

# Christopher (Chris) D. Lasher

chris.lasher@gmail.com  
http://www.gotgenes.com/

843 Valley Ave, Solana Beach, CA 92075  
+1-540-466-4007

## EDUCATION

**Ph.D., Genetics, Bioinformatics, and Computational Biology** August 2006 – September 2011  
Genetics, Bioinformatics, and Computational Biology Program of Blacksburg, Virginia, USA  
Virginia Tech

- ◇ Advisors: Prof. T. M. Murali (Dept. of Computer Science) and Prof. Padma Rajagopalan (Dept. of Chemical Engineering)
- ◇ Dissertation topic: Discovering contextual connections between biological processes using high-throughput gene expression data and interaction networks

**B.S. in Biology, *magna cum laude*** August 1999 – May 2003  
University of Georgia Athens, GA, USA

- ◇ Honors Thesis: “Using seeded clustering to append EST contigs while preserving UniGene sets”

## PUBLICATIONS

**Christopher D. Lasher**, Padmavathy Rajagopalan, and T. M. Murali. (2013) “Summarizing cellular responses as biological process networks.” *BMC Systems Biology* 7, 68: .

**Christopher D. Lasher**, Padmavathy Rajagopalan, and T. M. Murali. (2011) “Discovering Networks of Perturbed Biological Processes in Hepatocyte Cultures.” *PLoS ONE* 6, 1: e15247.

Yeonhee Kim, **Christopher D. Lasher**, Logan M. Milford, T. M. Murali, and Padmavathy Rajagopalan. (2010) “A Comparative Study of Genome-Wide Transcriptional Profiles of Primary Hepatocytes in Collagen Sandwich and Monolayer Cultures.” *Tissue Engineering Part C: Methods* 16, 6: 1449–1460.

**Christopher D. Lasher**, Christopher L. Poirel, and T. M. Murali. (2010) “Cellular Response Networks.” In *Problem Solving Handbook for Computational Biology and Bioinformatics*. Edited by Lenwood S. Heath and Naren Ramakrishnan. Springer-Verlag. 233–252.

**Chris Lasher**, Glen Dyszynski, Karin Everett, Jennifer Edmonds, Wenying Ye, Wade Sheldon, Shiyao Wang, Samantha B. Joye, Mary Ann Moran and William B. Whitman. (2009) “The Diverse Bacterial Community in Intertidal, Anaerobic Sediments at Sapelo Island, Georgia.” *Microbial Ecology* 58, 2: 244–261.

## CONFERENCE PRESENTATIONS

Yeonhee Kim, **Christopher D. Lasher**, Logan M. Milford, T. M. Murali, and Padmavathy Rajagopalan. (2010) “A Comprehensive Profiling of Genome-Wide Transcriptional Programs of Primary Hepatocytes *in Vitro* Cultures.” *American Institute of Chemical Engineers Annual Meeting*. Salt Lake City, Utah, USA.

**Christopher D. Lasher**, Yeonhee Kim, T. M. Murali, and Padmavathy Rajagopalan. (2010) “Temporal Cascades of Perturbed Biological Processes in Engineered Liver Mimics.” *Biomedical Engineering Society Annual Meeting*. Austin, Texas, USA.

## CAREER

### **Bioinformatics Analyst and Software Engineer**

September 2012 – present

5AM Solutions, Inc.

Rockville, MD, USA

Applying expertise in Python programming and bioinformatics to construct robust pipelines and custom validation software for our clients following Agile methodology.

- ◇ Refactored massively-multiplex, high-throughput targeted sequencing assay pipeline from BASH and Perl scripts into a robust, modularized Python 3 package interfacing with Oracle, MySQL, SQLite3, and tabix format databases.
- ◇ Maintained and improved efficiency of pipelines, deployed on Amazon Web Services (AWS), including EC2, S3, and RDS services.
- ◇ Architected and implemented a RESTful API and backend in Django and Tastypie powering JavaScript-based visualization tool for a biotech startup augmenting next generation sequencing technologies.
- ◇ Crafted an integration test suite and fixed deep-seated bugs in a legacy C++ codebase responsible for calling and annotating variants for a client company specializing in human genome sequencing.
- ◇ Constructed a software pipeline in Python to model next generation sequencing data for validating software by a large biotech company for identifying clinically relevant variants.

### **IRTA Postdoctoral Fellow**

January 2012 – August 2012

NIH / NLM / NCBI

Bethesda, MD, USA

As an Intramural Research Training Award (IRTA) fellow, developed computational methods for discovering architectures of mouse and human regulatory elements through the integration of sequence and epigenetic data.

- ◇ Constructed pipelines in Python to identify transcription factor binding sites in putative enhancer regions identified through ChIP-seq data.
- ◇ Implemented hidden Markov models for sequence feature detection in Python and Cython.

### **Graduate Research Assistant**

January 2009 – September 2011

Murali and Rajagopalan groups, Virginia Tech

Blacksburg, VA, USA

Produced novel computational methods for quickly summarizing genome wide changes in gene expression.

- ◇ Developed algorithms to summarize significant perturbations in biological networks by integrating gene expression, gene interaction, and gene annotation data; implemented algorithms in Python using NumPy, SciPy and NetworkX.
- ◇ Produced visualizations of biological networks and relevant data using NetworkX, Graphviz, and matplotlib
- ◇ Retrieved gene expression data sets and performed differential expression analyses in R using bioconductor.
- ◇ Gained practical experience with computational techniques such as Markov chain Monte Carlo (MCMC), Bayesian networks, empirical distribution construction, and multiple testing correction.
- ◇ Collaborated with chemical and tissue engineers in analyzing time series of genome-wide gene expression data from hepatocyte tissue cultures used for drug metabolism and toxicology studies.

### **Graduate Research Assistant**

August 2006 – December 2008

Virginia Bioinformatics Institute

Blacksburg, VA, USA

Investigated methods to elucidate the complicated evolutionary histories of the primary and secondary chromosomes and plasmids of prokaryotes in the Rhizobiaceae family.

- ◇ Prototyped graphical models to identify conserved blocks of orthologous genes within genomes exposed to frequent horizontal gene transfer events, and produced implementations in Python using NetworkX.

- ◇ Produced plots summarizing genomic features using Python with matplotlib.

**Research Technician**

August 2003 – July 2006

University of Georgia Depts. of Marine Science and Microbiology,  
Sapelo Island Microbial Observatory (SIMO)

Athens, GA, USA

Performed field and wet lab work and bioinformatics analysis for the Sapelo Island Microbial Observatory.

- ◇ Surveyed bacterial community composition and flux in one of the few remaining undisturbed coastal salt marshes in the USA.
- ◇ Collected samples from field quarterly and performed DNA extractions.
- ◇ Developed phylogenetic and rarefaction analysis pipelines in Perl and Python.

**Undergraduate Student Researcher**

June 2002 – May 2003

Pratt Laboratory for Genomics and Bioinformatics, University of  
Georgia

Athens, GA, USA

Assisted wet lab and bioinformatics pipelines for the sorghum expressed sequence tags (ESTs) project.

- ◇ Performed plasmid extraction and preparation for Sanger sequencing of ESTs.
- ◇ Prototyped algorithms in Perl to accelerate expressed sequence tag clustering in a bioinformatics pipeline.

## TECHNOLOGY EXPERIENCE

**Languages:** Python (primary) (Python 2 and Python 3), Perl, R, Ruby, SQL, C, C++, HTML, CSS, JavaScript

**Python Libraries:** Python standard library (including collections, functools, itertools, multiprocessing), NetworkX, NumPy/SciPy, matplotlib, Biopython, Cython, Django

**Django Libraries:** South (DB migrations), Tastypie (RESTful APIs), factory boy (fixtures replacement), django-bootstrap-toolkit

**R Libraries:** Bioconductor

**Databases:** PostgreSQL, MySQL, SQLite3, OracleDB (limited)

**Documentation:** Sphinx Docs,  $\LaTeX$

**Version Control Systems:** Git (preferred), Subversion, Bazaar VCS, Mercurial

**Systems Administration:** Apache, Nginx, gunicorn, upstart

**Operating Systems:** OS X, Ubuntu GNU/Linux, CentOS