

# Curriculum Vitae

## Fabio Vandin

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Department of Information Engineering  
University of Padova  
Via Gradenigo 6/B, I-35131 Padova, Italia  
*E-mail:* [fabio.vandin@unipd.it](mailto:fabio.vandin@unipd.it)  
*WWW:* [www.dei.unipd.it/~vandinfra/index.html](http://www.dei.unipd.it/~vandinfra/index.html)  
*Phone:* +39-049-827-7946

### Current Position

**Professor**  
**Coordinator of the Ph.D. program in Information Engineering**  
Department of Information Engineering  
University of Padova  
Italy

### 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

<b>Professor</b> Department of Information Engineering University of Padova, Italy.	<i>02/2020-current</i>
<b>Coordinator of the Ph.D. program in Information Engineering</b> Department of Information Engineering University of Padova, Italy.	<i>02/2023-current</i>
<b>Associate Professor</b> Department of Information Engineering University of Padova, Italy.	<i>07/2015-02/2020</i>
<b>Adjunct Associate Professor</b> Department of Department of Mathematics and Computer Science University of Southern Denmark, Denmark.	<i>11/2015-present</i>
<b>Assistant Professor</b> Department of Mathematics and Computer Science University of Southern Denmark, Denmark.	<i>01/2014-06/2015</i>
<b>Adjunct Assistant Professor of Computer Science (Research)</b>	<i>10/2013-12/2013</i>

- 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, E. Upfal. **Data Mining and Knowledge Discovery**, ECML PKDD 2010 special issue, Volume 21, Number 2, 2010.
- [2] F. Vandin, E. Upfal, 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, 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, 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, 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, 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, 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 1<sup>st</sup> 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. Kandath<sup>†</sup>, M.D. McLellan<sup>†</sup>, 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, F. Vandin. Identifying driver mutations in sequenced cancer genomes: computational approaches to enable precision medicine. **Genome Medicine**, 6:5 (2014).
- [16] K. A. Hoadley, C. Yau, D. M. Wolf, A. D. Cherniack, D. Tamborero, S. Ng, M. D. Leiserson, B. Niu, M. D. McLellan, V. Uzunangelov, J. Zhang, C. Kandath, R. Akbani, H. Shen, L. Omberg, A. Chu, A. A. Margolin, L. J. Van't Veer, N. Lopez-Bigas, P. W. Laird, B. J. Raphael, L. Ding, A. G. Robertson, L. A. Byers, G. B. Mills, J. N. Weinstein, C. Van Waes, Z. Chen, E. A. Collisson, The Cancer Genome Atlas Research Network, C. C. Benz, C. M. Perou, J. M. Stuart. 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, F. Silvestri. **Journal of Parallel and Distributed Computing**, Volume 76, Pages 58-65 (2015).
- [19] B. J. Raphael, F. Vandin<sup>‡</sup>. 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<sup>†</sup>, F. Vandin<sup>†</sup>, 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<sup>†</sup>, H.-T. Wu<sup>†</sup>, F. Vandin, B. J. Raphael. CoMET: A Statistical Approach to Identify Combinations of Mutually Exclusive Alterations in Cancer. **Genome Biology**, 16:160 (2015).
- [23] M. Chen, J. Baumbach, F. Vandin, R. Rottger, E. Barbosa, M. Dong, M. Frost, L. Christiansen, Q. Tan. Differentially Methylated Genomic Regions in Birth-Weight Discordant Twin Pairs. **Annals of Human Genetics** (2016).
- [24] F. Vandin<sup>‡</sup>, B. Raphael, 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 Human-Methylation450 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] F. Vandin. Computational Methods for Characterizing Cancer Mutational Heterogeneity. **Frontiers in Genetics**, 8 (2017).
- [30] R. Shrestha, E. Hodzic, T. Sauerwald, P. Dao, K. Wang, J. Yeung, S. Anderson, F. Vandin, G. Haffari, C. C. Collins, S. C. 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 M. Ceccarello, C. Fantozzi, A. Pietracaprina, G. Pucci. **PVLDB**, 4 (11):472-484 (2017).
- [33] R. Sarto Basso, D. Hochbaum, and F. Vandin<sup>‡</sup>. Efficient Algorithms to Discover Alterations with Complementary Functional Association in Cancer. **PLOS Computational Biology**, 15(5): e1006802 (2019).
- [34] M. H. Chalabi, V. Tsiamis, L. Käll, F. Vandin, V. Schwämmle. CoExpresso: assess the quantitative behavior of protein complexes in human cells. **BMC Bioinformatics** 20 (1), 17 (2019).

- [35] F. Altieri, T. V. Hansen, F. Vandin<sup>‡</sup>. NoMAS: A Computational Approach to Find Mutated Subnetworks Associated with Survival in Genome-Wide Cancer Studies. **Frontiers in Genetics**, 10, 265 (2019).
- [36] M. C. Hajkarim, E. Upfal, F. Vandin<sup>‡</sup>. Differentially mutated subnetworks discovery. **Algorithms for Molecular Biology**, 14 (1), 10 (2019).
- [37] W. Li, J. Baumbach, A. Mohammadnejad, C. Brasch-Andersen, F. Vandin, J. O. Korb, Q. Tan. Enriched power of disease-concordant twin-case-only design in detecting interactions in genome-wide association studies. **European Journal of Human Genetics**, 27, 631-636 (2019).
- [38] L. Pellegrina, C. Pizzi, and F. Vandin<sup>‡</sup>. Fast Approximation of Frequent k-mers and Applications to Metagenomics. **Journal of Computational Biology**, 27 (4), 534-549 (2020).
- [39] M. Riondato, F. Vandin<sup>‡</sup>. MiSoSouP: Mining Interesting Subgroups with Sampling and Pseudodimension. **ACM Transactions on Knowledge Discovery from Data**, 14 (5), 1-31 (2020).
- [40] L. Pellegrina, F. Vandin<sup>‡</sup>. Efficient Mining of the Most Significant Patterns with Permutation Testing. **Data Mining and Knowledge Discovery**, 34, 1201-1234 (2020).
- [41] D. Santoro, A. Tonon, F. Vandin<sup>‡</sup>. Mining Sequential Patterns with VC-Dimension and Rademacher Complexity. **Algorithms**, 13, 123 (2020).
- [42] M. Comin, B. Di Camillo, C. Pizzi, F. Vandin. Comparison of microbiome samples: methods and computational challenges. **Briefings in Bioinformatics**, bbaa121 (2020).
- [43] Y.-A. Kim, D. Wojtowicz, R. Sarto Basso, I. Sason, W. Robinson, D. S. Hochbaum, M. DM Leiserson, R. Sharan, F. Vandin, T. M. Przytycka. Network-based approaches elucidate differences within APOBEC and clock-like signatures in breast cancer. **Genome Medicine**, 12, 1-12 (2020).
- [44] Y.-A. Kim, R. Sarto Basso, D. Wojtowicz, A. S. Liu, D. S. Hochbaum, F. Vandin, T. M. Przytycka. Identifying drug sensitivity subnetworks with netphix. **IScience**, 23(10), 101619 (2020).
- [45] D. Buffelli, F. Vandin<sup>‡</sup>. Attention-Based Deep Learning Framework for Human Activity Recognition with User Adaptation. **IEEE Sensors Journal** (2021).
- [46] D. Buffelli, F. Vandin<sup>‡</sup>. The impact of global structural information in graph neural networks applications. **Data**, 7(1), 10 (2022).
- [47] F. Vandin. Technical perspective: Evaluating sampled metrics is challenging. **Communications of the ACM**, 65(7), 74 (2022).
- [48] D. Santoro, L. Pellegrina, M. Comin, F. Vandin<sup>‡</sup>. SPRISS: approximating frequent k-mers by sampling reads, and applications. **Bioinformatics**, 38(13), 3343-3350 (2022).
- [49] L. Pellegrina, C. Cousins, F. Vandin, M. Riondato. MCRapper: Monte-Carlo Rademacher averages for poset families and approximate pattern mining. **ACM Transactions on Knowledge Discovery from Data**, 16(6), 1-29 (2022).
- [50] A. Tonon, F. Vandin<sup>‡</sup>. gRosSo: mining statistically robust patterns from a sequence of datasets. **Knowledge and Information Systems**, 64(9), 2329-2359 (2022).
- [51] L. Pellegrina, F. Vandin<sup>‡</sup>. Discovering significant evolutionary trajectories in cancer phylogenies. **Bioinformatics**, 38(Supplement.2), ii49-ii55 (2022).
- [52] A. Tonon, F. Vandin<sup>‡</sup>. caSPiTa: mining statistically significant paths in time series data from an unknown network. **Knowledge and Information Systems**, 65(6), 2347-2374 (2023).

### Conference Papers (*Peer-Reviewed*)

- [53] Efficient Incremental Mining of Top-K Frequent Closed Itemsets, with A. Pietracaprina. In Proceedings 10<sup>th</sup> International Conference on Discovery Science (**DS**), LNCS 4755, pages 275-280, 2007.
- [54] An Efficient Rigorous Approach for Identifying Statistically Significant Frequent Itemsets, with A. Kirsch, M. Mitzenmacher, A. Pietracaprina, G. Pucci, E. Upfal. In Proceedings 28<sup>th</sup> ACM Symposium on Principles of Database Systems (**PODS**), pages 117-126, 2009.
- [55] MADMX: A Novel Strategy for Maximal Dense Motif Extraction, with R. Grossi, A. Pietracaprina, N. Pisanti, G. Pucci, E. Upfal. In Proceedings 9<sup>th</sup> Workshop on Algorithms in Bioinformatics (**WABI**), LNCS 5724, pages 362-374, 2009.
- [56] F. Vandin, E. Upfal, B. J. Raphael. Algorithms for Detecting Significantly Mutated Pathways in Cancer. In Proceedings 14<sup>th</sup> International Conference on Research in Computational Molecular Biology (**RECOMB**), LNCS 6044, pages 506-521, 2010.
- [57] F. Vandin, E. Upfal, B. J. Raphael. *De novo* Discovery of Mutated Driver Pathways in Cancer. In Proceedings 15<sup>th</sup> International Conference on Research in Computational Molecular Biology (**RECOMB**), LNCS 6577, pages 499-500, 2011.
- [58] F. Vandin, E. Upfal, B. J. Raphael. Finding Driver Pathways in Cancer: Models and Algorithms. In Proceedings 11<sup>th</sup> Workshop on Algorithms in Bioinformatics (**WABI**), LNCS 6833, pages 314-325,

- 2011.
- [59] F. Vandin, P. Clay, E. Upfal, B. J. Raphael. Discovery of Mutated Subnetworks Associated with Clinical Data in Cancer. In Proceedings Pacific Symposium on Biocomputing (**PSB**), pages 55-66, 2012.
  - [60] Algorithms on Evolving Graphs, with A. Anagnostopoulos, R. Kumar, M. Mahdian, E. Upfal. In Proceedings 3<sup>rd</sup> Innovations in Theoretical Computer Science Conference (**ITCS**), pages 149-160, 2012.
  - [61] L. He, F. Vandin, G. Pandurangan, C. Bailey-Kellogg. BALLAST: A Ball-based Algorithm for Structural Motifs. In Proceedings 16<sup>th</sup> International Conference on Research in Computational Molecular Biology (**RECOMB**), LNCS 7262, pages 79-93, 2012.
  - [62] F. Vandin, A. Papoutsaki, B. Raphael, E. Upfal. Genome-Wide Survival Analysis of Somatic Mutations in Cancer. In Proceedings 17<sup>th</sup> International Conference on Research in Computational Molecular Biology (**RECOMB**), LNCS 7821, pages 285-286, 2013. *Best Paper Award*.
  - [63] Space-Efficient Parallel Algorithms for Combinatorial Search Problems, with A. Pietracaprina, G. Pucci, F. Silvestri. In Proceedings 38<sup>th</sup> International Symposium on Mathematical Foundations of Computer Science (**MFCS**), LNCS 8087, pages 717-728, 2013.
  - [64] B. J. Raphael, F. Vandin<sup>‡</sup>. Simultaneous Inference of Cancer Pathways and Tumor Progression from Cross-Sectional Mutation Data. Proceedings 18<sup>th</sup> International Conference on Research in Computational Molecular Biology (**RECOMB**), pages 250-264, 2014.
  - [65] M. Riondato, F. Vandin<sup>‡</sup>. Finding the True Frequent Itemsets. Proceedings SIAM International Conference on Data Mining (**SDM**), pages 497-505, 2014.
  - [66] M. D. M. Leiserson, H.-T. Wu, F. Vandin, B. J. Raphael. CoMET: A Statistical Approach to Identify Combinations of Mutually Exclusive Alterations in Cancer. In Proceedings 19<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), pages 202-204, 2015.
  - [67] F. Vandin<sup>‡</sup>, B. Raphael, E. Upfal. On the Sample Complexity of Cancer Pathways Identification. In Proceedings 19<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), pages 326-337, 2015.
  - [68] T. Hansen, F. Vandin<sup>‡</sup>. Finding Mutated Subnetworks Associated with Survival Time in Cancer. 20<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), 2016.
  - [69] The Second Decade of the International Conference on Research in Computational Molecular Biology, with F. Hormozdiari, F. Hormozdiari, C. Kingsford, P. Medvedev. 20<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), 2016.
  - [70] Reconstructing Hidden Permutations Using the Average-Precision (AP) Correlation Statistic, with L. De Stefani, A. Epasto, E. Upfal. 13<sup>th</sup> AAAI Conference on Artificial Intelligence (**AAAI**), 2016.
  - [71] A. Bomersbach, M. Chiarandini, F. Vandin<sup>‡</sup>. An Efficient Branch and Cut Algorithm to Find Frequently Mutated Subnetworks in Cancer. 16<sup>th</sup> Workshop on Algorithms in Bioinformatics (**WABI**), 2016.
  - [72] R. Sarto Basso, D. Hochbaum, F. Vandin<sup>‡</sup>. Efficient Algorithms to Discover Alterations with Complementary Functional Association in Cancer. 22<sup>nd</sup> Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), 2018.
  - [73] M. Riondato, F. Vandin<sup>‡</sup>. MiSoSouP: Mining Interesting Subgroups with Sampling and Pseudodimension. 24<sup>th</sup> ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (**KDD**), pages 2130-2139, 2018.
  - [74] L. Pellegrina, F. Vandin<sup>‡</sup>. Efficient Mining of the Most Significant Patterns with Permutation Testing. 24<sup>th</sup> ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (**KDD**), pages 2070-2079, 2018.
  - [75] M. C. Hajkarim, E. Upfal, F. Vandin<sup>‡</sup>. Differentially Mutated Subnetworks Discovery. 18<sup>th</sup> Workshop on Algorithms in Bioinformatics (**WABI**), pages 18:1–18:14, 2018.
  - [76] L. Pellegrina, M. Riondato, and F. Vandin<sup>‡</sup>. SPuManTE: Significant Pattern Mining with Unconditional Testing. 25<sup>th</sup> ACM SIGKDD conference on Knowledge Discovery and Data Mining (**KDD**), pages 1528-1538, 2019.
  - [77] L. Pellegrina, C. Pizzi, and F. Vandin<sup>‡</sup>. Fast Approximation of Frequent k-mers and Applications to Metagenomics. 23<sup>rd</sup> Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), pages 208-226, 2019.
  - [78] A. Tonon and F. Vandin<sup>‡</sup>. Permutation Strategies for Mining Significant Sequential Patterns. 19<sup>th</sup> IEEE International Conference on Data Mining (**ICDM**), pages 1330-1335, 2019.
  - [79] L. Pellegrina, C. Cousins, F. Vandin, M. Riondato. MCRapper: Monte-Carlo Rademacher Averages

- for Poset Families and Approximate Pattern Mining. 26<sup>th</sup> ACM SIGKDD conference on Knowledge Discovery and Data Mining (**KDD**), pages 2165-2174, 2020.
- [80] A. Tonon, F. Vandin<sup>‡</sup>. GRosSo: Mining Statistically Robust Patterns from a Sequence of Datasets. In 2020 IEEE International Conference on Data Mining (**ICDM**), pages 551-560, 2020.
- [81] Scalable distributed approximation of internal measures for clustering evaluation with F. Altieri, A. Pietracaprina, G. Pucci. In Proceedings of the 2021 SIAM International Conference on Data Mining (**SDM**), pages 648-656, 2021.
- [82] I. Sarpe, F. Vandin<sup>‡</sup>. PRESTO: Simple and Scalable Sampling Techniques for the Rigorous Approximation of Temporal Motif Counts. In Proceedings of the 2021 SIAM International Conference on Data Mining (**SDM**), pages 145-153, 2021.
- [83] D. Santoro<sup>†</sup>, L. Pellegrina<sup>†</sup>, F. Vandin<sup>‡</sup>. SPRISS: Approximating Frequent  $k$ -mers by Sampling Reads, and Applications. 25<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (**RECOMB**), 2021.
- [84] I. Sarpe, F. Vandin<sup>‡</sup>. odeN: Simultaneous Approximation of Multiple Motif Counts in Large Temporal Networks. 30<sup>th</sup> ACM International Conference on Information and Knowledge Management (**CIKM**), 2021.
- [85] A. Tonon, F. Vandin<sup>‡</sup>. CASPITA: Mining Statistically Significant Paths in Time Series Data from an Unknown Network. 21<sup>st</sup> IEEE International Conference on Data Mining (**ICDM**), 2021.
- [86] D. Buffelli, F. Vandin<sup>‡</sup>. Graph representation learning for multi-task settings: a meta-learning approach. In 2022 IEEE International Joint Conference on Neural Networks (**IJCNN**), 2022.
- [87] D. Simionato, F. Vandin<sup>‡</sup>. Bounding the Family-Wise Error Rate in Local Causal Discovery Using Rademacher Averages. In Machine Learning and Knowledge Discovery in Databases: European Conference (**ECML PKDD**), 2022.
- [88] D. Buffelli, P. Liò, F. Vandin<sup>‡</sup>. Sizeshiftreg: a regularization method for improving size-generalization in graph neural networks. In Advances in Neural Information Processing Systems (**NeurIPS**), 2022.
- [89] P. Pellizzoni, F. Vandin<sup>‡</sup>. VC-dimension and Rademacher Averages of Subgraphs, with Applications to Graph Mining. In 39<sup>th</sup> IEEE International Conference on Data Engineering (**ICDE**), 2023.

### **Abstract/Poster in International Conferences**

- F. Vandin, E. Upfal, and B. J. Raphael. Identification of Significantly Mutated Pathways in Cancer. RECOMB Reg. Genomics/Sys. Biology/DREAM5, 2009
- F. Vandin, E. Upfal, and B. J. Raphael. Detection of Mutated Pathways in Cancer. 18<sup>th</sup> International Conference on Intelligent Systems for Molecular Biology (ISMB), 2010.
- 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
- F. Vandin, H.-T. Wu, E. Upfal, and B. J. Raphael. Algorithms for Automated Discovery of Mutated Pathways in Cancer. The Cancer Genome Atlas' 1<sup>st</sup> Annual Scientific Symposium: Enabling Cancer Research Through TCGA, 2011.
- F. Vandin, E. Upfal, and B. J. Raphael. Algorithms for Discovery of Mutated Pathways in Cancer. 2<sup>nd</sup> Workshop on Computational Advances for Next Generation Sequencing (CANGS) 2012, Las Vegas, NV, 2012.
- F. Vandin, H-T. Wu, E. Upfal, and B. J. Raphael. Algorithms to Find Mutated Pathways in Cancer. 16<sup>th</sup> International Conference on Research in Computational Molecular Biology (RECOMB), Barcelona, Spain, 2012.
- M. Leiserson, H.-T. Wu, D. Blokh, F. Vandin, R. Sharan, B. J. Raphael. Methods for Identifying Driver Pathways in Cancer. 3<sup>rd</sup> Annual Beyond the Genome Conference, Boston, USA, 2012.
- 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' 2<sup>nd</sup> Annual Scientific Symposium: Enabling Cancer Research Through TCGA, 2012.
- 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.
- 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.
- F. Vandin, and B. Raphael. Reconstructing Cancer Pathways and Their Mutation Order from Cross-Sectional Data. ISMB 2014, Boston, USA, 2014.
- 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.
- L. Andersen, F. Vandin. Efficient Methods for Reference-free Identification of SNVs, *1<sup>st</sup> Annual Danish Bioinformatics conference*, 2015.
  - M. C. Hajkarim, F. Vandin. GraDe-SVM: Graph-Diffused Classification for the Analysis of Somatic Mutations in Cancer. ROCKY 2015, Aspen (Colorado), USA, 2015.
  - M. C. Hajkarim, F. Vandin, V. Schwämmle. Computational Approaches to Decipher Composition and Regulation of Complexes by Large-scale Analysis of Mass Spectrometry (MS) Data, ISMB 2016.
  - W. Li, F. Vandin, J. Baumbach, Q. Tan. Enriched power of case-only design in detecting gene-gene interaction using disease concordant twins. International Symp. 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

Ministero dell'Università e della Ricerca (MUR), **PRIN EXPAND: scalable algorithms for Exploratory Analyses of heterogeneous and dynamic Networked Data**. Role: PI. Total amount: €388,337. *09/2023-09/2025.*

European Union, **Brainteaser: BRinging Artificial INTElligence home for a better cARE of amyotrophic lateral sclerosis and multiple SclERosis**. Role: participant. Total UniPD amount: €732,250. *2021-2024.*

Ministero dell'Istruzione, dell'Università e della Ricerca (MIUR), **PRIN AHeAD: efficient Algorithms for HARnessing networked Data**. Role: co-PI. Total amount: €784,860. *08/2019-08/2022.*

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.*

## Awards

Test of Time award, <b>RECOMB 2023</b> .	<i>2023</i>
Best Paper award, <b>ECML-PKDD 2022</b> .	<i>2022</i>
Above and Beyond award, <b>RECOMB 2021</b> .	<i>2021</i>
Knowledge and Information Systems, <b>Special Issue for ICDM 2020</b> .	<i>2020</i>
ACM Transactions on Knowledge Discovery from Data, <b>Special Issue for KDD 2018</b> .	<i>2018</i>
Algorithms for Molecular Biology, <b>Special Issue for WABI 2018</b> .	<i>2018</i>

<b>Research Fellow</b> , Simons Institute for the Theory of Computing, Berkeley, USA.	1-5/2016
<b>Lecturer Training Program</b> , Faculty of Science, University of Southern Denmark.	06/2015
<b>Teaching Award</b> , Faculty of Science, University of Southern Denmark.	10/2014
<b>Best Paper Award</b> , 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
Algorithms for Molecular Biology, <b>Special Issue for WABI 2011</b> .	2011
Premio “Sergio Gambi” for <b>best Ph.D. thesis</b> , University of Padova.	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
Data Mining and Knowledge Discovery, <b>Special Issue for ECML-PKDD 2010</b> .	2010
Borsa di Studio fondazione “Ing. Aldo Gini”, Padova.	01/2010.

## Invited Presentations

- Scalable Approximation of Internal Measures for Clustering Evaluation*, Workshop on Algorithmic Aspects of Clustering and Related Problems (ALACARTE 2023), Bertinoro BICI, 11/09/2023.
- Discovering Significant Evolutionary Trajectories in Cancer Phylogenies*, NCI Spring School on Algorithmic Cancer Biology (SSACB 2023), 17/03/2023.
- Approximating Frequent k-mers by Sampling*, Workshop on Pan-genome Graph Algorithms and Data Integration (PANGAIA), 24/01/2022.
- Fast Approximations of Frequent k-mers and Applications*, 20<sup>th</sup> IEEE International Workshop on High Performance Computational Biology (HiCOMB 2021), 17/05/2021.
- Computational Methods for the Identification of Cancer Pathways*, IFOM-IEO, Milan, Italy, 17/02/2020.
- Algorithms to Discover Alterations with Functional Association in Cancer*, CGSI, UCLA, USA, 30/07/2019.
- Fast Approximation of Frequent k-mers and Applications to Metagenomics.*, Workshop On Pangenomics Algorithms for Omics Data, Università Milano-Bicocca, Italy, 21/06/2019.
- Finding Patterns in Cancer Genomes: Challenges and Algorithms*, BITS2019-Analysis of Big Omics Data, Palermo, Italy, 26/06/2019.
- Finding Patterns in Cancer Genomes: Algorithms and Challenges*, Workshop on the Future of Algorithms in Biology, Carnegie Mellon University (CMU), USA, 28/09/2018.
- MiSoSouP: Mining Interesting Subgroups with Sampling and Pseudodimension*, Workshop on Foundations of Learning from Data, Bertinoro BICI, 11/09/2018.
- Computational methods to discover significant mutations in cancer genomes*, UNIBO-UCSD Cooperation Project Workshop, University of Bologna, 29/05/2018.
- Efficient Algorithms to Find Statistically Significant Patterns*, European Center for Living Technology (ECLT), University of Venice, 05/04/2018.
- Computational Methods for Survival Analysis in Genome-Wide Cancer Studies*, CGSI, UCLA, USA, 24/07/2017.
- Algorithms for Cancer Mutation Networks*, Computability in Europe, Turku, Finland, 15/06/2017.
- Computational Methods to Discover Significant Mutations in Cancer Genomes*, Sorbonne University, France, 01/06/2017.
- Inference of Mutated Pathways in Cancer*, University of Southern Denmark, 28/04/2017.
- Finding Mutated Subnetworks Associated with Survival Time in Cancer*, University of Palermo, 19/01/2017.
- Algorithms for Combinatorial Problems Arising in the Analysis of Cancer Mutation Networks*, Simons Institute for Theory of Computing, UC Berkeley, USA, 12/04/2016.
- Algorithms for Finding Significantly Mutated Pathways in Cancer*, Pennsylvania State University, USA, 23/03/2016.
- Computational Methods for Finding Significantly Mutated Pathways in Cancer*, Genome Center, UC Davis, USA, 03/02/2016.
- Finding Mutated Subnetworks Associated with Survival in Cancer*, Simons Institute for Theory of Computing, UC Berkeley, USA, 02/02/2016.
- Computational Methods for Identifying Significant Mutations In Cancer Genomes*, ETH Zurich, Switzerland, 18/12/2015.

*Algorithms for Identifying Significant Mutations in Cancer Genomes*, Bertinoro Computational Biology, Italy, 17/06/2015.

*On the Sample Complexity of Cancer Pathways Identification*, ITU, Copenhagen, Denmark, 18/05/2015.

*Algorithms for Identifying Significant Mutations in Cancer Genomes*, KTH, Sweden, 11/05/2015.

*Algorithms for Identifying Significant Mutations in Cancer Genomes*, Simon Fraser University, Vancouver, Canada, 23/01/2015.

*Algorithms to Find Significant Mutations and Pathways in Cancer Genomes*, PhD programme in Computer Science, University of Pisa, Pisa, Italy, 22/09/2014.

*How to Distinguish Driver Mutations from Passenger Mutations*, Clinical Institute, Odense, Denmark, 10/06/2014.

*Computational Methods for Cancer Genomics*, Bioinformatics Symposium, SDU, Odense, Denmark, 10/04/2014.

*Finding Somatic Mutations Associated with Survival Time in Cancer*, Mandrup Seminar, SDU, Odense, Denmark, 27/03/2014.

*Computational Cancer Genomics*, Bioinformatics Plenary Talk, SDU, Odense, Denmark, 14/03/2014.

*Accurate Computation of Survival Statistics in Genome-Wide Cancer Studies*, Bioinformatics Seminar, SDU, Odense, Denmark, 10/03/2014.

*Computational Problems in Cancer Genomics*, NII Shonan Meeting, Japan, 18/03/2014.

*Models and Algorithms to Find Driver Pathways in Cancer*, University of Padova, Italy, 09/10/2013.

*Computational Methods to Discover Significantly Mutated Pathways in Cancer*, IFOM-IEO, Milan, Italy, 08/10/2013.

*Identifying Significant Mutations in Large Cohorts of Cancer Genomes*, BigLS 2013, 13/06/2013.

*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, 31/05/2013.

*Algorithms for Identifying Significant Mutations in Cancer*, University of Southern Denmark, 17/03/2013.

*Computational Problems in Cancer Genomics*, IT University of Copenhagen, 06/03/2013.

*Algorithms for Identifying Significant Mutations in Cancer*, Worcester Polytechnic Institute, 01/02/2013.

*Discovery of Significantly Mutated Subnetworks in Cancer*, Network Links Workshop (University of Minnesota - IMA), 29/02/2012.

*Algorithms for Discovery of Mutated Pathways in Cancer*, CANGS 2012, 24/02/2012.

## Teaching

2022-current: **Instructor**: *Elements of Bioinformatics*, University of Padova.

2021-current: **Instructor**: *Learning from Networks*, University of Padova.

2018-current: **Instructor**: *Innovazione, progettazione e valutazione delle politiche e dei servizi (II level master)*, University of Padova.

2016-current: **Instructor**: *Machine Learning*, University of Padova. *Machine learning e big data nella medicina di precisione e nella ricerca biomedica (II level master)*, University of Padova.

2020: **Instructor**: *Learning from Networks* (Ph.D course), University of Padova.

2016-2022: **Instructor**: *Algorithms and Data Structures*, University of Padova. *Advanced Topics in Computational Biology*, University of Padova.

2015: **Instructor**: *Data Mining and Statistical Learning*, University of Southern Denmark. *Advanced Algorithms for Computational Biology*, University of Southern Denmark.

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).

## Supervision

**Postdocs**: Federico Altieri (2018-2020), Bui Van Thach (2019-2021), Leonardo Pellegrina (2020-2023) University of Padova;

**Ph.D students:** Morteza Chalabi Hajkarim (2014-2017, co-supervised with Prof. V. Schwämmle), University of Southern Denmark; Leonardo Pellegrina (2017-2020), Andrea Tonon (2018-2021), Davide Buffelli (2019-2023), Ilie Sarpe (2019-2023), Diego Santoro (2019-2023), Dario Simionato (from 2020), Antonio Collesei (from 2020), University of Padova.

**Master Students:** University of Padova: Matteo Riondato (2009), Federico Alberton (2016), Tommaso Scarpa (2017), Stefano Pelizzaro (2017), Simone Bettio (2017), Mattia Donami (2017), Matteo Mistura (2017), Leonardo Pellegrina (2017), Andrea Tonon (2018), Davide Dalle Pezze (2018), Davide Buffelli (2019), Enrico Vianello (2019), Marco Sansoni (2019), Ilie Sarpe (2019), Diego Santoro (2019), Dario Simionato (2019), Barutta Elena (2019), Andrea Rossi (2019), Matteo Terranova (2020), Marco Dalla Mutta (2020), Marco Barison (2021), Federico Soldà (2021), Samuele Benfatti (2022), Alessandro Chimetto (2022), Federica Vettor (2022), Davide Peressoni (2022), Matteo Visonà (2022), Paolo Pellizzoni (2022), Paola Donolato (2023), Cristian Boldrin (2023), Giorgio Venturin (2023), Leonardo Sforzin (2023), Giacomo Seno (2023), Giulia Pisacreta (2023), Paolo Bresolin (2023), Matteo Pozzer (2023). University of Southern Denmark: Felix Emil Drud (2014), Lars Andersen (2015), Mike Rostermund (2016), Anna Bomersbach (2016), Tommy Hansen (2016).

**Bachelor Students:** University of Padova: Stefano Gennari (2016), Riccardo Galiazzo (2016), Enrico Vianello (2016), Davide Dalle Pezze (2016), Alessandro Bianciardi (2016), Zanato Angelica (2017), Matilde Boschiero (2017), Marco Miola (2017), Marco Giraldo (2017), Laura Manduchi (2017), Ignazio Bovo (2017), Francesco Andrace (2017), Diego Santoro (2017), Matteo Terranova (2018), Roberto Rossini (2018), Mattia Avanzi (2018), Nicola Sartore (2018), Alexandru Enache (2018), Marco Rossi (2019), Tommaso Lunardon (2019), Luca Dolci (2019), Samuele Benfatti (2019), Filippo Ronco (2020), Federico Berton (2021), Thomas Zilio (2021). University of Southern Denmark: Daniel Arnfeldt Andersen (2014).

## **Professional Activities**

### **Editorial Service**

Since 2021: ACM Transactions on Intelligent Systems and Technology (Editorial Board member)

Since 2017: Systems Medicine (Editorial Board member)

Since 2016: BMC Bioinformatics (Associate Editor)

Since 2016: Journal of Graph Algorithms and Applications (Associate Editor)

### **Scientific Boards**

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

### **Referee**

**Journals (main)** (2007-present): 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; Nature Communication; Nature Cancer; IEEE Transactions on Knowledge and Data Engineering.

**Conferences (main)** (2007-present): 14<sup>th</sup> International Colloquium on Structural Information and Communication Complexity (SIROCCO 2007); 20<sup>th</sup> ACM Symposium on Parallelism in Algorithms and Architectures (SPAA 2008); 22<sup>nd</sup> IEEE International Parallel and Distributed Processing Symposium (IPDPS 2008); 50<sup>th</sup> Annual IEEE Symposium on Foundations of Computer Science (FOCS 2009); 16<sup>th</sup> IEEE International Conference on High Performance Computing (HiPC 2009); 24<sup>th</sup> IEEE International Parallel and Distributed Processing Symposium (IPDPS 2010); 21<sup>st</sup> Annual Symposium on Combinatorial Pattern Matching (CPM2010); 9<sup>th</sup> European Conference on Computational Biology (ECCB 2010); 1<sup>st</sup> IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS 2011); 23<sup>th</sup> ACM Symposium on Parallelism in Algorithms and Architectures (SPAA 2011); International Workshop on Combinatorial Algorithms 2011 (IWOCA 2011); 15<sup>th</sup> International Workshop on Randomization and Computation (RANDOM 2011); 16<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB 2012); 2<sup>nd</sup> Annual RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-seq 2012); 2<sup>nd</sup> IEEE International Conference

on Computational Advances in Bio and Medical Sciences (ICCABS 2012); 11<sup>th</sup> European Conference on Computational Biology (ECCB 2012); Pacific Symposium on Biocomputing (PSB) 2013; 17<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB 2013); 18<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB 2014); 22<sup>nd</sup> 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-PKDD) 2014; 26<sup>th</sup> International Conference on Scientific and Statistical Database Management (SSDBM 2014).

**Ph.D theses:** Marine LeMorvan (MINES ParisTech, 2018); Yael Silberberg (Tel Aviv University, 2017); Simona Cristea (ETH Zurich, 2016); Riccardo Vicedomini (Università di Udine, 2016).

**Research Proposals:** National Science Foundation (USA), Wellcome Trust, The Royal Society (UK), Natural Sciences and Engineering Research Council (Canada), Polish National Science Centre (NCN).

### *Program Committee*

**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).

**ACM-BCB**, 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**, International Conference on Research in Computational Molecular Biology 2017 (PC Member).

**RECOMB-CCB**, RECOMB Satellite Workshop on Computational Cancer Biology 2017 (PC Member).

**ACM-BCB**, ACM Conference on Bioinformatics, Computational Biology and Biomedicine 2017 (PC Member).

**ISMB**, International Conference on Intelligent Systems for Molecular Biology 2017 (PC Member).

**RECOMB**, International Conference on Research in Computational Molecular Biology 2018 (PC Member).

**RECOMB-CCB**, RECOMB Satellite Workshop on Computational Cancer Biology 2018 (PC Member).

**ISMB**, International Conference on Intelligent Systems for Molecular Biology 2018 (PC Member).

**RECOMB**, International Conference on Research in Computational Molecular Biology 2019 (PC Member).

**RECOMB-seq**, RECOMB Satellite Workshop on Massively Parallel Sequencing 2019 (PC Member).

**RECOMB-CCB**, RECOMB Satellite Workshop on Computational Cancer Biology 2019 (PC Member).

**ISMB**, International Conference on Intelligent Systems for Molecular Biology 2019 (PC Member).

**ACM-BCB**, ACM Conference on Bioinformatics, Computational Biology and Biomedicine 2019, 2020 (PC Member).

**KDD**, ACM SIGKDD Conference on Knowledge Discovery and Data Mining 2019 (PC Member).

**KDD**, ACM SIGKDD Conference on Knowledge Discovery and Data Mining 2020 (Senior PC Member).

**AAAI**, AAAI Conference on Artificial Intelligence 2020 (PC Member).

**RECOMB**, International Conference on Research in Computational Molecular Biology 2020 (PC Member).

**IJCAI**, International Joint Conference on Artificial Intelligence 2020 (PC Member).

**ECML-PKDD**, European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases 2020 (PC Member).

**NeurIPS**, Conference on Neural Information Processing Systems 2020 (PC Member).  
**ICDM**, IEEE International Conference on Data Mining 2020 (PC Member).  
**ACM-BCB**, ACM Conference on Bioinformatics, Computational Biology and Biomedicine 2021 (PC Member).  
**AAAI**, AAAI Conference on Artificial Intelligence 2021 (PC Member).  
**RECOMB**, International Conference on Research in Computational Molecular Biology 2021 (PC Member).  
**ISMB**, International Conference on Intelligent Systems for Molecular Biology 2021 (PC Member).  
**SDM**, SIAM International Conference on Data Mining 2021 (PC Member).  
**ECML-PKDD**, European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases 2021 (PC Member).  
**TheWebConf**, The Web Conference 2021 (PC Member).  
**KDD**, ACM SIGKDD Conference on Knowledge Discovery and Data Mining 2021 (Senior PC Member).  
**ICDM**, IEEE International Conference on Data Mining 2021 (PC Member).  
**ICML**, International Conference on Machine Learning 2021 (PC Member).  
**NeurIPS**, Conference on Neural Information Processing Systems 2021 (PC Member).  
**SDM**, SIAM International Conference on Data Mining 2022 (Senior PC Member).  
**RECOMB**, International Conference on Research in Computational Molecular Biology 2022 (PC Member).  
**ISMB**, International Conference on Intelligent Systems for Molecular Biology 2022 (PC Member).  
**KDD**, ACM SIGKDD Conference on Knowledge Discovery and Data Mining 2022 (Senior PC Member).  
**ECML-PKDD**, European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases 2022 (PC Member).  
**ICDM**, IEEE International Conference on Data Mining 2022 (PC Member).  
**NeurIPS**, Conference on Neural Information Processing Systems 2022 (PC Member).  
**WSDM**, ACM International WSDM Conference 2022 (PC Member).  
**ISMB**, International Conference on Intelligent Systems for Molecular Biology 2023 (PC Member).  
**RECOMB**, International Conference on Research in Computational Molecular Biology 2023 (PC Member).  
**ECML-PKDD**, European Conference on Machine Learning and Principles and Practice of Knowledge Discovery in Databases 2023 (PC Member).  
**KDD**, ACM SIGKDD Conference on Knowledge Discovery and Data Mining 2023 (Senior PC Member).  
**TheWebConf**, The Web Conference 2023 (PC Member).  
**WSDM**, ACM International Web Search and Data Mining Conference 2023 (Senior PC Member).  
**IDA**, Symposium on Intelligent Data Analysis 2023 (PC Member).  
**ICDM**, IEEE International Conference on Data Mining 2023 (PC Member).  
**SDM**, SIAM International Conference on Data Mining 2024 (Senior PC Member).  
**WSDM**, ACM International Web Search and Data Mining Conference 2024 (Senior PC Member).

## Organization of International Conferences

**RECOMB 2021**, International Conference on Research in Computational Molecular Biology (General chair).  
**RECOMB 2020**, International Conference on Research in Computational Molecular Biology (General chair).  
**RECOMB-CCB**, RECOMB Satellite Workshop on Computational Cancer Biology 2016 (PC chair).  
**Future Perspectives in Computational Pan-Genomics** (co-organiser), 2015, Lorentz Center (Netherlands).  
**The Future of Algorithmic Computational Biology 2015** (co-organiser), 2015, Bertinoro BiCi (Italy).

## Tutorials at International Conferences

**Multiple Hypothesis Testing and Statistically-sound Pattern Mining**, Leonardo Pellegrina, Matteo Riondato, Fabio Vandin, Proceedings of the 25<sup>th</sup> ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (**KDD 2019**). <https://doi.org/10.1145/3292500.3332286>  
**Multiple Hypothesis Testing and Statistically-sound Pattern Mining**, Leonardo Pellegrina, Matteo Riondato, Fabio Vandin, Proceedings of the 2021 SIAM International Conference on Data Mining (**SDM 2021**). [https://meetings.siam.org/session/dsp\\_programsess.cfm?SESSIONCODE=71922](https://meetings.siam.org/session/dsp_programsess.cfm?SESSIONCODE=71922)

## **(Some) Software Packages**

RAveL (<https://github.com/VandinLab/RAveL>)  
MASTRO (<https://github.com/VandinLab/MASTRO>)  
SPRISS (<https://github.com/VandinLab/SPRISS>)  
odeN (<https://github.com/VandinLab/odeN>)  
SILVAN (<https://github.com/VandinLab/SILVAN>)  
PRESTO (<https://github.com/VandinLab/PRESTO>)  
SPuManTE (<https://github.com/VandinLab/SPuManTE>)  
gRosSo (<https://github.com/VandinLab/gRosSo>)  
MCRapper (<https://github.com/VandinLab/MCRapper>)  
VCRadSPM (<https://github.com/VandinLab/VCRadSPM>)  
PROMISE (<https://github.com/VandinLab/PROMISE>)  
SAKEIMA (<https://github.com/VandinLab/SAKEIMA>)  
DAMOKLE (<https://github.com/VandinLab/DAMOKLE>)  
TopKWY (<https://github.com/VandinLab/TopKWY>)  
UNCOVER (<https://github.com/VandinLab/UNCOVER>)  
NoMAS (<https://github.com/VandinLab/NoMAS>)  
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 (<http://compbio.cs.brown.edu/projects/survival/>)  
MADMX (disponibile su richiesta)  
TopKMiner (disponibile su richiesta)

## **Patents**

*Heat diffusion based genetic network analysis* (WO2016054270, *pending*).