

# Shoujun Gu, Ph.D

Current Visa Status: Adjust Status Pending

Rockville, Maryland

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## Technical Skills

### **Programing Language:**

Python: Numpy, Pandas, Matplotlib, SQLAlchemy, Flask, Scikit-learn, Keras

R: DESeq, EdgeR, maSigPro

### **Interactive Data Visualization & Webpage:**

Javascript: D3js, Plotly, Leaflet

HTML: Bootstrap

### **Database:**

MySQL, MongoDB

### **Bioinformatics & Next Generation Sequencing (NGS):**

Data mining from various biology databases: NCBI, Ensembl, TCGA, cBioportal

Hands-on experience in NGS data analysis workflow

## Projects

- **The Cancer Genome Atlas (TCGA) data mining and analysis project**

The manuscript of this project entitled 'A Pan-Cancer Atlas of Genomic, Epigenomic and Transcriptomic Alterations in the TGF- $\beta$  Pathway' is under reviewing.

- **Built a machine learning model to predict the significance of a research project based on its abstract**

Details available at: [https://github.com/shoujungu/Impact\\_Factor\\_Pred](https://github.com/shoujungu/Impact_Factor_Pred)

Sample app available at: <https://if-pred.herokuapp.com>

- **Interactive visualization of US healthcare providers data**

Details available at: [https://github.com/shoujungu/US\\_Healthcare\\_Providers](https://github.com/shoujungu/US_Healthcare_Providers)

Sample app available at: <http://hcproviders.herokuapp.com>

- **Data mining and analysis on all healthcare publications (Year: 2017) in PubMed database**

Details available at: [https://github.com/shoujungu/2017\\_Pubmed\\_Analysis](https://github.com/shoujungu/2017_Pubmed_Analysis)

## Experience

### **The George Washington University, Washington, DC**

Oct 2015 –

Jan 2018

Postdoctoral Researcher

- Discovered an aberrant regulation pathway between TGF- $\beta$  signaling and cancer biomarker CEA in colon adenomas by using both whole genomic sequencing and whole transcriptome sequencing methods <sup>1</sup>;
- Discovered that Vitamin D promotes liver tumor progression in TGF-beta deficient environment by using both in vivo mouse model and bioinformatics tools <sup>2</sup>;
- Published a review article entitled "Alcohol, stem cells and cancer" <sup>3</sup>;
- TCGA data mining and analyzing of Pan-Cancer Atlas in the TGF- $\beta$  signaling (under review).

### **National Institutes of Health, Bethesda, MD**

Oct 2012 –

Sept 2015

Visiting Fellow

- Discovered that Wnt5a-induced Vangl2 phosphorylation is a key step for planar cell polarity (PCP) signaling initiation and establishment by showing phosphorylated Vangl2 exhibits altered interaction with other PCP proteins and forms self-aggregation;
- Generated myc-Prickle1 knock-in mice by using CRISPR/Cas9 genome editing technique;
- Discovered that Casein Kinase 1  $\epsilon/\delta$  conditional knockout mice exhibit significantly shortened long bones and delayed limb development.

## Education

### **The George Washington University, Washington, DC**

Oct 2017 –

Apr 2018

Data Analytics Boot Camp

- An intensive 24-week long boot camp dedicated to Data Mining and Analytics Skills on a variety of real-world problems.

### **UT Health Science Center at San Antonio**

Aug 2005 –

May 2012

Ph.D. Department of Biochemistry

- Oral presentation in American Society for Bone and Mineral Research 2008 Annual Meeting;
- Discovered that the Twist1 inhibits Sox9 transactivation through protein-protein interaction between Twist1 C-terminal domain and Sox9 DNA binding domain, which results in negative regulation of chondrogenesis <sup>4</sup>.

## Publications

1. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4839765/>
2. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4960540/>
3. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5724803/>
4. <https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3375531/>