

Joshua A. McCoy

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RESEARCH INTERESTS

My research interests reside in resource efficient graphical rendering and grid/parallel scientific computing. In scientific computing, my areas of interest are data mining and representation, Bayesian analysis, and molecular dynamics.

EDUCATION

UC Santa Cruz
Ph.D. program in Computer Science
Santa Cruz, CA
Currently Attending

Earlham College
B.A. in Computer Science
Richmond, IN
May 2004

Earlham College
B.A. in Sociology/Anthropology
Richmond, IN
May 2004

RESEARCH EXPERIENCE

2001-2005

Earlham College Cluster Computing Research Group
<http://cluster.earlham.edu>

Research I have performed with this group revolves around scientific computing and beowulf clusters. Topics include benchmarking and tuning the GROMACS molecular dynamics package, design and implementation of Folding@Clusters (a grid resource sibling of [Folding@Home](#)), Bayesian analysis for the phylogenic reconstruction of DNA/RNA, lowering the latency of the linux kernel v2.6 network stack for TCP/IP-based secure clusters, curriculum for teaching scientific and cluster computing, development of a low cost clusters for pedagogical use, and general cluster system administration. I have been a member of this group since May of 2001 and have served as a full time member since May of 2004.

2004-2005

Habitus - Game Development and Graphics Research Group

My work in this group covers a large selection of topics revolving around game development and current graphic techniques. The focus of this group is to learn and research through creating compelling, substantial, open source video games. My contributions have been writing graphics engines, physical simulation (collision detection, light modelling, etc), software design, and user interaction. I started and have lead this group since February of 2004.

2003-2004

Undergraduate Thesis <http://cs.earlham.edu/~mccoyjo/ndopengl/>

The topic of my undergraduate thesis was the research and implementation of a high dimensional rendering wrapper to OpenGL. The main focus of this project was generalizing the vector mathematics used in 2D and 3D render to be used in any dimension greater than the third.

2002-2004

Pedagogical Tools Group

This group's primary responsibilities are the development and maintenance of the programming tools, software libraries, and other software systems the computer science department uses in teaching programming and other aspects of computer science. I was with this group as a part time work-study position from January of 2002 to May of 2004.

TEACHING EXPERIENCE

Fall 2005

Substitute Instructor: In the absence of the instructor, I have periodically taught the course Programming and Problem Solving. I had full responsibilities including the preparation and grading of lectures, labs, and assignments.

Fall 2004 - Fall 2005

Teaching Assistant: I have been an active teaching assistant for the following courses: Networks and Networking, Database Systems, Principles of Computer Organization, Parallel and Distributed Computation, Operating Systems, and Programming and Problem Solving.

CONFERENCE PRESENTATIONS

Simulations of Interaction Through a Game Model at MidWest Student Sociology Conference, 11-12 April 2003.

High Dimensional Rendering in OpenGL at 2004 Butler Undergraduate Research Conference.

Benchmarking and Tuning the GROMACS Molecular Dynamics Package on Beowulf Clusters at Ohio Linuxfest 2004.

CONFERENCE POSTER PRESENTATIONS

Folding@Clusters: Harnessing Grid-Based Parallel Computing Resources for Molecular Dynamics Simulations at the SIAM 2005 Conference on Computational Science and Engineering.

Calculating $1/\sqrt{x}$ for Molecular Dynamics Packages on Commodity Vector Architectures at the SIAM 2005 Conference on Computational Science and Engineering.

Benchmarking and Tuning the Gromacs Molecular Dynamics Package on Beowulf Clusters at the SIAM 2004 Conference on Parallel Processing for Scientific Computing (this poster was the poster contest winner).

PUBLICATIONS

Charles Peck, Joshua Hursey, Josh McCoy, and Vijay Pande. "Building Internet Distributed Computing applications Using Existing Scientific Cores" *Dr. Dobb's Journal* Volume 378, November 2005.

SOFTWARE

Folding@Clusters <http://cluster.earlham.edu/detail/project/folding-at-clusters/>

Folding@Clusters is an adaptive framework for harnessing low latency parallel compute resources for protein folding research. It combines capability discovery, load balancing, process monitoring, and checkpoint/re-start services to provide a platform for molecular dynamics simulations on a range of grid-based parallel computing resources including clusters, SMP machines, and clusters of SMP machines. The software uses open source building blocks, such as the GROMACS molecular dynamics package and the LAM/MPI communications library, to provide the lowest-level functionality. Building on this foundation we construct a three tier architecture: cluster, node, and science core. This provides a basis on which to abstract the process of performing a molecular dynamics simulation. This includes work unit preparation, distribution, checkpointing, failure recovery, and result aggregation, on a compute resource with arbitrary capabilities (CPU speed, CPU count, memory, etc.).