

Research Publications, peer reviewed:

1. K. Hua and S. Hannenhalli: Parallel transitive closure computations using topological sort. Proc. of Intl. Conf. on Parallel and Distributed Information Systems 1991.
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5. S. Hannenhalli and P. Pevzner: Transforming men into mice (polynomial algorithm for genomic distance problem). 36th Annual IEEE Symposium on Foundations of Computer Science Page: 581-592, 1995.
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8. P. Berman and S. Hannenhalli: Fast sorting for reversal. Combinatorial Pattern Matching Page: 168-185, 1996.
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16. V. Bafna, S. Hannenhalli, K. Rice and L. Vawter: Ligand-receptor pairing via tree comparison. Journal of Computational Biology 7: 59-70, 2000.
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18. S. Levy, S. Hannenhalli and C. Workman: Enrichment of regulatory signals in conserved non-coding genomic sequence. Bioinformatics 1: 1-7, 2001.
19. Venter et al: The human genome. Science 291: 1304-1351, 2001.
20. P. Berman, S. Hannenhalli and M. Karpinski: Approximation algorithm for sorting by reversals. ESA 1: 375, 2002.
21. S. Hannenhalli and S. Levy: Predicting transcription factor synergism. Nucleic Acids Research 30: 4278-4284, 2002.
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26. J. Wang and S. Hannenhalli*: Generalized Markov models for sequence classification. BMC Bioinformatics 6(1): 219-230, 2005.
27. L.S. Wang, S.T. Jensen, S. Hannenhalli*: An Interaction-dependent model for transcription factor binding. RECOMB-Regulation 2005.
28. M. K. Lewinski, D. Bisgrove, P. Shinn, H. Chen, S. Hannenhalli, E. Verdin, C. C. Berry, J. R. Ecker, and F. D. Bushman: Genome-wide analysis of chromosomal feature repressing HIV transcription. J. Virology 79(11): 6610-6619, 2005.
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44. S. Vardhanabhuti, J. Wang, S. Hannenhalli*: Position and distance specificity are important determinants of cis-regulatory motifs in addition to evolutionary conservation. NAR 35: 3339-3354, 2007.
45. Shuzhang Yang, Kai Wang, Otto Valladares, Sridhar Hannenhalli and Maja Bucan: Genome-wide expression profiling and bioinformatics analysis of diurnally regulated genes in the mouse prefrontal cortex. Genome Biology 8(11): R247, 2007.
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55. Matthew Hansen, Logan Everett, Larry Singh, Sridhar Hannenhalli: Mimosa - Mixture model of co-expression to detect modulators of regulatory interaction Algorithms in Mol Biology. Stephen Salzberg and Tandy Warnow (eds.). (in press), September 2009 Notes: Accepted at the conference "Workshop on Algorithms in Bioinformatics"
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2. Hannenhalli, S.: Eukaryotic transcription factor binding sites--modeling and integrative search methods. Bioinformatics 24(11): 1325-31, 2008.
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