

Jiawei Gu

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Summary

I am a four years experienced bioinformatician in academic and industry. I obtained a **MS in biology** and a **MS in computer science** from University of Texas at Dallas. It gives me advantage in combining biology knowledge with programming skills in data engineering and analysis. With a Certificate from **Amazon Web Service**, I can boost your development and production in the era of cloud.

Work Experience

Bioinformatics Analyst, Navican Genomics, Inc. Salt Lake City, 08/2018-Present

- **Production & Automation**
 - Daily clinical control sequencing quality assurance.
 - Implemented and improved the **Tumor Mutation Burden(TMB)** calculation algorithm within the bioinformatics team inspired by
 - Built an **automated pipeline** for clinical control assurance in **python**. It connected multiple **cloud service platforms**(Philips IntelliSpace Genomics Medicine, Salesforce, SeraCare IQ, Slack, and Amazon AWS) via **API**.
 - Created an **Illumina BaseSpace Native APP** for sequencing quality control using **Docker**.
- **Data Engineering**
 - Created tools to query and clean data from **cloud service platforms** (Philips IntelliSpace Genomics Medicine, Salesforce, Clarity LIMS) via **API** for ETL and R&D.
 - Designed a Bioinformatics **Variant Database** to store clinical mutations.
- **Data Analysis**
 - Implemented and run validation workflows for Illumina TruSight™ Tumor 170 Sequencing Assay.
 - Designed statistical tests for lab operation quality metrics.
 - Help with other ad-hoc data analysis requests.

Research Assistant, Biology Department, UTD 01/2014-12/2016

I focused on the research of Next-Generation Sequencing analysis, especially on ChIP-seq, RNA-seq, and ChIA-PET Seq result analysis, and using machine learning tools to analyze and predict from data.

- Machine Learning Prediction for RNA-chromosome interaction
 - Collect **genomic and epigenomic data** from online resources by a self coded **web crawler**.
 - Cleaned data and used Random Shuffle to generate more negative data points.
 - Applied **Support Vector Machine()** to generate a model
- DNA Sequencing Analysis of Brg1 in Cancer Cell, UTD
 - Built pipelines for data process and ChIP-seq analysis using Linux bash shell
 - Implemented a protein binding motif scan and enrichment analysis program in R
 - Analyzed and Visualized data in **R** and **Python**
 - **Article publication:** Shi, X., et al. "SMARCA4/Brg1 coordinates genetic and epigenetic networks underlying Shh-type medulloblastoma development." [Oncogene \(2016\)](#).

Skills

Programming languages

Python, Java, JavaScript, R, SAS, SQL

Machine Learning & Statistical model

Support Vector Machine (SVM), Random Forest, Deep Learning, Hidden Markov Model (HMM), Expectation Maximization(EM)

NGS(Next Generation Sequencing) Analysis

ChIP-Seq Analysis ,RNA-Seq Analysis, GATK toolkit ,Gene Ontology Enrichment Analysis, ChIA-PET Analysis, Motif Analysis

Frameworks & Tools

- BigData: Apache Spark, Apache Hadoop
- Web: MEAN stack(MongoDB, Express JS, Angular JS, Node.js), Java Spring
- Deep Learning: TensorFlow, Keras
- Containerization: Docker, Kubernetes
- Cloud Service: **Amazon Web Service**(certified)

Certification

- [AWS Certified Solutions Architect - Associate](#)
Credential ID: 6WQVVZSKE24EQLK9
- [Coursera Deep Learning Specialization](#)
- [SAS Certified Base & Advanced Programmer for SAS 9](#)
- [edX Verified Certificate for Big Data Analysis with Apache Spark](#)

Education

01/2017-05/2018

MS, Computer Science; University of Texas at Dallas(UTD); **3.91/4**

08/2013-12/2016

MS, Bioinformatics; University of Texas at Dallas(UTD); **3.73/4** Performed two and a half years (05/2014 -12/2016) of studies in pursuit of Ph.D.

Side Project

[Dog Breed Identification, Kaggle.com](#) 05/2018

- A Kaggle machine learning competition Project
 - Design and built a **convolutional neural network(CNN)** in **keras** to determine the breed of a dog in an image
 - Applied a **integrated model** of Xception and InceptionV3 to extract bottleneck features from image
 - Used three fully connected layers with **drop out** and **batch normalization** to get predicted probabilities
 - Used **Adam** optimization algorithm to train the final model with **cross entropy** as loss function
 - Get the final validation **accuracy of 99.76%**, rank 102 out of 1286 teams**
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