eighth Annual International Conference on Computational Molecular Biology* (RECOMB 04), pp. 282–289 (2004).
294. G. Kimmel, R. Shamir, "The incomplete perfect phylogeny haplotype problem". Proc. RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotypes pp. 59–70 (2004).

295. T. Barzuza, J. S. Beckmann, R. Shamir and I. Pe'er, "Computational problems in perfect phylogeny haplotyping: XOR-genotypes and tag SNPs". Proceedings CPM 2004, LNCS 3109 pp. 14–31 (2004).
296. I. Gat-Viks, A. Tanay, R. Shamir, "Modeling and analysis of heterogeneous regulation in biological networks". Proceedings of the first RECOMB satellite workshop on Regulatory Genomics, E. Eskin and C. Workman (editors), Lecture Notes in Bioinformatics, Vol. 3318 pp. 98–113, Springer, Berlin (2005).
297. I. Gat-Viks, A. Tanay, D. Rajzman, R. Shamir, "Factor graph network models for biological systems". Proceedings RECOMB 2005, pp. 31-47, Lecture Notes in Bioinformatics 3500, Springer, Berlin (2005).
298. E. Halperin, G. Kimmel, R. Shamir, "Tag SNP selection in genotype data for maximizing SNP prediction accuracy". *Proceedings ISMB 05. Bioinformatics* Vol. 21 Suppl. 1 pp. i195-i203 (2005).
299. M. Ozery-Flato and R. Shamir, "An $O(n^{3/2}\sqrt{\log(n)})$ algorithm for sorting by reciprocal translocations". *Proceedings CPM 2006*, LNCS Vol. 4009 pp. 258–269 (2006).
300. M. Ozery-Flato, R. Shamir, "Sorting by translocations via reversals theory". *Proceedings of the 4th RECOMB Satellite on Comparative Genomics*, Lecture Notes in Computer Science Vol. 4205, pp. 87–98, Springer, Berlin (2006).
301. M. Ozery-Flato, R. Shamir, "Rearrangements in genomes with centromeres part I: translocations". Proceedings of the 11th Annual International Conference on Computational Molecular Biology (RECOMB 2007), LNCS vol. 4453, 339–353, Springer (2007).
302. M. Ozery-Flato, R. Shamir, "On the frequency of genome rearrangement events in cancer karyotypes". *Proceedings RECOMB satellite on Computational Cancer Biology* (2007).
303. I. Ulitsky, R. M. Karp, R. Shamir, "Detecting disease-specific dysregulated pathways via analysis of clinical expression profiles". Proceedings RECOMB 2008, pp. 347–359, LNBI 4955, Springer, Berlin (2008).
304. I. Ulitsky, R. Shamir, "Detecting pathways transcriptionally correlated with clinical parameters". Proceedings of the 7th Annual International Conference on Computational Systems Bioinformatics (CSB 08), pp. 249–258, Imperial College Press, London, UK (2008).
305. M. Ziv-Ukelson, I. Gat-Viks, Y. Wexler, R. Shamir, "A faster algorithm for RNA co-folding". Proceedings of the 8th International Workshop pm Algorithms in Bioinformatics (WABI), Keith A. Crandall and Jens Lagergren (Eds.), LNBI 5251, 174–185, Karlsruhe, Germany, September 15-17, (2008).
306. M. Ozery-Flato, R. Shamir, "Sorting cancer karyotypes by elementary operations". Proceedings RECOMB Satellite on Comparative Genomics, Paris, France, October 13-15 2008. Lecture Notes in Computer Science, Volume 5267, pp. 211-225, Springer (2008).
307. S. Bruckner, F. Hueffner, R. M. Karp, R. Shamir, R. Sharan, "Topology-free querying of protein interaction networks". *Proceedings RECOMB 2009*, LNCS 5541 74-89 (2009).
308. I. Ulitsky, L. Laurent, R. Shamir, "Towards Computational prediction of microRNA Function and activity". *Proceedings RECOMB Satellite conference on Regulatory Genomics*, Boston, Mass. (2009).
309. M. S. Bansal, P. Gogarten, R. Shamir, "Detecting highways of horizontal gene transfer". *Proceedings RECOMB satellite meeting on Comparative Genomics*, LNBI 6398, pp. 109–120. Springer, Heidelberg (2010).
310. Y. Orenstein, E. Mick, R. Shamir, "RAP: Accurate and fast motif finding based on protein microarray data". Proceedings RECOMB conference on Regulatory and Systems Genomics, San Francisco (2012).
311. R. Rozov, R. Shamir, E. Halperin, "Fast lossless compression via cascading Bloom filters". *BMC Bioinformatics* 15 (Suppl 9):S7, RECOMB-seq proceedings paper (2014).

312. D. Amar, D. Yekutieli, A. Maron-Katz, T. Hendler, R. Shamir. “A hierarchical Bayesian model for flexible module discovery in three-way time series data”. *Bioinformatics* 31 (12) i17–i26, ISMB/ECCB 2015 proceedings paper (2015).
313. R. Zeira, R. Shamir. “Sorting by cuts, joins and duplications”. Proceedings of CPM 2015, (F. Cicalese, E. Porat, U. Vaccaro, editors). LNCS 9133 pp. 396–409 (2015).
314. R. Rozov, A. Kav Brown, D. Bogumil, E. Halperin, I. Mizrahi, R. Shamir. “Recycler: an algorithm for detecting plasmids from de novo assembly graphs” BioRxiv doi: <http://dx.doi.org/10.1101/029926> (26 Oct 2015) *RECOMB-seq* 2016.
315. R. Shamir, M. Zehavi, R. Zeira. “A linear-time algorithm for the Copy Number Transformation Problem”. Proceedings of CPM 2016, R. Grossi and M. Lewenstein (Editors), LIPIcs, vol. 54, pp. 16:1–16:13. Dagstuhl, Germany. (2016).
316. Y. Orenstein, D. Pellow, G. Marcais, R. Shamir, C. Kingsford. “Compact universal k-mer hitting sets”. Proceedings of WABI 2016, Aarhus, Denmark, August, 2016. LNCS 9838 pp. 257–268 (2016).
317. M. El-Kebir, B. Raphael, R. Shamir, R. Sharan, S. Zaccaria, M. Zehavi, R. Zeira. “Copy-Number Evolution Problems: Complexity and Algorithms”. Proceedings of WABI 2016, Aarhus, Denmark, August, 2016. LNCS 9838 pp. 137–149 (2016).
318. G. Marcais, D. Pellow, D. Bork, Y. Orenstein, R. Shamir, C. Kingsford. “Improving the performance of minimizers and winnowing schemes”. *Bioinformatics* special issue of ISMB/ECCB 2017, Vol. 33, i110–i117 doi: 10.1093/bioinformatics/btx235 (2017).
319. R. Rozov, G. Goldshlager, R. Shamir, E. Halperin. “Faucet: streaming de novo assembly graph construction”. RECOMB-seq 2017. BiorXiv <https://doi.org/10.1101/125658>, April 2017.
320. R. Zeira, R. Shamir. “Sorting cancer karyotypes using double-cut-and-joins, duplications and deletions”. *RECOMB Computational Cancer Biology* (2018).
321. O. Noy*, D. Coster*, M. Metzger, I. Attar, S. Shenhar-Tsafraty, S. Berliner, G. Rahav, O. Rogowski, R. Shamir. A machine learning model for predicting deterioration of COVID-19 inpatients International Conference on Learning Representations (ICLR) 2021 Workshop: Machine Learning for Preventing and Combating Pandemics (online) May 8, 2021.
322. Y. Ben-Ari, D. Flomin, L. Pu, Y. Orenstein, R. Shamir. “Improving the efficiency of de Bruijn graph construction using compact universal hitting sets”. Proc. ACM Conference on Bioinformatics, Computational Biology and Health Informatics (ACM-BCB) August 2021, Article 4, pp 1–9 <https://doi.org/10.1145/3459930.3469520>
323. L. Pu, R. Shamir. “3CAC: improving the classification of phages and plasmids from metagenomic assemblies using assembly graphs”. *Bioinformatics* 38 (Supplement 2) ii56–ii61. doi: 10.1093/bioinformatics/btac468
324. D. Pellow, L. Pu, B. Ekim, L. Kotlar, R. Shamir, Y. Orenstein “Efficient minimizer orders for large values of k using minimum decycling sets”. BioRxiv doi: <https://doi.org/10.1101/2022.10.18.512682> Proc. *RECOMB* 2023.
325. O. Noy, R. Shamir. “Time-Dependent Iterative Imputation for Multivariate Longitudinal Clinical Data” Accepted to International Conference on Learning Representation (ICLR) workshop on Time Series Representation Learning for Health Kigali Rwanda May 1 — 5, 2023. arXiv:2304.07821
326. D. Coster, E. Fisher, S. Shenhar-Tsafraty, T. Menes, S. Berliner, E. Halperin, S. Rosset, M. Gorfine, R. Shamir. “Risk modeling of time-varying covariates using an ensemble of survival trees: Predicting future cancer events”. Proc. AAAI conference, Symposium ‘SPACA: Survival Prediction Algorithms, Challenges & Applications’ (2023). MedRxiv 2021.01.11.21249491 (2021).

327. Omer Noy Klein, Alihan Hüyük, Ron Shamir, Uri Shalit, Mihaela van der Schaar. “Towards Regulatory-Confirmed Adaptive Clinical Trials: Machine Learning Opportunities and Solutions”. To appear in the 28th International Conference on Artificial Intelligence and Statistics (AISTATS 2025).