Curriculum Vitae
Fabio Vandin

March 2018

Department of Information Engineering
University of Padova
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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

Associate Professor *07/2015-present*
Department of Information Engineering
University of Padova, Italy.

Adjunct Associate Professor *11/2015-present*
Department of Department of Mathematics and Computer Science
University of Southern Denmark, Denmark.

Adjunct Associate Professor of Computer Science (Research) *08/2015-present*
Department of Computer Science
Brown University.

Assistant Professor *01/2014-06/2015*
Department of Mathematics and Computer Science
University of Southern Denmark, Denmark.

Adjunct Assistant Professor of Computer Science (Research) *10/2013-12/2013*
Department of Computer Science, and Center for Computational Molecular Biology,
Brown University.

Assistant Professor of Computer Science (Research) *09/2011-08/2013*
Department of Computer Science, and Center for Computational Molecular Biology,
Brown University.

Postdoctoral Research Associate *08/2010-08/2011*
Center for Computational Molecular Biology, Brown University.
Mentors: Prof. B. J. Raphael, Prof. E. Upfal.

Postdoctoral Research Associate *05/2010-08/2011*
Department of Computer Science, Brown University.
Mentors: Prof. B. J. Raphael, Prof. E. Upfal.

Research Associate *02/2010-04/2010*

Department of Computer Science, Brown University.
Mentors: Prof. B. J. Raphael, Prof. E. Upfal.

Visiting Scholar *09/2008-01/2010*

Department of Computer Science, Brown University.

Research Assistant *11/2006-12/2006*

Department of Information Engineering, University of Padova.
Project: *Adaptive Software for Data Mining.*

Publications

Corresponding and senior author publications are denoted with "‡".
Equal contributions are denoted with "†".
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. *Recommended by F1000.*

[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).

[15] B. J. Raphael, J. R. Dobson, L. Oesper and F. Vandin. Identifying driver mutations in sequenced cancer genomes: computational approaches to enable precision medicine. **Genome Medicine**, 6:5 (2014).

[16] Hoadley K. A., Yau C., Wolf D. M., Cherniack A. D., Tamborero D., Ng S., Leiserson M. D., Niu B., McLellan M. D. , Uzunangelov V., Zhang J., Kandoth C., Akbani R., Shen H., Omberg L., Chu A., Margolin A. A., Van't Veer L. J., Lopez-Bigas N., Laird P. W., Raphael B. J., Ding L., Robertson A. G., Byers L. A., Mills G. B., Weinstein J. N., Van Waes C., Chen Z., Collisson E. A., The Cancer

Genome Atlas Research Network, Benz C. C., Perou C. M., Stuart J. M. Multiplatform analysis of 12 cancer types reveals molecular classification within and across tissues of origin. **Cell**, 158 (4), 929-944 (2014).

[17] The Cancer Genome Atlas Research Network. Integrated Genomic Characterization of Papillary Thyroid Carcinoma. **Cell**, 159 (3), 676 - 690 (2014).

[18] Space-Efficient Parallel Algorithms for Combinatorial Search Problems, with A. Pietracaprina, G. Pucci, and F. Silvestri. **Journal of Parallel and Distributed Computing**, Volume 76, Pages 58-65 (2015).

[19] B. J. Raphael and F. Vandin[‡]. Simultaneous Inference of Cancer Pathways and Tumor Progression from Cross-Sectional Mutation Data. **Journal of Computational Biology**, 22(6):510-27 (2015).

[20] M. D. M. Leiserson[†], F. Vandin[†], H.-T. Wu, J. R. Dobson, J. V. Eldridge, J. L. Thomas, A. Papoutsaki, Y. Kim, B. Niu, M. McLellan, M. S. Lawrence, A. Gonzalez-Perez, D. Tamborero, Y. Cheng, G. A. Ryslik, N. Lopez-Bigas, G. Getz, L. Ding, B. J. Raphael. Pan-Cancer Network Analysis Identifies Combinations of Rare Somatic Mutations across Pathways and Protein Complexes. **Nature Genetics**, 47(2):106-14 (2015).

[21] F. Vandin, A. Papoutsaki, B. J. Raphael, E. Upfal. Accurate Computation of Survival Statistics in Genome-wide Studies. **PLOS Computational Biology**, 11(5):e1004071 (2015).

[22] M. D. M. Leiserson, H.-T. Wu, F. Vandin and B. J. Raphael. CoMEt: A Statistical Approach to Identify Combinations of Mutually Exclusive Alterations in Cancer. **Genome Biology**, 16:160 (2015).

[23] Chen M., Baumbach J., Vandin F., Rttgr R., Barbosa E., Dong M., Frost ., Christiansen L., Tan Q. Differentially Methylated Genomic Regions in Birth-Weight Discordant Twin Pairs. **Annals of Human Genetics** (2016).

[24] F. Vandin[‡], B. Raphael and E. Upfal. On the Sample Complexity of Cancer Pathways Identification. **Journal of Computational Biology**, 23, 1:30-41 (2016).

[25] D. Almeida, I. Skov, J. Lund, A. Mohammadnejad, A. Silva., F. Vandin, Q. Tan, J. Baumbach, R. Rottger. Jllumina-A comprehensive Java-based API for statistical Illumina Infinium HumanMethylation450 and Infinium MethylationEPIC BeadChip data processing. **Journal of Integrative Bioinformatics**, 13 (4), 29 (2016).

[26] The Computational Pan-Genomics Consortium. Computational pan-genomics: status, promises and challenges. **Briefings in Bioinformatics**, bbw089 (2016).

[27] Q. Tan, W. Li, F. Vandin. Disease Concordant Twins Empower Genetic Association Studies. **Annals of Human Genetics** (2017).

[28] D. Almeida, I. Skov, A. Silva, F. Vandin, Q. Tan, R. Rottger, J. Baumbach. Efficient detection of differentially methylated regions using DiMmeR. **Bioinformatics**, btw657 (2017).

[29] Vandin F. Computational Methods for Characterizing Cancer Mutational Heterogeneity. **Frontiers in Genetics**, 8 (2017).

[30] Raunak Shrestha, Ermin Hodzic, Thomas Sauerwald, Phuong Dao, Kendric Wang, Jake Yeung, Shawn Anderson, Fabio Vandin, Gholamreza Haffari, Colin C Collins, S Cenk Sahinalp. HIT'nDRIVE: patient-specific multidriver gene prioritization for precision oncology. **Genome Research**, 27 (9), 1573-1588 (2017).

[31] N. Alcaraz, M. List, R. Batra, F. Vandin, H.J. Ditzel, J. Baumbach. De novo pathway-based biomarker identification. **Nucleic Acids Research**, Nucleic Acids Research, 45 (16), e151 (2017).

[32] Clustering Uncertain Graphs, with Matteo Ceccarello, Carlo Fantozzi, Andrea Pietracaprina, Geppino Pucci. **PVLDB**, 4 (11):472-484 (2017).

Conferences Papers

[33] 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.

[34] 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.

[35] 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.

[36] 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.

[37] 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.

[38] 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.

[39] 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.

[40] 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.

[41] 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.

[42] 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.***

[43] 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.

[44] B. J. Raphael and F. Vandin‡. Simultaneous Inference of Cancer Pathways and Tumor Progression from Cross-Sectional Mutation Data. Proceedings 18th International Conference on Research in Computational Molecular Biology (**RECOMB**), pages 250-264, 2014.

[45] M. Riondato, F. Vandin‡. Finding the True Frequent Itemsets. Proceedings SIAM International Conference on Data Mining (**SDM**), pages 497-505, 2014.

[46] M. D. M. Leiserson, H.-T. Wu, F. Vandin and B. J. Raphael. CoMEt: A Statistical Approach to Identify Combinations of Mutually Exclusive Alterations in Cancer. In Proceedings 19th Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), pages 202-204, 2015.

[47] F. Vandin‡, B. Raphael and E. Upfal. On the Sample Complexity of Cancer Pathways Identification. In Proceedings 19th Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), pages 326-337, 2015.

[48] T. Hansen and F. Vandin‡. Finding Mutated Subnetworks Associated with Survival Time in Cancer. 20th Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), 2016.

[49] Farhad Hormozdiari, Fereydoun Hormozdiari, Carl Kingsford, Paul Medvedev, Fabio Vandin. The Second Decade of the International Conference on Research in Computational Molecular Biology (**RECOMB**), 2016.

[50] Reconstructing Hidden Permutations Using the Average-Precision (AP) Correlation Statistic, with L. De Stefani, A. Epasto, E. Upfal. 13th AAAI Conference on Artificial Intelligence (**AAAI**), 2016.

[51] Bomersbach, A, Chiarandini, M., Vandin, F‡. An Efficient Branch and Cut Algorithm to Find Frequently Mutated Subnetworks in Cancer. 16th Workshop on Algorithms in Bioinformatics (**WABI**), 2016.

[52] R. Sarto Basso, D. Hochbaum, and F. Vandin‡'. Efficient Algorithms to Discover Alterations with Complementary Functional Association in Cancer. *Accepted at* 22nd Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), 2018.

Abstracts

[53] F. Vandin, E. Upfal, and B. J. Raphael. Identification of Significantly Mutated Pathways in Cancer. RECOMB Reg. Genomics/Sys. Biology/DREAM5, 2009

[54] F. Vandin, E. Upfal, and B. J. Raphael. Detection of Mutated Pathways in Cancer. 18th International Conference on Intelligent Systems for Molecular Biology (ISMB), 2010.

[55] L. He, F. Vandin, G. Pandurangan, and C. Bailey-Kellogg. Ball-based Algorithms for Structural Motifs. 3DSIG, Structural Bioinformatics and Computational Biophysics, ISMB Satellite Meeting, Vienna (Austria), 2011

[56] F. Vandin, H.-T. Wu, E. Upfal, and B. J. Raphael. Algorithms for Automated Discovery of Mutated Pathways in Cancer. The Cancer Genome Atlas' 1st Annual Scientific Symposium: Enabling Cancer

Research Through TCGA, 2011.

[57] F. Vandin, E. Upfal, and B. J. Raphael. Algorithms for Discovery of Mutated Pathways in Cancer. 2nd Workshop on Computational Advances for Next Generation Sequencing (CANGS) 2012, Las Vegas, NV, 2012.

[58] F. Vandin, H-T. Wu, E. Upfal, and B. J. Raphael. Algorithms to Find Mutated Pathways in Cancer. 16th International Conference on Research in Computational Molecular Biology (RECOMB), Barcelona, Spain, 2012.

[59] M. Leiserson, H.-T. Wu, D. Blokh, F. Vandin, R. Sharan, B. J. Raphael. Methods for Identifying Driver Pathways in Cancer. 3rd Annual Beyond the Genome Conference, Boston, USA, 2012.

[60] M. Leiserson, H.-T. Wu, A. Deschamps, F. Vandin, B. J. Raphael. Pathway and Network Analysis of Somatic Mutations Across Cancer Types in TCGA. The Cancer Genome Atlas' 2nd Annual Scientific Symposium: Enabling Cancer Research Through TCGA, 2012.

[61] M. Leiserson, H.-T. Wu, F. Vandin, B. J. Raphael. Network analysis of mutations across cancer types. 17th International Conference on Research in Computational Molecular Biology (RECOMB), Beijing, China, 2013.

[62] F. Vandin, A. Papoutsaki, B. Raphael, and E. Upfal. Accurate Genome-Wide Survival Analysis of Somatic Mutations in Cancer. ISMB ECCB 2013, Berlin, Germany, 2013.

[63] F. Vandin, and B. Raphael. Reconstructing Cancer Pathways and Their Mutation Order from Cross-Sectional Data. ISMB 2014, Boston, USA, 2014.

[64] M. D. Leiserson, F. Vandin, H. T. Wu, J. R. Dobson, and B. Raphael. Pan-cancer identification of mutated pathways and protein complexes. *Cancer Research*, 74(19) 5324-5324, 2014.

[65] L. Andersen, F. Vandin. Efficient Methods for Reference-free Identification of SNVs, 1st *Annual Danish Bioinformatics conference*, 2015.

[66] Morteza Chalabi, F. Vandin. GraDe-SVM: Graph-Diffused Classification for the Analysis of Somatic Mutations in Cancer. ROCKY 2015, Aspen (Colorado), USA, 2015.

[67] Morteza Chalabi, F. Vandin, Veit Schwämmle. Computational Approaches to Decipher Composition and Regulation of Complexes by Large-scale Analysis of Mass Spectrometry (MS) Data, ISMB 2016.

[68] W Li, F Vandin, J Baumbach, Q Tan. Enriched power of case-only design in detecting gene-gene interaction using disease concordant twins. International Symposium on Integrative Bioinformatics, 2017.

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.

Research Grants

University of Padova, **STARS: Algorithms for Inferential Data Mining**. Role: PI. Total amount: €140,000. *03/2018-03/2020.*

University of Padova, **Algorithms for Networks Analysis and Bioinformatics Applications**. Role: PI. Total amount: €54,000. *09/2017-09/2019.*

University of Padova, **From Single-Cell to Multi-Cells Information Systems Analysis**. Role: Co-PI (PI: Barbara Di Camillo). Total amount: €220,000. *09/2017-09/2020.*

National Science Foundation, **BIGDATA: Mid-Scale: Analytical Approaches to Massive Data Computation with Applications to Genomics**. Role: co-PI (PI: Eli Upfal). Total amount: $1,566,685. *10/2012-09/2018.*

National Science Foundation, **AF: Small: Algorithmic Problems in Protein Structure Studies**. Role: PI for the last two years of the award, total amount: $225,001. Collaborative with Gopal Pandurangan, and Chris Bailey-Kellogg. *06/2011-08/2013.*

Honors/Awards

Research Fellow, Simons Institute for the Theory of Computing, Berkeley.	*1-5/2016*
Lecturer Training Program, Faculty of Science, University of Southern Denmark.	*06/2015*
Teaching Award, Faculty of Science, University of Southern Denmark.	*10/2014*
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

On the Sample Complexity of Cancer Pathways Identification, RECOMB 2015, 04/14/2015.
Reconstructing Cancer Pathways and Their Mutation Order from Cross-Sectional Data, (Poster) ISMB 2014, 07/13/2014.
Simultaneous Inference of Cancer Pathways and Tumor Progression from Cross-Sectional Mutation Data, RECOMB 2014, 04/05/2014.
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 1^{st} 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

Algorithms for Combinatorial Problems Arising in the Analysis of Cancer Mutation Networks, Simons Institute for Theory of Computing, UC Berkeley, 04/12/2016.
Algorithms for Finding Significantly Mutated Pathways in Cancer, Pennsylvania State University, 03/23/2016.
Computational Methods for Finding Significantly Mutated Pathways in Cancer, Genome Center, UC Davis, 02/03/2016.
Finding Mutated Subnetworks Associated with Survival in Cancer, Simons Institute for Theory of Computing, UC Berkeley, 02/02/2016.
Computational Methods for Identifying Significant Mutations In Cancer Genomes, ETH Zurich, Switzerland, 12/18/2015.
Algorithms for Identifying Significant Mutations in Cancer Genomes, Bertinoro Computational Biology, Italy, 06/17/2015.
On the Sample Complexity of Cancer Pathways Identification, ITU, Copenhagen, Denmark, 05/18/2015.
Algorithms for Identifying Significant Mutations in Cancer Genomes, KTH, Sweden, 05/11/2015.

Algorithms for Identifying Significant Mutations in Cancer Genomes, Simon Fraser University, Vancouver, Canada, 01/23/2015.
Algorithms to Find Significant Mutations and Pathways in Cancer Genomes, PhD programme in Computer Science, University of Pisa, Pisa, Italy, 09/22/2014.
How to Distinguish Driver Mutations from Passenger Mutations, Clinical Institute, Odense, Denmark, 06/10/2014.
Computational Methods for Cancer Genomics, Bioinformatics Symposium, SDU, Odense, Denmark, 04/10/2014.
Finding Somatic Mutations Associated with Survival Time in Cancer, Mandrup Seminar, SDU, Odense, Denmark, 03/27/2014.
Computational Cancer Genomics, Bioinformatics Plenary Talk, SDU, Odense, Denmark, 03/14/2014.
Accurate Computation of Survival Statistics in Genome-Wide Cancer Studies, Bioinformatics Seminar, SDU, Odense, Denmark, 03/10/2014.
Computational Problems in Cancer Genomics, NII Shonan Meeting, Japan, 18/3/2014.
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

2015: **Instructor**: *Data Mining and Statistical Learning*, University of Southern Denmark. *Advanced Algorithms for Computational Biology*, University of Southern Denmark. *Algorithms and Data Structures*, University of Padova. *Advanced Topics in Computational Biology*, University of Padova. *Machine Learning*, University of Padova.
2014: **Instructor**: *Data Mining*, University of Southern Denmark.
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

Editorial Service

2017 - now: Systems Medicine (Editorial Board member)
2016 - now: BMC Bioinformatics (Associate Editor)
2016 - now: Journal of Graph Algorithms and Applications (Associate Editor)

Scientific Boards

2017 - now: Bertinoro international Center for informatics - BiCi (Scientific Advisory Board member)

Referee

2007 - now: **Journals**: Data & Knowledge Engineering; Journals of Zhejiang University SCIENCE; Journal of Discrete Algorithms; BMC Bioinformatics; PLOS Computational Biology; Bioinformatics (Oxford Journals); Genome Medicine; Human Mutation; Data Mining and Knowledge Discovery;

Journal of Computational Biology; BMC Genomics; ACM Transactions on Algorithms; Nature Scientific Reports; ACM Transactions on Bioinformatics and Computational Biology; Nature Methods.
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); 18th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2014); 22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2014); European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases (ECML-PKKD) 2014; 26th International Conference on Scientific and Statistical Database Management (SSDBM 2014); ; 22th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2018).

International Conferences and Workshops Organization

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).
ACM BCB, ACM Conference on Bioinformatics, Computational Biology and Biomedicine 2012 (PC Member).
RECOMB, International Conference on Research in Computational Molecular Biology 2014 (PC Member).
BigLS, ACM International Workshop on Big Data in Life Sciences 2014 (PC Member).
ISMB, International Conference on Intelligent Systems for Molecular Biology 2014 (PC Member).
RECOMB, International Conference on Research in Computational Molecular Biology 2015 (PC Member; Poster co-chair).
ISMB, International Conference on Intelligent Systems for Molecular Biology 2015 (PC Member).
Future Perspectives in Computational Pan-Genomics (Workshop co-organiser), 2015, Lorentz Center (Netherlands).
The Future of Algorithmic Computational Biology 2015 (Workshop co-organiser), 2015, Bertinoro BiCi (Italy).
ACMBCB, ACM Conference on Bioinformatics, Computational Biology and Biomedicine 2015 (PC Member).
SWAT, Scandinavian Symposium and Workshops on Algorithm Theory 2016 (PC Member).
RECOMB, International Conference on Research in Computational Molecular Biology 2016 (PC Member; Poster chair).
RECOMB-CCB, RECOMB Satellite Workshop on Computational Cancer Biology 2016 (PC chair).
RECOMB, International Conference on Research in Computational Molecular Biology 2017 (PC Member).
RECOMB-CCB, RECOMB Satellite Workshop on Computational Cancer Biology 2017 (PC member).
ACMBCB, ACM Conference on Bioinformatics, Computational Biology and Biomedicine 2017 (PC Member).
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RECOMB-CCB, RECOMB Satellite Workshop on Computational Cancer Biology 2018 (PC member).
ISMB, International Conference on Intelligent Systems for Molecular Biology 2018 (PC Member).

Memberships

EATCS European Association for Theoretical Computer Science
ISCB International Society for Computational Biology

Supervision of Graduate Students

University of Southern Denmark: one Ph.D. student (Morteza Chalabi Hajkarim, 2017) and four Master students (Lars Andersen, 2015; Mike Rostermund, 2016; Tommy Hansen, 2016; Anna Bomersbach, 2016). University of Padova: one Ph.D. student (Leonardo Pellegrina, expected 2020) and four Master student (Mattia Donami, 2016; Federico Alberton, 2016; Simone Bettio, 2017; Tommaso Scarpa, 2017).

Software Packages

`CoMEt` (`https://github.com/raphael-group/comet/releases`)
`HotNet2` (`https://github.com/raphael-group/hotnet2/releases`)
`Dendrix` (`http://compbio.cs.brown.edu/projects/dendrix/`)
`HotNet` (`http://compbio.cs.brown.edu/projects/hotnet/`)
`ExaLT` (`thttp://compbio.cs.brown.edu/projects/survival/`)
`MADMX` (available upon request)
`TopKMiner` (available upon request)