

Skills

Programming	R (dplyr, tidyr, ggplot), Python, Perl, bash, Shiny, RMarkdown, knitr, Jupyter, HTML, CSS Working knowledge of Airflow, Spark, Hadoop
Warehousing	SQL, Snowflake; Working knowledge of Redshift, Hive, MongoDB, BaseX
Other technologies	Tableau, Jira, Confluence, Git, Unix/Linux environments, AWS, REDCap

Professional Experience

Senior Bioinformatics Scientist, RTI International, Research Triangle Park, NC	Jun 2015 - present
<ul style="list-style-type: none"><li>Supervise multiple teams of analysts and developers as program manager and technical task lead</li><li>Responsible for designing and building extract, transform and load (ETL) pipelines to ingest and warehouse data, enhance data interoperability, and automate warehousing solutions</li><li>Use R to implement data transformations (dplyr, tidyr) and create novel visualizations (ggplot)</li><li>Utilize Snowpipe to ingest Twitter JSON data into Snowflake, where data is queried and transformed</li><li>Create intermediate tables from raw data to support ad-hoc analyses and reporting</li><li>Design and create tools and pipelines to support analytics needs and facilitate analysis and insights</li><li>Design and configure AWS framework to host ETL tools and Shiny applications</li><li>Interface with both technical and non-technical stakeholders to resolve complex business and technical issues</li></ul>	
Data Engineer (Consultant), Animal Cancer DX, LLC, Raleigh, NC	Jun 2021 - present
<ul style="list-style-type: none"><li>Designed and created an ETL pipeline to aggregate and warehouse experimental data on AWS S3, and automatically generate and distribute reports with statistical analyses to stakeholders</li><li>Designed and configured AWS framework (EC2, S3, RDS) to host a Shiny application</li><li>Designed and built data browser dashboard using Shiny and ggplot</li></ul>	
Bioinformatics Data Scientist, Johns Hopkins Medical Institutions, Baltimore, MD	Aug 2013 - Jun 2015
<ul style="list-style-type: none"><li>Completed 2-year data mining project in 10 weeks using R, SQL, and bash</li><li>Designed and created an ETL batch process to stage public health datasets and ingest into a SQL database</li><li>Used Python to implement data transformations (pandas) and create novel visualizations (matplotlib, ggplot)</li><li>Designed and implemented analysis pipelines for large genomic datasets for exploratory analysis and publication</li><li>Established unsupervised machine learning methods into quality control process</li></ul>	
Bioinformatics Analyst, Johns Hopkins Medical Institutions, Baltimore, MD	Oct 2011 - Aug 2013
<ul style="list-style-type: none"><li>Designed and created an ETL pipeline to ingest and transform public health data sources for analytic use, increasing the efficiency by 700% over the legacy workflow</li></ul>	
Bioinformatics Researcher, Putonti Lab, Loyola University, Chicago, IL	Jan 2010 - Jan 2011
<ul style="list-style-type: none"><li>Created pipeline to aggregate and analyze genomic data extracted from NCBI repository</li></ul>	

Education

Johns Hopkins University M.Sc. Bioinformatics	Baltimore, MD Aug 2013
Loyola University B.Sc. Bioinformatics	Chicago, IL May 2011

Publications

Gern, J. E., Jackson, D. J., Lemanske, R. F., Seroogy, C. M., Tachinardi, U., Craven, M., **Hwang, S. Y.**, ... Bacharier, L. B. (2019). The Children's Respiratory and Environmental Workgroup (CREW) Birth Cohort Consortium: Design, methods, and study population. *Respiratory Research*, 20(1), 115. doi:10.1186/s12931-019-1088-9

Vaz, M., **Hwang, S. Y.**, Kagiampaki, I., Phallen, J., Patil, A., O'Hagan, H. M., ... Baylin, S. B. (2017). Chronic cigarette smoke-induced epigenomic changes precede sensitization of bronchial epithelial cells to single-step transformation by KRAS mutations. *Cancer Cell*, 32, 360–376. doi:10.1016/j.ccell.2017.08.006