Amy Paguirigan

Seattle, WA • amypag.com

I have led and played consulting or support roles on a variety of data-intensive research projects mainly in the cancer genomics space. I most enjoy the interplay between data, analysis and technology. I have found myself drawn to exploring the systems and approaches to making science happen at a pace consistent with the evolution of data, while balancing investments in laying "track" as projects and programs develop. Roles of interest to me would touch on these realms of my expertise, including addressing overall data and analysis strategy and integration of supportive technologies to facilitate a wider array of reproducible biomedical research that makes a difference.

SKILLS

Experimental: single cell genomics, targeted/exome/genome sequencing, RNA sequencing, clinical datasets, data integration, flow cytometry, tissue culture.
Computational: GitHub, R, Unix/Linux, Docker, WDL, SLURM, AWS, Shiny, REDCap, Python, REST API
General: grant writing, publication writing, strategic planning, project management, experimental design, data analysis, personnel management and mentoring

WORK EXPERIENCE

SENIOR STAFF SCIENTIST **10/2016 – present**
Fred Hutchinson Cancer Research Center (Seattle, WA)

- Lead a research group using microfluidic device development and bioinformatic workflow design/optimization for single cell genotyping as well as bulk intratumoral genetic heterogeneity analyses (targeted DNA sequencing up to exome level); developed pipelines for image analysis in R.
- Received a K01 award (2015-2021) to support additional training to develop and improve ability to effectively manage, manipulate and analyze big datasets with a primary focus on genomics and bioinformatics.
- Lead creation and evolution of sciwiki.fredhutch.org, a Biomedical Data Science oriented Fred Hutch documentation site that is developed by collaborating with Fred Hutch researchers to develop and review content.
- Lead and developed the Translational Genomics Repository, a cross-divisional, collaborative data management and analysis system supporting ongoing translational genomics research at the Fred Hutch. This work focuses on the use of strategic on-prem and cloud (AWS/Google) based data storage, harmonized collection of associated clinical and scientific metadata across groups, and the use of workflow managers (Cromwell/Nextflow) plus containerization for reproducible bioinformatic analyses (WDL) using both on-prem (SLURM) and cloud (AWS Batch) based computing resources.
- Built R packages and R Shiny applications facilitating expert/non-expert use of compute resources via workflow manager (Cromwell) API as well as straightforward access to processed datasets for analysis. Supported training and use of python for supporting infrastructure and staff interactions with AWS from graduate students to bioinformatic analyst/staff scientist use.
- Created a data management structure that supported cloud-based (primarily AWS S3) genomic data storage (including indexing and tagging of related datasets) of 1500+ research datasets and managed the associated clinical, experimental and laboratory metadata (including ontology development and harmonization across projects) across 8 collaborative projects and across 5 investigators.

DATA STRATEGIST **09/2016 – 02/2018**
Fred Hutchinson Cancer Research Center (Seattle, WA)

- Served as an advisor regarding institutional data strategy with a focus on genomics data, primarily via the evaluation of multiple solutions for deploying bioinformatic workflows to cloud based computing resources, including the evaluation of multiple workflow manager software options in conjunction with Fred Hutch IT.

STAFF SCIENTIST **11/2013 - 10/2016**

Fred Hutchinson Cancer Research Center (Seattle, WA)

- Lead and performed laboratory and computational research into the integration of novel biotechnological techniques for single cell analysis and large scale bulk sequencing to clinical studies of clonal evolution in leukemia.
- Generated new grant applications and publication of work performed for several types of funding agencies (NIH, private nonprofit organizations, private corporations). Received two NIH 5 year R01 grants (one $3.4M, one $6M), for single cell analysis technique development and multi-modal data analysis, as well as many smaller pilot projects.
- Managed a 3-4 person team of laboratory and computational based staff as well as facilitated multiple collaborations with CLIA laboratories as well as microfluidics research labs. Mentored multiple short term and full time staff members in developing requisite data intensive skills such as R, python, git/GitHub and containerization/Docker usage.

POSTDOCTORAL RESEARCHER **06/2008 – 10/2013**

Fred Hutchinson Cancer Research Center (Seattle, WA)

- Optimized and validated a range of fundamental protocols for use with single cells after such as multiplexed QPCR and genotyping to accurately study multiple aspects of cellular function in individual cells concurrently. Developed and applied microfluidic devices for handling and isolating single cells or microvolume PCR reactions. Interfaced with CLIA laboratory to optimize approaches such that they could be applied to clinical specimens.
- Skills included: molecular biology laboratory techniques, qPCR/digital PCR/highly multiplexed PCR, next generation sequencing (primarily Illumina), tissue culture, laboratory material and personnel management, project management, grant writing, project planning.

GRADUATE FELLOW **05/2003 – 05/2008**

University of Wisconsin (Madison, WI)

- Adapted Western blotting techniques to quantify protein expression and quantify cellular stress responses (in-cell Western) in microfluidic cultures via in situ infrared and visible antibody imaging.
- Developed a technique for fabricating biocompatible microfluidic devices based on micromolding of enzymatically crosslinked extracellular matrix materials; natural polymer chemistry for biocompatibility; PDMS microdevice fabrication and design.
- Developed a mathematical model (via MATLAB) of stem cell control mechanisms in normal and preneoplastic mammary epithelia. Analyzed effects of different potential methods of stem and progenitor cell regulation on the overall population demographic.
- Skills included: Multicolor confocal imaging, multicolor laser scanner analysis, microfabrication, Western blotting, tissue culture, primary cell culture, experimental design, statistical analysis.

DESIGN ENGINEER INTERN **04/2001 – 05/2003**

iCyt Visionary Bioscience (Champaign, IL)

- Worked as a design engineer on the design of prototype flow cytometers and assisted in development and preliminary marketing of customized flow cytometers for use in industry, primarily for large agribusiness organizations.

EDUCATION **Academic Publications (available via NCBI MyBibliography)**

Doctor of Philosophy in Biomedical Engineering **2008**

University of Wisconsin (Madison, WI); Concentration: Microfluidic System Design, Optimization of Biological Assays, Cancer Biology

Master of Science in Biomedical Engineering **2005**

University of Wisconsin (Madison, WI); Concentration: Modeling of Dynamic Biological Systems, Biopolymer/Polymer Science

Bachelor of Science in Mechanical Engineering **2003**

University of Illinois (Urbana, IL); Concentration: Flow Cytometry, Biofluid Dynamics, Microhemodynamics

Bachelor of Science in Biology **2003**

University of Illinois (Urbana, IL); Concentration: Bioengineering and Biophysics