

## Objectives

To conduct PhD research in the fields of systems biology, computational biology, and bioinformatics. To model and predict the functions of complex biomolecular systems using novel theoretical approaches. To validate and expand upon models and analyses using quantitative experimental techniques. To develop new methods to acquire and analyze quantitative data from cellular systems.

## Education

**Ph.D., Bioinformatics and Integrative Genomics. (In Progress).** Massachusetts Institute of Technology. Harvard-MIT Division of Health Sciences and Technology.

**Whitaker International Bioengineering Fellow.** University of Cambridge. Cambridge, United Kingdom. 2008-2009. Advisor: Dr. Simon Tavaré.

**B.S., Bioengineering: Bioinformatics.** University of California, San Diego (UCSD). La Jolla, California. 2003-2008. GPA: 3.58.

## Awards

Whitaker International Bioengineering Fellow	2008-2009
NSF Graduate Research Fellowship	2009
Eleanor Roosevelt College at UCSD, Provost Honors	2003-2007
Best Poster, Algorithmic Biology Conference	2006
Pacific Rim Undergraduate Experience (PRIME) Award Recipient	2006
Google Summer of Code Project Showcase	2005
National Merit Commended Scholar	2002

## Publications

- “Product Length, Dye Choice, and Detection Chemistry in the Bead-Emulsion Amplification of Millions of Single DNA Molecules in Parallel.” I. Tiemann-Boege, C. Curtis, D. N. Shinde, **D. B. Goodman**, S. Tavaré, N. Arnheim. *Analytical Chemistry*. 81:5770-5776, 2009
- “Comparative Proteogenomics: Combining Mass Spectrometry and Comparative Genomics to Analyze Multiple Genomes.” N. Gupta, J. Benhamida, V. Bhargava, **D. Goodman**, E. Kain, I. Kerman, N. Nguyen, N. Ollikainen, J. Rodriguez, J. Wang, M. S. Lipton, M. Romine, V. Bafna, R. D. Smith, P. Pevzner. *Genome Res*. 18:1133-1142, 2008
- “Baculovirus Phylogeny Based on Genome Rearrangements.” **D. Goodman**, N. Ollikainen, C. Sholley. *Lecture Notes in Computer Science*, Vol 4751, 69-82. Springer, 2007.
- “Automated Multiplexed Multidensity Microfluidic (M3) Cell Sensing Based on Electrical Gain measurements.” J. Collins, D. Lavigne, Y. Lin, **D. Goodman**, P. Irwan, A. P. Lee. Conference Paper: IEEE EMBS Special Topic Conference on Microtechnologies in Medicine and Biology, May 2005.
- “Nanofluidic channel engineering using laminar flow layer-by-layer deposition of polyelectrolytes.” J. Collins, **D. Goodman**, P. Delhaes, A.P. Lee. Conference Paper: ASME Integrated Nanosystems & Nanotechnology Showcase, September 2004.

## Presentations / Posters

- “Cambridge iBrain: Foundations for an Artificial Nervous System using Self-Organizing Electrical Patterning.” L. Boettger, **D. Goodman**, E. O’Neill, X. Yan. Presentation and Poster. iGEM Jamboree 2008. Cambridge, MA, USA. November 2008
- “Genome Wide Identification of Off-site Protein Targets for Major Pharmaceuticals using Functional Site Similarity and Protein-Ligand Docking.” L. Xie, J. Wang, J. Chung, **D. Goodman**, N. Ollikainen, P. E. Bourne. Presentation. ISMB 2007. Vienna, Austria. July 2007
- “Genome Rearrangements In Baculovirus Genomes.” **D. Goodman**, N. Ollikainen, C. Sholley. Award Winning Poster: Algorithmic Biology 2006. La Jolla, CA, USA, November 2006. November 2006
- “High-Throughput Virtual Screening of a Novel Kinase on the Grid: Homology Modeling and Template-based techniques.” **D. Goodman**, M. Levesque. Presentation. Supercomputing 2006. Tampa Bay, FL, USA, September 2006. September 2006
- “Impedance Based Sensing of Biological Cells in Multiplexed 16 Channel Microwells.” J. Collins, **D. Goodman**, A.P. Lee. LabAutomation 2005. January 2005

## Research Experience

- Whitaker International Bioengineering Fellowship. University of Cambridge, UK. Advised by Dr. Simon Tavaré.** 2008 - Present
- Built microfluidics platform to automate sequential oligo-probe steps in a custom-built flow cell device
  - Developed image analysis software in C++/R/Matlab to analyze terabytes of fluorescent bead image data
  - Developing a novel experimental method for identifying methylation patterns in single cells using emulsion PCR, florescent microscopy, and image analysis
- International Genetically Engineered Machine Competition, University of Cambridge Team. Advised by Drs. Jim Haseloff, Gos Micklem, Jim Ajioka.** 2008
- Led a team of undergraduate engineers, mathematicians, biologists
  - Built a bacterial genetic system from standardized parts
  - Designed a two-component signaling system to produce Turing Patterns
  - Extensive lab work including PCR, microbial culture, DNA manipulation
  - Work was self-directed: students planned research, resources, timeline, methodology, protocols, and budget
- Genome Rearrangement Phylogeny Project. University of California, San Diego. Advised by Dr. Pavel Pevzner.** 2005 -2008
- Wrote software to determine phylogeny of small genomes based on gene order
  - Presented poster at Algorithmic Biology 2006
  - Published work at RECOMB 2007
- De Novo Mass Spectra Linker Project. University of California, San Diego. Advised by Drs. Nuno Bandiera and Pavel Pevzner. (2007 – Present)** 2007 - 2008
- Developed software to integrate and validate mass spectrometry data
  - Used software to increase resolution of de novo mass spectrometry
  - Used C++ extensively

2007-2008

**Research Consortium in Comparative Proteomics. University of California, San Diego. Advised by Drs. Pavel Pevzner and Vineet Bafna.**

- Developed software tools to validate genome annotations via comparative genomics and mass spectrometry data
- Published work in Genome Research

**Protein Functional Site Homology Project. Protein Data Bank. Advised by Drs. Phillip E. Bourne and Lei Xie.** 2005-2007

- Functional site characterization/analysis, mining data from Protein Data Bank
- Used protein docking software (DOCK, Autodock) to identify binding profiles
- Profiles analyzed to find potential off-site targets for major pharmaceuticals
- Presented work at ISMB 2007 in Vienna, Austria

**UCSD Bioeng. Honors Undergraduate Research Project. University of California, San Diego. Advised by Drs. Shankar Subramaniam and Brian Saunders.** 2004-2007

- Wrote software tools that gather gene homology data into a unified schema
- Wrote a web interface so that others could use this resource
- Used Oracle, Perl extensively

**Pacific Rim Undergraduate Experience (PRIME). Osaka University, Osaka, Japan. Advised by Drs. Shinji Shimojo and Phillip E. Bourne.** 2006

- Used automated docking software (DOCK) in a Grid environment
- Performed virtual ligand screening on a novel human kinase target
- Developed Grid-aware software to interface with DOCK
- Presented research at Supercomputing 2006

**BioMiNT Laboratory. University of California, Irvine. Advised by Dr. Abraham P. Lee.** 2004-2006

- Conducted cell-sensing experiments using microfluidic devices
- Designed and fabricated microfluidics devices in a cleanroom environment
- Assembled hardware for microfluidic flow control
- Wrote software for microfluidic device data acquisition
- Used some C++, Labview extensively
- Published work in two conference proceedings

**Google Summer of Code. Advised by Drs. Shankar Subramaniam and Brian Saunders.** 2005

- Created an online searchable database of gene and protein homology data
- Released the source code on the open-source community SourceForge
- Demo presented at OSCON 2005
- Used Perl extensively

## Publicly Available Software

### MULGOR (MULTiple Genome Order)

Automated and comprehensive tool to generate gene-order-based phylogeny of small genomes. Written in Perl and C. Publicly available at <http://realm.sdsc.edu/MULGOR>.

### Gene Homology Database (GHDB)

Open Database Schema to unify several disparate gene homology format. Includes web tools to display and search for data, and perform multiple alignments. Written in Perl. Publicly available at <http://sourceforge.net/projects/genehomology>.

**DOCK BioGrid Tools (DBGT)**

Unix command-line tools to distribute and monitor DOCK jobs in a Grid environment. Written in Perl, Bash, and C++. Source available on request.

**Activities / Organizations / Teaching****Salk Mobile Science Laboratory.**

2007-2008

- Visited local middle school science classes, grades 6 to 8
- Taught students about genetics, DNA, and biotechnology

**Biology Teaching Assistant. University of California, San Diego.**

2007

- Taught groups of 20-30 students for upper-div Cell Bio course
- Held office hours and review sessions for student questions

**Tau Beta Pi Engineering Honors Society.**

2005 - Present

- Weekly Elementary School Outreach
- Tutoring Fellow Engineering Students in Math/Science

**UCSD Biomedical Engineering Society.**

2005-2008

- Organized Student Research Presentations
- Bioinformatics Liason 2006-2008

**Relevant Coursework****Bioinformatics**

Applied Genomic Technologies  
 Biological Data & Analysis  
 Biological Databases  
 Computational Molecular Biology  
 Molecular Sequence Analysis  
 Systems Biology

**Biology**

Biochemical Techniques  
 Cell Biology  
 Cellular Neurobiology  
 Evolution  
 Metabolic Biochemistry  
 Molecular Biology  
 Organismic & Evol. Biology  
 Protein Evolution  
 Protein Folding & Human Disease  
 Recombinant DNA Techniques  
 Functional Genomics (HMS)  
 Population Genetics & Genomics (MIT)

**Computer Science**

Advanced Data Structures  
 Algorithm & Systems Analysis  
 Data Structures and OO Design  
 Design & Analysis of Algorithms  
 Intro to A.I.: Statistical Approaches  
 Neural Networks  
 Object Oriented Design  
 Computational Systems Biology (MIT)  
 Machine Learning (MIT)

**Physics/Chemistry**

Organic Chemistry Laboratory  
 Organic Chemistry (2 quarters)  
 Statistical & Thermal Physics  
 Molecular Biophysics

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**Streaming presentations, papers, source code, and more information about past research can be found at my website: <http://www.dbgoodman.com>**