

FERHAT AY

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EDUCATION

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| University of Washington (UW) Computing Innovation Fellow (Postdoctorate) <i>Noble Lab., Dept. of Genome Sciences</i> | Seattle, WA <i>September 2011</i> |
| University of Florida (UF) Ph.D. in Computer Science | Gainesville, FL <i>2007-2011</i> |
| Massachusetts Institute of Technology (MIT) Visiting Student at CSAIL <i>Computational Biology Group of Manolis Kellis</i> | Cambridge, MA <i>Summer 2010</i> |
| Middle East Technical University (METU) B.S. in Computer Engineering B.S. in Mathematics | Ankara, Turkey <i>2003-2007</i> <i>2004-2007</i> |

RESEARCH INTERESTS

My primary research areas are bioinformatics, computational biology, epigenetics and regulatory genomics. I am specifically interested in modeling genome architecture of various organisms and cell lines using datasets from high throughput methods such as chromosome conformation capture (3C) and its variants. I have an ongoing interest of analyzing topological structures of large scale biological networks and developing methods for mining biological network databases for conserved connectivity patterns.

DISSERTATION

Title: "A Comparative Study on Biological Networks: Alignment and Structural Properties"
Advisor: Assoc. Prof. Tamer Kahveci

ACADEMIC HONORS AND AWARDS

- NSF Computing Innovation Fellowship, University of Washington, September 2011 (Awarded \$140,000 for the first year of postdoctoral study).
- UF-HHMI Science for Life Graduate Student Mentor Award, University of Florida, March 2011.
- Alumni Fellowship, UF, 2007-2011.
- Alec Courtelis Award for Academic Excellence, UF, 2008.
- Outstanding Student Achievement Award, UF, 2008.
- Best Paper Award in the International Conference on Computational Systems Biology (CSB), 2008.
- METU Scholarship, Turkey, 2002-2007.
- Ranked 445th in University Entrance Exam (\approx 1.5 million attendees), Turkey, 2002.
- Third place in Mathematics Contest, Istanbul Technical University, Turkey, 2001.

PUBLICATIONS

JOURNAL PAPERS

1. The modENCODE Consortium, S. Roy*, J. Ernst*, P.V. Kharchenko*, P. Kheradpour*, N. Negre*, M.L. Eaton*, J.M. Landolin*, C.A. Bristow*, L. Ma*, M.F. Lin*, S. Washiet*, B.I. Arshinoff*, **F. Ay***, P.E. Meyer*, N. Robine*, N. L Washington*, L.D. Stefano*, et. al., S.E. Celniker, S. Henikoff, G.H. Karpen, E.C. Lai, D.M. MacAlpine, L.D. Stein, K.P. White and M.Kellis (*** co-first author**). Identification of functional elements and regulatory circuits by *Drosophila* modENCODE . *Science*, 330(6012):1787–1797, 2010.
2. **F. Ay**, M. Kellis and T. Kahveci. SubMAP: Aligning metabolic pathways with subnetwork mappings. *Journal of Computational Biology (JCB)*, 18(3):1-17. 2011.
3. **F. Ay**, F. Xu, and T. Kahveci. Scalable steady state analysis of Boolean biological regulatory networks. *PLoS ONE*, 4(12):e7992, 2009.
4. **F. Ay**, T. Kahveci, and V. de Crecy-Lagard. A fast and accurate algorithm for comparative analysis of metabolic pathways . *Journal of Bioinformatics and Computational Biology (JBCB)*, 7(3):389–428, 2009.

CONFERENCE PAPERS

5. M. Dang, **F. Ay** and T. Kahveci. A novel framework for large scale metabolic network alignments by compression (**Honorary Best Paper**). To appear in *Proceedings of 2nd ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB) 2011*.
6. **F. Ay** and T. Kahveci. SubMAP: Aligning metabolic pathways with subnetwork mappings. In *Proceedings of 14th International Conference on Research in Computational Molecular Biology (RECOMB)*, LNCS, volume 6044, pages 15–30, 2010.
7. **F. Ay** and T. Kahveci. Functional similarities of reaction sets in metabolic pathways. In *Proceedings of 1st ACM International Conference On Bioinformatics and Computational Biology (ACM-BCB)*, volume 1, pages 102–111, 2010.
8. **F. Ay***, T. Dinh*, M. Thai and T. Kahveci (*** co-first author**). Dynamic modular structure of regulatory networks. In *Proceedings of 10th International Conference on Bioinformatics and Bioengineering (IEEE BIBE)*, pages 136–143, 2010.
9. **F. Ay**, G. Gülsoy and T. Kahveci. Finding steady states of large scale regulatory networks through partitioning. In *9th IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS)*, 2010.
10. **F. Ay**, F. Xu and T. Kahveci. Scalable steady state analysis of Boolean biological regulatory networks. In *RECOMB-Satelite Conference on Regulatory Genomics (RECOMB-SAT)*, 2009.
11. **F. Ay**, T. Kahveci and V. de Crecy-Lagard. Consistent alignment of metabolic pathways without abstraction (**Best Paper**). In *Proceedings of 7th Annual Conference on Computational Systems Bioinformatics (CSB)*, volume 7, pages 237–248, 2008.

BOOK CHAPTERS

12. **F. Ay**, G. Gülsoy and T. Kahveci. Mining biological networks for similar patterns. To appear in “Data Mining: Foundations and Intelligent Paradigms”, editor Dawn Holmes, *Springer*.

PENDING PAPERS

13. **F. Ay**, M. Dang and T. Kahveci. Metabolic Network Alignment in Large Scale by Network Compression. Accepted to *BMC Bioinformatics*.
14. D. Marbach, S. Roy, P. Meyer, **F. Ay**, R. Candeias, T. Kahveci, C. Bristow and M. Kellis. Predictive regulatory models in *Drosophila Melanogaster* by integrative inference of transcriptional networks. Submitted to *Genome Research*.

INDUSTRY EXPERIENCE

- **Candidate Software Engineer, Radar Electronic Communication Group, ASELSAN, Turkey,** Jan. 2007 - Jul. 2007. ASELSAN is the leading high technology and multi-product defence electronics company of Turkey that introduces state-of-the-art equipment and systems solutions for both military and professional applications.
- **Summer Intern, Software Research and Development Center (SRDC), METU, Turkey,** Summer 2006. SRDC is established by the Scientific and Technical Research Council of Turkey (TUBITAK) in October 1991 and is operating under the Faculty of Engineering in METU. The aim of the center is to transfer the academic knowledge and know-how to industry through industrial collaborative projects.
- **Assistant System Administrator, Computer Engineering Department, METU, Turkey,** 2005 - 2006.
- **Summer Intern, HAVELSAN, Turkey,** Summer 2005. HAVELSAN is a software and systems company that presents global solutions in Defense and IT sectors.
- **Student Computer Lab Operator, Computer Center, METU, Turkey,** 2002 - 2005.

RESEARCH EXPERIENCE

- **Postdoctoral Fellow, UW,** Sep 2011 - Present
Genome architecture modeling and chromatin structure: Developing a computational pipeline for generating three-dimensional genome architecture models for various organisms (yeast, human, malaria) and cell lines. Participating in the improvement of statistical methods that extract relatively short-range intra-chromosomal interactions from the chromosome conformation capture data. Participating in the development of new experimental assays for genome architecture modeling and the development of validation techniques to assess the biological relevance of the inferred three-dimensional genome architecture models.
- **Research Assistant, UF,** Aug. 2007 - Aug. 2011.
Comparative analysis of biological networks: Developed novel computational techniques for aligning metabolic pathways with the goal of identifying functionally similar and evolutionary conserved parts across different species. Led the development of different algorithms that examine steady states and modular structure of dynamic regulatory networks using statistical methods, graph partitioning and graph compression techniques.
- **Visiting Student, MIT,** May - Sep 2010.
Topological analysis of *D. melanogaster* regulatory network: Integrated transcriptional and post-transcriptional regulations to analyze global and local structural properties of the genome-wide regulatory network of fruit fly. Participated in development of novel methods for predicting gene functions and expression, and integrating different experimental data to create a functional regulatory network.

TEACHING EXPERIENCE

- **Teaching Assistant.** COP-3530: *Data Structures and Algorithms*, Spring 2011, UF.
- **Teaching Assistant.** COT-5405: *Analysis of Algorithms*, Assoc. Prof. Arunava Banerjee, Spring 2008, UF.
- **Tutor.** *Academic Tutoring Center*, Fall 2007, UF.
- **Student Assistant.** CENG-230: *Introduction to C Programming*, Fall 2006, METU.

PRESENTATIONS/POSTERS

CONFERENCE PRESENTATIONS

1. *Multiple 3C (MC) and Modeling the Architectures of Yeast and Human Genomes*, **PSB 2012, Workshop on the Structure and Function of Chromatin and Chromosomes**, The Big Island, HI, Jan. 2012.
2. *A Novel Framework for Large Scale Metabolic Network Alignments by Compression*, **ACM-BCB 2011**, Chicago, IL, Aug. 2011.
3. *Finding steady states of large scale regulatory networks through partitioning*, **GENSIPS 2010**, Cold Spring Harbor, NY, Nov. 2010.
4. *SubMAP: Aligning metabolic pathways with subnetwork mappings*, **RECOMB 2010**, Lisbon, Portugal, Aug. 2010.

5. *Functional similarities of reaction sets in metabolic pathways*, **ACM-BCB 2010**, Niagara Falls, NY, Aug. 2010.
6. *Dynamic modular structure of regulatory networks*, **IEEE BIBE 2010**, Philadelphia, PA, Jun. 2010.
7. *Scalable steady state analysis of Boolean biological regulatory networks*, **RECOMB-SAT 2009**, Cambridge, MA, Dec. 2009.
8. *Consistent alignment of metabolic pathways without abstraction*, **CSB 2008**, Stanford, CA, Aug. 2008.

TALKS

- *A Comparative Study on Biological Networks: Alignment and Structural Properties*, Computational Biology Group at MIT, *Hosted by Dr. Manolis Kellis*, Cambridge, MA, May. 2011.
- *A Comparative Study on Biological Networks: Alignment and Structural Properties*, Bioengineering Department at UCSD, *Hosted by Dr. Shankar Subramaniam*, San Diego, CA, May. 2011.
- *A Comparative Study on Biological Networks: Alignment and Structural Properties*, National Institute of Environmental Health Sciences (NIEHS), *Hosted by Dr. Raja Jothi*, Research Triangle Park, NC, May. 2011.
- *A Comparative Study on Biological Networks: Alignment and Structural Properties*, Computational Biology Center at Memorial Sloan-Kettering Cancer Center, *Hosted by Dr. Chris Sander*, New York, NY, Apr. 2011.
- *Comparative analysis of biological networks*, Computer Engineering Department at Middle East Technical University (METU), *Hosted by Dr. Tolga Can*, Ankara, Turkey, May. 2010.

POSTERS

- *Ferhat Ay, Sushmita Roy, Manolis Kellis*
Global and local topological properties of genome-wide regulatory network of D. melanogaster, **RECOMB-SAT 2010**, New York, NY, Nov. 2010.
- *Ferhat Ay, Fei Xu, Tamer Kahveci*
Identifying Steady States of Boolean Biological Regulatory Networks, **RECOMB-SAT 2009**, Cambridge, MA, Dec. 2009.

PROFESSIONAL ACTIVITIES

- Member of the International Society for Computational Biology (ISCB), 2010.
- Member of ACM Special Interest Group in Bioinformatics, Computational Biology, Biomedical Informatics (ACM SIGBioinformatics), 2011.
- Reviewed scholarly articles for
 - Bioinformatics
 - BMC Systems Biology
 - Computers in Biology and Medicine
 - RECOMB 2012
 - CSB 2009
 - ACM-BCB 2009
 - PAKDD 2010

OTHER ACTIVITIES

- Captain of a co-ed Soccer Team in Intramural Sports, 2008-2010.
- Benton Engineering Council Representative for the Assoc. of Graduate Students in CISE Dept., UF, 2008.
- Webmaster and Officer of Turkish Students Association, UF, 2007.
- Organizer of Departmental Soccer Tournament, METU, 2006.
- Top Scorer of CENGCUP'06 Soccer Tournament, 2006.
- Student Representative of Junior Class, METU, 2005.
- Member of Scouts Club, METU, 2003.

REFERENCES

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