KELLY A. MCGLYNN

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TECHNICAL SKILLS

Data Science

Programming Languages	Python, R
Python Packages	pandas, numpy, scikit-learn, seaborn, requests, beautifulsoup, sqlalchemy, tensorflow (basic)
Techniques	Data cleaning, web scraping, machine learning classification models (logistic regression, random forest)
Tools	PyCharm, Git, Jupyter, R shiny, Flask (Python + HTML app development)

Biology & Biochemistry

Disease area expertise	Oncology (leukemia), hematology, epigenetics
Biochemistry & Biological Software	PyMOL (protein structure modeling), SWISS-MODEL, DNA/cloning software (Snapgene, SeqBuilder). Familiar with biological databases such as TCGA and ENCODE.
Wet-lab skills	7 years molecular biology and cloning experience, mutagenesis, CRISPR-Cas9. Mammalian cell culture and functional assays, Western blot, enzyme activity assays. Mouse models of leukemia, multicolor flow cytometry.

EDUCATION

2018 **Ph.D.**, Pharmacology, *University of Rochester Medical Center, Rochester, NY*
2012 **B.S.**, Molecular Biology, *University of Wisconsin – La Crosse, La Crosse, WI*

EXPERIENCE

2020 – Present | **Insight Health Data Science Fellow**
Insight Data Science, Boston, MA

- Created "AdhereID," a tool for doctors to predict patient non-adherence to prescription medications.
- Collected and cleaned a survey dataset on medication adherence, and webscraped a dataset of self-reported medication reviews; evaluated machine learning models using scikit-learn and implemented a binary logistic regression model for classifying patient medication adherence as high-risk or low-risk.
- Implemented and deployed a web app for AdhereID using Flask and AWS EC2 (*adhere-id.com*).

2019 – 2020 | **Postdoctoral Researcher**
Wilmot Cancer Center, University of Rochester Medical Center, Rochester, NY

- Designed a single-cell RNA sequencing experiment and prepared cell samples, generating 200 GB (~1.1 billion reads) of high-quality sequencing data which can be used to investigate single-cell differences in gene expression during the cellular transition from a normal to invasive state (not involved in NGS data analysis)

2012 – 2018 | **Ph.D. Student**
University of Rochester Medical Center, Rochester, NY

- Independently wrote a NIH National Cancer Institute (NCI) fellowship grant to support graduate research, securing a 3-year, $130,000 grant, and submitted annual progress reports to the NIH. Trained 12 undergraduate and graduate students in molecular lab techniques.
- Designed, cloned and contributed 7 recombinant DNA plasmids to the global plasmid repository Addgene, which have been requested 50+ times and shipped to labs around the world.

Graduate Research Projects:

EVI1 interacts with the SWI/SNF subunit BAF57 in acute leukemia.

- Developed a novel epitope-tagged leukemic mouse model overexpressing PRDM3/EVI1. Performed serial bone marrow transplantation into irradiated recipient mice to expand leukemic

cells. Harvested spleen tissue from transplant recipient mice to perform epitope tag pulldowns and mass spectrometry analysis.
- Identified a novel protein-protein interaction between EVI1 and the SWI/SNF chromatin remodeling complex in leukemic tissue, and confirmed the interaction via co-IP in multiple cell types.
- Employed ChIP-qPCR to confirm novel co-localization between EVI1 and the SWI/SNF chromatin remodeling complex.

***Prdm3* and *Prdm16* cooperatively maintain hematopoiesis with dependence on the PR domain**
- Initiated project to generate and characterize a novel mouse model containing tamoxifen-inducible double knockout of two transcription factor genes involved in hematopoiesis, *Prdm3* and *Prdm16*.
- Coordinated data collection in collaboration with other team members to characterize the bone marrow failure phenotype of double knockout mice.
- Established a cell culture functional assay (soft agar colony formation assay) to demonstrate that addback of wild-type *Prdm3* or *Prdm16*, but not *Prdm3* with specific point mutations in its putative enzymatic domain, rescues the phenotype.
- Performed *in silico* structural analysis of the putative enzymatic domain, examining evolutionary conservation in the binding pockets, predicted catalytic residues, and potential consequences of our specific addback point mutations on PRDM3's ligand binding sites.

[Collaboration project] **Analysis of AmpD enzyme and Omp36 porin mutations in clinical outbreak strains of carbapenem-resistant *Enterobacter aerogenes***
- Performed *in silico* structural analysis (PyMOL) of antibiotic importer proteins with clinical strain mutations to predict the potential functional significance of point mutations for bacterial antibiotic resistance.

DATA SCIENCE PROJECTS

Sources of the restriction enzymes used in molecular biology: an exploration of bacterial and environmental sample diversity. mcglynnk.shinyapps.io/rebase_shiny/ [2019]
- Used BeautifulSoup to collect restriction enzyme data from New England Biolabs' public database, added additional data to the table by querying a bacterial metadata database (BacDive API)
- Utilized leaflet in R to map bacterial isolation sources, and overlayed data on bacterial growth temperature, research publications per country, and global volcanic activity. and extracted insights on environmental sample sources through text mining and natural language processing (NLP).
- Extracted insights on most common environmental sample sources through text mining and natural language processing (NLP) via the tidytext and topicmodels packages, and deployed the project to a Shiny web app as a fun, exploratory tool for molecular biologists.

PUBLICATIONS AND PRESENTATIONS

Malek, A., McGlynn, K., Taffner, S., Fine, L., Tesini, B., Wang, J., Mostafa, H., Petry, S., Perkins, A., Graman, P., *et al*. (2019). Next-Generation-Sequencing-Based Hospital Outbreak Investigation Yields Insight into Klebsiella aerogenes Population Structure and Determinants of Carbapenem Resistance and Pathogenicity. Antimicrobial agents and chemotherapy *63*.

Ph.D. Thesis, available online: McGlynn K. *Cooperative and mechanistic roles of Mecom in hematopoiesis.* University of Rochester; 2018. http://hdl.handle.net/1802/34859.

McGlynn K., Sun R., Vonica A., Rudzinskas S., Zhang Y., and Perkins AS. *Prdm3* and *Prdm16* cooperatively maintain hematopoiesis with dependence on the PR domain. *[Submitted to Haematologica – impact factor 7.7]*

McGlynn K., Sun R., Vonica A., Rudzinskas S., Zhang Y., and Perkins AS. Prdm3 and Prdm16 contribute to hematopoietic stem cell regulation. (*Poster, national Keystone Symposium on Epigenetics & Cancer*) (2017)

McGlynn K., Zhang, Y., and Perkins, A. Characterization of Prdm3-containing protein complex in MLL leukemia. (*Poster, national EpiCypher conference on Clinical Frontiers in Epigenetics*) (2016)

McGlynn K., Zhang, Y., and Perkins, A. The Zinc Finger Transcription Factor Mds1-Evi1 Forms a Novel Protein Complex in MLL leukemia. (*Poster, national Keystone Symposium on Epigenetics & Cancer*) (2015)