

Elena Yavorska Harris

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RESEARCH INTERESTS Bioinformatics, Computational biology,
Data mining, Machine learning, Biostatistics.

EDUCATION

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

PROFESSIONAL EXPERIENCE 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 2005 – June 2007: Associate Instructor, Department of Computer Science and Engineering, University of California, Riverside.

PEER REVIEWED JOURNAL PAPERS [J1] E. Y. Harris, N. Ponts, A. Levchuk, K. Le Roch and S. Lonardi, “BRAT: Bisulfite-treated Reads Analysis Tool”, *Bioinformatics*, 2009.
DOI:10.1093/bioinformatics/btp706. (Impact factor: 4.328)
<http://genome.cshlp.org/content/early/2010/01/05/gr.101063.109.abstract?cited-by=yes&legid=genome;gr.101063.109v1>

[J2] N. Ponts*, 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: 10.176).
<http://bioinformatics.oxfordjournals.org/cgi/content/abstract/btp706?>

[J3] N. Ponts, 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: 3.223).
<http://linkinghub.elsevier.com/retrieve/pii/S1567134810002145>

PEER
REVIEWED
CONFERENCE
PAPERS

[C1] 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/>

[C2] N. Pokhriyal, N. Ponts, 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>

UNIVERSITY
COURSES
TAUGHT

- Intermediate Data Structures and Algorithms, July-August, 2008
- Discrete Structures, September-December, 2007

PROFESSIONAL
REVIEWER

- Computational Systems Bioinformatics (CSB08)
- Workshop on Algorithms in Bioinformatics (WABI08, WABI09)
- IEEE International Conference on Data Mining (ICDM08)
- SIAM Data Mining (SDM08)
- Combinatorial Pattern Matching (CPM08)
- International Symposium on Bioinformatics Research and Applications (ISBRA09)
- Transactions on Knowledge and Data Engineering (2009)
- BMC Bioinformatics (2009, 2010)

REFERENCES

- Stefano Lonardi, Associate Professor, Computer Science and Engineering, University of California, Riverside, CA 92521.
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