

# David Michael Alber

---

17476 NE 40th Place  
Redmond, WA 98052

alber.david@gmail.com  
<http://davidalber.net/>  
Tel: +1.217.390.1479

## EDUCATION

### University of Illinois at Urbana-Champaign

Ph.D. in Computer Science, May 2007

- Dissertation: *Efficient Setup Phase Algorithms for Parallel Algebraic Multigrid*

M.S. in Computer Science, May 2004

- Thesis: *Computational Local Fourier Mode Analysis in the Multigrid Solution of Coupled Systems*

### University of Iowa

B.S. in Biological Science and Computer Science, December 1999

## WORK EXPERIENCE

**Senior Software Development Engineer**, Technical Computing, Microsoft Corporation (June 2010 – current)

- Drive the implementation of statistical functions for a math library through the complete software development process. Implementation is done in native C++.
- Extra duties taken on: proposing and writing new tools in C#; adapted existing infrastructure tools to the team's needs; assisting manage automated builds in TFS Team Build System.
- Promoted from Software Development Engineer to Senior Software Development Engineer in August 2011 for consistently achieving all commitments and through contributions to make the group, as a whole, successful.

**Research Scientist**, Manycore Incubator Group, Microsoft Corporation (February 2009 – June 2010)

- Defined project plans and conducted in-depth research on fill-reducing reordering in sparse direct linear solvers. Designed and implemented a multilevel nested dissection algorithm in native C++ using a policy-based approach. Additional reordering algorithms and container classes for use by the group were implemented in native C++ and C#.
- Wrote Python code for extracting and presenting data on online sparse matrix collections in a much easier-to-use format; first in Excel and later in Microsoft PivotViewer.

**Postdoctoral Researcher**, National Renewable Energy Laboratory (May 2007 – February 2009)

Conducted research for a high-performance computational systems biology project studying bio-hydrogen production by the green alga *Chlamydomonas reinhardtii* [P3, P4].

- Wrote software in C for translating a metabolic model represented in the Systems Biology Markup Language (SBML) to C++. This model translation software has much better performance than the previously-used translation package in part due to the use of automatic differentiation.
- Driver software – including genetic algorithm optimization and improved and extended ODE integration and optimization – was written in C.
- Several tools for SBML models were written in Python. A deep understanding of SBML and was developed by this work. The tools experience culminated in the design and implementation of a plug-in manager for systems biology tools called SBTools [P5].
- Improved process by developing best practices. Replaced the manually-defined build system with a build based on Automake and Autoconf. Explored options for and improved the documentation of the project's software.
- Provided regular assistance in maintaining shared packages and administering the TORQUE resource manager and Maui scheduler on the Laboratory's primary cluster.

**Summer Intern**, Lawrence Livermore National Laboratory (Summers 2002 – 2004)

Research and development on multigrid methods. Topics included Fourier analysis, study of systems of PDEs (developed into Masters thesis), and multigrid for electromagnetics. Programming work was done in C and Matlab.

**Programmer**, University of Iowa College of Business (May 1998 – July 2000)

Developed the Iowa Electronic Markets, a real-time, real-money market, which offers twenty-four hour trading to an audience of several thousand users. Server was built in MS Visual C++ with a SQL database backend. Additional tools built include deadlock detector and trading engine test client.

**Laboratory Technician**, University of Iowa College of Medicine (June 1994 – January 1998)

Conducted experiments (Southern blots, PCR, gel runs, darkroom work, analysis) and maintained the lab (prepared chemical solutions, gels, computer work, cleaning, autoclaving).

- RESEARCH
- ◇ High-performance systems biology. Creation of tools to assist in developing a metabolic model for the green alga *Chlamydomonas reinhardtii*, and designing and engineering a suite of high-performance software for model integration, function and derivative evaluation, and optimization [P3, P4, P5].
  - ◇ Theoretical framework for selection based coarse-grid selection algorithms. Demonstrated the invariance of coarse-grid selection under certain conditions, and used this theoretical work in the creation of the Bucket Sorted Independent Sets (BSIS) selection algorithm [P6].
  - ◇ Parallel coarse-grid selection for algebraic multigrid. Developed algorithms and data structures to yield improvements in operator complexity, convergence factors, and computational efficiency for distributed memory coarse-grid selection algorithms. Implementation was done primarily in C++ using MPI [P1, P2].
  - ◇ Multigrid for electromagnetics. Contributions to multigrid solvers for problems arising from definite and indefinite forms of Maxwell's equations.
  - ◇ Local Fourier Analysis for systems of PDEs. Implemented feature-rich software package to predict convergence factors for multigrid on scalar and system PDE problems.
  - ◇ Computational Modeling of Protein Tertiary Structure. Produced software to assist in clustering protein backbone angle data and software for real-time visualization of solution during solve phase.

- PUBLICATIONS
- [P1] D. M. Alber. Modifying CLJP to select grid hierarchies with lower operator complexities and better performance. *Numer. Linear Algebra Appl.*, **13**:87–104, 2006.
  - [P2] D. M. Alber and L. N. Olson. Parallel coarse grid selection. *Numer. Linear Algebra Appl.*, **14**:611–643, 2007.
  - [P3] C. Chang, D. Alber, P. Graf, K. Kim, and M. Seibert. Addressing unknown constants and metabolic network behaviors through petascale computing: understanding H<sub>2</sub> production in green algae. *J. Phys.: Conf. Ser.*, **78** 012011, 2007.
  - [P4] C. H. Chang, P. Graf, D. M. Alber, K. Kim, G. Murray, M. Posewitz, and M. Seibert. Photons, photosynthesis, and high-performance computing: challenges, progress, and promise of modeling metabolism in green algae. *J. Phys.: Conf. Ser.*, **125** 012048, 2008.
  - [P5] D. M. Alber. SBTools Usage and Development Guide. Manual, <https://outreach.scidac.gov/frs/download.php/368/sbtools-0.5.pdf>, 2010.
  - [P6] D. M. Alber and L. N. Olson. Coarsening invariance and bucket-sorted independent sets for algebraic multigrid. *Electron. Trans. Numer. Anal.*, **37**:367–385, 2010.
  - [P7] M. Lunacek, A. Nag, D. M. Alber, K. Gruchalla, C. H. Chang, and P. A. Graf. Simulation, characterization, and optimization of metabolic models with the High Performance Systems Biology Toolkit. *SIAM J. Sci. Comput.*, **33**:3402–3424, 2011.