Christopher (Chris) D. Lasher

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CAREER

Bioinformatics Analyst and Software Engineer   September 2012 – present
5AM Solutions, Inc.   Rockville, MD, USA
Applying expertise in software engineering, Python programming, and bioinformatics to construct robust
pipelines and custom validation software for our clients following Agile methodology.

◇ Technical lead on public-facing next-generation sequencing assay design pipeline for international biotech
firm, including requirements gathering, technical risk management, architectural oversight, and personnel
training in software design principles.

◇ 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,   Athens, GA, USA
Sapelo Island Microbial Observatory (SIMO)

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   Athens, GA, USA
Georgia

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, Cython, C, C++, R, Ruby, SQL, HTML, CSS, JavaScript

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

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

R Libraries: Bioconductor

Databases: PostgreSQL, MySQL, OracleDB, SQLite3

Documentation: Sphinx Docs, LaTeX

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

Systems Administration: Apache, Nginx, gunicorn, upstart

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

Additional Tools: Jenkins CI, Travis CI, JIRA, Stash

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"

CERTIFICATIONS AND ACCOMPLISHMENTS

- ◇ Software Carpentry Bootcamp Instructor (2013)
- ◇ Certified ScrumMaster (CSM) (2012)
- ◇ Top 5% Stack Overflow Reputation

SELECTED 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.

"Brick walls are there for a reason: they let us prove how badly we want things." – Prof. Randy Pausch

"`import antigravity`" – Randall Munroe