Stephen Y. Hwang

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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

- Supervise multiple teams of analysts and developers as program manager and technical task lead
- Responsible for designing and building extract, transform and load (ETL) pipelines to ingest and warehouse data, enhance data interoperability, and automate warehousing solutions
- Use R to implement data transformations (dplyr, tidyr) and create novel visualizations (ggplot)
- Utilize Snowpipe to ingest Twitter JSON data into Snowflake, where data is queried and transformed
- Create intermediate tables from raw data to support ad-hoc analyses and reporting
- Design and create tools and pipelines to support analytics needs and facilitate analysis and insights
- Design and configure AWS framework to host ETL tools and Shiny applications
- Interface with both technical and non-technical stakeholders to resolve complex business and technical issues

Data Engineer (Consultant), Animal Cancer DX, LLC, Raleigh, NC   Jun 2021 - present

- 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
- Designed and configured AWS framework (EC2, S3, RDS) to host a Shiny application
- Designed and built data browser dashboard using Shiny and ggplot

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

- Completed 2-year data mining project in 10 weeks using R, SQL, and bash
- Designed and created an ETL batch process to stage public health datasets and ingest into a SQL database
- Used Python to implement data transformations (pandas) and create novel visualizations (matplotlib, ggplot)
- Designed and implemented analysis pipelines for large genomic datasets for exploratory analysis and publication
- Established unsupervised machine learning methods into quality control process

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

- 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

Bioinformatics Researcher, Putonti Lab, Loyola University, Chicago, IL   Jan 2010 - Jan 2011

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

Education

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