Jeremy Gresham

Phone	(336) 972-6733
Email	greshjs@gmail.com
Github	https://github.com/IHautaI
LinkedIn	https://www.linkedin.com/in/JSGresham
Website	https://ihautai.github.io

Technical Skills

- Python programming, data analysis with Pandas, machine learning with Scikit-Learn, Django, django-rest-framework
- C++11/14/17 programming, STL and Boost
- Scala programming, including Akka framework
- Experience with Amazon Web Services EC2, S3, Glacier
- Experience with container technologies including Docker and Singularity
- R programming
- Experience with JavaScript, including D3, TopoJSON, GeoJSON/shapefiles, Node.js with Express.js and Jade/Pug
- Technical Writing
- Proficient with LaTeX, a technical typesetting language
- Proficient with Maple and Matlab, mathematics and modeling software
- 2D/3D CAD/CAM, Blender
- Comfortable with the GNU/Linux, Mac and Windows families of operating systems
- Basic electronics, soldering, experience with Arduino and BeagleBone Black

Education

Master of Science (MS), Mathematics   2011
University of North Carolina Wilmington

Bachelor of Science (BS), Mathematics Minor in Physics   2007
North Carolina State University

Employment

Duke Cancer Institute, Bioinformatics Shared Resource   Durham, NC
Scientific Programmer   *November 2015 - Present*

- Developed reproducible pipelines for preprocessing and analysis of Next-Generation Sequencing data from a variety of platforms
- Adapted preprocessing and analysis pipelines for use on Amazon Web Services using Docker and Singularity containers
- Developed command-line tools for creation of reproducible pipelines using Docker and Singularity image metadata

- Collaboration with cancer researchers and statisticians including:

  - Contributed to bcSeq software package for fast sequence alignment for high-throughput shRNA and CRISPR Screens
  - Developing (in progress) C++ software and simulations for Compmix, a new statistical method for calling mutations from cell-free DNA libraries that does not require a paired germline control

- Provided independent validation of analysis results generated by colleagues for various research groups

- Programmed in a variety of environments and languages including Python, Scala, C/C++, R, Bash

ShopBot Tools, Inc. Durham, NC
Support Technician *November 2013 - May 2015*

- Provided technical support for hardware, software, and mechanical aspects of CNC tools for ShopBot customers

- Collected information about customer issues with construction and installation, operation, configuration, customization, and usage of tools and software. Identify problems, investigate causes, generate tests, and analyze test results. Research technical issues to resolve complex issues. Provide specific instructions and guidance to customers to troubleshoot and resolve issues.

- Was responsible for supporting a range of technical issues, including machine repair, parts replacement, wiring instructions, general tool use, calibration, tool path generation (2D/3D CAD/CAM), coding, and integration into manufacturing processes

- Tracked new product development to prepare for new systems, tools and accessories and understand how they function and how they will be integrated with existing software.

- Assisted in general software testing and suggest improvements to user interface

Wake Forest Baptist Medical Center Winston-Salem, NC
WakeOne Credential Trainer *June-October, 2012*

- Facilitated specialized one-day training sessions for physicians and surgeons to orient them in the use of a new heavily customized Electronic Medical Record (EMR), focusing on accurate documentation of patient visits and surgical consultations

- Provided in-person follow-up support to medical teams upon system implementation

- Analyzed system roll-out and implementation and provided recommendations to programmers regarding design issues and bugs

Publications

As Co-Author:

- Lin J, Gresham J, Xie J and Owzar K (2017). bcSeq: Fast Sequence Alignment for High-Throughput shRNA and CRISPR Screens. R package version 1.0.1, https://github.com/jl354/bcSeq.

- Thomas Longo, Kathleen F. McGinley, Jennifer A. Freedman, Wiguins Etienne, Yuan Wu, Alexander Sibley, Kouros Owzar, Jeremy Gresham, Christopher Moy, Stephen Szabo, Joel Greshock, Hui Zhou, Yuchen Bai, Brant A. Inman, Targeted Exome Sequencing of the Cancer Genome in Patients with Very High-risk Bladder Cancer, European Urology, Volume 70, Issue 5, 2016, Pages 714-717, ISSN 0302-2838, https://doi.org/10.1016/j.eururo.2016.07.049. (http://www.sciencedirect.com/science/article/pii/S0302283816304638)

Professional Training

The Iron Yard   Durham, NC
Python Programming   May 2015 - July 2015

Final Project: 'Moovn On' webapp
Description of Responsibilities:
Heroku management and deployment, creation of a django back-end with read-only RESTful API, data gathering, data cleaning, data visualization with D3.js, map making and bubble-charting
Technologies Used:
Python3, Django, django-rest-framework, GIS data from Census.gov and Zillow, ogr2ogr, GeoJSON, TopoJSON, D3.js, JavaScript, jQuery, HTML, Heroku, PostgreSQL, SVG