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Education

- **Ph.D. in Computer Science**, 1995, University of Colorado, Boulder.
- **M.S. in Computer Science**, 1990, University of Colorado, Boulder.

Professional Experience

- **Staff Scientist**, Computational Research Division, Lawrence Berkeley National Laboratory (July 2003-present).
- **Computer System Engineer III**, Computational Research Division, Lawrence Berkeley National Laboratory (Nov. 2001-June 2003).
- **Physical Biosciences Postdoctoral Fellow**, Lawrence Berkeley National Laboratory (1999- 2001).
- **NERSC Postdoctoral Fellow**, Lawrence Berkeley National Laboratory (1997-1999).
- **Research Associate**, University of Colorado at Boulder (1995-1997).
- **Research Assistant**, University of Colorado at Boulder (1988-1995).

Research Projects

- **Infrastructure for Improving Protein Structure Prediction in Computational Biology** This project concerns the development of an interactive visualization tool for the prediction of tertiary structure of proteins using concepts from robotics and animation.
- **Knowledge-Based Methods for Protein Structure Prediction**
This project concerns the development of methods for protein structure prediction based on structural homology and global optimization.
- **A Modeling and Steering Tool for Protein Prediction**
This project concerns the development of an infrastructure for enhancing the process of experimentation and discovery in protein research.

Memberships and Synergistic Activities

- Member of SIAM and ACM.
- Member of the Program Committee of the International Parallel and Distributed Processing Symposium, IPDPS 2004.

Collaborators

Wes Bethel, Lawrence Berkeley National Laboratory.

Prof. Bobby Schnabel, Prof. Richard Byrd, and Betty Eskow, Dept. of Computer Science, University of Colorado, Boulder.

Prof. Teresa Head-Gordon, Bioengineering Dept., University of California, Berkeley.

Prof. Bernd Hamann and Prof. Nelson Max, Dept. of Computer Science, University of California, Davis.

Dr. Juan Meza, Head of the Computational Research Division, Lawrence Berkeley Laboratory.

Graduate Students and Postdoctoral Fellows

Dr. Jinhui Ding (Postdoctoral Fellow), Ph.D. in Biology.
Dr. James Lu (Postdoctoral Fellow), Ph.D. in Computer Science.
Dr. Oliver Kreylos (Postdoctoral Fellow), Ph.D. in Computer Science.
Dr. Ricardo Oliva (Postdoctoral Fellow).
Clark Crawford (Grad. Student, UC Davis).

Publications

1. S. Crivelli, O. Kreylos, B. Hamann, N. Max, and W. Bethel (2004). *ProteinShop: A Tool for Interactive Protein Manipulation*. Accepted for publication in: Journal of Computer-Aided Molecular Design and Modeling.
2. S. Crivelli and T. Head-Gordon (2004). *A New Load Balancing Strategy for the Solution of Dynamical Large Tree Search Problems Using a Hierarchical Approach*. Accepted for publication in: the IBM Journal of Research and Development.
3. E. Eskow, B. Bader, R. Byrd, S. Crivelli, T. Head-Gordon, V. Lamberti, and R. Schnabel (2004). *An Optimization Approach to the Problem of Protein Structure Determination*. Accepted for publication in Mathematical Programming.
4. O. Kreylos, N. Max, B. Hamann, S. Crivelli, and W. Bethel (2003). *Interactive Protein Manipulation*. Proceedings of IEEE Visualization 2003 ApplicationTrack.
5. S. Crivelli, B. Bader, R. Byrd, E. Eskow, V. Lamberti, R. Schnabel, and T. Head-Gordon (2002). *A Physical Approach to Protein Structure Prediction*. Biophysical Journal **82**, 36-49.
6. T. Head-Gordon, S. Crivelli, O. Kreylos, E. Eskow, H. Choi, R. Byrd, and R. Schnabel (2002). *A Physical Approach to Protein Structure Prediction*, in: J. Moult, K. Fidelis, A. Zemla, and T. Hubbard, eds., Proceedings of CASP5 – Fifth Meeting on the Critical Assessment of Techniques for Protein Structure Prediction, Pacific Grove, California, December 1-5, A76-A78.
7. O. Kreylos, N. Max, and S. Crivelli (2002). *ProtoShop: Interactive Design of Protein Structures*, in: J. Moult, K. Fidelis, A. Zemla, and T. Hubbard, eds., Proceedings of CASP5 – Fifth Meeting on the Critical Assessment of Techniques for Protein Structure Prediction, Pacific Grove, California, December 1-5, A213-A214.
8. S. Crivelli, T.M. Philip, R. Byrd, E. Eskow, R. Schnabel, R.C. Yu, T. Head-Gordon (2000). *A Global Optimization Strategy for Predicting Protein Tertiary Structure: α -helical Proteins*. Computers & Chemistry **24**, 489-497.
9. A. Azmi, R.H. Byrd, E. Eskow, R. Schnabel, S. Crivelli, T.M. Phillips, T. Head-Gordon (2000). *Predicting Protein Tertiary Structure Using a Global Optimization Algorithm with Smoothing*. Optimization in Computational Chemistry and Molecular Biology: Local and Global Approaches, C.A. Floudas and P.M. Pardalos (eds.). Kluwer Academic Publishers, Netherlands, 1-18.
10. T. Head-Gordon, S. Crivelli, E. Eskow, B. Bader, V. Lamberti, R. Byrd, and R. Schnabel (2000). *Predicting Protein Tertiary Structure Using a Global Optimization Algorithm*, in: J. Moult, K.

- Fidelis, A. Zemla, and T. Hubbard, eds., Proceedings of CASP4 – Fourth Meeting on the Critical Assessment of Techniques for Protein Structure Prediction, Pacific Grove, California, December 3-7, A43-A44.
11. S. Crivelli, T. Head-Gordon, R.H. Byrd, E. Eskow, R. Schnabel (1999). *A Hierarchical Approach for Parallelization of a Global Optimization Method for Protein Structure Prediction*. Lecture Notes in Computer Science, Euro-Par '99, P. Amestoy, P. Berger, M. Dayde, I. Duff, V. Frayssé, L. Giraud, D. Ruiz (eds.), 578-585.
 12. S. Crivelli & E.R. Jessup (1999). *The PMESC Programming Library for Distributed-Memory MIMD Computers*. Journal of Parallel and Distributed Computing **57**, 295-321.
 13. S. Crivelli & E.R. Jessup (1996). *An Introduction to the PMESC Parallel Programming Paradigm and Library for Task Parallel Computation*. Wuhan University Journal of Natural Sciences **1**, No.3/4, 386-391.
 14. S. Crivelli & E.R. Jessup (1996). *Task Parallelism: What a Tool Can Provide and What Should Be Left to the User*. Lecture Notes in Computer Science Series, Euro-Par'96. Springer-Verlag.
 15. S. Crivelli & E.R. Jessup (1995). *The Cost of Eigenvalue Computation on Distributed-Memory MIMD Multiprocessors*, Parallel Computing **21**, 401-422.
 16. S. Crivelli & E.R. Jessup (1995). *An Introduction to the PMESC Parallel Programming Paradigm and Library for Task Parallel Computation*. Proceedings of ICPA '95, The International Conference on Parallel Algorithms.
 17. S. Crivelli & E.R. Jessup (1995). *The PMESC Parallel Programming Paradigm and Library*. Parallel Processing for Scientific Computing, ed. D. Bailey et al. SIAM.
 18. S. Crivelli & E.R. Jessup (1993). *A Programming Paradigm for Distributed-Memory Computers*. Parallel Processing for Scientific Computing, R. Sincovec, D. Keyes, M. Leuze, L. Petzold, and D. Reed (eds.), SIAM.
 19. S. Crivelli & E.R. Jessup (1993). *Optimal Eigenvalue Computation on a Mesh Multiprocessor*. Parallel Processing for Scientific Computing, R. Sincovec, D. Keyes, M. Leuze, L. Petzold, and D. Reed (eds.), SIAM.
 20. S. Crivelli & E.R. Jessup (1991). *Toward an Efficient Parallel Implementation of the Bisection Method for Computing Eigenvalues*. Proceedings of the Sixth Distributed Memory Computing Conference, Q. Stout and M. Wolfe (eds.), IEEE Computer Society Press.

Presentations

A New Approach to Protein Structure Prediction. Presented at the *Statistics and Genomics Seminars, School of Public Health*, University of California, Berkeley, Fall 2002.

An Ab Initio Approach to Protein Structure Prediction. Presented at the *Blanch-Prausnitz Group Seminars*, University of California, Berkeley, Fall 2001.

The Protein Structure Prediction Problem. Presented at the *Computer Science Departmental Colloquia*, Old Dominion University, Spring 2001.

An Approach to the Protein Structure Prediction Problem. Presented at the *Department of Computer Sciences Colloquia*, Purdue University, Spring 2001.

A Global Optimization Approach to Protein Structure Prediction. Presented at the *Computer Science and Engineering Seminar Series*, University of Notre Dame, Spring 2001.

The Protein Folding Problem (Designing Life: Proteins 1, Computers 0). Presented at *Distinguished Lecturer Series and Colloquia*, Computer Science Department, UC Davis, Spring 2001.

A Physical Approach to Protein Structure Prediction. Presented at *IBM Research Division*, Spring 2001.

A Hierarchical Approach for Parallelization of a Global Optimization Method for Protein Structure Prediction. Presented at *EuroPar'99, Toulouse, France, 1999.*

Phases of the Global Optimization Method for Protein Structure Prediction. Presented at *Supercomputing '98.*

Task Parallelism: What a tool can provide and what should be left to the user. Presented at *EuroPar'96, Lyon, France, August 1996.*

The PMESC Library. Presented at *Centre Europeen de Recherche et de Formation Avancee en Calcul Scientifique (CERFACS)*, Toulouse, France, August 1996.

The PMESC Parallel Programming Paradigm and Library. Presented at *the Seventh SIAM Conference on Parallel Processing for Scientific Computing*, San Francisco, California, 1995.

Implementing Dynamic Problems on Distributed-Memory Computers. Presented at *Seminar Series* organized by the Department of Mathematics, Rensselaer Polytechnic Institute, December 1994.

A Programming Paradigm for Distributed-Memory Computers. Presented at the *Sixth SIAM Conference on Parallel Processing for Scientific Computing*, Norfolk, Virginia, March 1993.

Optimal Eigenvalue Computation on a Mesh Multiprocessor. Presented at the *Sixth SIAM Conference on Parallel Processing for Scientific Computing*, Norfolk, Virginia, March 1993.