

Professional Experience

Senior Bioinformatics Scientist, Program Manager

RTI International, Research Triangle Park, NC
Jun 2015 - present

GenOmics, Bioinformatics, & Translational (GOBOT) Research Center

- Supervise multiple teams of data analysts
- Responsible for designing and building "Extract, Transform, and Load" (ETL) pipelines to clean and aggregate data, enhance data interoperability & automate warehousing solutions
- Utilize Snowpipe to ingest Twitter data into Snowflake to directly query and transform JSON data
- Design and create analysis pipelines to clean and query experimental data, automatically generate daily reports using RMarkdown and distribute findings of statistical testing to stakeholders
- Design and configure Amazon Web Services (AWS) Elastic Compute Cloud (EC2) & Relational Database Service (RDS) to host ETL pipelines and Shiny web applications
- Create meaningful visualizations from large data volumes (examples can be found in 2019 publication)
- Interface with both technical and non-technical stakeholders to resolve complex business and technical issues
- Migrated legacy Oracle systems to AWS EC2 and RDS (MySQL)

Data Engineer (Consultant)

Animal Cancer DX, LLC, Raleigh, NC
May 2021 - Sep 2021

- Individually designed and created an ETL pipeline to aggregate, clean and warehouse experimental data on AWS RDS, automatically generate daily reports with statistical analyses and distribute the reports to stakeholders
- Individually designed and configured AWS framework to host a Shiny application
- Individually designed and created data browser dashboard built using Shiny and ggplot

Bioinformatics Data Scientist

Johns Hopkins Medical Institutions, Baltimore, MD
Aug 2013 - Jun 2015

Sidney Kimmel Comprehensive Cancer Center

- Served as systems administrator for high-performance computing cluster
- Completed 2-year data mining project in 10 weeks using R, SQL, and bash
- Individually designed and created a complex ETL pipeline to populate a SQL database
- Designed and implemented analysis pipelines for large genomic datasets generated from clinical trials
- Incorporated machine learning methods to quality control processes where applicable
- Individually created novel visualizations from large genomic datasets (examples can be found in 2017 publication)

Bioinformatics Analyst

Johns Hopkins Medical Institutions, Baltimore, MD
Oct 2011 - Aug 2013

Pediatrics Infectious Diseases

- Individually designed and created an ETL pipeline, increasing the efficiency of the legacy workflow by over 700%

Bioinformatics Researcher

Loyola University, Chicago, IL
Jan 2010 - Jan 2011

Putonti Lab

- Created ETL pipeline to aggregate and analyze sequence data extracted from NCBI repository

Education

Johns Hopkins University

Baltimore, MD
Aug 2013

M.Sc. Bioinformatics

Loyola University

Chicago, IL
May 2011

B.Sc. Bioinformatics

Skills

Programming

R (dplyr, tidyr, ggplot), SQL, Python, Perl, bash, Shiny, RMarkdown, knitr, Jupyter, HTML, CSS

Technologies

Tableau, Snowflake, Hive, Jira, Confluence, AWS (EC2, RDS, S3), Git/Subversion, REDCap
Working knowledge of Airflow, Spark, Hadoop, AWS EMR, CDE/LOINC/OMOP standards

Published Visualizations

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

References

Available upon request