Keenan Graham

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EXPERIENCE

Department of Genetics, Stanford University School of Medicine —
Principal Investigator: Mike Cherry, Ph.D.

May 2017 - Present

- **Develop software** and wrangle data at the **ENCODE Data Coordination Center** including:
    - *Backend.* Develop and maintain the ENCODE Portal's (https://www.encodeproject.org) Python/Pyramid application, **following proper Git workflows, Jira Sprints, unit and integration tests, and code reviews.**
    - *Backend.* **Troubleshoot failures** and upgrade deployment environment (Ubuntu, Postgres, Elasticsearch). Integrate database migration tool. **Write documentation for new features.**
    - *Frontend.* **Design and implement QANCODE**, an automated image-based comparison tool for regression testing in the browser.
    - *Pipelines.* **Modify genomic analysis pipeline accessioning code** to support wider variety of assay types. Introduce documentation tools to pipeline group.
    - *Pipelines.* Develop a general quality metric reporting tool that **performs complex data scraping and manipulation** and creates reproducibly formatted Google Sheets for use by consortium working groups.
    - *External scripts.* Maintain and update *pyencoded-tools*, scripts used by wranglers to submit and modify data, **in accordance with wranglers' specification.**
- **Design with lead data wranglers software solutions for modeling ENCODE objects**, controlling status, and synchronizing datastores in AWS and Google Cloud. Implement new features to significantly lower AWS storage costs.
- Act as resource for group members on backend permissions and views, metadata questions, Postgresql database inquiries, and DNAnexus failures. **Guide new group members in setting up development environment.**
- Analyze biosample, experiment, file and quality metric metadata.
- Present tutorial on JSON objects and interaction with the portal.

Department of Microbiology and Parasitology, Genova Diagnostics — *Laboratory Director: James Kelton, Ph.D.*

2015 - April 2017

- Write, revise, and execute custom automation scripts to extract data from the laboratory information system for use in research projects and

TECHNICAL SKILLS

Data analysis and software development **in Python** and JavaScript

Custom dashboards with **D3.js**, HTML, CSS, Jupyter Notebooks, and Markdown

Database creation and **querying in SQL and Elasticsearch**

Web applications with Pyramid/Flask/Django, React

Git, Bash, AWS, Emacs

LABORATORY SKILLS

Diagnostic parasitology and microscopy

Bacterial culture and antibiotic sensitivity assays

MALDI-TOF mass spectrometry

Western blot

PCR and DNA sequencing

INTERESTS

Bioinformatics

Hierarchical **Bayesian analysis and statistical modelling**

Interactive data visualization

Machine/deep learning

laboratory monitoring including:

- ○ All parasitology results from 2014 and 2015 (over 120,000 samples) and patient demographics (age, gender, location)
- ○ All negative parasitology results since 2001
- ○ All *Clostridium difficile* results since 2010
- Clean, transform, calculate summary statistics, and **perform complex analysis on data with Python** and Jupyter notebook.
- Create publication-quality visualizations and reports to share with supervisors and display in the laboratory.
- Implement classical statistical hypothesis tests and Bayesian analysis to answer epidemiological questions.
- Liaise with IT Department to create custom SQL queries of the backend database in order to monitor the daily input and output of the laboratory.
- **Build daily parasitology monitoring tools** and interactive, web-ready visualizations in D3.js, JavaScript, HTML, and CSS.

2013 - April 2017

- Examine via light microscopy trichrome-stained slides and iodine-stained concentrated wet mount preparations in order to **identify intestinal protozoa and parasitic helminths/ova in patient samples submitted for clinical diagnostics.**
- Complete >20 hours of continuing education per year and participate quarterly in College of American Pathologists proficiency testing and in-house quality assurance.
- Cross-train in bacteriology methods of sterile plating, Vitek 2 identification and antibiotic sensitivity assays, and MALDI-TOF mass spectrometry.
- **Have resulted more than 20,000 patient samples.**

Department of Clinical Genetics, Fullerton Genetics Center, Mission Hospital — *Laboratory Director: Jack Tarleton, Ph.D., FACMG*

2013 **(Volunteer Project)**

- Identify novel mutations in the *CLCN1* gene leading to myotonia congenita.
- Converse regularly with the laboratory director on general topics of clinical genetics and NGS technology and specific topics of project-related data and goals.
- **Correct inconsistencies between lookup table of point mutations and raw DNA exon sequences of the gene.**

Department of Epidemiology, UNC Chapel Hill Gillings School of Global Public Health — *Principal Investigator: Carla Cerami Hand, M.D./Ph.D.*

2010 - 2011

- Determine parasitemia in blood samples infected with the malaria parasite *Plasmodium falciparum.*
- Isolate the non-erythropoietic, tissue-protective erythropoietin heteroreceptor.
- Collaborate and attend laboratory meetings with practicing research scientists, Ph.D. candidates, and laboratory technicians.
- **Senior research thesis based on experiments performed in this laboratory.**

EDUCATION

University of North Carolina at Chapel Hill, Chapel Hill, NC —
Bachelor of Science in Biology

2011

Coursework in the Biology of Blood Diseases, Molecular Biology, Genetics, Organic Chemistry, Biochemistry, Modern Physics, Ordinary Differential Equations, Linear Algebra, Advanced Mathematical Methods.

RECENT SOFTWARE PROJECTS

HapPyNet — *Haplotype-block-based dimensionality reduction for complex variant-disease associations.*

NCBI-UCSC Genomics Hackathon, Santa Cruz, CA, April 2-4, 2018.

More at https://github.com/NCBI-Hackathons/HapPyNet

Biosynthetic Gene Cluster Data and k-Mer Search Portal — *Applying k-mers to find similar DNA sequences in the Minimum Information about a Biosynthetic Gene cluster (MIBiG) data repository.*

October 2016.

More at https://biosynthetic-kmers.herokuapp.com

The Epidemiology of Intestinal Parasites — *The Prevalence of Protozoal Infection in 120,000+ Clinical Fecal Samples, United States, United Kingdom, Northern Europe, Canada, Australia.*

Genova Diagnostics, Asheville, NC, 2014- 2015.

More at http://keenangraham.github.io/project/project.html