

Sarah Aerni

E-mail sarah@computationalbio.com

Website: <http://www.computationalbio.com>

Education

In Progress Fall 2006 Stanford University Stanford, CA

Ph.D. Biomedical Informatics

- Primary advisor Serafim Batzoglou
- Co-advisor Stuart Kim

2001-2005 University of California, San Diego La Jolla, CA

B. S. Biology with Specialization in Bioinformatics, magna cum laude

- Minor in French Literature

Research Interests

My current research is focused on single-cell expression profiling of organisms (specifically *C. elegans*) using image analysis and machine learning techniques. Generally, I am interested in creating and applying novel analytical tools and refinement of current techniques for research in gene regulation, aging and cancer.

Awards received

National Science Foundation Graduate Research Fellowship

Stanford Graduate Fellowship (William R. Hewlett Fellow)

Phi Beta Kappa Society Member

2006 Finalist for Computing Research Association's Outstanding Undergraduate Award Program

Caledonian Honor Society at Muir College, UCSD

Provost's Honors

Publications

Xiao Liu, Fuhui Long, Hanchuan Peng, **Sarah J Aerni**, Min Jiang, Adolfo Sanchez-Blanco, John I. Murray, Robert H. Waterston, Serafim Batzoglou, Eugene W Myers, Stuart K. Kim "Molecular signatures and gene expression at the single cell level in *C. elegans*", (in preparation for submission)

Sarah J Aerni, Doron Lipson, Stas Volik, Collin C. Collins, Michael Barrett, Zohar Yakhini, Benjamin J. Raphael "Combined Analysis of Copy Number Changes and Structural Rearrangements in Cancer Genomes", (in preparation for submission to PLoS CompBio)

Benjamin J Raphael, Stanislav Volik, Peng Yu, Chunxiao Wu, Guiqing Huang, Elena V Linardopoulou, Barbara J Trask, Frederic M Waldman, Joseph Costello, Kenneth Pienta, Gordon Mills, Krystyna Bajsarowicz, Yasuko Kobayashi, Sridharan Shivanranjani, Pamela Paris, Quanzhou Tao, **Sarah J Aerni**, Raymond P Brown, Ali Bashir, Joe W Gray, Jan-Fang Cheng, Pieter de Jong, Mikhail Nefedov, Thomas Ried, Hesed M Padilla-Nash, Colin Collins "A sequence-based survey of the complex structural organization of tumor genomes", *Genome Biology* 2008, 9:R59.

Bradley T Messmer, Benjamin J Raphael **Sarah J Aerni**, George F Widhopf, Laura Z Rassenti, Traci L Toy, and Thomas J Kipps "Identification of Extensive Ig Sequence Archetypes Among Both Mutated And Unmutated Sequences in Chronic Lymphocytic Leukemia", (in preparation for resubmission)

Sarah J. Aerni, Eleazar Eskin "10 Years of the International Conference on Research in Computational Molecular Biology (RECOMB)", RECOMB 2006: 546-562 ([electronic edition](#))

Research experience

Bioinformatics Intern

July 2005-Sept 2006 Wold Lab, California Institute of Technology Pasadena, CA

- Created 3 Python-based motif finders for Cistematic package, implementing Greedy, Gibb's Sampler and Expectation maximization algorithms including background modeling using Markov models
- Used Cistematic package to identify possible motifs in ENCODE region for use in presentations at committee meetings

Computational Research Assistant

Jan 2005-Sept 2006 Bioinformatics Laboratory, UCSD La Jolla, CA

- Created programs using Perl, Python and C to analyze sequence data from tumor genomes and determine areas of interest based on results
- Developed software for VDJ analysis of CLL patients
- Completed annotation of VDJ junction analysis of leukemia patients using Perl and Java
- Performed analysis of sequence homology of antibodies using blast tools and clustering

Lab Assistant at Geological Data Center

June 2003 – Jan 2005 Scripps Institute of Oceanography La Jolla, CA

- Harvested, managed and compiled data of Scripps scientific cruises for SIO Explorer website (SIO Cruise archives) part of the National Science Digital Library – nsdl.sdsc.edu
- Programming in Perl, C-shell, and Awk in the Unix environment

Abstracts and posters

Bradley T Messmer, Benjamin J Raphael, **Sarah J Aerni**, George F Widhopf, Laura Z Rassenti, Traci L Toy, and Thomas J Kipps “A Bioinformatic Approach To CLL IGHV Sequence Analysis Identifies Extensive Ig Sequence Archetypes Among Both Mutated And Unmutated Sequences”, (The 2005 American Society of Hematology Annual Meeting – abstract published in BLOOD (Vol 106, Number 11, Nov16, 2005, pg25a))

Benjamin J Raphael, **Sarah J Aerni**, George F. Widhopf, Thomas J Kipps, Bradley T Messmer “Advanced Tools For Analysis Of Large CLL IgV Gene Sequence Collections”, (XI International Workshop on CLL <http://www.iwcll.org/> - abstract published in supplement to Leukemia & Lymphoma (Vol 46, Suppl 1, 2005))

Teaching and educational activities

BMI 212 course TA, Fall 2008 – Introduction to Biomedical Informatics Research Methodology (Profs Russ Altman, Betty Cheng, Teri Klein). Evaluated grant writing and presentation skills of groups, helped student teams complete projects.

BMI 214 course TA, Spring 2008 –Representations and Algorithms for Computational Molecular Biology (Prof Russ Altman). Created problem sets, helped students with programming and understanding concepts, grading. Oversaw AMIA 10x10 students.

The Science Bus, after-school science program for East Palo Alto Charter School, student tutor.

Undergraduate computer science course tutor, Fall 2003-Winter 2005 – Selected by professors of introductory computer science courses at UCSD (Prof Paul Kube and Beth Simon).

Assisted students in programming assignments in introductory Java and fluency in information technology, grading, proctoring exams, led lab sections.

Enduring Resources for Earth Science Education Teacher Workshop – member of GDC Team
Stanford Biomedical Informatics Training Program executive committee student representative (admissions committee member, industry panels organizer)

10th annual Biomedical Computing at Stanford (BCATS) organizing committee member

Stanford Association for Multi-Disciplinary Medicine and Science (S.A.M.M.S.) founding and signatory member, Biomedical Informatics program representative

Stanford-South Africa BioMedical Informatics Students Seminar Series organizer

Southern California Bioinformatics Summer Institute – NIH/NSF funded summer education and internship program for students pursuing a career in Bioinformatics, two-year participant (instructional1.calstatela.edu/jmomand2/)

10th annual International Conference on Research in Computational Biology (RECOMB 2006) - Serving on the anniversary committee

Scripps Institute of Oceanography’s Geological Data Center Open House– Presenter

Memberships

Golden Key International Honour Society
International Society for Computational Biology

References

Upon request, please email sarah@computationalbio.com

Skills and Qualifications

- Computer programming (experience in Java, ANSI C, C++, Matlab, R, Python, Perl, csh/awk, bash, Scheme)
- Unix, Macintosh and Windows Environment
- Microsoft Word, Excel, PowerPoint
- Biochemical and Molecular Biology laboratory experience

Languages

Fluency in English, German and a Swiss dialect, competence in French