

Elena Yavorska Harris

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RESEARCH INTERESTS Bioinformatics, Algorithms, Data mining

EDUCATION

- **University of California, Riverside, CA.**
Doctor of Philosophy, Computer Science, 2005-2010.
- **California State University, San Bernardino, CA.**
Master of Arts, Mathematics, 2003-2005.
- **California State University, San Bernardino, CA.**
Master of Science, Computer Science, 2000-2003.
- **Odessa Polytechnic State University, Ukraine.**
Bachelor of Science, Nuclear Engineering, 1983-1988.

PROFESSIONAL EXPERIENCE

August 2013 – present: Assistant Professor, Computer Science Department, California State University, Chico.

March 2012 – June 2013: Temporary Faculty, Computer Science Department and Engineering Technology Department, Cal Poly Pomona

August 2011 – July 2013: Visiting postdoc, Algorithms and Computational Biology Lab, Computer Science Department, University of California, Riverside.

July 2010 – July 2011: Research Associate, Molecular and Computational Biology section, Division of Biological Sciences, University of Southern California.

January 2008 – June 2010: Graduate Research Assistant, Department of Computer Science and Engineering, University of California, Riverside.

September – December 2007: Associate Instructor, Department of Computer Science and Engineering, University of California, Riverside.

May – June 2007: Associate Instructor, Department of Computer Science and Engineering, University of California, Riverside.

PEER
REVIEWED
JOURNAL
PAPERS

[J1] E. Y. Harris, N. Pons, K. Le Roch and S. Lonardi, "BRAT-BW: efficient and accurate mapping of bisulfite-treated reads", *Bioinformatics*, 2012.

DOI:10.1093/bioinformatics/bts264. (Impact factor: 5.468)

<http://bioinformatics.oxfordjournals.org/content/28/13/1795.abstract>

[J2] E. Y. Harris, N. Pons, K. G. Le Roch, S. Lonardi, "Chromatin-driven *de novo* discovery of DNA binding motifs in the human malaria parasite." *BMC Bioinformatics*, 2011.

DOI:10.1186/1471-2164-12-601. (Impact factor: 4.4).

<http://www.biomedcentral.com/1471-2164/12/601/abstract>

[J3] N. Pons*, E. Y. Harris*, J. Prudhomme, I. Wick, C. Eckhardt, G. Hicks, G. Hardiman, S. Lonardi, and K. Le Roch, "Nucleosome landscape and control of transcription in the human malaria parasite", *Genome Research*, 2010.

DOI:10.1101/gr.101063.109. (Impact factor: 13.608).

<http://bioinformatics.oxfordjournals.org/cgi/content/abstract/btp706?>

[J4] N. Pons, E. Y. Harris, S. Lonardi, K. G. Le Roch, "Nucleosome occupancy at transcription start sites in the human malaria parasite: A hard-wired evolution of virulence?" *Infection, Genetics and Evolution*, 2010.

DOI:10.1016/j.meegid.2010.08.002. (Impact factor: 3.166).

<http://linkinghub.elsevier.com/retrieve/pii/S1567134810002145>

[J5] E. Y. Harris, N. Pons, A. Levchuk, K. Le Roch and S. Lonardi, "BRAT: Bisulfite-treated Reads Analysis Tool", *Bioinformatics*, 2009.

DOI:10.1093/bioinformatics/btp706. (Impact factor: 5.468)

<http://genome.cshlp.org/content/early/2010/01/05/gr.101063.109.abstract?cited-by=yes&legid=genome;gr.101063.109v1>

PEER
REVIEWED
CONFERENCE
PAPERS

[C1] N. Pokhriyal, N. Pons, E. Y. Harris, K. G. Le Roch, S. Lonardi, "Novel Gene Discovery in the Human Malaria Parasite using Nucleosome Positioning Data." CSB 2010 - Computational Systems Bioinformatics Conference, pp. 124-135, Stanford, CA, 2010, Proceedings.

(Acceptance Rate: 27%).

<http://www.lifesciencesociety.org/CSB2010/toc/124.2010.html>

[C2] E. B. Fernandez, E. Harris, W. Najjar, S. Lonardi, "Exploration of short reads mapping in hardware." FPL 2010 - International Conference on Field Programmable Logic and Applications, pp. 360-363, Milano, Italy, 2010. Proceedings.

<http://www.lifesciencesociety.org/CSB2010/toc/>

[C3] E. Y. Harris, T. Lecroq, G. Kucherov and S. Lonardi, "CPM's 20th Anniversary: A Statistical Retrospective." CPM 2009 - Annual Symposium on Combinatorial Pattern Matching, pp.1-11, Lille, France, 2009, Proceedings.

(Acceptance Rate: 42.9%).

<http://www.springerlink.com/content/dj5211416833017g/>

CONFERENCE
TALKS

[C1] "Analysis of high-resolution and genome-scale DNA methylation data." X-Gen Congress & Expo, 14-18 March, 2011, San Diego, CA.

[C2] "Novel Gene Discovery in the Human Malaria Parasite using Nucleosome Positioning Data." CSB 2010 - Computational Systems Bioinformatics Conference, 16-18 August, 2010, Stanford, CA.

UNIVERSITY
COURSES
TAUGHT

- Introduction to Artificial Intelligence, August-December, 2013
- Programming and Algorithms I, August-December, 2013
- Discrete Structures, August-December, 2013
- Computer Applications for Engineering Technology, January-June, 2013
- Data Structures and Algorithms II, September-December, 2012
- Discrete Structures, September-December, 2012
- Programming Languages, March-June, 2012
- Intermediate Data Structures and Algorithms, July-August, 2008
- Discrete Structures, September-December, 2007

PROFESSIONAL
REVIEWER

- Nucleic Acid Research (2013)
- Asia Pacific Bioinformatics Conference (APBC 2013)
- Conference on Research in Computational Molecular Biology (RECOMB 2013)
- BMC Bioinformatics (2009, 2010, 2012)
- Transactions on Knowledge and Data Engineering (2009)
- International Symposium on Bioinformatics Research and Applications (ISBRA09)
- Combinatorial Pattern Matching (CPM08)
- SIAM Data Mining (SDM08)
- IEEE International Conference on Data Mining (ICDM08)
- Workshop on Algorithms in Bioinformatics (WABI08, WABI09)
- Computational Systems Bioinformatics (CSB08)

AWARDS

Dean's Graduate Fellowship award at the University of California, Riverside (2005-2007)

REFERENCES

- Stefano Lonardi, Professor and Associate Chair, Computer Science and Engineering, 900 University Ave., University of California, Riverside, CA 92521.
Phone: (951) 827-2203
Email: stelo@cs.ucr.edu
- Tao Jiang, Professor, Department of Computer Science & Engineering, 900 University Ave., University of California, Riverside, CA 92521.
Phone: (951) 827-2991
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