

Melissa Suzanne Cline

Education

- Ph.D., Computer Science**, University of California, Santa Cruz 9/1995 – 6/2000
- Concentration: bioinformatics. Advisor: David Haussler
 - Thesis: *“Protein sequence alignment reliability: prediction and measurement”*
 - Coursework in machine learning, neural networks, algorithm theory, molecular biology.
- M.S., Computer Science**, University of California, Santa Cruz 9/1993 – 6/1995
- Concentration: software engineering. Advisor: Lydia Gregoret
 - Thesis: *An empirical study of the affected branch coverage of different fault classes*
- B.S., Computer Engineering**, Rensselaer Polytechnic Institute 9/1981 – 5/1986

Bioinformatics Research Experience

Postdoctoral Researcher Pasteur Institute, Paris, France 3/2005 - Present

Cytoscape Project

- Developing software to visualize and analyze protein interaction and association networks. Development performed in collaboration with U.C. San Diego, the Institute for Systems Biology, and Memorial Sloan Kettering.
- Extending Cytoscape to indicate changes in network topology induced by splice variation.

Staff Scientist Affymetrix, Inc. Emeryville, CA USA 6/2001 – 12/2004

Alternative Splicing Project

- Developed ANOSVA, a statistical method to identify alternative splicing from expression data. Validated successfully on spiked clone experiments. Published at ISMB2005.
- Analyzed the effects of alternative splicing on protein transmembrane and signal peptide regions. Observed that while such regions are often spliced out entirely in a short-form protein, they interrupted by splice variation significantly less often than expected. Observed that introns are rare in the transmembrane region of 1-TM signaling proteins. Published at PSB2004.
- Managed an external collaboration to explore the effects of alternative splicing on the signal transduction pathways involved in cardiomyopathy, premature labor, and other tissue remodeling events.
- Participated in the design group for the Affymetrix Human Exon Expression array by
 - developing and assessing methods to measure nonspecific background from a population of probes instead of a single mismatch probe.
 - Assessing the relation between probe set size and signal quality.

Chip Design and Genotyping

- Assessed the relationship between genotyping probe performance and predictors of probe performance, including probe scoring estimates and GC content.

NetAffx Web Resource

- Developed HMM-based protocols for protein recognition by SCOP structural family, enzyme class, and GPCR subfamily. Incorporated the protocols into the NetAffx annotation pipeline.
- Assessed public domain data repositories for possible integration with NetAffx. In particular, investigated data repositories and integration methods for incorporating data on biological pathways and interactions.

Independent Consultant Affymetrix, Inc. Emeryville, CA USA 1/2001 – 6/2001

- Assessed protein homology recognition frameworks involving SAM and Pfam (HMMER).

Graduate Student Researcher University of California, Santa Cruz, USA 1/1995 - 6/2000

- Developed software methods for HMM homology recognition. Applied the methods in the CASP2, CASP3, and CASP4 protein structure prediction competitions as part of the UCSC team. All three times, the UCSC team was judged one of the most successful fold recognition groups, and was invited to submit a paper to the special issue of *Proteins*.
- Applied information-theoretic and predictive methods to assess patterns of pairwise contacts in protein structures. Developed neural networks for beta-sheet contact prediction.

Teaching Experience

Bioinformatics Instructor UCSC Extension, Santa Clara, CA USA 4/2001 - 12/2001

- Taught “Data Analysis, Modeling, and Visualization for Bioinformatics”, covering probability models, information theory, neural networks, k-means and hierarchical clustering, self-organizing maps, mixture models, decision trees, Markov chains, HMMs.

Visiting Researcher Bioinformatics group, Högskolan Skövde, Sweden 4/1997 - 6/1997

- Advised master's students on bioinformatics thesis research. Provided input on development of an undergraduate bioinformatics curriculum.

Teaching Assistant University of California, Santa Cruz, CA USA (various dates)

- Assisted with “Artificial Intelligence” and “Introduction to Programming in C”.

Other Related Experience

Senior Software Engineer Abbott Laboratories, Santa Clara, CA USA 9/1990-7/1993

- Developed data analysis and management software for hematology analysis instruments.

Software Engineer GenRad, Concord, MA USA 9/1986-8/1990

- Developed quality management software for application in electronics manufacturing.

Honors and Awards

- Alfred P. Sloan Foundation postdoctoral fellowship in computational biology, 2000
- Graduate Assistance in Areas of National Need (GAANN) Fellowship, 1995-1999

Invited Presentations

- **Cline M.** *Systems biology technology platforms: the challenges to industry.* IBC Systems Biology 2004.
- **Cline M.** *Alternative splicing discovery with exon tiling arrays.* ACS Advanced Microarray Strategies for Biopharmaceuticals 2004.
- **Cline M.** *Building a better systems biology toolbox.* IBC Systems Biology 2003.
- **Cline M, C. Barrett. K. Karplus.** *Making the most of your hidden Markov models.* Tutorial presentation, Intelligent Systems for Molecular Biology, 1999.

Peer-Reviewed Publications

1. Ule J, Ule A., Spencer J., Williams A., Hu JS, **Cline M**, Wang H, Clark T, Fraser C, Ruggiu M, Zeeberg BR, Kane D, Weinstein JN, Blume J, Darnell RB. *Nova regulates brain-specific splicing to shape the synapse.* Nat Genet. 2005 37(8):844-52.
2. **Cline M.**, Blume J., Cawley S., Clark TA, Hu JS, Lu G., Salomonis N., Wang H., Williams A., *A statistical method for detecting splice variation from expression data.* Bioinformatics. 2005 Suppl 1:i107-i115.
3. **Cline MS**, Shigeta R., Wheeler R., Siani-Rose M., Kulp D., Loraine AE, *The effects of alternative splicing on transmembrane proteins in the mouse genome,* Pacific Symposium on Biocomputing, 2004;:17-28.
4. Karchin R., **Cline M.**, Karplus K., *Evaluation of local structure alphabets based on residue burial,* Proteins, 2004; 55(3):508-18.

5. Cheng J, Sun S, Tracy A, Hubbell E, Morris J, Valmeekam V, Kimbrough A, **Cline MS**, Liu G, Shigeta R, Kulp D, Siani-Rose MA. *NetAffx Gene Ontology Mining Tool: A visual approach for microarray data analysis*, Bioinformatics 2004; 20(9):1462-3.
6. Cheng J, **Cline M**, Martin J, Finkelstein D, Awad T, Kulp D, Siani-Rose MA., *A knowledge-based clustering algorithm driven by Gene Ontology*, Journal of Biopharmaceutical Statistics 2004, 14(3).
7. Loraine AE, Helt GA, **Cline MS**, Siani-Rose MA, *Exploring alternative transcript structure in the human genome using BLOCKS and InterPro*, Journal of Bioinformatics and Computational Biology, 2003 Jul; (2) 289-306.
8. Wang H, Hubbell E, Hu JS, Mei G, **Cline M**, Lu G, Clark T, Siani-Rose MA, Ares M, Kulp DC, Haussler D. *Gene structure-based splice variant deconvolution using a microarray platform*. Bioinformatics 2003; Suppl 1:I315-I322
9. Karchin R, **Cline M**, Mandel-Gutfreund Y, Karplus K. *Hidden Markov models that use predicted local structure for fold recognition: Alphabets of backbone geometry*. Proteins, 2003; 51(4):504-1.
10. Shigeta R, **Cline M**, Liu G, Siani-Rose MA.. *GPCR-GRAPA-LIB-a refined library of hidden Markov Models for annotating GPCRs*. Bioinformatics, 2003; 19(5):667-8.
11. Liu G, Loraine AE, Shigeta R, **Cline M**, Cheng J, Valmeekam V, Sun S, Kulp D, Siani-Rose MA.. *NetAffx: Affymetrix probesets and annotations*. NAR, 2003; 31(1):82-6
12. **Cline M**, Karplus K, Lathrop R, Smith T, Rogers R Jr., Haussler D. *Information-theoretic dissection of pairwise contact potentials*. Proteins, 2002; 49(1):7-14.
13. Loraine AE, Helt G, **Cline M**, Siani-Rose M. *Protein-based analysis of alternative splicing in the human genome*. IEEE Bioinformatics 2002; 118-27.
14. **Cline M**, Liu G, Loraine AE, Shigeta R, Cheng J, Mei G, Kulp D, Siani-Rose MA. *Structure-based comparison of four eukaryotic genomes*. Pacific Symposium on Biocomputing, 2002; 127-38.
15. **Cline M**, Hughey R, Karplus K. *Predicting reliable regions in protein sequence alignments*. Bioinformatics, 2002; 18(2):306-14.
16. Karplus K, Karchin R, Barrett B, Tu S, **Cline M**, Diekhans M, Grate L, Casper J, Hughey R. *What is the value added by human intervention in protein structure prediction?* Proteins, 2001; Suppl 5:86-91.
17. Karplus K, Barrett C, **Cline M**, Diekhans M, Grate L, Hughey R. *Predicting protein structure using only sequence information*. Proteins. 1999; Suppl 3:121-5.
18. **Cline M**, Werner L, *An empirical study of the branch coverage of different fault classes*. California Software Symposium CSS'95, pages 41-53.

Other Professional Activities

- W3C Semantic Web for Life Sciences task force
- New England BioLabs Molecular Biology Summer Workshop, Smith College, 2004.
- Referee: Bioinformatics, Journal of Theoretical Biology, NAR, Proteins, IEEE Transactions on Computational Biology, Pacific Symposium on Biocomputing, IEEE Computational and Systems Biology, Briefings in Bioinformatics.

Computational Skills

- Programming in C, C++, Java, Perl, SQL (Postgresql, MySQL), XML, RDF.
- Statistical analysis in R (S-Plus) and Matlab.