

Fabio Vandin

Department of Computer Science, and Center for Computational Molecular Biology
Brown University
115 Waterman St., 4th Floor, Providence, RI 02912 USA
Mobile: +1-401-286-1402, *Fax:* +1-401-863-7657
E-mail: fabio_vandin@brown.edu
WWW: www.cs.brown.edu/~vandinfa/home.html

Education

Ph.D. in Information Engineering, University of Padova, 04/2010.

Thesis Title: *Mining of Significant Patterns: Theory and Practice*.

Advisor: Prof. A. Pietracaprina.

M.S. in Computer Engineering (*Laurea Specialistica*), University of Padova, *summa cum laude*, 10/2006.

Thesis Title: *On the Top-K Frequent Closed Itemsets Mining Problem*, in Italian.

Advisors: Prof. A. Pietracaprina, Prof. G. Pucci.

My thesis work has been officially deemed as *distinguished* by the thesis committee.

B.S. in Computer Engineering (*Laurea triennale*), University of Padova, *summa cum laude*, 07/2004.

Final Project Title: *Models and Methods for the Evaluation of Runway Capacity*, in Italian.

Advisor: Prof. L. Brunetta.

Professional Appointments

Research Assistant Professor of Computer Science	<i>09/2011-present</i>
Department of Computer Science, and Center for Computational Molecular Biology, Brown University.	
Postdoctoral Research Associate	<i>08/2010-08/2011</i>
Center for Computational Molecular Biology, Brown University. Mentors: Prof. B. J. Raphael, Prof. E. Upfal.	
Postdoctoral Research Associate	<i>05/2010-08/2011</i>
Department of Computer Science, Brown University. Mentors: Prof. B. J. Raphael, Prof. E. Upfal.	
Research Associate	<i>02/2010-04/2010</i>
Department of Computer Science, Brown University. Mentors: Prof. B. J. Raphael, Prof. E. Upfal.	
Visiting Scholar	<i>09/2008-01/2010</i>
Department of Computer Science, Brown University.	
Research Assistant	<i>11/2006-12/2006</i>
Department of Information Engineering, University of Padova. Project: <i>Adaptive Software for Data Mining</i> .	

Publications

Author lists denoted using “with” are alphabetical.

Journals

- [1] Mining Top-K Frequent Itemsets Through Progressive Sampling, with A. Pietracaprina, M. Riondato, and E. Upfal. **Data Mining and Knowledge Discovery**, ECML PKDD 2010 special issue, Volume 21, Number 2, 2010.

- [2] F. Vandin, E. Upfal, and B. J. Raphael. Algorithms for Detecting Significantly Mutated Pathways in Cancer. **Journal of Computational Biology**, 18(3):507-22, 2011.
- [3] MADMX: A Strategy for Maximal Dense Motif Extraction, with R. Grossi, A. Pietracaprina, N. Pisanti, G. Pucci, and E. Upfal. **Journal of Computational Biology**, 18(4):535-45, 2011.
- [4] The Cancer Genome Atlas Project Network. Integrated Genomic Analyses of Ovarian Carcinoma. **Nature**, 474, 609-615 (30 June 2011).
- [5] F. Vandin, E. Upfal, and B. J. Raphael. De novo Discovery of Mutated Driver Pathways in Cancer. **Genome Research**, 22(2):375-85, 2012. Epub 2011 Jun. 7.
- [6] F. Vandin, E. Upfal, B. J. Raphael. Algorithms and Genome Sequencing: Identifying Driver Pathways in Cancer. **IEEE Computer**, March 2012, vol. 45 no. 3, pp.39-46.
- [7] An Efficient Rigorous Approach for Identifying Statistically Significant Frequent Itemsets, with A. Kirsch, M. Mitzenmacher, A. Pietracaprina, G. Pucci, and E. Upfal. **Journal of the ACM**, Volume 59 Issue 3, June 2012,12:1-12:22.
- [8] C. Grasso, Y. Wu, D. Robinson, X. Cao, S. Dhanasekaran, A. Khan, M. Quist, X. Jing, R. Lonigro, J. C. Brenner, I. Asangani, B. Ateeq, S. Chun, J. Siddiqui, L. Sam, M. Anstett, R. Mehra, J. Prensner, N. Palanisamy, G. Ryslik, F. Vandin, B. J. Raphael, L. Kunju, D. Rhodes, K. Pienta, A. M. Chinnaiyan, S. A. Tomlins. The Mutational Landscape of Lethal Castrate Resistant Prostate Cancer. **Nature** 487, 239-243 (12 July 2012).
- [9] F. Vandin, E. Upfal, and B. J. Raphael. Finding Driver Pathways in Cancer: Models and Algorithms. **Algorithms for Molecular Biology**, 7(1):23, 2012.
- [10] L. He, F. Vandin, G. Pandurangan, and C. Bailey-Kellogg. BALLAST: A Ball-based Algorithm for Structural Motifs. **Journal of Computational Biology**, 20(2):137-51, 2013.
- [11] The Cancer Genome Atlas Research Network. Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. **New England Journal of Medicine**, May 1st 2013.
- [12] The Cancer Genome Atlas Research Network. Comprehensive molecular characterization of clear cell renal cell carcinoma. **Nature**, 499, 43-9 (4 July 2013).
- [13] The Cancer Genome Atlas Research Network. The Cancer Genome Atlas Pan-Cancer analysis project. **Nature Genetics**, 45(10):1113-20 (26 September 2013).
- [14] C.Kandoth*, M.D. McLellan*, F. Vandin, K.Ye, B. Niu, C. Lu, M. Xie, Q. Zhang, J.F. McMichael, M.A. Wyczalkowski, M.D.M. Leiserson, C.A. Miller, J.S. Welch, M.J. Walter, M.C. Wendl, T.J. Ley, R.K. Wilson, B.J. Raphael, L. Ding. Mutational landscape and significance across 12 major cancer types. **Nature**, 502, 333-339 (17 October 2013).

Conferences Papers

- [15] Efficient Incremental Mining of Top-K Frequent Closed Itemsets, with A. Pietracaprina. In Proceedings 10th International Conference on Discovery Science (**DS**), LNCS 4755, pages 275-280, 2007.
- [16] An Efficient Rigorous Approach for Identifying Statistically Significant Frequent Itemsets, with A. Kirsch, M. Mitzenmacher, A. Pietracaprina, G. Pucci, and E. Upfal. In Proceedings 28th ACM Symposium on Principles of Database Systems (**PODS**), pages 117-126, 2009.
- [17] MADMX: A Novel Strategy for Maximal Dense Motif Extraction, with R. Grossi, A. Pietracaprina, N. Pisanti, G. Pucci, and E. Upfal. In Proceedings 9th Workshop on Algorithms in Bioinformatics (**WABI**), LNCS 5724, pages 362-374, 2009.
- [18] F. Vandin, E. Upfal, and B. J. Raphael. Algorithms for Detecting Significantly Mutated Pathways in Cancer. In Proceedings 14th International Conference on Research in Computational Molecular Biology (**RECOMB**), LNCS 6044, pages 506-521, 2010.
- [19] F. Vandin, E. Upfal, and B. J. Raphael. *De novo* Discovery of Mutated Driver Pathways in Cancer. In Proceedings 15th International Conference on Research in Computational Molecular Biology (**RECOMB**), LNCS 6577, pages 499-500, 2011.
- [20] F. Vandin, E. Upfal, and B. J. Raphael. Finding Driver Pathways in Cancer: Models and Algorithms. In Proceedings 11th Workshop on Algorithms in Bioinformatics (**WABI**), LNCS 6833, pages 314-325, 2011.
- [21] F. Vandin, P. Clay, E. Upfal, and B. J. Raphael. Discovery of Mutated Subnetworks Associated with Clinical Data in Cancer. In Proceedings Pacific Symposium on Biocomputing (**PSB**), pages 55-66, 2012.
- [22] Algorithms on Evolving Graphs, with A. Anagnostopoulos, R. Kumar, M. Mahdian, and E. Upfal. In Proceedings 3rd Innovations in Theoretical Computer Science Conference (**ITCS**), pages 149-160, 2012.

- [23] L. He, F. Vandin, G. Pandurangan, and C. Bailey-Kellogg. BALLAST: A Ball-based Algorithm for Structural Motifs. In Proceedings 16th International Conference on Research in Computational Molecular Biology (**RECOMB**), LNCS 7262, pages 79-93, 2012.
- [24] F. Vandin, A. Papoutsaki, B. Raphael, and E. Upfal. Genome-Wide Survival Analysis of Somatic Mutations in Cancer. In Proceedings 17th International Conference on Research in Computational Molecular Biology (**RECOMB**), LNCS 7821, pages 285-286, 2013. *Best Paper Award*.
- [25] Space-Efficient Parallel Algorithms for Combinatorial Search Problems, with A. Pietracaprina, G. Pucci, and F. Silvestri. In Proceedings 38th International Symposium on Mathematical Foundations of Computer Science (**MFCS**), LNCS 8087, pages 717-728, 2013.

Conferences Abstracts/Posters

- [26] F. Vandin, E. Upfal, and B. J. Raphael. Identification of Significantly Mutated Pathways in Cancer. (Abstract) RECOMB Reg. Genomics/Sys. Biology/DREAM5, 2009
- [27] F. Vandin, E. Upfal, and B. J. Raphael. Detection of Mutated Pathways in Cancer. (Poster) 18th International Conference on Intelligent Systems for Molecular Biology (ISMB), 2010.
- [28] L. He, F. Vandin, G. Pandurangan, and C. Bailey-Kellogg. Ball-based Algorithms for Structural Motifs. (Poster) 3DSIG, Structural Bioinformatics and Computational Biophysics, ISMB Satellite Meeting, Vienna (Austria), 2011
- [29] F. Vandin, H.-T. Wu, E. Upfal, and B. J. Raphael. Algorithms for Automated Discovery of Mutated Pathways in Cancer. (Poster/Abstract) The Cancer Genome Atlas' 1st Annual Scientific Symposium: Enabling Cancer Research Through TCGA, 2011.
- [30] F. Vandin, E. Upfal, and B. J. Raphael. Algorithms for Discovery of Mutated Pathways in Cancer. (Abstract) 2nd Workshop on Computational Advances for Next Generation Sequencing (CANGS) 2012, Las Vegas, NV, 2012.
- [31] F. Vandin, H.-T. Wu, E. Upfal, and B. J. Raphael. Algorithms to Find Mutated Pathways in Cancer. (Poster/Abstract) 16th International Conference on Research in Computational Molecular Biology (RECOMB), Barcelona, Spain, 2012.
- [32] M. Leiserson, H.-T. Wu, D. Blokh, F. Vandin, R. Sharan, B. J. Raphael. Methods for Identifying Driver Pathways in Cancer. (Poster) 3rd Annual Beyond the Genome Conference, Boston, USA, 2012.
- [33] M. Leiserson, H.-T. Wu, A. Deschamps, F. Vandin, B. J. Raphael. Pathway and Network Analysis of Somatic Mutations Across Cancer Types in TCGA. (Abstract) The Cancer Genome Atlas' 2nd Annual Scientific Symposium: Enabling Cancer Research Through TCGA, 2012.
- [34] M. Leiserson, H.-T. Wu, F. Vandin, B. J. Raphael. Network analysis of mutations across cancer types. (Poster) 17th International Conference on Research in Computational Molecular Biology (RECOMB), Beijing, China, 2013.
- [35] F. Vandin, A. Papoutsaki, B. Raphael, and E. Upfal. Accurate Genome-Wide Survival Analysis of Somatic Mutations in Cancer. (Poster) ISMB ECCB 2013, Berlin, Germany, 2013.

Theses

- F. Vandin. Mining of Significant Patterns: Theory and Practice. Ph.D. thesis, University of Padova, 2010.
Advisor: Prof. A. Pietracaprina.
- F. Vandin. On the Top-*K* Frequent Closed Itemsets Mining Problem (in Italian). *Laurea specialistica* thesis, University of Padova, 2006.
Advisors: Prof. A. Pietracaprina, Prof. G. Pucci.

Honors/Awards

Best Paper Award, RECOMB 2013.	04/2013
International Society for Computational Biology (ISCB) Travel Fellowship, RECOMB 2012.	04/2012
Pacific Symposium on Biocomputing Travel Award, PSB 2012.	01/2012
“Sergio Gambi” Best Ph.D. Thesis Award , University of Padova, Italy.	12/2011
Institute for Pure and Applied Mathematics (IPAM) Travel Fellowship, UCLA.	10/2011

International Society for Computational Biology (ISCB) Travel Fellowship, RECOMB 2011. 03/2011
CCMB Travel Award, Brown University, RECOMB 2010. 08/2010
“Ing. Aldo Gini” Foundation Fellowship, Padova, Italy. 01/2010

Presentations

International Conferences

Genome-Wide Survival Analysis of Somatic Mutations in Cancer, RECOMB 2013, 04/08/2013.
Algorithms for Find Mutated Pathways in Cancer, (Poster) RECOMB 2012, 04/22/2012.
A Ball-based Algorithm for Structural Motifs, RECOMB 2012, 04/22/2012.
Algorithms on Evolving Graphs, ITCS 2012, 01/08/2012.
Discovery of Mutated Subnetworks Associated with Clinical Data in Cancer, PSB 2012, 01/04/2012.
Algorithms for Automated Discovery of Mutated Pathways in Cancer, (Poster) TCGA 1st Annual Scientific Symposium 2011, 11/17/2011.
Finding Driver Pathways in Cancer: Models and Algorithms, WABI 2011, 09/08/2011.
De novo Discovery of Mutated Driver Pathways in Cancer, RECOMB 2011, 03/30/2011.
Algorithms for Detecting Significantly Mutated Pathways in Cancer, RECOMB 2010, 08/12/2010.
Detection of Mutated Pathways in Cancer(Poster), ISMB 2010, 07/11/2010.
Identification of Significantly Mutated Pathways in Cancer (Poster), RECOMB Reg. Genomics/Sys. Biology/DREAM5 2009, 12/04/2009.
MADMX: A Novel Strategy for Maximal Dense Motif Extraction, WABI 2009, 09/13/2009.
An Efficient Rigorous Approach for Identifying Statistically Significant Frequent Itemsets, PODS 2009, 06/30/2009.

Invited

Computational Methods to Discover Significantly Mutated Pathways in Cancer, IFOM-IEO, Milan, Italy, 10/8/2013.
Models and Algorithms to Find Driver Pathways in Cancer, University of Padova, Italy, 10/9/2013.
Identifying Significant Mutations in Large Cohorts of Cancer Genomes, BigLS 2013, 06/13/2013.
Accurate Genome-Wide Survival Analysis of Somatic Mutations in Cancer: Nanyang Technological University, Singapore, 04/16/2013; National University of Singapore, 04/16/2013; University of Padova, 05/31/2013.
Algorithms for Identifying Significant Mutations in Cancer, University of Southern Denmark, 03/17/2013.
Computational Problems in Cancer Genomics, IT University of Copenhagen, 03/06/2013.
Algorithms for Identifying Significant Mutations in Cancer, Worcester Polytechnic Institute, 02/01/2013.
Discovery of Significantly Mutated Subnetworks in Cancer, Network Links Workshop (University of Minnesota - IMA), 02/29/2012.
Algorithms for Discovery of Mutated Pathways in Cancer, CANGS 2012, 02/24/2012.

Teaching

2013: **Instructor**: *Probabilistic Methods in Computer Science*, Brown University.
2010-2012: **Guest Lecturer**: *Probabilistic Methods in Computer Science*, *Introduction to Probability and Computing* (Prof. E. Upfal), *Introduction to Discrete Structures and Probability*, *Computational Molecular Biology*, *Topics in Computational Biology* (Prof. B. J. Raphael), Brown University.
01-02/2008: **Teaching Assistant**: course *Algorithms and Data Structures 1* (Prof. A. Pietracaprina), University of Padova (Italy).

Professional Activities

Referee

2007 - now: **Journals**: Data & Knowledge Engineering; Journals of Zhejiang University SCIENCE; Journal of Discrete Algorithms; BMC Bioinformatics; PLOS Computational Biology.
2007 - now: **Conferences**: 14th International Colloquium on Structural Information and Communication Complexity (SIROCCO 2007); 20th ACM Symposium on Parallelism in Algorithms and Architectures

(SPAA 2008); 22nd IEEE International Parallel and Distributed Processing Symposium (IPDPS 2008); 50th Annual IEEE Symposium on Foundations of Computer Science (FOCS 2009); 16th IEEE International Conference on High Performance Computing (HiPC 2009); 24th IEEE International Parallel and Distributed Processing Symposium (IPDPS 2010); 21st Annual Symposium on Combinatorial Pattern Matching (CPM2010); 9th European Conference on Computational Biology (ECCB 2010); 1st IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS 2011); 23th ACM Symposium on Parallelism in Algorithms and Architectures (SPAA 2011); International Workshop on Combinatorial Algorithms 2011 (IWOCA 2011); 15th International Workshop on Randomization and Computation (RANDOM 2011); 16th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2012); 2nd Annual RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-seq 2012); 2nd IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS 2012); 11th European Conference on Computational Biology (ECCB 2012); Pacific Symposium on Biocomputing (PSB) 2013; 17th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2013).

Program Committees

SPIRE, International Symposium on String Processing and Information Retrieval 2011 (PC Member).
RECOMB-seq, Second Annual RECOMB Satellite Workshop on Massively Parallel Sequencing 2012 (PC Member).

ACMBCB, ACM Conference on Bioinformatics, Computational Biology and Biomedicine 2012 (PC Member).

RECOMB, International Conference on Research in Computational Molecular Biology 2014 (PC Member).

Memberships

EATCS European Association for Theoretical Computer Science

ISCB International Society for Computational Biology

Software Packages

Dendrix (<http://compbio.cs.brown.edu/projects/dendrix/>)

HotNet (<http://compbio.cs.brown.edu/projects/hotnet/>)

MADMX (available upon request)

TopKMiner (available upon request)