

# Addam Hardy

Software Engineer

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## Goal

To find a secure position in a small team environment passionate about innovation, communication and test driven development, that is focused on results and progress instead of process. Less a job and more a group of close friends that work well together and are driven to push each other past their limits.

## Education

- **University of Arkansas** Fayetteville, AR  
*B.Sc Computer Science (current), B.Sc Electrical Engineering (current)* 2010 - 2012(projected)
- **Defense Language Institute** Monterey, CA  
*A.Arts Korean Language, Korean Basic Course* 2004-2006

## Skills

- **Development:** C/C++, Python, CUDA, JavaScript, Ruby (Rails), Java, FORTRAN, MATLAB
- **Numerical Analysis:** Optimization, Linear Algebra, ODEs, PDEs, Monte Carlo, Computational Physics, Complex Systems, Iterative Methods, Tomology
- **Computer Science:** Machine Learning, Data Mining, Parallel Programming, Data Structures, Artificial Intelligence, Operating Systems
- Discovering and implementing new ideas. Give me an API and a problem and I will figure it out.
- Diverse background in Math, Computer Science, Physics and Biology allows me to communicate to a wide scientific and general audience and begin contributing to any group immediately.
- I have worked in many places in a myriad of fields. I can readily learn and adapt to a new discipline, area or environment and start pushing real results quickly.

## Research and Work Experience

- **Bloomberg LP** New York, NY  
*Financial Software Development Intern* Summer 2011
  - Developed end-to-end reporting software in C++ and javascript
  - Implemented statistical models to perform forward and backward portfolio analysis
- **DOE Joint Genome Institute (Lawrence Berkeley National Lab)** Walnut Creek, CA  
*Researcher in Analysis Group under Dr. Zhong Wang* Summer 2010
  - Created **open source** genome validation software tool in python and C
  - Used machine learning to mine TBs of genome data efficiently using novel likelihood function
- **Los Alamos National Laboratory** Los Alamos, NM  
*Researcher in Metagenomics Group under Dr. Nick Hengartner* Summer 2009
  - Wrote **open source** alignment algorithm software tool in python, C and CUDA
  - Used statistical models to discover sequence alignments using parallel algorithms on GPUs
- **Oregon State University** Corvallis, OR  
*Research Assistant under Prof. Malgorzata Peszynska and Prof. Rubin Landau* 2005-2008

- Finite element analysis with uncertainty and web-based teaching in **Java**

- **Max Plank Institute for the Physics of Complex Systems**  
*NSF REU Research Assistant under Prof. Steven Tomsovic*
  - Research on extreme value statistics in **MATLAB** and **FORTRAN**

Dresden, Germany  
*Summer 2007*

- **University of California: Davis**  
*NSF REU Research Assistant under Prof. Daniel Cox*
  - Computational biophysics research as applied to protein folding in **Java**

Davis, CA  
*Summer 2006*

## Selected Open Source Projects and Publications ([github.com/addamh](https://github.com/addamh))

- **ALE: Assembly Likelihood Estimator**  
*Probabalistic evaluation of genome assemblies*
  - Uses statistical likelihood function to score and rank genome assemblies
  - Publication being prepared for Genome Research
  - Presented at several conferences including SIAM Scientific Computing
- **Velvetrope**  
*A parallel statistical algorithm for finding homologous regions within sequences*
  - Profiled in DEIXIS Magazine, Publication submitted to BMC Bioinformatics
  - Presented at several conferences including Supercomputing and Q-bio
- **BetaHelix**  
*Computes various statistics about a left or right handed beta helix*
  - Published in Prion: Left handed  $\beta$  helix models for mammalian prion fibrils.

C, Python  
*2010 - Current*

Python, C, CUDA  
*2009 - 2010*

Java  
*2006 - 2007*