FERHAT AY

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EDUCATION

2007-2011	University of Florida (UF), Gainesville, FL
	Ph.D. in Computer Science
Summer 2010	Massachusetts Institute of Technology (MIT), Cambridge, MA
	Visiting Student
2003-2007	Middle East Technical University (METU), Ankara, Turkey
	B.S. in Computer Engineering
2004-2007	Middle East Technical University (METU), Ankara, Turkey
	B.S. in Mathematics

PROFESSIONAL APPOINTMENTS

Jan 2016 –	La Jolla Institute for Allergy and Immunology (LIAI), La Jolla, CA
	Institute Leadership Assistant Professor of Computational Biology
	Division of Vaccine Discovery
Mar 2015 – Dec 2015	Northwestern University (NU), Chicago, IL
	Research Assistant Professor
	Department of Preventive Medicine – Health and Biomedical Informatics
Dec 2014 – Feb 2015	University of Washington (UW), Seattle, WA
	Acting Assistant Professor
	Department of Genome Sciences
Sep 2011 – Nov 2014	University of Washington (UW), Seattle, WA
	Computing Innovation Fellow (Postdoctorate)
	Department of Genome Sciences

RESEARCH SUPPORT

07/01/2016–06/31/2021 (Pending)	*Mechanisms regulating lncRNA short and long range signaling.* **NIH R01. Role: Co-Investigator (PI: Jhumku Kohtz, Northwestern)**
09/01/2016–08/31/2021 (Pending)	*Characterization of the dynamic nuclear organization of hepatocytes.* **NIH R01. Role: Co-Investigator (PI: Karine Le Roch, UC Riverside)**
07/01/2016–06/31/2021 (Completed)	*Computing Innovation Fellowship, 2011.* http://cifellows.org NSF/Computing Research Association (CRA).

HONORS & AWARDS

2011	HHMI Science for Life Graduate Student Mentor Award, University of Florida. https://sfl.aa.ufl.edu/press/GSA2011.pdf
2008	Alec Courtelis Award for Academic Excellence, University of Florida.
2008	Outstanding Student Achievement Award, University of Florida.
2008	Best Paper Award, International Conference on Computational Systems Biology (CSB), 2008. http://csb2008.org
2007	Alumni Fellowship, University of Florida.
2002	Middle East Technical University Scholarship, Turkey.

PUBLICATIONS

Journal Articles

1) **F. Ay** and W. S. Noble. Analysis methods for studying the 3D architecture of the genome. *Genome Biology*, 16:183, 2015.

2) X. Deng, W. Ma, V. Ramani, A. Hill, F. Yang, **F. Ay**, J. Berletch, C. A. Blau, J. Shendure, Z. Duan, W. S. Noble and C. Disteche Bipartite structure of the inactive mouse X chromosome. *Genome Biology*, 16:152, 2015.

3) R. M. Gittelman, E. Hun, **F. Ay**, J. Madeoy, L. Pennacchio, W. S. Noble, R. D. Hawkins and J. M. Akey Comprehensive identification and analysis of human accelerated regulatory DNA. *Genome Research*, 25(9): 1245–1255, 2015.

4) S. Roy, A. F. Siahpirani, D. Chasman, S. Knaack, **F. Ay**, R. Stewart, M. D. Wilson and R. Sridharan. A predictive modeling approach for cell-line specific long-range regulatory interactions. *Nucleic Acids Research (NAR)*, 2015 (Accepted).

5) V. Dileep, **F. Ay**, J. Sima, W. S. Noble and D. M. Gilbert. Topologically-associating domains and their long- range contacts are established during early G1 coincident with the establishment of the replication timing program. *Genome Research*, 25(8):1104–1113, 2015.

6) N. Varoquaux, I. Liachko, **F. Ay**, J. N. Burton, J. Shendure, M. Dunham, J.-P. Vert and W. S. Noble. Accurate identification of centromere locations in yeast genomes using Hi-C. *Nucleic Acids Research (NAR)*, 43(11):5331–5339, 2015.

7) M. W. Libbrecht, **F. Ay**, M. M. Hoffman, D. M. Gilbert, J. A. Bilmes and W. S. Noble. Joint annotation of chromatin state and chromatin conformation reveals relationships among domain types and identifies domains of cell type-specific expression. *Genome Research*, 25(4):544–557, 2015.

8) **F. Ay**, T. H. Vu, M. J. Zeitz, N. Varoquaux, J. E. Carette, J.-P. Vert, A. R. Hoffman and W. S. Noble. Identifying multi-locus chromatin contacts in human cells using tethered multiple 3C. *BMC Genomics*, 16:121, 2015.

9) W. Ma, **F. Ay**, C. Lee, G. Gulsoy, X. Deng, S. Cook, J. Hesson, C. B. Ware, A. Krumm, J. Shendure, C. A. Blau, C. Disteche, W. S. Noble and Z. J. Duan. Fine-scale chromatin interaction maps reveal the cis-regulatory landscape of lincRNA genes in human cells. *Nature Methods*, 12(1):71–78, 2015.

10) **F. Ay***, E. M. Bunnik*, N. Varoquaux, J.-P. Vert, W. S. Noble and K. G. Le Roch. Multiple dimensions of epigenetic gene regulation in the malaria parasite *Plasmodium falciparum*. *Bioessays*, 37(2):182–194, 2015.

11) **F. Ay***, E. M. Bunnik*, N. Varoquaux*, S. M. Bol, J. Prudhomme, J.-P. Vert, W. S. Noble and K. G. Le Roch. Three-dimensional modeling of the *P. falciparum* genome during the erythrocytic cycle reveals a strong connection between genome architecture and gene expression. *Genome Research*, 24(6):974–988, 2014.

12) **F. Ay**, T. L. Bailey and W. S. Noble. Statistical confidence estimation for Hi-C data reveals regulatory chromatin contacts. *Genome Research*, 24(6):999–1011, 2014.

13) N. Varoquaux, **F. Ay**, J.-P. Vert and W. S. Noble. A statistical approach for inferring the 3D structure of the genome. **Accepted, ISMB 2014**. *Bioinformatics*, 30(12):i26–i33, 2014.

14) M. J. Zeitz, P. L. Lerner, **F. Ay**, E. V. Nostrand, J. D. Heidmann, W. S. Noble and A. R. Hoffman. Implications of COMT long-range interactions on the phenotypic variability of 22q11.2 deletion syndrome. *Nucleus*, 4(6):487–493, 2013.

15) M. J. Zeitz, **F. Ay**, J. D. Heidmann, P. L. Lerner, W. S. Noble, B. N. Steelman and A. R. Hoffman. Genomic interaction profiles in breast cancer reveal altered chromatin architecture. *PLoS ONE*, 8(9):e73974, 2013.

16) D. Marbach, S. Roy, **F. Ay**, P. Meyer, R. Candeias, T. Kahveci, C. Bristow and M. Kellis. Predictive regulatory models in *Drosophila Melanogaster* by integrative inference of transcriptional networks. *Genome Research*, 22(7):1334–1349, 2012.

17) **F. Ay**, M. Dang and T. Kahveci Metabolic Network Alignment in Large Scale by Network Compression. *BMC Bioinformatics*, 13(Suppl 3):S2, 2012.

18) **F. Ay**, M. Kellis and T. Kahveci. SubMAP: Aligning metabolic pathways with subnetwork mappings. *Journal of Computational Biology (JCB)*, 18(3):1–17. 2011.

19) 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. Washielt*, 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. Identification of functional elements and regulatory circuits by Drosophila modENCODE. *Science*, 330(6012):1787–1797, 2010.

20) **F. Ay**, F. Xu and T. Kahveci. Scalable steady state analysis of Boolean biological regulatory networks. **Accepted to RECOMB-SAT 2009**. *PLoS ONE*, 4(12):e7992, 2009.

21) **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*, 7(3):389–428, 2009.

Conference Proceedings

22) M. Dang, **F. Ay** and T. Kahveci. A novel framework for large-scale metabolic network alignments by compression **(Honorary Best Paper)**. In *Proceedings of the 2nd ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB) 2011*.

23) **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.

24) **F. Ay** and T. Kahveci. Functional similarities of reaction sets in metabolic pathways. In *Proceedings of the 1st ACM International Conference On Bioinformatics and Computational Biology (ACM-BCB)*, volume 1, pages 102–111, 2010.

25) **F. Ay***, T. Dinh*, M. Thai and T. Kahveci. Dynamic modular structure of regulatory networks. In *Proceedings of 10th International Conference on Bioinformatics and Bioengineering (IEEE BIBE)*, pages 136–143, 2010.

26) **F. Ay**, G. Gulsoy 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.

27) **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

28) **F. Ay**, G. Güsoy and T. Kahveci. Mining biological networks for similar patterns. In *"Data Mining: Foundations and Intelligent Paradigms (Vol 3)"*, *Springer*, Dawn E. Holmes, Lakhmi C. Jain (Eds.), 2012 (ISBN 78-3-642-23150-6).

TEACHING EXPERIENCE

Winter 2013   **Instructor.** BIO-285: Directed Study/Research, Department of Biology, UW Bothell. University of Washington Future Faculty Fellows program. *Genetically modified organisms and applications of genetic engineering* **Overall student evaluation:** 4.8/5.0 (detailed report available upon request).

Spring 2011   **Teaching Assistant.** COP-3530: Data Structures and Algorithms, Computer Science. University of Florida.

Spring 2008   **Teaching Assistant.** COT-5405: Analysis of Algorithms, Computer Science. University of Florida.

PRESENTATIONS/POSTERS

Conference Presentations

1) Identifying centromere locations of multiple yeast genomes using Hi-C contact maps, **Midwest Yeast Meeting**, Evanston, IL, Sep 2014.
2) Genome architecture in action: Gene regulation via 3D chromatin organization in a malarial parasite, **Seattle Genetic Instability and Cancer Symposium**, Seattle, WA, Apr 2014.
3) Modeling the genome architectures of a haploid and a diploid human cell line using Tethered-Multiple 3C, **CSHL Meeting on Dynamic Organization of Nuclear Function**, Cold Spring Harbor, NY, Sep 2012.
4) 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.
5) A Novel Framework for Large Scale Metabolic Network Alignments by Compression, **ACM-BCB 2011**, Chicago, IL, Aug 2011.
6) Finding steady states of large-scale regulatory networks through partitioning, **GENSIPS 2010**, Cold Spring Harbor, NY, Nov 2010.
7) SubMAP: Aligning metabolic pathways with subnetwork mappings, **RECOMB 2010**, Lisbon, Portugal, Aug 2010.
8) Functional similarities of reaction sets in metabolic pathways, **ACM-BCB 2010**, Buffalo, NY, Aug 2010.
9) Dynamic modular structure of regulatory networks, **IEEE BIBE 2010**, Philadelphia, PA, Jun 2010.
10) Scalable steady state analysis of Boolean biological regulatory networks, **RECOMB-SAT 2009**, Cambridge, MA, Dec 2009.
11) Consistent alignment of metabolic pathways without abstraction, **CSB 2008**, Stanford, CA, Aug 2008.

Invited Talks

12) Genome architecture in action: Gene regulation via 3D chromatin organization in a malarial parasite, **Midwest Chromatin and Epigenetics Meeting** , Madison, WI, May 2014.
13) Genome architecture in action: Gene regulation via 3D chromatin organization, **Computational Biology Dept. at Carnegie Mellon University**, Hosted by Dr. Carl Kingsford, Pittsburgh, PA, Feb 2015.
14) Genome architecture in action: Gene regulation via 3D chromatin organization, **College of Natural and Agricultural Sciences at University of California-Riverside**, Hosted by Dr. Thomas Girke, Riverside, CA, Feb 2015.
15) Genome architecture in action: Gene regulation via 3D chromatin organization, **Biostatistics and Biomedical Informatics, Morgridge Institute at University of Wisconsin-Madison**, Hosted by Dr. Michael Newton, Madison, WI, Feb 2015.
16) Genome architecture in action: Gene regulation via 3D chromatin organization, **Institute for Genomic Biology at University of Illinois-Urbana Champaign**, Hosted by Dr. Jian Ma, Urbana, IL, Feb 2015.
17) Genome architecture in action: Gene regulation via 3D chromatin organization, **Biofrontiers Institute at University of Colorado-Boulder**, Hosted by Dr. Robin Dowell, Boulder, CO, Jan 2015.

18) Genome architecture in action: Gene regulation via 3D chromatin organization, **La Jolla Institute for Allergy and Immunology**, Hosted by Dr. Bjoern Peters, San Diego, CA, Jan 2015.

19) Genome architecture in action: Gene regulation via 3D chromatin organization, **The Institute of Bioinformatics at University of Georgia**, Hosted by Dr. Jessica Kissinger, Athens, GA, Jan 2015.

20) Genome architecture in action: Gene regulation via 3D chromatin organization, **Google[x]**, Mountain View, CA, Oct 2014.

21) Genome architecture in action: Gene regulation via 3D chromatin organization, **Clinical and Translation Sciences Institute at Northwestern University**, Hosted by Dr. Ramana Davuluri, Chicago, IL, Sep 2014.

22) Genome architecture in action: Gene regulation via 3D chromatin organization in human, mouse and malarial parasites, **Biophysics/Soft Matter Seminar Series, Simon Fraser University**, Hosted by Dr. David Sivak, Burnaby, BC, Canada, Dec 2014.

23) Genome architecture in action: Gene regulation via 3D chromatin organization, **Center for Regenerative Medicine at Washington University-St Louis**, Hosted by Dr. L. Solnica-Krezel, St Louis, MO, Mar 2014.

24) Genome architecture in action: Gene regulation via 3D chromatin organization, **The Jackson Laboratory for Genomic Medicine**, Hosted by Dr. Krishna Karuturi, Farmington, CT, Jan 2014.

25) A Comparative Study on Biological Networks: Alignment and Structural Properties, **Department of Genome Sciences at University of Washington**, Hosted by Dr. William Noble, Seattle, WA, May 2011.

26) A Comparative Study on Biological Networks: Alignment and Structural Properties, **SAGE Bionetworks**, Hosted by Dr. Bin Zhang, Seattle, WA, May 2011.

27) A Comparative Study on Biological Networks: Alignment and Structural Properties, **CSAIL MIT**, Hosted by Dr. Manolis Kellis, Cambridge, MA, May 2011.

28) A Comparative Study on Biological Networks: Alignment and Structural Properties, **Bioengineering Department at UCSD**, Hosted by Dr. Shankar Subramaniam, San Diego, CA, May 2011.

29) A Comparative Study on Biological Networks: Alignment and Structural Properties, **National Institute of Environmental Health Sciences (NIEHS)**, Hosted by Dr. Raja Jothi, Research Triangle, NC, May 2011.

30) 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.

31) Comparative Analysis of Biological Networks, **Dow AgroSciences**, Hosted by Dr. Daniel Caraviello, Indianapolis, IN, Oct 2010.

32) Comparative analysis of biological networks, **Computer Engineering Department at Middle East Technical University (METU)**, Hosted by Dr. Tolga Can, Ankara, Turkey, May 2010 (Invited Talk).

Posters

1) Genome architecture in action: Gene regulation via 3D chromatin organization in a malarial parasite, **The Biology of Genomes, CSHL**, NY, May 2014.

2) Analysis of genome architecture data reveals regulatory chromatin contacts in human and mouse cell lines, **Seattle Genetic Instability and Cancer Symposium**, Seattle, WA, Apr 2013.

3) Assigning statistical confidence estimates to DNA-DNA interactions from genome-wide chromosome conformation capture assays, **ISMB 2012**, Long Beach, LA, Jul 2012.

4) Global and local topological properties of genome-wide regulatory network of D. melanogaster, **RECOMB-SAT 2010**, New York, NY, Nov 2010.

5) Identifying Steady States of Boolean Biological Regulatory Networks, **RECOMB-SAT 2009**, Cambridge, MA, Dec 2009.

PROFESSIONAL MEMBERSHIPS

– Member of the International Society for Computational Biology (ISCB), since 2010.
– Member of ACM Special Interest Group in Bioinformatics and Computational Biology, since 2011.
– Member of the National Postdoctoral Association (NPA), since 2012.

PROFESSIONAL ACTIVITIES

- Program committee member, The International Conference on Intelligent Systems for Molecular Biology (ISMB) 2016.
- Tutorial Organizer, Analysis methods for 3D nucleome data at the ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM BCB), 2015 http://noble.gs.washington.edu/proj/3DNtutorial2015.
- Program committee member, International Workshop on Computational Network Biology at the ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM BCB), 2014, 2015.
- Publicity chair, Workshop on epigenomics and cell function at the ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics (ACM BCB), 2013.
- Publicity chair, Epigenomics session at the Pacific Symposium on Biocomputing (PSB), 2013.
- Program committee member, IEEE International Workshop on Genomic Signal Processing and Statistics (GENSIPS), 2012, 2013.
- Session chair, Algorithms for Sequence Analysis at ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM BCB) 2012.
- Co-chair of the University of Washington Postdoctoral Association (UWPA), 2012.
- Reviewed scholarly articles for:
    - **Journals**: Nature Methods, Genome Research, Genome Biology, PLoS Computational Biology, Scientific Reports, Bioinformatics, Epigenetics and Chromatin, Chromosoma, PLoS ONE, Nucleic Acids Research (NAR), BMC Genomics, Journal of Cell Biology, Cell Research, FEBS Letters, WIREs Systems Biology, BMC Bioinformatics, BMC Systems Biology, IEEE TCBB, Database, Journal of Bioinformatics and Computational Biology.
    - **Conference Proceedings**: ISMB 2016, PSB 2013, RECOMB 2012, ISMB 2012, 2013, 2014, ICDM 2011, ACM-BCB 2010.